Databases & tools for Biochemistry, Molecular Biology, Biology, Chemistry, etc.

(a non-exhaustive list of some of the main sources of data, analysis tools, and other tools I've found useful)

Bri Bibel (the bumbling biochemist); updated 8/6/26
Blog version: https://bit.ly/databases_guide
YouTube playlist: https://www.youtube.com/playlist?list=PLUWsCDtjESrGkBl0waJHJVYZk6rZC6LoJ

Main go-tos which can serve as launch pads, providing links to take you to other more specialized sites:

- Protein stuff: **UniProt** https://www.uniprot.org/
- Macromolecular structures: **PDB** https://www.rcsb.org/
- Nucleic acids: **NCBI Nucleotide** (which contains GenBank, RefSeq, etc.) https://www.ncbi.nlm.nih.gov/nucleotide/ **, BLAST** https://blast.ncbi.nlm.nih.gov/Blast.cgi
- Genome-level stuff: **Ensembl** https://uswest.ensembl.org/index.html
- Chemicals: **PubChem** https://pubchem.ncbi.nlm.nih.gov/, **ChemSpider** http://www.chemspider.com/
- Random stats (concentrations, sizes, rates, etc.): **BioNumbers: The Database of Useful Biological Numbers:** it looks for published data on your query https://bionumbers.hms.harvard.edu/search.aspx
    - They have a cheat sheet with key numbers: https://bionumbers.hms.harvard.edu/keynumbers.aspx

Other things

- Papers: **PubMed** https://pubmed.ncbi.nlm.nih.gov/ and **PubMed Central (PMC)** (free to read articles): https://pmc.ncbi.nlm.nih.gov/**, Google Scholar** https://scholar.google.com/**, bioRxiv** (preprints) https://www.biorxiv.org/
- Free books, book chapters, and other documents: **NCBI Bookshelf** https://www.ncbi.nlm.nih.gov/books
- Free code: **bio.code** (curated database with information about and links to lots of different software programs), **GitHub** https://github.com/ **, Bioconductor** (R scripts) https://www.bioconductor.org/ **, Galaxy** (web-based server with programs for genomics, etc.) https://usegalaxy.org/ , **CRAN** (R packages) https://cran.r-project.org/, **Python Package Index (PyPI**) https://pypi.org/ & **Anaconda Package Repository** (Python packages) https://anaconda.org/anaconda/repo

Some more specialized ones…

Proteins

<u>Protein databases</u>

- **UniProt:** basics (functions, length, sequence(s), isoforms, structures, interactions, etc.: lots of links to more detailed databases for each) https://www.uniprot.org/
    - Consists of:
        - **UniProtKB** (annotated entries, with reviewed entries in UniProtKB/Swiss-Prot and unreviewed entries in UniProtKB/TrEMBL)
        - **UniRef** (data is clustered by % sequence identity (100, 90, or 50), then each cluster is represented by a reference entry for efficient searching, etc.)
        - **UniParc** (archives for all non-redundant protein sequence data)
    - More about it here: https://bit.ly/uniprotprotparam & YouTube: https://youtu.be/f75f6QCe1gA
- **Human Protein Atlas**: mass spec, antibody evidence, mRNA-seq, etc. showing where different proteins are expressed in humans, and even within cells https://www.proteinatlas.org/
- **Human Proteoform Atlas:** mass spectrometry data for what forms of what proteins are expressed when and where http://human-proteoform-atlas.org/
    - More here: https://thebumblingbiochemist.com/365-days-of-science/protein-isoforms/
- **ExplorEnz:** official IUBMB info about enzymes and their classification https://www.enzyme-database.org/
    - More about it here: https://bit.ly/ec_numbers & YouTube: https://youtu.be/8yO1XEzoVIE

- **BRENDA:** additional information about enzymes w/links to other sites https://www.brenda-enzymes.org/
- **M-CSA** (Mechanism and Catalytic Site Atlas): info about enzyme mechanisms https://www.ebi.ac.uk/thornton-srv/m-csa/

