SHORT COMMUNICATIONS

THE CONFORMATIONAL CHAIN PLOT AND THE ANALYSIS OF PROTEIN CONFORMATIONS

G. RAGHUNATHAN AND R. BALASUBRAMANIAN
Department of Crystallography and Biophysics,
University of Madras, Guindy Campus,
Madras 600 025, India.

THE backbone conformation of a protein molecule can be completely specified by the twin dihedral angles ϕ and ψ around the single bonds N-C^{α} and C^{α}–C' respectively. The allowed and disallowed combinations of ϕ and ψ values are readily recognized from the "Ramachandran map"[1-2]. Several representatiives of structural data have been reported in the literature[3-13]. The sequential folding of the molecule, the occurrence of the various secondary structural domains and the structural transitions are succinctly represented by plotting ϕ and ψ values against the corresponding residue numbers in the form of a linear plot proposed by Balasubramanian[14]. The secondary structures like α-helices, β-strands and the various types of β-bends[15] or turns are seen as characteristic patterns in this chain plot[14]. From such characteristic patterns, the various secondary structural regions along the length of a protein chain are readily discernable from a mere inspection of the chain plot and one gets an immediate picture of the secondary folding of the molecule. Further from a comparison of the plots for different proteins one is able to assess the degree of structural homology between them. This would give an insight into the functional and evolutionary relationships between the two protein molecules. A similar representation[16] has been suggested later in which ϕ and ψ values are plotted along the radius of a circle instead of in a linear way. The linear representation enjoys the advantage of serving as a tool to compare two proteins directly when they are stacked, one atop the other and moved along the sequence in the search for homologous regions.

Haemoglobin is a tetramer composed of two α and two β-chains. The α and β-sub-units are folded in the same way. The α-chain has 141 residues and the β-chain 146. Figure 1 gives the linear plot for the two chains. The residue numbers and names in one letter notation are given along the abcissa. The ordinate represents the ϕ and ψ values and these are shown by symbols Δ and ∇ respectively. The eight helices from out of which the molecule is constructed are denoted by the letters A, B, C, D, E, F, G and H. These are

