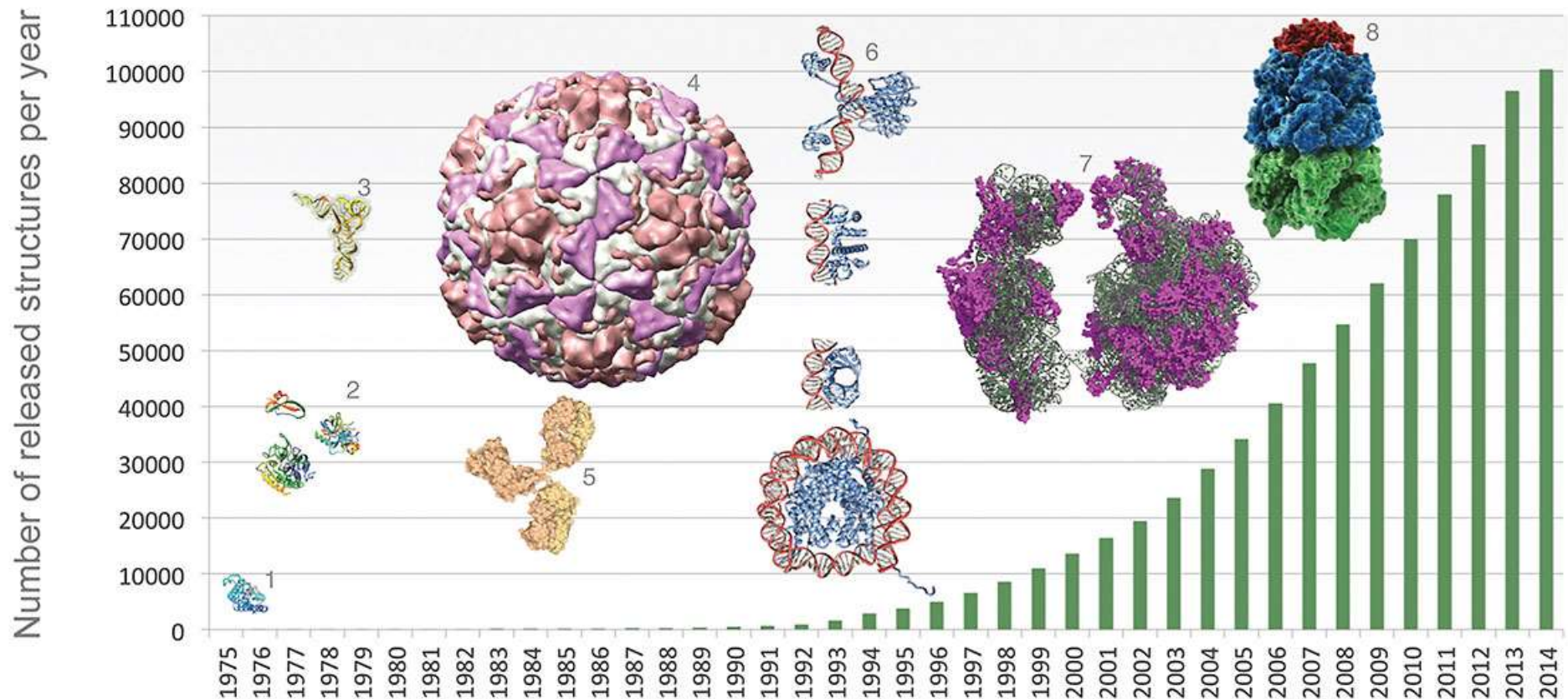


Introduction:

Why structural studies?

Corso di Biocristallografia e Microscopia Elettronica

rdezorzi@units.it



Contents

Introduction

- Structure function relationships
- Elements of protein structure
- Visualization software and databanks of protein structures

Protein samples for structural studies

- Recombinant proteins
- Expression and purification
- Evaluation of sample quality and purity
- Analysis of conformational stability

Practical experiences

- Crystallization of a protein sample
- Sample preparation for data collection
- Data collection at the Elettra Synchrotron
- Data analysis, structure solution and refinement

Biocrystallography

- Crystallization of proteins
- Symmetry in crystals
- Non-crystallographic symmetries
- Basic concepts of diffraction physics
- Instruments
- Diffraction data collection techniques
- Phase problem in crystallography
- Refinement of the structural model
- Validation

Transmission electron microscopy

- Basic concepts of optics for TEM
- Instruments
- Single particle techniques
- Image analysis
- 3D reconstruction from images
- Validation
- Electron crystallography

Objectives of the course

Knowledge of:

- Basic elements of 3D structure of proteins
- Main characteristics of crystals and crystallization techniques
- Physical basis of X-ray diffraction
- X-ray data collection techniques, structural determination and refinement
- Techniques of structural determination by electron microscopy
- Electron microscopy data analysis up to structure validation

Apply knowledge to:

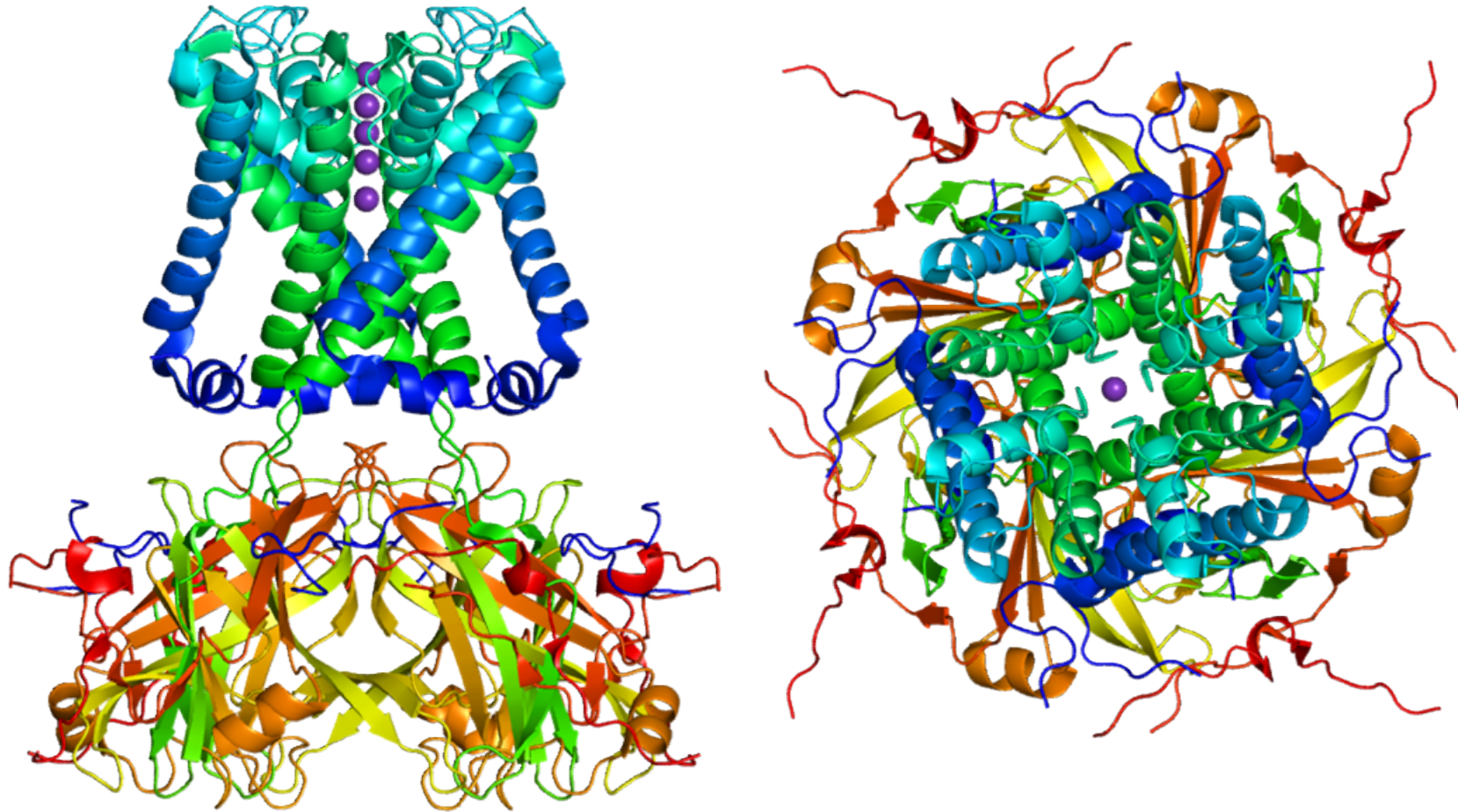
- Describe the 3D structure of a protein
- Plan a X-ray diffraction or electron microscopy experiment, from expression to structure
- Highlight main reasons to chose a structural biology technique over the others
- Recognize crucial factors that can improve/hamper a structural biology experiment
- Identify significant information that can be obtained from a protein structure
- Evaluate quality and reliability of a protein structure obtained through crystallography or EM

Communicate:

- Read and understand a structural biology paper, discussing critical aspects
- Obtain useful information from the available online databases of protein structures
- Present a structural biology study, highlighting useful information obtained from structures
- Obtain images of a protein structure to describe its main features
- Highlight structure-function relationships

