

Fig. 5. Long-range distance restraints in the experimental NMR data set for the protein cyclophilin A (Ottiger et al. 1997). Restraints between atoms five or more residues apart in the sequence are represented by lines going from upper left to lower right (restraints between side-chain atoms), or from lower left to upper right (restraints involving backbone atoms). On the left and right hand sides the amino acid sequence of cyclophilin A is given.

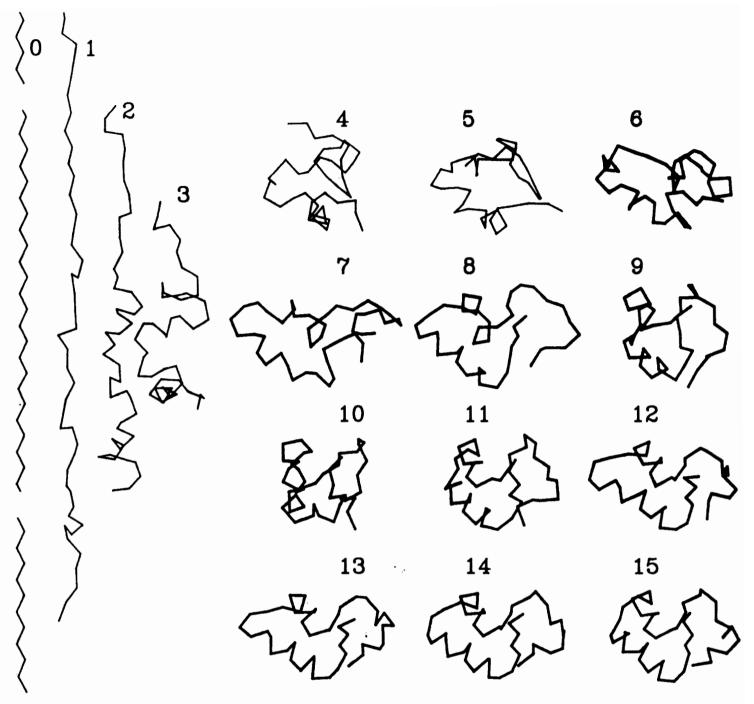
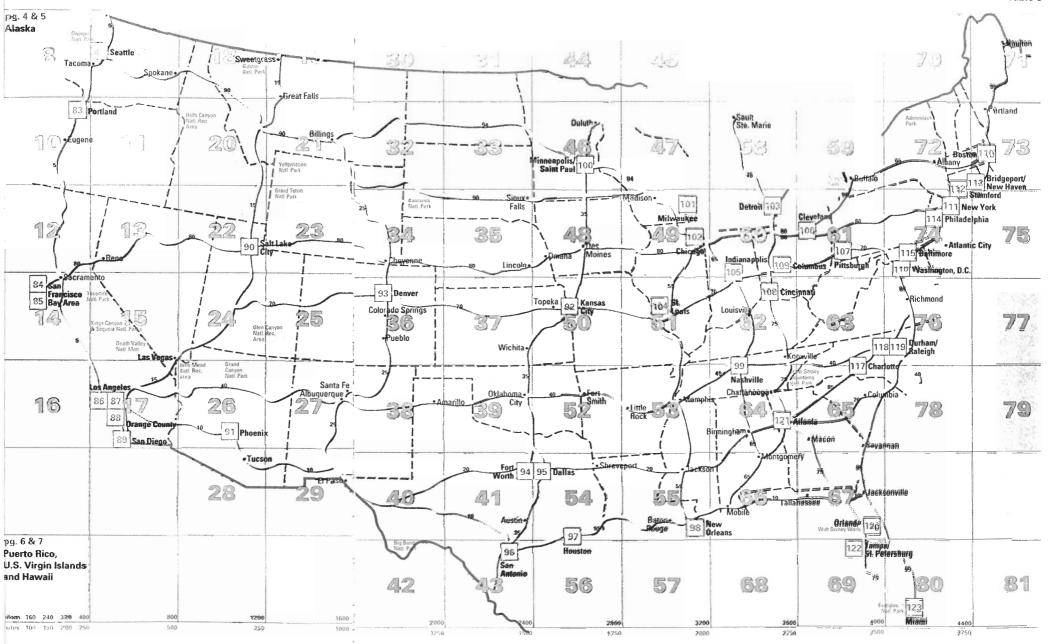


Figure 1. Pathway of SA for the structure determination of crambin starting with an extended β -strand using interproton distance data. Simulated interproton distance data were used that could realistically be obtained by two-dimensional NOE spectroscopy. Snapshots of the C^{α} backbone are shown at 1-ps intervals. During the first 5 ps (thin lines), only interproton distance restraints between residues $i, i \pm 1, i \pm 2, i \pm 3, i \pm 4,$ and $i \pm 5$ were taken into account, while all interproton distances were used during the following stages (thick lines).

