



STUDENT WORKSHEET

LKPD

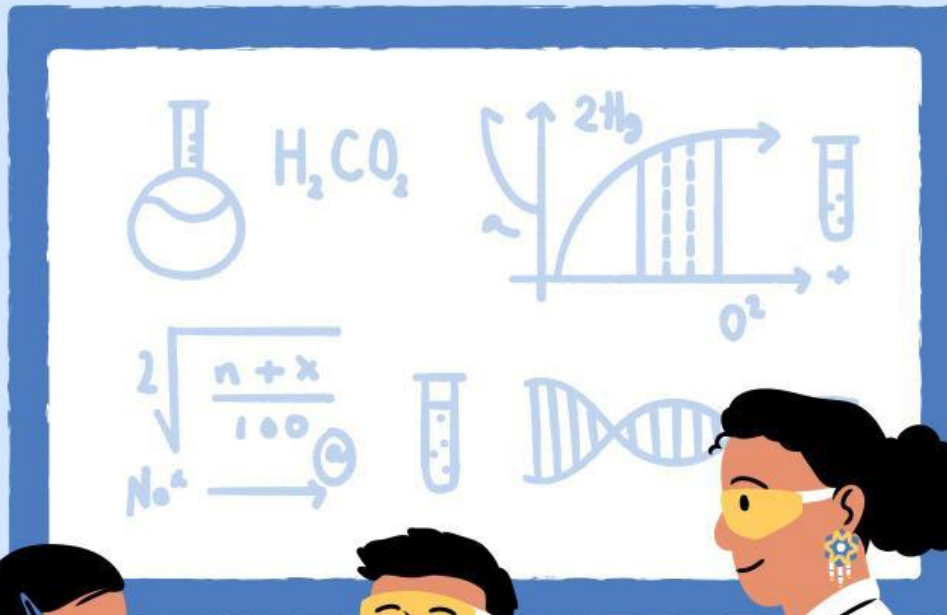
GENETICS

"GENETIC ENGINEERING"

NAME :

CLASS :

GROUP :



FOR UNDERGRADUATE STUDENTS

INTRODUCTION

A. Apperception

Question	Answer
What do you know about genetics?	
Do you know and have you ever used SMS?	
Do you know and have you ever used NCBI?	
What genetic diseases do you know?	
What do you know about obesity?	
What is the role of biotechnology in medicine development?	

