

База данных структуры белков

Лекция по Молекулярной
Биофизике

Юрий Андреевич Владимиров
yuvlad@mail.ru

Фрагмент окна Белковой Базы Данных (PDB)

<http://www.rcsb.org/pdb/>

Поиск белка

DEPOSIT data
DOWNLOAD files
browse LINKS
BETA TEST new features
BETA mmCIF files

Current Holdings

20254 Structures
Last Update: 04-Mar-2003
[PDB Statistics](#)



Molecule of the Month:
lac Repressor

The Protein Data Bank (PDB) is operated by Rutgers, The State University of New Jersey; the San Diego Supercomputer Center at the University of California, San Diego; and the Center for Advanced

PROTEIN DATA BANK

Welcome to the PDB, the single worldwide repository for the distribution of 3-D biological macromolecular structure data

[ABOUT PDB](#) | [DATA UNIFORMITY](#) | [RECENT FEATURES](#) | [STRUCTURAL GENOMICS](#) | [PUBLIC](#)

Search the Archive

Enter a PDB ID or keyword

Query Tutorial

superoxide dismutase Find a structure

query by PDB id only match exact word
 remove sequence homologs

[SearchLite](#) keyword search form with examples
[SearchFields](#) customizable search form
[Status Search](#) find entries awaiting release

PI
**Pl
San
Rut
Nati
Can
Nati
Osa
Univ
Max
Gen

Фрагмент окна результатов поиска в PDB

PDB Query Result - Microsoft Internet Explorer

Файл Правка Вид Избранное Сервис Справка

Назад Поиск Избранное Журнал

Адрес C:\WINDOWS\Рабочий стол\PDB\PDB Query Result.htm

PDB Home

Query Result Browser

Help PDB Home Contact us

Your query found **106** structures in the current PDB release and you have selected **0** structures so far. (There are currently **2** structures being processed or "on hold" matching your query!) You can select specific structures by clicking on the checkbox next to their id. If you do not select any structures, certain options will default to all structures. To examine an individual structure select the Explore link!

Pull down to select option: New Search Go

1-20

<input type="checkbox"/>	1AP5	Deposited: 24-Jul-1997 Exp. Method: X-ray Diffraction Resolution: 2.20 Å	(EXPLORE)
Title	Tyr34->Phe Mutant Of Human Mitochondrial Manganese Superoxide Dismutase		
Classification	Oxidoreductase		
Compound	Mol_Id: 1; Molecule: Manganese Superoxide Dismutase; Chain: A, B; Ec: 1.15.1.1; Engineered: Yes; Mutation: Y34F; Biological_Unit: Homotetramer		

Нажать здесь

Фрагмент окна результатов выбора белка 1

PDB
PROTEIN DATA BANK

Structure Explorer - 1AR5

Summary Information

View Structure

Download/Display File

Structure Neighbors

Geometry

Other Sources

Sequence Details

Title: X-Ray Structure Of The Cambialistic Superoxide Dismutase From Propionibacterium Shermanii Active With Fe Or Mn

Compound: **Mol_Id:** 1; **Molecule:** Superoxide Dismutase; **Chain:** A, B; **Synonym:** Sod; **Ec:** 1.15.1.1; **Biological_Unit:** Homotetramer

