BT 3040: BIOINFORMATICS

Assignment 2

Atharva Mandar Phatak | BE21B009
Department of Biotechnology

Indian Institute of Technology
Madras

Q1) How many “Homo sapiens” sequences deposited in DDBJ? Compare with Genbank and

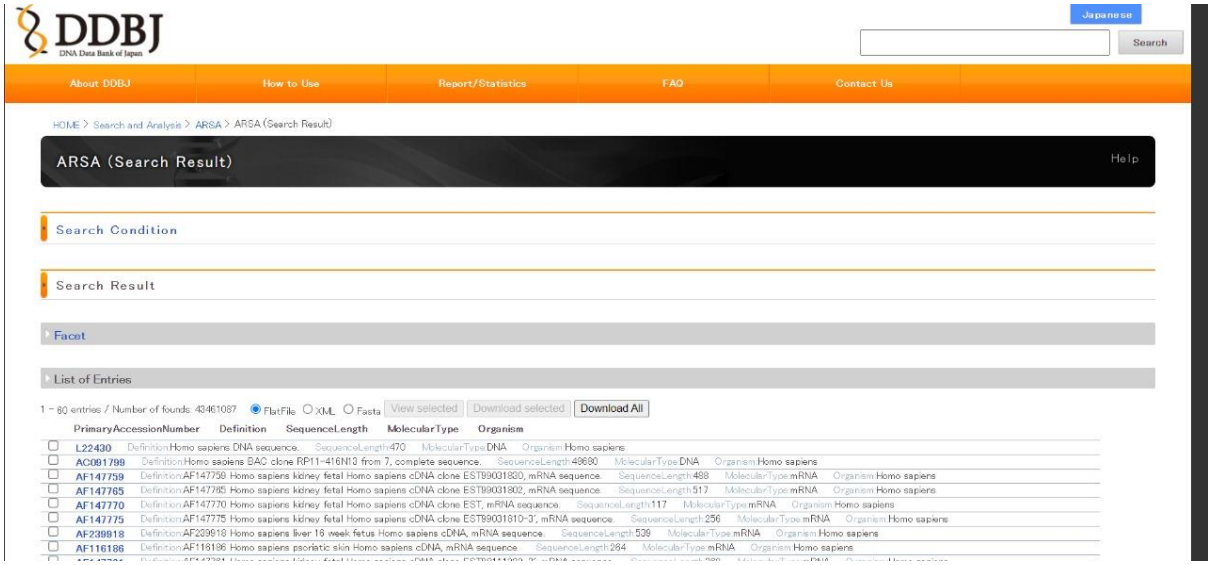
EMBL

http://www.ddbj.nig.ac.jp/

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

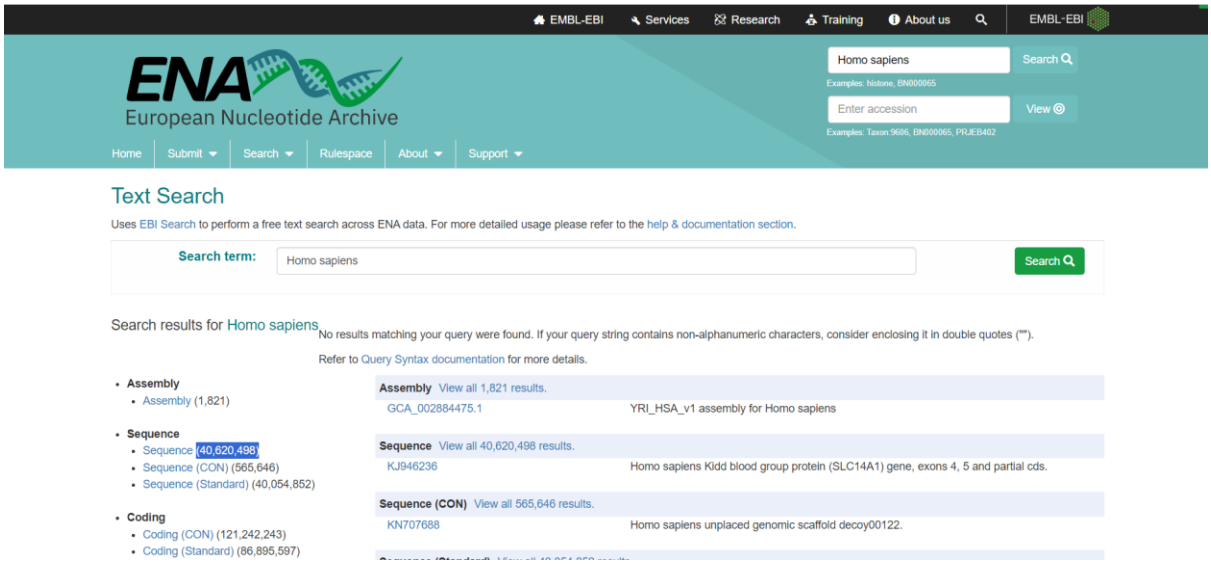
http://www.ebi.ac.uk/embl/