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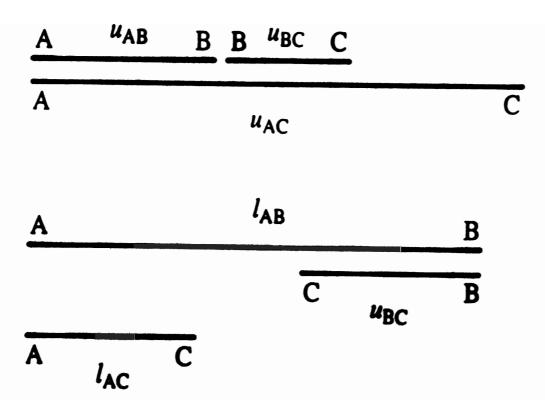


Fig. 8.14 The two triangle inequalities used in distance geometry.

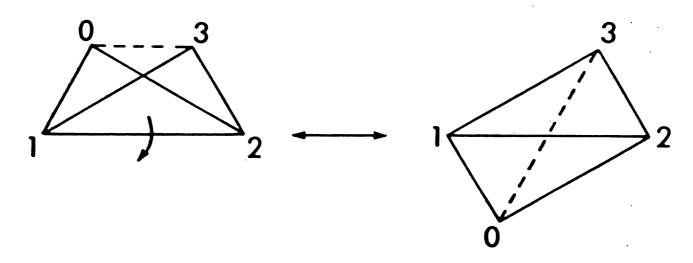
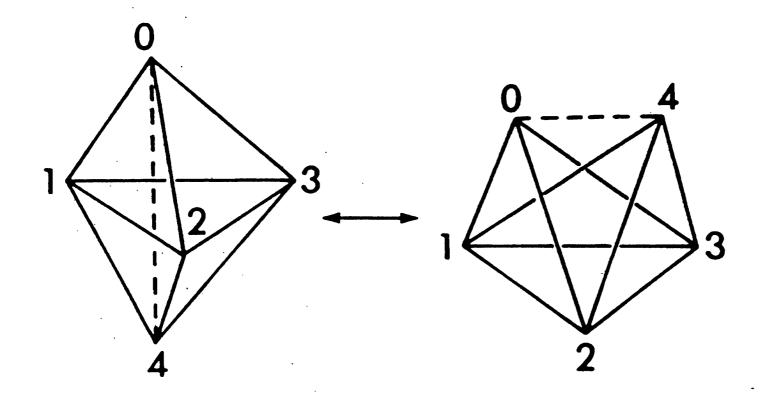


Figure 1. The two possible solutions of the tetrangle equality for a configuration of four points.



The two possible solutions of the pentangle equality for a configuration of five points.

DISTANCE GEOMETRY PROTOCOL

INPUT

Distance, Chirality and Torsion Constraints

BOUNDS SMOOTHING

Upper Triangle, Lower Triangle, Quadrangle

TRIAL DISTANCE SELECTION

Choose Distances between the Bounds

EMBEDDING

Compute Centroid, Metric Matrix, Principal Components, then Atomic Coordinates

REFINEMENT

Nonlinear Optimization to satisfy Constraints

KEY EQUATIONS

Metric Matrix =
$$g_{ij} = x_i * x_j$$

 $d_{i0}^2 = 1/N \sum d_{ij}^2 - 1/N^2 \sum d_{jk}^2$
 $g_{ij} = (d_{i0}^2 + d_{j0}^2 - d_{ij}^2) / 2$
 $g_{ij} = \sum x_{ik} x_{jk} = \sum w_{ik} w_{jk} \lambda_k$
 $x_{ik} = \lambda_k^{1/2} * w_{ik}$

METRIZATION METHODS

Random Fractional Triangle Correlated Ordered Atom Based Four-Point Atom-Based Random Pair-Based (*)

