Monte Carlo Calculations on Polypeptide Chains. VIII. Distribution Functions for the End-to-End Distance and Radius of Gyration for Hard-Sphere Models of Randomly Coiling Poly(glycine) and Poly(L-alanine)

Darrow E. Neves and Roy A. Scott III*

Department of Biochemistry, The Ohio State University, Columbus, Ohio 43210.

Received September 10, 1974

ABSTRACT: A Monte Carlo study of the distribution functions for the end-to-end distance and radius of gyration for hard-sphere models of poly(glycine) and poly(L-alanine) random coils has been conducted in the chain-length range $n = 3$ to 100 monomer units for both unperturbed chains and chains perturbed by long-range interactions (excluded volume effects). The distribution functions for the radius of gyration in all cases have been very precisely calculated, those for the perturbed end-to-end distance less precisely, and those for the unperturbed end-to-end distance least precisely. Empirical distribution functions of the form $W(\rho) = a\rho^b \exp(-c\rho^d)$ for the reduced end-to-end distance $\rho = r/\langle r^2\rangle^{1/2}$ and a similar form for the reduced radius of gyration could be least-squares fit to the Monte Carlo data. The expansion factors α_r and α_s were calculated vs. chain length and were used to test various versions of the two-parameter theory of the excluded volume effect. To be consistent with the chain-length dependence of α_r and α_s as determined by the Monte Carlo calculations, each of these theories required two different binary cluster integrals, a β_r based on α_r and a β_s based on α_s, both of which were strongly chain-length dependent. Both of these results suggest that the two-parameter theory is not applicable to the models used in this study. It was also found that, except for very short chain lengths, plots of ln α_r vs. ln n were linear, and thus that α_r could be estimated for long chain lengths. Comparison of these estimates with the experimental data on four polypeptide chains in non-Θ solvents suggests that the hard-sphere models used in this study yield expansion factors that do not seriously overestimate the magnitude of the excluded volume effect.

In a recent report from this laboratory[1] a preliminary Monte Carlo study of the distribution functions for the end-to-end distance and radius of gyration for hard-sphere models of randomly coiling poly(glycine) and poly(L-alanine) chains of length 5 and 20 residues was presented for both unperturbed chains and chains perturbed by long-range interactions (excluded volume effects). As expected, the distribution functions for these very short unperturbed chains were non-Gaussian; however, they appeared to be approaching Gaussian behavior with increasing chain length, the more flexible poly(glycine) chains more rapidly than the poly(L-alanine) chains. The distribution functions for the perturbed chains were distinct from those for unperturbed chains even at such short chain lengths and showed no evidence of approaching Gaussian behavior.

In this study we present a continuation of the early one on distribution functions,[1] but covering a range of chain lengths from 3 to 100 units in length. We find that empirical distribution functions of the form $W(\rho) = a\rho^b \exp(-c\rho^d)$, where the reduced end-to-end distance $\rho = r/\langle r^2\rangle^{1/2}$ and $\langle r^2\rangle$ is the mean-square end-to-end distance, and similar functions for the radius of gyration can be fit to the data for both perturbed and unperturbed chains. Also, using several versions of the two-parameter theory of long-range interactions,[2] we find that for these theories to be consistent with our Monte Carlo estimates of expansion factors α_r for the end-to-end distance and α_s for the radius of gyration requires two binary cluster integrals β_r and β_s which are strongly increasing functions of chain length over the range studied. Finally, we find that plots of ln α_r vs. ln n are linear which allows us to estimate α_r at long chain lengths. By comparing these estimates with the experimental values for four polypeptides in non-Θ solvents, it is shown that the hard-sphere model does not seriously overemphasize the excluded volume effect.

