Protein Data Bank

Quarterly Newsletter

Number 60 April 1992

April Update

The April 1992 PDB release includes 56 new atomic coordinate entries (see Table 3), bringing the total number of coordinate entries to 906. In addition to these 906 entries, 101 pre-release entries from the pending list (Table 8) are included in DATAPRTP. The size of the atomic coordinate and bibliographic entry database (DATAPRTP) is now 236 Mbytes.

Be sure to visit the PDB at booth 19 during the Sixth Symposium of the Protein Society in San Diego, July 25-29, 1992.

The PDB Newsletter is available in text and PostScript formats from the PDB anonymous FTP and e-mail server.

Data preprocessing requires approximately three weeks, after which time depositors will be notified of their idcode(s), or apprised of any questions or problems related to their data.

Data will not be accepted for preprocessing until the coordinates, deposition form, and preprints/reprints have been received.

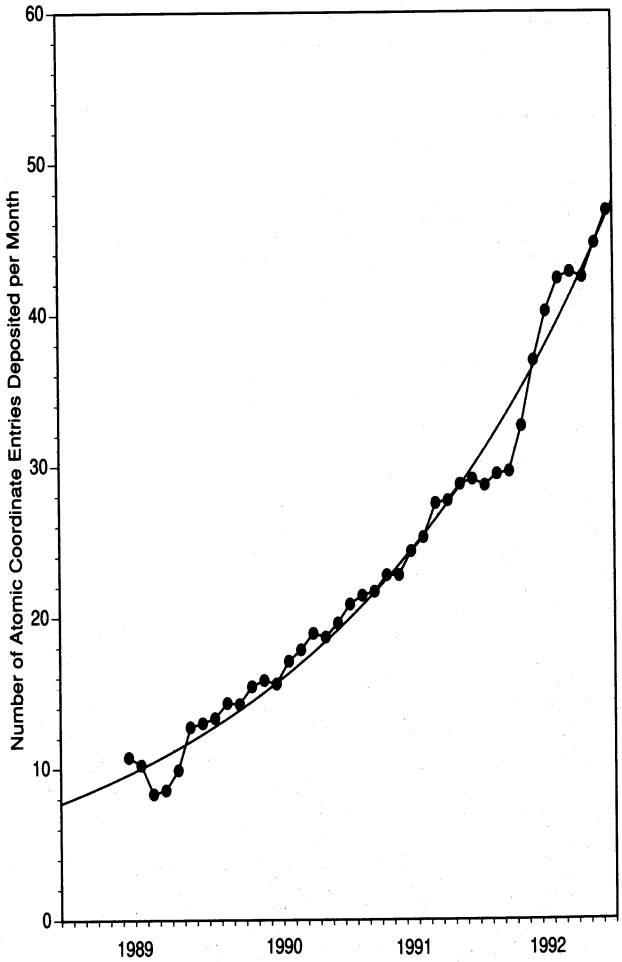
We anticipate that future releases of the DATAPRTP UNIX distribution will be set up with entries located in a single directory instead of tape1, tape2, ..., and tape8 as they are now. If you have any comments or suggestions, please contact John Skora via e-mail to skora@bnl.gov, voice mail at +1 516-282-5750 or fax at +1 516-282-5751.

Pre-release of Pending Entries

In total, 101 atomic coordinate entries are now available in pre-release and additional entries will be loaded as soon as they are ready.

Due to the preliminary nature of pre-release entries it is suggested that those using them check the PDB anonymous FTP server for update notices. Pre-release entries are available from the PDB anonymous FTP server as well as from the PDBSA centers listed on page 9. Pre-release entries ready at the time a new master release tape is prepared will be included as part of the regular DATAPRTP distribution.

Pre-release entries carry 5-character IDENT CODES, which begin with the letter 'P' in column 62 for easy identification.



Running 12-month average number of atomic coordinate entries deposited per month since 1989. The curve shows an exponential fit to the experimental data points.

Table of Contents

A number of tables in this April 1992 Newsletter are abbreviated and contain only new or updated information. Full versions of all tables are available from the PDB anonymous FTP and e-mail server or by regular mail upon request.

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Statement of Support

The PDB is supported by a combination of Federal Government Agency funds (work supported by the U.S. National Science Foundation; the U.S. Public Health Service, National Institutes of Health, National Center for Research Resources, National Institute of General Medical Sciences, and National Library of Medicine; and the U.S. Department of Energy under contract DE-AC02-76CH00016) and user fees.

The Protein Data Bank as an International Resource

Frank Hartel and John Wooley
Biological Instrumentation and Resources Division
National Science Foundation

The Protein Data Bank's growing importance for research in wide areas of contemporary biology and chemistry is well established. It is arguable that the ultimate success of the genome projects (from "model" organisms to higher plants and humans) depends critically on the understanding of structure-function relationships, and that this sound theoretical understanding in turn can only come from the coupling of computational simulation, experimental advances in structural biology, and increased sophisticated usage of the key, relevant scientific database, PDB. The continuing impact of molecular biology on x-ray crystallography, the growing role of synchrotron light sources and other instrumentation advances, and the developing power of NMR structural determination, will all serve to increase the value of PDB, and at the same time produce more stress on the "system" - the staff, the federal agencies involved in funding, and the investigators. PDB will not only have to solve the crises brought on by the rapid introduction of new structures and increased usage by non-structural biologists who need "friendlier interfaces", but will also have to evolve to meet the need to provide linkages to other key scientific databases like GenBank and Protein Identification Resource and incorporate new information technologies as they evolve.

The National Science Foundation (through the Biological Directorate), the National Institutes of Health (through the National Institute of General Medical Sciences, the National Center for Research Resources, and the National Center for Biotechnology Information in the National Library of Medicine) and the Department of Energy (through the Office of Health and Environmental Research), have all contributed to the recent development of PDB. NSF has historically been the central point for PDB activities, and over the past year we have worked closely with our colleagues at the other agencies, and with the scientific community, to assist PDB staff in solving the immediate concerns and in looking toward the future. Toward that end we have encouraged sessions devoted to PDB at the meetings of professional societies; added ex officio membership from the professional societies to the PDB advisory committee; developed workshops to provide collective advice to PDB staff on solving the backlog issue; involved the international community in the planning process and on the PDB advisory committee; collectively provided significantly increased funding to enable PDB to deal with the new demands and opportunities; started prototype projects by computer scientists and others to look toward the future in terms of increased functionality for PDB. Agency staff will continue to work together, with the scientific community both in the US and around the world, and with PDB staff, to ensure PDB will be able to meet the needs of the scientific community and play a central role in the continuing revolution in our understanding of biological machinery.

These comments are strictly an informal statement on the current issues facing PDB and the central importance of this resource for contemporary science. That is, this article is not a government policy document in any fashion, nor an official statement by any agency. It does not necessarily reflect the specific viewpoint or policy of the Federal Government nor any of the participating agencies, nor of their staff members. Instead, this is simply a communication to the frequent users of the PDB, who have regularly expressed concerns about the future of PDB to many government staff members of the cognizant agencies. The article, as a bottom line, is intended to indicate the recognition by government staff members - at a number of collaborating agencies - of the importance of PDB as a national and international research resource, a central scientific database facing difficult challenges today and greater challenges tomorrow, in order to meet the needs of researchers. Full responsibility for the specific statements above lie only with the authors. Full reports of the workshops held to advise PDB, and of other advisory committee meetings are available from either PDB staff or from NSF. (Electronic mail address: dba@nsf.gov - dba represents Scientific DataBase Activities, the programmatic activity providing the core funding.)

PDB Format Upgrade Committee

The following are the members of the PDB Format Upgrade Committee:

Russell Athay	BIOSYM Technologies, Inc.
Helen Berman	Rutgers University
Paula Fitzgerald	Merck Sharp and Dohme Research
Angela Gronenborn	NIH, National Institute of Diabetes and Digestive and Kidney Diseases
Alwyn Jones	University of Uppsala
Yukiteru Katsube	Osaka University
Irwin Kuntz	Univ. of California, San Francisco
Jane Richardson	Duke University
Robert Robbins	Welch Medical Library
Raymond Salemme	Sterling Winthrop Pharmaceuticals
Janet Thornton	University of London
Keith Watenpaugh	Upjohn
Shoshana Wodak	University of Brussels
John Wootton	National Library of Medicine, National Center for Biotechnology Information

This standing committee is assisting the PDB in implementing a comprehensive upgrade of our interchange format, in order to better serve the future needs of the community.

Suggestions and comments on our efforts to upgrade the PDB format are welcome. Please send correspondence to Enrique Abola using the Internet e-mail address abola@pb3.pdb.bnl.gov.

François Major from the National Library of Medicine, National Center for Biotechnology Information is collaborating with us in converting the current contents of the PDB into the ISO standard abstract syntax notation (ASN.1) format.

Sending New Data

Frances Bernstein

We continue to experience a rapid growth in the number of data sets being deposited. It would simplify and speed up the handling of new data if all entries and printed material were sent to the proper computer account and/or address (see How to Deposit Guide on page 6 for details).

Some helpful hints that facilitate data deposition:

1. Include a few lines at the top of each data file indicating its contents, depositor names, etc., so that it can be readily identified. For e-mail, the inclusion of appropriate subject descriptors can be very informative.
2. Do NOT send duplicates of your data to more than one person or computer account.
3. Use +1 516-282-3629 for phone inquiries on data deposition.
4. Atomic coordinate data files, structure factor files, NMR restraint files, and deposition forms each are handled differently. It is more convenient for us if these are not combined in one FTP or e-mail file.
5. It is very important that we be informed if a deposition replaces an existing PDB entry. Please provide us with the PDB entry IDENT CODE(s) of the old entries.
6. Please do NOT combine multiple coordinate sets in one file. The only exception to this is for NMR structures where the multiple models should be in one file and should be separated by MODEL and ENDMDL records. Multiple NMR models should always be specified in identical coordinate frames.

Sixth Symposium of the Protein Society

A PDB users group meeting will be held during the next Protein Society Symposium which will take place from July 25-29, 1992 in San Diego, CA. During the week, we will also be presenting some of our work at Exhibitor Booth Number 19. At that time, we plan to demonstrate how we process data and how to access information available from the PDB as well as details on the upgrade of the PDB format.

1992 Annual Meeting of the American Crystallographic Association

Members of the PDB staff will be attending the 1992 Annual Meeting of the American Crystallographic Association which is being held jointly with the 50th Annual Scientific Meeting of the Pittsburgh Diffraction Society in Pittsburgh, PA from August 9-14, 1992. An electronic poster will be presented in which we plan a demonstration similar to the one we will be giving in San Diego. An overview of the PDB will also be given as part of an oral session on Crystallographic Computing organized by the ACA Crystallographic Data and Computing Committee.

Description of Atom Records

The following atom record specification was adapted from the PDB document "Atomic Coordinate and Bibliographic Entry Format Description". This document is available from the PDB anonymous FTP server or by mail if requested.

ATOM Atomic coordinate records for "standard" groups

HETATM Atomic coordinate records for "non-standard" groups

Cols.	1 - 4	ATOM
or	1 - 6	HETATM
	7 - 11	Atom serial number(i)
	13 - 16	Atom name(ii)
	17	Alternate location indicator(iii)
	18 - 20	Residue name(iv,v)
	22	Chain identifier, e.g., A for hemglobin α chain
	23 - 26	Residue sequence number
	27	Code for insertions of residues, e.g., 66A, 66B, etc.
	31 - 38	X }
	39 - 46	Y } Orthogonal Å coordinates
	47 - 54	Z }
	55 - 60	Occupancy
	61 - 66	Temperature factor(vi)
	68 - 70	Footnote number

FORMAT (6A1,I5,1X,A4,A1,A3,1X,A1,I4,A1,3X,3F8.3,2F6.2, 1X,I3)

Notes: (i) Residues occur in order of their sequence numbers which always increase starting from the N-terminal residue for proteins and the 5'-terminal residue for nucleic acids. Within each residue the atoms are ordered as indicated in note (ii) below. If the residue sequence is known, certain atom serial numbers may be omitted to allow for future insertion of any missing atoms. If the sequence is not reliably known, these serial numbers are simply ordinals

(ii) Amino Acids: The atom names follow the IUPAC-IUB rules[1] except:

a) Greek letter remoteness codes are transliterated as follows: α-A, β-B, γ-G, δ-D, ε-E, ζ- Z, η-H.

b) Atoms for which some ambiguity exists in the crystallographic results are designated A. This will usually apply only to the terminal atoms of asparagine and glutamine and to the ring atoms of histidine.

Within each residue the atoms occur in the order specified by the superscripts found in the figure "Atom Names, Remoteness Codes, and Order Indicators for the Common Amino Acids" in Appendix B of the document "Atomic Coordinate and Bibliographic Entry Format Description".

The extra oxygen atom of the carboxy terminal amino acid is designated OXT.

Four characters are reserved for these atom names. They are assigned as follows:

1-2 Chemical symbol - right justified
3 Remoteness indicator (alphabetic)
4 Branch designator (numeric)

c) For protein coordinate sets containing hydrogen atoms, the IUPAC-IUB rules[1] have been followed. Recommendation rule number 4.4 has been modified as follows: When more than one hydrogen atom is bonded to a single atom, the hydrogen atom number designation is given as the first character of the atom name rather than as the last character (e.g. $H^{\beta 1}$ is denoted as 1HB). Exceptions to these rules may occur in certain data sets at the depositors' request. Any such exceptions will be delineated clearly in FTNOTE and REMARK records.

Nucleic Acids: Atom names employed for polynucleotides generally follow the precedents set for mononucleotides. The following points are worthy of note.

a) The prime character (') commonly used to denote atoms of the ribose originally was avoided because of non-uniformity of its external representation. An asterisk (*) therefore was used in its place in entries released through January 1992.

Within each residue the atoms occur in the order specified by the superscripts in the figure "Atom Names and Order Indicators for the Common Ribonucleotides" in Appendix B of the document "Atomic Coordinate and Bibliographic Entry Format Description".

b) Of the four characters reserved for atom names, the left-most two are reserved for the chemical symbol (right justified) and the remaining two denote the atom's position.

c) Atoms exocyclic to the ring systems have the same position identifier as the atom to which they are bonded except if this would result in identical atom names. In this case an alphabetic character is used to avoid ambiguity.

d) The ring-oxygen atom of the ribose is denoted O4 rather than O1.

e) The extra oxygen atom at the free 5' phosphate terminus is designated OXT. This atom will be placed first in the coordinate set.

For nucleotides which are simple derivatives (e.g., methyl or acetyl) of the parent nucleotide, the modifying atoms or groups occur immediately after the atom to which they are bonded. In the case of an acetyl modifier, the three atoms are ordered carbonyl carbon, carbonyl oxygen, methyl carbon.

(iii) Alternate locations for atoms may be denoted here by A, B, C, etc.

(iv) Standard residue names are given in Appendix C of the document "Atomic Coordinate and Bibliographic Entry Format Description"; other components are defined in HET records.

(v) HETATM records are used for water molecules and atoms contained in HET groups.

(vi) Normally, the isotropic B value appears in this field. However, if anisotropic temperature factors have been provided, the temperature factor field of the corresponding ATOM or HETATM record will contain the equivalent U-isotropic [U(eq)] which is calculated by

$$U(eq) = 1/3[U(1,1) + U(2,2) + U(3,3)] \times 10^{-4}$$

where the integers U(i,j) stored on the corresponding ANISOU record are $U_{ij} \times 10^4$.

[1] IUPAC-IUB Commission on Biochemical Nomenclature. "Abbreviations and Symbols for the Description of the Conformation of Polypeptide Chains. Tentative Rules (1969)", J. Biol. Chem. 245, 6489 (1970).

The 1974 recommendations on the "Nomenclature of α–Amino Acids" (Biochemistry, 14, 449 (1975)) provides a scheme based on normal rules for organic compounds, but this scheme will not be used here.

Amino Acid Side-Chain Nomenclature

Enrique Abola

New procedures have been implemented to ensure that amino acid atom names fully conform to IUPAC-IUB recommendations (J. Biol. Chem. 245, 6489 (1970)). Atom labels that may be affected are those for side-chain atoms of ASP, GLU, ARG, PHE and TYR. For example, in the case of the residue ASP, the rule specifies which atom to label OD1 and which to label OD2. New and replaced atomic coordinate entries listed in the April 1992 PDB release have been checked for compliance with these rules. Corrections to other atomic coordinate entries will be done as time permits.

