

Quick Bio Review

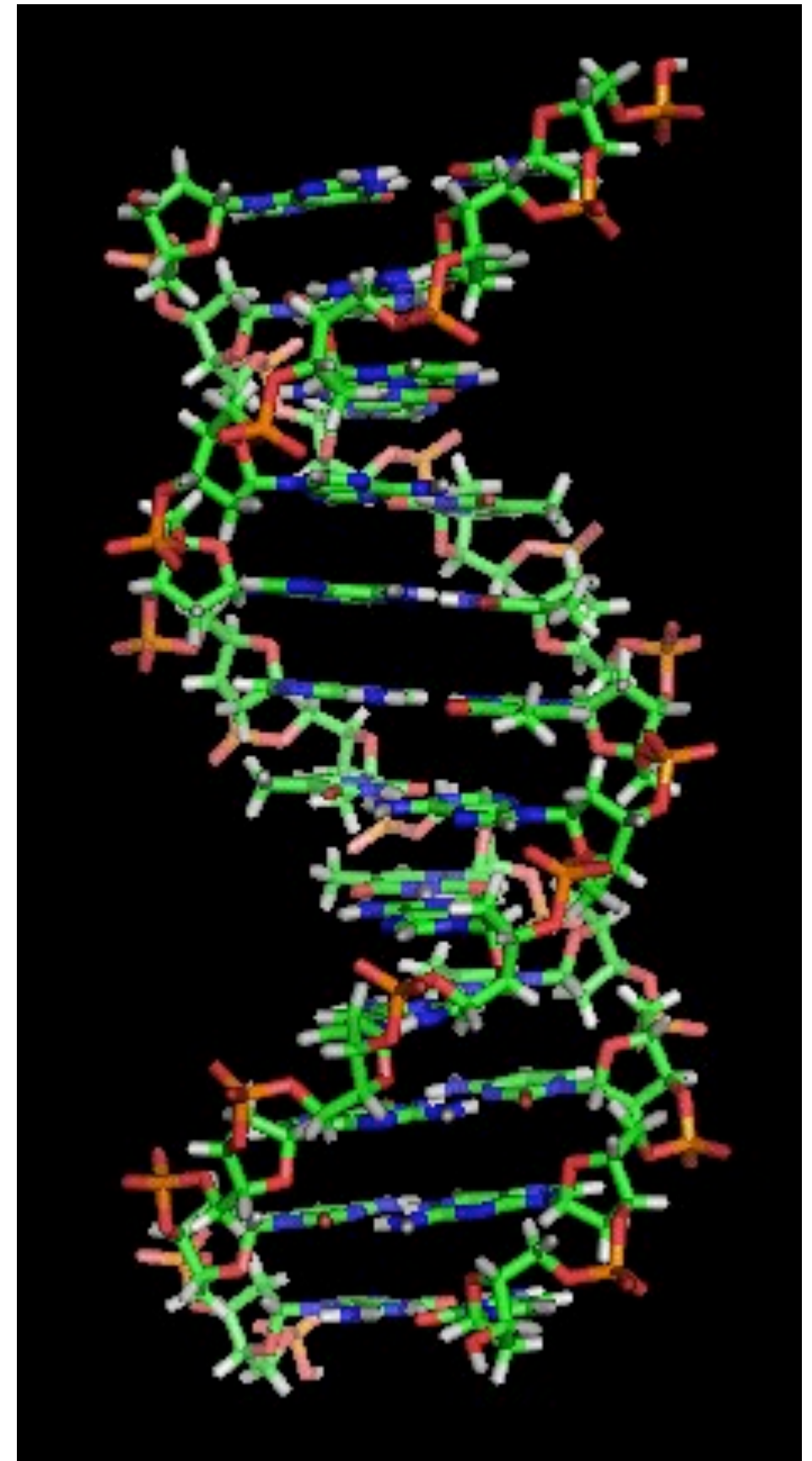
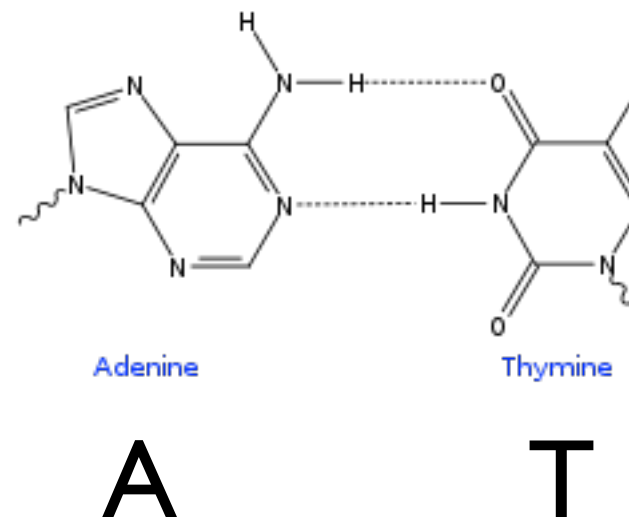