Protein analysis tools

- **Expasy ProtParam**: protein stats (amino acid composition (e.g. # of each amino acid, isoelectric point (pI) (for predicting overall charge at different pHs), extinction coefficient (for getting concentration from UV), etc.) can also use for custom sequences you copy and paste: great for recombinant expression constructs https://web.expasy.org/protparam/
    - More about it here: https://bit.ly/uniprotprotparam & YouTube: https://youtu.be/taVHOa7XnHg
- **AlUpred:** for predicting intrinsically disordered regions of proteins https://aiupred.elte.hu/
    - More here: https://thebumblingbiochemist.com/365-days-of-science/idrs/
- **PSIPRED:** this will do things like predict secondary structure, domains, & disordered regions for proteins: http://bioinf.cs.ucl.ac.uk/psipred/
- **PhosphoSitePlus:** lets you find information about the post-translational modifications of a protein of interest. As the name suggests, it tells you about phosphorylation, but also things like acetylation, ubiquitinylation, & other modifications. Info includes strength of the evidence, putative suspects (modifying enzymes) etc. https://www.phosphosite.org/homeAction.action
- **H++:** Free web-based tool that takes a pdb file of a protein and predicts the protonation state of each amino acid residue at a pH of your choosing http://newbiophysics.cs.vt.edu/H++/index.php
    - More about it here: https://bit.ly/hplusplus
- **MPI Bioinformatics Toolkit:** this has lots of tools for structural prediction, homology finding, etc. https://toolkit.tuebingen.mpg.de/

Protein comparison tools

- If you want to **find proteins that are similar**:
    - *In sequence:*
        - **BLAST (specifically blastp)**: This searches protein databases for protein sequences. and takes into account both sequence identity (are the amino acids in the sequences identical at a given location) and similarity (are the amino acids in the sequences biochemically similar at a given location)
            - You can access it directly or through UniProt ("Tools" → "BLAST") https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome
    - *In structure:*
        - **Foldseek**: It compares structures against one another to find similar ones. What's even cooler is that it searches both experimentally-determined structures (housed in the PDB) and AI-predicted (AlphaFold Protein Structure DataBase (AFDB)) structures.
            - You can access the web version of it here: https://search.foldseek.com/search
            - Or the open-access code to run it in command line is here: https://github.com/steineggerlab/foldseek
            - It's also integrated into the AlphaFold database so you can get results there too https://alphafold.ebi.ac.uk/
        - **Foldseek multimer:** Goes beyond a single chain – it searches for complexes with similar structures https://search.foldseek.com/multimer
        - **PDB Advanced Search Query Builder** https://www.rcsb.org/search/advanced
            - More here: https://youtu.be/iSM6orTve-Y
        - **ENDscript** https://endscript.ibcp.fr/ESPript/ENDscript/index.php
            - This will find sequences to align and also get their PDB codes and structural information.

- If you're looking to create and/or visualize (interactively or for figures) **protein *sequence* alignments**:
    - For **creating sequence alignments:**
        - **Clustal Omega:** https://www.ebi.ac.uk/jdispatcher/msa/clustalo

        - You can also access it through the “Tools” → “Align” button in UniProt: https://www.uniprot.org/
    - For **visualizing sequence alignments interactively**:
        - **JalView**JS (web version) or JalView desktop version: https://www.jalview.org/jalview-js/JalviewJS/
        - For quickly comparing sequences in a clustal alignment and finding what number in one sequence corresponds to what number in another sequence, etc. here’s a simple Jupyter/GoogleColab notebook: https://github.com/bribibel/clustal_comparer/blob/ab4cd7391b9add2857e20798d2da60c2f5caacfd/clustal_alignment_comparer.ipynb
    - For **making nice pretty sequence alignment figures**, including with overlying secondary structural information, etc.:
        - **ESPript** https://espript.ibcp.fr/ESPript/ESPript/index.php
    - More here: https://bit.ly/proteinalignments