File Server and Anonymous FTP

At Brookhaven, the PDB has an e-mail file server available for your use. This server provides PDB general information and documentation files. For more information, send an e-mail message to fileserv@pb1.pdb.bnl.gov and include the following text:

send info your_e-mail_address.

The PDB also has an anonymous FTP account available on the system pdb.pdb.bnl.gov with Internet address 130.199.144.1. It is possible to transfer files to and from this system using "anonymous" as the FTP user name and your real user name as the password. PDB general information and documentation files, as well as pre-release atomic coordinate entries, are available for downloading. You also can upload any files that you may wish to send to the PDB. Those using VMS may need to place quotes around file names.

Anyone experiencing problems or having questions related to the above network service should send an e-mail message to skora@bnl.gov.

To Contact the PDB

Please include your telephone number, facsimile number, mailing address, and e-mail address in all correspondence.

Mail: Protein Data Bank
Chemistry Department, Building 555
Brookhaven National Laboratory
Upton, NY 11973 USA

Phone: +1 516-282-3629

Fax: +1 516-282-5751

e-mail: pdb@bnlchm.bitnet
or pdb@chm.chm.bnl.gov

How to Deposit Guide

Karen Bailey

A PDB data deposition has three essential components, all of which must be received at Brookhaven before we can proceed to process a submission. These are:

1. *Deposition Form.* A PDB data deposition form must be completed. If you prefer, you may enter the relevant information in your computer and e-mail or FTP it to us. The deposition form is available via the PDB e-mail server or anonymous FTP. Please let us know if you would like us to mail you a printed copy of the data deposition form.

2. *Reprints and Preprints.* In order to complete our file on your structure, we must have copies of all relevant papers that are to be cited in your PDB entry. We realize that this means a bit of extra work for you, but it allows us to achieve significant time savings in processing your data.

3. *Data Files.* Data files should be in PDB format and may be sent via FTP or e-mail, floppy disk, or tape as described in the data deposition form. If you FTP the data, instructions are provided when you carry out the remote FTP. If you e-mail to pdb@bnlchm.bitnet or pdb@chm.chm.bnl.gov, please send each file twice, so that we can detect transmission errors, which occasionally do occur.

Items to be mailed should be addressed to:

Protein Data Bank Depositions
Chemistry Department, Building 555
Brookhaven National Laboratory
Upton, NY 11973 USA

Citing the PDB

Frances Bernstein

Any researcher making use of information from the PDB should reference the data as follows:

1. The original authors and publication should be cited. Each entry has one or more AUTHOR records with the official author list for the PDB entry. If there is a paper describing the coordinates deposited with the PDB, it is presented on JRNL records. If there are no JRNL records the entry may be cited as a "private communication".

2. The PDB should be cited. The appropriate references are F. C. Bernstein, T. F. Koetzle, G. J. B. Williams, E. F. Meyer, Jr., M.D. Brice, J. R. Rodgers, O. Kennard, T. Shimanouchi, and M. Tasumi, "The Protein Data Bank: A Computer-based Archival File for Macromolecular Structures", J. Mol. Biol., 112, 535-542 (1977) and E. E. Abola, F. C. Bernstein, S. H. Bryant, T. F. Koetzle, and J. Weng, "Protein Data Bank" in Crystallographic Databases - Information Content, Software Systems, Scientific Applications, eds. F. H. Allen, G. Bergerhoff, and R. Sievers, Data Commission of the International Union of Crystallography, Bonn/Cambridge/Chester, 1987, pp. 107-132.

SAMPLE CITATION:

We used coordinates[1] for molecule x[2] obtained from the Protein Data Bank[3] at Brookhaven National Laboratory.

[1] Entry 1ABC, version of July 1987
[2] J. Smith, S. Doe, journal reference
[3] (a) F. C. Bernstein, ...
(b) E. E. Abola, ...

We would appreciate receiving reprints of all publications making use of data from the PDB. Please send them to Ms. Frances C. Bernstein, Protein Data Bank, Chemistry Department, Building 555, Brookhaven National Laboratory, Upton, NY 11973 USA.

Nucleic Acid Database

The following description of the Nucleic Acid Database is a contribution from the staff of the NDB project. NDB staff are collaborating with the PDB in processing nucleic acid atomic coordinate depositions.

1. *Introduction.* The Nucleic Acid Database (NDB) Project has been established by Helen M. Berman and Wilma K. Olson of Rutgers University and David L. Beveridge of Wesleyan University, with the goal to assemble and distribute structural information about nucleic acids.

   Data from the literature and from the PDB have been put into a relational database. For the present, reports (tables) describing several important properties of the structures and coordinate files are available via e-mail and anonymous ftp. In the future, NDB plans to make the software available to produce reports describing any of the stored properties of any subset of the structures in the database.

   At this time, the Nucleic Acid Database has stored information on 192 DNA and RNA crystal structures, including 130 entries having atomic coordinates. The primary experimental information contained in NDB includes atomic coordinates, crystal data, bibliographic references, crystallization conditions, data collection methods, refinement information, and various structural descriptions. The derivative information is calculated from the atomic coordinates and includes chemical bond lengths and angles, torsion angles, virtual bond lengths and angles involving phosphorus atoms, and base morphology parameters calculated according to various algorithms.

   Currently, the coordinate files and reports produced at the Nucleic Acid Database Project are placed into an electronic library for public access, maintained at NDB. The reports are updated regularly to include information about all newly released structures. The regularly released NDB newsletter contains information on the current contents of the library and detailed access instructions.

2. *Subscription.* Subscription to the NDB newsletter may be initiated by sending an e-mail message to ndblib@helix.rutgers.edu. It is necessary to include the word "subscribe" in the subject line, as it is read automatically by the mail server.

3. *NDB Library.* The Nucleic Acid Database Library is divided into the following directories:

   newsletter -- containing the present and all previous newsletters. The presently available newsletters are: news.dec91, news.feb92, news.apr92.

   reports_ascii -- containing reports in ascii format on the primary experimental information of all structures. The presently available reports are: names (naming conventions and short descriptors for each structure), citations (primary references), structure summary (sequences, structure_types, modifications, drugs, mismatches), drugs (details on bound drugs), mismatches, base_modifiers, phosphate_modifiers, and cell_dimensions.

   reports_ps -- containing the same reports as reports_ascii, but in PostScript format.

   coordinates -- coordinate files for all structures where released.

   torsions -- containing reports on torsion angles of most structures.

4. *Mail Server Instructions.* To obtain files through the mail server, the user must send an e-mail message to the library at ndblib@helix.rutgers.edu.

   The mail server will read the subject line sent to this address and automatically reply by posting the requested file to the user's directory. The subject line MUST be in the following format:

   Subject: send <filename> from <directory>

   where <directory> is replaced by one of the five mentioned above, and <filename> is replaced by the name of the requested file. Each directory contains a file called 'index' which lists and explains the contents of that directory. For example, to get a listing of all newsletters, the subject line must look like this:

   Subject: send index from newsletter

   To get the current NDB newsletter, the subject line must look like this:

   Subject: send news.apr92 from newsletter

   To get a description of the reports available in ascii format, send the following subject line:

   Subject: send index from reports_ascii

To obtain one of these reports, for example the one called names.ascii, send this line:

Subject: send names.ascii from reports_ascii

To obtain coordinate files, the same kind of subject line can be sent, with 'coordinates' as the directory and the NDB name of the structure as file name. The following line will request the coordinate file for the structure with NDB name bdl001:

Subject: send bdl001 from coordinates

(for a list of NDB names, refer either to the 'index' in the coordinates directory or to the report called 'names.ascii' and 'names.ps').

Obtaining files from the directories 'reports_ps' and 'torsions' is similar to the above examples.

5. *Anonymous FTP Instructions.* The Nucleic Acid Database Library can also be accessed by anonymous FTP. Start the FTP program by typing:

ftp helix.rutgers.edu

Once the proper connection to helix is established, the following command has to be issued in order to log in:

user anonymous

Then FTP will request a password, to which your own user name should be typed. After getting into the proper session, it is necessary to type 'cd pub' as the first command, and then to enter one of the following commands to choose the directory with the files to be transferred:

cd newsletter
cd reports_ascii
cd reports_ps
cd coordinates
cd torsions

(The 'ls' command will list the files in the current directory.) To obtain any of the files in the current directory, issue a get statement in the form of:

get <filename>

(It is a good idea to type 'get index' to obtain a description of the current directory.)

The FTP session ends with the 'quit' command.

6. *Staff.*

Helen M. Berman, Wilma K. Olson, David L. Beveridge, Principal Investigators
John Westbrook, Director, Center for Computational Chemistry, Rutgers University
Anke Gelbin, Database Coordinator
Tamas Demeny, Database Programmer
Shu-Hsin Hsieh, Database Programmer

Inquiries should be addressed to:

ndbadmin@helix.rutgers.edu

7. *Acknowledgment.* This project is funded by grant DIR N012772 from the National Science Foundation.

If you use any reports or data from NDB, please use this citation: The Nucleic Acid Database: A Guide to the Use of a Relational Database of Nucleic Acid Crystal Structures, 1991. Technical Report. Helen M. Berman, Wilma K. Olson, John Westbrook, Anke Gelbin, Tamas Demeny, Shu-Hsin Hsieh, Center for Computational Chemistry, Rutgers University, New Brunswick, NJ and David L. Beveridge, Wesleyan University, Middletown, CT.

Affiliated Centers

Eleven affiliated centers offer DATAPRTP for distribution. These centers, listed immediately below, are members of the Protein Data Bank Service Association (PDBSA). Centers designated with an asterisk(*) distribute DATAPRTP on magnetic media; those without an asterisk are on-line DATAPRTP distributors.

CAN/SND
Canadian Scientific Numeric Data Base Service
Ottawa, Ontario, Canada
Roger Gough
613-993-3294
cansnd@vm.nrc.ca

CAOS/CAMM
Dutch National Facility for Computer-Assisted Chemistry
Nijmegen, The Netherlands
Jan Noordik
31-80-653386
noordik@caos.caos.kun.nl

CINECA
NE Italy Interuniversity Computing Center
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Salvatore Rago
39-51-598411
argo@icineca.bitnet

EMBL
European Molecular Biology Laboratory
Heidelberg, Germany
Peter Rice
49-6221-387-247
peter.rice@embl-heidelberg.de

*JAICI
Japan Association for International Chemical Information
Tokyo, Japan
Hideaki Chihara
81-3-816-3389

NCSA
National Center for Supercomputing Applications
University of Illinois at Urbana-Champaign
Champaign, Illinois
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217-244-2756
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*Osaka University
Institute for Protein Research
Osaka, Japan
Yukiteru Katsube
81-6-877-5111 ext 3912.

Pittsburgh Supercomputing Center
Pittsburgh, Pennsylvania
Hugh Nicholas
412-268-4960
nicholas@cpwpsca.bitnet

Prophet
BBN Systems and Technologies Corporation
Cambridge, Massachusetts
Wayne Rindone
617-873-2669
prophet-help@bbn.com

SDSC
San Diego Supercomputer Center
San Diego, CA
Lynn Ten Eyck
619-534-8189
teneyckl@sdsc.bitnet

SEQNET
Daresbury Laboratory
Warrington, United Kingdom
User Interface Group
44-925-603351
uig@daresbury.ac.uk

TABLE 1 - PROTEIN DATA BANK, INFORMATION AVAILABLE ON MAGNETIC TAPE

CODE	ITEM
DATAPRTP	*ALL AVAILABLE COORDINATE ENTRIES (TABLE 3), BIBLIOGRAPHIC ENTRIES (TABLE 4 - NO COORDINATES IN BIB ENTRIES), AND SOME COMPUTER PROGRAMS (TABLE 2, PART A)
PDBPGMTP	ALL COMPUTER PROGRAMS AND MISCELLANEOUS FILES (TABLE 2, PARTS A AND B)
NONST1TP	STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 1)
NONST2TP	STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 2)
NONST3TP	STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 3)
NONST4TP	STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 4)
NONST5TP	STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 5)
NONST6TP	STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 6)
NONST7TP	STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 7)
NONST8TP	STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 8)
NONST9TP	*STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 9)
NONST10TP	*STRUCTURE FACTOR ENTRIES (TABLE 5 - PART 10)
NMRRS1TP	NMR EXPERIMENTAL DATA ENTRIES (TABLE 6)

* CONTAINS NEW OR REPLACEMENT ENTRIES SINCE JAN-1992 NEWSLETTER

TABLE 2 - PROTEIN DATA BANK, COMPUTER PROGRAMS AND MISCELLANEOUS FILES

NAME	PURPOSE	AUTHOR(S)	REV DATE/ SUPPORTED	
PART A - AVAILABLE ON DATAPRTP, PDBPGMTP				
BENDER	PARAMETERS FOR BENT-WIRE MODELS	G.WILLIAMS	4/82	YES
BLDKIT	MODEL BUILDER'S KIT	E.ABOLA	2/84	YES
BRUKTP	MAKE VAX/VMS FILES FROM PDB TAPE	H.BOSSHARD	8/85	NO
CONECT	GENERATE FULL CONNECTIVITY	F.BERNSTEIN	7/89	YES
CONTNT	GENERATE PDB CONTENTS LIST	H.NICHOLAS JR.	4/91	NO
CONTCT	INTERMOLECULAR CONTACTS	L.ANDREWS	5/83	NO
DGPLOT	DIAGONAL PLOTS ON PRINTER	E.SWANSON,F.BERNSTEIN	1/83	YES
DIHDRL	COMPLETE TORSION ANGLES	E.ABOLA	3/80	YES
DRCTRY	DIRECTORY OF PDB DISTRIBUTION TAPE	E.ABOLA	7/86	YES
DSTNCE	CALC DISTANCES FROM CONECT RECORDS	F.BERNSTEIN	8/82	YES
FISIPL	PHI/PSI PLOTS ON PRINTER	F.BERNSTEIN	5/79	YES
LSM	COLOR-CODED ALPHA-CARBON MODELS	R.MATELA,R.FLETTERICK	3/82	NO
NAMOD	BALL-AND-STICK MODEL DISPLAY	Y.BEPPU	4/89	NO
PHIPSI	MAIN-CHAIN TORSION ANGLES	ANDREWS,WILLIAMS,BERNSTEIN	2/79	YES
REFMTE	REFORMAT DATA FOR SUPERTAB,SUPERB	L.RELLICK,J.DUANE	12/83	NO
STEREO	EXTRACT X,Y,Z FROM STEREO DIAGRAMS	M.ROSSMANN	6/79	NO
TAPDIR	PRINT DIRECTORY OF TAPE CONTENTS	H.BERNSTEIN,F.BERNSTEIN	11/79	YES
THEOD	MEASURE COORDINATES WITH THEODOLITE	L.LEBIODA	1/82	NO
TORSRU	COMPLETE TORSION ANGLES	G.REEKE	10/79	NO
TOTALS	VALIDATION OF MASTER RECORD	L.ANDREWS,F.BERNSTEIN	3/82	YES
PART B - AVAILABLE ON PDBPGMTP ONLY				
ALB	SECONDARY STRUCT. CALC.,PREDICTION	A.FINKELSTEIN,O.PTITSYN	10/85	NO
CRYSTAL	DATA BASE-PROTEIN CRYSTALLIZATION	G.GILLILAND	12/84	NO
NDB	NUCLEIC ACID DATA BASE + PROGRAMS	H.BERMAN ET AL.	9/89	NO
NEWHEL92	DNA HELIX ANALYSIS	R.DICKERSON ET AL.	2/92	NO
NUPARM	NUCLEIC ACID PARAMETER DETERMINATN	M.BANSAL,D.BHATTACHARYYA	5/90	NO
SEARCHDB	SEQUENCE SEARCH OF PDB ENTRIES	D.BLOCH	6/88	NO
TABLES	DISPLAY SPACE-GROUP SYMMETRY IN 3D	C.ABAD-ZAPATERO,T.O'DONNELL	12/87	NO

* NEW OR REPLACEMENT ENTRY SINCE JAN-1992 NEWSLETTER

SUPPORTED PROGRAMS ARE THOSE FOR WHICH STAFF OF THE PROTEIN DATA BANK WILL PROVIDE CORRECTIONS FOR DEMONSTRATED ERRORS.