Watch the following video

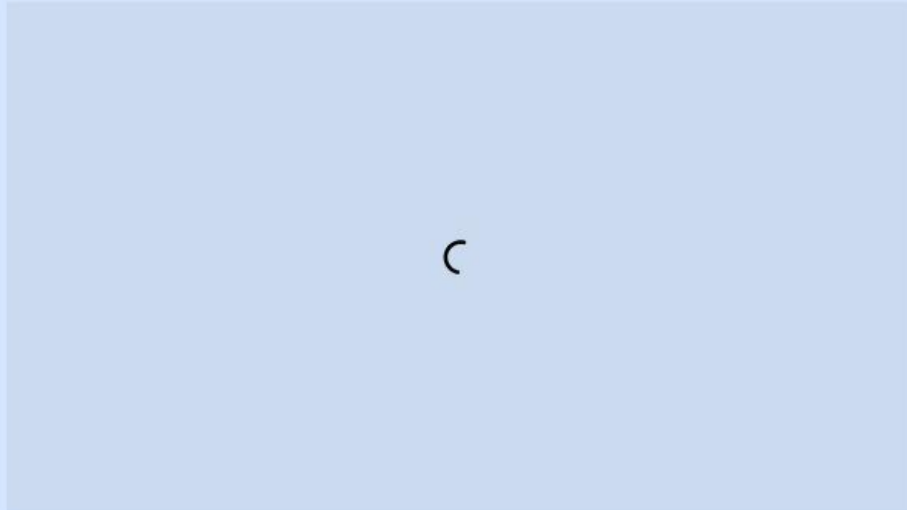
a) Genetics

https://youtu.be/-i1_JagCL1U?si=OWFgYK3u3_vpm2pK

C

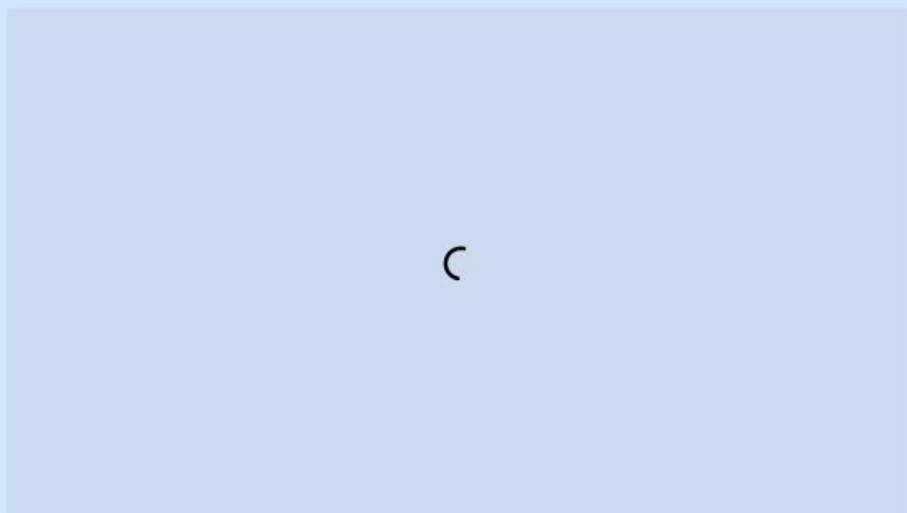
b) Obesity Gene

https://youtu.be/jufMNsJxD-4?si=fw_y7cOnXVMqyrlk



c) Medicine Development Biotechnology

<https://youtu.be/u-mXH4U29Hs?si=YpA8fczdb3yQYLCB>



INVESTIGATION

Obesity, or being overweight, is a major health problem worldwide. It not only makes people uncomfortable but also increases the risk of serious diseases such as diabetes, heart disease, and cancer. In addition to diet and lifestyle, scientists have also discovered that genes (hereditary factors) play a role in causing obesity. This means that some people are simply more prone to obesity due to genetic factors.

Obesity is a growing global problem and contributes to various chronic diseases such as type 2 diabetes, cardiovascular disease, and cancer. Genetic factors are known to play a significant role in the predisposition to obesity, but many genes remain incompletely characterized.

a. Identification and Exploration of Obesity Genes

1. Identifying the FTO, PPARG, ADRB3, and FABP2 genes involved in obesity by researching their location, function, and association with metabolic diseases.
2. Downloading the FTO, PPARG, ADRB3, and FABP2 gene sequences in FASTA format, both DNA and protein sequences.

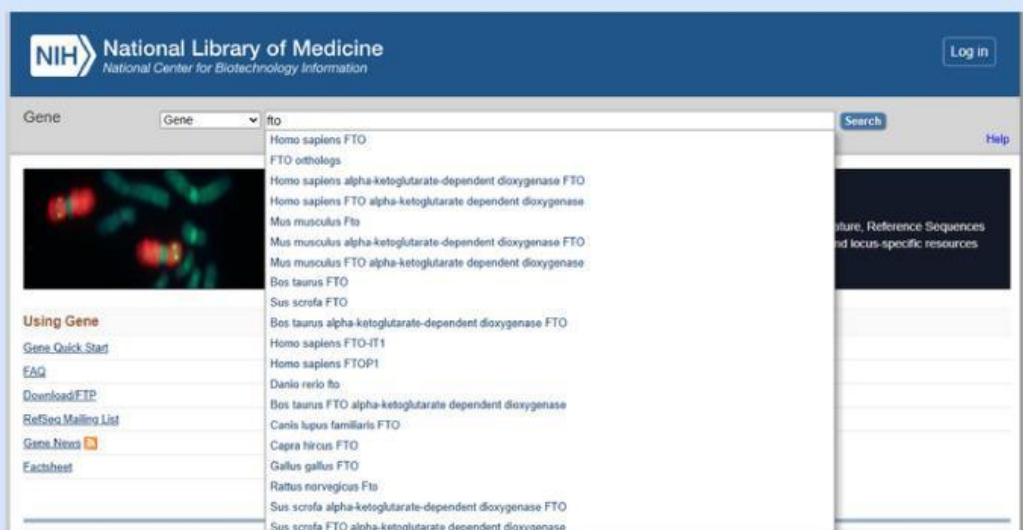
The following is data regarding each obesity gene in humans.