a) DDBJ: **43461087 sequences**



b) Gen bank: **64311072 sequences**

c) EMBL: **40620498**



Comparison (based on number of sequences) :

DDBJ	GenBank	EMBL
43461087	**64311072**	**40620498**

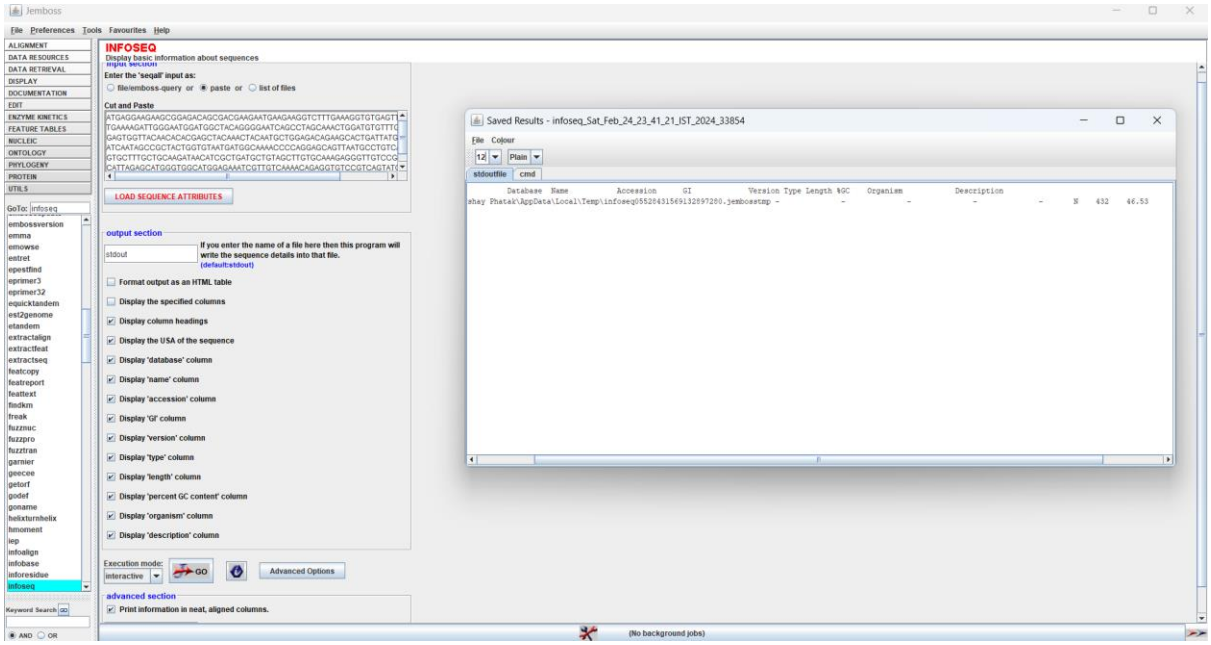
Thus GenBank has the highest number of deposited "Homo Sapiens" sequences

GenBank>DDBJ>EMBL

*Based on number of sequences

Q2) What is the GC-content of the AY330867?