(*) Uses a Modified Murchland Shortest Path Update Algorithm

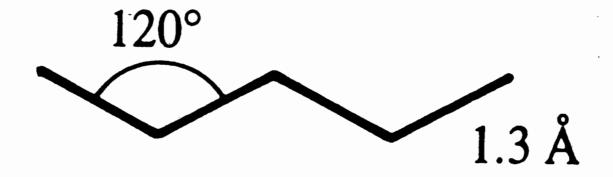


Fig. 8.15 Five-carbon fragment to illustrate distance geometry

initial bounds matrix

1	0.0	1.3	2.2517	3.4395	99.0
	1.3	0.0	1.3	2.2517	3.4395
	2.2517	1.3	0.0	1.3	2.2517
	2.6	2.2517	1.3	0.0	1.3
	2.8	2.6	2.2517	1.3	0.0

smoothed bounds matrix

$\int 0.0$	1.3	2.2517	3.4395	4.5033
1.3	0.0	1.3	2.2517	3.4395
2.2517	1.3	0.0	1.3	2.2517
2.6	2.2517	1.3	0.0	1.3
2.8	2.6	2.2517	1.3	0.0

randomly assigned distance matrix

$$\begin{pmatrix}
0.0 & 1.3 & 2.25 & 3.11 & 3.42 \\
0.0 & 1.3 & 2.25 & 2.85 \\
0.0 & 1.3 & 2.25 \\
0.0 & 1.3 \\
0.0
\end{pmatrix}$$

We calculate the *metric matrix*, G, each of whose elements (i, j) is equal to the scalar product of the vectors from the origin to atoms i and j:

$$G_{ii} = \mathbf{i}.\mathbf{j} \tag{8.4}$$

The elements G_{ij} can be calculated from the distance matrix using the cosine rule:

$$G_{ij} = (d_{io}^2 + d_{jo}^2 - d_{ij}^2)/2 (8.5)$$

 d_{io} is the distance from the origin to atom i and d_{ij} is the distance between atoms i and j.

It is usual to take the centre of the molecule as the origin of the coordinate system. The distance of each atom from the centre can be calculated directly from the interatomic distances using the following expression:

$$d_{io}^{2} = \frac{1}{N} \sum_{j=1}^{N} d_{ij}^{2} - \frac{1}{N^{2}} \sum_{j=2}^{N} \sum_{k=1}^{j-1} d_{jk}^{2}$$
 (8.6)

The metric matrix G is a square symmetric matrix. A general property of such matrices is that they can be decomposed as follows:

$$\mathbf{G} = \mathbf{V}\mathbf{L}^2\mathbf{V}^{\mathsf{T}} \tag{8.7}$$

The diagonal elements of L^2 are the eigenvalues of G and the columns of V are its eigenvectors. The atomic coordinates can be derived from the metric matrix by rewriting equation (8.4) as

$$\mathbf{G} = \mathbf{X}\mathbf{X}^{\mathsf{T}} \tag{8.8}$$

X is a matrix containing the atomic coordinates. Equating equations (8.7) and (8.8) gives X = VL

$$X = VL (8.9)$$

As L has only diagonal entries, the matrix L is identical to its transpose: $L = L^{T}$. The atomic coordinates are thus obtained by multiplying the square roots of the eigenvalues by the eigenvectors.

metric matrix

$$\begin{pmatrix} 3.571 & 1.569 & -0.427 & -2.276 & -2.436 \\ 1.569 & 1.256 & 0.105 & -1.122 & -1.808 \\ -0.427 & 0.105 & 0.644 & 0.261 & -0.583 \\ -2.276 & -1.122 & 0.261 & 1.569 & 1.569 \\ -2.436 & -1.808 & -0.583 & 1.569 & 3.259 \end{pmatrix}$$