Authors: M. Schmidt, B. Meier, F. Parak

Exp. Method: X-ray Diffraction

Classification: Oxidoreductase

EC Number: 1.15.1.1

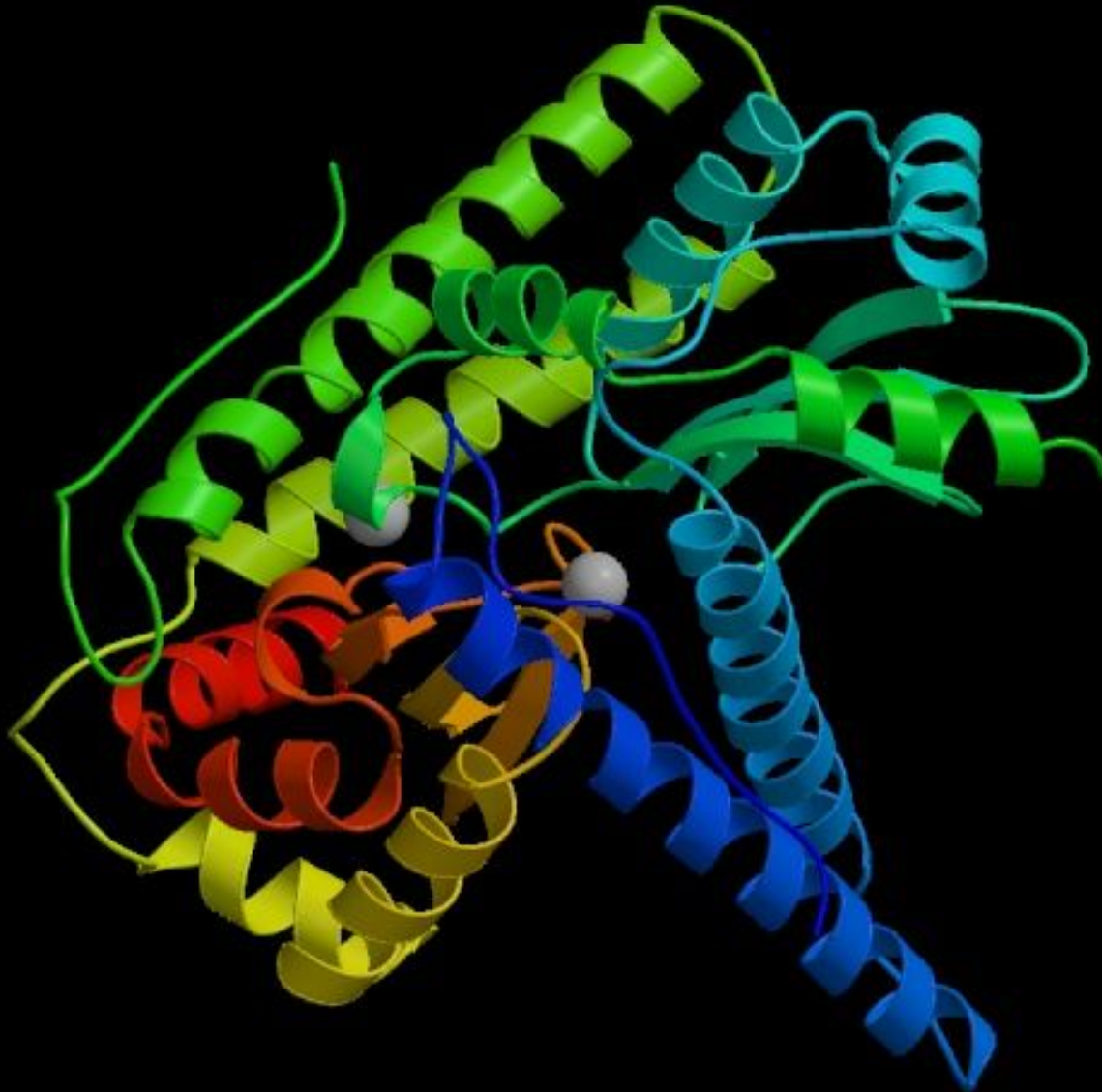
Source: Propionibacterium freudenreichii subsp. shermanii

Просмотр структуры

Загрузка файла структуры

Общая информация

Экспорт неподвижной картины структуры



альфа-спирали

петли

Фрагмент окна результатов выбора белка 2

The screenshot shows a web browser window titled "Structure Explorer - 1BZO - Microsoft Internet Explorer". The address bar shows the URL "C:\WINDOWS\Рабочий стол\PDB\View structure.htm". The main content area displays the PDB logo and the title "Structure Explorer - 1BZO". Below the title, the protein name is "Three-Dimensional Structure Of Prokaryotic Cu, Zn Superoxide Dismutase From P. Leiognathi, Sed By X-Ray Crystallography." The classification is "Oxidoreductase", the compound is "Mol_Id: 1; Iecule: Superoxide Dismutase; Chain: A; Ec: 1.15.1.1; Engineered: Yes", and the experimental method is "X-ray Diffraction". A "View Structure" section offers interactive 3D display options: VRML (default options), VRML (custom options, full screen display), Rasmol, and Swiss-PdbViewer. A "Download Help" section provides links for VRML and Rasmol.