Structure-function relationship

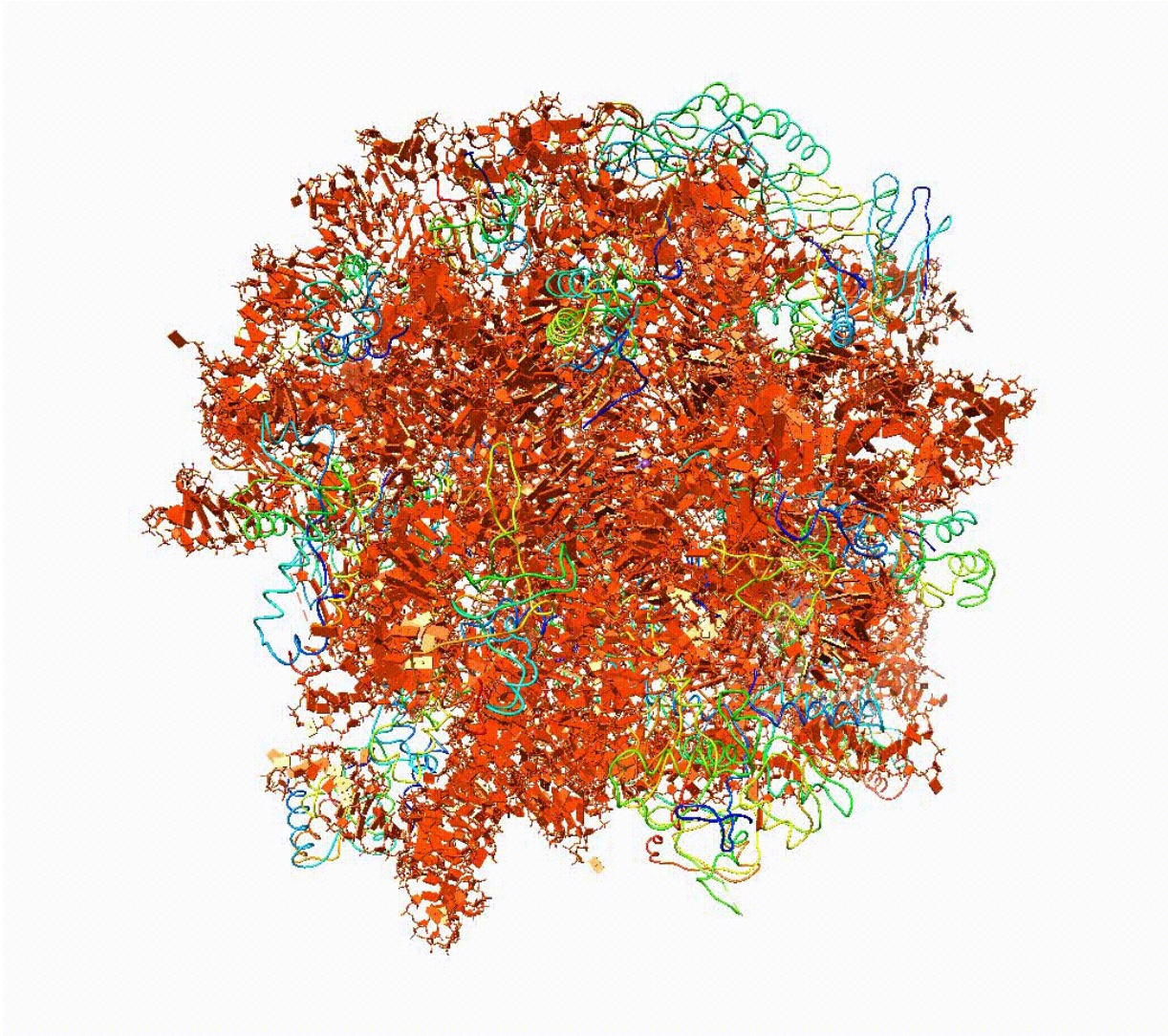
- Mechanisms of biologically relevant proteins and complexes: e.g. Potassium channel



PDB: 3zrs

Structure-function relationship

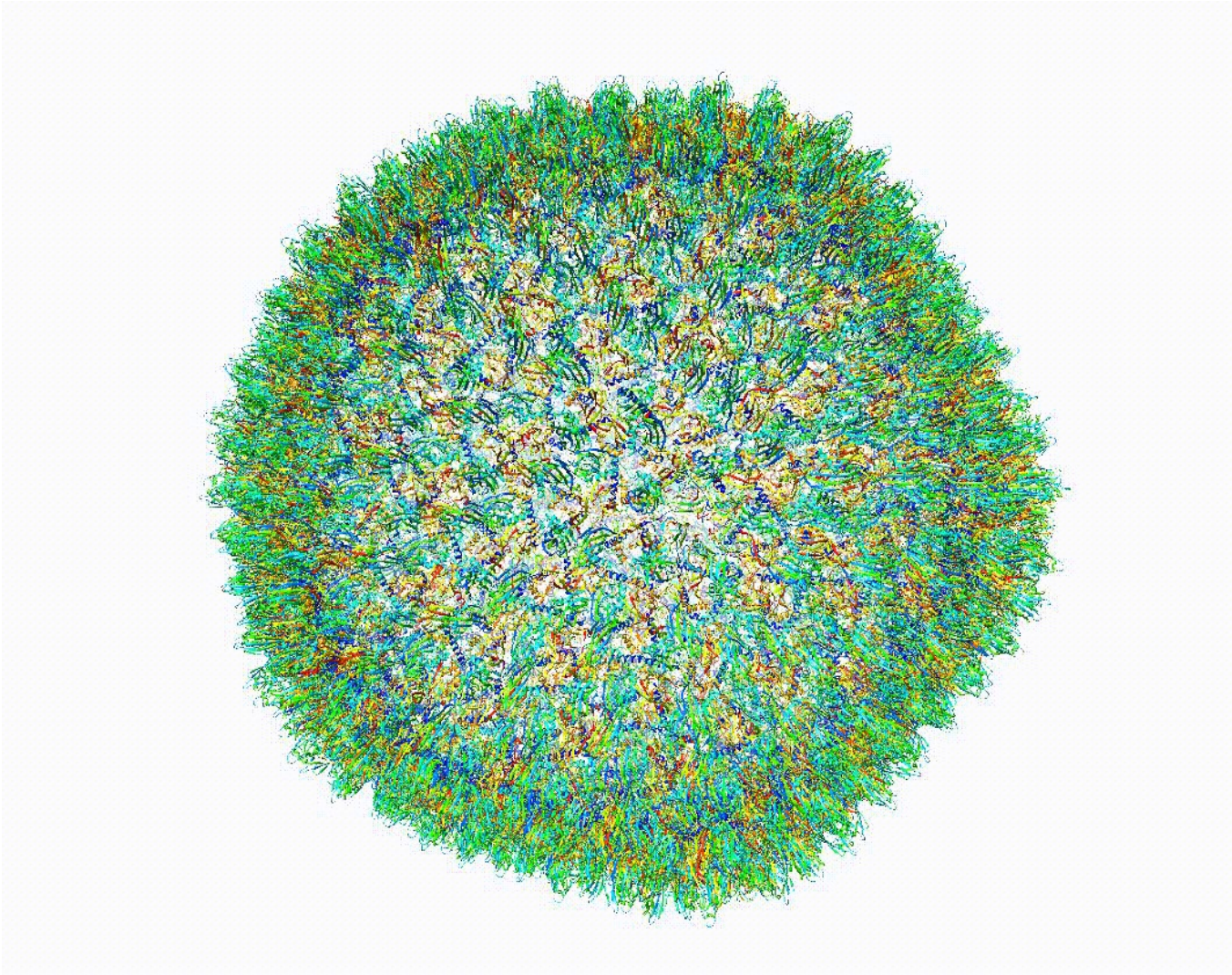
- Mechanisms of biologically relevant proteins and complexes: e.g. ribosome



PDB: 1fft

Structure-function relationship

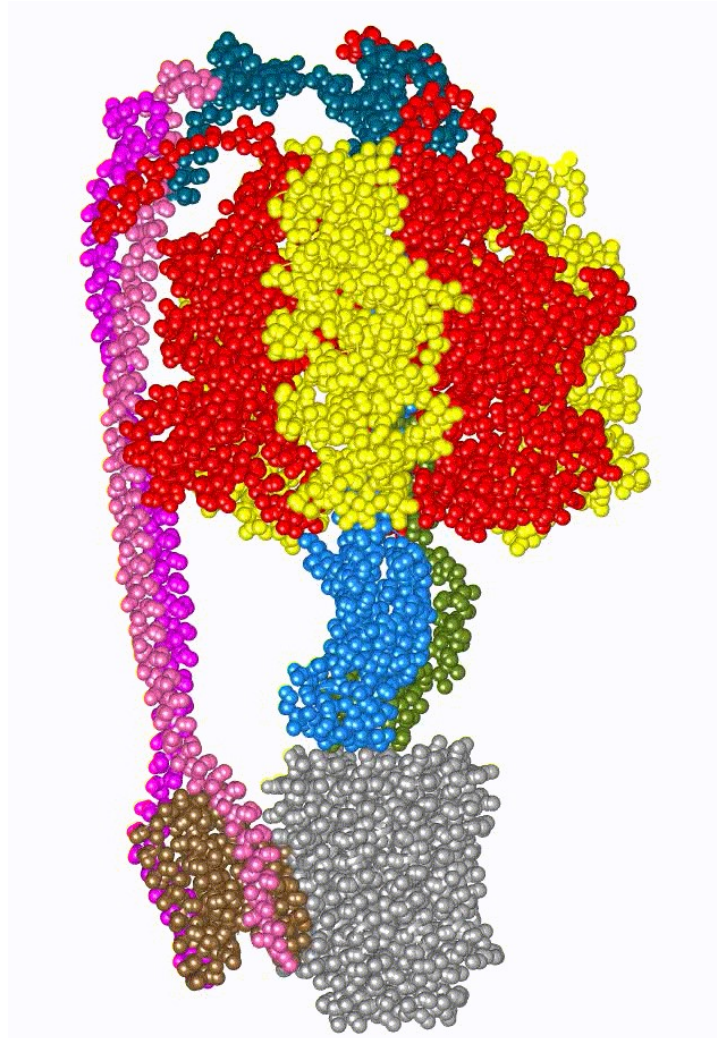
- Mechanisms of biologically relevant proteins and complexes: e.g. virus



PDB: 1w8x

Structure-function relationship

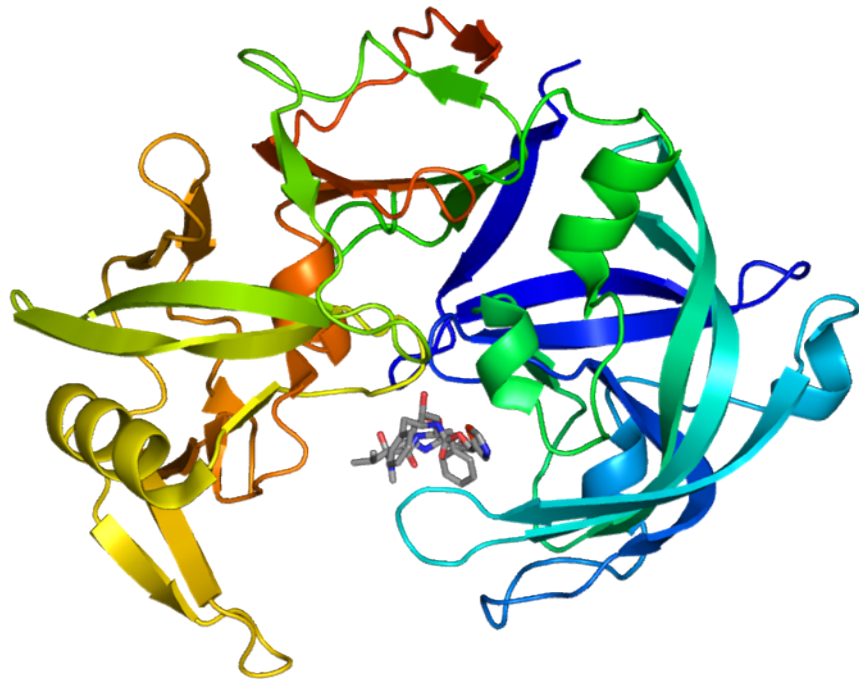
- Mechanisms of biologically relevant proteins and complexes: e.g. ATP-synthase