TABLE 3 - PROTEIN DATA BANK ATOMIC COORDINATE ENTRIES (AVAILABLE)

new or replacement data only

IDENT CODE	MOLECULE	DEPOSITOR(S)	DATE/ STATUS	
8GCH	*GAMMA-CHYMOTRYPSIN(-183 DEG C)(BOVINE)	M.HAREL,I.SILMAN,J.SUSSMAN	3/91	
1HCC	*16TH COMPLEMENT CONTROL PROTEIN(NMR)	NORMAN,BARLOW,CAMPBELL	11/90	
1D29	*DNA(CGTGAATTCACG,SYNTHETIC,0 DEG C)	LARSEN,KOPKA,DICKERSON	1/91	
1D30	*DNA(CGCGAATTCGCG,SYNTHETIC)/DAPI	LARSEN,DICKERSON ET AL.	1/91	
1D32	*DNA(CGCG)/DITERCALINIUM	A.RICH ET AL.	1/91	
1D33	*DNA(CGCGCG)/DAUNOMYCIN/HCHO	A.WANG	2/91	
2D34	*DNA(CGTDCG)/DAUNOMYCIN/HCHO	A.WANG	5/91	
1D35	*DNA(CGTDCG)/MAR 70	A.WANG ET AL.	4/91	
1D36	*DNA(CGTACG)/MAR 70	A.WANG ET AL.	4/91	
1D37	*DNA(CGATCG)/4ODEMETHYL11DEOXYOXORUBICIN	A.WANG ET AL.	4/91	
1D38	*DNA(CGATCG)/IDARUBICIN	A.WANG ET AL.	4/91	
1D39	*DNA(CGCGCG)/CUCL2	T.KAGAWA,P.HO ET AL.	5/91	
1D40	*DNA((5MC)GUA(5MC)G)/CUCL2	B.GEIERSTANGER,P.HO ET AL.	5/91	
1D41	*DNA((5MC)GUA(5MC)G)	G.ZHOU,P.HO	5/91	
1D43	*DNA(CGCGAATTCGCG)/HOECHST 33258/0C UP	QUINTANA,LIPANOV,DICKERSON	5/91	
1D44	*DNA(CGCGAATTCGCG)/HOECHST 33258/0C DOWN	QUINTANA,LIPANOV,DICKERSON	5/91	
1D45	*DNA(CGCGAATTCGCG)/HOECHST 33258/-25C	QUINTANA,LIPANOV,DICKERSON	5/91	
1D46	*DNA(CGCGAATTCGCG)/HOECHST 33258/-100C	QUINTANA,LIPANOV,DICKERSON	5/91	
2D47	*DNA(CCCCCGCGGGGG)/SPERMINE	VERDAGUER,SUBIRANA ET AL.	10/91	
1D48	*DNA(CGCGCG)/SPERMINE	EGLI,WILLIAMS,GAO,RICH	9/91	
1D49	*DNA(CGATTAATCG)	QUINTANA,DICKERSON ET AL.	9/91	
4EST	*ELASTASE/DIFLUOROKETONE INHIBTR COMPLEX	E.MEYER JR. ET AL.	5/89	
5EST	*ELASTASE/BORONIC ACID INHIBITOR COMPLEX	E.MEYER JR. ET AL.	5/89	
3ENL	*ENOLASE(YEAST)	L.LEBIODA	11/90	R
4ENL	*ENOLASE(YEAST)/ZN	L.LEBIODA	11/90	
5ENL	*ENOLASE/CA2+/2-PHOSPHO-D-GLYCERIC ACID	L.LEBIODA	11/90	
6ENL	*ENOLASE(YEAST)/ZN2/PHOSPHOGLYCOLATE	L.LEBIODA	11/90	
7ENL	*ENOLASE(YEAST)/MG2+/2-PHOSPHO-D-GLYCERAT	L.LEBIODA	11/90	
1FBP	*FRUCTOSE-1,6-BISPHOSPHATASE/F6P/AMP/MG	H.KE,Y.ZHANG,W.LIPSCOMB	5/90	
2FBP	*FRUCTOSE-1,6-BISPHOSPHATASE	W.LIPSCOMB ET AL.	6/90	
3FBP	*FRUCTOSE-1,6-BISPHOSPHATASE/F6P	W.LIPSCOMB ET AL.	6/90	
9HVP	*HIV-1 PROTEASE/INHIBITOR A-74704	D.NEIDHART,J.ERICKSON	11/90	
1HSD	*HYDROXYSTEROID DEHYDROGENASE	D.GHOSH,W.DUAX	8/91	
1IGF	*IGG1 FAB' FRAGMENT B13I2	R.STANFIELD,I.WILSON	3/91	
2IGF	*IGG1 FAB' FRAGMENT B13I2/EVVPHKK PEPTIDE	R.STANFIELD,I.WILSON	3/91	
1HIG	*INTERFERON-GAMMA(HUMAN)	S.EALICK ET AL.	10/91	A
1RIG	*INTERFERON-GAMMA(RABBIT)	SAMUDZI,BURTON,RUBIN	8/91	A
21BI	*INTERLEUKIN 1B(HUMAN) MUTANT(C71A)	VEERAPANDIAN,POULOS ET AL.	3/91	
31BI	*INTERLEUKIN 1B(HUMAN) MUTANT(C71S)	VEERAPANDIAN,POULOS ET AL.	3/91	
41BI	*INTERLEUKIN 1B(HUMAN) MUTANT(C8A)	VEERAPANDIAN,POULOS ET AL.	2/92	
1LHM	*LYSOZYME MUTANT(C77A,C95A)(HUMAN)	K.INAKA,M.MATSUSHIMA	10/91	
2LHM	*LYSOZYME MUTANT(Q86D,A92D)(HUMAN)(APO)	K.INAKA,M.MATSUSHIMA	10/91	
3LHM	*LYSOZYME MUTANT(Q86D,A92D)(HUMAN)(HOLO)	K.INAKA,M.MATSUSHIMA	10/91	
1BN2	*NEUROPHYSIN II(BOVINE)/P-IODO-F-Y AMIDE	B.-C.WANG	8/90	A
1NRD	*NITRITE REDUCTASE	J.GODDEN,E.ADMAN,S.TURLEY	4/91	A
1OVA	*OVALBUMIN(CHICKEN)	P.STEIN,A.LESLIE	11/90	
1PCD	*PROTOCATECHUATE 3,4-DIOXYGENASE	DUPONT PROTEIN CRYSTLLGRPY	9/90	
1SAR	*RIBONUCLEASE SA(STREP.AUREOFACIENS)	J.SEVCIK,E.DODSON,G.DODSON	12/90	
2SAR	*RIBONUCLEASE SA(STREP.AUREOFACIENS)/GMP	J.SEVCIK,E.DODSON,G.DODSON	12/90	
9PTI	*TRYPSIN INHIBITOR(BOVINE,MET 52 OXIDIZD)	EIGENBROT,RANDAL,KOSSIAKFF	4/91	
3CTI	*TRYPSIN INHIBITOR(SQUASH)(NMR,6 STRCTRS)	T.HOLAK,M.NILGES ET AL.	3/91	
1PI2	*BOWMAN-BIRK TRYPSIN INHIBITOR PI-2	P.CHEN,J.ROSE,B.C.WANG	3/91	
1PHV	*HIV-2 PROTEASE/ACETYL PEPSTATIN MODEL	A.GUSTCHINA,I.WEBER	2/91	
2PHV	*HIV-2 PROTEASE/RENIN INHIBTR H261 MODEL	A.GUSTCHINA,I.WEBER	2/91	
1MCA	*MCAF/MCP-1(HUMAN) MODEL	A.GRONENBORN,G.CLORE	4/91	
1SDG	*SORBITOL DEHYDROGENASE MODEL	H.EKLUND ET AL.	8/90	

* NEW OR REPLACEMENT ENTRY SINCE JAN-1992 NEWSLETTER

TABLE 4 - PROTEIN DATA BANK, BIBLIOGRAPHIC ENTRIES (NO COORDINATES)

Unchanged. All full tables are available from the PDB anonymous FTP and e-mail server or by regular mail upon request.

TABLE 5. PROTEIN DATA BANK, STRUCTURE FACTOR ENTRIES (AVAILABLE)

new data only (parts 1-8 unchanged)

IDENT CODE	MOLECULE	DEPOSITOR(S)	DATE/ CODE
PART 9 - AVAILABLE ON NONST9TP			
R1C2RSF	*CYTOCHROME C2(RHODOBACTER CAPSULATUS)	H.HOLDEN ET AL.	3/91 SF
R1D26SF	*DNA(GCCC(G3P)GGC)	U.HEINEMANN ET AL.	9/90 SF
R1D29SF	*DNA(CGTGAATTCACG,SYNTHETIC,0 DEG C)	LARSEN,KOPKA,DICKERSON	1/91 SF
R1D30SF	*DNA(CGCGAATTCGCG,SYNTHETIC)/DAPI	LARSEN,DICKERSON ET AL.	1/91 SF
R1D39SF	*DNA(CGCGCG)/CUCL2	T.KAGAWA,P.HO ET AL.	5/91 SF
R1D40SF	*DNA((5MC)GUA(5MC)G)/CUCL2	GEIERSTANGER,HO ET AL.	5/91 SF
R1D41SF	*DNA((5MC)GUA(5MC)G)	G.ZHOU,P.HO	5/91 SF
R1D43SF	*DNA(CGCGAATTCGCG)/HOECHST 33258/0C	R.DICKERSON ET AL.	5/91 SF
R1D45SF	*DNA(CGCGAATTCGCG)/HOECHST 33258/-25C	R.DICKERSON ET AL.	5/91 SF
R1D46SF	*DNA(CGCGAATTCGCG)/HOECHST 33258/-100C	R.DICKERSON ET AL.	5/91 SF
R1D49SF	*DNA(CGATTAATCG)	R.DICKERSON ET AL.	9/91 SF
R3EBXSF	*ERABUTOXIN B(SEA SNAKE)	B.LOW ET AL.	1/88 SF
R2PRKSF	*PROTEINASE K(TRITIRACHIUM ALBUM LIMBER)	BETZEL,PAL,SAENGER	11/87 SF
PART 10 - AVAILABLE ON NONST10TP			
R4ESTSF	*ELASTASE/DIFLUOROKETONE INHIBTR COMPLEX	E.MEYER JR. ET AL.	5/89 SF
R5ESTSF	*ELASTASE/BORONIC ACID INHIBITOR COMPLEX	E.MEYER JR. ET AL.	5/89 SF
R1LHMSF	*LYSOZYME MUTANT(C77A,C95A)(HUMAN)	K.INAKA,M.MATSUSHIMA	10/91 SF
R2LHMSF	*LYSOZYME MUTANT(Q86D,A92D)(HUMAN)(APO)	K.INAKA,M.MATSUSHIMA	10/91 SF
R3LHMSF	*LYSOZYME MUTANT(Q86D,A92D)(HUMAN)(HOLO)	K.INAKA,M.MATSUSHIMA	10/91 SF
R1SARSF	*RIBONUCLEASE SA(STREP.AUREOFACIENS)	SEVCIK,DODSON,DODSON	1/91 SF
R2SARSF	*RIBONUCLEASE SA(STREP.AUREOFACIENS)/GMP	SEVCIK,DODSON,DODSON	1/91 SF
R9PTISF	*TRYPSIN INHIBITOR(BOVINE,MET 52 OXIDIZD)	C.EIGENBROT ET AL.	4/91 SF

* NEW OR REPLACEMENT ENTRY SINCE JAN-1992 NEWSLETTER

CODES

SF STRUCTURE FACTORS

TABLE 6. PROTEIN DATA BANK, NMR EXPERIMENTAL DATA ENTRIES (AVAILABLE)

new data only

IDENT CODE	MOLECULE	DEPOSITOR	DATE/ CODE
R1HCCMR	*16TH COMPLEMENT CONTROL PROTEIN(NMR)	NORMAN,BARLOW,CAMPBELL	11/90 M
R3CTIMR	*TRYPSIN INHIBITOR(SQUASH)(NMR)	T.HOLAK,M.NILGES ET AL	3/91 M

* NEW OR REPLACEMENT ENTRY SINCE JAN-1992 NEWSLETTER

CODES

M NMR RESTRAINTS AND OTHER NMR EXPERIMENTAL DATA

TABLE 7 - CORRECTIONS TO COORDINATE ENTRIES AND PROGRAMS

THE FOLLOWING DATA SETS HAVE HAD CORRECTIONS APPLIED. PLEASE CONSULT A COPY OF THE PROTEIN DATA BANK ATOMIC COORDINATE AND BIBLIOGRAPHIC ENTRY FORMAT DESCRIPTION FOR A FULL DESCRIPTION OF REVDAT RECORDS.

REVDAT	9	15-APR-92	3PGKH	3	ATOM
REVDAT	4	15-APR-92	1BDSC	1	EXPDTA
REVDAT	4	15-APR-92	1HVPC	1	SEQRES
REVDAT	2	15-APR-92	1MBAA	3	ATOM
REVDAT	3	15-APR-92	1PHYB	1	JRNL
REVDAT	4	15-APR-92	2BDSC	1	EXPDTA
REVDAT	2	15-APR-92	2ENLA	3	OBSLTE
REVDAT	5	15-APR-92	2HFLD	1	REMARK
REVDAT	2	15-APR-92	2MBAA	3	ATOM
REVDAT	2	15-APR-92	3MBAA	3	ATOM
REVDAT	2	15-APR-92	4MBAA	3	ATOM
REVDAT	3	15-APR-92	4MDHB	3	ATOM
REVDAT	3	15-APR-92	1MRBB	1	REMARK
REVDAT	4	15-APR-92	2MRBC	1	REMARK SEQRES HET
REVDAT	4	15-APR-92	2PHHC	1	JRNL
REVDAT	3	15-APR-92	4ER4B	1	JRNL
REVDAT	2	15-APR-92	1AAPA	1	REMARK
REVDAT	2	15-APR-92	1ALDA	1	REVDAT JRNL
REVDAT	2	15-APR-92	1C2RA	1	REVDAT
REVDAT	2	15-APR-92	1GSGA	1	REMARK
REVDAT	2	15-APR-92	2FGFA	1	JRNL