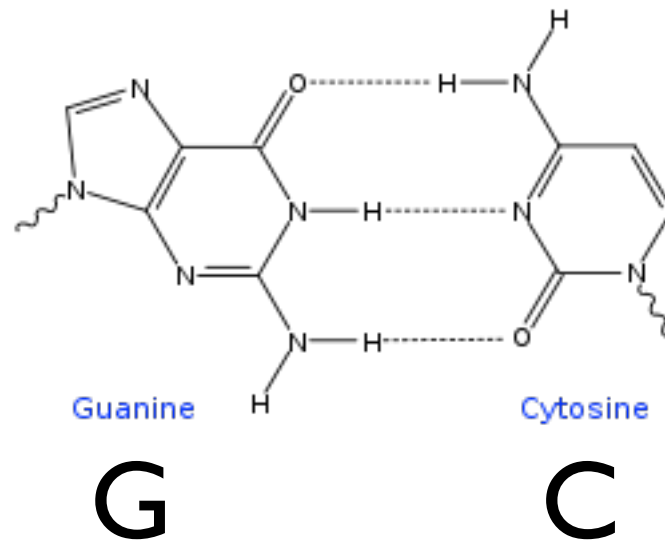
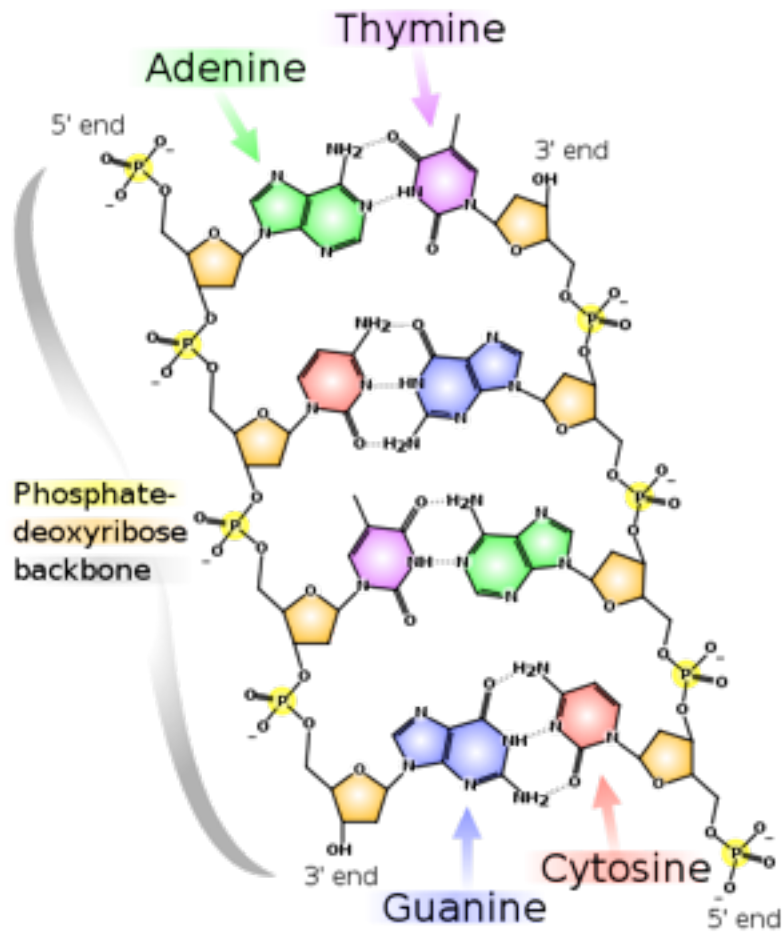
CMSC 423