Models and Methods of Calculation

The hard-sphere models for poly(glycine) and poly(L-alanine) used in this study are similar to those used previously in this laboratory.[1,3] Briefly, all bond lengths and bond angles are held rigidly fixed, the peptide bonds are fixed in the planar trans configuration, and internal rotations about the angles φ and ψ for respectively the backbone N–C$^\alpha$ and C$^\alpha$–C′ single bonds are free of any inherent rotational potentials. Atoms or groups of atoms separated from each other by four or more intervening chemical bonds interact by means of hard-sphere potential functions. The bond lengths, bond angles, and hard-sphere potential functions are those used previously in this laboratory.[4,5]

The sterically allowed states per chain unit are determined at 10° increments of rotation about the internal rotational angles φ and ψ (i.e., from a Ramachandran map) and are then used to generate by random selection Monte Carlo samples of both perturbed and unperturbed chains by methods used previously,[3] except that in this study the samples at chain lengths 50 and 100 residues were generated by the dimerization method of Alexandrowicz[6] and the polypeptide chains at all chain lengths were assumed to begin and end at α-carbon atoms. The end-to-end distance is then taken to be from the first to the last α-carbon atom. The number of residues n is defined to be equal to the number of pairs of φ and ψ rotational angles and the number of polymer segments to be equal to $n + 1$, the number of peptide units.

At each chain length the total sample of chains was subdivided into ten equal sized subsamples. All average properties and distribution function curves were determined ten times, once for each subsample. These ten estimates were then averaged to obtain a final mean value and a 90% confidence limit. Most of the chain samples consisted of 100,000 chains except the perturbed poly(glycine) chains of length 100 residues which consisted of 67,000, the unperturbed poly(L-alanine) chains of length 18 residues which consisted of 125,000, and those of lengths 25, 34, and 50 residues which consisted of 200,000.

Empirical distribution functions of the form

$$W(\rho) = a\rho^b \exp(-c\rho^d) \tag{1}$$

for the reduced end-to-end distance and

Table I
Comparison of Exact Theoretical and Monte Carlo Estimates of $\langle r^2\rangle_0$ and $\langle s_2\rangle_0$ for Unperturbed Poly(glycine)

	$\langle r^2\rangle_0$		$\langle s^2\rangle_0$	
n	Monte Carlo	Theoretical	Monte Carlo	Theoretical
3	104.1 ± 0.2	103.80	17.06 ± 0.01	17.048
4	136.8 ± 0.4	136.91	22.03 ± 0.03	22.037
6	204.3 ± 0.6	203.75	32.44 ± 0.05	32.373
10	339.2 ± 0.8	337.83	53.9 ± 0.1	53.779
18	605 ± 3	606.06	97.8 ± 0.3	97.648
25	842 ± 3	840.77	136.5 ± 0.3	136.420
34	1145 ± 4	1142.50	186.4 ± 0.4	186.460
50	1676 ± 5	1679.00	275.1 ± 0.6	275.630
100	3360 ± 15	3355.50	556 ± 1	554.760

Table II
Comparison of Exact Theoretical and Monte Carlo Estimates of $\langle r_2\rangle_0$ and $\langle s_2\rangle_0$ for Unperturbed Poly(L-alanine) Chains

	$\langle r^2\rangle_0$		$\langle s^2\rangle_0$	
n	Monte Carlo	Theoretical	Monte Carlo	Theoretical
3	110.1 ± 0.2	110.35	16.98 ± 0.02	17.010
4	153.1 ± 0.3	153.32	22.57 ± 0.03	22.579
6	245.4 ± 0.6	245.97	34.84 ± 0.05	34.854
10	444 ± 1	443.16	62.56 ± 0.1	62.432
18	849 ± 2	847.72	123.4 ± 0.2	123.530
25	1196 ± 4	1202.90	179.2 ± 0.3	179.740
34	1651 ± 4	1659.70	252.9 ± 0.3	253.570
50	2463 ± 7	2471.70	386.1 ± 0.7	386.680
100	5000 ± 19	5009.20	807 ± 2	806.970