THE FOLLOWING DATA SETS HAVE BEEN REPLACED

		OLD ENTRY	NEW ENTRY
OBSLTE	15-APR-92	2ENL	3ENL

* NEW OR REPLACEMENT ENTRY SINCE JAN-1992 NEWSLETTER

TABLE 8 - COORDINATE AND STRUCTURE FACTOR AND NMR EXPERIMENTAL DATA ENTRIES IN PREPARATION

IDENT CODE	MOLECULE	DEPOSITOR(S)	DATE/ STATUS	
2AAA	ACID ALPHA-AMYLASE(ASPERGILLUS NIGER)	G.DODSON ET AL.	2/91	P
7ACN	ACONITASE/ISOCITRATE	C.D.STOUT ET AL.	9/91	P
8ACN	ACONITASE/NITROISOCITRATE	C.D.STOUT ET AL.	9/91	P
1AEC	*ACTINIDIN/E-64	K.VARUGHESE	2/92	H
1ATN	ACTIN/DEOXYRIBONUCLEASE I	W.KABSCH ET AL.	3/91	N
1ACP	ACYL CARRIER PROTEIN(NMR,2 MODELS)	J.PRESTEGARD,Y.KIM	7/90	P
1APS	ACYLPHOSPHATASE(NMR,5 STRUCTURES)	V.SAUDEK ET AL.	2/91	P
1AKE	ADENYLATE KINASE(E.COLI)/AP5A	C.MUELLER,G.SCHULZ	11/91	P
1CWG	*WHEAT GERM AGGLUTININ(ISOLECTIN 1)/T-5	C.WRIGHT	2/92	P
2HUD	ALCOHOL DEHYDROGENASE(HUMAN)	M.AMZEL,T.HURLEY ET AL.	9/91	P
2P07	ALPHA-LYTIC PROTEASE MUTANT(M(192)A)	R.BONE,D.AGARD	10/90	RN
1P11	ALPHA-LYTIC PROTEASE/PHOSPHONATE ESTER	R.BONE,D.AGARD	10/90	N
1P12	ALPHA-LYTIC PROTEASE/PHOSPHONATE ESTER	R.BONE,D.AGARD	10/90	N
1LPR	ALPHA-LYTIC PROTSE MUTANT(M(192)A)/INHBTR	R.BONE,D.AGARD	8/91	P
2LPR	ALPHA-LYTIC PROTSE MUTANT(M(192)A)/INHBTR	R.BONE,D.AGARD	8/91	P
3LPR	ALPHA-LYTIC PROTSE MUTANT(M(192)A)/INHBTR	R.BONE,D.AGARD	8/91	P
4LPR	ALPHA-LYTIC PROTSE MUTANT(M(192)A)/INHBTR	R.BONE,D.AGARD	8/91	P
5LPR	ALPHA-LYTIC PROTSE MUTANT(M(213)A)/INHBTA	A.FUJISHIGE,R.BONE,D.AGARD	8/91	P
6LPR	ALPHA-LYTIC PROTSE MUTANT(M(213)A)/INHBTR	R.BONE,D.AGARD	8/91	P
7LPR	ALPHA-LYTIC PROTSE MUTANT(M(213)A)/INHBTA	A.FUJISHIGE,R.BONE,D.AGARD	8/91	P
8LPR	ALPHA-LYTIC PROTSE MUTANT(M(213)A)/INHBTA	A.FUJISHIGE,R.BONE,D.AGARD	8/91	P
9LPR	ALPHA-LYTIC PROTEASE/MSUC-A-A-P-L-BORONCR	R.BONE,D.AGARD	8/91	P
1ACH	ALPHA1 ANTICHYMOTRYPSIN(HUMAN)	U.BAUMANN,R.HUBER ET AL.	1/91	H
1HOM	ANTENNAPEDIA HOMEODOMAIN(NMR,19 STRCTRS)	K.WUTHRICH ET AL.	10/91	P
2HOA	*A. HOMEODOMAIN(NMR,20STRCTS)MUTANT(C39S)	K.WUTHRICH ET AL.	4/92	P
1LPE	APOLIPOPROTEIN E3(LDL RECEPTR-BNDNG DMN)	C.WILSON,D.AGARD	8/91	P

1LE2	APOLIPOPROTEIN E2(LDL RECEPTR-BNDNG DMN)	C.WILSON,D.AGARD	8/91	P
1LE4	APOLIPOPROTEIN E4(LDL RECEPTR-BNDNG DMN)	C.WILSON,D.AGARD	8/91	P
5ABP	ARABINOSE-BINDING PROTEIN/D-GALACTOSE	F.QUIOCHO,D.WILSON,N.VYAS	12/90	P
1AOZ	ASCORBATE OXIDASE(ZUCCHINI)	A.MESSERSCHMIDT ET AL.	1/92	H
1AMA	ASPARTATE AMINOTRANSFERASE/AMA	J.JANSONIUS ET AL.	2/92	P
7AAT	ASPARTATE AMINOTRANSFERASE/PLP(PH 7.5)	MCPHALEN,VINCENT,JANSONIUS	12/91	P
8AAT	ASPARTATE AMINOTRANSFERASE/PLP(PH 5.1)	MCPHALEN,VINCENT,JANSONIUS	12/91	P
9AAT	ASPARTATE AMINOTRANSFERASE/PMP(PH 7.5)	MCPHALEN,VINCENT,JANSONIUS	12/91	P
1AT2	ASPARTATE CARBAMOYLTRANSFERASE(B.SUBTLS)	STEVENS,REINISCH,LIPSCOMB	6/91	H
1LIG	*ASPARTATE RECEPTOR(LIGAND-BINDING DOMN)	S.KIM ET AL.	4/92	P
2AZU	AZURIN(P.AERUGINOSA) MUTANT(H35L)	NAR,MESSERSCHMIDT,HUBER	1/91	H
3AZU	AZURIN(P.AERUGINOSA) MUTANT(H35Q)	MESSERSCHMIDT,NAR,HUBER	1/91	H
4AZU	AZURIN(P.AERUGINOSA) (PH 5.5)	NAR,MESSERSCHMIDT,HUBER	6/91	H
5AZU	AZURIN(P.AERUGINOSA) (PH 9.0)	NAR,MESSERSCHMIDT,HUBER	6/91	H
1RNB	BARNASE/D(GPC) (BAC. AMYLOLIQUEFACIENS)	J.JANIN,S.BAUDET	3/91	P
1BW1	BARWIN(NMR,20 STRUCTURES)	F.POULSEN	11/91	P
1BW2	BARWIN(NMR,20 STRUCTURES)	F.POULSEN	11/91	P
1NBT	BUNGAROTOXIN(NEURONAL)(NMR,12 STRUCTURS)	R.OSWALD,M.SUTCLIFFE ET AL	10/91	P
2SCP	SARCOPLASMIC CALCIUM-BINDING PROTEIN	W.COOK,S.VIJAY-KUMAR	8/91	P
4ICB	CALBINDIN D9K(BOVINE)	L.A.SVENSSON	8/91	P
1CB1	CALBINDIN D9K(PORCINE)(NMR,14 STRUCTURS)	AKKE,DRAKENBERG,CHAZIN	12/91	P
4CLN	CALMODULIN(DROSOPHILA MELANOGASTER)	J.SACK	6/91	P
4CA2	CARBONIC ANHYDRASE II(HUMAN RECOMBINANT)	R.ALEXANDER,D.CHRISTIANSON	6/91	P
5CA2	CARBONIC ANHYDRASE II MUTANT(T200S)	R.ALEXANDER,D.CHRISTIANSON	6/91	P
6CA2	CARBONIC ANHYDRASE II MUTANT(V143F)	R.ALEXANDER,D.CHRISTIANSON	7/91	P
7CA2	CARBONIC ANHYDRASE II MUTANT(V143G)	S.NAIR,D.CHRISTIANSON	7/91	P
8CA2	CARBONIC ANHYDRASE II MUTANT(V143H)	R.ALEXANDER,D.CHRISTIANSON	7/91	P
9CA2	CARBONIC ANHYDRASE II MUTANT(V143Y)	R.ALEXANDER,D.CHRISTIANSON	7/91	P
4CAC	CARBONIC ANHYDRASE C(PH 6)	A.LILJAS ET AL.	9/91	P
5CAC	*CARBONIC ANHDRASE C/SO3	A.LILJAS ET AL.	3/92	P
7CPA	CARBOXYPEPTIDASE A/ZFVP(O)F	H.KIM,W.LIPSCOMB	5/91	P
8CPA	CARBOXYPEPTIDASE A/ZAGP(O)F	H.KIM,W.LIPSCOMB	5/91	P
1CBX	CARBOXYPEPTIDASE A/L-BENZYLSUCCINATE	MANGANI,CARLONI,ORIOLI	10/91	P
1PBA	CARBOXYPEPTIDASE B(ACTIVATION DOMAIN)	K.WUTHRICH ET AL.	11/91	P
1CD8	CD8(HUMAN)	LEAHY,AXEL,HENDRICKSON	1/91	P
3CHY	CHE Y(ESCHERICHIA COLI)	K.VOLZ,P.MATSUMURA	4/91	P
3CMS	CHYMOSIN B MUTANT(V111F)(BOVINE)	T.BLUNDELL ET AL.	2/90	N
1ACB	ALPHA-CHYMOTRYPSIN(BOVINE)/EGLIN C	M.BOLOGNESI ET AL.	11/91	P
3CI2	CHYMOTRYPSIN INHIBITOR 2(NMR,20 STRCTRS)	F.POULSEN	9/91	P
1CGI	ALPHA-CHYMOTRYPSINOGEN A/PSTI VARIANT 3	H.HECHT ET AL.	10/91	P
1CGJ	ALPHA-CHYMOTRYPSINOGEN A/PSTI VARIANT 4	H.HECHT ET AL.	10/91	P
1CCD	CLARA CELL 17 KDA PROTEIN(RAT)	T.UMLAND ET AL.	9/91	P
2CTX	ALPHA COBRATOXIN(NAJA NAJA SIAMENSIS)	W.SAENGER,C.BETZEL ET AL.	9/91	P
1COL	COLICIN(C-TERMINAL DOMAIN)(E.COLI)	M.PARKER ET AL.	7/91	P
4CNA	CONCANAVALIN A/ALPHA-METHYL-MANNOSIDE	Z.DEREWENDA ET AL.	10/90	N
1CTG	MU-CONOTOXIN GIIIA(NMR,MIN AVRGE STRCTR)	LANCELIN,KOHDA,INAGAKI	8/91	P
2CTG	MU-CONOTOXIN GIIIA(NMR,32 STRUCTURES)	LANCELIN,KOHDA,INAGAKI	8/91	P
1CMH	P-CRESOL METHYLHYDROXYLASE	F.S.MATHEWS	5/90	H
1BB2	BETA-B2 CRYSTALLIN(BOVINE)	C.SLINGSBY ET AL.	7/91	P
1CPL	CYCLOPHILIN(HUMAN T CELL)	KE,ZYDOWSKY,LIU,WALSH	9/91	H
1CYA	*CYCLOPHILIN/CYCLOSPORIN A(NMR,MIN AV ST)	S.FESIK	2/92	P
1CYB	*CYCLOPHILIN/CYCLOSPORIN A(NMR,20 STRCTS)	S.FESIK	2/92	P
2CYS	*CYCLOPHILIN/CYCLOSPORIN A(NMR)	K.WUTHRICH ET AL.	3/92	P
2YCC	CYTOCHROME C(YEAST,ISO-1,OXIDIZED)	A.BERGHUIS,G.BRAYER	1/91	N
1YEA	CYTOCHROME C(YEAST,ISO-2,REDUCED)	M.MURPHY,G.BRAYER	10/91	P
1YEB	CYTOCHROME C(YEAST B-2036 COMPOST,REDCD)	M.MURPHY,G.BRAYER	10/91	P
1C53	CYTOCHROME C553(DESULFOVIBRIO VULGARIS)	A.NAKAGAWA ET AL.	8/91	P
1CP4	CYTOCHROME P450CAM(PHENYL RADICAL)	R.RAAG,T.POULOS	6/91	P
2CP4	CYTOCHROME P450CAM MUTANT(T252A)	R.RAAG,T.POULOS	6/91	P
3CP4	CYTOCHROME P450CAM(11 WEEK ADAMANTANE)	R.RAAG,T.POULOS	6/91	P
4CP4	CYTOCHROME P450CAM(RECOMBINANT)	R.RAAG,T.POULOS	6/91	P
1SCC	*CYTOCHROME P450SCC(BOVINE)	S.VIJAYAKUMAR,J.SALERNO	1/92	P
1DFN	DEFENSIN HNP-3(HUMAN)	HILL,YEE,SELSTED,EISENBERG	1/91	P
1DTB	*DELTATOXIN(NMR,7 STRUCTURES)	BLADON,BLADON,PARKINSON	3/92	P
1DRC	DIHYDROFOLATE REDUCTASE(E.COLI CLONED)	S.OATLEY,J.KRAUT	6/91	P
2DRC	DIHYDROFOLATE REDUCTASE MUTANT(W22F)	K.BROWN,J.KRAUT	6/91	P
1DHR	*DIHYDROPTERIDINE REDUCTASE(RAT LIVER)	K.VARUGHESE	3/92	H
1D42	DNA(GTATATAC) (NMR)	U.SCHMITZ,T.JAMES	5/91	P
1D53	DNA(CGCICICG)	V.KUMAR ET AL.	11/91	P
1D54	DNA(TGTACA)/4'-EPIADRIAMYCIN	G.LEONARD,T.BROWN,W.HUNTER	1/92	P
1D55	DNA(GAAGCTTC)/ACTINOMYCIN D	S.KAMITORI,F.TAKUSAGAWA	2/92	H
1D56	*DNA(CGATATATCG)/CALCIUM	YUAN,QUINTANA,DICKERSON	2/92	P
1D57	*DNA(CGATATATCG)/MAGNESIUM	YUAN,QUINTANA,DICKERSON	2/92	P
1D59	*DNA(GGGGTTTTGGGG)	C.KANG,A.RICH	2/92	P
1D63	*DNA(CGCAAATTTGCG)/BERENIL	D.BROWN,S.NEIDLE ET AL.	3/92	P
1D64	*DNA(CGCGAATTCGCG)/PENTAMIDINE	EDWARDS,JENKINS,NEIDLE	3/92	P
1D65	*DNA(CGCAAATTTGCG)	K.EDWARDS,S.NEIDLE ET AL.	3/92	P
1CGC	DNA(CCGGCGCCGG)	U.HEINEMANN,M.BANSAL	1/92	P