PDB
PROTEIN DATA BANK

Structure Explorer - 1BZO

Title Three-Dimensional Structure Of Prokaryotic Cu, Zn Superoxide Dismutase From P. Leiognathi, Sed By X-Ray Crystallography.

Classification Oxidoreductase

Compound Mol_Id: 1; Iecule: Superoxide Dismutase; Chain: A; Ec: 1.15.1.1; Engineered: Yes

Exp. Method X-ray Diffraction

View Structure

[Summary Inform.](#)

[View Structure](#)

[Download/Displae](#)

[Structural Neighb](#)

[Geometry](#)

[Other Sources](#)

Interactive 3D Display:

Choose from the following [display options](#):

- [VRML \(default options\)](#): Interactive immersive ribbon diagram
- [VRML \(custom options, full screen display\)](#): Interactive immersive ribbon or cylinder diagram with ligands
- [Rasmol](#)
- [Swiss-PdbViewer](#)

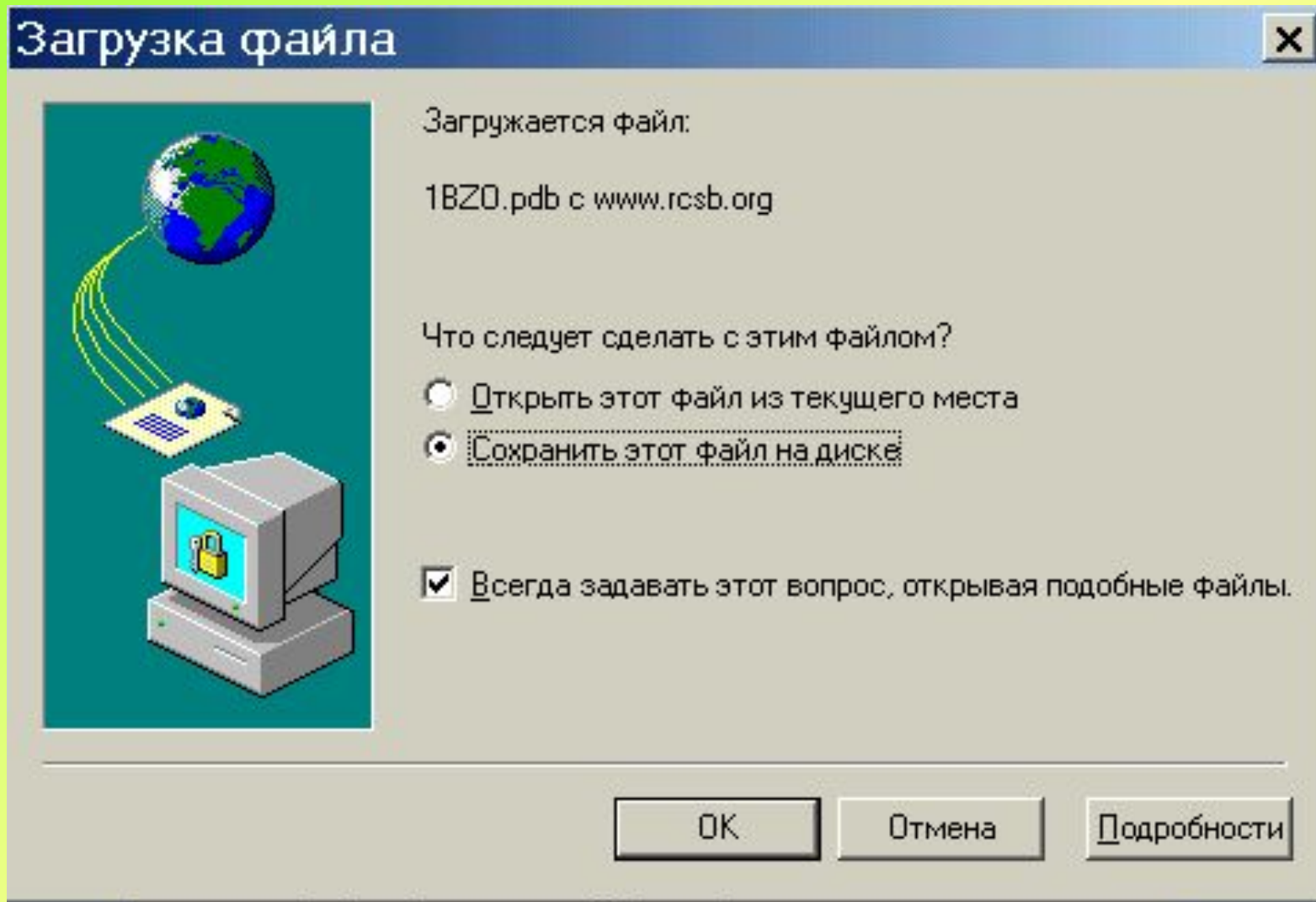
[HELP](#)

