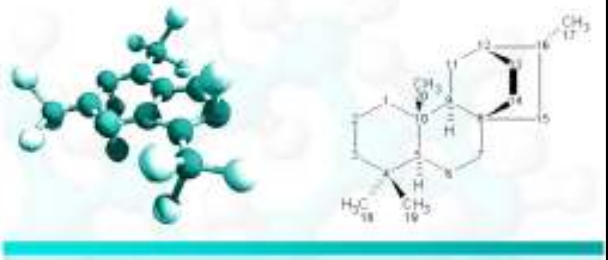

# MB11: Bioinformatics Fundamentals

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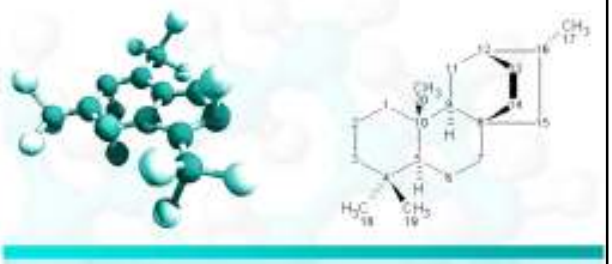


## Unit #2

## Biological Databases

## Contents

- Protein Sequence and Structural Databases
- Nucleotide Sequence Databases
  - EMBL
  - GenBank
  - DDBJ
- Swiss PROT
- PIR
- Protein Data Bank (PDB)
- UniGene
- Saccharomyces Genome Database (SGD)
- PubMed



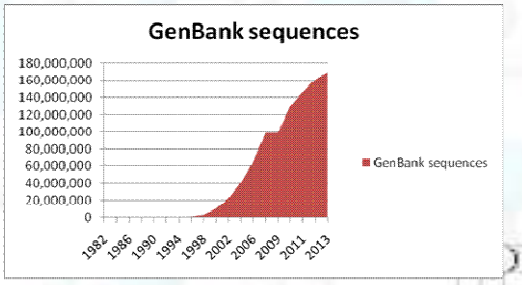
## Nucleotide sequence databases

- GenBank, EMBL, and DDBJ are the **three primary nucleotide sequence databases**
- **EMBL** www.ebi.ac.uk/embl/
- **GenBank** www.ncbi.nlm.nih.gov/Genbank/
- **DDBJ** www.ddbj.nig.ac.jp

## Genbank

- An **annotated collection of all publicly available nucleotide and proteins**.
- Set up in 1979 at the LANL (Los Alamos).
- Maintained since 1992.
- It is part of the ***International Nucleotide Sequence Database Collaboration*** (INSDC).
- INSDC comprises the DNA DataBank of Japan (**DDBJ**), the European Molecular Biology Laboratory (**EMBL**), and **GenBank** at NCBI.
- These three organizations exchange data on a daily basis.

## Growth of Genbank sequences



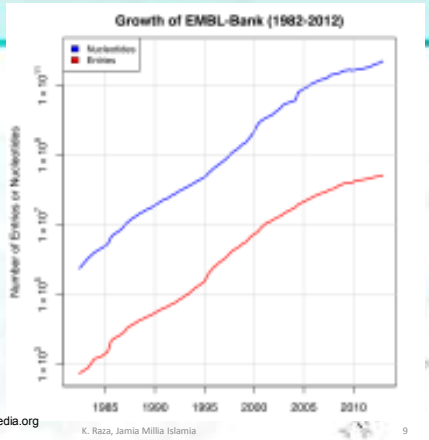
## Access to GenBank

- Several ways to search and retrieve data from GenBank.
- Search for sequence identifiers and annotations with **Entrez Nucleotide**.
- It is divided into three divisions:
  - **CoreNucleotide** (the main collection),
  - **dbEST** (Expressed Sequence Tags), and
  - **dbGSS** (Genome Survey Sequences).
- Searching and alignment is done using BLAST.
- BLAST searches CoreNucleotide, dbEST, and dbGSS independently.
- Search, link, and download sequences programatically using **NCBI e-utilities**.