eigenvalues

8.18, 1.74, 0.26, 0.10 and 0.0

matrix of eigenvectors

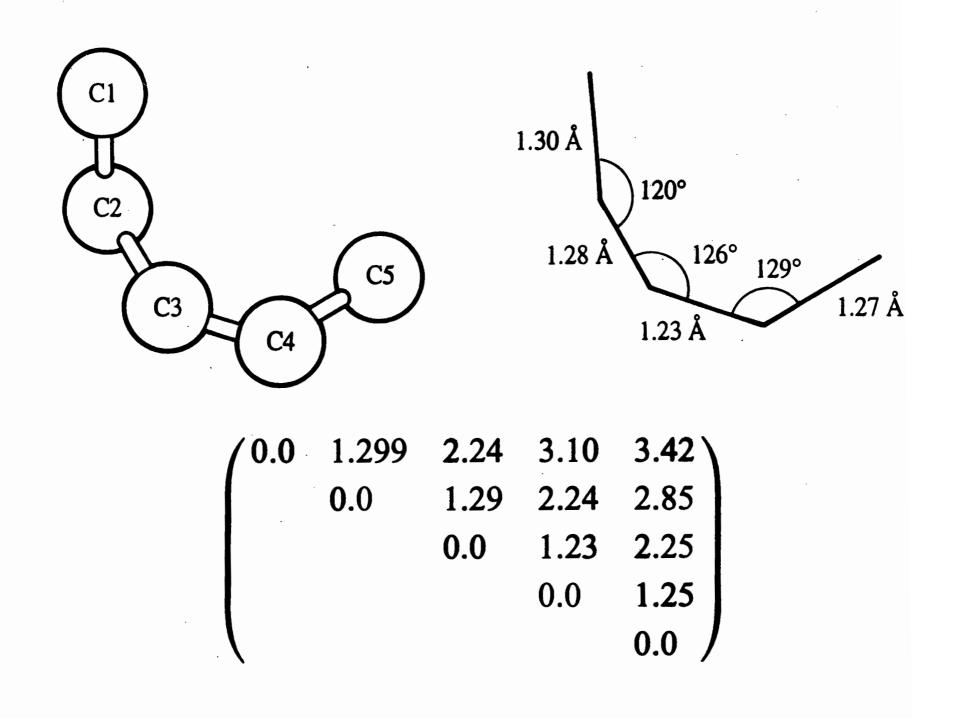
$$\mathbf{W} = \begin{pmatrix} 0.621 & 0.455 & -0.425 & 0.164 \\ 0.355 & -0.184 & 0.800 & 0.020 \\ 0.0 & -0.573 & -0.368 & -0.580 \\ -0.408 & -0.287 & -0.153 & 0.727 \\ -0.567 & 0.590 & 0.145 & -0.330 \end{pmatrix}$$

$$x_{i} = \sqrt{\lambda_{1} W_{i1}}$$

$$y_{i} = \sqrt{\lambda_{2} W_{i2}}$$

$$z_{i} = \sqrt{\lambda_{3} W_{i3}}$$

Atom	x coordinate	y coordinate	z coordinate
1	1.777	0.601	-0.218
2	1.014	-0.244	0.410
3	-0.001	-0.757	-0.188
4	-1.166	-0.379	-0.079
5	-1.623	0.799	0.075



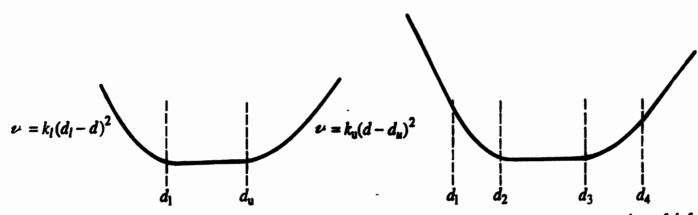


Fig. 8.23 A restraining potential that does not penalise structures in which the distance lies between the lower and upper distances d_l and d_u and uses harmonic functions outside this range (left). The harmonic potentials may also be replaced by linear restraints further from this region (right).

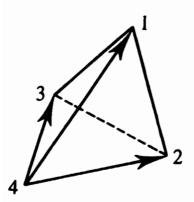


Fig. 8.17 The stereochemistry about tetrahedral atoms can be maintained with an appropriate chiral constraint.

