# Biochemistry

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### Editorial: Computer System for *Biochemistry*

Lo aid in the selection of the most appropriate reviewers and to accelerate the processing of manuscripts, a microcomputer system was developed and recently installed in the Editorial Office of *Biochemistry*. One of the most important steps in the evaluation of a manuscript is the selection of competent reviewers. With more than 3000 reviewers in our file, it is almost impossible to recall the names of all those who could judge a manuscript and would be available to do so at a given time. Inevitably, the most frequently used reviewers come to mind first and the least frequently used ones are seldom recalled. The computer system developed by Dr. Lorrin Garson of the American Chemical Society, Book and Journals Division, Research and Development Department, provides for up to 100 topical categories. Each reviewer currently serving Biochemistry has been asked to select from about 70 categories up to five that most closely correspond to his/her scientific expertise. (See questionnaire on next page.) The questionnaire represents a first attempt to identify the categories which most closely correspond to the topics covered in *Biochemistry*. We intend to revise it as dictated by experience (categories 69-73) were added after the questionnaires were returned), and therefore it should not be considered a final selection.

When a manuscript is received in the Editorial Office, those categories are identified which in the judgment of the Editors represent most closely the subject of the manuscript. Upon command, the computer displays the names of the reviewers and their availability at any given time. Two are chosen by the Editors from this list. The computer reviewer file includes the names, addresses, telephone numbers, areas of expertise, editors' comments, dates unavailable for reviewing, reviewers' recommendations concerning manuscripts, and other ancillary information. The manuscript file includes the names and addresses of the corresponding authors and the dates when manuscripts are received, sent to the reviewers, returned for revision, and published. The computer is also capable of monitoring the assignment of manuscripts to members of the Editorial Advisory Board and printing form letters, self-adhesive mailing labels, manuscript control documents, and the copyright release document. Other programs also provide monthly statistical reports on the number of manuscripts received, rejected, and published, the average time elapsed before papers were published or rejected, and the average time reviewers had manuscripts in their possession. The photograph of the "MENU", which appears on the CRT as a prompt, shows the functions available. The computer system is also used as a word processing unit by staff of the Editorial Office.

Hardware. The computer is an Alpha Microsystems Model AM100 which is based on the Western Digital WD1600 16 bit microprocessor. The system has 128K of random excess

#### MENU

#### Editorial Files for the ACS Journal BIOCHEMISTRY

The date today is: June 1, 1979

REVIEWER FILE COPYRIGHT FORM PROGRAM Enter New Record 13 Access Program Select to Review PROCESSING LABEL Locate a Record **PROGRAM** Print Address Label 14 Access Program Find Overdue Reviews STATISTICAL PROGRAMS ADVISORY BOARD FILE 15 Access Program List Enter New Record SET DATE 16 Access Date Program Select to Review LETTER FILE Manuscript Status of 17 Access File Locate a Record EXIT TO MONITOR 10 Print Address Label

18 Exit

11 Enter New Record 12 Locate a Record

MANUSCRIPT/AUTHOR FILE

ENTER THE NUMBER OF THE FUNCTION YOU WISH PER-FORMED:■

memory, of which 32K are assigned to each of three Lear-Siegler ADM-3 terminals and 32K are at systems level. A Control Data Corporation Model 856-14 cartridge disk drive provides 10 megabytes of storage (5 megabytes on the fixed disk and 5 megabytes on the removable cartridge). The system also has a Diablo Model 1620 printer/terminal. The system is set up so that three users can simultaneously access data files and run programs. Simultaneous access to specific records and certain files is prevented by a check/lock subroutine. System software, provided by the Alpha Microsystems, consists of 91 programs occupying 135K of disk storage.

Software. There are 23 programs (requiring 144K of storage) for each of the three terminals plus three command files and two temporary data files (requiring 3K of storage). Other miscellaneous programs and files require 17K of storage, bringing the total disk storage required to 450K. The programs were written in Basic and are used by reading the compiled versions from the disk into the users memory partition. Program execution is generally accomplished in 1 to 2 seconds or less.