Download Help

[VRML](#)

[Rasmol](#)

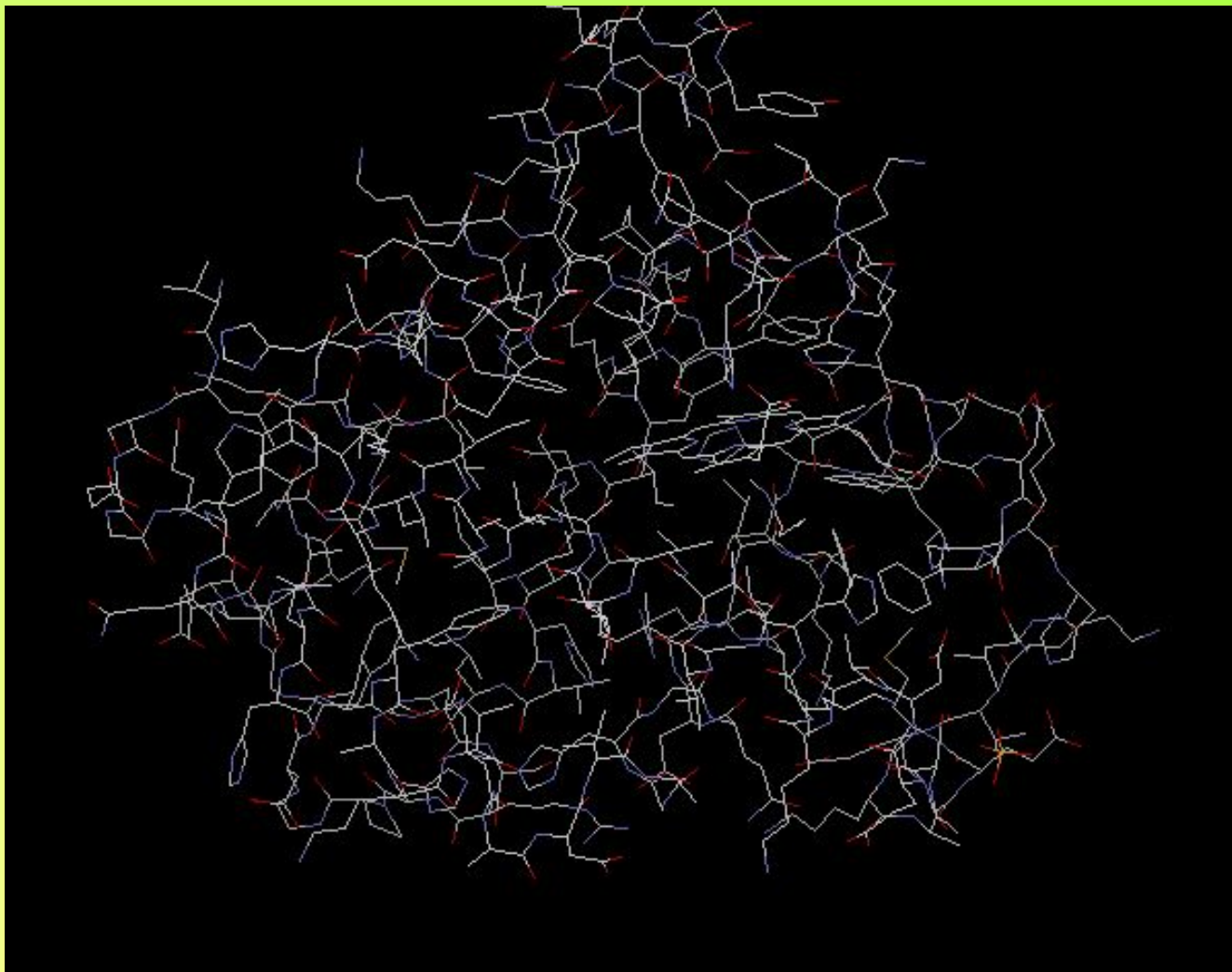
Загрузка файла белковой базы данных (*.pdb)