E. coli

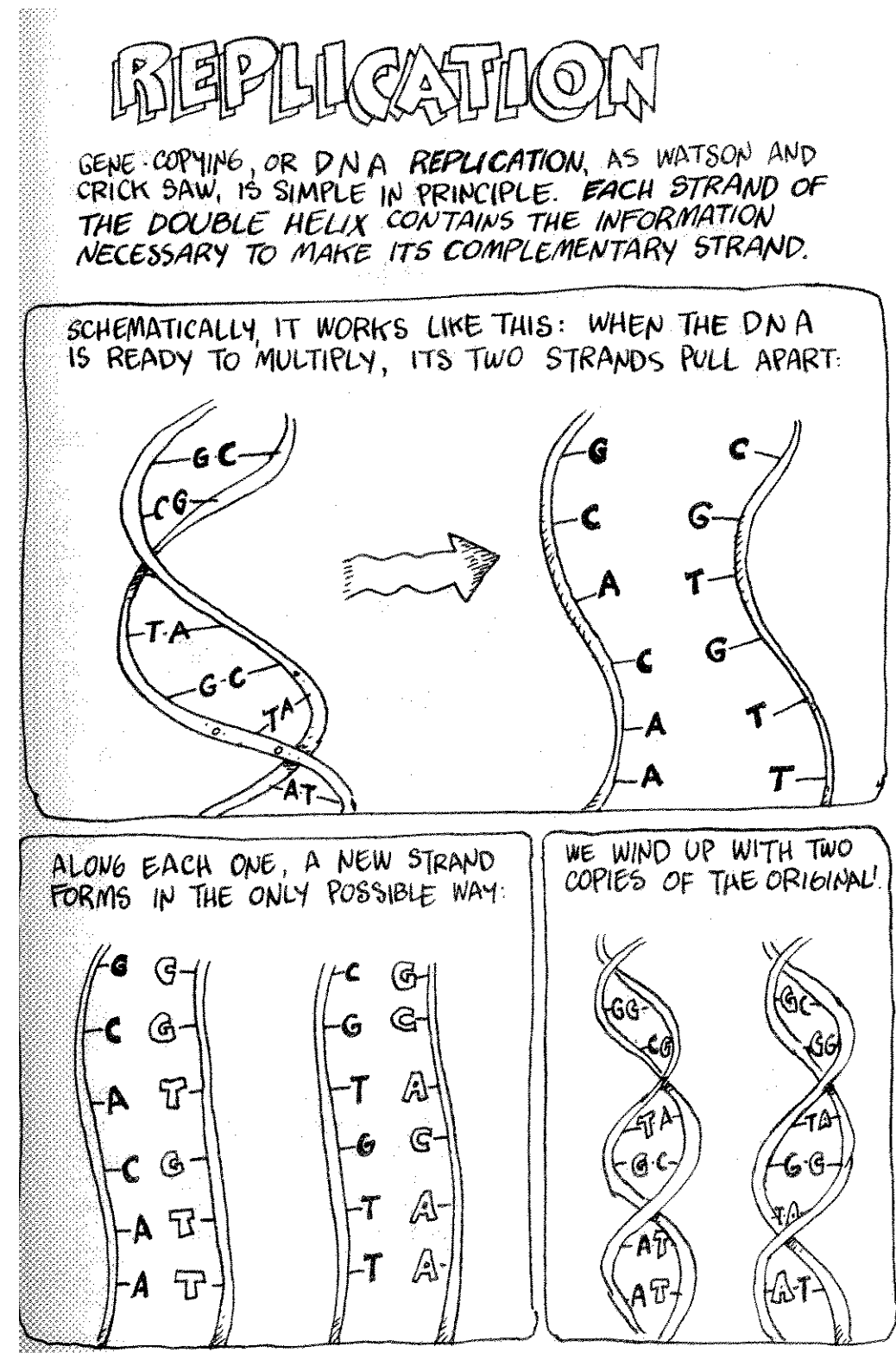