Simbol	Nama	Lokasi	Jaringan/Ekspresi	Fungsi	Patologi Penyakit
FTO	FTO α -ketoglutarate dependent dioxygenase	16q12.2	Otak, kelenjar adrenal, dan 25 jaringan lainnya	Membalikkan kerusakan DNA dan RNA terakumulasi oleh demetilasi oksidatif	Hubungan yang kuat dengan BMI, risiko obesitas dan T2DM
PPARG	peroxisome proliferasi activated receptor γ	3p25.2	Ekspresi bias pada lemak, kandung kemih, usus besar, lambung, dan sembilan jaringan lainnya	Membantu dalam mengatur transkripsi berbagai gen; pengatur diferensiasi adiposit	obesitas, DM, aterosklerosis, kanker
ADRB3	adrenergic receptor β 3	8p11.23	Ovarium, kandung kemih, plasenta, dan dua jaringan lainnya	Memediasi aktivasi adenilat siklase yang diinduksi katekolamin melalui aksi protein G; terlibat dalam regulasi lipolisis dan termogenesis	obesitas dan gangguan terkait berat badan
FABP2	fatty acid-binding protein 2	4q26	Usus halus, usus dua belas jari, usus besar	Protein pengikat asam lemak, penyerapan metabolisme intraseluler, pengangkutan asam lemak rantai panjang; dapat bertindak sebagai sensor lipid untuk mempertahankan homeostasis energi	obesitas, penyakit ginjal, gangguan metabolisme

b. Steps for downloading obesity genes (FTO, PPARG, ADRB3, and FABP2) in fasta format on NCBI

1. Open the NCBI website via the Google Chrome browser or access it directly via the following link: <https://www.ncbi.nlm.nih.gov/gene>.
2. In the search bar, type the name of a gene associated with obesity, for example, "FTO."
3. Once the search results are displayed, select the FTO gene, which originates from Homo sapiens.
4. Scroll down the page until you find the section labeled "FASTA," then click on the link.
5. Once the FASTA page opens, click the "Send to" button, usually located in the upper right corner.
6. Select the "Gene Features" option from the menu provided.
7. Finally, click the "Create File" button to download the file in FASTA format.

Step 2.



Step 3



Genomic regions, transcripts, and products

Go to [reference sequence details](#)

Genomic Sequence: **NC_000016.10** Chromosome 16 Reference GRCh38 p14 Primary Assembly ▾

Go to nucleotide: [Graphics](#) [FASTA](#) [GenBank](#)

NC_000016.10 ▾ Find:

Genes, RefSeq Project (release v1.4)

FTO

HP_000043223

HP_000072961

HP_000014054

HP_000014055

HP_000014056

HP_000014057

HP_000014058

HP_000014059

HP_000014060

HP_000014061

HP_000014062

HP_000014063

HP_000014064

HP_000014065

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HP_000014268

HP_000014269

HP_000014270

HP_000014271

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HP_000014274

HP_000014275

HP_000014276

HP_0

Nucleotide [Advanced](#)

FASTA

Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly

NCBI Reference Sequence: NC_000016.10

[GenBank](#) [Graphics](#)