- If you’re looking to create and visualize **3D protein structural alignments**:
    - **RCSB PDB Pairwise Structure Alignment Tool** https://www.rcsb.org/alignment
        - You can choose from a variety of alignment methods based on how similar the proteins &/or their structures are. Choose a rigid method to directly superimpose the structures without altering them (good if very similar) or a flexible method (which breaks the structure up and aligns parts) for ones with large structural differences.
        - This will also allow you to download mmCIF files of them overlaid.
        - More here: https://youtu.be/MOBMBuAIAKo
    - **FoldMason MSTA:** Unlike a pairwise alignment tool, FoldMason MSTA does Multiple Structure Alignment, finding the best alignment for a group of sequences, rather than comparing each structure to the same reference structure https://search.foldseek.com/foldmason

- More on tools for working with proteins: https://thebumblingbiochemist.com/365-days-of-science/proteintools/

Nucleic acids

Nucleic acid sequence databases

- **NCBI nucleotide** (which contains GenBank, RefSeq, etc.) https://www.ncbi.nlm.nih.gov/nucleotide/
    - **GenBank**: “all” public sequencing data (lots of duplicates) https://www.ncbi.nlm.nih.gov/genbank/
    - **RefSeq**: more polished data w/no duplicates https://www.ncbi.nlm.nih.gov/refseq/
- **Ensembl** (from EMBL-EBI): all sorts of genomics stuff: sequences, evolution, etc. https://uswest.ensembl.org/Homo_sapiens/Info/Index
- **miRBase: the microRNA database:** the place to go if you want to search for a microRNA (miRNA). It gives you info about the sequence as well as how confident you can be that it’s legit and not a false positive (misannotation) (look to # of reads for a good indication). Note that human miRNAs will start with “hsa-“ and then miR-… https://www.mirbase.org/

Nucleic acid sequence viewing tools

- **UCSC genome browser**: can look at lots of different data about specific areas of genomes as “tracks” you can customize https://genome.ucsc.edu/cgi-bin/hgGateway
- **Integrative Genomics Viewer (IGV)**: good for visualizing sequencing data, zooming in and out, etc.; web-based and desktop versions; can import from public databases or upload your own data https://software.broadinstitute.org/software/igv/

Tools for nucleic acid analysis, etc.

- **BLAST**: for sequence alignment and finding where sequences come from, also tools for making primers, etc. https://blast.ncbi.nlm.nih.gov/Blast.cgi

    - The NCBI has a BLAST Program Selection Guide you can look at if you want all the details https://www.ncbi.nlm.nih.gov/blast/BLAST_guide.pdf But here's the gist
        - **nucleotide blast (aka blastn):** this is for searching for/comparing nucleotide (DNA or RNA) sequences.
        - **blastx:** this is for if you want to put in "translated nucleotides" and figure out what protein they correspond to - remember "x" for "exons" or "expressed."
        - **tblastn:** this is the opposite of blastx. Here you're taking a protein sequence and trying to find genes that code for it (or similar proteins).
        - **tblastx:** this searches translated nucleotides against translated nucleotides
        - **protein blast (blastp):** this searches protein databases for protein sequences
        - **Primer-BLAST:** for designing primers that avoid off-target binding (and/or incorporate other desired features) https://www.ncbi.nlm.nih.gov/tools/primer-blast/
    - More about it here: http://bit.ly/sequencetermstools
- **ViennaRNA Web Services:** lots of tools for studying RNA - things like predicting RNA folding (e.g., RNAfold Server); binding thermodynamics & kinetics; and sequence design http://rna.tbi.univie.ac.at/
- **The Sequence Manipulation Suite:** this site has a bunch of tools, but what I've used it most for is generating the reverse-complement, the reverse, and the complement of DNA sequences: https://www.bioinformatics.org/sms/index.html
- **Expasy Translate:** this will translate a nucleic acid sequence to amino acids in the various reading frames: https://web.expasy.org/translate/
- **Biologics International Corp Codon Usage Table:** https://www.biologicscorp.com/tools/CodonUsage
- **Targetsscan:** a database of predicted target sites for miRNAs along with info about confidence, whether there's published experimental evidence, evolutionary conservation, etc. You can search a specific miRNA or miRNA family to find target genes or search a target gene to find miRNAs that target it. http://www.targetscan.org/vert_71/