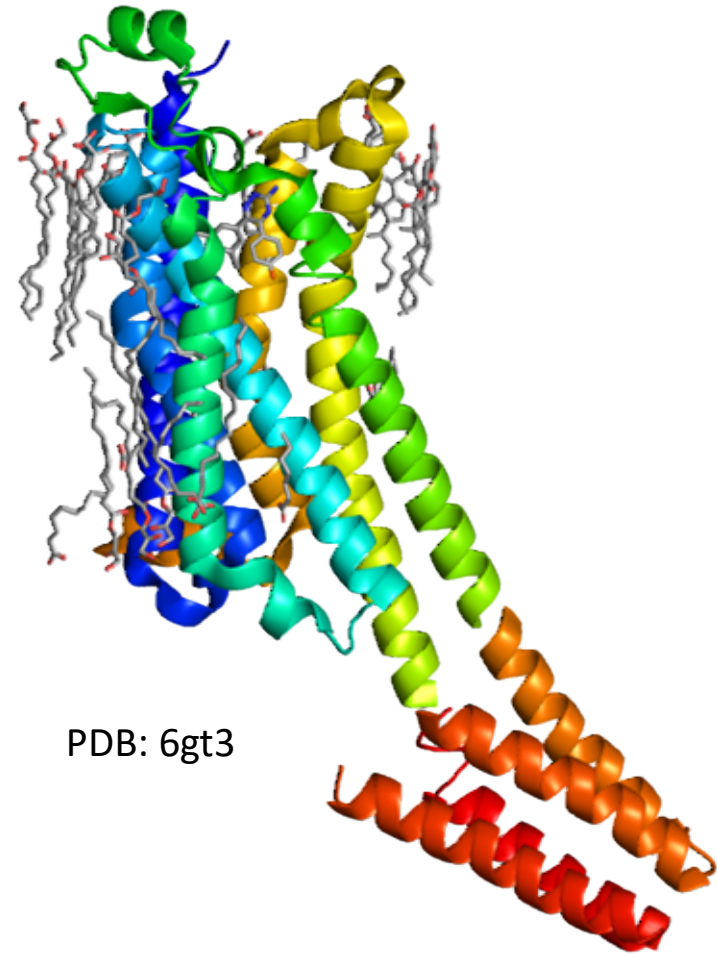
PDB: 5are, 5fil,
5fij, 5fik, 5ara,
5ari, 5arh

Structure-function relationship

- Drug design: e.g. HIV protease inhibitors, GPCR receptors



PDB: 3q70



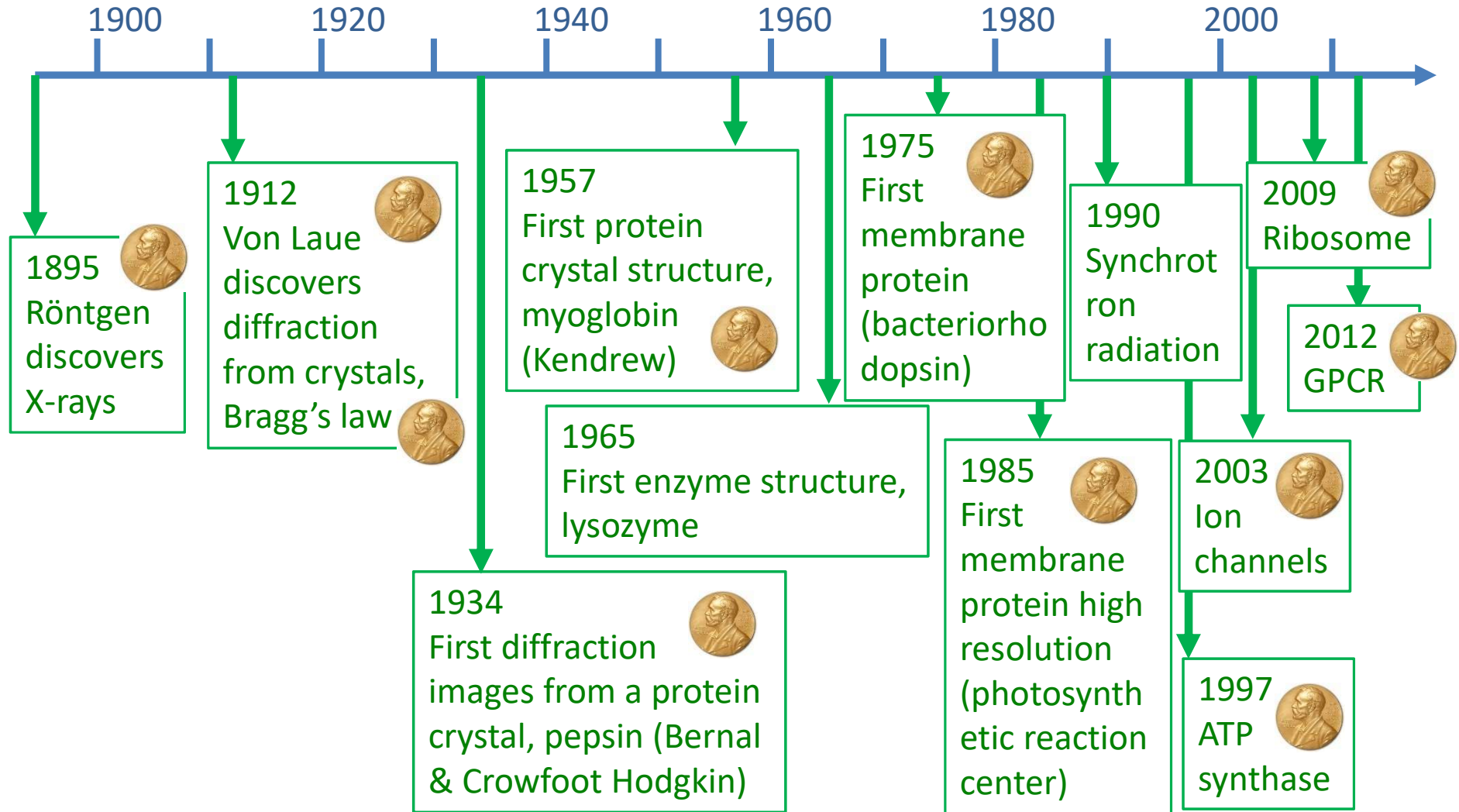
PDB: 6gt3

Structural biology: techniques

	X-ray crystallography	NMR	Electron Microscopy
Protein size	No limitation	< 80 KDa	> 50 kDa
Resolution	Atomic	Atomic	< 2 Å
First structure	1957	1985	Low res: 1975 Medium res: 1990 High res: 2015
Dynamics	No	Yes	(Yes)
Main bottlenecks	Crystallization	Isotope enrichment	Image analysis, model validation

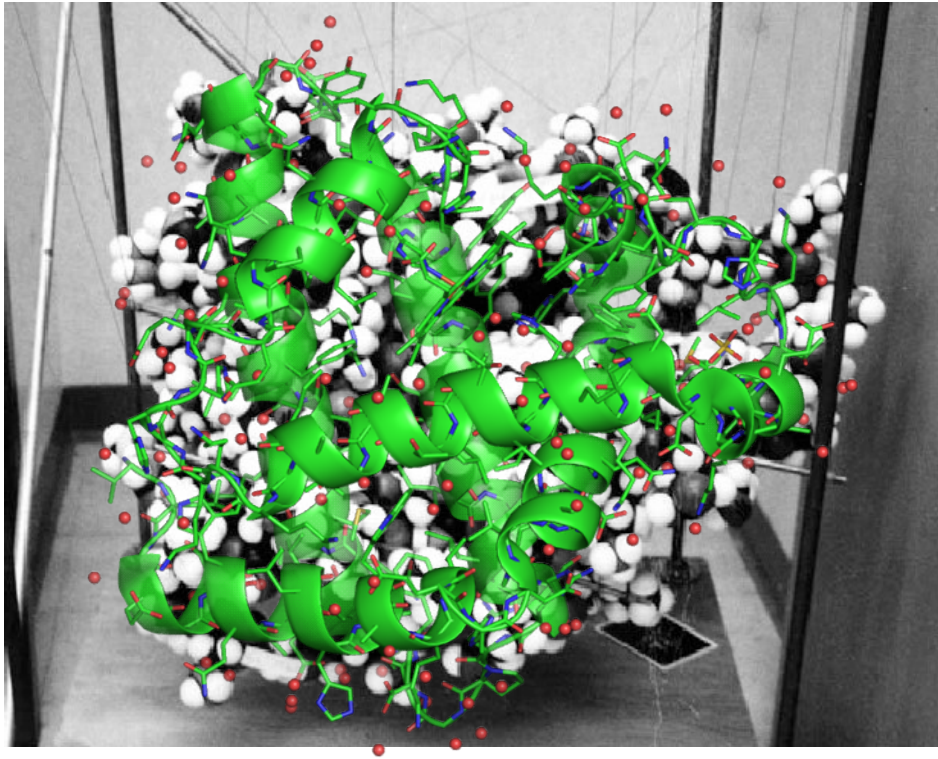
Different structural biology techniques give complementary results!!