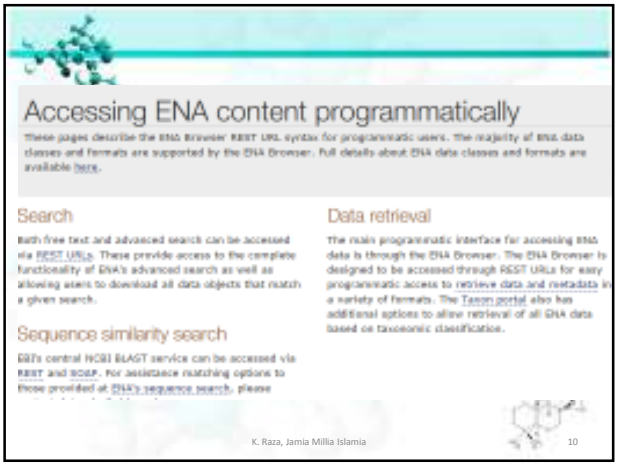
## EMBL Nucleotide Sequence Database

- An annotated collection of all publicly available nucleotide and protein sequences.
- Created in 1980 at the *EMBL* in Heidelberg, Germany.
- Maintained since 1994 by EBI- Cambridge.
- Also known as **EMBL-Bank.**
- Now, EMBL Nucleotide Sequence is a section of Nucleotide Sequence Archive.
- http://www.ebi.ac.uk/ena/
- Increased in size from around 600 entries in 1982 to over **$2.5\times10^8$** by December 2012.
- Uncompressed file size of 1.6 terabytes




Source: https://en.wikipedia.org








## DNA Data Bank of Japan (DDBJ)

- An annotated collection of all publicly available nucleotide and protein sequences.
- Started, 1984 at the ***National Institute of Genetics*** (NIG).
- http://www.ddbj.nig.ac.jp

## Sequence submission

- Data mainly direct submissions from the authors.
- Submissions through the Internet:
  - Web forms
  - Email
- Sequences shared/exchanged between the 3 centers on a daily basis:
  - The sequence content of the banks is identical.

## Sequence Retrieval Tools

- Various tools to get sequences of interests from databases
  - Entrez in NCBI http://www.ncbi.nlm.nih.gov/Entrez
  - SRS for EMBL and other DBs **http://srs.ebi.ac.uk**
  - Fetch in GCG package
  - Seqret in EMBOSS

## Derived databases

- CUTG Codon usage tabulated from GenBank http://www.kazusa.or.jp/codon/
- Genetic Codes Deviations from the standard genetic code in various organisms and organelles http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi?mode=c
- UniGene Unified clusters of ESTs and full-length mRNA sequences http://www.ncbi.nlm.nih.gov/UniGene/

## Protein Databases

- General Sequence databases
- Protein properties
- Protein localization and targeting
- Protein sequence motifs and active sites
- Protein domain databases; protein classification
- Databases of individual protein families

## Protein Databases

- **General Sequence databases**
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http://www.ncbi.nlm.nih.gov/protein

## NCBI Protein database

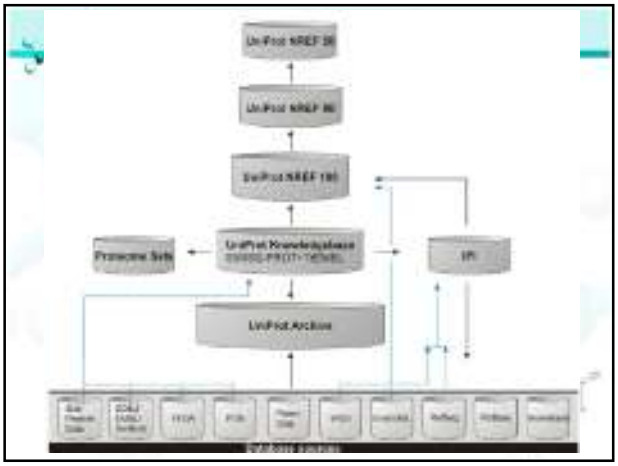
- The NCBI Entrez Protein database are from:
  - SwissProt,
  - Protein Information Resource,
  - Protein Research Foundation,
  - Protein Data Bank, and
  - translations from annotated coding regions in the GenBank and RefSeq databases.

## Swiss-Prot

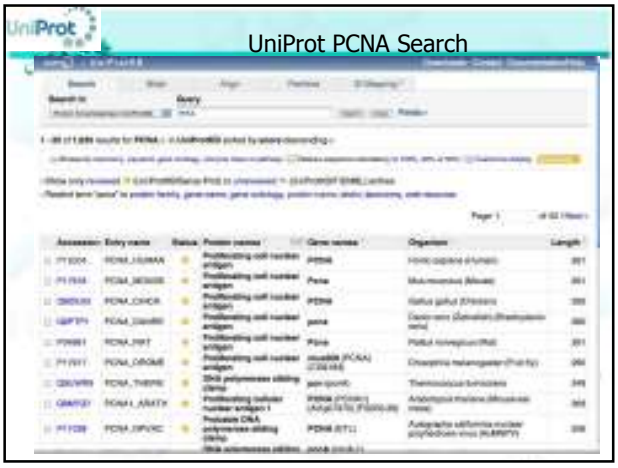
- The Swiss-Prot Protein Knowledgebase is a curated protein sequence database established in 1986.
- Provides a high level of annotation, such as:
  - description of protein function,
  - domains structure,
  - post-translational modifications,
  - variants, etc.
- *A minimal level of redundancy and high level of integration with other databases*.
- Now, a part of **UniProt**, a "one-stop shop" that allows easy access to all publicly available information of protein sequence annotation.