Table III
Monte Carlo Estimates of $\langle r^2\rangle$ and $\langle s^2\rangle$ for Perturbed Poly(glycine) and Poly(L-alanine)

n	$\langle r^2\rangle_{\mathrm{Gly}}$	$\langle s^2\rangle_{\mathrm{Gly}}$	$\langle r^2\rangle_{\mathrm{Ala}}$	$\langle s^2\rangle_{\mathrm{Ala}}$
3	104.8 ± 0.1	17.12 ± 0.01	111.4 ± 0.2	17.10 ± 0.02
4	141.1 ± 0.3	22.41 ± 0.03	159.3 ± 0.3	23.12 ± 0.03
6	222.3 ± 0.6	34.17 ± 0.04	266.4 ± 0.5	36.76 ± 0.04
10	400.1 ± 0.8	60.5 ± 0.1	514 ± 1	69.2 ± 0.1
18	799 ± 2	120.9 ± 0.1	1067 ± 3	146.8 ± 0.2
25	1182 ± 4	179.4 ± 0.4	1590 ± 5	223.9 ± 0.5
34	1708 ± 6	260.7 ± 0.5	2303 ± 6	331.9 ± 0.5
50	2717 ± 9	416.7 ± 0.8	3653 ± 13	540.2 ± 0.9
100	6274 ± 22	1009 ± 2	8309 ± 28	1326 ± 3

$$W(\sigma) = a'\sigma^{b'} \exp(-c'\sigma^{d'}) \quad (2)$$

for the reduced radius of gyration were least-squares fit to the Monte Carlo data. Here the reduced end-to-end distance $\rho = r/\langle r^2\rangle^{1/2}$ and the reduced radius of gyration $\sigma = s/\langle s^2\rangle^{1/2}$, where $\langle r^2\rangle$ and $\langle s^2\rangle$ are respectively the mean-square end-to-end distance and mean-square radius of gyration. We will also distinguish properties and parameters for unperturbed chains by a subscript 0 (i.e., a_0, b_0, c_0, d_0, a_0', b_0', c_0', d_0', $\langle r^2\rangle_0$, $\langle s^2\rangle_0$, etc.) The least-squares fitting was accomplished by adjustment of the parameters a, b, c, and d in eq 1 and a', b', c', and d' in eq 2. This was also done ten times, once for each subsample, to produce a mean curve with 90% confidence limits for the distribution functions and mean values and 90% confidence limits for the adjustable parameters.

The expansion factors $\alpha_r = (\langle r^2\rangle/\langle r^2\rangle_0)^{1/2}$ and $\alpha_s = (\langle s^2\rangle/\langle s^2\rangle_0)^{1/2}$ were calculated from the Monte Carlo estimates of $\langle r^2\rangle$, $\langle r^2\rangle_0$, $\langle s^2\rangle$, and $\langle s^2\rangle_0$, again using the ten subsamples to calculate a final mean value and a 90% confidence limit. Using these Monte Carlo estimates for the expansion factors and four versions of the two-parameter theory of the excluded volume effect, the binary cluster integrals β were calculated at each chain length. We have distinguished between a β_r calculated from α_r and a β_s calculated from α_s. The four versions of the two-parameter theory used were the theories of Flory, Yamakawa-Tanaka, Ptitsyn, and Fixman as given by Yamakawa.[7] According to these theories there is only a single binary cluster integral (i.e., $\beta_r = \beta_s = \beta$) which should be independent of chain length.

Results and Discussion

In Tables I and II are shown the Monte Carlo estimates with 90% confidence limits for the mean-square end-to-end distance and radius of gyration at the nine chain lengths studied for unperturbed poly(glycine) and poly(L-alanine) chains. Also included are the exact theoretical values for these quantities as calculated for our models by the methods developed by Flory and coworkers.[8] Examination of the data in these tables demonstrates the validity of our method of sample generation, since in the majority of cases the correct theoretical value lies within the 90% confidence range of the Monte Carlo estimate and in the other cases is only marginally outside this range. In Table III are shown the Monte Carlo estimates and 90% confidence limits for the same properties for chains perturbed by long-range interactions. As expected, the dimensions of the perturbed chains are expanded relative to those for unperturbed chains, and the dimensions of the more flexible poly(glycine) chains are less than those of poly(L-alanine) chains for both the perturbed and unperturbed samples.