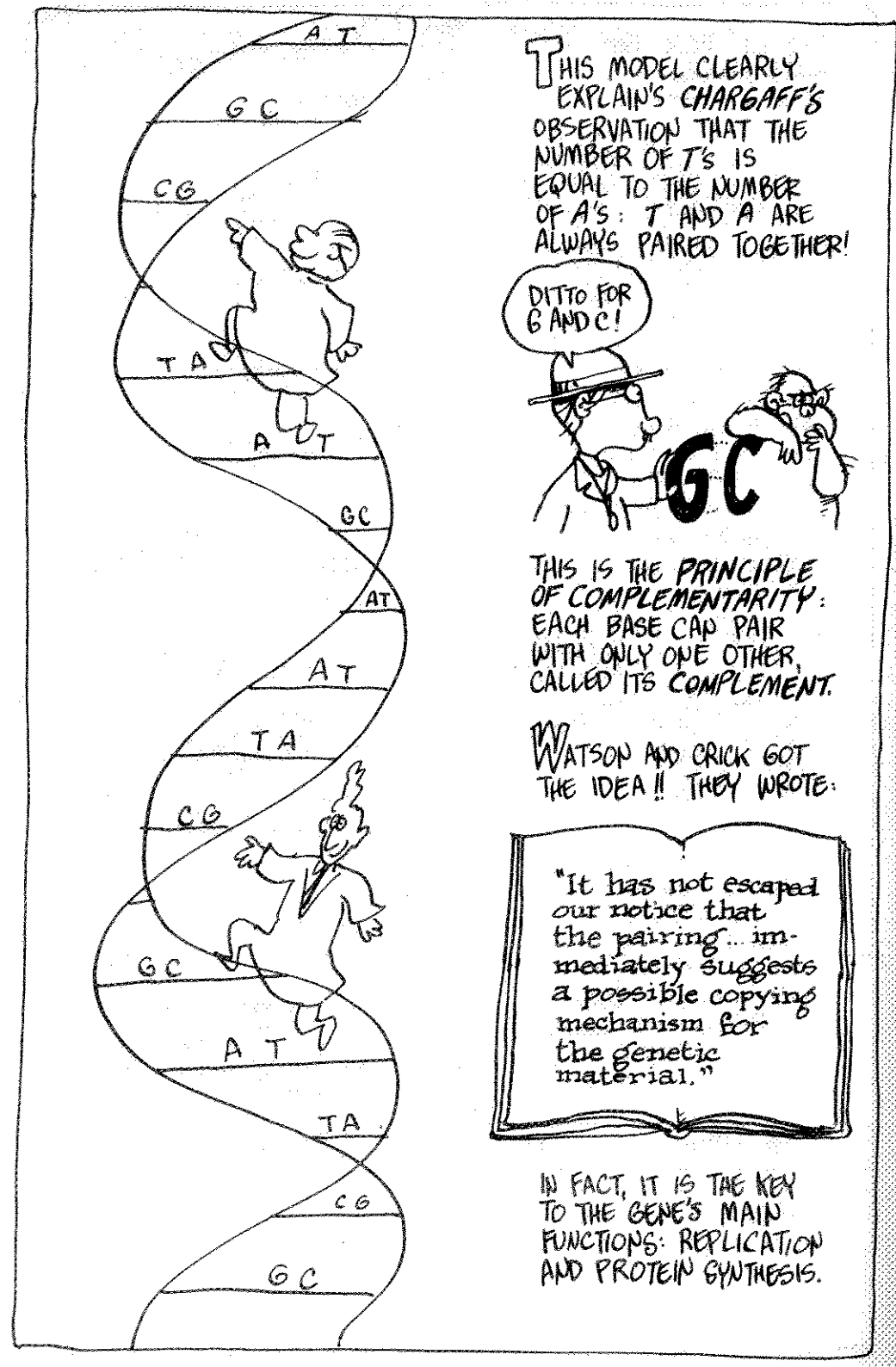
- E. coli is an example of a bacterium.