Biocrystallography



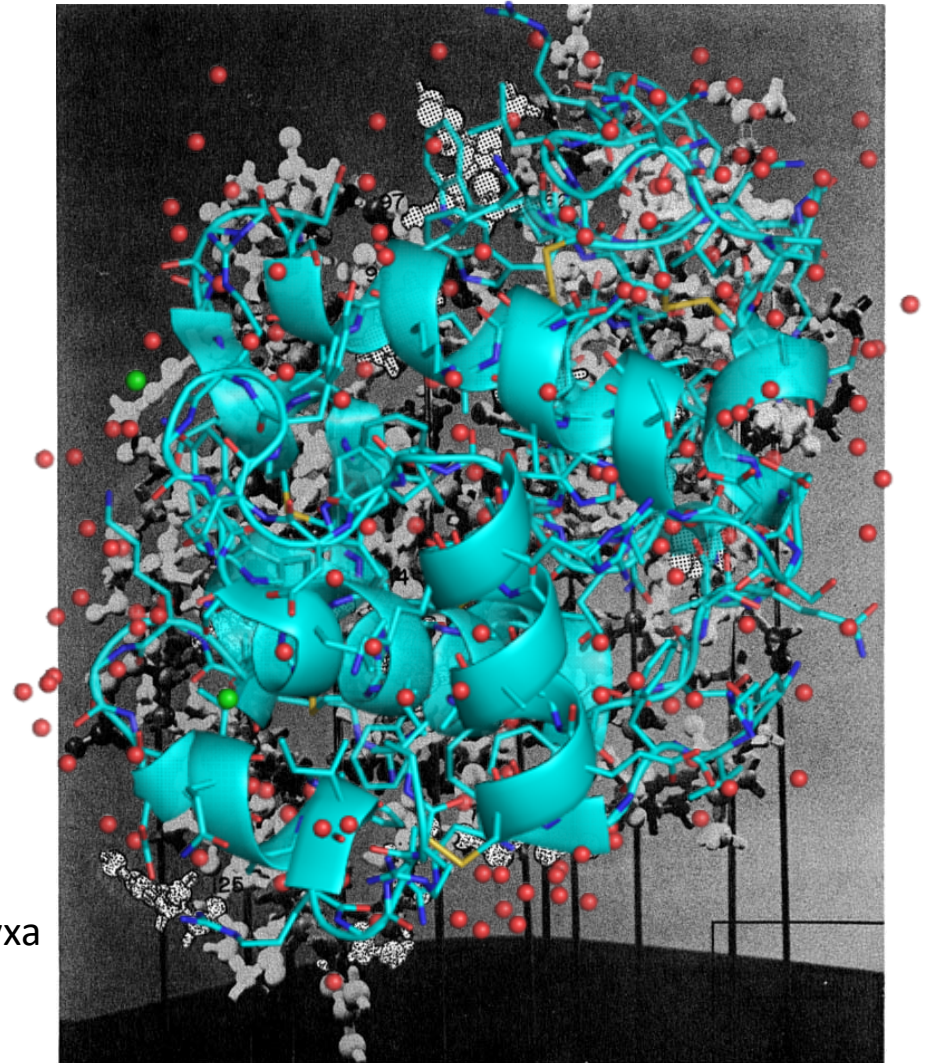
First protein structures determined by X-ray crystallography

- Myoglobin from sperm whale



PDB: 1vxa

- Lysozyme from chicken egg whites

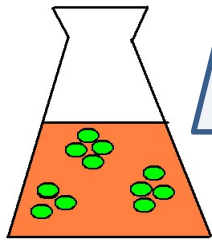


PDB: 1vxa

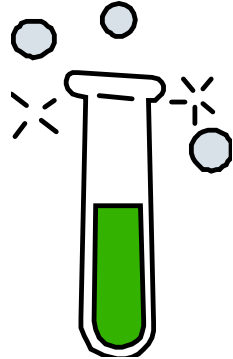
Bioinformatics

A biocrystallography experiment

Molecular biology

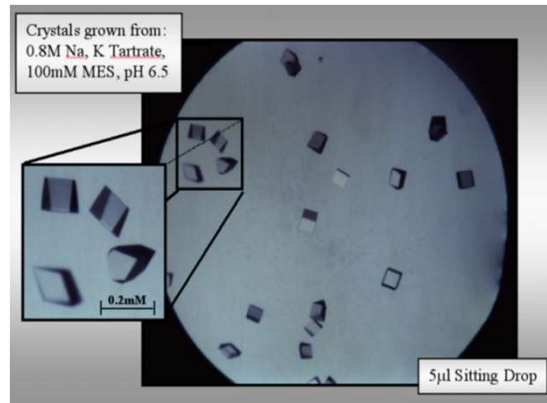
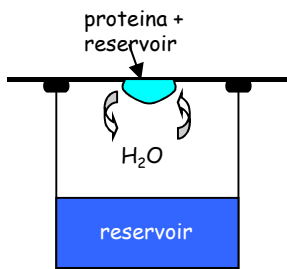


Expression and purification



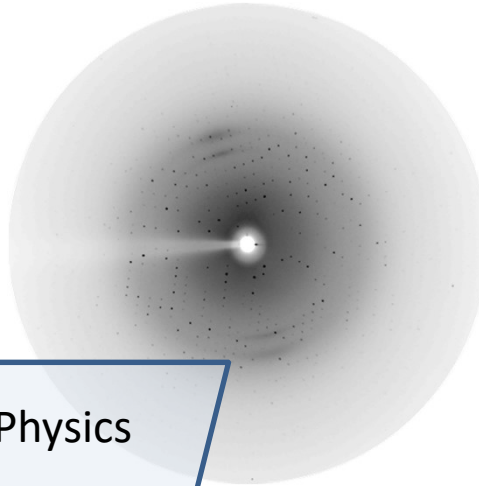
Chemistry

Crystallization

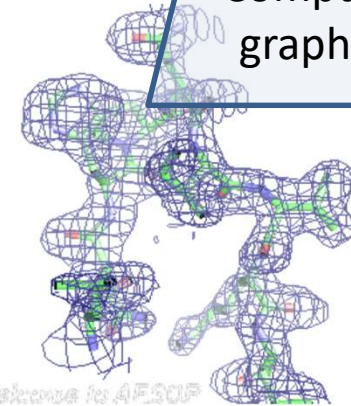


Physics

Diffraction data collection



Computer graphics



Structure refinement

Biology

Biochemistry

10 days to 10 years

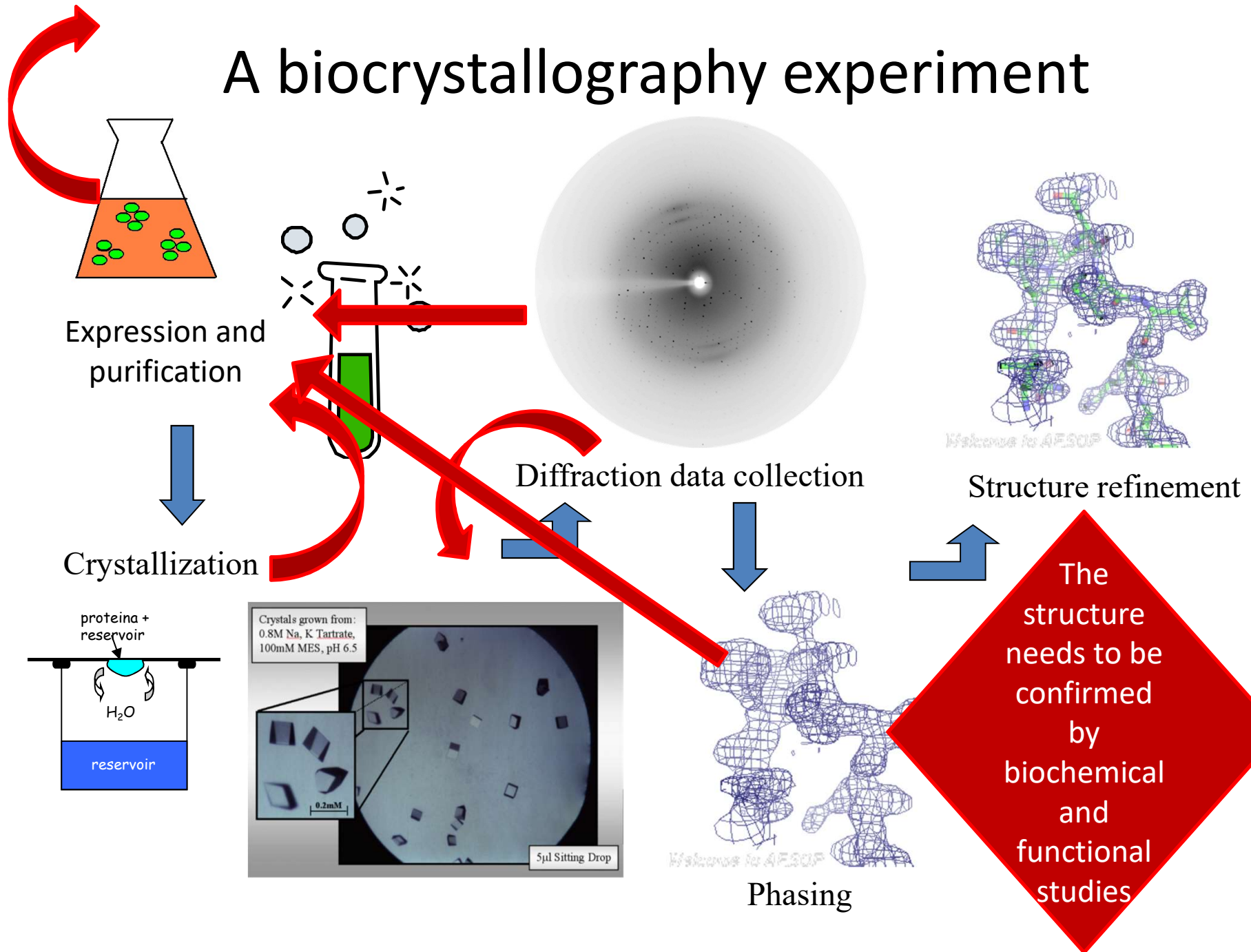
Software development

Mathematics

Statistics

Phasing

A biocrystallography experiment



Databank resources: PDB (www.rcsb.org)

RCSB PDB

Deposit ▾

Search ▾

Visualize ▾

Analyze ▾

Download ▾

Learn ▾

More ▾

MyPDB

Experimental Data & Validation

Experimental Data

Method: X-RAY DIFFRACTION

Resolution: 1.16 Å

R-Value Free: 0.157

R-Value Work: 0.138

Space Group: [I 4](#)

Unit Cell:

Length (Å)	Angle (°)
a = 124.872	$\alpha = 90.00$
b = 124.872	$\beta = 90.00$
c = 175.683	$\gamma = 90.00$

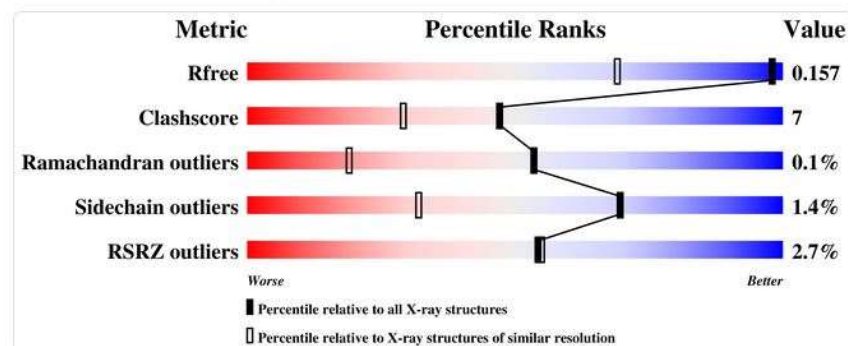
Software Package:

Software Name	Purpose
MOLREP	phasing
HKL-2000	data reduction
PHENIX	refinement
HKL-2000	data scaling

[View more in-depth experimental data](#)


Structure Validation


View [Full Validation Report](#) or [Ramachandran Plots](#)



Contact Us

Databank resources: EMDB (www.ebi.ac.uk/pdbe/emdb/)