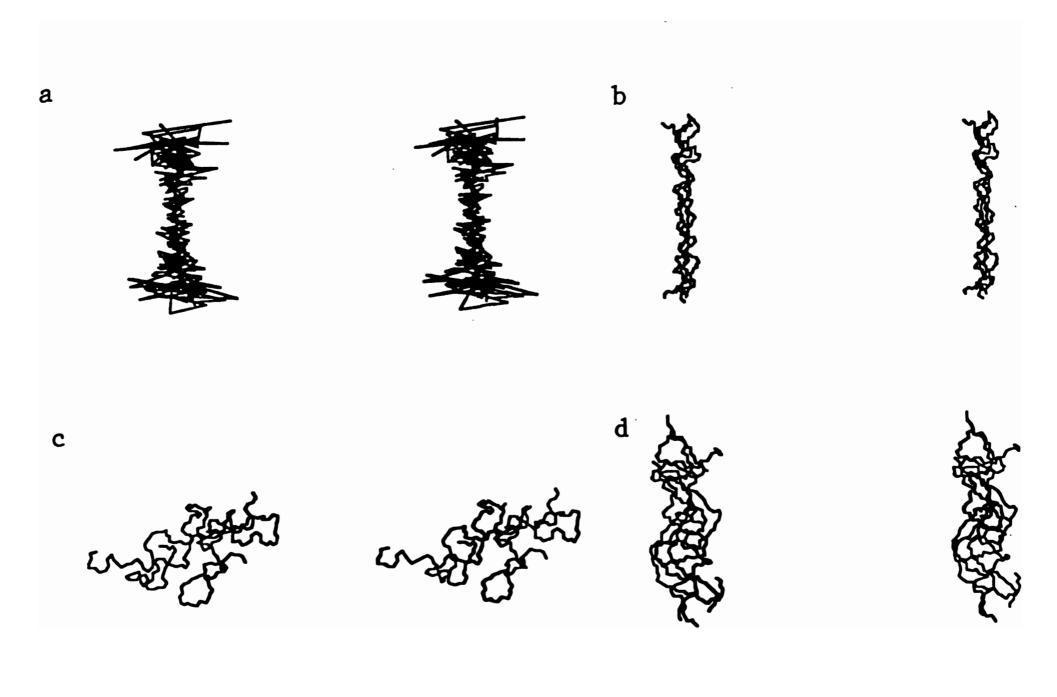
During the optimisation of the structure against the distance constraints it is usual to incorporate chiral constraints. These are used to ensure that the final conformation is the desired stereoisomer. Chiral constraints are necessary because the interatomic distances in two enantiomeric conformations are idential and as a consequence the 'wrong' isomer may quite legitimately be generated. Chiral constraints are usually incorporated into the error function as a chiral volume, calculated as a scalar triple product. For example, to maintain the correct stereochemistry about the tetrahedral atom number 4 in Figure 8.17, the following scalar triple product must be positive:

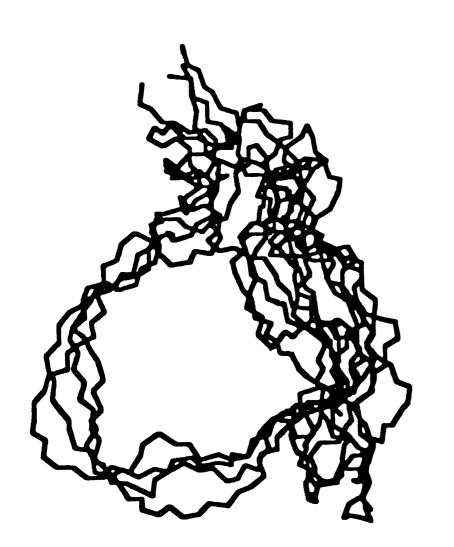
$$(v_1 - v_4).[(v_2 - v_4) \times (v_3 - v_4)]$$
 (8.21)

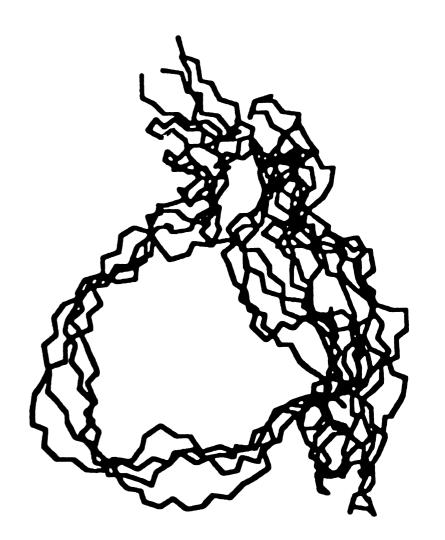
The other stereoisomer corresponds to a negative chiral volume. Chiral constraints are included in the penalty function by adding terms of the following form:

$$(V_{\rm ch} - V_{\rm ch}^*)^2$$
 (8.22)

 $V_{\rm ch}^*$ is the desired value of the chiral constraint. Chiral constraints can also be used to force groups of atoms to lie in the same plane by requiring the chiral volume to have a value of zero.