	% total dry weight	
DNA	3.1	} Algorithms are used to understand these important components.
RNA	20.5	
Protein	55.0	
Lipid	9.1	

DNA



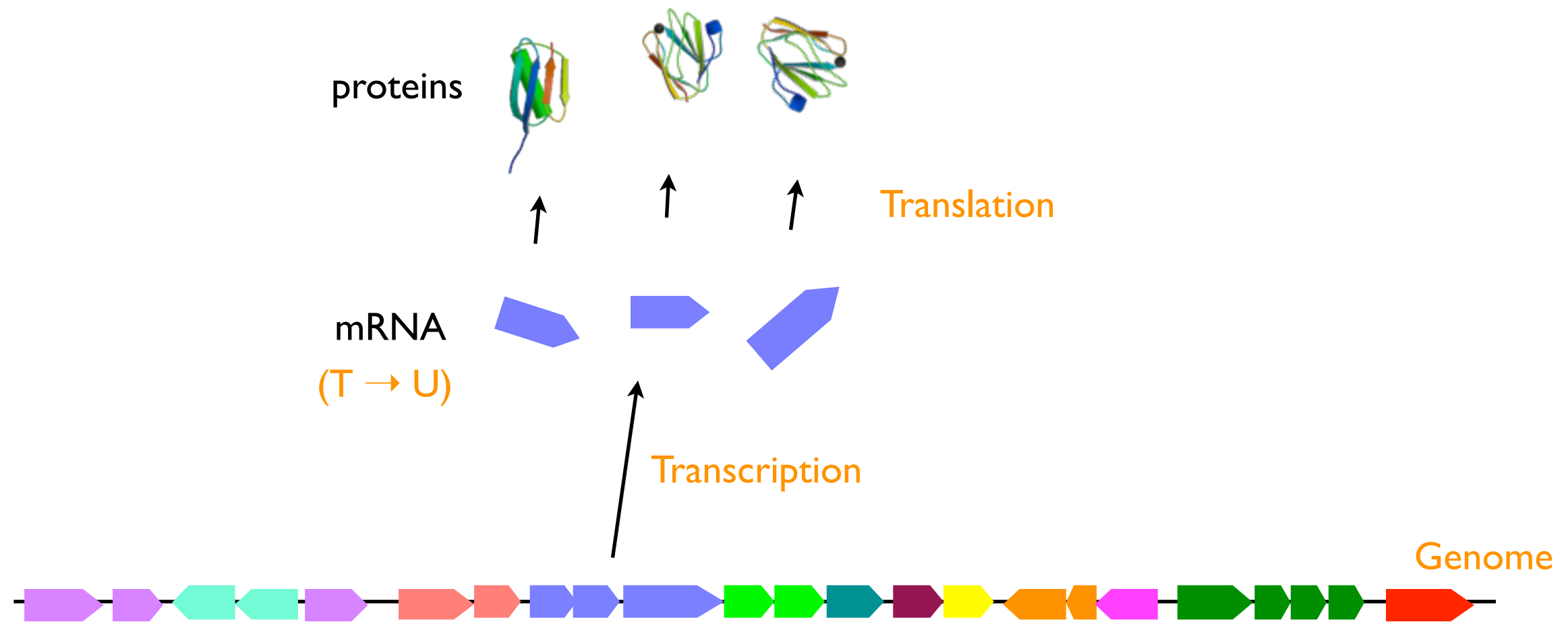
DNA Replication



Most Genes Encode For Proteins

- Make up structural components of the cell.
- Pass signals from environment to the cell and between locations within the cell.
- Act as *enzymes*: catalyze reactions.
- Work as molecular motors
- Many other functions...


"Central Dogma" of Biology



DNA =

- double-stranded, linear molecule
- each strand is string over $\{A, C, G, T\}$

- strands are complements of each other ($A \leftrightarrow T$; $C \leftrightarrow G$)