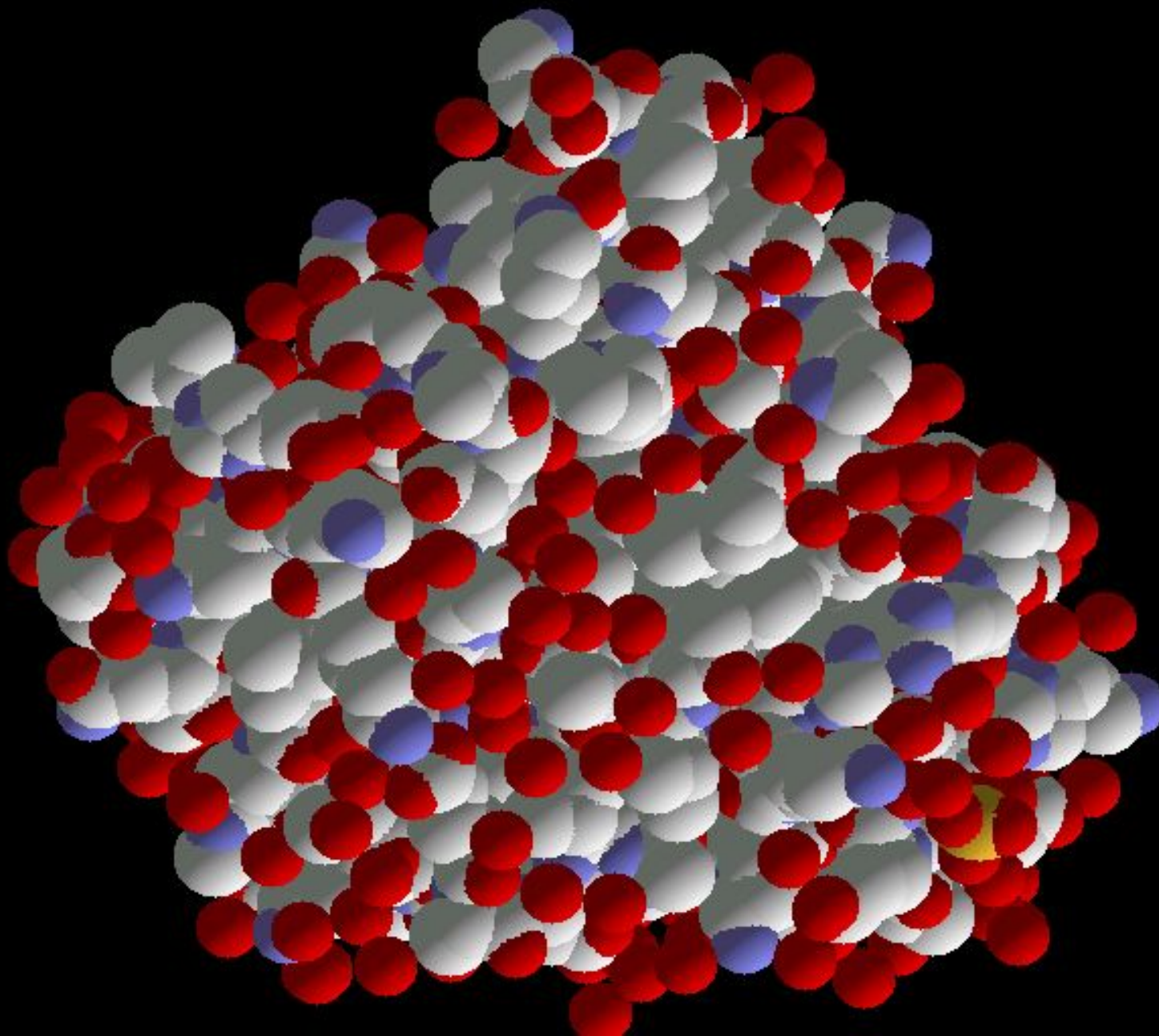
Просмотр структуры с помощью Ras Top.exe