>NC_000016.10:53703963-54121941 Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly

```
CTACGCTCTTCAGCTGCTCGGACCTGGGAAATCTCTCTGTGCTAAATCCCTGGGCTCGCGGGTGTGCG
CGCGGTGCACTCTGGGAGTGTGATGTTTTCTACTCAGAGGGAGAAATGCTCTCAGACGGGACGAGGACGC
TGAGAGAACTACATGCAAGGAGCGGGGCTCAGGGCGAGGGATCTACGCGAGCTTGCAGTGGCGAAGCGGCG
TTTAGTGGCAGCATGAAGCGCACCCCGACTGCGAGGAAACGAGAGCGCAGAGCTAAGGATATGTCGGGCTC
CCGGGCGCTGAGATCTTCGTGCGCTGTGAGCAAGGATCAGGGAACGGAAAGGCTTGGTTGATGGCGGA
CGCGATGCGCGGTTAAATTAAGGGATGACAGGGCTTGTGACGCAAGGACCTGGAGATATTAGAGGGG
ATGTTACAAATTCGTGCTCTCAGGATCGAGGCCGAGCTTGTGGATCGGCTCAAAAATGAGAGCGCAAG
ATACCCATCTCTCTGCTCTCTCTGCTCATTTCTTGGTAAATTTGTGCGCATCCCTGTGCTCTCAAGT
TTACGGGATCTCAGATGACTGTGATCATACCAAGCTGTGCTTCTCATATGGTCTCTGAGGACAGATG
CGGCTAGATGAAATATCTGTGCACTGCTGCTTCTTGGAAACATTTGCTCCGTGACCGGCTGATA
ACAGTTGTGCTTTTAGCGCTGTGGATATGAATCTTAACTACATTTGCTCTCTACCTTTGATGTTCT
AGCTCTGGTAGTGCCATTCCATGGGATGACATAATAATGGCAACAGAGATTTAAAGGCAATTTATT
GTGGGTGAGGCACTGTTAAGTGCATAATATTTAAATATTTCAATCATTTGTCACAGCAGATGCAAG
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TTGAGTGTGTTCTTCTCTCATCTCCCAAACTCAGATCGCTGTGATTTGCTACGATATATTGGGAAATG
CCCACTTTTTTTTTTTCATCTCCACTACCTTGGACCAAGCTACCATATTCTTTAATAGACGTGTGG
AATAGCTATTGATTGGCTACACTCACTCTACACCCCTAACTTAACTCTCTCTCACTCTCTCTCTCTCT
CTCAACTACCATCTCTCTCTGACACCATAGAGTAAGATCTCGTGAAATGCAATATAAATATGTCCTC
TTTCTTTCTCTTACTCTGCAACCACTGTTTTTAAATATTTCCATGCTCTCTGCTCTCTAGGATA
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GATATGACACTCTGCTCTGCTCAGCAGCTCACTTTGGCTCTTAAAGGCTCACTCTTCACTATACTTTA
TCGGGCTCTCAGGGCTTTGACATGTGCTTGTGCTCTACTCTATGTTAGGCAAAATTTGGCAGTGAATA
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GCAATACACTAAGGATTTAAATATAAAATCTGCTCTATATGACCTGAGTATTGTCAGTATTCTGTAAG
GAGGAGTAAAGGTTTCTAGTGTAGGCTGATATGATGTCGATATATATTAAGATAGCTCAAGAGAG
```