Macromolecular Structures

Structure databases

- **PDB (Protein Data Bank)**: protein (and other macromolecule) structures https://www.rcsb.org/ (US-maintained site), https://www.ebi.ac.uk/pdbe/ (European-maintained site)
    - More about it here: http://bit.ly/thepdb & https://bit.ly/pdbstructures (emphasis on x-ray crystallography entries) & YouTube: https://youtu.be/klB4T0X-sVU (overview) & https://youtube.com/playlist?list=PLU1mvOopp1Ik&si=LLBBOZkQfvOX-YIe (playlist)
    - Features include **3D sequence annotation viewer**, **PDB validation reports**, **advanced search query builder** (including searching by structure or structural motif), **structure grouping**, and **structural alignment**.
- **EMDB (Electron Microscopy Data Bank):** electron microscopy structure data, validation information, 3D viewing: https://www.ebi.ac.uk/emdb/
    - More: http://bit.ly/cryoemxray & https://youtu.be/G57aBLsBgOk
- **SASB (Small Angle Scattering Biological Data Bank):** data from small angle x-ray scattering (SAXS) and small angle neutron scattering experiments https://www.sasbdb.org/
- **AlphaFold Protein Structure Database (AFDB)**: contains pre-computed predicted structures of single chains of proteins https://alphafold.ebi.ac.uk/

Molecular structure viewers

- **PyMOL:** https://PyMOL.org/ (paid (incentive) version) – free for educational use & https://github.com/schrodinger/pymol-open-source (totally free (but more limited) open-source version)
    - More here: https://bit.ly/PyMOLintro & https://youtu.be/CeTTmm5DI_k & https://www.youtube.com/playlist?list=PLUWsCDtjESrG-46VDvPZfYPQyyXhZbGCN
    - Consult their wiki for help: https://pymolwiki.org/
- **ChimeraX:** https://www.cgl.ucsf.edu/chimerax/
    - Consult their wiki for help: https://www.rbvi.ucsf.edu/chimerax/tutorials.html

- Note: less powerful, but convenient, browser-based alternatives include iCN3D and Mol*
    - **iCN3D:** https://www.ncbi.nlm.nih.gov/Structure/icn3d/full.html
    - **Mol*:** https://molstar.org/
        - It has a stand-alone browser version and is also integrated into the PDB and UniProt
- Here's an OER I helped write showing how to do different basic tasks in the different software tools: Acevedo, R., & Procko, K. (Eds.). (2025). Seeing the Invisible: Learning to Teach with Biomolecular Visualization. The University of Texas at Austin. https://doi.org/10.15781/m4zd-7691

Tools for investigating structures

- **PDB Validation Reports**: you can download full reports and/or view map &/or model quality mapped onto the structure. https://www.rcsb.org/docs/general-help/assessing-the-quality-of-3d-structures
    - More here: https://thebumblingbiochemist.com/365-days-of-science/structurequality/ https://youtu.be/0AswlZBLpKw
- **PDB 3D Sequence Annotation Viewer**: view a variety of annotations mapped onto the structure https://www.rcsb.org/docs/sequence-viewers/sequence-annotations-viewer
    - More here: https://youtu.be/6zKBBkzl-4A
- **PDBSum**: Easy way to automatically generate protein topology & domain diagrams & investigate interfaces https://www.ebi.ac.uk/thornton-srv/databases/pdbsum/
    - Just upload or fetch a PDB file and it'll generate a bunch of things including: domain architecture diagram, secondary structure diagrams, topology map, diagram of and information about ligand-protein and protein-protein interactions (distances, types, etc.), information about pockets, tunnels, and channels
    - *Note: Their server is down as of this writing, but there's a stand-alone version you can download from GitHub.*
    - More here: https://youtu.be/AFmN4CKU1uE

- **3D bio notes:** you put in the PDB code for a structure, then this site integrates a ton of information about the protein from various sources and lets you see sites of mutations, etc. in 3D. Also good for a quick overview or on the go look when you don't want to open PyMOL. http://3dbionotes.cnb.csic.es/ws

Tools for experimentally determining structures (note: this is just a small portion of the tools out there!)