GC content = **46.53%**



Q3 Compare the contents in DDBJ, Genbank and EMBL

DDBJ	GenBank	EMBL
I. LOCUS II. DEFINITION III. ACCESSION IV. VERSION V. DBLINK VI. KEYWORDS VII. SOURCE a. ORGANISM VIII. REFERENCE a. AUTHORS b. TITLE c. JOURNAL IX. COMMENT X. FEATURES XI. BASE COUNT XII. ORIGIN	I. LOCUS II. DEFINITION III. ACCESSION IV. VERSION V. KEYWORDS VI. SOURCE a) ORGANISM VII. REFERENCE a) AUTHORS b) TITLE c) JOURNAL	I. Submit entries II. Search options – i. Text search ii. Advanced search iii. Sequence search iv. Xref search v. Sequence versions III. Rulespace IV. General info a. EMBL ENA b. Research c. Industry d. Training

The contents of EMBL will be nearly identical, although the main sources of nucleoid sequences are direct submissions from individual researchers, genome sequencing projects and patent application. Another notable distinction between the databases is that GeneBank doesn't show base count while DDBJ, EMBL show it.

Q4) Get the papers about "discrimination of beta barrel membrane proteins".

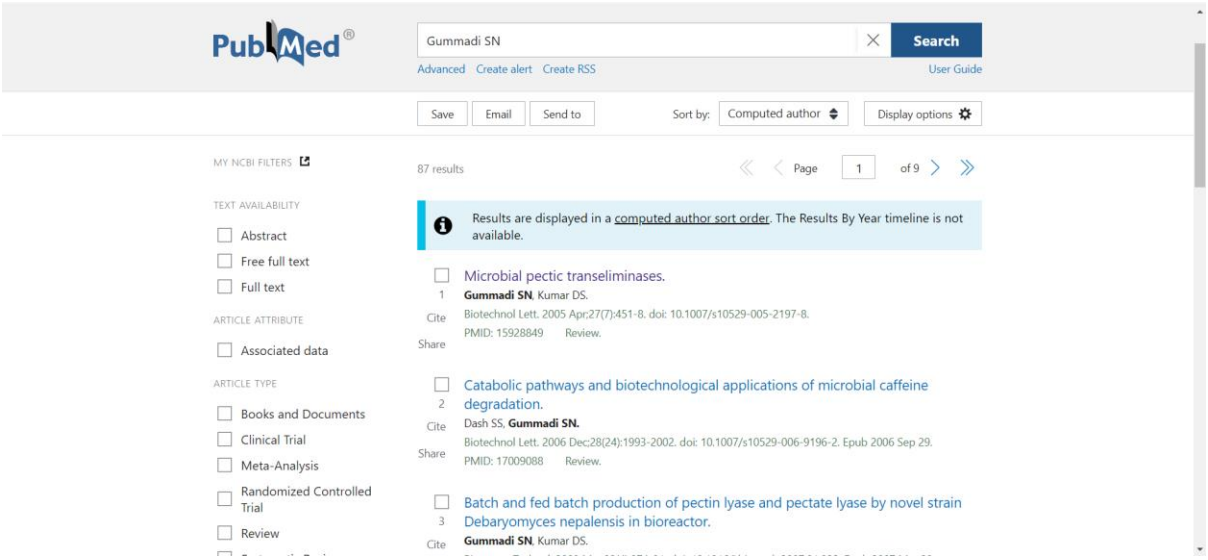
https://pubmed.ncbi.nlm.nih.gov/

These two articles (out of 53) were found by **citation matching**

a) TMBETADISC-RBF: Discrimination of beta-barrel membrane proteins using RBF networks and PSSM profiles.
Ou YY, et al. Comput Biol Chem. 2008. PMID: 18434251

b) Current developments on beta-barrel membrane proteins: sequence and structure analysis, discrimination and prediction.
Gromiha MM, et al. Curr Protein Pept Sci. 2007. PMID: 18220845 Review.

Q5) The papers published by Dr. Sathyanarayana N Gummadi Sir.