In Figure 1 are shown plots of the distribution functions for the reduced end-to-end distance, $W(\rho)$ vs. ρ, at four of the nine chain lengths studied for respectively unperturbed poly(glycine) and unperturbed poly(L-alanine). Also shown in these figures are the least-squares best fit of eq 1 to the Monte Carlo data. Both curves are shown in the form of 90% confidence bands as calculated by the methods discussed in the previous section. For the shortest chain lengths the Monte Carlo estimates of the distribution functions are very precise for all values of ρ except those near the origin. These distribution functions are characterized by a maximum in the vicinity of ρ = 0.9–1.1 and a plateau region to the left of the maximum. The least-squares best fit of eq 1 to these short chain length distribution functions produces curves which fit the Monte Carlo curves quite well in the vicinity of the maximum and at larger ρ values. Of course the form of eq 1 cannot produce the plateau region to the left of the maximum, but rather decreases continuously to zero at the origin. As the chain length increases the plateau region disappears, the maximum begins to shift toward the origin, and the 90% confidence bands become wider for both the Monte Carlo curve and the fit curve, especially at smaller values of ρ. Also eq 1 appears to fit the Monte Carlo data over a wider range of ρ. It is well known that the distribution functions for unperturbed chains approach Gaussian behavior as $n \rightarrow$ large,[9] and this appears to be occurring in Figure 1, more rapidly for the more flexible poly(glycine) chains than for poly(L-alanine). Unfortunately, for the longer chain lengths the 90% confidence bands become extremely wide as $\rho \rightarrow 0$. To overcome this problem would require much larger samples. Since the

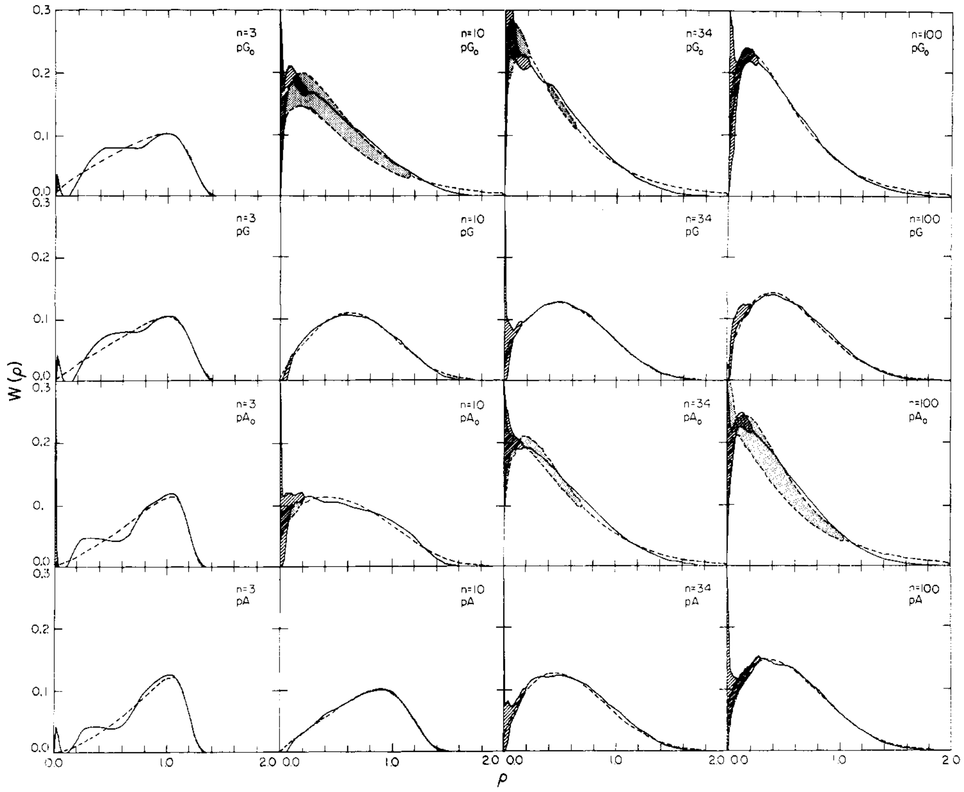

Figure 1. Plots of $W(\rho)$ vs. ρ at chain lengths 3, 10, 34, and 100 for unperturbed poly(glycine) chains (first row, labeled pG$_0$), perturbed poly(glycine) chains (second row, labeled pG), unperturbed poly(L-alanine) chains (third row, labeled pA$_0$), and perturbed poly(L-alanine) chains (fourth row, labeled pA).

distribution functions for perturbed end-to-end distances and perturbed and unperturbed radii of gyration are much better defined with the present samples, larger samples for the unperturbed end-to-end distance were not attempted in the present study. Even with the large confidence bands it is evident that neither polymer model has reached Gaussian behavior at $n = 100$.