- **Phenix:** Great for x-ray crystallographic phasing, model building and automated refinement. http://www.phenix-online.org/ They also have some great tutorials on YouTube: https://www.youtube.com/c/phenixtutorials
- **Coot:** This is the software I use for manual refinement https://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/ This cheatsheet is a definite must! https://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/web/docs/crib-sheet.pdf
- Those are integrated with each other, along with **MolProbity** which tells you about things like clashes and awkward geometry https://molprobity.biochem.duke.edu/
    - MolProbity is also used as part of PDB Validation
- **CryoSparc:** for some of the steps of cryo-EM processing; they also have great tutorials https://cryosparc.com/

Tools for predicting structures and/or structural features, designing constructs, etc.

- **AlphaFold:** Predicts the structure of proteins, nucleic acids, and complexes. The server has more limited options than the stand-alone (GitHub) and **ColabFold** (Python notebook-based) versions, but uses the latest version of AlphaFold https://alphafoldserver.com/
    - More here: https://thebumblingbiochemist.com/365-days-of-science/interpreting-alphafold-predictions/
- **Institute for Protein Design Software** including **RFdiffusion** – can design new protein backbones (basically, the skeletons of proteins); **ProteinMPNN** – can predict sequences likely to fold into specific shapes (such as those predicted by RFdiffusion); **RoseTTAFold** – "classical" structure from sequence; **FoldIt** – crowdsourced protein folding game https://www.ipd.uw.edu/software/

- **SWISS-MODEL:** I used this for homology modeling in undergrad. It's good for when there's a solved structure of a highly similar protein to one you want to know the structure of (such as if there's a structure of the mouse one but you're interested in the human one) https://swissmodel.expasy.org/
- **HawkDock:** Models protein-protein interactions and analyzes strength of interactions at a residue level basis (for either predicted structures or already-prepared PDB files) https://cadd.zju.edu.cn/hawkdock/
- **MPI Bioinformatics Toolkit:** this has lots of tools for structural prediction, homology finding, etc. https://toolkit.tuebingen.mpg.de/
- **Crystallisation Construct Designer2 (CCD^2):** helps you design protein constructs to attempt to crystallize - good for figuring out where to make truncations & stuff (e.g. identify domain boundaries & remove predicted disordered regions at the end) https://ccd.rhpc.nki.nl/tutorial
- **CHARM-GUI**: for molecular dynamics (MD) https://www.charmm-gui.org/
    - Check out their "lecture" series of tutorials for help: https://www.charmm-gui.org/?doc=lecture

Gene Expression databases

- **Human Protein Atlas**: mass spec, antibody evidence, mRNA-seq, etc. showing where different proteins are expressed in humans, and even within cells https://www.proteinatlas.org/
- **EMBL-EBI Expression Atlas**: protein expression in multiple species https://www.ebi.ac.uk/gxa/home
- **Gene Expression Omnibus (GEO)**: datasets from high-throughput assays including microarrays, RNA-seq, etc.; people deposit their data which can be accessed through their "GEO accession numbers": look for them at the end of papers https://www.ncbi.nlm.nih.gov/geo/
- **SRA (Sequence Read Archive)**: similar to GEO, but with just high throughput sequencing data https://www.ncbi.nlm.nih.gov/sra