EMBL-EBI  [Services](#) [Research](#) [Training](#) [About us](#)

 **Protein Data Bank in Europe**
Bringing Structure to Biology

Search [Advanced search](#)
Examples: [hemoglobin](#), [BRCA1_HUMAN](#)

[Feedback](#)

EMDB > EMD-0632

Rotavirus A-VP3 (RVA-VP3)

Source organism: [Rotavirus A](#) [28875]

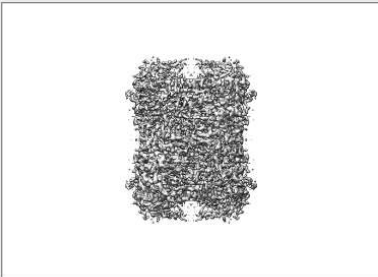
Fitted atomic model: [6o6b](#)

3Dbionotes: [available for this entry](#)

To be published

Single particle reconstruction
2.7Å resolution

Map released:
2020-03-11



Quick links

- [EMD-0632 overview](#)
- [Function and Biology](#)
- [Experiments and Validation](#)
- [View](#)
- [Downloads](#)
- [Volume viewer](#)
- [Volume slicer](#)
- [Visual analysis](#)

Function and Biology [Details](#) | **Experimental Information** [Details](#)

Sample name:	VP3	Resolution:	2.7Å
Ligand:	GUANOSINE-5'-MONOPHOSPHATE	Resolution method:	FSC 0.143 CUT-OFF
Proteins:	VP3, Protein VP3	Applied symmetry:	D2
		Reconstruction software:	RELION
		Microscope:	JEOL 3200FSC
		Detector:	GATAN K2 SUMMIT (4k x 4k)

Related entries

- [By authors](#)
- [By sample](#)
- [By organism](#)

Structure atomic coordinates: pdb file

RCSB PDB Deposit Search Visualize Analyze Download Learn More MyPDB

RCSB PDB 161470 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education
PROTEIN DATA BANK

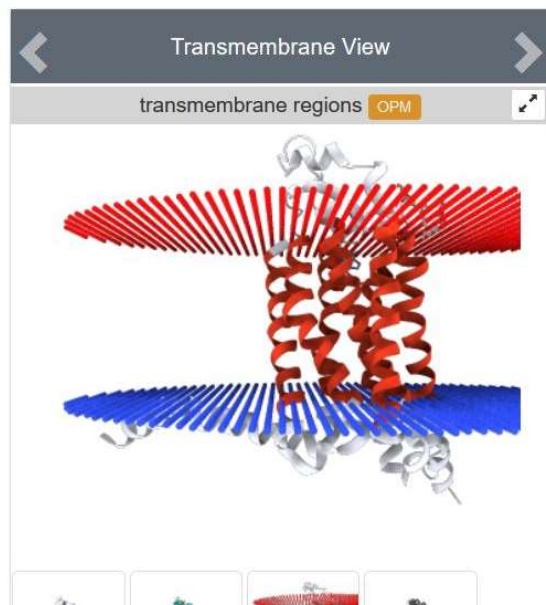
Search by PDB ID, author, macromolecule, sequence, or ligands Go

Advanced Search | Browse by Annotations

PDB-101 WORLDWIDE PDB PROTEIN DATA BANK EMDatabank Unified Data Resource for ISEM NDB NUCLEIC ACID DATABASE Worldwide Protein Data Bank Foundation

f t y d

- Structure Summary
- 3D View
- Annotations
- Sequence
- Sequence Similarity
- Structure Similarity
- Experiment



2YDO

Thermostabilised HUMAN A2a Receptor with adenosine

DOI: [10.2210/pdb2YDO/pdb](https://doi.org/10.2210/pdb2YDO/pdb)

Classification: [RECEPTOR](#)

Organism(s): [Homo sapiens](#)

Expression System: [Trichoplusia ni](#)

Mutation(s): 5

Deposited: 2011-03-23 Released: 2011-05-18

Deposition Author(s): [Lebon, G.](#), [Warne, T.](#), [Edwards, P.C.](#), [Bennett, K.](#), [L...](#)

Experimental Data Snapshot

Method: X-RAY DIFFRACTION

Resolution: 3 Å

R-Value Free: 0.269

R-Value Work: 0.244

wwPDB Validation

Metric	Value
Clashscore	1.8
Ramachandran outliers	0.0%
Sidechain outliers	0.0%

Display Files Download Files

- FASTA Sequence
- PDB Format
- PDB Format (gz)
- PDBx/mmCIF Format
- PDBx/mmCIF Format (gz)
- PDBML/XML Format (gz)
- Biological Assembly 1
- Structure Factors (CIF)
- Structure Factors (CIF - gz)

Structure atomic coordinates: pdb file

```
2ydo.pdb - Blocco note di Windows
File Modifica Formato Visualizza ?
HEADER RECEPTOR 23-MAR-11 2YDO
TITLE THERMOSTABILISED HUMAN A2A RECEPTOR WITH ADENOSINE BOUND
COMPND MOL_ID: 1;
COMPND 2 MOLECULE: ADENOSINE RECEPTOR A2A;
COMPND 3 CHAIN: A;
COMPND 4 FRAGMENT: RESIDUES 1-317;
COMPND 5 SYNONYM: THERMOSTABILISED HUMAN A2A RECEPTOR;
COMPND 6 ENGINEERED: YES;
COMPND 7 MUTATION: YES
SOURCE MOL_ID: 1;
SOURCE 2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE 3 ORGANISM_COMMON: HUMAN;
SOURCE 4 ORGANISM_TAXID: 9606;
SOURCE 5 TISSUE: BRAIN;
SOURCE 6 EXPRESSION_SYSTEM: TRICHOPLUSIA NI;
SOURCE 7 EXPRESSION_SYSTEM_COMMON: CABBAGE LOOPER;
SOURCE 8 EXPRESSION_SYSTEM_TAXID: 7111;
SOURCE 9 EXPRESSION_SYSTEM_CELL_LINE: HIGH FIVE;
SOURCE 10 EXPRESSION_SYSTEM_VECTOR_TYPE: BACULOVIRUS;
SOURCE 11 EXPRESSION_SYSTEM_PLASMID: PBACPAK8
KEYWDS RECEPTOR, G PROTEIN COUPLED RECEPTOR, SEVEN-HELIX RECEPTOR, AGONIST
KEYWDS 2 BOUND FORM, THERMOSTABILISING POINT MUTATIONS, GPCR, 7TM RECEPTOR
EXPDTA X-RAY DIFFRACTION
AUTHOR G. LEBON, T. WARNE, P. C. EDWARDS, K. BENNETT, C. J. LANGMEAD, A. G. W. LESLIE,
AUTHOR 2 C. G. TATE
REVDAT 4 03-APR-19 2YDO 1 SOURCE
REVDAT 3 22-JUN-11 2YDO 1 JRNL
REVDAT 2 01-JUN-11 2YDO 1 REMARK MASTER
REVDAT 1 18-MAY-11 2YDO 0
JRNL AUTH G. LEBON, T. WARNE, P. C. EDWARDS, K. BENNETT, C. J. LANGMEAD,
JRNL AUTH 2 A. G. W. LESLIE, C. G. TATE
JRNL TITL AGONIST-BOUND ADENOSINE A(2A) RECEPTOR STRUCTURES REVEAL
JRNL TITL 2 COMMON FEATURES OF GPCR ACTIVATION.
JRNL REF NATURE V 474 521 2011
```

Information
about the
protein

Information
about the
publication

Structure atomic coordinates: pdb file

```
2ydo.pdb - Blocco note di Windows
File Modifica Formato Visualizza ?
REMARK 200
REMARK 200 EXPERIMENTAL DETAILS
REMARK 200 EXPERIMENT TYPE : X-RAY DIFFRACTION
REMARK 200 DATE OF DATA COLLECTION : 09-DEC-10
REMARK 200 TEMPERATURE (KELVIN) : 100
REMARK 200 PH : 7.6
REMARK 200 NUMBER OF CRYSTALS USED : 2
REMARK 200
REMARK 200 SYNCHROTRON (Y/N) : Y
REMARK 200 RADIATION SOURCE : DIAMOND
REMARK 200 BEAMLINE : I24
REMARK 200 X-RAY GENERATOR MODEL : NULL
REMARK 200 MONOCHROMATIC OR LAUE (M/L) : M
REMARK 200 WAVELENGTH OR RANGE (A) : 0.9778
REMARK 200 MONOCHROMATOR : NULL
REMARK 200 OPTICS : NULL
REMARK 200
REMARK 200 DETECTOR TYPE : PIXEL
REMARK 200 DETECTOR MANUFACTURER : DECTRIS PILATUS 6M
REMARK 200 INTENSITY-INTEGRATION SOFTWARE : MOSFLM
REMARK 200 DATA SCALING SOFTWARE : SCALA
REMARK 200
REMARK 200 NUMBER OF UNIQUE REFLECTIONS : 10556
REMARK 200 RESOLUTION RANGE HIGH (A) : 3.000
REMARK 200 RESOLUTION RANGE LOW (A) : 79.340
REMARK 200 REJECTION CRITERIA (SIGMA(I)) : 0.000
REMARK 200
REMARK 200 OVERALL.
REMARK 200 COMPLETENESS FOR RANGE (%) : 93.9
REMARK 200 DATA REDUNDANCY : 2.600
REMARK 200 R MERGE (I) : 0.10000
REMARK 200 R SYM (I) : NULL
REMARK 200 <I/SIGMA(I)> FOR THE DATA SET : 7.1000
```