Also shown in Figure 1 are the distribution functions for the reduced end-to-end distance, $W(\rho)$ vs. ρ, for poly(glycine) and poly(L-alanine) chains perturbed by long-range interactions. For $n = 3$ the distribution functions and the least-squares fits of eq 1 are very similar to those for unperturbed chains, but as the chain lengths increase the effect of long-range interactions becomes very noticeable. Even by chain length 10 the effects are obvious and become more so at longer chain lengths. With increasing chain length the maxima in the distribution functions shift toward smaller values of ρ and $W(\rho) \rightarrow 0$ both for $\rho \rightarrow$ large and $\rho \rightarrow$ small. Except for the shortest chain lengths, eq 1 fits the Monte Carlo data quite well over the entire range of ρ. For both polymers the parameter d decreases with increasing chain length and appears to be approaching a value near or slightly less than 2 at the longer chain lengths. The parameter a increases with increasing chain length for both polymers; however, there is no indication that it has reached a limiting value at the longest chain lengths studied. b appears to decrease with increasing chain length whereas c increases, and neither of these two parameters appears to have reached a limiting value except perhaps the parameter b for poly(glycine) which has nearly the same value for chain lengths 50 and 100. Based on the above results we conclude that eq 1 fits the distribution functions quite well at all chain lengths studied from $n = 4$ to 100, but that longer chain lengths would be required to determine if the parameters a, b, c, and d approach limiting values.

In Figure 2 are shown plots of the distribution functions for the reduced radius of gyration $W(\sigma)$ vs. σ for respectively unperturbed poly(glycine) and poly(L-alanine) chains, and similar plots for both polymers when their dimensions are perturbed by long-range interactions. It is evident from examination of this figure that these distribution functions have been determined very precisely, the 90% confidence bands being too small to be noticeable. For most practical purposes these curves can be considered to be the exact curves for all four cases. It is also evident from these figures that eq 2 fits the data quite well for all four cases at all chain lengths studied. At short chain lengths these distribution functions are relatively sharp with a maximum near $\sigma = 1.0$. With increasing chain length they broaden, become more skewed to the right, and have their maxima shifted toward $\sigma = 0.8$. It is very difficult to distinguish between the four models by examination of the figure; however, the differences become somewhat more evident by examining the least-squares adjusted parameters for eq 2. The parameters a_0' and a' have values between 37.3 and 38.9 for all four cases at all chain lengths studied. The parameters b_0' and b' are strongly chain-length dependent, decreasing from values in the range 18.0–20.5 at $n = 3$ to a value of about 7.7 for the unperturbed chains and a value in the range of 9.4–9.8 for the perturbed chains. There is no indication that b_0' and b' have reached limiting values. The parameters c_0' and c' are mildly dependent upon chain length, increasing from about 4.8–4.9 at $n = 3$ to 5.4–5.7 at $n = 100$.

According to the two parameter theories of the excluded volume effect,[7] the expansion factors $\alpha_r = (\langle r^2\rangle/\langle r^2\rangle_0)^{1/2}$ and $\alpha_s = (\langle s^2\rangle/\langle s^2\rangle_0)^{1/2}$ are functions of a parameter $z = (3/2\pi\langle r^2\rangle_0)^{3/2}\beta(n + 1)^2$, where β is the binary cluster integral and $n + 1$ is the number of polymer segments. For a given polymer in a particular solvent at a fixed temperature, β is