1DRI	*D-RIBOSE-BINDING PROTEIN(E.COLI)	S.MOWBRAY,L.B.COLE	2/92	H
1RVE	*ECO RV ENDONUCLEASE	F.WINKLER ET AL.	2/92	P
1IXA	EGF-LIKE MODULE OF HUMAN FACTOR IX	D.NORMAN ET AL.	11/91	P
8EST	ELASTASE/GUANIDINIUM ISOCOUMARIN	R.RADHAKRISHNAN,E.MEYER JR	2/90	P
9EST	ELASTASE(PORCINE)/PEPTIDYL BENZOXALOSE	E.MEYER JR. ET AL.	1/91	H
2R1E	ECO RI ENDONUCLEASE/TCGCGAATTCGCG	J.ROSENBERG	9/90	N
1EDP	*ENDOTHELIN-1	N.ANDERSEN,C.CHEN	12/91	P
1EPS	5-ENOL-PYRUVYL-3-PHOSPHATE SYNTHASE	W.STALLINGS	4/91	AH
1EGF	*EPIDERMAL GROWTH FACTOR(MOUSE)(NMR,32)	MONTELIONE,SCHERAGA ET AL.	10/91	P
1EPG	*EPIDERMAL GROWTH FACTOR(NMR,PH 2.0,AVRG)	D.KOHDA,F.INAGAKI	3/92	P
1EPH	*EPIDERMAL GROWTH FCTR(NMR,PH 2.0,10 STS)	D.KOHDA,F.INAGAKI	3/92	P
1EPI	*EPIDERMAL GROWTH FACTOR(NMR,PH 6.8,AVRG)	D.KOHDA,F.INAGAKI	3/92	P
1EPJ	*EPIDERMAL GROWTH FACTR(NMR,PH 6.8,5 STS)	D.KOHDA,F.INAGAKI	3/92	P
6EBX	ERABUTOXIN B(LATICAUDA SEMIFASCIATA)	T.PRANGE,P.SALUDJIAN	5/91	P
3FIS	FIS(E.COLI)	R.DICKERSON ET AL.	8/91	P
4FIS	FIS(E.COLI) MUTANT(R89C)	R.DICKERSON ET AL.	8/91	P
1FIA	*FIS(E.COLI)	W.SAENGER ET AL.	12/91	P
1FXD	FERREDOXIN II(DESULFOVIBRIO GIGAS)	C.KISSINGER ET AL.	4/91	P
1FXA	FERREDOXIN(ANABAENA 7120)	H.HOLDEN	1/91	P
1FHA	FERRITIN(HUMAN,H CHAIN)	P.ARTYMIUK,P.HARRISON	12/90	P
1FPA	FIBRINOPEPTIDE A FRAGMENT(NMR)	F.NI,K.GIBSON,H.SCHERAGA	12/90	P
2FPA	FIBRINOPEPTIDE A FRGMT MUTANT(G12V)(NMR)	F.NI,K.GIBSON,H.SCHERAGA	12/90	P
2FX2	FLAVODOXIN(D.VULGARIS,ROOM TEMPERATURE)	W.WATT,K.WATENPAUGH	10/91	P
3FX2	FLAVODOXIN(D.VULGARIS,-150C,OXIDIZED)	W.WATT,K.WATENPAUGH	10/91	P
4FX2	FLAVODOXIN(D.VULGARIS,-150C,SEMIQUINONE)	W.WATT,K.WATENPAUGH	10/91	P
5FX2	FLAVODOXIN(D.VULGARIS,-150C,HYDROQUINON)	W.WATT,K.WATENPAUGH	10/91	P
4FBP	FRUCTOSE-1,6-BISPHOSPHATASE/AMP	KE,LIANG,ZHANG,LIPSCOMB	2/91	P
5FBP	FRUCTOSE-1,6-BISPHOSPHATASE/F6P	KE,ZHANG,LIANG,LIPSCOMB	2/91	P
1FPB	FRUCTOSE-1,6-BISPHOSPHATASE/FRU-2,6-P2	W.LIPSCOMB ET AL.	2/92	H
1D66	*GAL4(RESIDUES 1-65)/CCGGAGGACAGTCCTCCGG	R.MARMORSTEIN,S.HARRISON	3/92	P
1CGP	CATABOLITE GENE ACTIVATOR PROTEIN/DNA	SCHULTZ,SHIELDS,STEITZ	8/91	H
1GLY	GLUCOAMYLASE(ASPERGILLUS AWAMORI)	R.HONZATKO ET AL.	1/92	P
1GPR	GLUCOSE PERMEASE(IIA DOMAIN)(B.SUBTILIS)	D.-I.LIAO,O.HERZBERG	9/91	H
1GST	*GLUTATHIONE S-TRANSFERASE/GLUTATHIONE	GILLILAND,ARMSTRONG,JI	3/92	P
1EGO	GLUTAREDOXIN(OXIDIZED)(E.COLI)(NMR)	K.WUTHRICH ET AL.	10/91	P
1EGR	GLUTAREDOXIN(REDUCED)(E.COLI)(NMR)	K.WUTHRICH ET AL.	10/91	P
1GGA	G-GLYCERALDEHYDE-PHOSPHATE DEHYDROGENASE	F.VELLIEUX,J.HAJDU,W.HOL	10/91	H
1GPA	GLYCOGEN PHOSPHORYLASE A(R STATE)	BARFORD,HU,JOHNSON	11/90	P
1GPB	GLYCOGEN PHOSPHORYLASE B	JOHNSON,ACHARYA,STUART	6/90	P
2GPB	GLYCOGEN PHOSPHORYLASE B/GLC	J.MARTIN,L.JOHNSON	6/90	P
3GPB	GLYCOGEN PHOSPHORYLASE B/G1P	J.MARTIN,L.JOHNSON	6/90	P
4GPB	GLYCOGEN PHOSPHORYLASE B/GFP	J.MARTIN,L.JOHNSON	6/90	P
5GPB	GLYCOGEN PHOSPHORYLASE B/GMP/GLC	J.MARTIN,L.JOHNSON	6/90	P
6GPB	GLYCOGEN PHOSPHORYLASE B/H2P	L.JOHNSON,K.ACHARYA	6/90	P
7GPB	GLYCOGEN PHOSPHORYLASE B(R STATE)/AMP	BARFORD,HU,JOHNSON	11/90	P
8GPB	GLYCOGEN PHOSPHORYLASE B(T STATE)/AMP	BARFORD,HU,JOHNSON	11/90	P
9GPB	GLYCOGEN PHOSPHORYLASE B(R STATE)	BARFORD,JOHNSON	12/90	P
2GMA	GRAMICIDIN A	B.WALLACE,K.RAVIKUMAR	10/89	N
1GMF	*GRANULOCYTE-MACROPHAGE COLONY-STIM FCTR	P.A.KARPLUS,K.DIEDERICHS	12/91	P
1RGM	*GRANULOCYTE-MACROPHAGE COLONY-STIM FCTR	WALTER,COOK,EALICK ET AL.	3/92	P
1HHR	GROWTH HORMONE/RECEPTOR EXTRACELLR DOMN	DE VOS,ULTSCH,KOSSIAKOFF	1/92	H
1GKY	GUANYLATE KINASE(BAKER'S YEAST)/GMP	T.STEHLE,G.SCHULZ	12/91	P
1HAD	HALOALKANE DEHALOGENASE	B.DIJKSTRA ET AL.	4/91	N
1HGD	HEMAGGLUTININ MUTANT(G135(A)R)	D.WILEY ET AL.	11/91	P
1HGE	HEMAGGLUTININ MUTANT(G135(A)R)/NEU5AC2ME	D.WILEY ET AL.	11/91	P
1HGF	HEMAGGLUTININ	D.WILEY ET AL.	11/91	P
1HGG	HEMAGGLUTININ/ALPHA(2,3)SIALYLLACTOSE	D.WILEY ET AL.	11/91	P
1HGH	HEMAGGLUTININ/NEU5AC(ALPHA)2BAC	D.WILEY ET AL.	11/91	P
1HGI	HEMAGGLUTININ/4-ACETYL-NEU5AC(ALPHA)2ME	D.WILEY ET AL.	11/91	P
1HGJ	HEMAGGLUTININ/9-AMINO-NEU5AC(ALPHA)2ME	D.WILEY ET AL.	11/91	P
1HCY	HEMOCYANIN(PANULIRUS INTERRUPTUS)	A.VOLBEDA,W.HOL	5/91	P
1HC1	HEMOCYANIN(P.INTERRUPTUS) SUBUNIT 1	A.VOLBEDA,W.HOL	5/91	P
1HC2	HEMOCYANIN(P.INTERRUPTUS) SUBUNIT 2	A.VOLBEDA,W.HOL	5/91	P
1HC3	HEMOCYANIN(P.INTERRUPTUS) SUBUNIT 3	A.VOLBEDA,W.HOL	5/91	P
1HC4	HEMOCYANIN(P.INTERRUPTUS) SUBUNIT 4	A.VOLBEDA,W.HOL	5/91	P
1HC5	HEMOCYANIN(P.INTERRUPTUS) SUBUNIT 5	A.VOLBEDA,W.HOL	5/91	P
1HC6	HEMOCYANIN(P.INTERRUPTUS) SUBUNIT 6	A.VOLBEDA,W.HOL	5/91	P
1HBG	HEMOGLOBIN(GLYCERA DIBRANCHIATA,CO)	ARENTS,BRADEN,PADLAN,LOVE	2/91	N
2HBG	HEMOGLOBIN(GLYCERA DIBRANCHIATA,DEOXY)	G.ARENTS,W.LOVE	2/91	N
1NIH	HEMOGLOBIN(ALPHA-NICKEL,BETA-FERROUS)	B.LUISI,B.LIDDINGTON	3/90	P
1HBA	HEMOGLOBIN ROTHSCHILD MUTANT(W37(B)R)	J.KAVANAUGH,A.ARNONE	1/92	P
1HBB	HEMOGLOBIN(LOW SALT)	J.KAVANAUGH,A.ARNONE	1/92	P
1PBX	HEMOGLOBIN(PAGOTHENIE BERNACCHII)/CO	G.FERMI	11/91	P
1ITH	HEMOGLOBIN(URECHIS CAUPO)	KOLATKAR,ERNST,HACKERT	12/91	P
2HIP	HIPIP(ECTOTHIORHODOSPIRA HALOPHILA)	H.HOLDEN ET AL.	6/91	P
1HPA	HIPIP(CHROMATIUM VINOSUM)(REDUCED)	C.CARTER JR.	12/91	P
1HRG	HIRUDIN(C TERMINAL FRAGMENT)(NMR)	F.NI,K.GIBSON,H.SCHERAGA	12/90	P
1HTC	HIRUDIN(VARIANT 2)/THROMBIN COMPLEX	A.TULINSKY ET AL.	3/91	AP

2HTC	HIRUDIN(VARIANT 2)/THROMBIN COMPLEX	A.TULINSKY ET AL.	4/91	H
1HGT	HIRUGEN/THROMBIN COMPLEX	A.TULINSKY ET AL.	6/91	H
2HGT	HIRULOG 1/THROMBIN COMPLEX	A.TULINSKY,V.CARPEROS	6/91	H
1HIO	HISTONE OCTAMER(CHICKEN)	G.ARENTS,E.MOUDRIANAKIS	9/91	H
7HVP	HIV-1 PROTEASE/INHIBITOR JG-365	A.WLODAWER ET AL.	9/90	P
8HVP	HIV-1 PROTEASE/INHIBITOR U-85548E	A.WLODAWER ET AL.	10/90	P
4PHV	HIV-1 PROTEASE/INHIBITOR L-700,417	R.BONE	10/91	P
1HIV	*HIV-1 PROTEASE/INHIBITOR U75875	N.THANKI,A.WLODAWER	2/92	P
6FAB	FAB 36-71(MURINE ANTI-PHENYLARSONATE)	R.STRONG ET AL.	1/91	P
1BAF	AN02 FAB FRAGMENT(MOUSE)	LEAHY,BRUNGER,FOX,HYNES	1/92	P
1MAM	FAB(MOUSE MONOCLONAL ANTIBODY YST9.1)	D.ROSE	1/92	P
7FAB	IMMUNOGLOBULIN FAB' NEW	F.SAUL,R.POLJAK	11/91	RP
8FAB	*IGG1 FAB FRAGMENT HIL	F.SAUL,R.POLJAK	3/92	P
6INS	INSULIN(PIG,DES-B30,CROSSLINKED B29-A1)	G.DODSON ET AL.	3/91	P
7INS	INSULIN(PORCINE)/M-CRESOL/CLUPEINE Z	F.KORBER ET AL.	9/91	P
2GF1	INSULIN-LIKE GROWTH FACTOR 1(NMR,AVERAG)	COOKE,HARVEY,CAMPBELL	1/91	P
3GF1	INSULIN-LIKE GROWTH FACTOR 1(NMR,10 STR)	COOKE,HARVEY,CAMPBELL	1/91	P
1IFA	*INTERFERON-BETA(MOUSE)	Y.MITSUI ET AL.	10/91	P
2ILA	INTERLEUKIN 1A(HUMAN)	B.GRAVES,M.HATADA	5/91	AP
6I1B	INTERLEUKIN 1B(HUMAN)(NMR,AVERAGED STRC)	CLORE,WINGFIELD,GRONENBORN	1/91	P
7I1B	INTERLEUKIN 1B(HUMAN)(NMR,32 STRUCTURES)	CLORE,WINGFIELD,GRONENBORN	1/91	P
8I1B	INTERLEUKIN 1B(MOUSE)	DUPONT PROTEIN CRYSTLLGRPY	1/91	P
1MIB	INTERLEUKIN 1B(MOUSE)	J.PRIESTLE ET AL.	8/91	P
1ITL	INTERLEUKIN 4(HUMAN)(NMR)	C.DOBSON ET AL.	2/92	H
3IL8	INTERLEUKIN 8	A.WLODAWER	12/90	P
1IFC	*FATTY ACID BINDING PROTEIN(APO FORM 2)	SCAPIN,GORDON,SACCHETTINI	12/91	P
1IPD	3-ISOPROPYLMALATE DEHYDROGENASE	K.IMADA,M.SATO,Y.KATSUBE	1/92	P
4BLM	BETA-LACTAMASE(BACILLUS LICHENIFORMIS)	J.KNOX,P.MOEWS	5/91	P
1LDN	LACTATE DEHYDROGENSE/NADH/OXAMATE/F1,6BP	D.WIGLEY ET AL.	11/91	P
1LFH	LACTOFERRIN(HUMAN MILK,APO)	ANDERSON,BAKER,NORRIS	9/91	P
1LFG	LACTOFERRIN(HUMAN MILK,DIFERRIC)	BAKER,ANDERSON,HARIDAS	2/92	P
1LFI	*LACTOFERRIN(HUMAN MILK,COPPER)	SMITH,ANDERSON,BAKER,BAKER	2/92	P
1LMB	LAMBDA REPRESSOR/DNA	L.BEAMER,C.PABO	11/91	RP
1LTE	LECTIN(ERYTHRINA CORALLODENDRON)	B.SHAANAN,H.LIS,N.SHARON	6/91	P
1ZTA	LEUCINE ZIPPER(GCN4 TAP)(NMR,20 STRCTRS)	A.PASTORE ET AL.	10/90	P
2ZTA	LEUCINE ZIPPER(GCN4 TAP)	O'SHEA,KLEMM,KIM,ALBER	7/91	P
3LAD	LIPOAMIDE DEHYDROGENASE(A.VINELANDII)	MATTEVI,SCHIERBEEK,HOL	12/91	P
1LAO	LYS-,ARG-,ORNITHINE-BINDING PROTEIN(LAO)	S.-H.KIM	10/91	H
1HEW	LYSOZYME(HEN)/TRI-N-ACETYLCHITOTRIOSE	CHEETHAM,ARTYMIUK,PHILLIPS	1/92	P
1HEL	LYSOZYME(HEN)	WILSON,MALCOLM,MATTHEWS	1/92	P
1HEM	LYSOZYME(HEN) MUTANT(S91T)	WILSON,MALCOLM,MATTHEWS	1/92	P
1HEN	LYSOZYME(HEN) MUTANT(I55V,S91T)	WILSON,MALCOLM,MATTHEWS	1/92	P
1HEO	LYSOZYME(HEN) MUTANT(I55V)	WILSON,MALCOLM,MATTHEWS	1/92	P
1HEP	LYSOZYME(HEN) MUTANT(T40S,I55V,S91T)	WILSON,MALCOLM,MATTHEWS	1/92	P
1HEQ	LYSOZYME(HEN) MUTANT(T40S,S91T)	WILSON,MALCOLM,MATTHEWS	1/92	P
1HER	LYSOZYME(HEN) MUTANT(T40S)	WILSON,MALCOLM,MATTHEWS	1/92	P
4LZM	LYSOZYME(T4)(HIGH SALT)	B.MATTHEWS ET AL.	1/91	P
5LZM	LYSOZYME(T4)(MEDIUM SALT)	B.MATTHEWS ET AL.	1/91	P
6LZM	LYSOZYME(T4)(LOW SALT)	B.MATTHEWS ET AL.	1/91	P
7LZM	LYSOZYME(T4)(DITHIOTHREITOL)	B.MATTHEWS ET AL.	1/91	P
1L77	LYSOZYME(T4) MUTANT(M102L)	J.HURLEY,B.MATTHEWS	11/91	P
2L78	LYSOZYME(T4) MUTANT(V111I)	J.HURLEY,B.MATTHEWS	1/92	P
1L79	LYSOZYME(T4) MUTANT(L99F,V111I)	J.HURLEY,B.MATTHEWS	11/91	P
1L80	LYSOZYME(T4) MUTANT(L99F,M102L,V111I)	J.HURLEY,B.MATTHEWS	11/91	P
1L81	LYSOZYME(T4) MUT(L99F,M102L,V111I,F153L)	J.HURLEY,B.MATTHEWS	11/91	P
1L82	LYSOZYME(T4) MUTANT(L99F,M102L,F153L)	J.HURLEY,B.MATTHEWS	11/91	P
1L83	*LYSOZYME(T4) MUT(C54T,C97A,L99A)/BENZENE	A.ERIKSSON,B.MATTHEWS	1/92	P
1L84	*LYSOZYME(T4)MT(C54T,C97A,L99A,F153A)/BNZ	A.ERIKSSON,B.MATTHEWS	1/92	P
1L85	*LYSOZYME(T4) MUTANT(C54T,C97A,F153A)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L86	*LYSOZYME(T4) MUTANT(C54T,C97A,F153I)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L87	*LYSOZYME(T4) MUTANT(C54T,C97A,F153L)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L88	*LYSOZYME(T4) MUTANT(C54T,C97A,F153M)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L89	*LYSOZYME(T4) MUTNT(C54T,C97A,L99A,F153A)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L90	*LYSOZYME(T4) MUTANT(C54T,C97A,L99A)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L91	*LYSOZYME(T4) MUTANT(C54T,C97A,L99F)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L92	*LYSOZYME(T4) MUTANT(C54T,C97A,L99I)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L93	*LYSOZYME(T4) MUTANT(C54T,C97A,L99M)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L94	*LYSOZYME(T4) MUTANT(C54T,C97A,L99V)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L95	*LYSOZYME(T4) MUTANT(C54T,C97A,F153V)	A.ERIKSSON,B.MATTHEWS	1/92	P
1L96	*LYSOZYME(T4) MUTANT(I3P,P 32 2 1)	DIXON,SHEWCHUK,MATTHEWS	2/92	P
1L97	*LYSOZYME(T4) MUTANT(I3P,P 21 21 2)	DIXON,SHEWCHUK,MATTHEWS	2/92	P
3LZ2	LYSOZYME(TURKEY)	P.L.HOWELL ET AL.	9/91	P
1LZ3	LYSOZYME(TURKEY)	K.HARATA	11/91	P
2PTE	L-LYSYL-D-ALA-D-ALA/DD PEPTIDASE SITE	J.KNOX,R.PRATT	11/90	P
1VAN	L-LYSYL-D-ALA-D-ALA/VANCOMYCIN	J.KNOX,R.PRATT	11/90	P
2MCM	MACROMOMYCIN(STREPTOMYCES MACROMOMYCTCS)	P.VAN ROEY	5/91	P
1MBP	D-MALTODEXTRIN-BINDING PROTEIN/D-MALTOSE	J.SPURLINO,F.QUIOCHO	12/90	AP
1MNR	MANDELATE RACEMASE(PSEUDOMONAS PUTIDA)	D.NEIDHART,G.PETSKO	9/91	P