- substrings encode for genes 
most of which encode for proteins



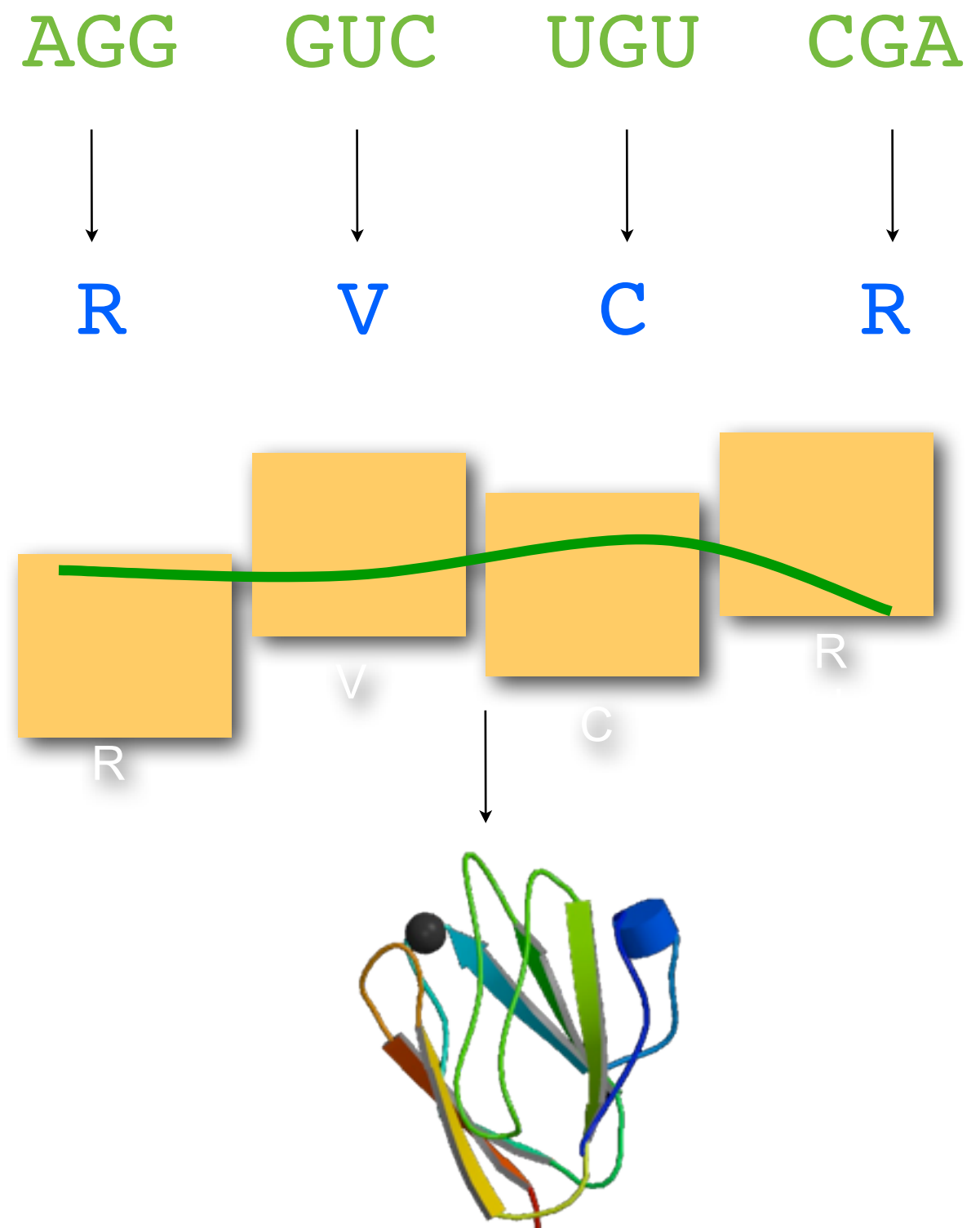
Proteins

mRNA
 $\Sigma = \{A, C, G, U\}$
↓
protein
 $|\Sigma| = 20$ amino acids

Amino acids with flexible
side chains strung
together on a backbone

Proteins are the Building
Blocks of Life

Their shape is instrumental in
determining their function.



Another View of the Genetic Code

- There are 20 different amino acids & 64 different codons.
- Lots of different ways to encode for each amino acid.
- The 3rd base is typically less important for determining the amino acid
- Three different “stop” codons that signal the end of the gene
- Start codons differ depending on the organisms, but AUG is often used.

		2nd base							
		U		C		A		G	
1st base	U	UUU	(Phe/F) Phenylalanine	UCU	(Ser/S) Serine	UAU	(Tyr/Y) Tyrosine	UGU	(Cys/C) Cysteine
		UUC	(Phe/F) Phenylalanine	UCC	(Ser/S) Serine	UAC	(Tyr/Y) Tyrosine	UGC	(Cys/C) Cysteine
		UUA	(Leu/L) Leucine	UCA	(Ser/S) Serine	UAA	Ochre Stop	UGA	Opal Stop
		UUG	(Leu/L) Leucine	UCG	(Ser/S) Serine	UAG	Amber Stop	UGG	(Trp/W) Tryptophan
	C	CUU	(Leu/L) Leucine	CCU	(Pro/P) Proline	CAU	(His/H) Histidine	CGU	(Arg/R) Arginine
		CUC	(Leu/L) Leucine	CCC	(Pro/P) Proline	CAC	(His/H) Histidine	CGC	(Arg/R) Arginine
		CUA	(Leu/L) Leucine	CCA	(Pro/P) Proline	CAA	(Gln/Q) Glutamine	CGA	(Arg/R) Arginine
		CUG	(Leu/L) Leucine	CCG	(Pro/P) Proline	CAG	(Gln/Q) Glutamine	CGG	(Arg/R) Arginine
	A	AUU	(Ile/I) Isoleucine	ACU	(Thr/T) Threonine	AAU	(Asn/N) Asparagine	AGU	(Ser/S) Serine
		AUC	(Ile/I) Isoleucine	ACC	(Thr/T) Threonine	AAC	(Asn/N) Asparagine	AGC	(Ser/S) Serine
		AUA	(Ile/I) Isoleucine	ACA	(Thr/T) Threonine	AAA	(Lys/K) Lysine	AGA	(Arg/R) Arginine
		AUG [A]	(Met/M) Methionine	ACG	(Thr/T) Threonine	AAG	(Lys/K) Lysine	AGG	(Arg/R) Arginine
	G	GUU	(Val/V) Valine	GCU	(Ala/A) Alanine	GAU	(Asp/D) Aspartic acid	GGU	(Gly/G) Glycine
		GUC	(Val/V) Valine	GCC	(Ala/A) Alanine	GAC	(Asp/D) Aspartic acid	GGC	(Gly/G) Glycine
		GUA	(Val/V) Valine	GCA	(Ala/A) Alanine	GAA	(Glu/E) Glutamic acid	GGA	(Gly/G) Glycine
		GUG	(Val/V) Valine	GCG	(Ala/A) Alanine	GAG	(Glu/E) Glutamic acid	GGG	(Gly/G) Glycine