Table IV
Values and 90% Confidence Limits for α_r and α_s for Poly(glycine) and Poly(L-alanine)

n	α_r(Gly)	α_s(Gly)	α_r(Ala)	α_s(Ala)
3	1.0036 ± 0.0008	1.0019 ± 0.0001	1.0061 ± 0.0003	1.0036 ± 0.0005
4	1.016 ± 0.003	1.009 ± 0.002	1.020 ± 0.003	1.012 ± 0.002
6	1.043 ± 0.003	1.026 ± 0.004	1.042 ± 0.003	1.027 ± 0.002
10	1.09 ± 0.01	1.059 ± 0.004	1.076 ± 0.004	1.053 ± 0.002
18	1.149 ± 0.004	1.112 ± 0.003	1.123 ± 0.003	1.091 ± 0.005
25	1.185 ± 0.004	1.146 ± 0.002	1.153 ± 0.003	1.118 ± 0.006
34	1.222 ± 0.001	1.183 ± 0.001	1.181 ± 0.002	1.146 ± 0.006
50	1.273 ± 0.002	1.231 ± 0.005	1.218 ± 0.005	1.183 ± 0.004
100	1.367 ± 0.004	1.347 ± 0.006	1.289 ± 0.005	1.282 ± 0.002

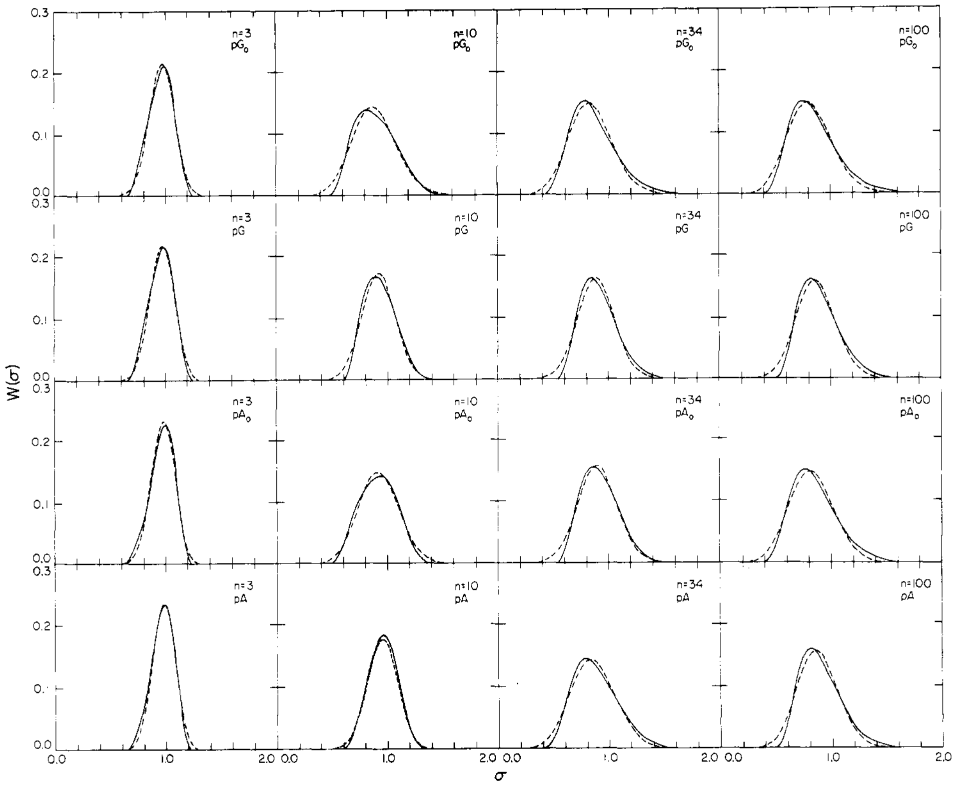

Figure 2. Plots of $W(\sigma)$ vs. σ at chain lengths 3, 10, 34, and 100 for unperturbed poly(glycine) chains (first row, labeled pG_0), perturbed poly(glycine) chains (second row, labeled pG), unperturbed poly(L-alanine) chains (third row, labeled pA_0), and perturbed poly(L-alanine) chains (fourth row, labeled pA).