Data Files. There are two main data files: one file of 2100K capacity for data on 4200 reviewers and members of the Editorial Advisory Board and the other a 1500K for data on 3000 manuscripts. Both are random access files. There are also 14 miscellaneous small files for temporary data storage. At present the reviewer file contains approximately 3100 active records (74% of capacity). The capacity of 3000 man-

# Research and Development Department/Books and Journals Division American Chemical Society/1155 16th Street, N.W./Washington, D.C. 20036

			<ol> <li>Are you willing to continue to review manuscripts for Biochemistry?</li> </ol>
r		٦	yes no There is no need to answer any further questions. Please return the questionnaire in the envelope provided.
L		٦	2. Please check the computer- generated address label to the left and make any necessary corrections. The number printed above your name is the reviewer number which has been assigned to your record; this number, as well as your name, will remain anonymous to authors.
manuscripts. Indicate the subject area	of highest competence	willingness with r	n you are competent and willing to review number one (1), the second highest with ion will determine, to a great extent, the
Amino Acid Sequence Analysis (1)	Growth Factors (25	5)	Polyamines (50)
Antibodies (2)	—— Hemoglobin (26)		Protein Chemistry (51)
Bacterial Metabolism (3)	Hemoproteins (27)		Protein Conformation (52)
Bio-Energetics (4)	Hormones (28)		Protein Hormones (53)
Biological Differentiation (5)	Lectins (29)		Protein Phosphorylation,
Bioluminescence (6)	Lipid Chemistry (30)		Dephosphorylation (54)
Blood Coagulation (7)	Lipid Metabolism (31)		Protein Synthesis, Degradation (55)
Carbohydrate Chemistry (8)	Lipoproteins (32)		Proteolytic Enzymes (56)
Carbohydrate Metabolism (9)	Luminescence (33)		Raman Scattering (57)
Cell Surfaces (10)	Membranes and Bi-Layers (34)		Ribosomes (58)
Chlorophyll (11)	Metal Binding (35)		RNA (59)
Chromatin, Chromosome, and Gene	Metallo-Proteins (36)		Steroid Chemistry, Enzomology (60)
Structure (12)	Microfilaments (37)		Steroid Hormones and Receptors
Collagen (13)	Microtubules (38)		(61)
DNA Replication (14)	Muscle Proteins (39)		Toxins (62) Transcription (63)
Endocrines (15)	NMR Spectroscopy (40)		Transcription (63)
Enzyme Purification and Structure (16)	Natural Products (41)		Tumorogenesis (65)
Enzyme Kinetics (17)	Nitrogen Fixation (42)		Viruses (66)
Enzyme Mechanism (18)	Nitrogen Metabolism (43)		Vitamins (67)
Enzyme Regulation (19)	Nucleic Acid Chemistry (44)		X-Ray Crystallography (68)
EPR Spectroscopy (20)	Oxidative Phosphorylation (45)		Visual Pigments (69)
Evolution (21)	Oxygenases (46)		Drugs & Related Compounds (70)
Fertilization (22)	P-450 (47)		Cyclic Nucleotides (71)
Fluorescence Spectroscopy (23)	Peptide Chemistry (48)		Immunochemistry (72)
Glycoproteins (24)	Photosynthesis (49)		Neurochemistry (73)
4. Would you please give one or two te through which we could contact you if ne		would not be avai	period during the next several months that you ilable to review manuscripts?
Telephone number:	☐ no (most direct number) ☐ yes plea		se indicate inclusive dates
Telephone number:	·		
		From (date)	To (date)

uscript records will allow the system to store over 2 years of manuscript data before older records will have to be purged onto an inactive archival cartridge.

Indexes. The reviewer file is accessed by searching the reviewer's last name/first initial or by the reviewer number. The 100 name indexes are based upon ASCII numeric equivalent of the first two letters of the last name. The reviewer number, which is automatically assigned by the computer, is directly tied to the record accession number of the main data file. Reviewers' records may also be accessed through a set of 100 indexes based upon areas of reviewer subject expertise.

Manuscript records are accessed by a corresponding author's last name/first initial or manuscript number. The 100 manuscript number indexes are based upon the last two digits of

the 9-digit manuscript number. In all, there are 400 index files requiring 474K of disk storage. The computer system cannot, nor was it intended to, replace human judgment or evaluation of manuscripts received. Nevertheless, in actual operation, the system has already proven its value by recalling reviewers for a given topic, regardless of frequency of their use, and by broadening the list of reviewers most appropriate for a given manuscript. The system also expedites the flow of manuscripts and greatly facilitates all of the operations for which it was designed. Although the system was specifically designed to be used by *Biochemistry*, it could be applicable with minor modifications to other journals.