☐ Complete Record
☐ Coding Sequences
☒ Gene Features

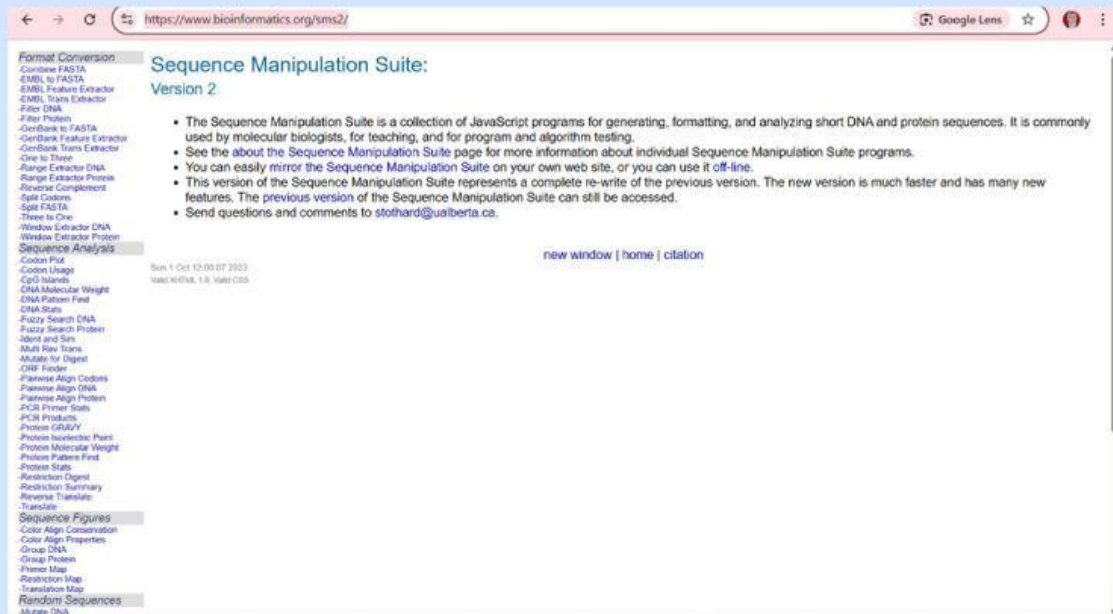
Download gene features.

Format

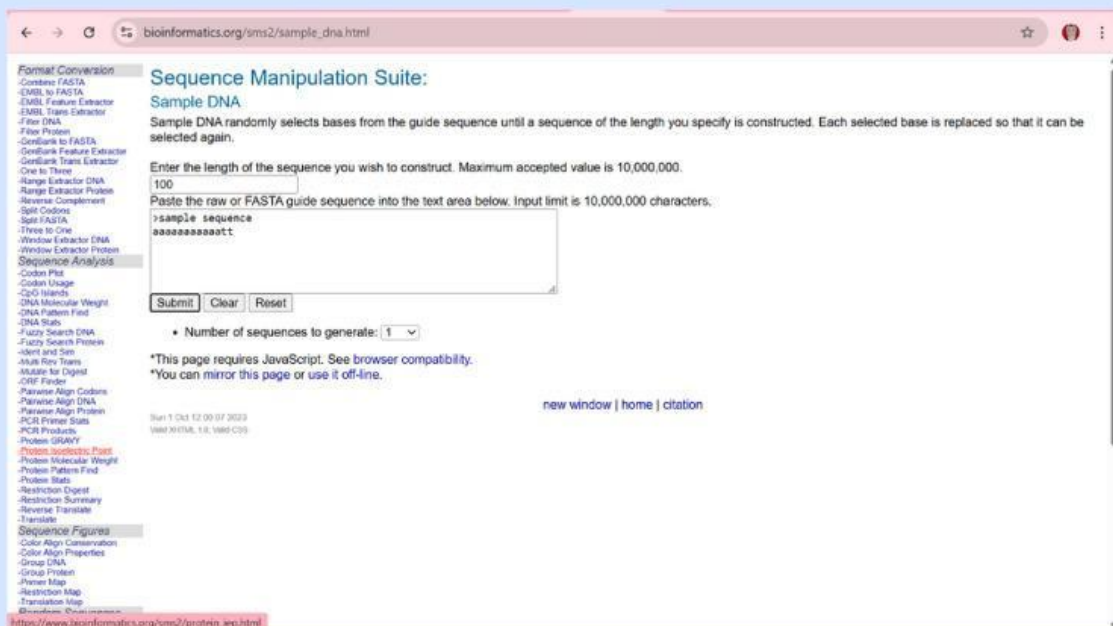
c. Stages of using SMS (Sequence Manipulate Suite)

1. Click the link to access the SMS (Sequence Manipulate Suite) website

<https://www.bioinformatics.org/sms2/>



2. Next, click DNA Sample



The screenshot shows a web browser window with the address bar displaying 'bioinformatics.org/sms2/sample_dna.html'. The page title is 'Sequence Manipulation Suite: Sample DNA'. The main content area contains the following text:

Sample DNA randomly selects bases from the guide sequence until a sequence of the length you specify is constructed. Each selected base is replaced so that it can be selected again.