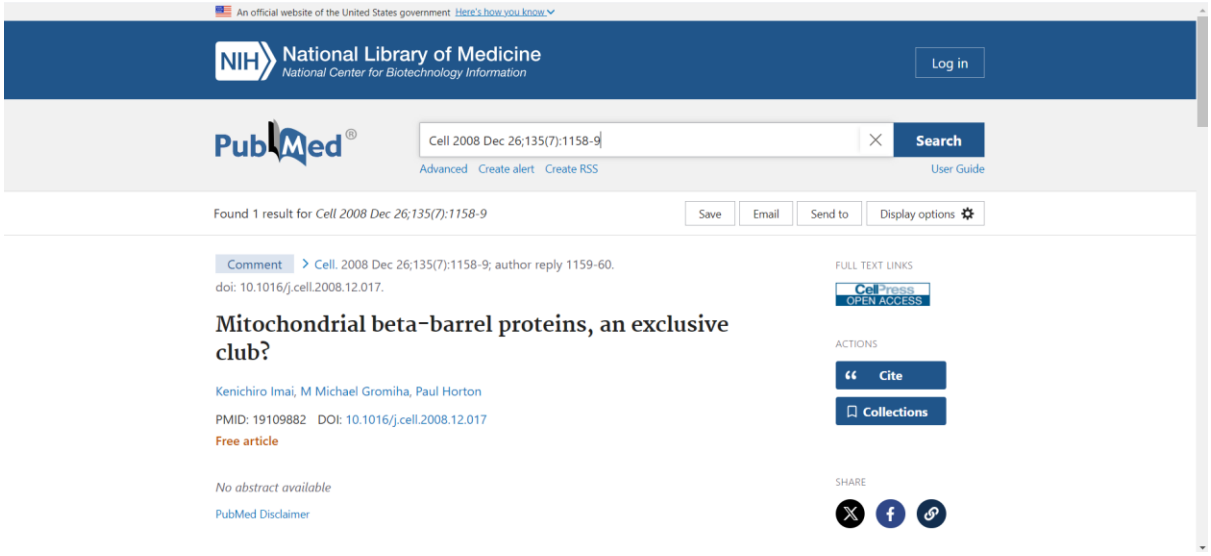


Q6) How many related articles are listed in PUBMED for the paper, Cell 2008 Dec 26;135(7):1158-9?

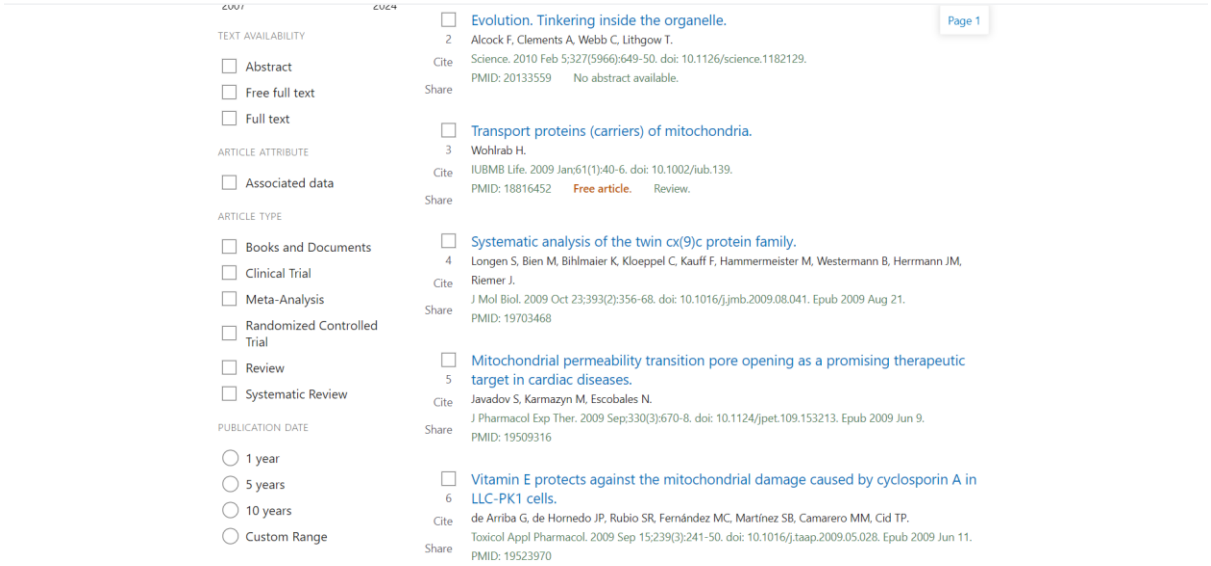
Following paper correspond to the given code.