Information
about the
crystallographic
experiment

Structure atomic coordinates: pdb file

```
File Modifica Formato Visualizza ?
SITE      3 AC1 11 HOH A2016  HOH A2017  HOH A2018
SITE      1 AC2  1 TYR A 179
SITE      1 AC3  5 GLY A 142  TRP A 143  ASN A 144  ASN A 145
SITE      1 AC3  5 GLN A 148
CRYST1    76.465  98.869  79.516  90.00  93.49  90.00 C 1 2 1 4
ORIGX1    1.000000  0.000000  0.000000  0.000000
ORIGX2    0.000000  1.000000  0.000000  0.000000
ORIGX3    0.000000  0.000000  1.000000  0.000000
SCALE1    0.013078  0.000000  0.000798  0.000000
SCALE2    0.000000  0.010114  0.000000  0.000000
SCALE3    0.000000  0.000000  0.012500  0.000000
ATOM      1  N  SER  A  6  -28.148  4.590  -7.800  1.00 113.33  N
ATOM      2  CA SER  A  6  -26.785  4.701  -7.207  1.00 115.91  C
ATOM      3  C  SER  A  6  -26.419  6.159  -6.970  1.00 114.54  C
ATOM      4  O  SER  A  6  -26.103  6.886  -7.915  1.00 110.10  O
ATOM      5  CB SER  A  6  -25.744  4.037  -8.113  1.00 116.34  C
ATOM      6  OG SER  A  6  -26.087  2.689  -8.379  1.00 121.40  O
ATOM      7  N  SER  A  7  -26.458  6.572  -5.703  1.00 116.37  N
ATOM      8  CA SER  A  7  -26.153  7.952  -5.306  1.00 112.95  C
ATOM      9  C  SER  A  7  -24.758  8.391  -5.751  1.00 109.79  C
ATOM     10  O  SER  A  7  -24.497  9.586  -5.902  1.00 104.20  O
ATOM     11  CB SER  A  7  -26.313  8.125  -3.794  1.00 113.79  C
ATOM     12  OG SER  A  7  -25.474  7.228  -3.088  1.00 117.64  O
ATOM     13  N  VAL  A  8  -23.879  7.409  -5.959  1.00 108.84  N
ATOM     14  CA VAL  A  8  -22.535  7.626  -6.501  1.00 108.75  C
ATOM     15  C  VAL  A  8  -22.622  8.258  -7.895  1.00 110.01  C
ATOM     16  O  VAL  A  8  -21.895  9.207  -8.205  1.00 105.91  O
ATOM     17  CB VAL  A  8  -21.739  6.295  -6.599  1.00 108.46  C
ATOM     18  CG1 VAL  A  8  -20.240  6.568  -6.638  1.00 107.74  C
ATOM     19  CG2 VAL  A  8  -22.087  5.355  -5.443  1.00 105.56  C
ATOM     20  N  TYR  A  9  -23.521  7.717  -8.719  1.00 108.80  N
ATOM     21  CA TYR  A  9  -23.812  8.252 -10.048  1.00 102.10  C
ATOM     22  C  TYR  A  9  -24.618  9.551  -9.966  1.00  98.51  C
ATOM     23  O  TYR  A  9  -24.331 10.506 -10.688  1.00  94.86  O
```

Unit cell
and
symmetry

List of atoms
with:

1. Atom name
2. Residue type and number
3. Chain
4. Cartesian coordinates
5. Occupancy
6. Thermal factor
7. Atom type

Structure atomic coordinates: mmCIF file

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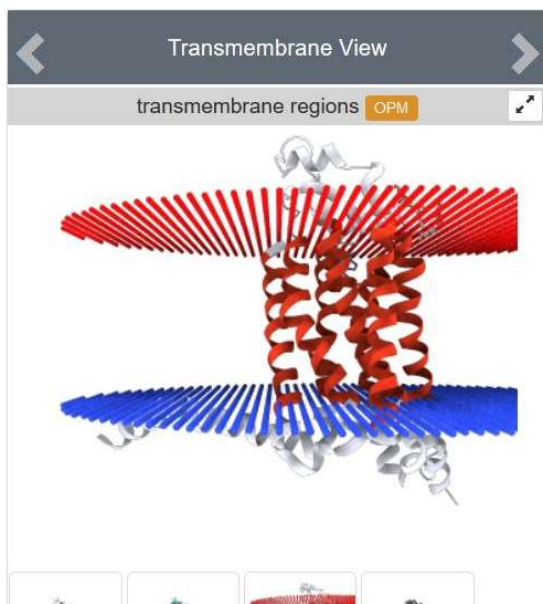
RCSB PDB PROTEIN DATA BANK 161470 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education

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PDB-101 WORLDWIDE PDB PROTEIN DATA BANK EMDatabank Unified Data Resource for SDEM NUCLEIC ACID DATABASE Worldwide Protein Data Bank Foundation

- Structure Summary
- 3D View
- Annotations
- Sequence
- Sequence Similarity
- Structure Similarity
- Experiment



2YDO

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Experimental Data Snapshot

Method: X-RAY DIFFRACTION

Resolution: 3 Å

R-Value Free: 0.269

R-Value Work: 0.244

wwPDB Validation

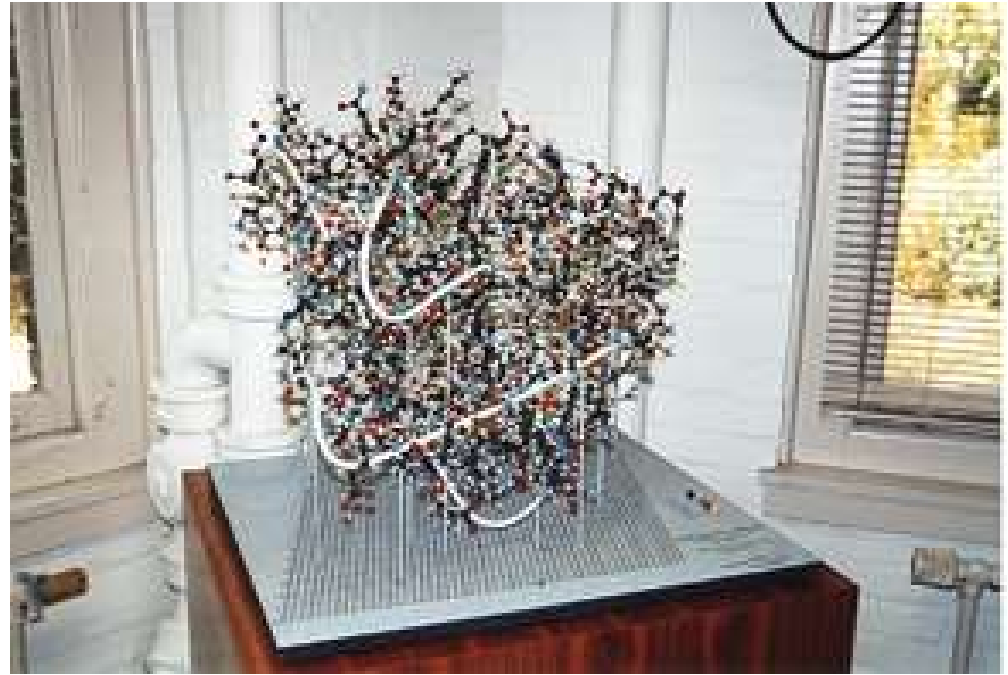
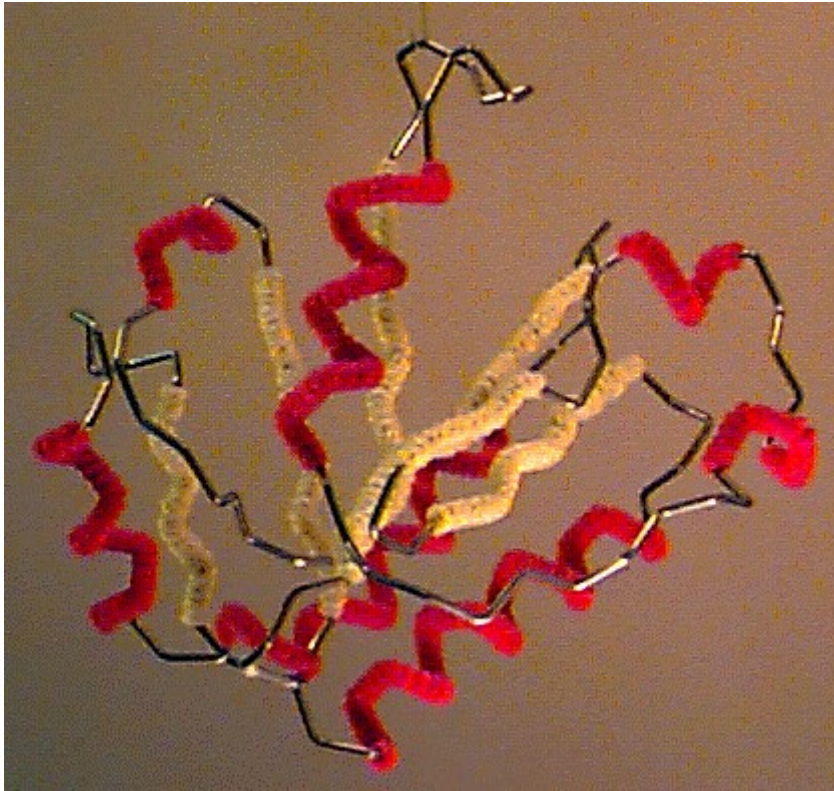
Metric	Value
Clashscore	1.8
Ramachandran outliers	0.0%
Rotamer outliers	0.0%