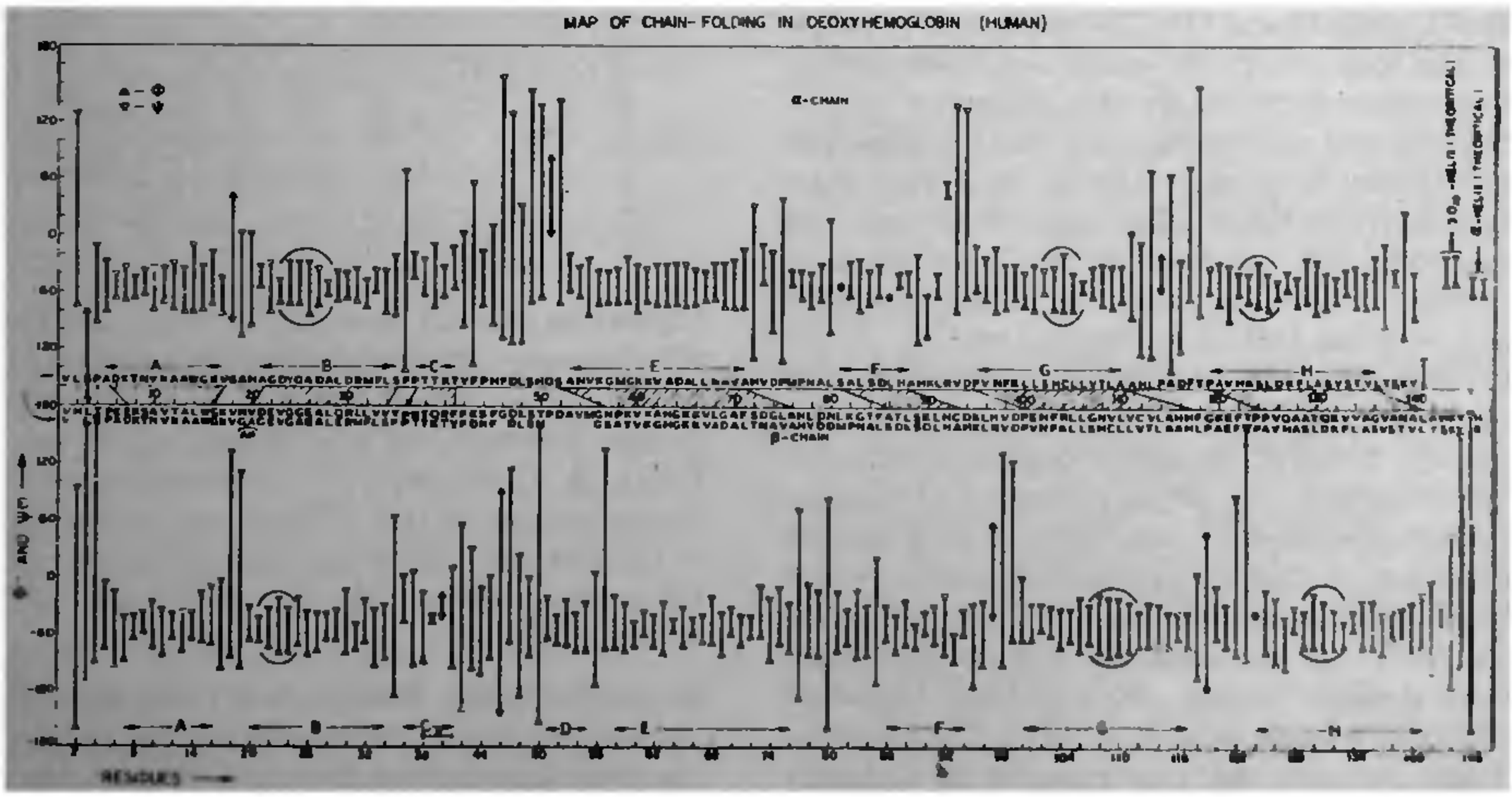


Figure 1. Linear plot of haemoglobin α and β-chains. α-chain is given at the top half of the figure and the β-chain at the bottom half. Δ refers to the value of ϕ and ∇ to that of ψ. The residue number and name are taken along the abscissa. The eight helices are marked by letters A to H and are recognised by stretches of short vertical lines around –60° (see text for further discussion).