https://pubmed.ncbi.nlm.nih.gov/19109882/

Authors: Kenichiro Imai, M Michael Gromiha, Paul Horton

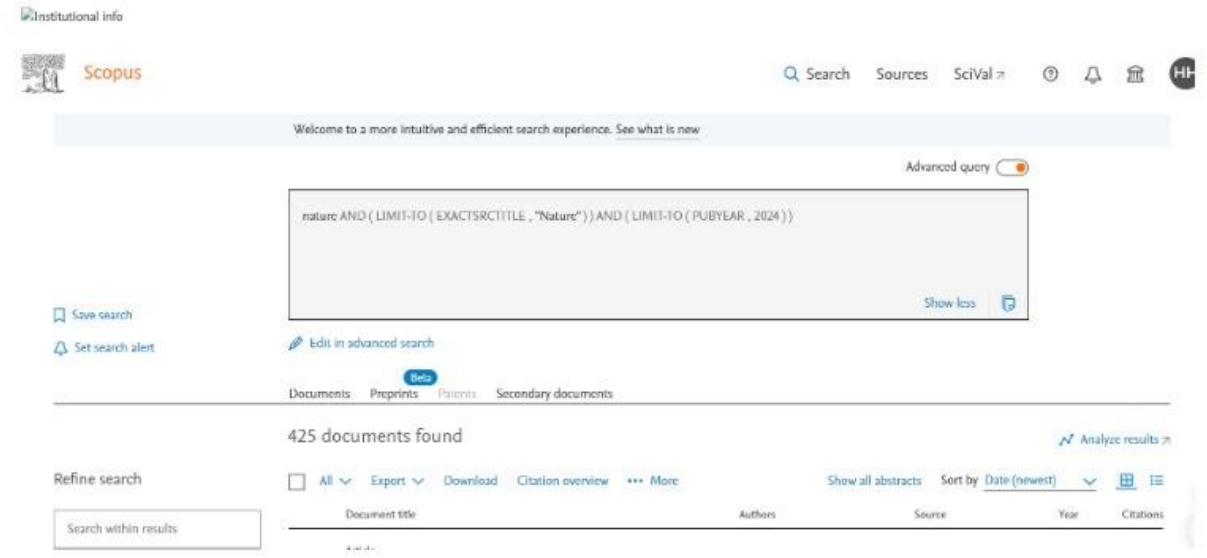


On scrolling down to the 'Similar Articles' section, total of **27** articles re found. The screenshot shows the **top 5** similar articles.

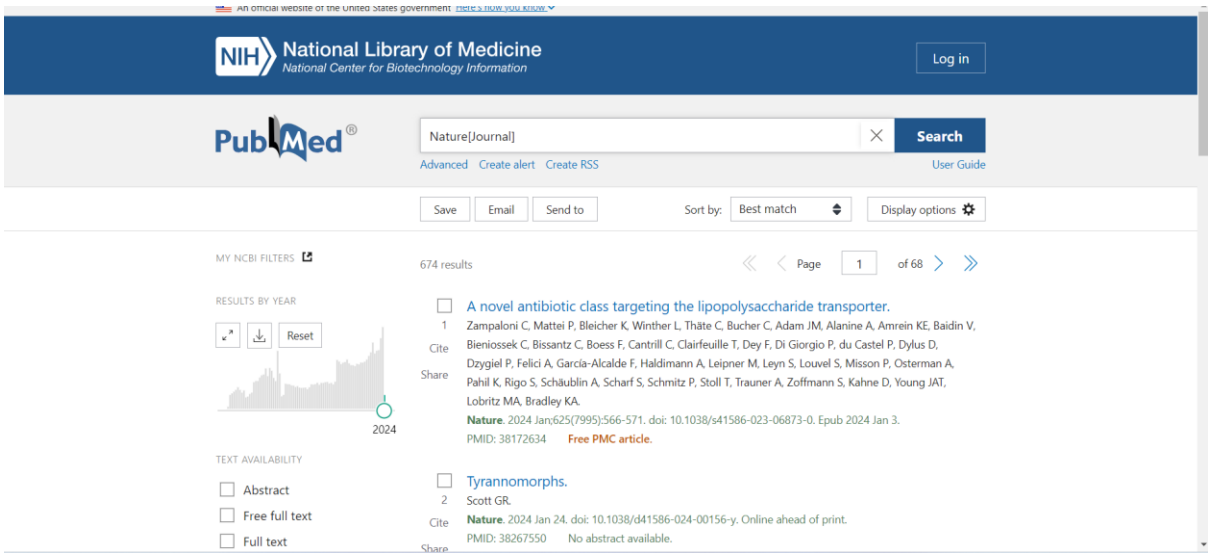


Q7) List the papers published in the journal "Nature" for the year 2024. Check the list in SCOPUS and PUBMED