Display Files Download Files

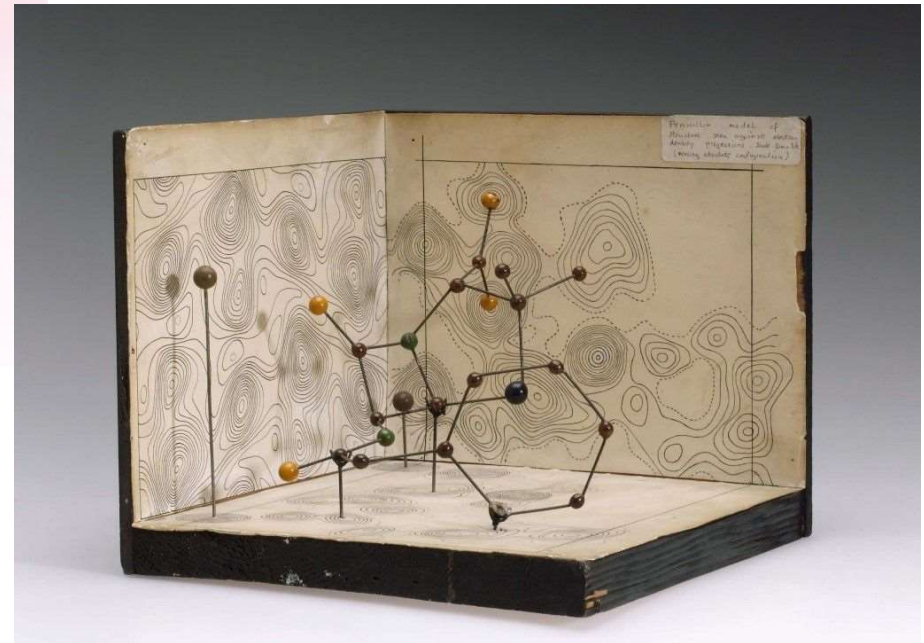
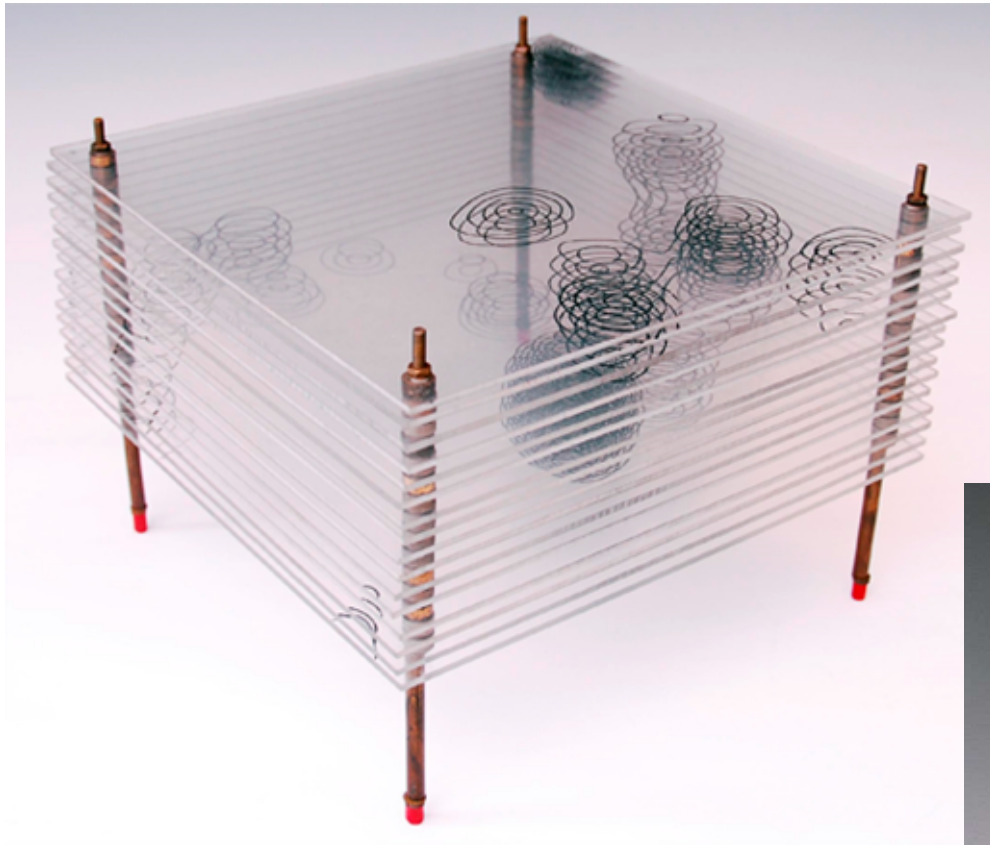
- FASTA Sequence
- PDB Format
- PDB Format (gz)
- PDBx/mmCIF Format**
- PDBx/mmCIF Format (gz)
- PDBML/XML Format (gz)
- Biological Assembly 1
- Structure Factors (CIF)**
- Structure Factors (CIF - gz)
- 2fo-fc Map (DMNA)

for the electron density!!!

Graphical software: in the old days...



Graphical software: in the old days...



Graphical software: in the old days...

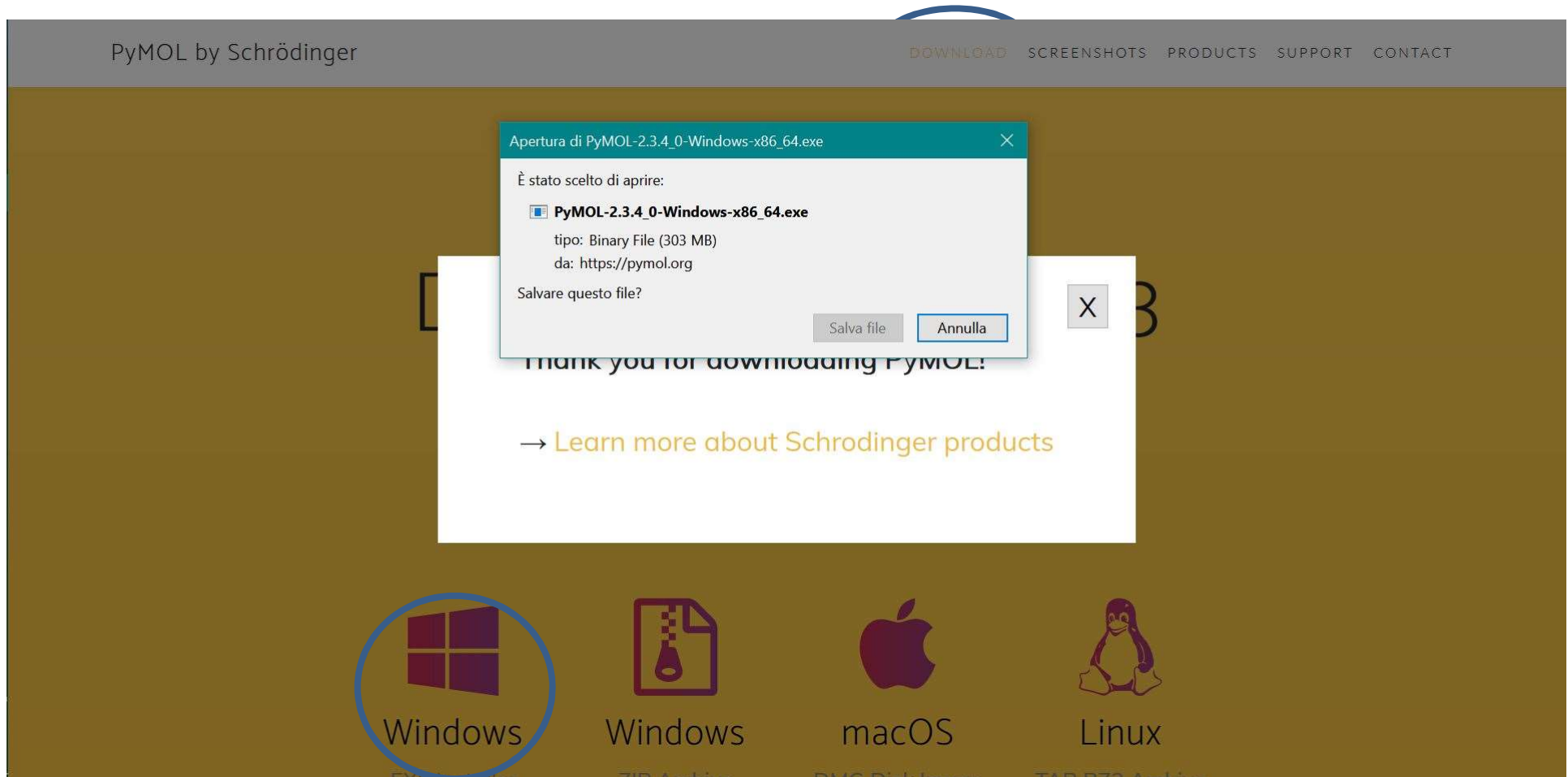


Graphical software:... today



Graphical software: Pymol

1. Download: <https://pymol.org/2/>



2. Open and load pdb file

The screenshot displays the PyMOL software interface. The top window, titled "PyMOL Tcl/Tk GUI", contains a command history window with the following text:

```
COMPND  MOL_ID: 1;  
COMPND  2 MOLECULE: INSULIN;  
COMPND  3 CHAIN: A, C;  
COMPND  4 MOL_ID: 2;  
COMPND  5 MOLECULE: INSULIN;  
COMPND  6 CHAIN: B, D  
ObjectMolecule: Read secondary structure assignments.  
ObjectMolecule: Read crystal symmetry information.  
Symmetry: Found 9 symmetry operators.  
CmdLoad: "C:/Users/Rita/Downloads/1zni.pdb" loaded as "1zni".
```

Below the command window is a toolbar with buttons for "Reset", "Zoom", "Draw", "Ray", "Rock", "Unpick", "Deselect", "Get View", navigation arrows, "Command", and "Builder".

The bottom window, titled "PyMOL Viewer", shows a 3D molecular structure of insulin. The structure is rendered in a stick representation with green and blue atoms. The background is black, and the structure is surrounded by red asterisks representing symmetry-related molecules.

On the right side of the viewer window is a legend table:

all	A	S	H	L	C
1zni	A	S	H	L	C

At the bottom right of the viewer window is a keyboard control menu:

```
Mouse Mode 3-Button Viewing  
Buttons L M R Wheel  
& Keys Rota Move MovZ Slab  
Shft +Box -Box Clip MovS  
Ctrl +/- PKAt Pk1 MvSZ  
CtSh Sele Orig Clip MovZ  
SnglClk +/- Cent Menu  
DblClk Menu - PKAt  
Selecting Residues  
Frame [ 1/ 11] 28/sec
```

3. Menu options

The image shows the PyMOL software interface. The top window, titled "PyMOL Tcl/Tk GUI", contains a menu bar (File, Edit, Build, Movie, Display, Setting, Scene, Mouse, Wizard, Plugin, Help, Tutorial) and a command console. The console displays the following text:

```
COMPND  MOL_ID: 1;  
COMPND  2 MOLECULE: INSULIN;  
COMPND  3 CHAIN: A, C;  
COMPND  4 MOL_ID: 2;  
COMPND  5 MOLECULE: INSULIN;  
COMPND  6 CHAIN: B, D  
ObjectMolecule: Read secondary structure assignments.  
ObjectMolecule: Read crystal symmetry information.  
Symmetry: Found 9 symmetry operators.  
CmdLoad: "C:/Users/Rita/Downloads/1zni.pdb" loaded as "1zni".
```

The bottom window, titled "PyMOL Viewer", displays a 3D ribbon representation of the insulin protein structure in green. A context menu is open over the structure, showing the following options:

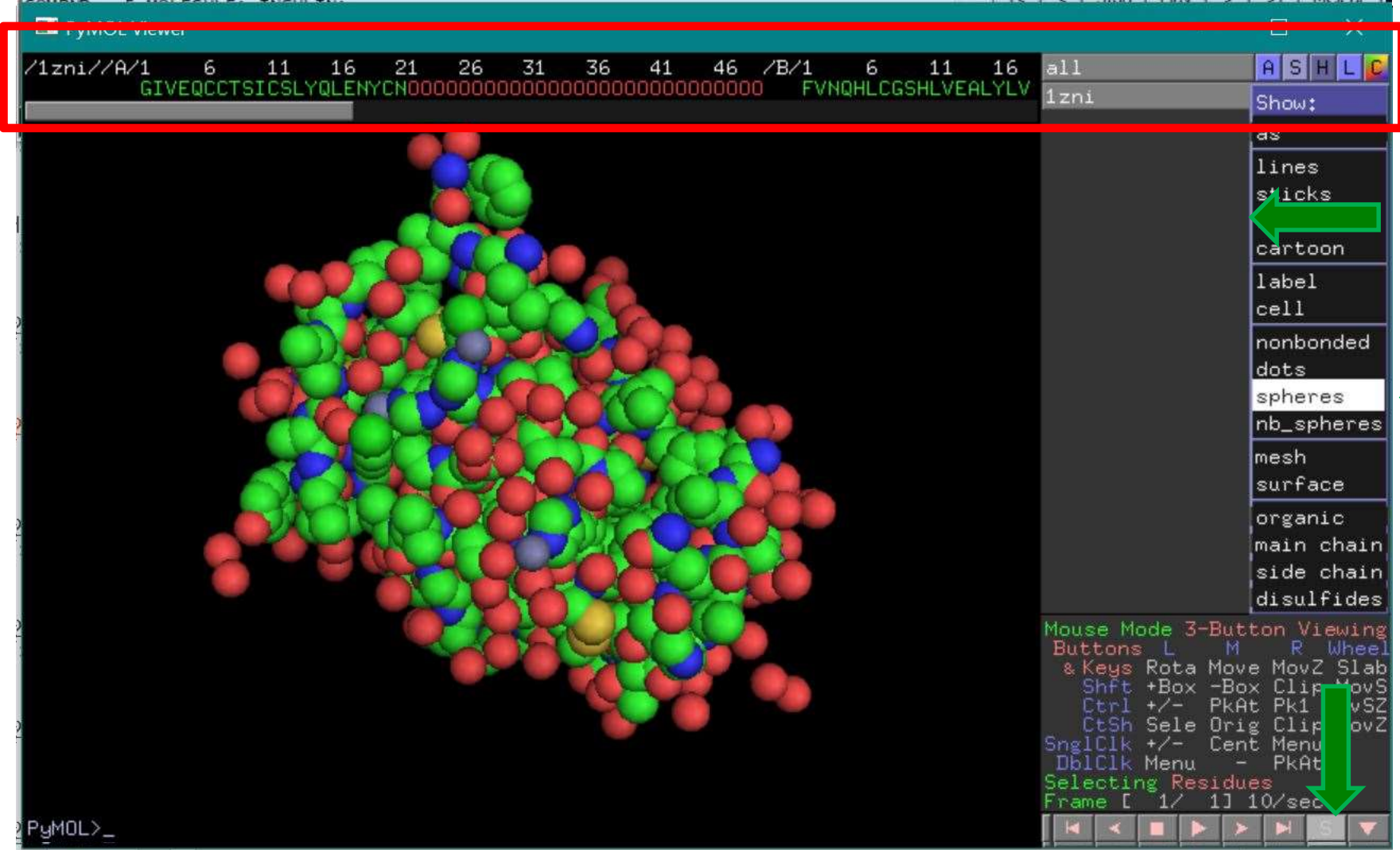
- all
- 1zni
- Color:
- by element
- by chain
- by ss
- spectrum
- auto
- reds
- greens
- blues
- yellows
- magentas
- cyans
- oranges
- tints
- grays

At the bottom of the viewer window, there is a mouse control menu:

```
Mouse Mode 3-Button Viewing  
Buttons L M R Wheel  
& Keys Rota Move MovZ Slab  
Shft +Box -Box Clip MovS  
Ctrl +/- PkAt Pk1 MvSZ  
CtSh Sele Orig Clip MovZ  
SnglClk +/- Cent Menu  
DblClk Menu - PkAt  
Selecting Residues  
Frame [ 1/ 1] 8/sec
```

Visualization options:

spheres



Graphical software: UCSF Chimera

1. Download: www.cgl.ucsf.edu/chimera/

UCSF CHIMERA
an Extensible Molecular Modeling System

Download Chimera

- [Daily Builds](#)
- [Snapshot Releases](#)
- [Unsupported Releases](#)
- [Old Releases](#)
- [Bug Tracking System](#)
- [Licensing Information](#)
- [Experimental Chimera Features](#)
- [Plug-ins on the Web](#)
- [Graphics Driver Bugs](#)
- [Benchmark Results](#)
- [Chimera Source Code](#)
- [Cygwin Source Code](#)

Current Production Releases

- See the [release notes](#) for a list of new features and other information.
- For [more recent changes](#), use the [snapshot](#) and [daily](#) builds; they are less tested but usually reliable.

- 64-bit Releases:**

Platform	Installer, Size, and Checksum	Date	Notes
Microsoft Windows 64-bit	chimera-1.14-win64.exe Size: 152229635 bytes MD5: a3eddc25f84e55c4c49ff6f6f7643b	Nov 13, 2019	Instructions Documentation Runs on Windows 7 or later.
Mac OS X 64-bit	chimera-1.14-mac64.dmg Size: 135741903 bytes MD5: c763aa87af928ae6dc7d39a8f6bf92d5	Nov 13, 2019	Instructions Documentation Runs on Mac OS X 10.10 or later.

2. Open and load pdb file



3. Load a map file (electron density!) (www.ebi.ac.uk/pdbe/emdb/)

EMBL-EBI Services Research Training About us

Protein Data Bank in Europe
Bringing Structure to Biology

Search [Advanced search](#)

Examples: [hemoglobin](#), [BRCA1_HUMAN](#)

Feedback

EMDB > EMD-0632

Rotavirus A-VP3 (RVA-VP3)

Source organism: [Rotavirus A](#) [28875]

Fitted atomic model: [6o6b](#)

3Dbionotes: [available for this entry](#)

To be published

Single particle reconstruction
2.7 Å resolution

Map released:
2020-03-11

Function and Biology [Details](#) | **Experimental Information** [Details](#)

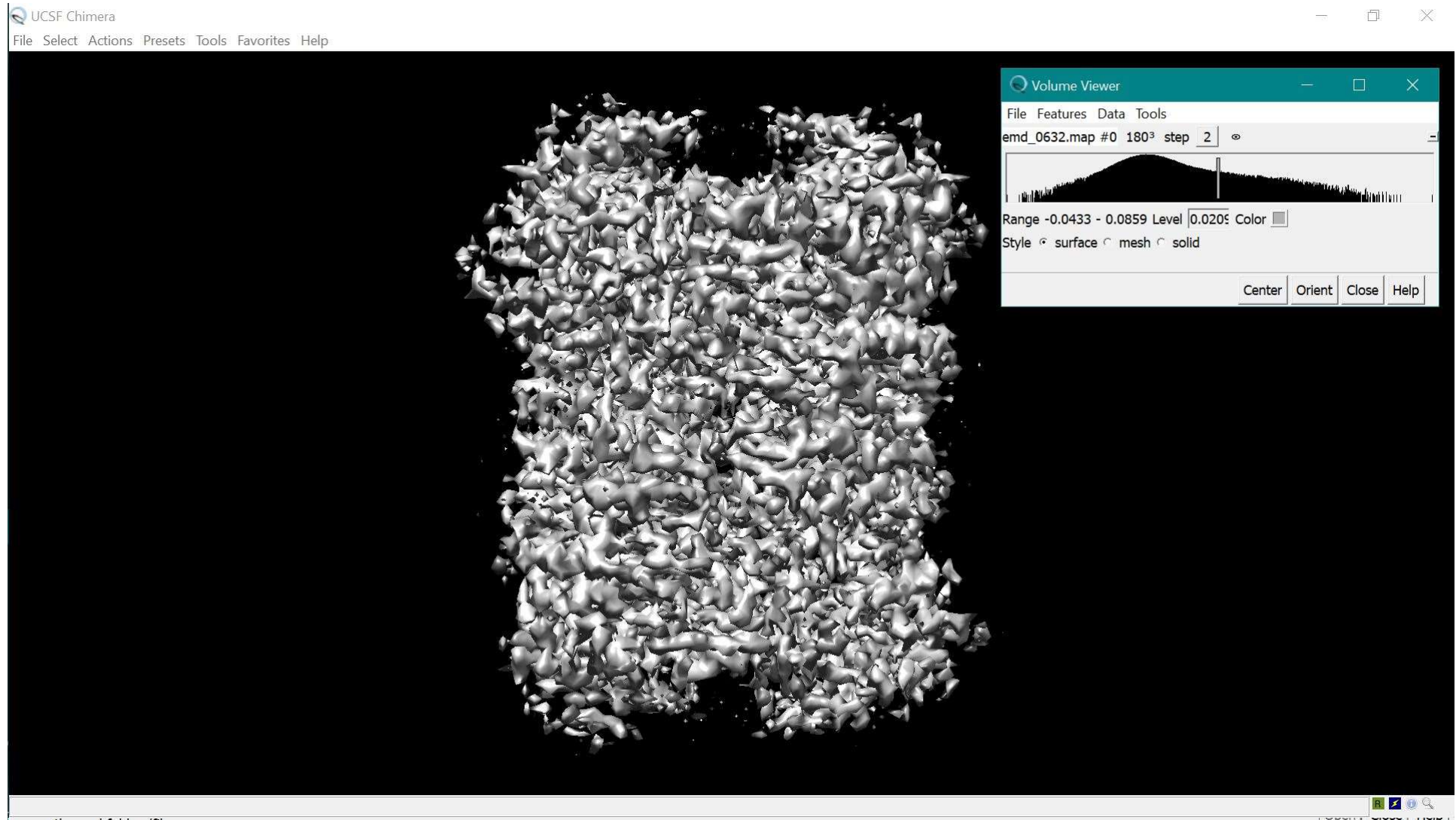
Sample name:	VP3	Resolution:	2.7 Å
Ligand:	GUANOSINE-5'-MONOPHOSPHATE	Resolution method:	FSC 0.143 CUT-OFF
Proteins:	VP3, Protein VP3	Applied symmetry:	D2
		Reconstruction software:	RELION
		Microscope:	JEOL 3200FSC
		Detector:	GATAN K2 SUMMIT (4k x 4k)

Quick links

- EMD-0632 overview
- [Function and Biology](#)
- [Experiments and Validation](#)
- View
- Downloads** ←
- Map (gz)
- Experimental metadata (xml)
- Bundle (tar.gz)
- Bundle (zip)
- Volume viewer
- Volume slicer
- Visual analysis

Related entries

3. Load a map file (electron density!)



99.Animation!

The image shows the UCSF Chimera software interface. The main window displays a protein structure as a yellow ribbon on a black background. The 'Animation' panel is open on the right, showing a timeline with four scenes labeled '1: 4', '2: 2', '3: 1', and '4: 1'. A red arrow points to the play button in the timeline controls, and another red arrow points to the stop button. The 'Actions' panel shows 'Rock' and 'Roll' actions. The status bar at the bottom indicates 'Movie saved to \C:Users\...\Bicristallografia\test_chimera.avi'.

UCSF Chimera
File Select Actions Presets Tools Favorites Help

Animation

Scenes

1 2 3 4

Actions

Rock Roll

Timeline

1: 4 2: 2 3: 1 4: 1

Timeline: 1 (4 of 4)

Movie saved to \C:Users\...\Bicristallografia\test_chimera.avi

99.Animation!