a measure of the effective volume excluded to one polymer segment by the presence of another segment and is supposed to be chain-length independent. We have used our Monte Carlo data to calculate α_r and α_s vs. n, and the results are shown along with the 90% confidence limits in Table IV. It can be seen that these expansion factors have been very precisely determined and that both α_r and α_s are slightly larger for poly(glycine) than for poly(L-alanine). Also for both polymers α_r is slightly larger than α_s. We have used these data and the four versions of two-parameter theory mentioned above to calculate binary cluster integrals, distinguishing a β_r from a β_s. The results are shown in Figure 3. In all cases β_r and β_s are found to be increasing functions of the number of polymer segments $n + 1$, and to differ from each other to some extent at each chain length. These results are not consistent with the definition of a single β which is independent of chain length and indicates that two-parameter theory is not applicable to our models.

In Figure 4 are shown plots of ln α_r vs. ln n for poly(glycine) and poly(L-alanine). Both plots show curvature over the short-chain-length range but become very nearly linear in the range n = 18–100, i.e., for the five longest chain lengths studied. From the slope and intercept of these plots we obtain the following empirical relationship between α_r and n for poly(glycine)

$$\alpha_r = 0.8548n^{0.1018} \qquad (3)$$

and for poly(L-alanine) the relationship

$$\alpha_r = 0.8897n^{0.0804} \qquad (4)$$

Using these two empirical relationships and assuming that they can be used to approximate α_r at chain lengths greater than n = 100, the results shown in Table V for α_r vs. chain length and molecular weight were calculated. It can be seen that α_r is a much more rapidly increasing function of n for poly(glycine) than for poly(L-alanine). In the former case α_r does not reach a value of 2 until n = 4,248 (molecular weight 242,379) whereas the latter case requires n = 23,630 (molecular weight 1,679,635).

In their investigation of the unperturbed dimensions of randomly coiling polypeptide chains, Brant and Flory[10] were forced to use experimental data in non-Θ solvents and apply polymer solution theory to correct the dimensions for

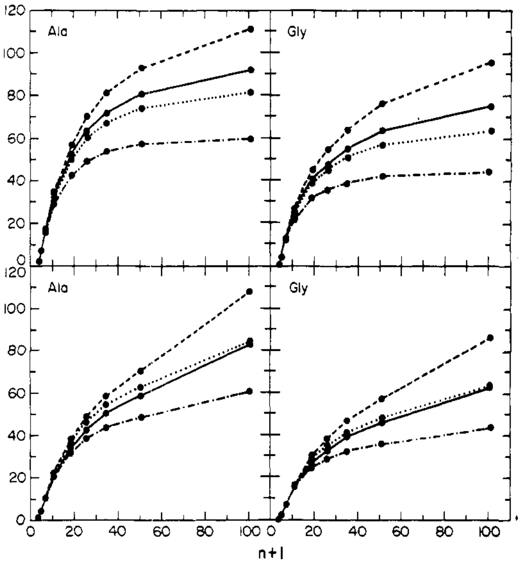

Figure 3. Plots of β_r and β_s vs. the number of chain segments ($n + 1$) for poly(glycine) and poly(L-alanine) chains as calculated from the expansion factors α_r and α_s in Table IV using the theories of Flory (- - -), Yamakawa-Tanaka (——), Pittsyn (· · ·), Fixman (- · -).

perturbation by the solvent. They selected solvent systems for which the perturbations were as small as possible, i.e., where α_r was not much greater than unity. For poly(β-benzyl-L-aspartate) in *m*-cresol at 100° and $n \approx 912$ they found $\alpha_r = 1.22$, for poly(L-glutamic acid) in aqueous 0.3 *M* sodium phosphate solution at pH 7.85 at 37° and $n \approx 454$ they found $\alpha_r = 1.34$, for poly(L-lysine) in aqueous 1.0 *M* sodium phosphate solution at pH 4.54 at 37° and $n \approx 550$ they found $\alpha_r = 1.51$. Comparison of these experimental data with the calculations shown in Table V shows that at corresponding chain lengths the calculated values of α_r are only slightly larger than the experimental. Considering that all four experimental values are for solutions relatively close to Θ conditions, this comparison suggests that the hard-sphere models do not vastly overemphasize the excluded volume effect.