Total of articles have been published in the year 2024 till now in "Nature".
a) Scopus: 425 papers

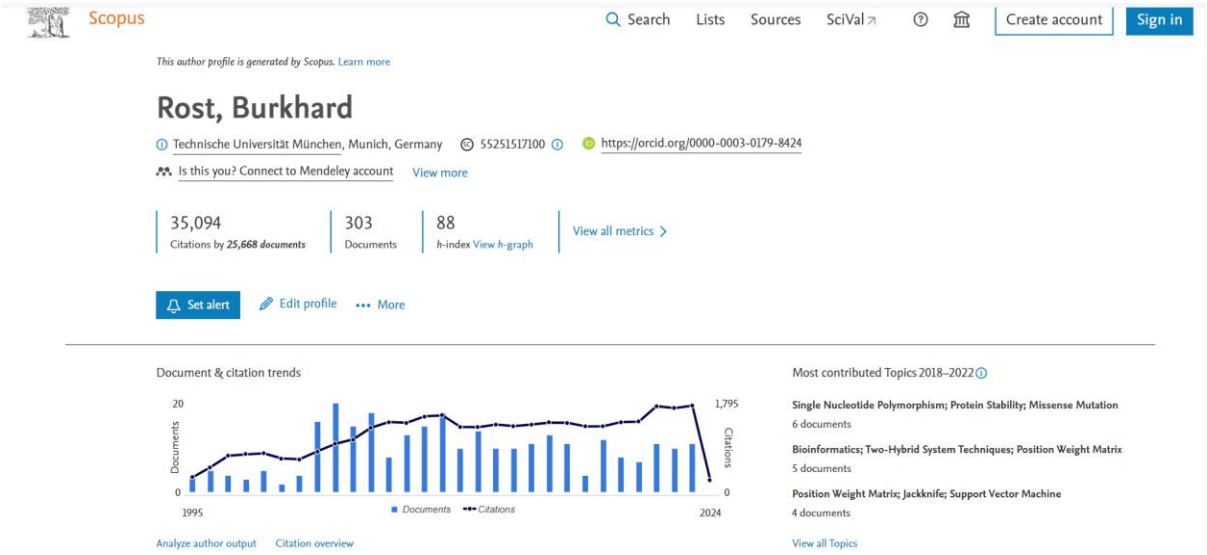


b) PubMed: 674 papers



Q8) Find the h-index and number of citations for “Burkhard Rost”.

The given screenshot shows the profile of “Burkhard Rost” on Scopus. “Burkhard Rost” has a h-index of **88.**