Миоглобин из мышцы кита

Backbone



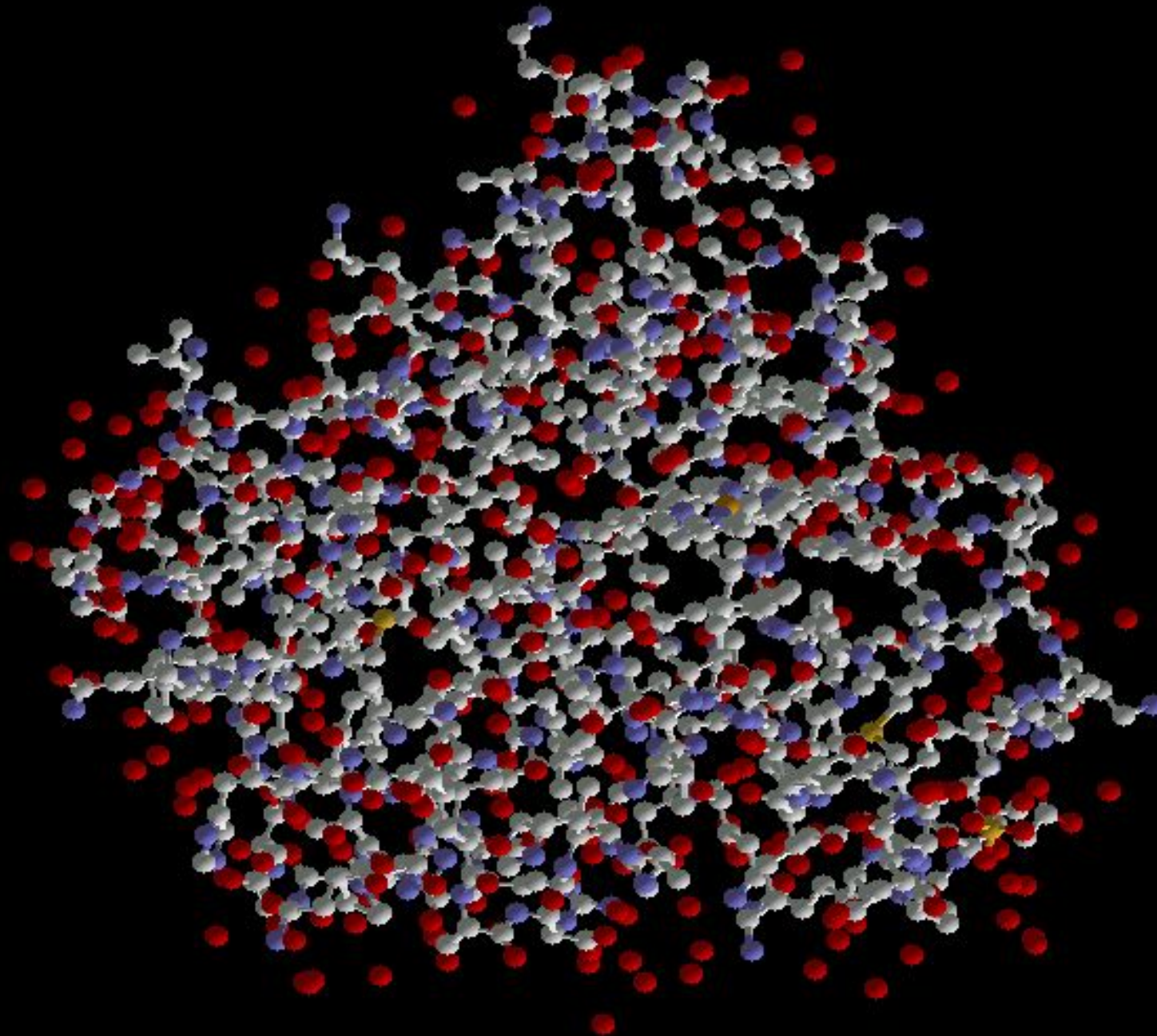
Просмотр структуры с помощью Rostop.exe



Atoms

Просмотр структуры с помощью Rostop.exe