## UniProt

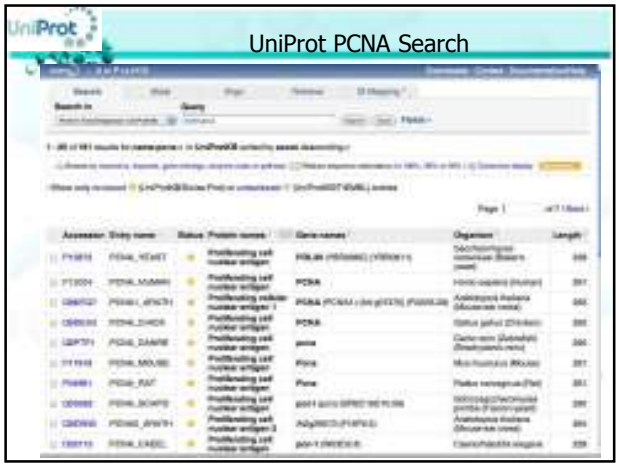
- The **Swiss-Prot**, **TrEMBL**, and **PIR** protein database have united to form the *Universal Protein Resource* (UniProt)
  - Uniprot Knowledgebase (UniprotKB): curated sequence information, annotations, linked to other databases.
  - Uniprot Reference Clusters (UniRef): removing sequence redundancy by merging sequences that are 100% (UniRef100), 90% (UniRef90) and 50% (UniRef50), linked to Knowledgebase and UniParc records.
  - Uniprot Archive (UniParc): history of sequences, no annotation, linked to source records.



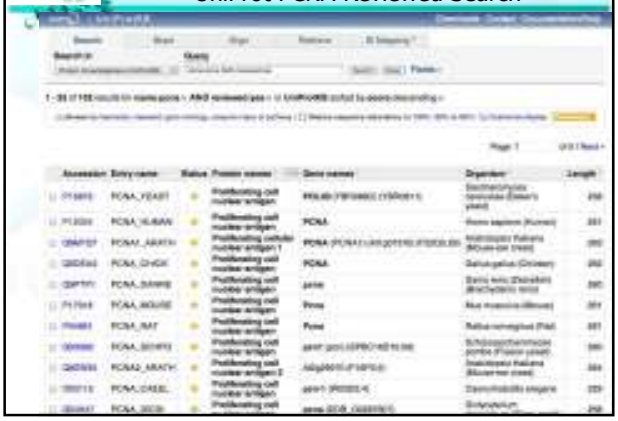

## UniProt PCNA Search




## UniProt PCNA Search

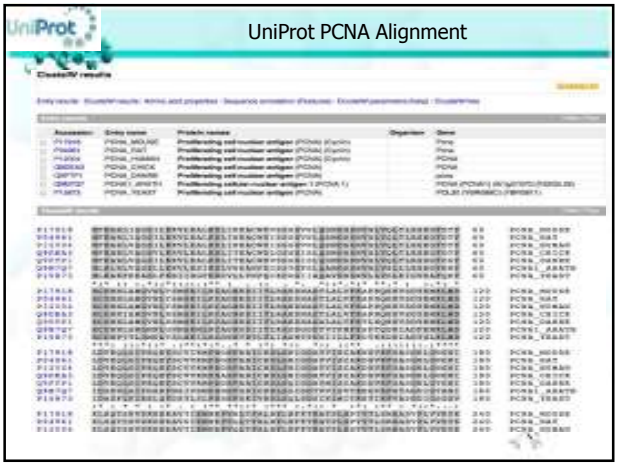


## UniProt PCNA Reviewed Search



## UniProt PCNA BLAST Search

## UniProt PCNA Alignment



## Protein Databases

- General Sequence databases
- **Protein properties**
- Protein sequence motifs and active sites
- Protein domain databases; protein classification
- Databases of individual protein families