It should be emphasized that the hard-sphere models connot be expected to agree with experimental data, since they are temperature and solvent independent as well as too crude in many other respects. The point of interest here is only whether these models have α_r and α_s values that do not vastly overemphasize the excluded volume effect. The above discussion suggests that they do not and that, in fact, they yield α_r values typical of an indifferent solvent or perhaps a good solvent,[11] but not of an unrealistically good solvent. It should also be emphasized that the results and conclusions of this study are not dependent upon the exact choice of bond lengths, bond angles, or atomic radii. Reasonable variations in the choice of these parameters would change somewhat the numerical results but not the essential nature of these results or the conclusions based upon them. In our work we have occasionally carried out calculations with other values for these parameters within a range of approximately 10% of the values used in this study to ensure ourselves that the results were not overly sensitive to such adjustments.

Table V
Expansion Factor α_r as Extrapolated to Longer Chain Lengths for Poly(glycine) and Poly(L-alanine)

Poly(glycine)			Poly(L-alanine)		
n	Mol wt	α_r	n	Mol wt	α_r
200	11,429	1.466	200	14,234	1.363
500	28,544	1.609	500	35,558	1.467
1,000	57,071	1.726	1,000	71,098	1.551
2,000	114,124	1.852	10,000	710,817	1.866
3,000	171,176	1.931	20,000	1,421,615	1.973
4,248	242,379	2.000	23,630	1,679,635	2.000

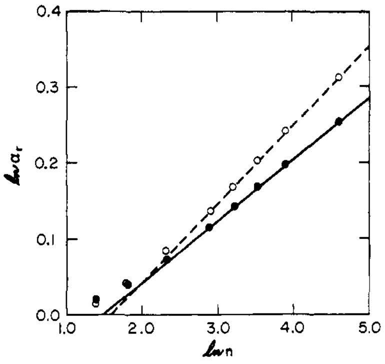

Figure 4. Plots of ln α_r vs. ln n for poly(glycine) chains (open circles) and poly(L-alanine) chains (closed circles). The dashed line is a least-squares straight line through the five points at n = 18, 25, 34, 50, and 100 for poly(glycine) and the solid line is a similar line for poly(L-alanine).

Acknowledgment. The authors wish to acknowledge the expert assistance of the staff of The Ohio State University Instruction and Research Computer Center in their work and also generous grants of computing time on the IBM 370-165 system. This work was supported by grants (GB-3057 x 1 and GB-3961) from the National Science Foundation. One of us (R.A.S.) is also a United States Public Health Service Career Development Awardee (GM-38-73/4).

References and Notes

(1) K. K. Knaell and R. A. Scott III, *Polym Prepr., Am. Chem. Soc., Div. Polym. Chem.*, **14**, 157 (1973).
(2) H. Yamakawa, "Modern Theory of Polymer Solutions," Harper and Row, New York, N.Y., 1971.
(3) H. E. Warvari, K. K. Knaell, and R. A. Scott III, *J. Chem. Phys.*, **55**, 2020 (1971).
(4) K. K. Knaell and R. A. Scott III, *J. Chem. Phys.*, **54**, 566 (1971).
(5) K. K. Knaell and R. A. Scott III, *J. Chem. Phys.*, **54**, 3556 (1971).
(6) F. Alexandrowicz, *J. Chem. Phys.*, **51**, 561 (1969).
(7) Reference 2, Chapter III.
(8) P. J. Flory, "Statistical Mechanics of Chain Molecules," Interscience, New York, N.Y., 1969, Chapter VII.
(9) Reference 8, Chapter VIII.
(10) D. A. Brant and P. J. Flory, *J. Am. Chem. Soc.*, **87**, 2788 (1965).
(11) C. Tanford, "Physical Chemistry of Macromolecules," Wiley, New York, N.Y., 1961, pp 163 and 201.