Q9) Find the class of the enzyme EC 1.7.2.3 and its function

http://www.brenda-enzymes.org/

1: Oxidoreductases

1.7: Acting on other nitrogenous compounds as donors

1.7.2: With a cytochrome as acceptor

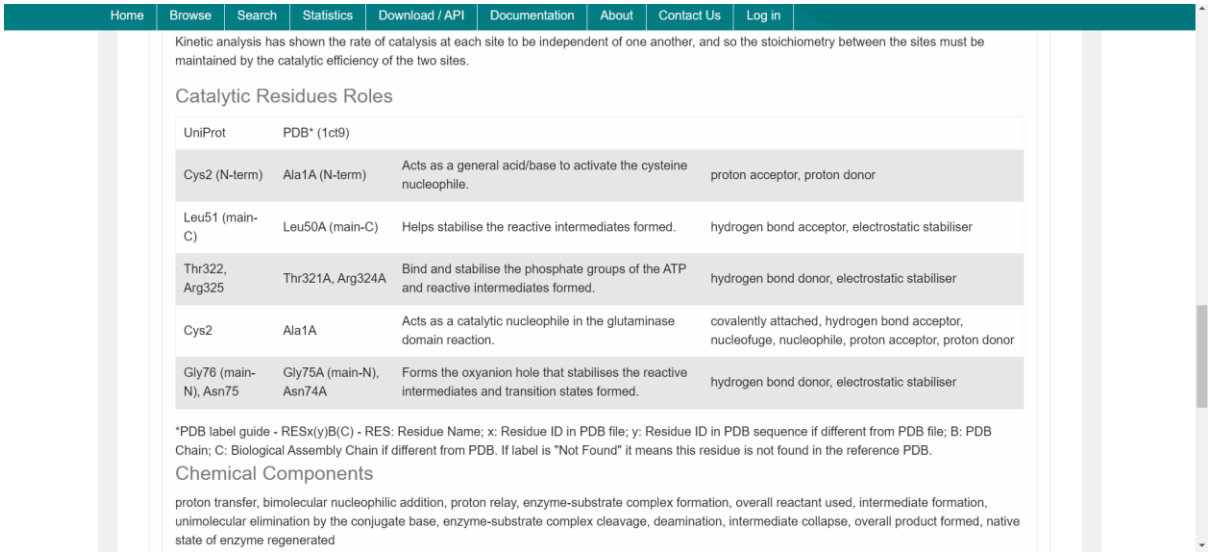
1.7.2.3: trimethylamine-N-oxide reductase

Function: It is the enzyme TMAO reductase, which reduces the cytochrome TorC . Also reduces dimethyl sulfoxide to dimethyl sulfide.

Q10) Find the catalytic site residues in Asparagine synthetase
Hint: Find the EC number and search in Catalytic site atlas
https://www.ebi.ac.uk/thornton-srv/m-csa/

The EC number of Asparagine Synthetase is **6.3.5.4**

The Catalytic Site Residues in Asparagine Synthetase as given in Catalytic Site atlas are.



Q11) Find the scientific name, the taxonomy ID and the number of chromosomes for the following organisms.
http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Root
Organisms: Human, Cat, Dog, domestic guinea pig, and Thale cress

Sr. No	Common Name	Scientific Name	Taxonomy ID	No. of Chromosomes (Total i.e 2n=)
1.	Human	*Homo sapiens* Linnaeus, 1758	9606	46
2.	Cat	*Felis catus* Linnaeus, 1758	9685	38
3.	Dog	*Canis lupus familiaris* Linnaeus, 1758	9615	78
4.	Domestic Guinea Pig	*Cavia porcellus*	10141	64
5.	Thale Cress	*Arabidopsis thaliana* (L.) Heynh., 1842	3702	10

Q12) What are NCBI E-utilities? Give the syntax for fetching a record in FASTA format using E-utilities. http://www.ncbi.nlm.nih.gov/books/NBK25500

The Entrez Programming Utilities (E-utilities) are a set of nine server-side programs that provide a stable interface into the Entrez query and database system at the National Center for Biotechnology Information (NCBI). The E-utilities use a fixed URL syntax that translates a standard set of input parameters into the values necessary for various NCBI software components to search for and retrieve the requested data. The E-utilities are therefore the structured interface to the Entrez system, which currently includes 38 databases covering a variety of biomedical data, including nucleotide and protein sequences, gene records, three-dimensional molecular structures, and the biomedical literature

Base URL

https://eutils.ncbi.nlm.nih.gov/entrez/eutils/einfo.fcgi

Syntax for fetching a record in FASTA format:

Downloading Full Records Go to:

Basic Downloading

```
efetch.fcgi?db=<database>&id=<uid_list>&rettype=<retrieval_type>
&retmode=<retrieval_mode>
```

Input: List of UIDs (&id); Entrez database (&db); Retrieval type (&rettype); Retrieval mode (&retmode)

Output: Formatted data records as specified

Example: Download nuccore GIs 34577062 and 24475906 in FASTA format

https://eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi?db=nuccore&id=34577062,24475906&rettype=fasta&retmode=text

Q13) List two databases under each of the following category. a. Protein properties, b. Small molecules (Structure related), c. Cancer gene databases Hint: Use Nucleic Acids Research (NAR) – 'database category list' https://www.oxfordjournals.org/our_journals/nar/database/c/

Two databases under the given category are as follows:

1.	**Protein Properties**	AAindex
		TOPPR
2.	**Small molecule (Structure related)**	BitterDB
		SuperToxic
3.	**Cancer Gene Database**	ArrayMap
		UMD-BRCA1/BRCA2 databases