Databases of Biological Data

- General Repositories
 - **GenBank** - USA
 - **EMBL** - Europe: <http://www.ebi.ac.uk/embl/>
- Specialized by data type
 - **NCBI Trace Archive** - raw reads from sequencing machines
 - **SwissProt** - curated protein information: <http://www.expasy.org>
 - **KEGG** - metabolic pathways: <http://www.genome.jp/kegg/>
 - **Gene Expression Omnibus (GEO)** - gene expression
 - **PDB** - protein structures
- Specialized by organism
 - **ZFIN** - zebrafish
 - **SGD** - yeast
 - **WormBase** - c. elegans
 - **FlyBase** - fruit fly

NCBI

GenBank:
central
repository
for genome
sequences

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DraftAssembly

Bacteria
Chromosome
Plasmid
DraftAssembly

Eukaryota
Chromosome
Plasmid
Organelles

Viruses
Phages

Viroids

All Plasmids

The Genome database provides views for a variety of genomes, complete chromosomes, sequence maps with contigs, and integrated genetic and physical maps. The database is organized in six major organism groups: [Archaea](#), [Bacteria](#), [Eukaryotae](#), [Viruses](#), [Viroids](#), and [Plasmids](#) and includes complete chromosomes, organelles and plasmids as well as draft genome assemblies.

Total species (6547)

Organism Group	Count
Viruses	2411
Eukaryota	2445
Bacteria	1512
Archaea	99
Viroids	41
Plasmids	39

Total records (12340)

Organism Group	Count
Viruses	3653
Eukaryota	1314 chromosomes 2438 organelles 43 plasmids
Bacteria	2440 chromosomes 2176 plasmids
Archaea	100 chromosomes 95 plasmids
Viroids	41
Plasmids	40

Genome Sequencing Milestone Reached! There are now 1000 complete Prokaryotic Genomes available in Entrez Genome. See the full list of [complete bacterial and archaeal genomes](#). [Microbial Resources](#) are available for search, retrieval, and analysis of all genomes.

