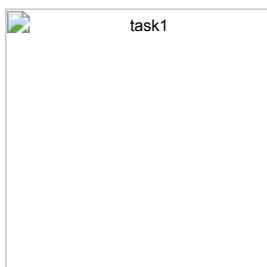


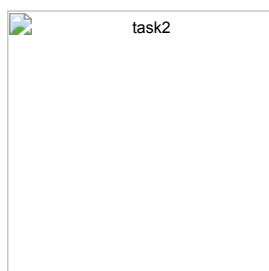
---

author: Batuhan Seyhan title: date: 12.05.2023 keywords: 11C  
geometry: margin = 2cm output: pdf\_document fontsize: 12pt  
lang: en

## TASK-1



## TASK2

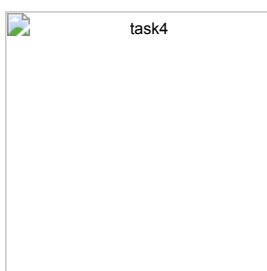


Executive: Colored 10 atoms. Executive: Colored 44 atoms.

## TASK3

not sure what the diffrence it can make though

## TASK4



## TASK5

12

## TASK6

2

## TASK7

--

# TASK8



# TASK9

YES, IT FOLDED.

# TASK10



# TASK11

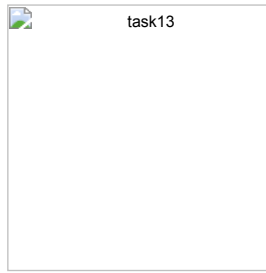


PyMOL(TM) 2.5.5 - Incentive Product Copyright (C) Schrodinger, LLC This Executable Build integrates and extends Open-Source PyMOL. Detected OpenGL version 2.1. Shaders available. Detected GLSL version 1.20. OpenGL graphics engine: GL\_VENDOR: Apple GL\_RENDERER: Apple M1 GL\_VF Detected 8 CPU cores. Enabled multithreaded rendering.

# Task12

sp|Q94KT8|COBRA\_ARATH Protein COBRA OS=Arabidopsis thaliana OX=3702 GN=COB PE=2 SV=1  
MESFFSRSTSIVSKLSFLALWIVFLISSSSFTSTEAYDALDPEGNITMKWDVMSWTPDGY  
VAVVTMFNFQKYRHIQSPGWTLGWKWAKKEVIWSMVGAQTTEQGDCSKYGNIPHCKCKD  
PTVVDLLPGTPYNQQIANCCKGGVMNSWVQDPATAASSFQISVGAAGTTNKTVRVPRNFT  
LMGPGPGYTCGPAKIVRPTKFVTTDTRRTTQAMMTWNITCTYSQFLAQRTPTCVSLSSF  
YNETIVGCPTCACGCQNNRTESGACLDPDTPHLASVVSPTTKGTVLPPLVQCTRHMCP  
RVHWHVKQNYKEYWRVKITITNFNYRLNYTQWNLVAQHPNLDNITQIFSFNYSKSLTPYAG  
LNDTAMLWGVKFYNDFLSEAGPLGNVQSEILFRKQDQSTFTFEKGWAFPRRIYFNGDNCVM PPPDSYPFLPNGGSRSQFSFVAAVLLPLLVFFFFSA

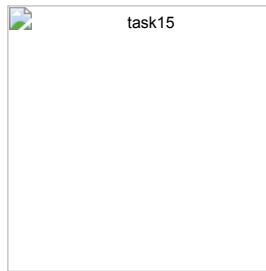
# TASK13



## Task14

The code performs a protein structure prediction using the AlphaFold model, it will generate graphs showing the multiple sequence alignment (MSA) and the predicted protein structure.

## TASK15



## Task16