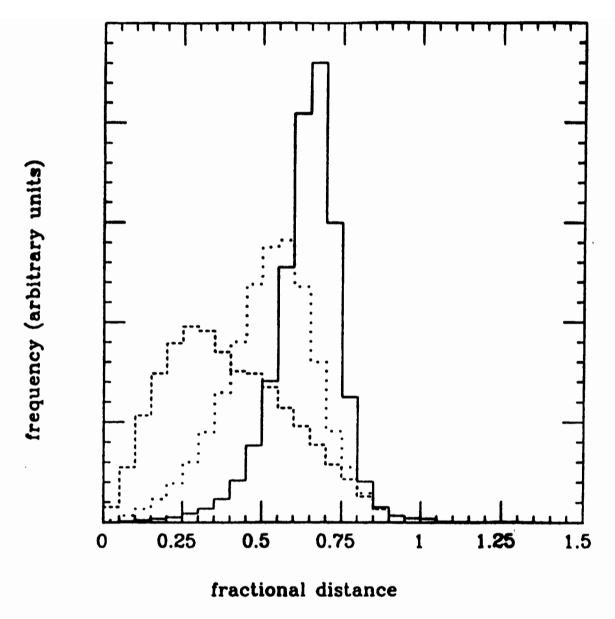


Figure 1. Histogram for the fractional distance, (distance (crystal) — lower bound)/(upper bound — lower-bound). Bounds taken from the all-(H-H) data set (solid line), 10% data set (dotted line) or disulfide-only data set (dashed line).

FOUR-ATOM METRIZATION UNIFORM TRIAL DISTRIBUTION

PAIRWISE-5% METRIZATION GAUSSIAN TRIAL DISTRIBUTION

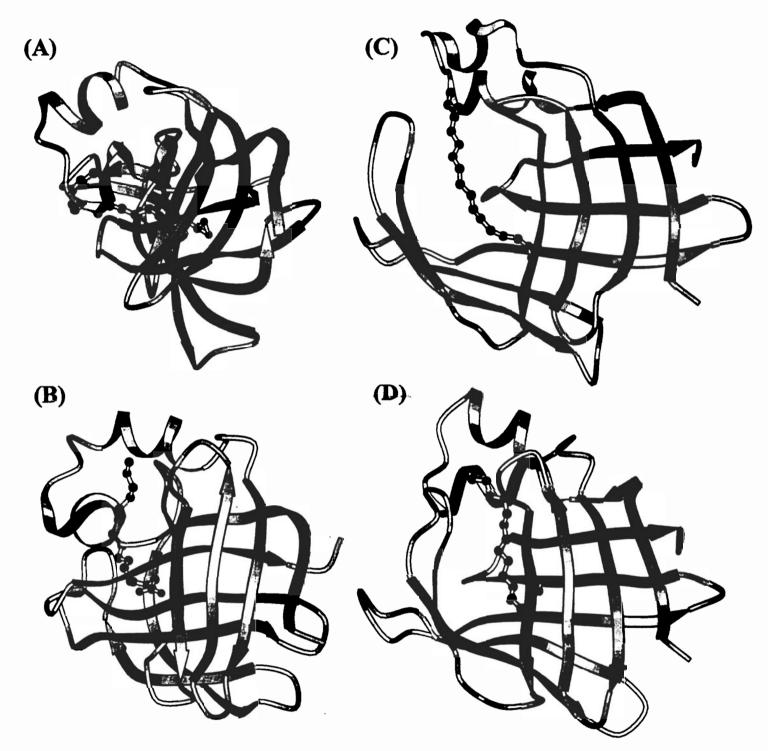


Figure 10. Ribbon diagrams illustrating the influence of the distance geometry metrization algorithm on the calculated structures both prior to ((A) and (C)) and after ((B) and (D)) simulated annealing refinement. All of the calculations were performed using DISTGEOM, which has the option of altering the trial distribution and the type of metrization employed. The structures in (A) and (B) were calculated using four-atom metrization with a uniform trial distribution; this is the type of algorithm implemented in X-PLOR version 3.1. The structures in (C) and (D) were controlled using pairwise-5% metrization with an optimized Gaussian trial distribution. This latter algorithm was used the current study. For reference, the correct positions of secondary structure elements, as defined by $^1H/^{13}C$ chemical shifts, are indicated in each ribbon diagram; this is not meant to imply that regions of the calculated structures shown here actually adopt ϕ/ψ angles consistent with regular α -helix and β -sheet, especially in the distorted structures shown on the left. All of the calculations used the final set of distance restraints listed in Table 3. The structures shown are examples from an ensemble of structures obtained for each set of calculations; other members of the ensemble showed the same general characteristics as shown here.