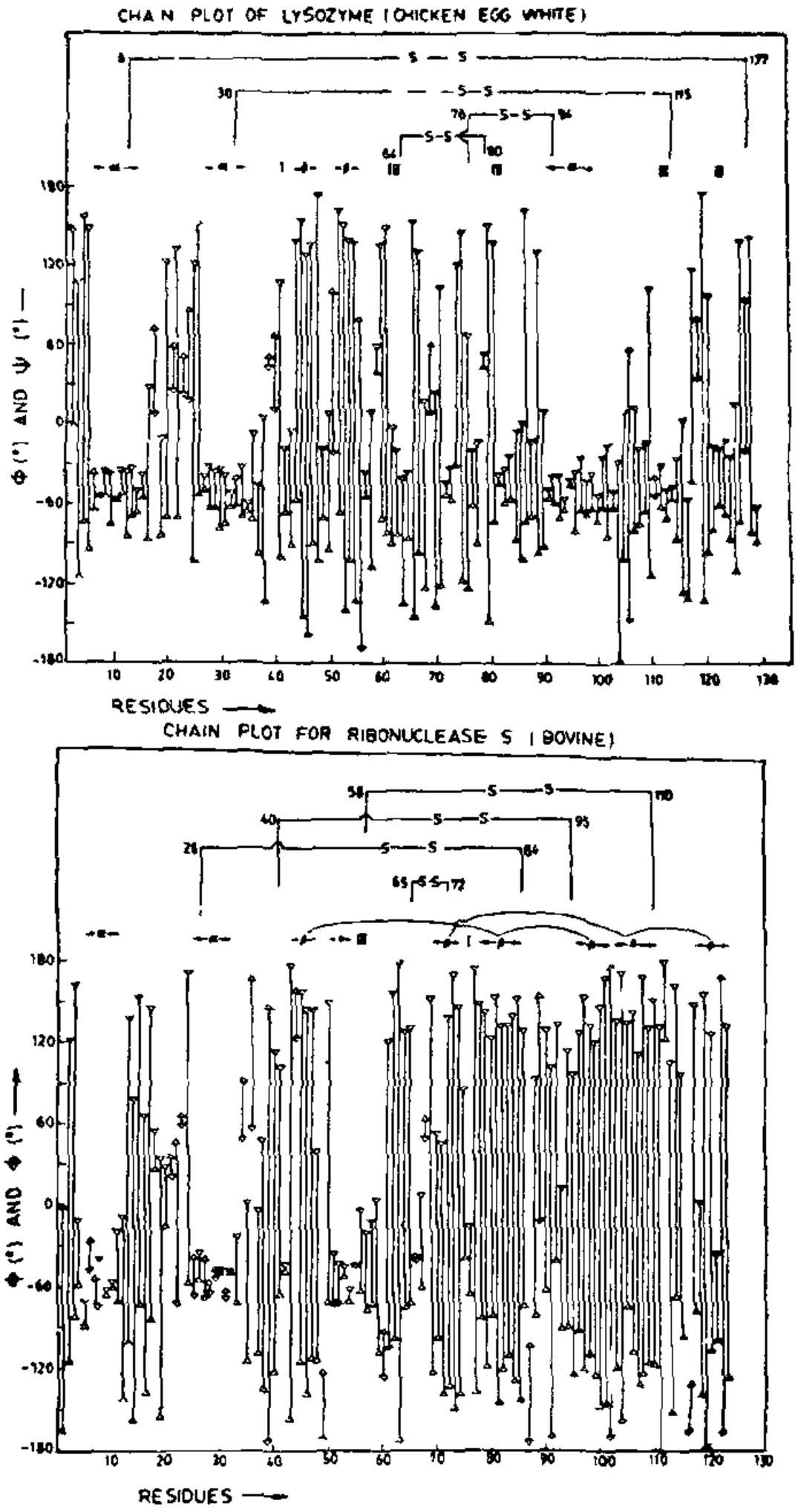
discernable by the stretches of short vertical lines around -60°. The similarity in the folding of the α and β-chains of the molecule is immediately visible. The absence of D helix in the α-chain is at once perceived. The C-helix is a 3.0_{10} helix. This stands out, since the vertical lines are longer than those for α-helix. The residue names in the two chains are shifted along the sequence in the two chains and are arranged for maximum homology in the primary structure. This is shown at the top of the plot for β-chain. Secondary structural homology brought about by similar folding of the two chains is illustrated by the hatched bands between the corresponding regions of the two chains. In both the chains, the helices are separated by long conformational lines ( ). These correspond to conformations that serve as hinges for giving the necessary turn to the adjacent helical segments. The occurrence of proline at the beginning of C, G and H helices of haemoglobin and in the various bends between the helices is also noticeable.

Figure 2a gives the linear plot for lysozyme. The various secondary structural regions are marked in the figure. The molecule has three helices (residues 6–14, 26–35 and 86–98). There are mainly two β-strends which are fairly long. The disulphide linkages are also marked. The chain plot for ribonuclease is given in figure 2b. The *N*-terminal half of the molecule consists of 3 segments of α-helices while the *C*-terminal half is dominated by β-sheets. The two β-sheets each consisting of three strands (residues 45–48, 80–86 and 94–104 and 68–73, 104–110 and 118–124) are shown by arrow heads. The four disulphide linkages and their corresponding residue numbers are also dilineated.

Lysozyme and ribonuclease are two proteins that are structurally a lot more similar than what their chemical activities would allow one to anticipate[17]. It is noteworthy that our plots for the two proteins at once reveal extensive similarity in structure especially at the *N*-terminal half of the two chains.

The linear representation for bovine trypsin DIP and porcine tosyl elastase are shown in figures 3a and 3b respectively. Elastase, though belonging to the same class of molecules (*viz.* serine proteases) as trypsin, differs significantly from the latter in its substrate specificity and in its ability to degrade elastin. Still it shares a high degree of structural homology with trypsin. As evidenced in figures 3a and 3b both have extensive β-sheets regions. Both of them terminate with the only α-helix present in them. The extensive homology between the two proteins is strikingly apparent from a cursory glance of the two plots. The four disulphide linkages in the two proteins neatly fall in place in the corresponding regions.