Hans Neurath Lorrin Garson

## Role of Cis-Trans Isomerism of the Peptide Bond in Protease Specificity. Kinetic Studies on Small Proline-Containing Peptides and on Polyproline<sup>†</sup>

Lung-Nan Lin and John F. Brandts\*

ABSTRACT: Aminopeptidase P, a proline-specific exopeptidase, was isolated from Escherichia coli, and the cis-trans specificity of its activity was critically tested by using L-phenylalanyl-L-proline, polyproline, and glycyl-L-prolyl-L-alanine as substrates, under conditions where a high ratio of enzyme activity to substrate concentration existed. The results of the study strongly suggest that aminopeptidase P, like prolidase [Lin, L.-N., & Brandts, J. F. (1979) Biochemistry 18, 43], can only hydrolyze the trans form of the X-L-Pro peptide bond, while the cis form has to isomerize before it can be cleaved. This study also shows that the isomeric specificity of aminopeptidase P is valuable for studying the conformation of proline-containing peptides preequilibrated in aqueous solution as well as in the solid form. The kinetic data for polyproline hydrolysis

show clearly that the cis-to-trans isomerization of polyproline I, when dissolved in water, begins step by step from the N-terminal end rather than the C-terminal end, as suggested by others from NMR data. It was also found that the rate of isomerization for glycyl-L-prolyl-L-alanine in aqueous solution is ~16 times faster than that of glycyl-L-proline, suggesting that the tripeptide could be a better model for proline isomerism in proteins. Finally, the experimental results indicate that the isomeric states of the C-terminal proline residue in L-leucyl-L-phenylalanyl-L-proline can be determined by using two aminopeptidases in tandem: one of which (leucine aminopeptidase) cleaves the Leu-Phe bond and the other of which (prolidase) cleaves the Phe-Pro bond.

 $oldsymbol{A}$  previous study from this laboratory (Lin & Brandts, 1979) on the stereospecificity of prolidase, a proline-specific dipeptidase, demonstrated that this enzyme hydrolyzes only the trans form of the X-L-Pro bond. The cis isomer is not a hydrolyzable substrate and has to isomerize before it can be cleaved. One important question raised from that study is whether other proteases will exhibit the same kind of isomeric specificity. Since the amount of cis form of the peptide bond for residues other than proline is probably less than 1% (Brandts et al., 1977; Lin & Brandts, 1978), it would be very difficult to detect stereospecificity for proteases which cleave only nonproline bonds. However, other proline-specific proteases should demonstrate such preference if the trans peptide bond is a general requirement for protease action. In order to test the generality of isomeric specificity and eventually to establish the use of proteases in conformational studies of

†From the Department of Chemistry, University of Massachusetts, Amherst, Massachusetts 01003. Received June 15, 1979. This work was supported by a grant (GM-11071) from the National Institutes of Health.

proline-containing peptides or proteins, we have isolated aminopeptidase P (Yaron & Mlynar, 1968; Yaron & Berger, 1970) from *Escherichia coli* (strain B) for the present study.

Both prolidase and aminopeptidase P are proline-specific exopeptidases which cleave the N-terminal X-Pro bond. Whereas prolidase is a dipeptidase, which can only hydrolyze X-L-proline or X-L-hydroxyproline bonds (Davis & Smith, 1957), aminopeptidase P can cleave the bond between any N-terminal amino acid (including proline) and a subsequent L-proline residue (but not hydroxyproline) irrespective of the size of polypeptide. In this communication, the stereospecificity of aminopeptidase P will be critically tested by using L-phenylalanyl-L-proline, polyproline, and glycyl-L-prolyl-Lalanine as substrates. As in the previous paper (Lin & Brandts, 1979), this study will be carried out at a high ratio of enzyme activity to substrate concentration. The crystalline substrates as well as those preequilibrated in aqueous solution will be subjected to hydrolysis. NMR data (Grathwohl & Wüthrich, 1976) have shown that L-phenylalanyl-L-proline and glycyl-L-prolyl-L-alanine exist as a mixture of cis and trans