Chemicals

- **PubChem**: database from NIH https://pubchem.ncbi.nlm.nih.gov/
- **ChemSpider**: database from RSC (Royal Society for Chemistry http://www.chemspider.com/
- **NIST Webbook:** thermodynamic and spectroscopic data of chemicals (great for o-chem class!) https://webbook.nist.gov/
- **DrugBank:** comprehensive information on drug molecules https://go.drugbank.com/
- **ChEMBL:** literature-extracted biological activity information (has info about how molecules interact with different proteins, etc.: can search by molecule or target) https://www.ebi.ac.uk/chembl/
- **Cambridge Crystallographic Data Centre (CCDC):** crystal structures of small molecules https://www.ccdc.cam.ac.uk/structures/
- **MassBank**: mass spectrometry data https://massbank.eu/MassBank/
- **MassIve:** mass spectrometry data https://massive.ucsd.edu/ProteoSAFe/static/massive.jsp?redirect=auth

Other

- Metabolic pathways
    - **KEGG Pathway Database** https://www.genome.jp/kegg/pathway.html
- Lots of things
    - **Expasy Swiss Bioinformatics Resource Portal** https://www.expasy.org/
    - **Page on my blog with resources I've found helpful:** https://bit.ly/bumblingbiochemisttoolbox

Laboratory tools and resources

- **Promega Biomath Calculators:** they have calculators that will let you do various concentration conversions for DNA and proteins https://www.promega.com/resources/tools/biomath/?calc=dnaprotein
- **GraphPad Molarity Calculator:** they have calculators for: mass from volume & concentration; volume from mass & concentration; molarity from mass & volume; diluting stock solutions https://www.graphpad.com/quickcalcs/Molarityform/
- **Sigma Calculators & Apps:** there's a TON of them… https://www.sigmaaldrich.com/US/en/support/calculators-and-apps
- **NEBioCalculator:** good mass to moles/moles to mass converter for various molecules. I like that you can convert by length https://nebiocalculator.neb.com

- **AAT Bioquest Serial Dilution Calculator and Planner:** this helps you plan out serial dilutions. It's really helpful when you're trying to figure out how much of what concentration you need to start when you're using awkward dilution factors. You give it your starting concentration & dilution factor (e.g. 2 for a 1:2 dilution where you're halving the concentration each time) OR you give it a concentration range. Then you give it your stock concentration, desired final volume for each dilution, & # of dilutions and it works out the math for you. https://www.aatbio.com/tools/serial-dilution
- **Good Calculators Significant Figures Calculator:** it will do the calculations for you, but it also explains how to do them and offers a quiz https://goodcalculators.com/sig-fig-significant-figures-calculator/
- **Omni Error Propagation Calculator:** https://www.omnicalculator.com/statistics/error-propagation
- **Wolfram Alpha:** I haven't really used it much since undergrad, but it was super helpful especially in math and physics because they work out solutions so you learn instead of just being fed the answers. https://www.wolframalpha.com/

Laboratory protocols, guides, and tutorials

- **OpenWetWare Protocols:** this is a wiki with tons of protocols including recipes for making reagents that typically come in kits so you can DIY it. The site has other features as well, but I've only used it for the protocols. https://openwetware.org/wiki/Protocols
- **Pipette Jockey Reagents/Recipes/Protocols**: more DIY stuff https://pipettejockey.com/reverse-engineering-reagentsrecipes/
- **Cold Spring Harbor Protocols:** this has tons of protocols. Some are free for everyone, others require that you or your institution are subscribed http://cshprotocols.cshlp.org/
- **Bio-protocol Journal**: its name basically says it for itself! https://bio-protocol.org/en
- **JoVe:** this site has a bunch of experimental protocols and video demonstrations - for basic experiments as well as super technical ones (but many are paywalled). https://www.jove.com/
- **LabXchange:** this site run by Harvard and amgen hosts a variety of free educational content (and even shares some of my stuff). They have a range of content - videos, text, infographics, and, coolest of all, interactive virtual labs. Teachers can use it to build course content and pathways but students can just use it freely as well and there are a range of pre-made "clusters" which are kinda like mini-courses that combine content from multiple different collaborators. https://www.labxchange.org/explore
- **Addgene blog, especially Plasmids 101:** everything you ever wanted to know about plasmids and molecular cloning including details and comparisons of various techniques. https://info.addgene.org/plasmids-101-topic-page
- **ThermoFisher Protein Expression Handbook:** discusses various strategies for expressing proteins and is a good place to start for people wanting to get into recombinant expression https://www.thermofisher.com/us/en/home/life-science/protein-biology/protein-biology-learning-center/protein-biology-resource-library/protein-expression-handbook.html
- **Cytiva (previously GE) Principles & Methodology Handbooks** (all free to download without registering or anything although they do include product information) https://www.cytivalifesciences.com/en/us/support/handbooks
    - There are lots of good ones but the Strategies for protein purification handbook is a great place to start for people interested in purification https://cdn.cytivalifesciences.com/dmm3bwsv3/AssetStream.aspx?mediaformatid=10061&destinationid=10016&assetid=15680