Thus the linear representation helps indentify domains of similar secondary folding between two



Figures 2a & b: a. Chain plot for lysozyme. The different secondary structural segments are marked in the figure. The disulphide linkages and the corresponding residue numbers are also shown at the top of the figure. **b.** Chain plot for ribonuclease. The plot is almost similar to that of lysozyme, especially at the N-terminal half, revealing the structural homology of these two proteins. The two sheets are marked by arrow heads.

protein molecules. Rossman and coworkers[18-22] superimpose two protein chains one over the other to study the three-dimensional homology between the chains. They calculate a search function representing the number of topologically equivalent residues plotted with respect to the three Eulerian angles. A unique fold common to the two proteins is characterised by a single large peak. The method developed by us makes

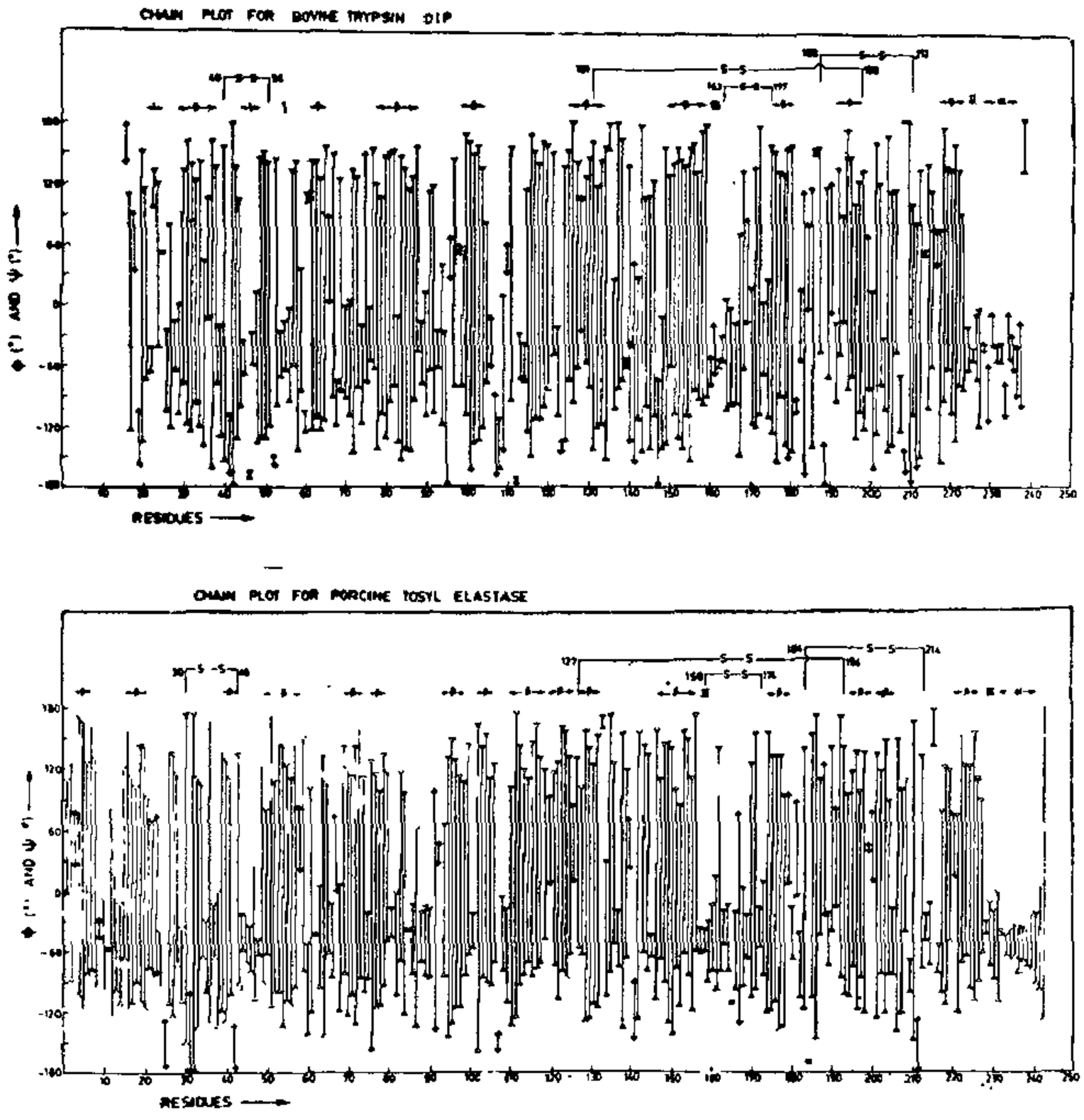


Figure 3a & b. a. Represenation for bovine trypsin DIP. **b.** Representation for porcine tosyl elastase. Major portion of the protein is made of β-sheets as in the case of trypsin. Similarity of this figure with figure 3a is readily perceived.

use of only two internal parameters, *viz* the interpeptide dihedral angles ϕ and ψ. The method is simple and direct to study and compare secondary structural domains between two proteins and it can be used as a first step for further elaborate search for homology in three dimensions.