1MEE	MESENTERICOPEPTIDASE/EGLIN C	Z.DAUTER,C.BETZEL,K.WILSON	4/91	P
3MT2	METALLOTHIONEIN(ISOFORM II,RAT LIVER)	A.ROBBINS,C.D.STOUT	8/91	P
1MDA	*METHYLAMINE DEHYDROGENASE/AMICYANIN	CHEN,DURLEY,F.S.MATHEWS	3/92	P
2MON	MONELLIN(SERENDIPITY BERRY)	F.JIANG,L.TONG,S.-H.KIM	6/90	RN
5MBA	MET MYOGLOBIN(A.LIMACINA)/AZIDE PH 7.0	M.BOLOGNESI ET AL.	1/91	RN
2MM1	MYOGLOBIN MUTANT(K45R,C110A)(HUMAN)	S.HUBBARD	2/91	P
1MYT	MYOGLOBIN(MET,YELLOWFIN TUNA)	BIRNBAUM,ROSE,PRZYBYLSKA	5/91	H
2SN3	*SCORPION NEUROTOXIN(VARIANT 3)	ZHAO,CARSON,EALICK,BUGG	2/92	RP
1NPC	NEUTRAL PROTEASE(BACILLUS CEREUS)	STARK,PAUPTIT,JANSONIUS	1/92	P
1NN2	NEURAMINIDASE N2(A/TOKYO/3/67)	J.VARGHESE,P.COLMAN	3/91	P
1NN9	NEURAMINIDASE N9	P.COLMAN ET AL.	3/91	P
2NN9	NEURAMINIDASE N9 MUTANT(S370L)	P.COLMAN ET AL.	3/91	P
3NN9	NEURAMINIDASE N9 MUTANT(N329D)	P.COLMAN ET AL.	3/91	P
4NN9	NEURAMINIDASE N9 MUTANT(I368R)	P.COLMAN ET AL.	3/91	P
5NN9	NEURAMINIDASE N9 MUTANT(A369D)	P.COLMAN ET AL.	3/91	P
6NN9	NEURAMINIDASE N9 MUTANT(K432N)	P.COLMAN ET AL.	3/91	P
1NCA	*NEURAMINIDASE N9/NC41 FAB	TULIP,VARGHESE,COLMAN	1/92	P
1NCB	*NEURAMINIDASE N9 MUTANT(N329D)/NC41 FAB	TULIP,VARGHESE,COLMAN	1/92	P
1NCC	*NEURAMINIDASE N9 MUTANT(I368R)/NC41 FAB	TULIP,VARGHESE,COLMAN	1/92	P
1NCD	*NEURAMINIDASE N9(PILOT WHALE)/NC41 FAB	TULIP,VARGHESE,COLMAN	1/92	P
1NSB	NEURAMINIDASE(INFLUENZA VIRUS)	BURMEISTER,RUIGROK,CUSACK	8/91	P
3OVO	OVOMUCOID 3RD DOMAIN CLVD(JAPANSE QUAIL)	D.MUSIL,W.BODE	5/91	P
4OVO	OVOMUCOID 3RD DOMAIN CLVD(SILVER PHSANT)	D.MUSIL,W.BODE	5/91	P
1PE6	PAPAIN/E-64-C	D.YAMAMOTO ET AL.	5/91	P
5PAL	PARVALBUMIN(ALPHA LINEAGE)(SHARK)	J.DECLERCQ ET AL.	9/91	P
1PDC	PDC-109 TYPE II B-DOMAIN(NMR)	LLINAS,CONSTANTINE,PATTHY	10/91	P
1PSA	PEPSIN/RENIN INHIBITOR	L.CHEN,C.ABAD-ZAPATERO	10/91	P
2PSG	PEPSINOGEN(PORCINE)	M.JAMES,A.SIELECKI	1/91	P
3PSG	PEPSINOGEN(PORCINE)	HARTSUCK,KOELSCH,REMINGTON	9/91	RP
1NPX	NADH PEROXIDASE(NON-NATIVE,OXIDIZED)	G.SCHULZ ET AL.	8/91	H
1F3G	PHOSPHOCARRIER III GLC FAST(E.COLI)	S.REMINGTON ET AL.	8/91	P
1PMG	PHOSPHOGLUCOMUTASE(RABBIT)	RAY,DAI,LIU,KONNO	1/92	P
1PGD	6-PHOSPHOGLUCONATE DEHYDROGENASE(SHEEP)	ADAMS,GOVER,PHILLPS,SOMERS	8/91	P
1BPQ	*PHOSPHOLIPASE A2(BOVINE)	M.SUNDARALINGAM	10/91	P
2BPP	*PHOSPHOLIPASE A2(BOVINE) MUTANT(K56M)	M.SUNDARALINGAM	1/92	P
1PK4	PLASMINOGEN KRINGLE 4	A.TULINSKY,A.MULICHAK	7/91	P
2PK4	PLASMINOGEN KRINGLE 4 COMPLEX	A.TULINSKY,A.MULICHAK	9/91	P
1PLC	*PLASTOCYANIN(POPLAR,CU2+)	J.M.GUSS,H.FREEMAN	3/92	RP
1POR	PORIN(RHODOBACTER CAPSULATUS)	M.WEISS,G.SCHULZ	10/91	P
1PII	PRA ISOMERASE:IGP SYNTHASE	WILMANNS,PRIESTLE,JANSNIUS	6/91	P
2RCR	PHOTOSYNTHETIC REACTION CNTR(RB.SPHAER.)	CHANG,NORRIS,SCHIFFER	2/91	P
4RCR	PHOTOSYNTHETIC REACTION CNTR(RB.SPHAER.)	REES,FEHER ET AL.	9/91	P
1CPC	C-PHYCOCYANIN(FREMYELLA DIPLOSIPHON)	DUERRING,SCHMIDT,HUBER	10/90	H
9PCY	PLASTOCYANIN(FRENCH BEAN)(NMR,16 STRCTS)	P.WRIGHT ET AL.	3/91	P
1PPO	*PROTEASE OMEGA(PAPAYA)	R.PICKERSGILL ET AL.	7/91	P
1GB1	PROTEIN G(B1 DOMAIN)(NMR,60 STRUCTURES)	CLORE,GRONENBORN ET AL.	5/91	P
2GB1	PROTEIN G(B1 DOMAIN)(NMR,MIN AVGD STRCT)	CLORE,GRONENBORN ET AL.	5/91	P
1PGX	*PROTEIN G(B2 DOMAIN)	WHITLOW,ACHARI,HOWARD	4/92	P
3PRK	*PROTEINASE K/MTHXSCCNL-AAPA-CHLRMTL KTN	W.SAENGER ET AL.	8/91	P
1PF1	PROTHROMBIN FRAGMENT 1(RESIDUES 1-156)	A.TULINSKY ET AL.	3/91	P
1PF2	PROTHROMBIN CA-FRAGMENT 1	A.TULINSKY ET AL.	12/91	H
1Q21	C-H-RAS P21 PROTEIN/GDP	S.-H.KIM	9/91	RP
2Q21	C-H-RAS P21 PROTEIN MUTANT(G12V)/GDP	S.-H.KIM	9/91	RP
3Q21	C-H-RAS P21 PROTEIN/GDPCP	S.-H.KIM	9/91	P
4Q21	C-H-RAS P21 PROTEIN(RESIDUES 1-188)/GDP	S.-H.KIM	9/91	P
5Q21	C-H-RAS P21 PROTEIN MUTANT(Q61L)/GDPCP	S.-H.KIM	9/91	P
121P	C-H-RAS P21 PROTEIN/GPPCP	U.KRENGEL ET AL.	6/91	P
221P	C-H-RAS P21 PROTEIN MUTANT(D38E)/GPPNP	U.KRENGEL ET AL.	6/91	P
321P	C-H-RAS P21 PROTEIN MUTANT(G12P)/GPPNP	U.KRENGEL ET AL.	6/91	P
421P	C-H-RAS P21 PROTEIN MUTANT(G12R)/GPPNP	U.KRENGEL ET AL.	6/91	P
521P	C-H-RAS P21 PROTEIN MUTANT(G12V)/GTP	U.KRENGEL ET AL.	6/91	P
621P	C-H-RAS P21 PROTEIN MUTANT(Q61H)/GPPNP	U.KRENGEL ET AL.	6/91	P
721P	C-H-RAS P21 PROTEIN MUTANT(Q61L)/GPPNP	U.KRENGEL ET AL.	6/91	P
1REA	REC A PROTEIN(E.COLI)/ADP	R.STORY,T.STEITZ	12/91	P
2REB	*REC A PROTEIN(E.COLI)	R.STORY,T.STEITZ	3/92	P
6RLX	RELAXIN(HUMAN)	C.EIGENBROT ET AL.	6/91	P
2REN	RENIN	A.SIELECKI,M.JAMES ET AL.	2/92	P
1RNE	RENIN(HUMAN)(GLYCOSYLATED,INHIBITED)	GRUETTER,RAHUEL,PRIESTLE	12/91	P
1PRA	R1-69 N-TERMINUS OF 434 REPRESSOR	K.WUTHRICH ET AL.	11/91	P
3SRN	RIBONUCLEASE A(SEMISYNTH.) MUTANT(D121N)	B.EDWARDS ET AL.	5/91	P
4SRN	RIBONUCLEASE A(SEMISYNTH.) MUTANT(D121A)	B.EDWARDS ET AL.	5/91	P
1RAT	RIBONUCLEASE A(BOVINE,98 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P
2RAT	RIBONUCLEASE A(BOVINE,130 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P
3RAT	RIBONUCLEASE A(BOVINE,160 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P
4RAT	RIBONUCLEASE A(BOVINE,180 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P
5RAT	RIBONUCLEASE A(BOVINE,220 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P
6RAT	RIBONUCLEASE A(BOVINE,240 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P
7RAT	RIBONUCLEASE A(BOVINE,260 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P

8RAT	RIBONUCLEASE A(BOVINE,300 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P
9RAT	RIBONUCLEASE A(BOVINE,320 K)	R.TILTON JR.,DEWAN,PETSKO	8/91	P
1RNC	*RIBONUCLEASE A(BOVINE)/2',5'-CPG	C.AGUILAR ET AL.	10/91	P
1RND	RIBONUCLEASE A(BOVINE)/3',5'-DCPDG	C.AGUILAR ET AL.	10/91	P
1RN2	RIBONUCLEASE H(E.COLI)	K.KATAYANAGI ET AL.	11/91	P
1RMS	RIBONUCLEASE MS/3'-GUANYLIC ACID	NONAKA,MITSUI,NAKAMURA	12/91	N
2RNS	*RIBONUCLEASE S(PH 4.75)	WYCKOFF,RICHARDS ET AL.	2/92	RP
1RNU	*RIBONUCLEASE S(PH 5.5)	WYCKOFF,RICHARDS ET AL.	2/92	P
1RNV	*RIBONUCLEASE S(PH 4.75,TRUNCATED S PEPT)	WYCKOFF,RICHARDS ET AL.	2/92	P
5RNT	RIBONUCLEASE T1/GUANOSINE-3',5'-BISPHSPH	SAENGER,HEINEMANN,LENZ	4/91	P
6RNT	RIBONUCLEASE T1/2'-AMP	W.SAENGER ET AL.	8/91	P
7RNT	RIBONUCLEAST T1 MUTANT(Y45W)/2'-AMP	W.SAENGER ET AL.	8/91	P
8RNT	RIBONUCLEASE T1/ZN++	DING,CHOE,GRANZIN,SAENGER	9/91	P
9RNT	RIBONUCLEASE T1	W.SAENGER ET AL.	9/91	P
1RN1	RIBONUCLEASE T1(GLN 25)	R.ARNI ET AL.	11/91	H
1RN4	RIBONUCLEASE T1(H92A)	W.SAENGER ET AL.	11/91	P
1RGL	*RIBONUCLEASE T1(E46Q)	J.GRANZIN ET AL.	2/92	P
1OFX	RNA(GCG)D(TATACCC)/D(GGGTATACGC)OKAZAKI	EGLI,USMAN,ZHANG,RICH	10/91	P
1ROP	ROP(COL E1)	M.KOKKINIDIS ET AL.	4/91	P
1RPP	*ROP(COL E1) (NMR)	W.EBERLE ET AL.	10/91	P
1RPR	*ROP(COL E1) (NMR,10 STRUCTURES)	W.EBERLE ET AL.	10/91	P
3RUB	RUBISCO(FORM III)	EISENBERG,SCHREUDER ET AL.	5/90	P
4RUB	RUBISCO(FORM IV)	EISENBERG,SCHREUDER ET AL.	5/90	P
8RUB	RUBISCO(SPINACH)/CABP	KNIGHT,ANDERSSON,BRANDEN	11/90	N
9RUB	RUBISCO(R.RUBRUM)/RIBULOSE-1,5-BISPHSPHT	T.LUNDQVIST,G.SCHNEIDER	11/90	P
8RXN	RUBREDOXIN(D.VULGARIS)	DAUTER,SIEKER,WILSON	8/91	P
1BST	SOMATOTROPIN(BOVINE GROWTH HORMONE)	CARLACCI,CHOU,MAGGIORA	2/91	P
2SNM	STAPH NUCLEASE MUTANT(V66K)	E.LATTMAN ET AL.	4/91	P
1ST3	SUBTILISIN BL(BACILLUS LENTUS)	D.GODDETTE	11/91	H
2SIC	SUBTILISIN BPN'/SSI COMPLEX	Y.MITSUI ET AL.	4/91	RP
3SIC	SUBTILISIN BPN'/SSI MUTANT(M73K)	Y.MITSUI ET AL.	8/91	P
5SIC	SUBTILISIN BPN'/SSI MUTANT(M70G,M73K)	MITSUI,TAKEUCHI,NAKAMURA	11/91	P
1SBN	SUBTILISIN NOVO/EGLIN C MUTANT(L45R)	GRUETTER,HEINZ,PRIESTLE	12/91	P
3SDP	FE SUPEROXIDE DISMUTASE(PSEUDMNS.OVALIS)	STODDARD,RINGE,PETSKO	5/91	P
3SOD	SUPEROXIDE DISMUTASE(BOVINE)	J.TAINER ET AL.	6/90	P
1COB	*SUPEROXIDE DISMUTASE(BOVINE,CO-SUBSTITD)	M.BOLOGNESI ET AL.	2/92	P
1SDY	SUPEROXIDE DISMUTASE(YEAST)	M.BOLOGNESI ET AL.	6/91	P
5TAA	TAKA-AMYLASE(ASPERGILLUS ORYZAE)	H.SWIFT ET AL.	5/91	H
1THM	*THERMITASE(THERMOACTINOMYCES VULGARIS)	A.TEPLYAKOV ET AL.	2/92	P
1TRB	THIOREDOXIN REDUCTASE(E.COLI)	J.KURIYAN,T.KRISHNA	9/91	P
1PK2	TISSUE PLASMINOGEN ACTVTR(KRINGLE2)(NMR)	M.LLINAS,I.BYEON	9/91	P
1TPK	TISSUE PLASMINOGEN ACTIVATOR(KRINGLE2)	A.DE VOS ET AL.	9/91	P
5TRA	TRANSFER RNA(YEAST,SER)	A.DOCK-BREGEON	2/90	N
1TFD	TRANSFERRIN(N-TERMINAL HALF-MOLECULE)	R.SARRA,P.LINDLEY	8/90	P
2TGF	TRANSFORMING GROWTH FACTOR(NMR,AVERAGE)	I.CAMPBELL ET AL.	1/91	P
3TGF	TRANSFORMING GROWTH FACTOR(NMR,4 STRCTS)	I.CAMPBELL ET AL.	1/91	P
1THA	*TRANSTHYRETIN(HUMAN THYROID)/(3,3'-T2)	A.WOJTCZAK,J.LUFT,V.CODY	11/91	P
5TGL	TRIACYLGLYCEROL LIPASE/INHIBITOR	VANDIEPEN,DEREWENDA ET AL.	10/91	P
3TGL	TRIACYLGLYCEROL ACYLHYDROLASE	Z.DEREWENDA	7/91	H
4TGL	TRIACYLGLYCEROL ACYLHYDROLASE COMPLEX	Z.DEREWENDA	7/91	H
1TMD	TRIMETHYLAMINE DEHYDROGENASE	F.S.MATHEWS,L.LIM,S.WHITE	1/91	P
4TIM	TIM(TRYPANOSOMAL)/2-PHOSPHOGLYCERATE	NOBLE,WIERENGA,HOL ET AL.	4/91	P
5TIM	TIM(TRYPANOSOMAL)/SULFATE	R.WIERENGA,W.HOL ET AL.	4/91	RP
6TIM	TIM(TRYPANOSOMAL)/GLYCEROL-3-PHOSPHATE	NOBLE,WIERENGA,HOL ET AL.	4/91	P
3YPI	TIM(YEAST) MUTANT(H95Q)/PGH	E.LOLIS,G.PETSKO	1/91	P
2TPR	TRYPANOTHIONE REDUCTASE	J.KURIYAN ET AL.	8/91	P
1GBT	TRYPSIN(GUANIDINOBENZOYL)	R.SWEET ET AL.	9/91	P
2TLD	TRYPSIN/SSI MUTANT(M70G,M73K)	Y.MITSUI ET AL.	9/91	N
1TIE	TRYPSIN INHIBITOR(ERYTHRINA CAFFRA)	S.ONESTI,P.BRICK,D.BLOW	2/91	P
1BTI	TRYPSIN INHIBITOR(BOVINE) MUTANT(F22A)	A.WLODAWER ET AL.	7/91	P
1BOV	VEROTOXIN-1(B SUBUNIT)(E.COLI)	P.STEIN ET AL.	10/91	H
1XIM	D-XYLOSE ISOMERASE(A.MIS.)/XYLITOL/CO	J.JANIN ET AL.	5/91	P
2XIM	D-XYLOSE ISOMERASE(A.MIS.)/XYLOSE/MG	J.JANIN ET AL.	5/91	P
3XIM	D-XYLOSE ISOMERASE(A.MIS.)/SORBITOL/CO	J.JANIN ET AL.	5/91	P
1XIS	D-XYLOSE ISOMERASE(S.RUBIGINOSUS)/MNCL2	M.WHITLOW,A.HOWARD	3/91	P
2XIS	D-XYLOSE ISOMERASE(S.RUB.)/XYLITOL	M.WHITLOW,A.HOWARD	3/91	P
3XIS	D-XYLOSE ISOMERASE(S.RUB.)/XYLOSE	M.WHITLOW,A.HOWARD	3/91	P
4XIS	D-XYLOSE ISOMERASE(S.RUB.)/XYLOSE/MNCL2	M.WHITLOW,A.HOWARD	3/91	P
1MS2	MS2 VIRUS(BACTERIOPHAGE)	K.VALEGARD,L.LILJAS	5/91	P
1MEC	MENGO VIRUS(LOW PH)	M.ROSSMANN	1/92	P
1DPV	PARVOVIRUS(CANINE,MONOCLINIC)	M.ROSSMANN ET AL.	11/90	P
1SNV	SINDBIS VIRUS CAPSID PROTEIN	M.ROSSMANN ET AL.	9/91	P
1TME	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS	R.GRANT,D.FILMAN,J.HOGLE	1/92	P
1TMF	*THEILER'S MURINE ENCEPHALOMYELITIS VIRUS	M.LUO,K.TOTH	2/92	P
5ZNF	ZINC FINGER(NMR,13 STRUCTURES)	KOCHOYAN,KEUTMANN,WEISS	8/91	P
7ZNF	ZINC FINGER(SWAP,NMR,12 STRUCTURES)	KOCHOYAN,KEUTMANN,WEISS	8/91	P
1CLG	COLLAGEN(3 CHAINS OF 12(G-P-P))(MODEL)	J.CHEN	9/91	P