## DBs based on Protein properties

- **AAindex:** A database of amino acid indices and amino acid mutation matrices.
- **Cybase:** Cyclic proteins
- **dbPTM**: protein post-translational modification (PTM) information
- **iProLINK**: Integrated Protein Literature, INformation and Knowledge
- **PFD** - Protein Folding Database
- **PINT**: Protein-protein Interactions Thermodynamic Database
- **MIPS, STRING**: Protein-protein Interactions Database
- **REFOLD**: Data related to refolding experiments

## Protein sequence motifs and active sites

- ASC - Active Sequence Collection
- Blocks
- COMe - Co-Ordination of Metals etc.
- CSA - Catalytic Site Atlas
- eBLOCKS
- eMOTIF
- InterPro
- Metalloprotein Site Database
- O-GLYCBASE
- PDBSite
- PhosphoELM Base
- PRINTS
- PROMISE
- ProRule
- PROSITE

## Protein domain databases; protein classification

- ADDA - Automatic Domain Decomposition Algorithm
- BAliBASE
- BIOZON
- CluSTr - Clusters of Swiss-Prot and TrEMBL proteins
- COG - Clusters of Orthologous Groups of proteins
- FusionDB
- HSSP
- InterDom
- InterPro <---- PROSITE, Pfam, PRINTS, Prodom, SMART, TIGRFAMs, PIR superfamily
- iProClass
- MulPSSM
- PALI
- Pfam
- ProDom <---- SP, TrEMBL
- SUPFAM

## Databases of individual protein families

- AARSDB
- ABCdb
- ARAMEMNON
- BacTregulators (formerly AraC/XylS database)
- CSDBase - Cold Shock Domain database
- DCCP - Database of Copper-Chelating Proteins
- DExH/D Family Database
- DSD
- Endogenous GPCR List
- EROP-Moscow
- ESTHER
- FUNPEP
- GPCRDB
- gpDB - G-protein database
- Histone Database
- HIV RT and Protease Sequence Database
- Homeobox Page
- Homeodomain Resource
- InBase
- KinG - Kinases in Genomes
- Knottins
- LGICdb
- Lipase Engineering Database
- Lipid MAPS
- MEROPS
- Nuclear Receptor Resource
- NucleaRDB
- NUREBASE
- PHYTOPROT
- Protein kinase resource
- Ribonuclease P Database
- RNRdb
- RTKdb - Receptor Tyrosine Kinase database

## Database Searching Tips

- Look for links to Help or Examples
- Always check update dates
- Level of curation
- Try Boolean searches
- Be careful with UK/US spelling differences
  - leukaemia vs leukemia
  - haemoglobin vs hemoglobin
  - colour vs color

## Protein Structures

**Tertiary protein structure prediction is possibly the Holy Grail of bioinformatics.**

**This houses a collection of 3D coordinates of each atom in a protein, allowing the structure to be displayed by viewing software.**

**Protein structures are submitted by individual researchers and have been determined by x-ray diffraction, or NMR.**



## Protein Structure Databases

- **PDB:** Protein DataBank, New Jersey, USA
  - http://www.rcsb.org/
- **EMSD:** EBI Macromolecular Structure Database
  - Management and distribution of data on macromolecular structures in close collaboration with the PDB.
  - http://www.ebi.ac.uk/msd/index.html
- **SCOP:** Structural Classification of Proteins
  - scop.mrc-lmb.cam.ac.uk/scop
- **CATH:** Classification, Architecture, Topology, Homology
  - http://www.biochem.ucl.ac.uk/bsm/cath_new/



## Protein Data Bank (PDB)

- A repository for 3-D biological macromolecular structure.
- It includes ***proteins***, ***nucleic acids*** and ***viruses***.
- Obtained by X-Ray crystallography (80%) or NMR spectroscopy (16%).
- Important in solving real problems in molecular biology.
- Established in 1972 at Brookhaven National Laboratory.
- Transferred to the **Research Collaboratory for Structural Bioinformatics** (RCSB) in 1998.
- Sole international repository of macromolecular structure data.
- URL: http://www.rcsb.org/

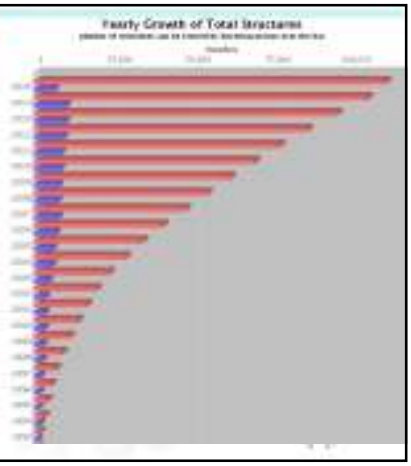
## Protein Data Bank (Structures)