The results presented in this paper were originally sent for publication as an invited contribution in the Festschrift Volume in honour of Prof G. N. Ramachandran, F.R.S. However, for reasons not clear to us, the paper was not published therein. We rededicate this paper to Prof GNR.

2 February 1983; Revised 6 April 1983

1. Ramachandran, G. N., Ramakrishnan, C. and Sasisekharan, V., *J. Mol. Biol.*, 1963, **7**, 95.
2. Ramachandran, G. N. and Sasisekharan, V., *Adv. Prot. Chem.*, 1968, **23**, 283.
3. Lewis, P. N., Momany, F. A. and Scheraga, H. A., *Biochem. Biophys. Acta.*, 1973, **303**, 211.
4. Dunn, J. B. R. and Klotz, I. M., *Arch. Biochem. Biophys.*, 1975, **167**, 615.
5. Kuntz, I.D., *J. Am. Chem. Soc.*, 1975, **97**, 4362.
6. Srinivasan, R., Balasubramanian, R. and Rajan, S. S., *J. Mol. Biol.*, 1975, **98**, 739.
7. Balasubramanian, R., *Biochem. J.*, 1976, **157**, 769.
8. Balasubramanian, R., *Indian J. Biochem. Biophys.*, 1976, **13**, 289.
9. Balasubramanian, R., *Indian J. Biochem. Biophys.*, 1976, **13**, 303.
10. Balasubramanian, R. and Srinivasan, R., *Curr. Sci.*, 1976, **45**, 397.
11. Levitt, M., *J. Mol. Biol.*, 1976, **104**, 59.
12. Levitt, M. and Chothia, C., *Nature (London)*, 1976, **261**, 552.
13. Balasubramanian, R., *Int. J. Polypep. Prot. Res.*, 1977, **9**, 157.
14. Balasubramanian, R., *Nature (London)*, 1977, **266**, 856.
15. Venkatachalam, C. M., *Biopolymers*, 1968, **6**, 1425.
16. Srinivasan, A. R. and Yathindra, N., *Biopolymers*, 1978, **17**, 1595.

17. Dickerson, R E. and Geis, I., In *The structure and action of proteins*, Harper and Row, New York, Evanston, London.
18. Rao, S. T. and Rossman, M. G., *J. Mol. Biol.*, 1973, **76**, 241.
19. Eventhoff, W. and Rossman, M. G., CRC *critical review of biochemistry*. (ed. Fasman, G. D.), 1975, (RC Press, Cleveland), **3**, 111.
20. Rossman, M. G. and Argos, P., *J. Biol. Chem.*, 1975, **250**, 7525.
21. Rossman, M. G. and Argos, P., *J. Mol. Biol.*, 1976, **105**, 75.
22. Rossman, M. G. and Argos, P., *J. Mol. Biol.*, 1977, **109**, 99.

CATALYTIC ACTIVITY OF Ln_2MnNiO_6 PEROVSKITES FOR ISO-PROPONOL DECOMPOSITION

R. RADHA AND C. S. SWAMY
Department of Chemistry, Indian Institute of Technology, Madras 600 036, India.

MULTIPLE ion-substituted perovskites of the type $A_2BB'O_6$ with transition metal ions at the B site show interesting solid state and catalytic properties. The preparation and characterization of perovskites of the type La_2TiMO_6 (M = Cu, Ni and Zn) have been reported earlier and tested for isopropanol and nitrous oxide decomposition[1,2]. The present communication deals with the catalytic activity of rare earth-substituted perovskites of the general formula Ln_2MnNiO_6 (Ln = La, Nd, Sm and Gd) for iso-propanol decomposition.