2CLG	COLLAGEN(3 CHNS 12(G-P-HYDRXYPRO)(MODEL)	J.CHEN	9/91	P
3CLG	COLLAGEN(15 CHAINS OF 12(G-P-P))(MODEL)	J.CHEN	9/91	P
4CLG	COLLAGEN(15CHS 12(G-P-HYDRXYPRO))(MODEL)	J.CHEN	9/91	P
5ZNA	DNA(Z,GCGCGCGCGCGCGC) MODEL	A.ANSEVIN,A.WANG	2/91	P
2IGE	IMMUNOGLOBULIN E(FC FRAGMENT) MODEL	E.PADLAN,B.HELM	10/90	P
1IPT	INTRON(CORE OF GROUP I INTRONS) MODEL	F.MICHEL,E.WESTHOF	5/91	P
1POM	*MYB ONCOPROTEIN(DNA-BINDING DOMAIN)MODEL	J.FRAMPTON,T.GIBSON ET AL.	11/91	P
1PAI	PROTEIN C INHIBITOR (2 MODELS)	L.KUHN,C.FISHER,J.TAINER	7/90	P
1RRN	5S RIBOSOMAL RNA MODEL	WESTHOF,ROMBY,EHRESMANN	6/91	P
1SLK	SILK I(POLY ALA-GLY) MODEL	H.SCHERAGA ET AL.	10/91	P
2SLK	SILK II(POLY ALA-GLY) MODEL	H.SCHERAGA ET AL.	10/91	P

R2AAASF	ACID ALPHA-AMYLASE(ASPERGILLUS NIGER)	G.DODSON ET AL.	3/91	SH
R1AKESF	ADENYLATE KINASE(E.COLI)/AP5A	C.MUELLER,G.SCHULZ	11/91	S
R1CWGSF	*WHEAT GERM AGGLUTININ(ISOLECTIN 1)/T-5	C.WRIGHT	2/92	S
R1ACHSF	ALPHA1 ANTICHYMOTRYPSIN(HUMAN)	BAUMANN,HUBER ET AL.	1/91	SH
R4ICBSF	CALBINDIN D9K(BOVINE)	L.A.SVENSSON	8/91	S
R2SCPSF	SARCOPLASMIC CALCIUM-BINDING PROTEIN	W.COOK,S.VIJAY-KUMAR	8/91	S
R4CACSF	CARBONIC ANHYDRASE C(PH 6)	A.LILJAS ET AL.	9/91	S
R5CACSF	*CARBONIC ANHYDRASE C/SO3	A.LILJAS ET AL.	9/91	S
R1CD8SF	CD8(HUMAN)	LEAHY,AXEL,HENDRICKSON	1/91	S
R3CHYSF	CHE Y(ESCHERICHIA COLI)	K.VOLZ,P.MATSUMURA	4/91	S
R1ACBSF	ALPHA-CHYMOTRYPSIN(BOVINE)/EGLIN C	M.BOLOGNESI ET AL.	11/91	S
R1CGISF	ALPHA-CHYMOTRYPSINOGEN A/PSTI VARIANT 3	H.HECHT ET AL.	10/91	S
R1CGJSF	ALPHA-CHYMOTRYPSINOGEN A/PSTI VARIANT 4	H.HECHT ET AL.	10/91	S
R1CCDSF	CLARA CELL 17 KDA PROTEIN(RAT)	T.UMLAND ET AL.	9/91	S
R1BB2SF	BETA-B2 CRYSTALLIN(BOVINE)	C.SLINGSBY ET AL.	7/91	S
R2YCCSF	CYTOCHROME C(YEAST,ISO-1,OXIDIZED)	A.BERGHUIS,G.BRAYER	1/91	S
R1YEASF	CYTOCHROME C(YEAST,ISO-2,REDUCED)	M.MURPHY,G.BRAYER	10/91	S
R1YEBSF	CYTOCHROME C(YEAST B-2036 COMPOST,REDCD)	M.MURPHY,G.BRAYER	10/91	S
R1DFNSF	DEFENSIN HNP-3(HUMAN)	D.EISENBERG ET AL.	1/91	S
R1D54SF	*DNA(TGTACA)/4'-EPIADRIAMYCIN	LEONARD,BROWN,HUNTER	1/92	S
R1D55SF	DNA(GAAGCTTC)/ACTINOMYCIN D	KAMITORI,TAKUSAGAWA	2/92	SH
R1D56SF	*DNA(CGATATATCG)/CALCIUM	YUAN,QUNTANA,DICKERSON	2/92	S
R1D57SF	*DNA(CGATATATCG)/MAGNESIUM	YUAN,QUNTANA,DICKERSON	2/92	S
R1D63SF	*DNA(CGCAAATTTGCG)/BERENIL	D.BROWN,S.NEIDLE ET AL.	3/92	S
R1D64SF	*DNA(CGCGAATTCGCG)/PENTAMIDINE	EDWARDS,JENKINS,NEIDLE	3/92	S
R1D65SF	*DNA(CGCAAATTTGCG)	EDWARDS,NEIDLE ET AL.	3/92	S
R1CGCSF	DNA(CCGGCGCCGG)	U.HEINEMANN,M.BANSAL	1/92	S
R1DRISF	*D-RIBOSE-BINDING PROTEIN(E.COLI)	S.MOWBRAY,L.B.COLE	2/92	S
R6EBXSF	*ERABUTOXIN B(LATICAUDA SEMIFASCIATA)	T.PRANGE,P.SALUDJIAN	8/91	S
R3FISSF	FIS(E.COLI)	R.DICKERSON ET AL.	9/91	S
R4FISSF	FIS(E.COLI) MUTANT(R89C)	R.DICKERSON ET AL.	9/91	S
R1FIASF	*FIS(E.COLI)	W.SAENGER ET AL.	12/91	S
R2FX1SF	FLAVODOXIN(D.VULGARIS,ROOM TEMPERATURE)	W.WATT,K.WATENPAUGH	1/91	S
R3FX1SF	FLAVODOXIN(D.VULGARIS,-150C,OXIDIZED)	W.WATT,K.WATENPAUGH	1/91	S
R4FX1SF	FLAVODOXIN(D.VULGARIS,-150C,SEMIQUINONE)	W.WATT,K.WATENPAUGH	1/91	S
R5FX1SF	FLAVODOXIN(D.VULGARIS,-150C,HYDROQUINON)	W.WATT,K.WATENPAUGH	1/91	S
R1GGASF1	G-GLYCERALDEHYDE-PHOSPHATE DEHYDROGENASE	VELLIEUX,HAJDU,HOL	10/91	S
R1GGASF2	G-GLYCERALDEHYDE-PHOSPHATE DEHYDROGENASE	VELLIEUX,HAJDU,HOL	10/91	S
R1GKYSF	GUANYLATE KINASE(BAKER'S YEAST)/GMP	T.STEHLE,G.SCHULZ	12/91	S
R1HGDSF	HEMAGGLUTININ MUTANT(G135(A)R)	D.WILEY ET AL.	11/91	S
R1HGESF	HEMAGGLUTININ MUTANT(G135(A)R)/NEU5AC2MED	D.WILEY ET AL.	11/91	S
R1HGFSF	HEMAGGLUTININ	D.WILEY ET AL.	11/91	S
R1HGGSF	HEMAGGLUTININ/ALPHA(2,3)SIALYLLACTOSE	D.WILEY ET AL.	11/91	S
R1HGHSF	HEMAGGLUTININ/NEU5AC(ALPHA)2BAC	D.WILEY ET AL.	11/91	S
R1HGISF	HEMAGGLUTININ/4-ACETYL-NEU5AC(ALPHA)2ME	D.WILEY ET AL.	11/91	S
R1HGJSF	HEMAGGLUTININ/9-AMINO-NEU5AC(ALPHA)2ME	D.WILEY ET AL.	11/91	S
R1HGKSF	HEMAGGLUTININ/ALPHA(2,3)SIALYLLACTOSE(2)	D.WILEY ET AL.	11/91	S
R1HGLSF	HEMAGGLUTININ/ALPHA(2,3)SIALYLLACTOSE(8)	D.WILEY ET AL.	11/91	S
R1HGMSF	HEMAGGLUTININ/ALPH(2,3)SIALYLLACTOSE(32)	D.WILEY ET AL.	11/91	S
R1HGNSF	HEMAGGLUTININ/ALPHA(2,6)SIALYLLACTOSE(2)	D.WILEY ET AL.	11/91	S
R1HGOSF	HEMAGGLUTININ/ALPHA(2,6)SIALYLLACTOSE(8)	D.WILEY ET AL.	11/91	S
R1HGPSF	HEMAGGLUTININ/ALPH(2,6)SIALYLLACTOSE(32)	D.WILEY ET AL.	11/91	S
R1HGQSF	HEMAGGLUTININ/NEU5AC(ALPHA)2MAC(50MM)	D.WILEY ET AL.	11/91	S
R1HGRSF	HEMAGGLUTININ/NEU5AC(ALPHA)2ME(2MM)	D.WILEY ET AL.	11/91	S
R1HGSSF	HEMAGGLUTININ/NEU5AC(ALPHA)2ME(100MM)	D.WILEY ET AL.	11/91	S
R1HCYSF	HEMOCYANIN(PANULIRUS INTERRUPTUS)	A.VOLBEDA,W.HOL	5/91	S
R1HBGSF	HEMOGLOBIN(GLYCERA DIBRANCHIATA,CO)	W.LOVE ET AL.	2/91	S
R2HBGSF	HEMOGLOBIN(GLYCERA DIBRANCHIATA,DEOXY)	W.LOVE ET AL.	2/91	S
R1HBASF	HEMOGLOBIN ROTHSCHILD MUTANT(W37(B)R)	J.KAVANAUGH,A.ARNONE	1/92	S
R1HBBSF	HEMOGLOBIN(LOW SALT)	J.KAVANAUGH,A.ARNONE	1/92	S
R1PBXSF	HEMOGLOBIN(PAGOTHENIE BERNACCHII)/CO	G.FERMI	11/91	S
R1HPASF	*HIPIP(CHROMATIUM VINOSUM)(REDUCED)	C.CARTER JR.	12/91	S
R1MAMSF	FAB(MOUSE MONOCLONAL ANTIBODY YST9.1)	D.ROSE	1/92	S
R6INSSF	*INSULIN(PIG,DES-B30,CROSSLINKED B29-A1)	G.DODSON ET AL.	5/91	S
R7INSSF	INSULIN(PORCINE)/M-CRESOL/CLUPEINE Z	F.KORBER ET AL.	9/91	S
R4BLMSF	BETA-LACTAMASE(BACILLUS LICHENIFORMIS)	J.KNOX,P.MOEWS	5/91	S