## PDB Contents

**PDB Current Holdings Breakdown**

| Exp. Method | Proteins | Nucleic Acids | Protein/NA Complexes | Other | Total |
|---|---|---|---|---|---|
| X-RAY | 92817 | 1649 | 4616 | 4 | **99086** |
| NMR | 9699 | 1126 | 227 | 8 | **11060** |
| ELECTRON MICROSCOPY | 602 | 29 | 199 | 0 | **830** |
| HYBRID | 70 | 3 | 2 | 1 | **76** |
| other | 166 | 4 | 6 | 13 | **189** |
| Total | 103354 | 2811 | 5050 | 26 | **1,11,241** |

## Growth of PDB



*As on Aug 11, 2015*

## Effective use of PDB

- Queries are of three types
  - PDB id - As quoted in paper
  - Search Lite - one or more keywords
  - Search Fields - A detailed query form
- Query results
  - Structure Explorer - details of the structure
  - Query Result Browser - for multiple structures
- PDB Viewer

## Structure Explorer

## PDB data formats

- PDB file format was used to contain the coordinates and related information.
- In the late 1990's, macromolecular Crystallographic Information file (**mmCIF**) evolved.
- mmCIF and PDBML
  - Push in to make structure files completely self-contained descriptions of the experiment and details of the structure determination.
  - ***PDB file format unstructured and obsolete***

## PDB File Format

- Text file – you can edit with a text editor e.g. WordPad
- Atomic co-ordinates
- Rich annotation
  - Citation
  - Experimental Method
  - Biological source e.
  - Etc.

## PDB: Example

- HEADER
- COMPND
- SOURCE
- AUTHOR
- DATE
- JRNL
- REMARK
- SECRES
- ATOM COORDINATES

```
HEADER    LYASE(OXO-ACID)                         01-OCT-91   12CA      12CA  2
COMPND    CARBONIC ANHYDRASE /II (CARBONATE DEHYDRATASE) (/HCA II)   12CA  3
COMPND    2 (E.C.4.2.1.1) MUTANT WITH VAL 121 REPLACED BY ALA (/V121A) 12CA  4
SOURCE    HUMAN (HOMO SAPIENS) RECOMBINANT PROTEIN                   12CA  5
AUTHOR    S.K.NAIR,D.W.CHRISTIANSON                                  12CA  6
REVDAT   1  15-OCT-92 12CA      0                                    12CA  7
JRNL        AUTH   S.K.NAIR,T.L.CALDERONE,D.W.CHRISTIANSON,C.A.FIERKE   12CA  8
JRNL        TITL   ALTERING THE MOUTH OF A HYDROPHOBIC POCKET.         12CA  9
JRNL        TITL 2 STRUCTURE AND KINETICS OF HUMAN CARBONIC ANHYDRASE   12CA  10
JRNL        TITL 3 /II$ MUTANTS AT RESIDUE VAL-121                     12CA  11
JRNL        REF    J.BIOL.CHEM.              V. 266 17320 1991        12CA  12
JRNL        REFN   ASTM JBCHA3  US ISSN 0021-9258              071  12CA  13
REMARK   1                                                     12CA  14
REMARK   2                                                     12CA  15
REMARK   2 RESOLUTION. 2.4  ANGSTROMS.                         12CA  16
REMARK   3                                                     12CA  17
REMARK   3 REFINEMENT.                                         12CA  18
REMARK   3   PROGRAM                PROLSQ                    12CA  19
REMARK   3   AUTHORS                HENDRICKSON,KONNERT       12CA  20
REMARK   3   R VALUE                0.170                     12CA  21
REMARK   3   RMSD BOND DISTANCES      0.011  ANGSTROMS        12CA  22
REMARK   3   RMSD BOND ANGLES         1.3    DEGREES          12CA  23
REMARK   4                                                     12CA  24
REMARK   4 N-TERMINAL RESIDUES SER 2, HIS 3, HIS 4 AND C-TERMINAL      12CA  25
REMARK   4 RESIDUE LYS 260 WERE NOT LOCATED IN THE DENSITY MAPS AND,   12CA  26
REMARK   4 THEREFORE, NO COORDINATES ARE INCLUDED  FOR THESE RESIDUES.  12CA  27
.....
```