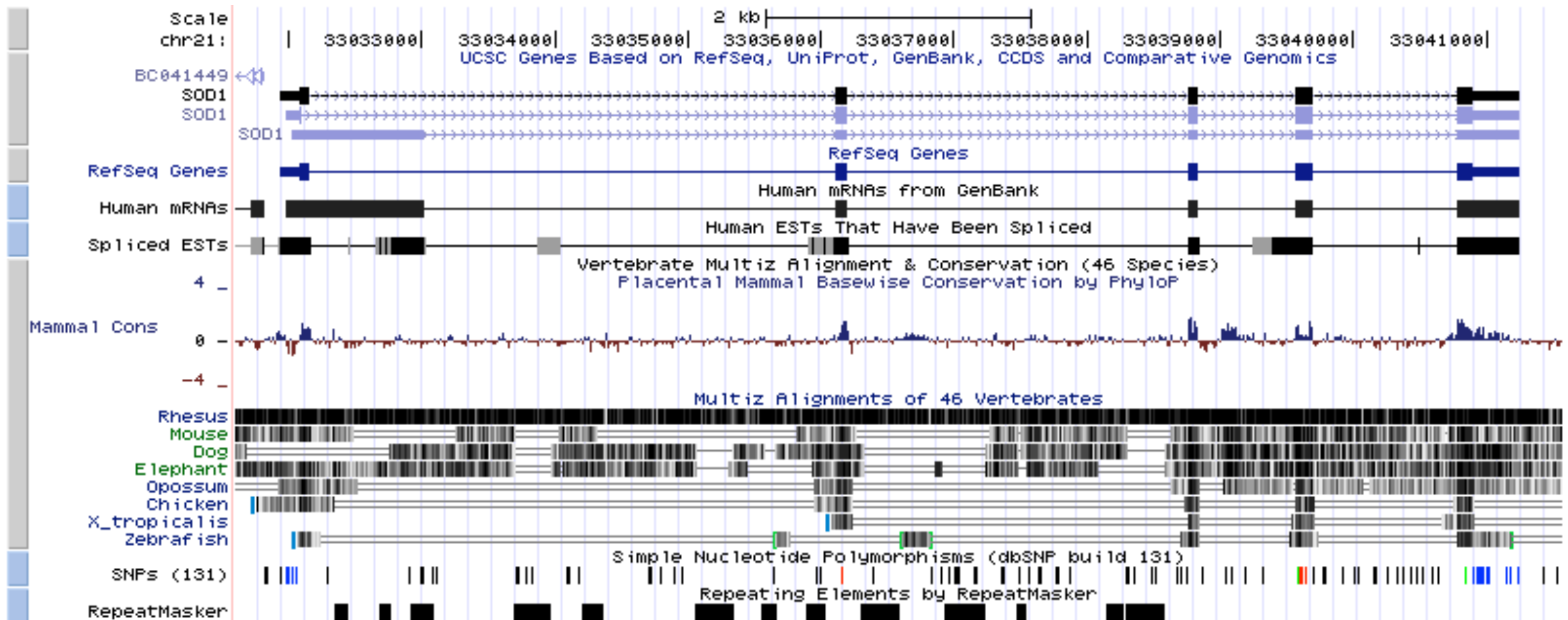
Microbial Genomes Resources presents public data from prokaryotic genome sequencing projects. The sequence collection contains data from finished genomes as well as draft assemblies. The analytical tools include specialized [BLAST](#) with microbial genomes, newly developed [Concise](#)

Related resources

- [Entrez Genome Project](#) complete and incomplete large-scale sequencing projects
- [Entrez Protein Clusters](#) a collection of related protein sequences
- [Eukaryotic genome projects and sequences](#)
- [Genomes of Bacillus anthracis](#) reference genome and related sequences
- [Influenza Virus Resource](#) sequence database and analyses
- [Microbial Genomes](#) reference sequences and resources
- [Organelle](#) reference sequences and tools
- [Plant Genomes Central](#) major plant genome projects
- [SARS Coronavirus Resource](#) sequence data and analyses
- [Salmonella SNPs](#) SNP data in two Salmonella enterica pathotypes
- [Viruses](#) reference sequences and

Human Genome Browser

- <http://genome.ucsc.edu/>



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Inter-molecular interactions in a 44 kDa interferon-receptor complex detected by asymmetric back-protonation and 2D NOESY

DOI:10.2210/pdb2kz1/pdb

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Primary Citation

Intermolecular interactions in a 44 kDa interferon-receptor complex detected by asymmetric reverse-protonation and two-dimensional NOESY.

Nudelman, I., Akabayov, S.R., Schnur, E., Biron, Z., Levy, R., Xu, Y., Yang, D., Anglister, J.

Journal: (2010) Biochemistry **49**: 5117-5133

PubMed: 20496919

DOI: 10.1021/bi100041f

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PubMed Abstract:

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Classification: Antiviral Protein

Structure Weight: 43587.80

Molecule: Interferon alpha-2

Polymer: 1 **Type:** polypeptide(L)

Length: 165

Chains: A

Molecule: Soluble IFN alpha/beta receptor

2KZ1

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Authors: Nudelman, I., Akabayov, S.R., Schnur, E., Biron, Z., Levy, R., Xu, Y., Yang, D., Anglister, J.

Recap

- Central dogma of biology: DNA -> RNA -> Proteins
 - DNA encodes genes, most of which encode for proteins (via the genetic code)
 - Proteins perform much of the work of the cell.
 - RNA acts as an intermediate step (it also has other functions as well)
- Huge amount of data now available, need algorithms to make sense of it.
- Next up: sequence comparison using dynamic programming.