The oxides Ln_2MnNiO_6 (Ln = La, Nd, Sm and Gd) were prepared by firing stoichiometric amounts of the corresponding oxalates at 950° C for 36 hr. A similar procedure had been employed by Blasse[3] to prepare a series of compounds La_2MnMO_6 (M = Cu, Co, Ni and Mg) and by Ganguly[4] to prepare $La_2MM'O_6$ (M, M' = Cr, Mn, Fe, Co, Ni, $M \neq M'$). The formation of single phase was checked by x-ray diffraction using CuK_α radiation. All the compounds crystallised in a cubic lattice and the lattice parameters were found to be approximately twice that of the ABO_3 perovskites (~3.9 Å). The lattice parameters are as follows:

La_2MnNiO_6 = 7.76 Å; Nd_2MnNiO_6 = 7.74 Å
Sm_2MnNiO_6 = 7.71 Å; Gd_2MnNiO_6 = 7.68 Å

Isopropyl alcohol (BDH spec pure) was distilled before use. The decomposition reactions were followed in a fixed bed-flow type integral reactor[5]. The reactant was fed into the reactor using a motor driven syringe pump. The liquid and gaseous products were analysed using gas chromatograph (Varian 1800) and Orsat gas analyser. It was found that heating in air (free of CO_2 and moisture) for 4 hr at 400° C restored the activity completely. The reactor was flushed with nitrogen for 10 min before each run to get an inert atmosphere.

The decomposition of isopropyl alcohol was studied in the temperature range 260–320° C and at contact times 0.2 to 4 sec. All the four catalysts promoted only dehydrogenation to the complete exclusion of dehydration. From the plots of contact time versus mole per cent conversion the initial rates were computed and these were used for making the Arrhenius plots (figure 1).

In order to understand the effect of products on the course of the decomposition, reactions were carried