## PDB (cont.)

```
SHEET    3  S10 PHE    66  PHE    70 -1  O  ASN    67   N  LEU    60   12CA 68
SHEET    4  S10 TYR    88  TRP    97 -1  O  PHE    93   N  VAL    68   12CA 69
SHEET    5  S10 ALA   116  ASN   124 -1  O  HIS   119   N  HIS    94   12CA 70
SHEET    6  S10 LEU   141  VAL   150 -1  O  LEU   144   N  LEU   120   12CA 71
SHEET    7  S10 VAL   207  LEU   212  1  O  ILE   210   N  GLY   145   12CA 72
SHEET    8  S10 TYR   191  GLY   196 -1  O  TRP   192   N  VAL   211   12CA 73
SHEET    9  S10 LYS   257  ALA   258 -1  O  LYS   257   N  THR   193   12CA 74
SHEET   10  S10 LYS    39  TYR    40  1  O  LYS    39   N  ALA   258   12CA 75
TURN     1  T1 GLN    28  VAL    31   TYPE VIB (CIS-PRO 30)          12CA 76
TURN     2  T2 GLY    81  LEU    84   TYPE II(PRIME) (GLY 82)        12CA 77
TURN     3  T3 ALA   134  GLN   137   TYPE I (GLN 136)               12CA 78
TURN     4  T4 GLN   137  GLY   140   TYPE I (ASP 139)               12CA 79
TURN     5  T5 THR   200  LEU   203   TYPE VIA (CIS-PRO 202)         12CA 80
TURN     6  T6 GLY   233  GLU   236   TYPE II (GLY 235)              12CA 81
CRYST1   42.700   41.700   73.000  90.00 104.60  90.00 P 21          2  12CA 82
ORIGX1      1.000000  0.000000  0.000000        0.00000             12CA 83
ORIGX2      0.000000  1.000000  0.000000        0.00000             12CA 84
ORIGX3      0.000000  0.000000  1.000000        0.00000             12CA 85
SCALE1      0.023419  0.000000  0.006100        0.00000             12CA 86
SCALE2      0.000000  0.023981  0.000000        0.00000             12CA 87
SCALE3      0.000000  0.000000  0.014156        0.00000             12CA 88
ATOM      1  N   TRP     5       8.519  -0.751  10.738  1.00 13.37    12CA 89
ATOM      2  CA  TRP     5       7.743  -1.668  11.585  1.00 13.42    12CA 90
ATOM      3  C   TRP     5       6.786  -2.502  10.667  1.00 13.47    12CA 91
ATOM      4  O   TRP     5       6.422  -2.085   9.607  1.00 13.57    12CA 92
ATOM      5  CB  TRP     5       6.997  -0.917  12.645  1.00 13.34    12CA 93
ATOM      6  CG  TRP     5       5.784  -0.209  12.221  1.00 13.40    12CA 94
ATOM      7  CD1 TRP     5       5.681   1.084  11.797  1.00 13.29    12CA 95
```

## Fragment of CIF example

```
#####################
# ATOM_SITE       #
#####################
loop_
_atom_site.label_seq_id
_atom_site.group_PDB
_atom_site.type_symbol
_atom_site.label_atom_id
_atom_site.label_comp_id
_atom_site.label_asym_id
_atom_site.auth_seq_id
_atom_site.label_alt_id
_atom_site.cartn_x
_atom_site.cartn_y
_atom_site.cartn_z
_atom_site.occupancy
_atom_site.B_iso_or_equiv
_atom_site.footnote_id
_atom_site.label_entity_id
_atom_site.id
1
 ATOM  N  N   GLY A   1  .  -8.863  16.944  14.289  1.00 21.88  1  1
       1
1
 ATOM  C  CA  GLY A   1  .  -9.929  17.026  13.244  1.00 22.85  1  1
       2
1
 ATOM  C  C   GLY A   1  .  -10.051 15.625  12.618  1.00 43.92  1  1
       3
1
 ATOM  O  O   GLY A   1  .  -9.782  14.728  13.407  1.00 25.22  1  1
```