Graphics

- **Vector graphics programs**
    - **Adobe Illustrator**
        - More here: https://bit.ly/adobe_illustrator_fundamentals & https://www.youtube.com/playlist?list=PLUWsCDtjESrHU5vdztBYlQ4hK3iiccSnH
    - **Inkscape** FREE https://inkscape.org/
    - More here: http://bit.ly/makinggraphics

- **Illustrator for Biological Sequences (IBS):** lets you make simple domain architecture graphics - you can enter domain start and end #s and it will illustrate them. helpful for making sure you get the scaling right! http://ibs.biocuckoo.org/
- **Draw.io**: great for making mind/concept maps, flow charts, etc. https://app.diagrams.net/
- **WikiMedia Commons:** freely usable images and graphics https://commons.wikimedia.org/wiki/Main_Page
- **bioicons** has free science vector graphics https://bioicons.com/
- A few other options I haven't played around with, which have free and paid options are **Figma**, **bioRendr**, and **Canva**

Other tools

- **Reference manager** with web browser and word processor extensions installed: Zotero, Mendeley, ReadCube, etc.
    - Zotero https://www.zotero.org/
    - Mendeley https://www.mendeley.com/reference-management/reference-manager
    - Endnote https://endnote.com/
    - ReadCube Papers https://www.digital-science.com/product/readcube/
    - More on reference managers: http://bit.ly/referencemanagementtools ; YouTube: https://youtu.be/p2G0LZThsfA
- **Clipboard manager:** to store things you copy so you can paste them even after you copied another thing
    - I use one called CopyClip
    - More here: https://youtu.be/3g1CEXyxFFY
- **Cloud storage desktop drive (Box Drive, Google Drive, etc.)** for backing up and quickly accessing cloud files just as if they were on your hard drive
    - More here: https://youtube.com/shorts/Rwj0PBDSCrY
- **PubPeer browser extension** to see if articles you visit or articles a visited article cites have been retracted or have had questions raised about them (usually, but not always, bad) https://pubpeer.com/
- **Unpaywall browser extension** to see if free versions of pay-walled articles are available when you visit an article's page https://unpaywall.org/
- **scite_:** I use this browser extension that generates a sidebar which tells you the number of positive, neutral, and negative/questioning citations. When you click on it you get a report that shows you snippets of where it's cited and links to see those full articles. In the free version you can't filter the results or anything though. I find it's really helpful in giving me a better idea of the wider context of any one work and how others in the field interpret the results. https://scite.ai/
- **RSS Reader** to stay up to date on new articles
    - **NewsBlur** https://newsblur.com/
    - **Feedly** https://feedly.com/
    - **The Old Reader** https://theoldreader.com/
    - **Inoreader** https://www.inoreader.com/
- **GraphPad Prism:** this isn't free, but if you have access to it, it's a great tool for graphing, modeling, and statistical analysis, of numerical data https://www.graphpad.com/

Resources page with a downloadable version of this, as well as a guide to my resources and others: https://thebumblingbiochemist.com/lets-talk-science/resources/

Page with these and other resources I've found helpful: https://bit.ly/bumblingbiochemisttoolbox

Tools for studying proteins: https://thebumblingbiochemist.com/365-days-of-science/proteintools/

Structural biology resources: https://bit.ly/structural_biology