Enter the length of the sequence you wish to construct. Maximum accepted value is 10,000,000.

100

Paste the raw or FASTA guide sequence into the text area below. Input limit is 10,000,000 characters.

K7906399.1 Synthetic construct Homo sapiens clone
 cc5broaden_15979 FTO gene, encodes complete protein
 GTTCCTGCAACAAATTGATGGGCAATGCTTTTATTAATGCCACCTTTGTACAAAAAGTT
 GGCATGCG
 ATGCCAGGCGAGAGAGGAGTGTGTTGGCCAGTCACGAATTGCCCAACATTACCTGCTGATC
 AGAAGCCA

Submit Clear Reset

Number of sequences to generate: 1

*This page requires JavaScript. See browser compatibility.

*You can mirror this page or use it off-line.

new window | home | citation

Sun 1 Oct 12:00:07 2023
 Valid XHTML 1.0 | Valid CSS

The sidebar on the left contains the following links:

- Format Conversion
 - Combine FASTA
 - EMBL to FASTA
 - EMBL Feature Extractor
 - EMBL Trunc Extractor
 - Filter DNA
 - Filter Protein
 - GenBank to FASTA
 - GenBank Feature Extractor
 - GenBank Trunc Extractor
 - One to Three
 - Range Extractor DNA
 - Range Extractor Protein
 - Reverse Complement
 - Split Codons
 - Split FASTA
 - Three to One
 - Window Extractor DNA
 - Window Extractor Protein
- Sequence Analysis
 - Codon Plot
 - Codon Usage
 - CpG Islands
 - DNA Molecular Weight
 - DNA Pattern Find
 - DNA Stats
 - Fuzzy Search DNA
 - Fuzzy Search Protein
 - Ident and Sites
 - Multi Rev Trans
 - Mutate for Top Blast
 - ORF Finder
 - Pairwise Align: Codons
 - Pairwise Align: DNA
 - Pairwise Align: Protein
 - PCR Primer Stats
 - PCR Products
 - Protein GRAVY
 - Protein Isoelectric Point
 - Protein Molecular Weight
 - Protein Pattern Find
 - Protein Stats
 - Restriction Digest
 - Restriction Summary
 - Reverse Translate
 - Translate
- Sequence Figures
 - Color Align Conservation
 - Color Align Properties
 - Group: DNA
 - Group: Protein
 - Primer Map
 - Restriction Map
 - Translation Map
- Random Sequences
 - Mutate DNA

6. Translate → Translates DNA sequences into proteins.

Reverse Complement → Understands DNA chain orientation.

ORF Finder → Finds open reading frames in target genes.

GC Content → Assesses gene stability based on GC content.

Protein Stats → Determines molecular weight and amino acid composition.

Purpose: Screen target candidates and prepare data for drug molecule docking.

7. Initial (Conceptual) medical Molecule Design and Modeling

Based on the target proteins of FTO, PPARG, ADRB3, and FABP2, the analyzed protein sequences can be used as the basis for drug design.

- Compounds can be selected based on the literature or drug databases such as DrugBank (this step is outside of NCBI/SMS, but is additional).

ANSWER

Please answer the following questions again.

Question	Answer
What do you know about genetics?	
Do you know and have you ever used SMS?	
Do you know and have you ever used NCBI?	
What genetic diseases do you know?	
What do you know about obesity?	
What is the role of biotechnology in medicine development?	

Let's review your answers before and after this activity. If your answers are now more complete and clear, congratulations! This means your understanding has improved.

However, if there hasn't been any change, don't worry. This means there's still room for learning. Please review the material again and don't hesitate to discuss it with your teacher or friends. Keep up the good work, because understanding will come with effort!