## Structure Visualization

PDB file =======➔

**Rasmol/Pymol/Jmol**

## Jmol View of 1VYM

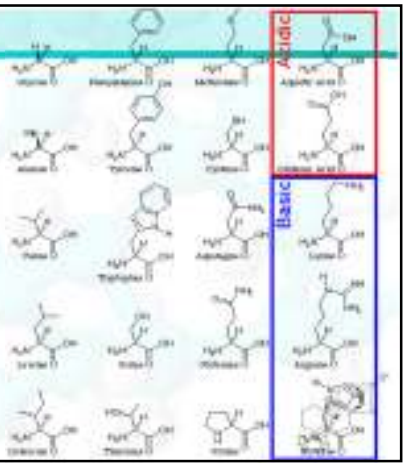

## 3-D Structure from PDB

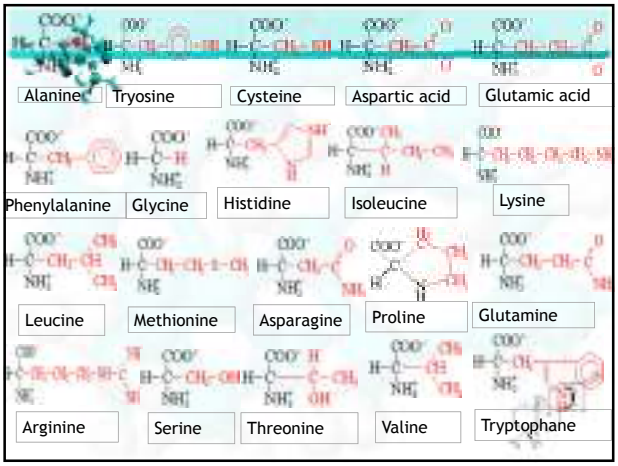
- 20 Amino acids

http://www.clunet.edu/BioDev/omm/aa/aa.htm

http://www.nyu.edu/pages/mathmol/library/life/

http://inquiry.uiuc.edu/bioweb/tutorial/amino_acids.htm




## How to Construct 3-D Molecule

- Read coordinates from PDB.
- Set up data structure of molecules
- Form bonds among atoms and groups
- Calculate secondary structure.
- Implement 3-D graphical algorithms.
- Render 3-D graph in various style, wires, sticks, balls, ribbons, and the like.

## Bonds among atoms

```
ATOM     20  N   LEU 1   4      30.279 -25.716 105.041  1.00 10.60      2MCG 249
ATOM     21  CA  LEU 1   4      31.406 -26.518 104.496  1.00  9.39      2MCG 250
ATOM     22  C   LEU 1   4      32.658 -25.786 105.165  1.00  8.90      2MCG 251
ATOM     23  O   LEU 1   4      32.890 -24.586 104.967  1.00  8.74      2MCG 252
ATOM     24  CB  LEU 1   4      31.615 -26.794 103.141  1.00  8.79      2MCG 253
ATOM     25  CG  LEU 1   4      31.552 -27.440 101.860  1.00  8.37      2MCG 254
ATOM     26  CD1 LEU 1   4      32.732 -26.945 100.970  1.00  7.99      2MCG 255
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```
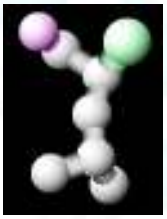
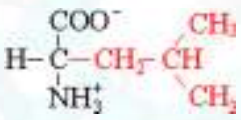



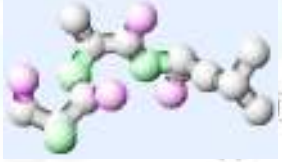


Leucine LEU L

Formula: $C_6 H_{13} N O_2$

## Bonds between groups