R8LDHSF	APO-M4-LACTATE DEHYDROGENASE/CITRATE	M.ROSSMANN ET AL.	1/88	S
R7LDHSF	LACTATE DEHYDROGENASE COMPLEXES	M.ROSSMANN ET AL.	1/88	S
R6LDHSF	APO-M4-LACTATE DEHYDROGENASE(DOGFISH)	M.ROSSMANN ET AL.	11/87	S
R1LDMSF	LACTATE DEHYDROGENASE/NADH/OXAMATE(DOGF)	J.GRIFFITH,M.ROSSMANN	11/87	S
R1LDNSF	LACTATE DEHYDROGENSE/NADH/OXAMATE/F1,6BP	D.WIGLEY ET AL.	11/91	S
R1LFHSF	LACTOFERRIN(HUMAN MILK,APO)	ANDERSON,BAKER,NORRIS	9/91	S
R1LAPSF	LEUCINE AMINOPEPTIDASE(BOVINE LENS)	W.LIPSCOMB ET AL.	8/90	SH
R1LADSF	LIPOAMIDE DEHYDROGENASE(A.VINELANDII)	MATTEVI,SCHIERBEEK,HOL	9/90	S
R1LZ3SF	LYSOZYME(TURKEY)	K.HARATA	2/92	S
R3LZ2SF	LYSOZYME(TURKEY)	P.L.HOWELL ET AL.	9/91	S
R2MCMSF	MACROMOMYCIN(STREPTOMYCES MACROMOMYCTCS)	P.VAN ROEY	5/91	S
R1MEESF	MESENTERICOPEPTIDASE/EGLIN C	DAUTER,BETZEL,WILSON	4/91	S
R1MADSF	METHYLAMINE DEHYDROGENASE	F.VELLIEUX,W.HOL	2/91	SH
R5MBASF	MET MYOGLOBIN(A.LIMACINA)/AZIDE PH 7.0	M.BOLOGNESI ET AL.	1/91	S
R2MM1SF	MYOGLOBIN MUTANT(K45R,C110A)(HUMAN)	S.HUBBARD	3/90	S
R1MYTSF	MYOGLOBIN(MET,YELLOWFIN TUNA)	BIRNBAUM,ROSE,PRZBLSKA	5/91	SH
R1NPXSF	NADH PEROXIDASE(NON-NATIVE,OXIDIZED)	G.SCHULZ ET AL.	8/91	SH
R1NPCSF	NEUTRAL PROTEASE(BACILLUS CEREUS)	J.JANSONIUS ET AL.	1/92	S
R1NN2SF	NEURAMINIDASE N2(A/TOKYO/3/67)	J.VARGHESE,P.COLMAN	3/91	SH
R1NN9SF	NEURAMINIDASE N9	P.COLMAN ET AL.	3/91	SH
R2NN9SF	NEURAMINIDASE N9 MUTANT(S370L)	P.COLMAN ET AL.	3/91	SH
R3NN9SF	NEURAMINIDASE N9 MUTANT(N329D)	P.COLMAN ET AL.	3/91	SH
R4NN9SF	NEURAMINIDASE N9 MUTANT(I368R)	P.COLMAN ET AL.	3/91	SH
R5NN9SF	NEURAMINIDASE N9 MUTANT(A369D)	P.COLMAN ET AL.	3/91	SH
R6NN9SF	NEURAMINIDASE N9 MUTANT(K432N)	P.COLMAN ET AL.	3/91	SH
R1NCASF	*NEURAMINIDASE N9/NC41 FAB	TULIP,VARGHESE,COLMAN	1/92	S
R1NCBSF	*NEURAMINIDASE N9 MUTANT(N329D)/NC41 FAB	TULIP,VARGHESE,COLMAN	1/92	S
R1NCCSF	*NEURAMINIDASE N9 MUTANT(I368R)/NC41 FAB	TULIP,VARGHESE,COLMAN	1/92	S
R1NCDSF	*NEURAMINIDASE N9(PILOT WHALE)/NC41 FAB	TULIP,VARGHESE,COLMAN	1/92	S
R2SN3SF	*SCORPION NEUROTOXIN(VARIANT 3)	ZHAO,CARSON,EALCK,BUGG	2/92	S
R1Q21SF	C-H-RAS P21 PROTEIN/GDP	S.-H.KIM	5/90	SH
R2Q21SF	C-H-RAS P21 PROTEIN MUTANT(G12V)/GDP	S.-H.KIM	5/90	SH
R3Q21SF	C-H-RAS P21 PROTEIN/GDPCP	S.-H.KIM	5/90	SH
R1PE6SF	PAPAIN/E-64-C	D.YAMAMOTO ET AL.	5/91	S
R1PSASF	PEPSIN/RENIN INHIBITOR	L.CHEN,C.ABAD-ZAPATERO	10/91	S
R1PGDSF	6-PHOSPHOGLUCONATE DEHYDROGENASE(SHEEP)	M.ADAMS ET AL.	8/91	S
R7PCYSF	PLASTOCYANIN(ENTEROMORPHA,CU2+)	COLLYER,GUSS,FREEMAN	9/89	S
R1PLCSF	*PLASTOCYANIN(POPLAR,CU2+)	J.M.GUSS,H.FREEMAN	3/92	S
R1PPOSF	*PROTEASE OMEGA(PAPAYA)	R.PICKERSGILL ET AL.	7/91	S
R3PRKSF	*PROTEINASE K/MTHXSCCNL-AAPA-CHLRMTL KTN	W.SAENGER ET AL.	8/91	S
R2PNPSF	PURINE NUCLEOSIDE PHOSPHORYLASE(HUMAN)	S.EALICK ET AL.	11/89	SH
R6RLXSF	RELAXIN(HUMAN)	C.EIGENBROT ET AL.	6/91	SH
R1RNCSF	*RIBONUCLEASE A(BOVINE)/2',5'-CPG	C.AGUILAR ET AL.	10/91	S
R1RNDSF	RIBONUCLEASE A(BOVINE)/3',5'-DCPDG	C.AGUILAR ET AL.	10/91	S
R5RNTSF	RIBONUCLEASE T1/GUANOSINE-3',5'-BISPHSPH	SAENGER,HEINEMANN,LENZ	4/91	S
R8RNTSF	*RIBONUCLEASE T1/ZN++	W.SAENGER ET AL.	11/91	S
R9RNTSF	RIBONUCLEASE T1	W.SAENGER ET AL.	9/91	S
R1RGLSF	*RIBONUCLEASE T1(E46Q)	J.GRANZIN ET AL.	2/92	S
R8RXNSF	RUBREDOXIN(D.VULGARIS)	DAUTER,SIEKER,WILSON	8/91	S
R2SNMSF	STAPH NUCLEASE MUTANT(V66K)	E.LATTMAN ET AL.	4/91	S
R1ST3SF	SUBTILISIN BL(BACILLUS LENTUS)	D.GODDETTE	11/91	SH
R3SODSF	SUPEROXIDE DISMUTASE(BOVINE)	J.TAINER ET AL.	6/90	SH
R1COBSF	*SUPEROXIDE DISMUTASE(BOVINE,CO-SUBSTITD)	M.BOLOGNESI ET AL.	2/92	S
R1SDYSF	SUPEROXIDE DISMUTASE(YEAST)	M.BOLOGNESI ET AL.	4/91	S
R4TAASF	TAKA-AMYLASE(ASPERGILLUS ORYZAE)	H.SWIFT ET AL.	2/91	SH
R1TRBSF	THIOREDOXIN REDUCTASE(E.COLI)	J.KURIYAN,T.KRISHNA	9/91	S
R2TPRSF	TRYPANOTHIONE REDUCTASE	J.KURIYAN ET AL.	8/91	S
R1MS2SF	MS2 VIRUS(BACTERIOPHAGE)	K.VALEGARD,L.LILJAS	5/91	S
R1R1ASF	RHINOVIRUS 1A	M.ROSSMANN ET AL.	12/88	S
R1RMUSF	RHINOVIRUS MUTANT((1)C199Y)	M.ROSSMANN ET AL.	10/88	S
R2RMUSF	RHINOVIRUS MUTANT((1)V188L)	M.ROSSMANN ET AL.	10/88	S
R2RR1SF	RHINOVIRUS/ANTIVIRAL AGENT 1R COMPLEX	M.ROSSMANN ET AL.	10/88	S
R2RS1SF	RHINOVIRUS/ANTIVIRAL AGENT 1S COMPLEX	M.ROSSMANN ET AL.	10/88	S
R2RM2SF	RHINOVIRUS/ANTIVIRAL AGENT 2 COMPLEX	M.ROSSMANN ET AL.	10/88	S
R2RS3SF	RHINOVIRUS/ANTIVIRAL AGENT 3S COMPLEX	M.ROSSMANN ET AL.	10/88	S
R2R04SF	RHINOVIRUS/ANTIVIRAL AGENT 4 COMPLEX	M.ROSSMANN ET AL.	10/88	S
R2RS5SF	RHINOVIRUS/ANTIVIRAL AGENT 5S COMPLEX	M.ROSSMANN ET AL.	10/88	S
R2R06SF	RHINOVIRUS/ANTIVIRAL AGENT 6 COMPLEX	M.ROSSMANN ET AL.	10/88	S
R2R07SF	RHINOVIRUS/ANTIVIRAL AGENT 7 COMPLEX	M.ROSSMANN ET AL.	10/88	S
R1R08SF	RHINOVIRUS/ANTIVIRAL AGENT 8 COMPLEX	M.ROSSMANN ET AL.	10/88	S
R1TMFSF	*THEILER'S MURINE ENCEPHALOMYELITIS VIRUS	M.LUO,K.TOTH	2/92	S
R1ACPMR	ACYL CARRIER PROTEIN(NMR)	J.PRESTEGARD,Y.KIM	7/90	M
R1APSMR	ACYLPHOSPHATASE(NMR)	V.SAUDEK ET AL.	2/91	M
R1HOMMR	ANTENNAPEDIA HOMEODOMAIN(NMR)	K.WUTHRICH ET AL.	10/91	M
R2HOAMR	*A. HOMEODOMAIN(NMR,20STRCTS)MUTANT(C39S)	K.WUTHRICH ET AL.	4/92	M
R1BW1MR	BARWIN(NMR,20 STRUCTURES)	F.POULSEN	11/91	M
R1BW2MR	BARWIN(NMR,20 STRUCTURES)	F.POULSEN	11/91	M

R1NBTMR	BUNGAROTOXIN(NEURONAL)(NMR)	OSWALD,SUTCLIFFE ET AL	10/91	M
R1CB1MR	CALBINDIN D9K(PORCINE)(NMR,14 STRUCTURS)	AKKE,DRAKENBERG,CHAZIN	12/91	M
R1PBAMR	CARBOXYPEPTIDASE B(ACTIVATION DOMAIN)	K.WUTHRICH ET AL.	11/91	M
R3CI2MR	CHYMOTRYPSIN INHIBITOR 2(BARLEY)(NMR)	F.POULSEN	9/91	M
R1CTGMR	CONOTOXIN GIIA(NMR)	LANCELIN,KOHDA,INAGAKI	8/91	M
R2CYSMR	*CYCLOPHILIN/CYCLOSPORIN A(NMR)	K.WUTHRICH ET AL.	3/92	M
R1D42MR	DNA(GTATATAC) (NMR)	U.SCHMITZ,T.JAMES	5/91	M
R1EDPMR	*ENDOTHELIN-1	N.ANDERSEN,C.CHEN	12/91	M
R1EGFMR	*EPIDERMAL GROWTH FACTOR(MOUSE)(NMR)	MONTELIONE,SCHERAGA	10/91	M
R1EPHMR	*EPIDERMAL GROWTH FACTOR(NMR,PH 2.0)	D.KOHDA,F.INAGAKI	3/92	M
R1EPJMR	*EPIDERMAL GROWTH FACTOR(NMR,PH 6.8)	D.KOHDA,F.INAGAKI	3/92	M
R1EGOMR	GLUTAREDOXIN(OXIDIZED)(E.COLI)(NMR)	K.WUTHRICH ET AL.	10/91	M
R1EGRMR	GLUTAREDOXIN(REDUCED)(E.COLI)(NMR)	K.WUTHRICH ET AL.	10/91	M
R2GF1MR	INSULIN-LIKE GROWTH FACTOR 1(NMR)	COOKE,HARVEY,CAMPBELL	1/91	M
R6I1BMR	INTERLEUKIN 1B(HUMAN)(NMR)	CLORE,GRONENBORN ET AL	1/91	M
R1ITLMR	INTERLEUKIN 4(HUMAN)(NMR)	C.DOBSON ET AL.	2/92	MH
R1ZTAMR	LEUCINE ZIPPER(GCN4 TAP)(NMR)	A.PASTORE ET AL.	10/90	M
R1PDCMR	PDC-109 TYPE II B-DOMAIN(NMR)	M.LLINAS ET AL.	10/91	M
R1PK2MR	PLASMINOGEN ACTIVATOR(KRINGLE 2 DOMAIN)	M.LLINAS,I.BYEON	9/91	M
R9PCYMR	PLASTOCYANIN(FRENCH BEAN)(NMR)	P.WRIGHT ET AL.	3/91	M
R1GB1MR	PROTEIN G(B1 DOMAIN)(GROUP G STREPTOCCS)	CLORE,GRONENBORN ET AL	7/91	M
R1PRAMR	R1-69 N-TERMINUS OF 434 REPRESSOR	K.WUTHRICH ET AL.	11/91	M
R1RPPMR	*ROP(COL E1) (NMR)	W.EBERLE ET AL.	10/91	M
R2TGFMR	TRANSFORMING GROWTH FACTOR(NMR)	I.CAMPBELL ET AL.	1/91	M

* NEW OR REPLACEMENT ENTRY SINCE JAN-1992 NEWSLETTER

STATUS CODES

A	ALPHA CARBON ATOMS ONLY
B	BACKBONE ONLY
H	HOLD FOR DELAYED RELEASE AS REQUESTED BY DEPOSITOR
M	NMR RESTRAINTS AND OTHER NMR EXPERIMENTAL DATA
N	NEW ENTRY AWAITING APPROVAL BY DEPOSITOR
P	IN PREPARATION
R	REPLACEMENT FOR ENTRY IN TABLE 3
S	STRUCTURE FACTORS

Name of User _____ Date _____

Address _____ Phone _____

_____ E-mail _____

_____ Fax # _____

DATAPRTP

(all available coordinate entries, bibliographic entries, and some computer programs)

	6250cpi	1600cpi	TK50	1/4"	8mm	DAT
VAX/VMS *backup*	[ ] $413	[ ] $877	[ ] $560			
VAX/VMS *copy*	[ ] $413	[ ] $877	[ ] $560			
Unlabeled *ASCII*	[ ] $413	[ ] $877				
Unlabeled *EBCDIC* . . .	[ ] $413	[ ] $877				
SGI/SUN/IBM/E&S UNIX *tar*				[ ] $348	[ ] $348	[ ] $348

PDBPGMTP

(all computer programs and miscellaneous files)

	6250cpi	1600cpi	TK50	1/4"	8mm	DAT
VAX/VMS *copy*	[ ] $336	[ ] $336	[ ] $359			
SGI/SUN/IBM/E&S UNIX *tar*				[ ] $348	[ ] $348	[ ] $348

STRUCTURE FACTOR ENTRIES

(experimental diffraction data)

Choose tape(s): [ ] NONST1TP [ ] NONST2TP [ ] NONST3TP [ ] NONST4TP
[ ] NONST5TP [ ] NONST6TP [ ] NONST7TP [ ] NONST8TP
[ ] NONST9TP [ ] NONST10TP

Choose one format for selection(s) shown above:

	6250cpi	1600cpi	TK50	1/4"	8mm	DAT
VAX/VMS *backup*	[ ] $336	[ ] $336	[ ] $359			
VAX/VMS *copy*	[ ] $336	[ ] $336	[ ] $359			
Unlabeled *ASCII*	[ ] $336	[ ] $336				
Unlabeled *EBCDIC* . . .	[ ] $336	[ ] $336				
SGI/SUN/IBM/E&S UNIX *tar*				[ ] $348	[ ] $348	[ ] $348

NMRRS1TP

(NMR experimental data entries)

	6250cpi	1600cpi	TK50	1/4"	8mm	DAT
VAX/VMS *backup*	[ ] $336	[ ] $336	[ ] $359			
VAX/VMS *copy*	[ ] $336	[ ] $336	[ ] $359			
Unlabeled *ASCII*	[ ] $336	[ ] $336				
Unlabeled *EBCDIC* . . .	[ ] $336	[ ] $336				
SGI/SUN/IBM/E&S UNIX *tar*				[ ] $348	[ ] $348	[ ] $348

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TOTAL CHARGES

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(Prices are valid until September 30, 1992) ***TOTAL COST*** . . . . . $ _____

PRINTED DOCUMENTATION (no charge)

[ ] Atomic Coordinate and Bibliographic Entry Format Description for DATAPRTP (Feb. 1992)
[ ] Complete List of Bibliographic Entries
[ ] Current DATAPRTP Directory
[ ] Data Deposition Form
[ ] Detailed Contents and Format Description for Each Structure Factor Entry
[ ] Latest Newsletter
[ ] Sources of Visual Aids for Macromolecular Structure (Feb. 1990)

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3. payment (use one of the methods listed below):

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⇒ Original hardcopy of purchase order payable to Brookhaven National Laboratory. After your order is processed, our Fiscal Division will invoice you.

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Acct. name: Brookhaven National Laboratory
Cust. Acct. : 076-51-912

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(NMR experimental data entries)

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