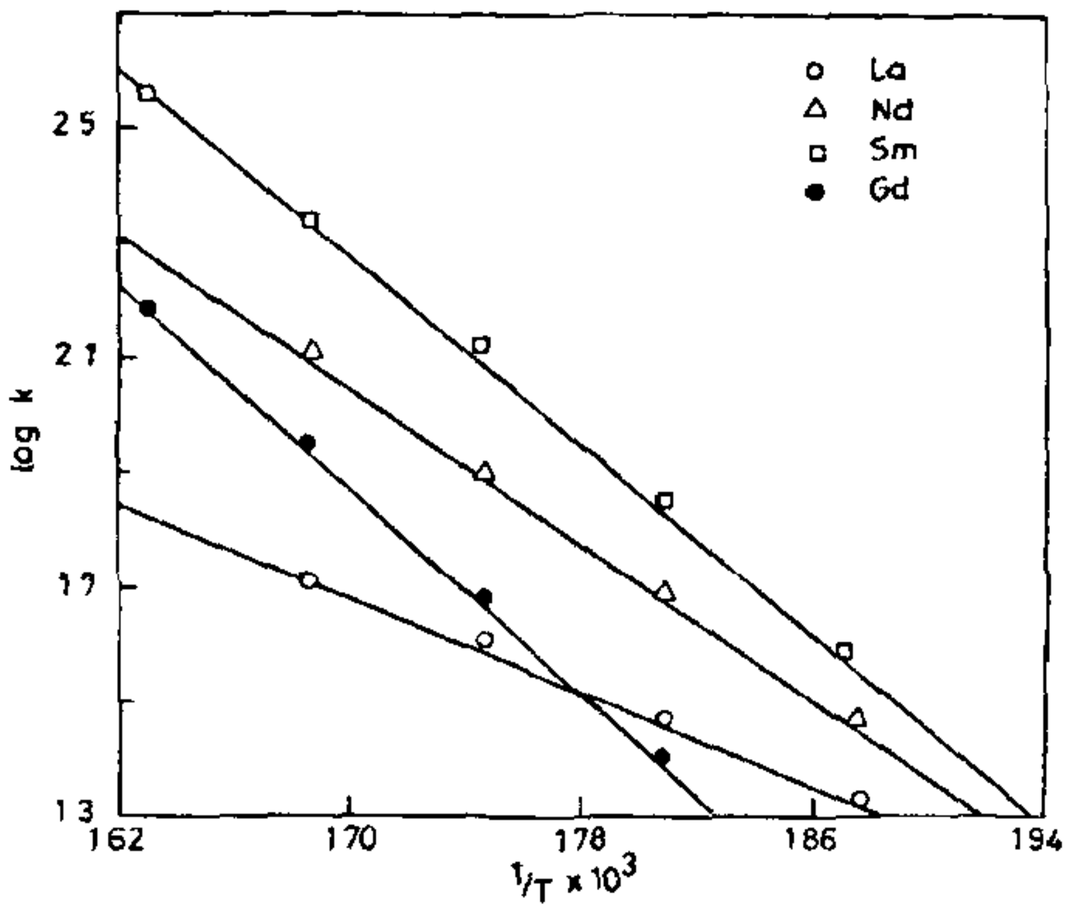


Figure. 1. Arrhenius plots for the decomposition of isopropyl alcohol on Ln_2MnNiO_6 (Ln = La, Nd, Sm, Gd).

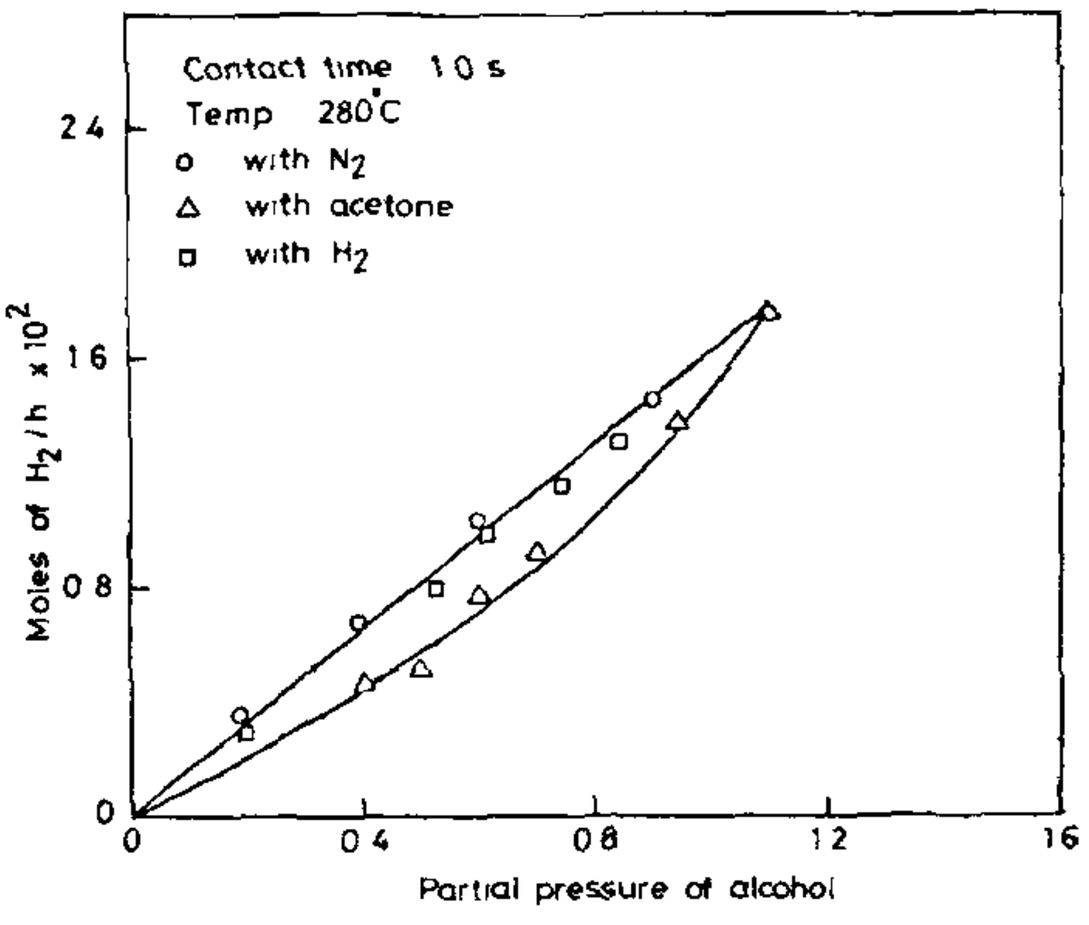


Figure. 2. Effect of products on the decomposition of iso-propyl alcohol on Gd_2MnNiO_6.