```
ATOM     9  N   SER 1   2      25.548 -22.930 103.333  1.00 16.05      2MCG 238
ATOM     10 CA  SER 1   2      26.608 -22.758 104.327  1.00 15.38      2MCG 239
ATOM     11 C   SER 1   2      27.351 -24.076 104.604  1.00 14.81      2MCG 240
ATOM     12 O   SER 1   2      27.530 -24.949 103.740  1.00 15.00      2MCG 241
ATOM     13 CB  SER 1   2      25.887 -22.406 105.682  1.00 15.73      2MCG 242
ATOM     14 OG  SER 1   2      25.193 -23.586 106.117  1.00 15.14      2MCG 243
ATOM     15 N   ALA 1   3      27.758 -24.228 105.876  1.00 13.72      2MCG 244
ATOM     16 CA  ALA 1   3      28.328 -25.397 106.456  1.00 12.33      2MCG 245
ATOM     17 C   ALA 1   3      29.255 -26.303 105.686  1.00 11.58      2MCG 246
ATOM     18 O   ALA 1   3      29.033 -27.552 105.641  1.00 11.28      2MCG 247
ATOM     19 CB  ALA 1   3      27.101 -26.228 106.998  1.00 12.39      2MCG 248
ATOM     20 N   LEU 1   4      30.279 -25.716 105.041  1.00 10.60      2MCG 249
ATOM     21 CA  LEU 1   4      31.406 -26.518 104.496  1.00  9.39      2MCG 250
ATOM     22 C   LEU 1   4      32.658 -25.786 105.165  1.00  8.90      2MCG 251
ATOM     23 O   LEU 1   4      32.890 -24.586 104.967  1.00  8.74      2MCG 252
ATOM     24 CB  LEU 1   4      31.615 -26.794 103.141  1.00  8.79      2MCG 253
ATOM     25 CG  LEU 1   4      31.552 -27.440 101.860  1.00  8.37      2MCG 254
ATOM     26 CD1 LEU 1   4      32.732 -26.945 100.970  1.00  7.99      2MCG 255
ATOM     27 CD2 LEU 1   4      31.706 -28.963 102.016  1.00  8.09      2MCG 256
```



## Nucleic Acid Database (NDB)

- NDB contains information about experimentally-determined nucleic acids and complex assemblies.
- Use the NDB to perform searches based on annotations relating to sequence, structure and function, and to download, analyze, and learn about nucleic acids.
- The NDB Project is funded by the National Science Foundation and the Department of Energy.
- The goal of NDBP is to assemble and distribute structural information about nucleic acids,
- The format of NDB is the same as PDB.

## Nucleic Acid Database (NDB)

**A Portal for Three-dimensional Structural Information about Nucleic Acids.**

**As of 12-Aug-2015 number of released structures: 7671**

## UniGene

- **UniGene** is an NCBI database of the transcriptome.
- Information on protein similarities, gene expression, cDNA clones, and genomic location is included with each entry.



## Saccharomyces Genome Database (SGD)

- Provides Internet access to the complete Saccharomyces cerevisiae (yeast) genomic sequence, its genes and their products, the phenotypes of its mutants, and the literature supporting these data.
- Currently the only complete sequence of a eukaryotic genome.
- Aids researchers by providing basic information and tools for sequence similarity searching, and finding relationships between genes.
- SGD presents information using a variety of user-friendly, dynamically created graphical displays illustrating physical, genetic and sequence feature maps.
- http://www.yeastgenome.org/



## PubMed

- Where we search for research from medical journals
- 13 million citations/abstracts
- 4,500 journals
  - From 1966
- Covers
  - Medicine
  - Nursing
  - Dentistry
  - Veterinary medicine
  - Healtchcare systems
  - Preclinical sciences

## More About PubMed

- Links to other databases
  - OLDMEDLINE (1950-1965)
  - International biomedical journals
    - 1,760,000 citations
- Not all journals are strictly scientific or medical
- Links (LinkOut) to the full-text of articles at participating publishers' web sites

## What Can You Do in PubMed?

- Search for articles (usually abstracts)
  - By keyword
  - By author
  - By Journal, etc
- Combine searches
- Link to related articles
- Link to outside sources
  - To purchase the full article
  - Look at related books (including pages in the books)
- Clinical queries

## The PubMed Homepage

http://www.ncbi.nlm.nih.gov/pubmed

## PubMed – Search Overview

- Search by keyword
  - E.g., thrombin, but you get 31,365 results
- Use a more specific keyword
  - Like "Thrombin-JMI", but now you only get 2 hits
- Additional tools
  - Limits
  - Search Field Tags
  - meSH (Medical Subject Heading)

## PubMed – Additional Tools

- Limits
  - Age, groups, gender, type of study, etc
- Search Field tags
  - Qualify terms, used in brackets [ta]
- Boolean Statements
  - And, OR, NOT
- meSH
  - The "vocabulary" of PubMed
  - Stands for Medical Subjects Headings
  - Used for indexing biomedical literature

## PubMed -- Limits


## PubMed -- Search Field Tags

- Search Field Tags also qualify terms
- Letters in brackets
  - Nature [ta] (title abbreviation)
  - Watson JD [au] (author)
  - 1953 [dp] (date of publication)
  - DNA [mh] (maSH)

## Boolean Statements

- Example: citations on DNA authored by Crick in 1993
  - Dna [mh] AND crick [au] AND 1993[dp]
- Effect of heat or humidity on surgical hemostasis
  - (heat OR humidity) AND surgical hemostasis

## PubMed -- The meSH Tree

- meSH organizes terms in a hierarchal manner


## MedlinePlus

- Information on over 650 diseases and conditions
- Medical encyclopedia and dictionary
- Information on prescription and nonprescription drugs
- Links to ClinicalTrials.gov
- Links to news
- Sponsored by the NIH.

**http://www.nlm.nih.gov/medlineplus/**

## References


- Rastogi et al., ***Bioinformatics: Methods & Applications***, PHI.
- Jin Xiong, ***Essential Bioinformatics***, Cambridge University Press.
- Several Online Resources….


## What's Next?

- **Data Analysis Tools**
  - DNA Sequence Analysis Tools
  - RNA analysis tools
  - Protein sequence and structure analysis tools
  - Microarray data analysis tools
  - Literature search tools