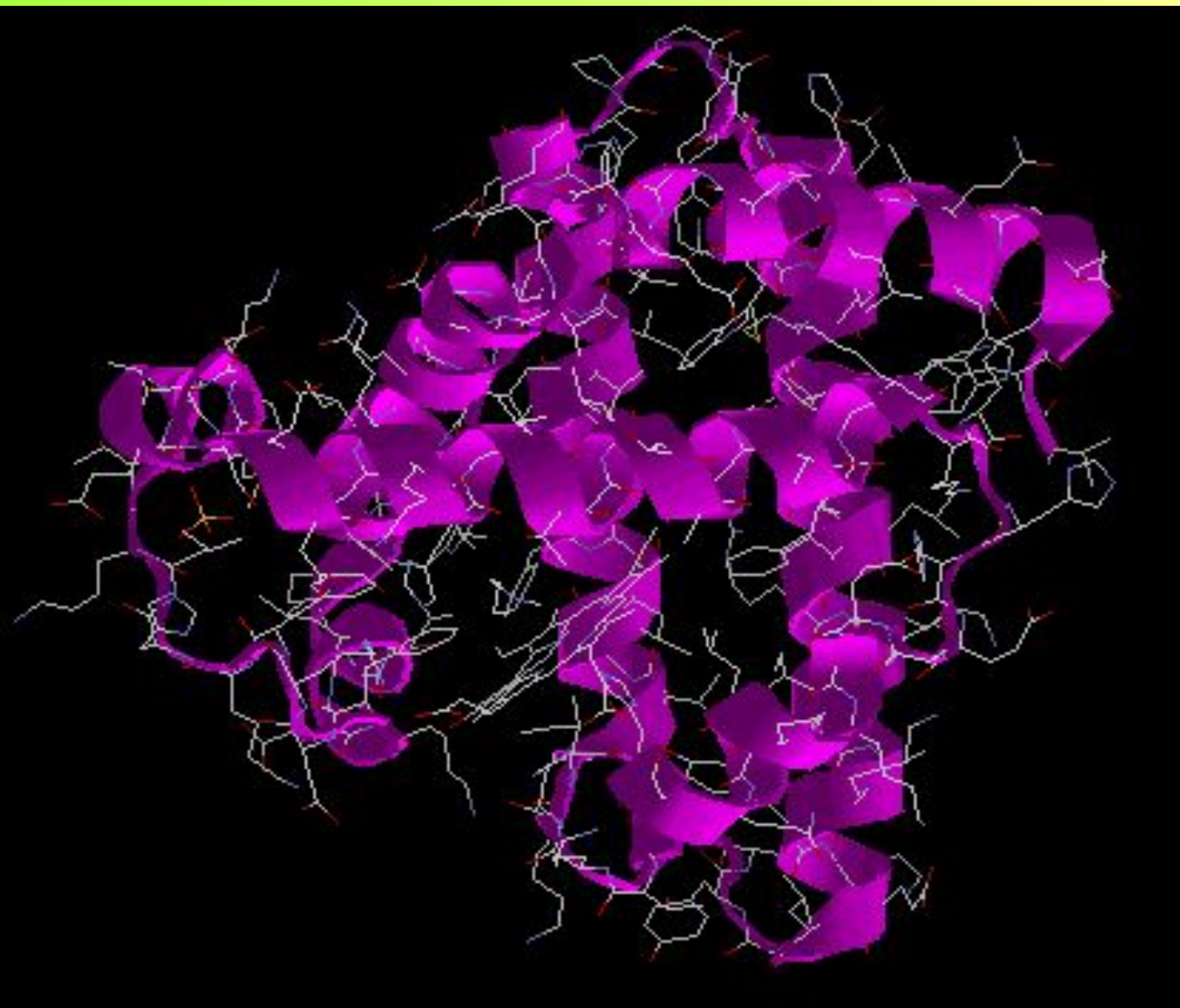
спермы кита



Bonds +
Small
atoms

Просмотр структуры с помощью Rostop.exe

Миоглобин из мышцы кита

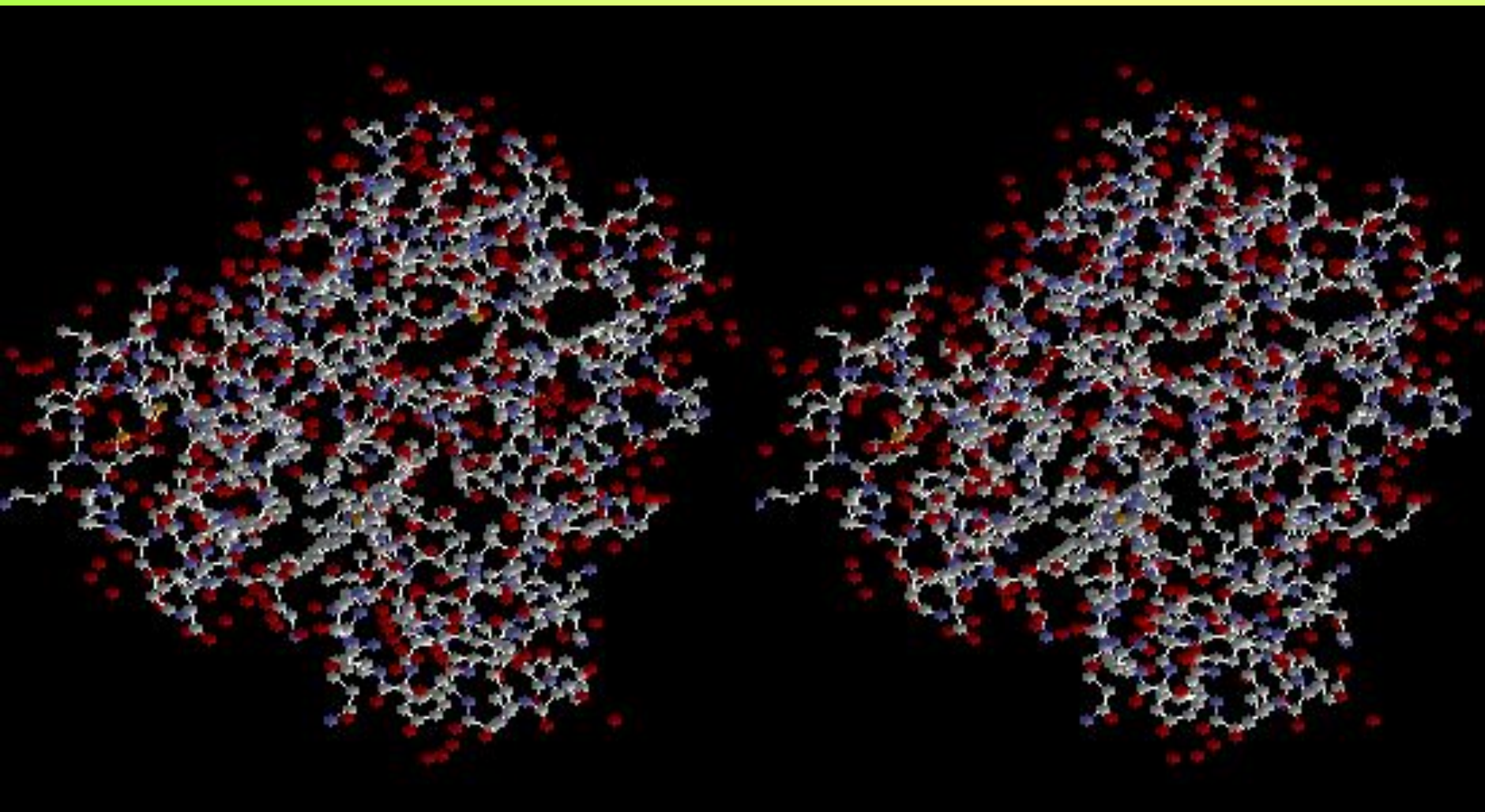


Backbone
+ Ribbon
(cartoon)

Просмотр структуры с помощью Rostop.exe

Миоглобин из мышцы кита

Stereo



Просмотр структуры с помощью Rostop.exe

Миоглобин из мышцы кита

Sticks stereo image