Protein Engineering: Map Distance Geometry Problem

Initial Table of Intercity Mileages:

	A	В	C	D	F	Ħ	×	P
A	0	1084	715	1519	860	875	814	776
В	1084	0	976	2008	1902	1961	1069	308
C	715	976	0	1017	970	1073	95	767
D	1519	2008	1017	0	763	1038	1036	1770
F	860	1902	970	763	0	236	1064	159 5
H	875	1961	1073	1038	236	0	1150	1648
M	814	1069	95	1036	1064	1150	0	849
P	776	308	767	1770	1595	1648	849	0

Applying Triangle Inequality to the Distances:

```
A to M Distance Changed from 814 to 810 via A --> C --> M B to H Distance Changed from 1961 to 1959 via B --> A --> H B to H Distance Changed from 1959 to 1956 via B --> P --> H B to D Distance Changed from 2008 to 1993 via B --> C --> D D to H Distance Changed from 1038 to 999 via D --> F --> H
```

Distance Geometry Metric Matrix:

	A	В	С	D	F	H	M	P
A	245203	159156	-108504	-512045	53837	117256	-126632	171728
В	159156	1248166	172302	-842907	-883683	-911418	131519	926866
C	-108504	172302	49014	26397	-144907	-173690	98811	80578
D	-512045	-842907	26397	1038068	528985	397501	61202	-697201
F	53837	-883683	-144907	528985	602071	650655	-186196	-620762
H	117256	-911418	-173690	397501	650655	754934	-204967	-630270
M	-126632	131519	98811	61202	-186196	-204967	157632	68631
	171728				_			

Distance from each City to the Map Centroid:

City	Distance to Centroid	
A	495	
В	1117	
C	221	
D	1019	
F	776	
H	869	
M	397	
P	837	

Eigenvalues and Eigenvectors of Metric Matrix:

-164207.0202	-31467.5657	0.0000	4993.2342
0.7015	-0.1262	0.3536	-0.2326
-0.2545	-0.4255	0.3536	-0.2421
0.0964	0.7715	0.3536	-0.22 94
0.3626	-0.2271	0.35 3 6	0.1407
-0.4811	0.0921	0.3536	-0.4662
-0.2226	-0.1110	0.3536	0.4979
-0.1213	-0.2468	0.3536	-0.05 69
-0.0811	0.2730	0.3536	0.5885
14258.5892	967 61.34 62	1028672.7147	3846507.8266
0.1134	0.0399	-0.5400	0.0821
-0.4188	-0.2519	0.0845	0.5697
-0.3758	0.1587	0.2177	0.0641
-0.0008	-0. 3 632	0.6044	-0.4182
0.3685	-0 .289 5	-0.2173	-0.3885
-0.4703	0.1887	-0.3910	-0.3944
0.3353	0.7708	0.2929	0.0617
0.4485	-0.2535	-0.0513	0.4236

Distance Geometry Generated Map Coordinates:

City	X-Coordinate	Y-Coordinate
λ	161	-548
В	1117	86
C	126	221
D	-820	613
F	-762	-220
H	-774	-397
×	121	297
P	831	-52

Final Table of Intercity Mileages:

	A	B	C	D	F	H	×	P
A	0	1147	769	1520	979	947	846	83 3
В	1147	0	1001	2008	1904	1951	1018	318
C	769	1001	0	1024	991	1091	76	756
D	1520	2008	1024	0	835	1011	993	1780
F	979	1904	991	835	0	177	1023	1602
H	947	1951	1091	1011	177	0	1132	1641
M	846	1018	76	993	1023	1132	0	791
P	833	318	756	1780	1602	1641	791	0

Map Showing the Locations of the Cities:

