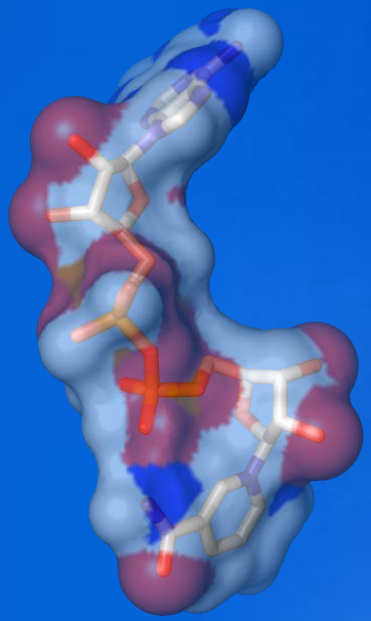
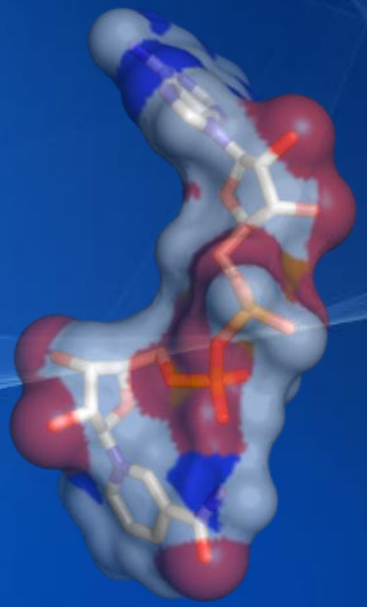
7600080 – Biologia Molecular Estrutural





Prof. Rafael V. C. Guido

rvcguido@ifsc.usp.br

Aula 03

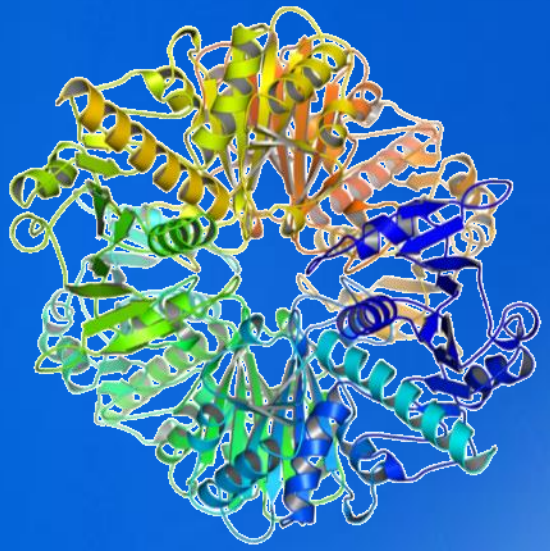
Bacharelado em Ciências Físicas e Biomoleculares

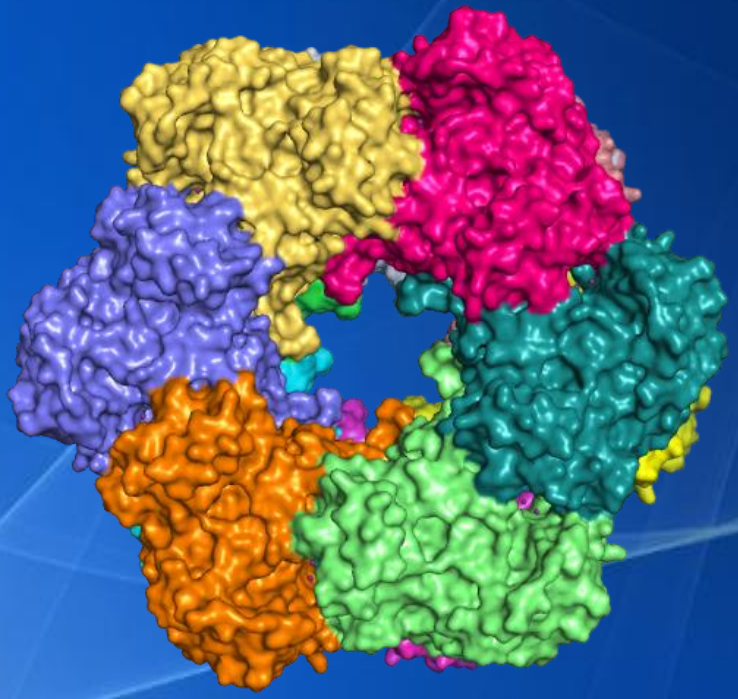
Instituto de Física de São Carlos - USP

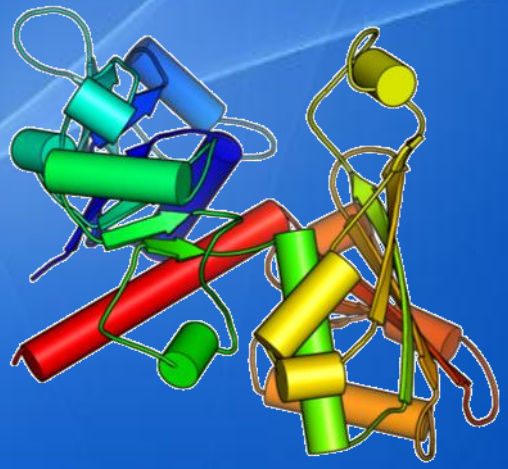
Objetivos

- Visualização de estruturas de macromoléculas
- Representação de estruturas de macromoléculas

Visualização e Representação de Estruturas







História

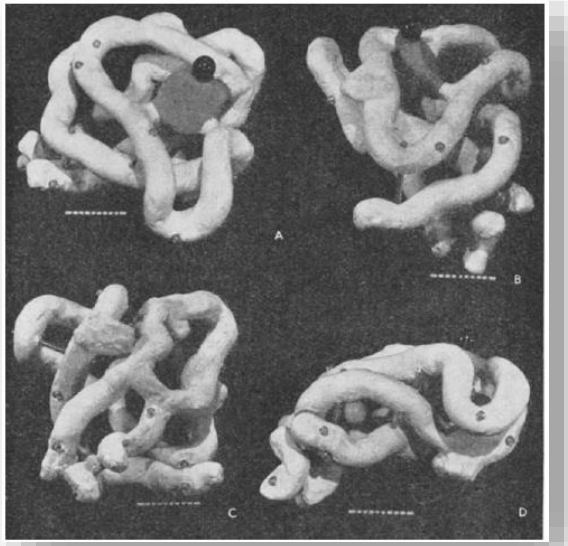
John Kendrew e Max Perutz e os modelos 3D de proteínas

Jonh Kendrew – Mioglobina (1958)

662 NATURE March 8, 1958 Vol. 181

A THREE-DIMENSIONAL MODEL OF THE MYOGLOBIN MOLECULE OBTAINED BY X-RAY ANALYSIS

By Drs. J. C. KENDREW, G. BODO, H. M. DINTZIS, R. G. PARRISH and H. WYCKOFF
Medical Research Council Unit for Molecular Biology, Cavendish Laboratory, Cambridge
AND
D. C. PHILLIPS
Davy Faraday Laboratory, The Royal Institution, London

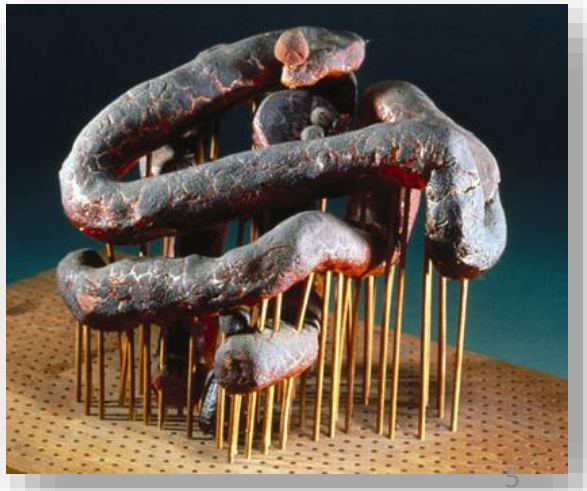


422 NATURE February 13, 1960 Vol. 185

STRUCTURE OF MYOGLOBIN

A THREE-DIMENSIONAL FOURIER SYNTHESIS AT 2 Å. RESOLUTION

By Drs. J. C. KENDREW, R. E. DICKERSON, B. E. STRANDBERG, R. G. HART and D. R. DAVIES*
Medical Research Council Unit for Molecular Biology, Cavendish Laboratory, Cambridge
AND
D. C. PHILLIPS and V. C. SHORE
Davy Faraday Laboratory, The Royal Institution, London



Max Perutz – Hemoglobina (1960)

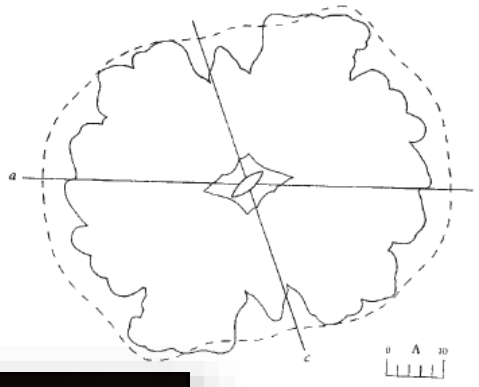
STRUCTURE OF HÆMOGLOBIN

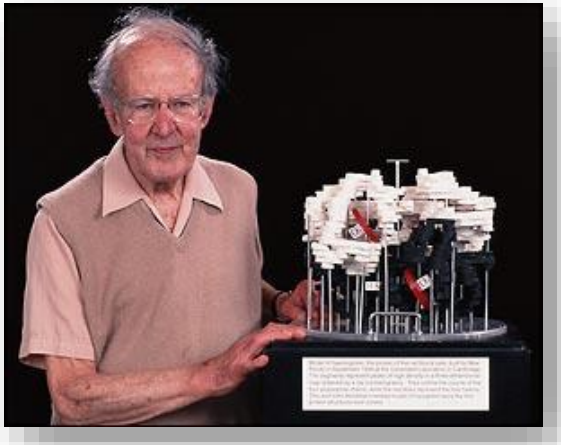
A THREE-DIMENSIONAL FOURIER SYNTHESIS AT 5·5-Å. RESOLUTION, OBTAINED BY X-RAY ANALYSIS

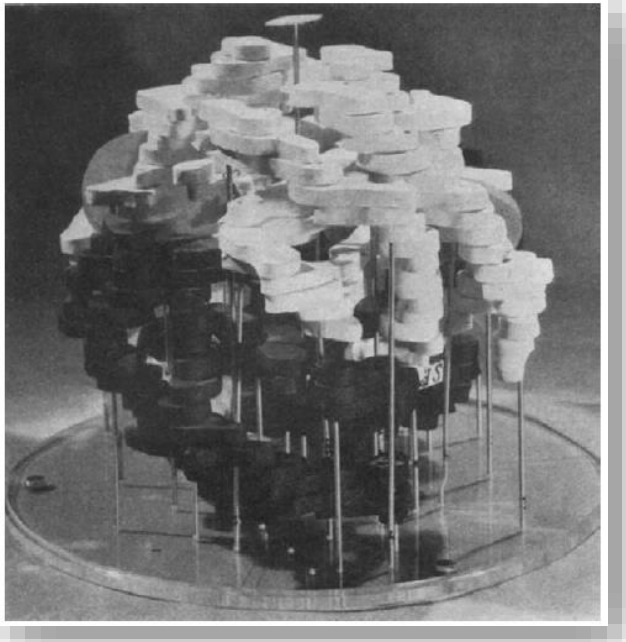
By Dr. M. F. PERUTZ, F.R.S., Dr. M. G. ROSSMANN, ANN F. CULLIS, HILARY MUIRHEAD and Dr. GEORG WILL
Medical Research Council Unit for Molecular Biology, Cavendish Laboratory, University of Cambridge
AND
Dr. A. C. T. NORTH
Medical Research Council External Staff, Davy Faraday Research Laboratory, Royal Institution, London, W.1

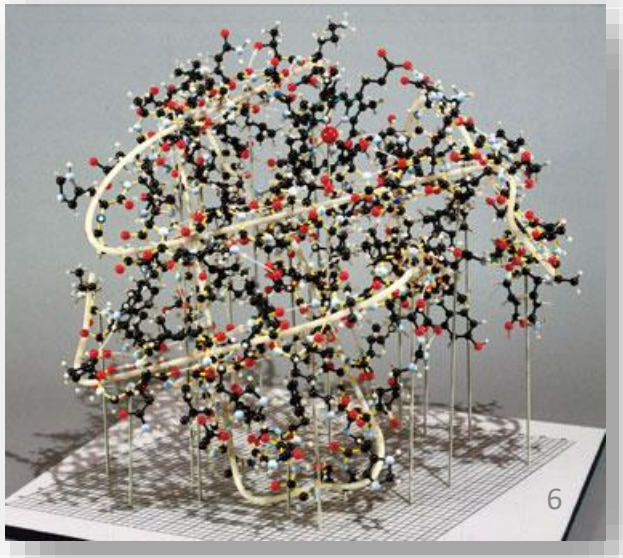
VERTEBRATE hæmoglobin is a protein of molecular weight 67,000. Four of its 10,000 atoms are iron atoms which are combined with protoporphyrin to form four hæm groups. The remaining atoms are in four polypeptide chains of roughly equal size, which are identical in pairs[1–3]. Their amino-acid sequence is still largely unknown.

We have used horse oxy- or met-hæmoglobin because it crystallizes in a form especially suited for X-ray analysis, and employed the method of isomorphous replacement with heavy atoms to determine the phase angles of the diffracted rays[4–7]. The Fourier synthesis which we have calculated shows that hæmoglobin consists of four sub-units in a tetrahedral array and that each sub-unit closely resembles Kendrew's model of sperm whale myoglobin[4]. The four hæm groups lie in separate pockets on the surface of the molecule.

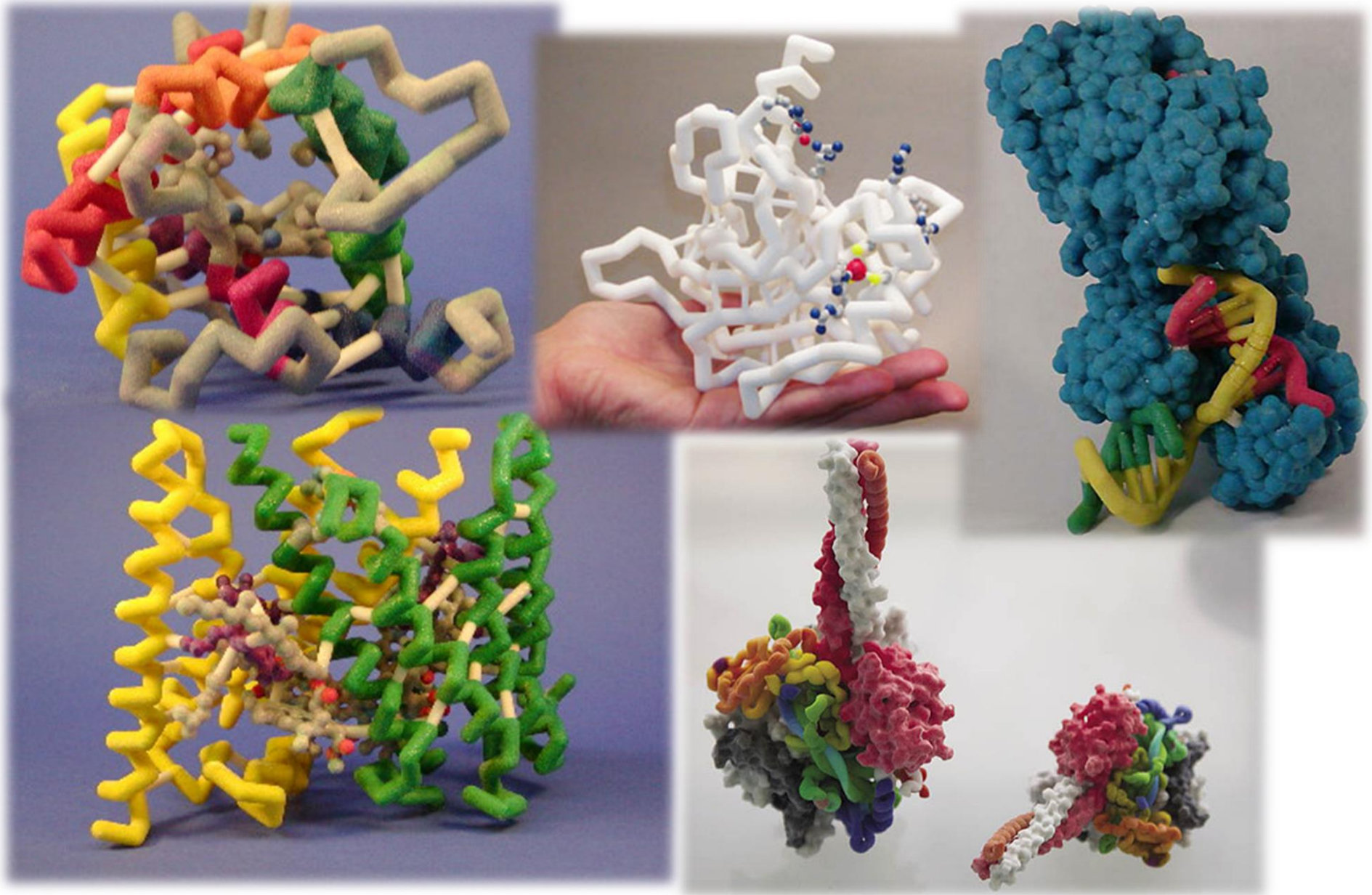




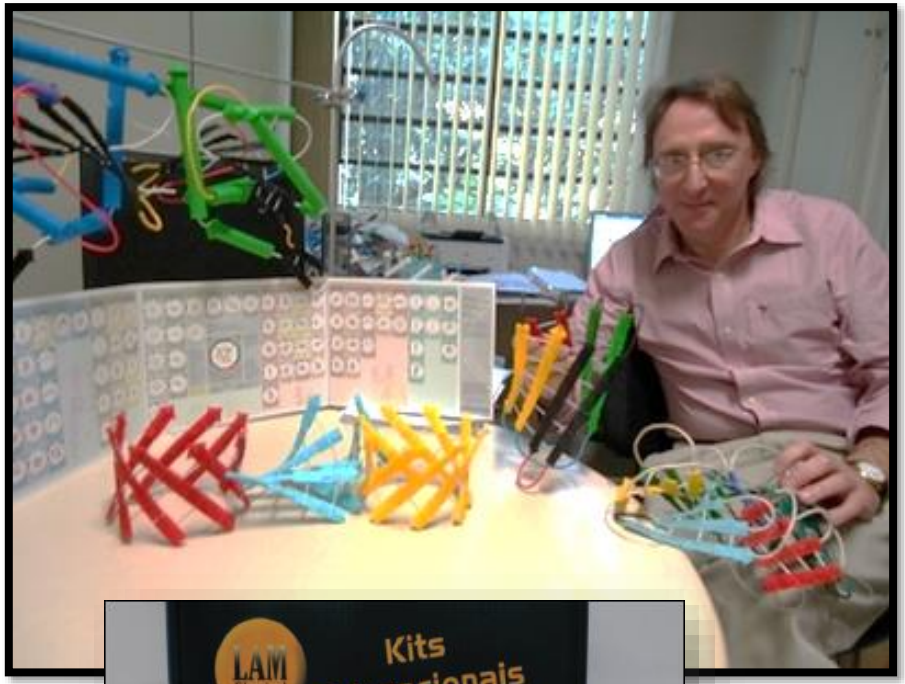


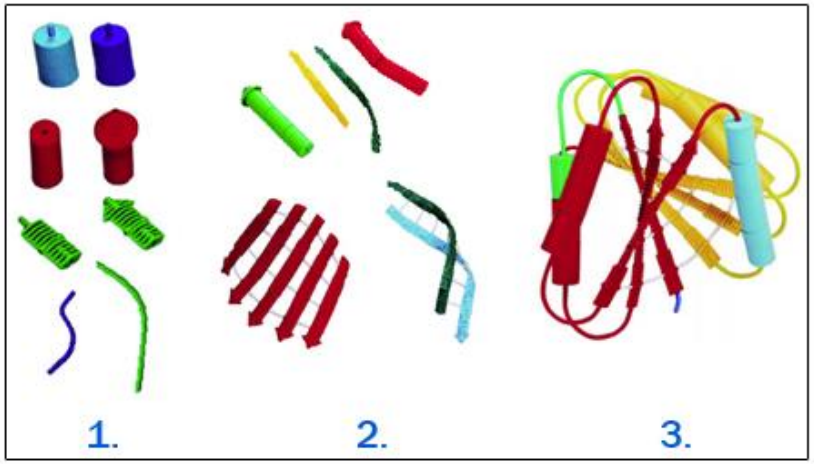


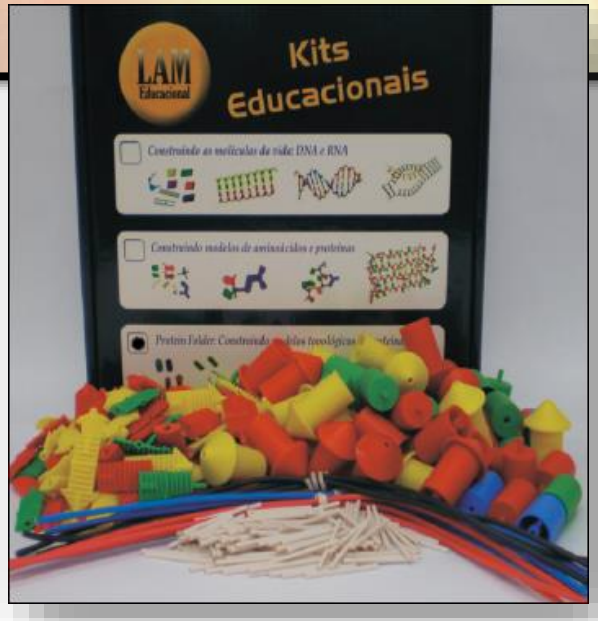
Modelos Físicos de Proteínas



Modelos Físicos de Proteínas

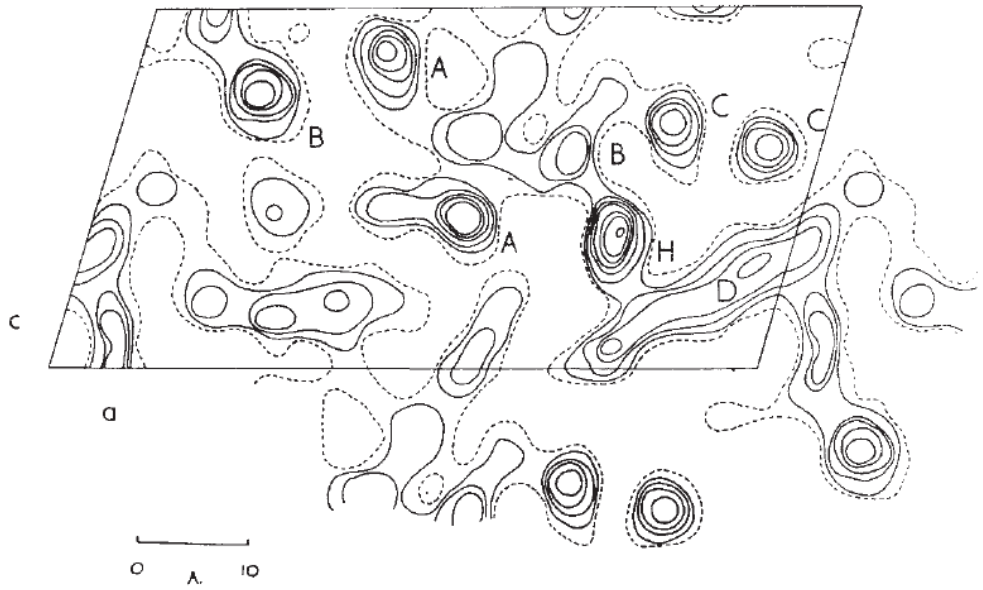


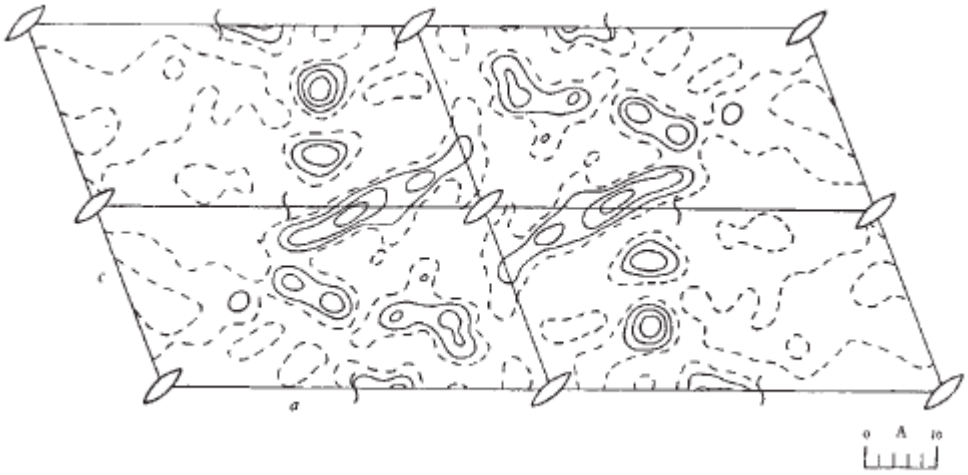




Visualização dos mapas de densidade eletrônica

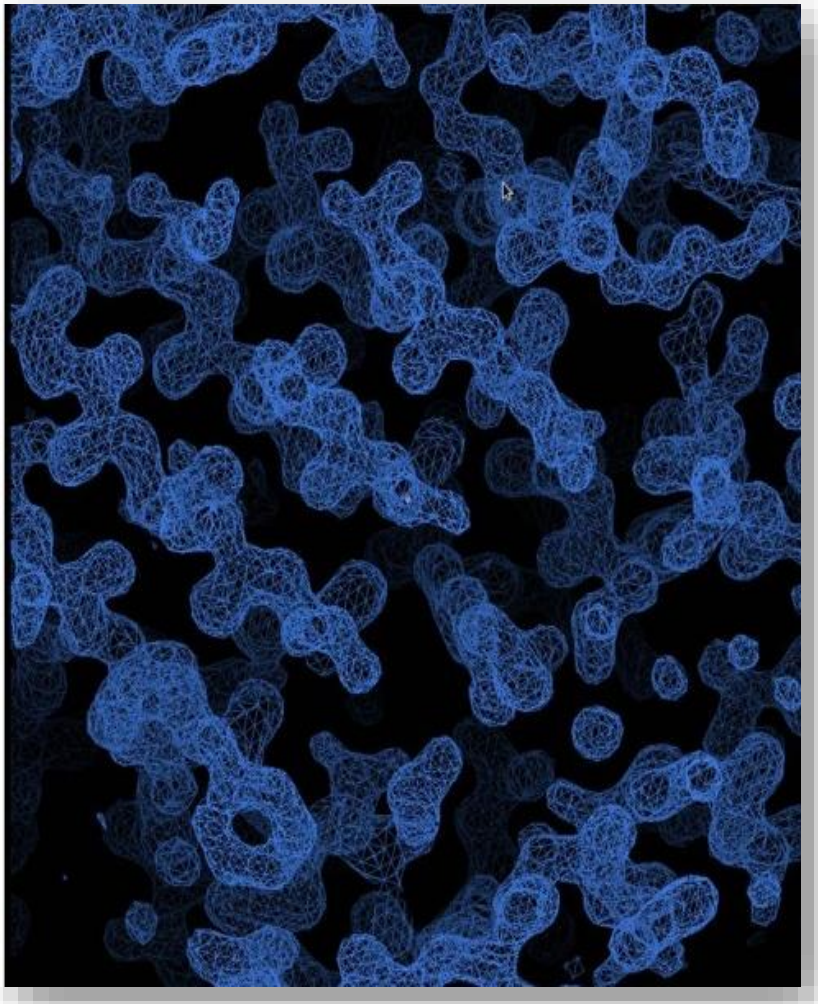
Kendrew *et al*, *Nature,*1958, **181**, 662

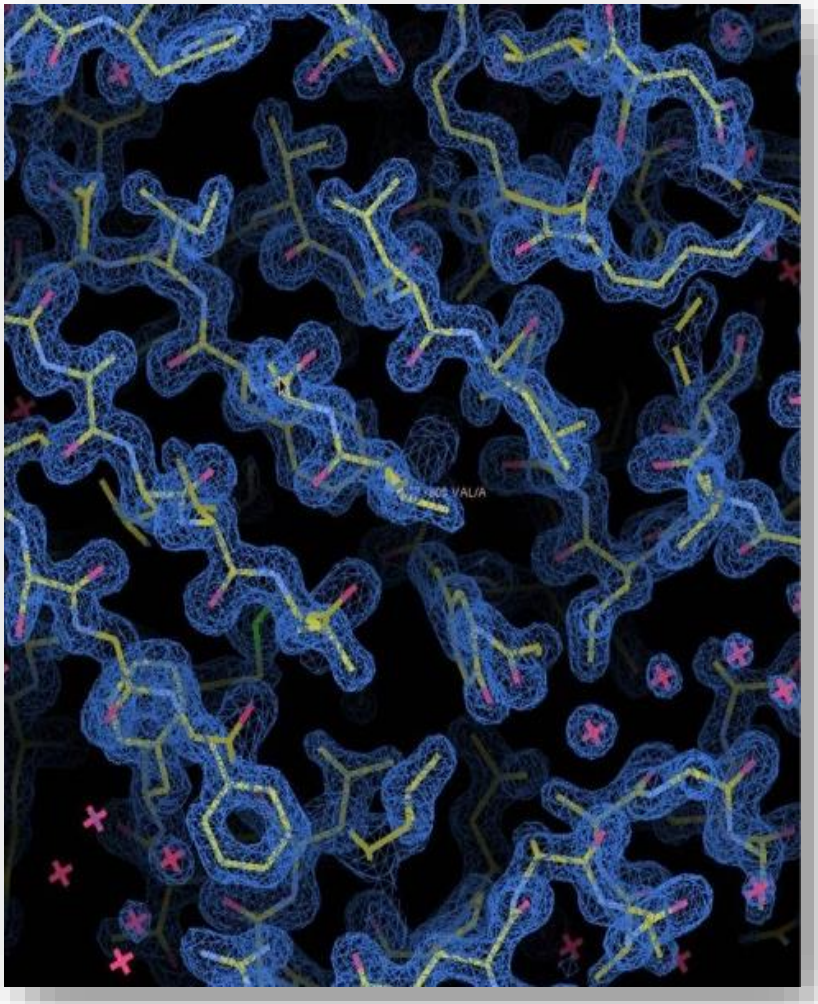




Perutz *et al, Nature*, 1960, **185**, 416

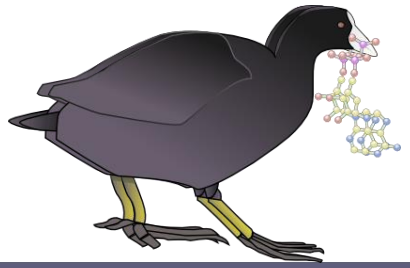
Visualização dos mapas de densidade eletrônica

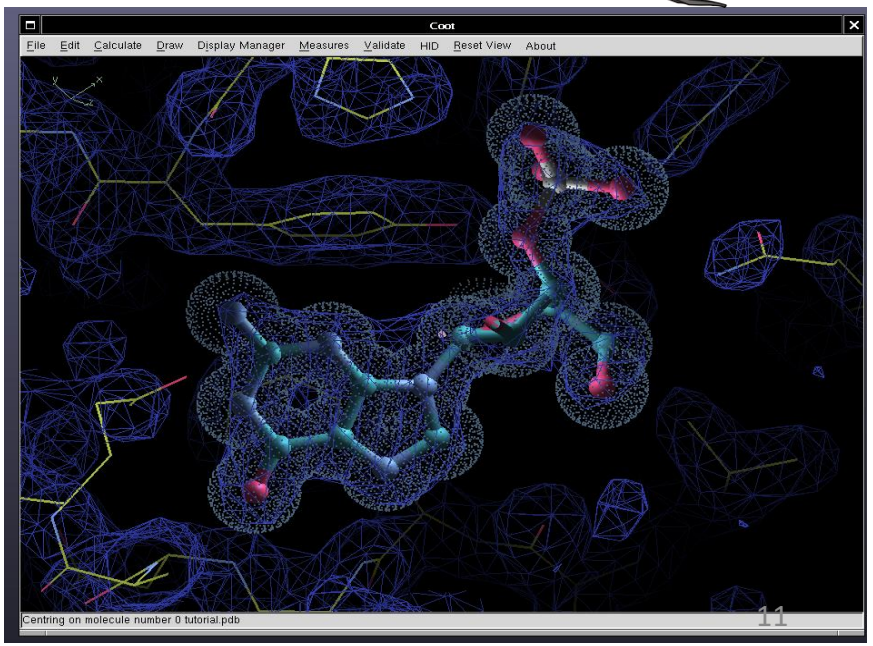




Visualização dos mapas de densidade eletrônica

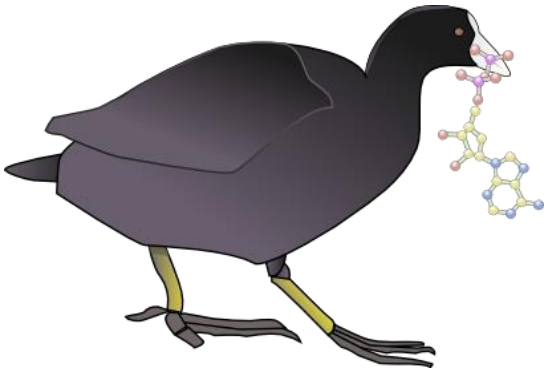
- Avanços nos hardwares
  - Refinamento de estruturas cristalográficas no espaço real, visualização de densidades eletrônicas
- FRODO (Alwyn Jones, 1978);
- *O* (Jones *et al*., 1991)
- Coot (Emsley & Cowtan, 2004)

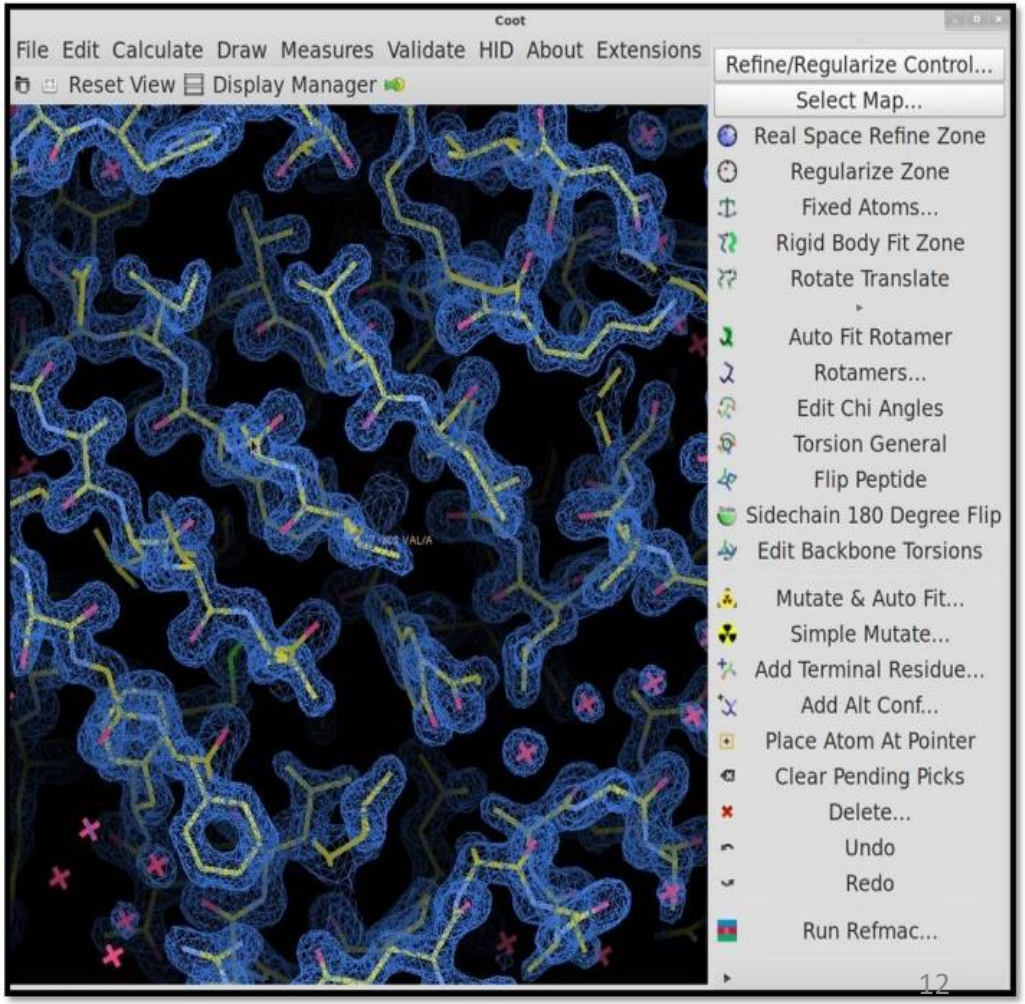




Coot

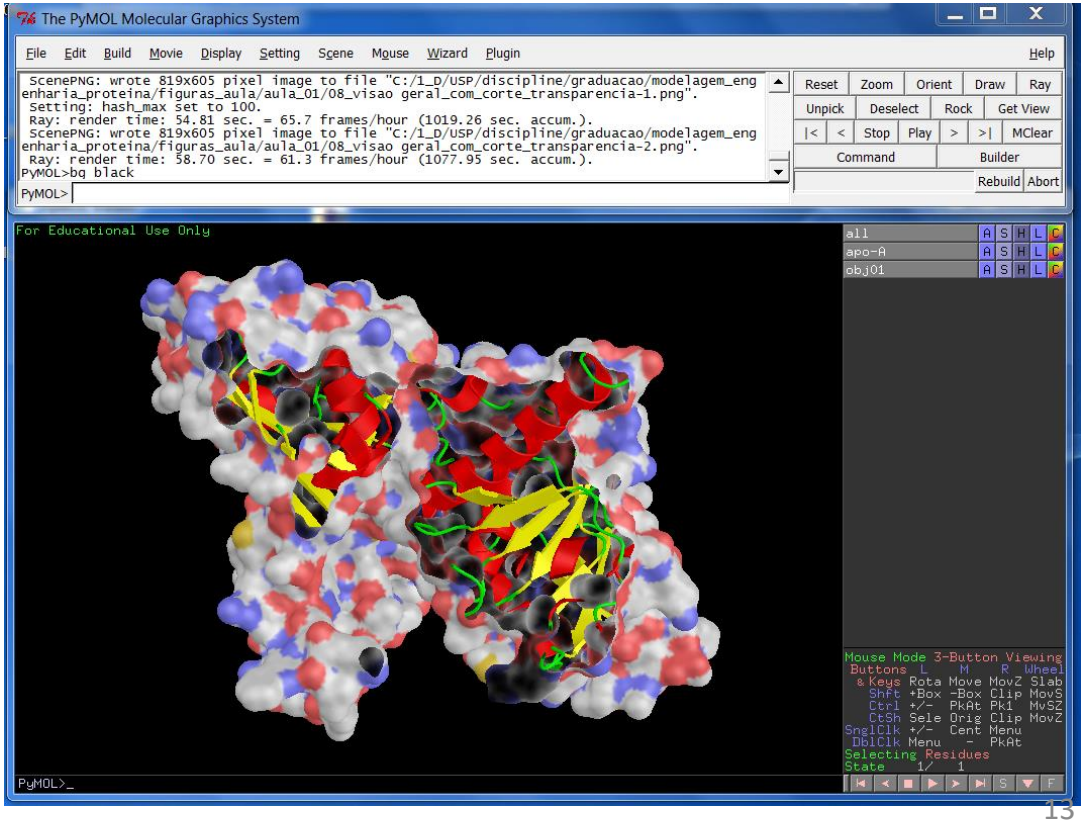
http://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/





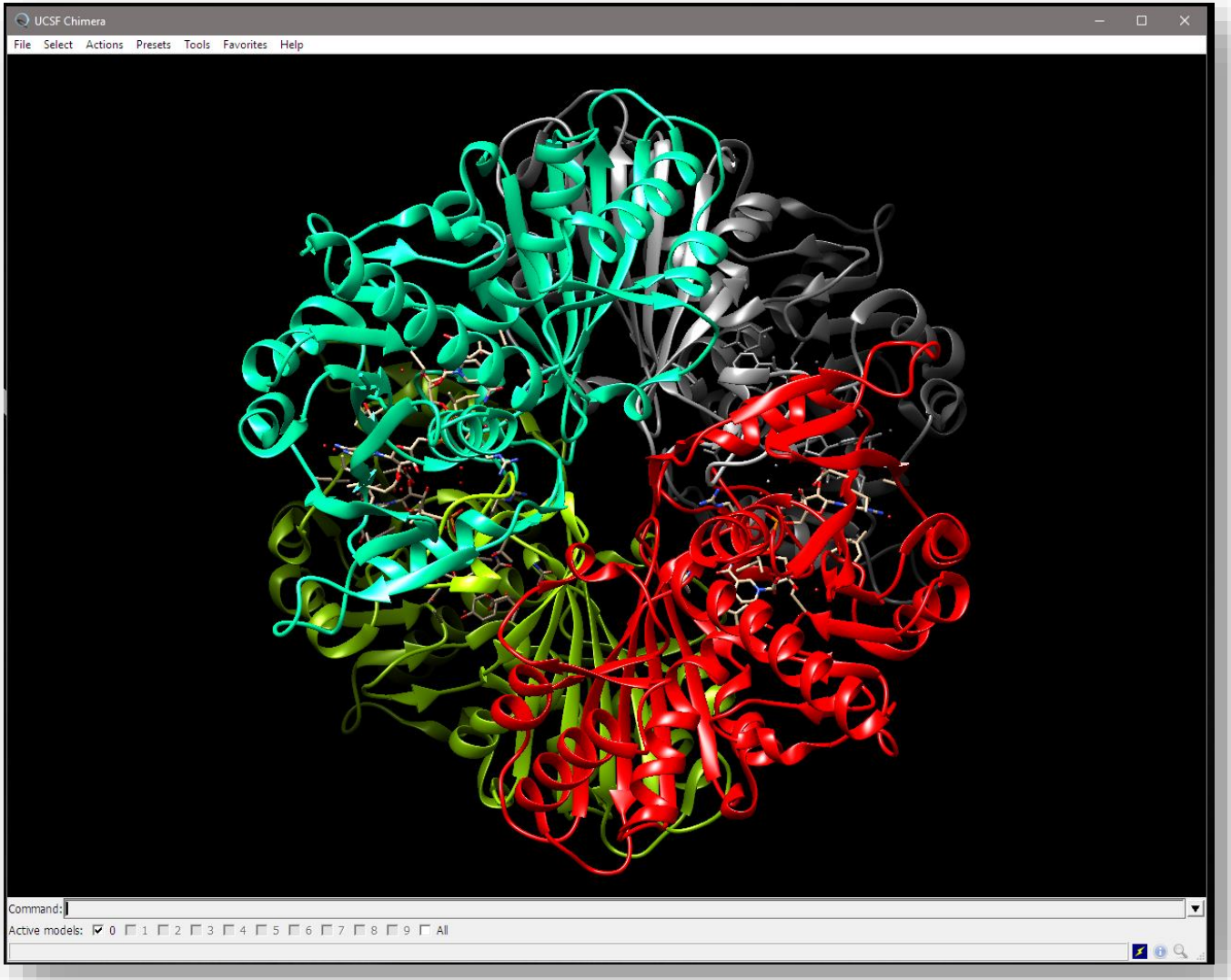
Pymol

- http://www.pymol.org
- Livre até a versão 0.99.
- Após a versão 1.0, livre para fins educacionais



ChimeraX

http://www.cgl.ucsf.edu/chimera/



Chimera

http://www.cgl.ucsf.edu/chimera/

RBVI

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Please note that UCSF Chimera is legacy software that is no longer being developed or supported. Users are strongly encouraged to try UCSF ChimeraX, which is under active development.

UCSF CHIMERA

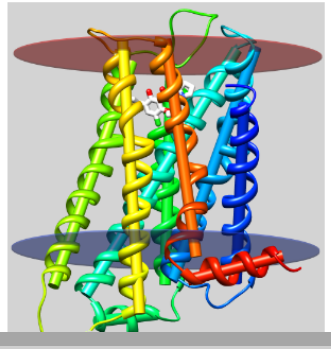
an Extensible Molecular Modeling System

UCSF Chimera is a program for the interactive visualization and analysis of molecular structures and related data, including density maps, trajectories, and sequence alignments. It is available free of charge for noncommercial use. Commercial users, please see Chimera commercial licensing.

We encourage Chimera users to try ChimeraX for much better performance with large structures, as well as other major advantages and completely new features in addition to nearly all the capabilities of Chimera (details...).

Chimera is no longer under active development. Chimera development was supported by a grant from the National Institutes of Health (P41-GM103311) that ended in 2018.

Feature Highlight



Axes and Planes

Axes, planes, and centroids can be calculated from sets of atoms using the Axes/Planes/Centroids tool or the command define. **Axes** can be shown as cylinders, **planes** as disks, and **centroids** as spheres, and any of these can be used in distance and angle measurements.

For example, the figure shows the dopamine D3 receptor and bound inhibitor (PDB entry 3pbl) as modeled into the membrane in the OPM database. The planes of the inner and outer membrane boundaries are shown as transparent blue and red disks, respectively. The protein ribbon is rainbow-colored from blue at the N-terminus to red at the C-terminus, and the axis of each helix is shown as a cylinder of matching color. The axis of the red helix forms an angle of 15.1° with the membrane and comes within 3.5 Å of the inner boundary.

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Recent Citations

Diverse modes of H3K36me3-guided nucleosomal deacetylation by Rpd3S. Guan H, Wang P *et al. Nature.* 2023 Aug 17;620(7974):669-675.

Structural basis for the binding of

Chimera Search

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News

April 19, 2023

Chimera production release 1.17.1 is now available, fixing an issue with 1.17 for Windows and Linux. See the release notes for details.

April 13, 2023

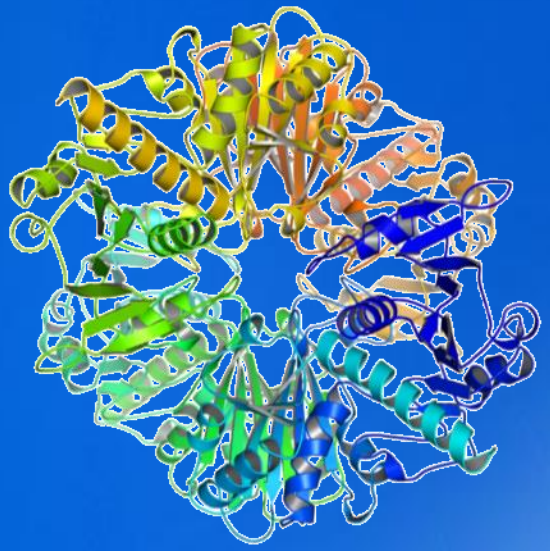
Chimera production release 1.17 is now available. Updating is required to keep using the tools that run Blast Protein, Modeller, and multiple sequence alignment with Clustal Omega or MUSCLE, as these will soon stop working in older versions. See the release notes for details.

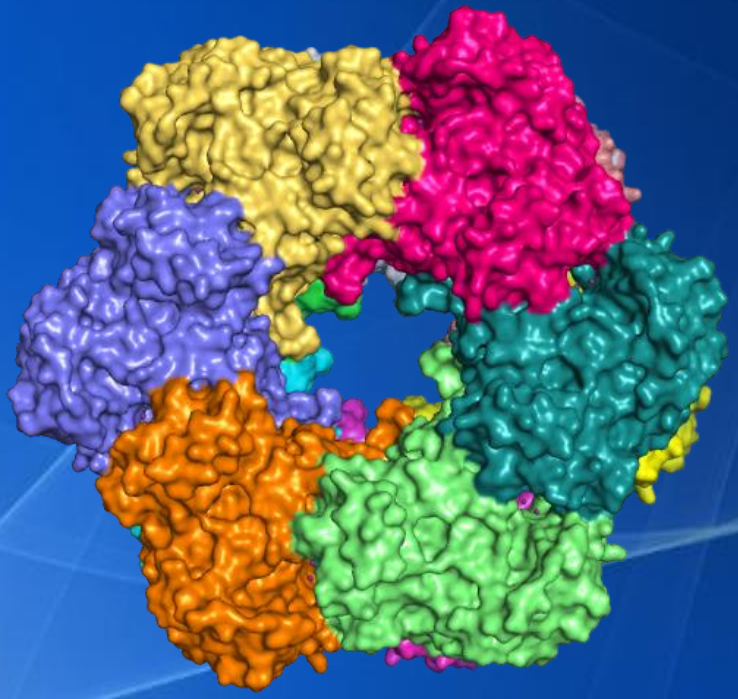
December 21, 2022

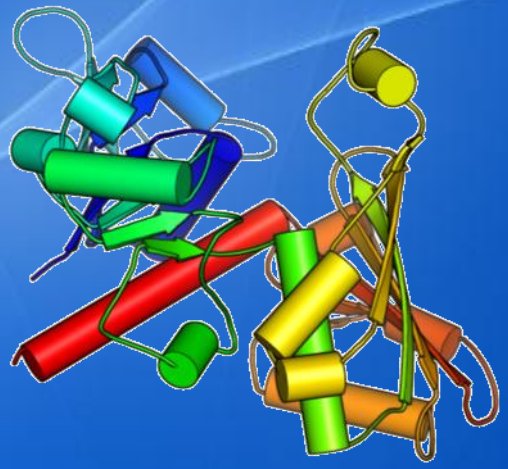
The RBVI wishes you a safe and happy holiday season! See our 2022 card and the gallery of previous cards back to 1985.

Previous news...

Modos de Representação Molecular







- Os modos de representação são divididos em dois grupos:
  - representação de todos os átomos (*e.g.*, linhas, bastões, esferas, esfera e bastão)
  - representações esquemáticas (*e.g.*, traço da cadeia principal; “cartoon” e superfície).
- As representações esquemáticas utilizam grupos específicos de átomos para o processamento dos modos de representação (*e.g.*, carbonos α da cadeia polipeptídica).

Níveis de representação molecular

Dimensão	Micromoléculas	Macromoléculas

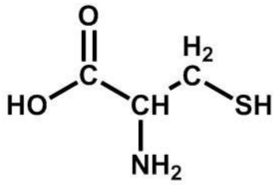
1D

Nomenclatura: L- Cisteína
Código SMILES: N[C@@H](CS)C(O)=O
Nomenclatura IUPAC: ácido (*R*)-2-amino-3-sulfanil-propanóico
Fórmula molecular: $C_3H_7NO_2S$

Nomenclatura: Gliceraldeído-3-fosfato desidrogenase
Código de 1 letra: M P I K V G I …
Código de 3 letras: Met Pro Ile Lys Val Gly Ile …

2D

Estrutura Química



Arquivo *mol*

```
L-Cysteine
 14 13  0  0  0  0  0  0  0  0999 V2000
  -0.9161   -1.9422   -0.4589 N   0  3  0  0  0  0  0  0  0
  -0.7560   -0.4201   -0.4087 C   0  0  2  0  0  0  0  0  0
   0.5229   -0.1100    0.4199 C   0  0  0  0  0  0  0  0  0
   1.1898   -1.1897    0.5674 O   0  0  0  0  0  0  0  0  0
  -2.0041    0.2065    0.1993 C   0  0  0  0  0  0  0  0  0
  -2.2447    1.9281   -0.3382 S   0  0  0  0  0  0  0  0  0
...
```

Arquivo *pdb*

```
HEADER    OXIDOREDUCTASE                  01-JUL-08   3DMT
TITLE     STRUCTURE OF GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
TITLE    2 T. CRUZI IN COMPLEX WITH THE IRREVERSIBLE IODOACETATE
TITLE    3 INHIBITOR
SOURCE    2 ORGANISM_SCIENTIFIC: TRYPANOSOMA CRUZI;
JRNL        AUTH   R.V.C.GUIDO,T.L.BALLIANO,A.D.ANDRICOPULO,G.OLIVA
REMARK    2 RESOLUTION.    2.30 ANGSTROMS
ATOM      1  N        MET A   1     -27.113  13.359   5.209  0.01 31.32           N
ATOM      2  CA       MET A   1     -26.624  14.514   6.015  0.01 31.32           C
ATOM      3  C        MET A   1     -25.361  14.157   6.787  0.01 31.31           C
ATOM      4  O        MET A   1     -24.843  13.047   6.667  0.01 31.31           O
...
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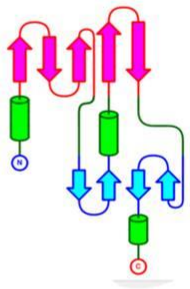
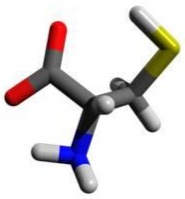
Topologia



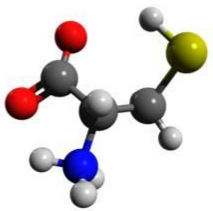
Esquema da Distribuição das Estruturas Primária e Secundária

3D

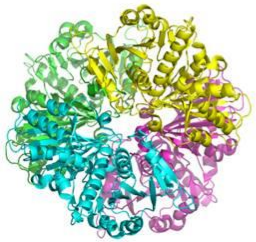
Bastões



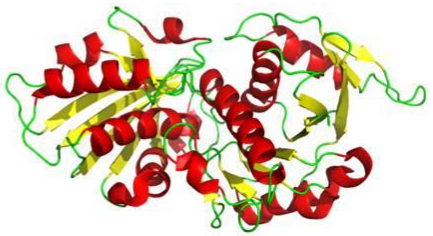
Esferas e Bastões



"Cartoon" (Tetrâmero)



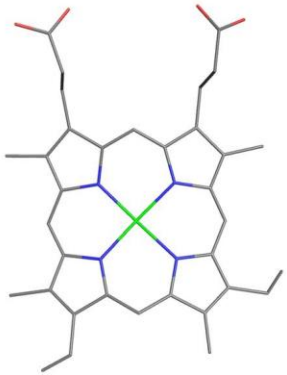
"Cartoon" (Monômero)



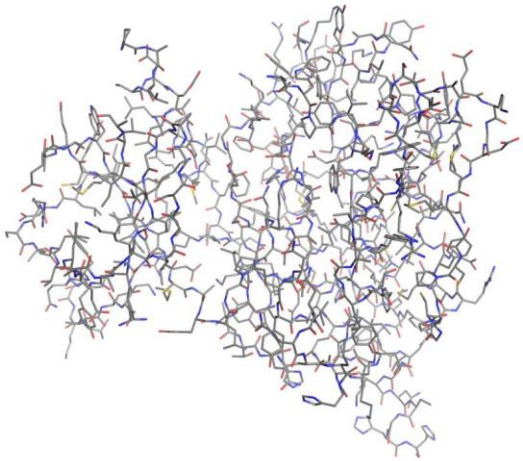
Linhas

- Representação molecular mais simples disponível é denominada “linhas” (do inglês, *wireframe* ou *lines*)
- As ligações químicas são indicadas por linhas retas e os átomos constituintes da molécula pelos vértices. Devido à baixa demanda de processamento, simplicidade de representação e rápida renderização esse modo é utilizado como padrão pela maioria dos programas de visualização molecular.

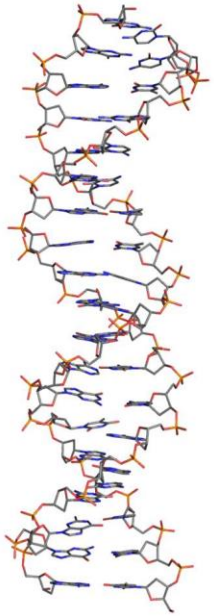
Micromolécula



Proteína



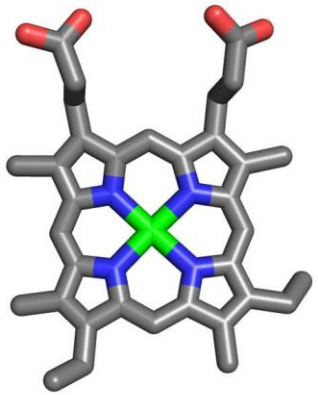
DNA



Bastões

- O modo de representação molecular “bastões” (do inglês, *sticks*) é uma variante do modo linhas, sendo frequentemente indicado por cilindros de raio variado.

Micromolécula



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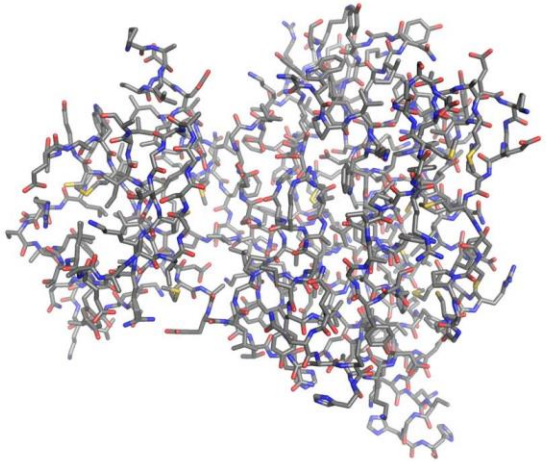
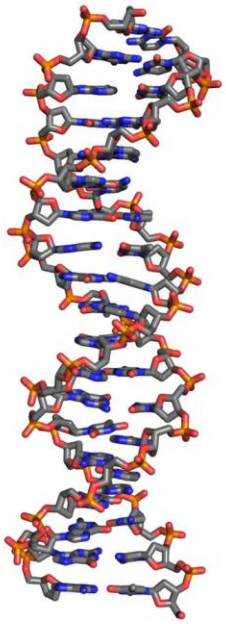


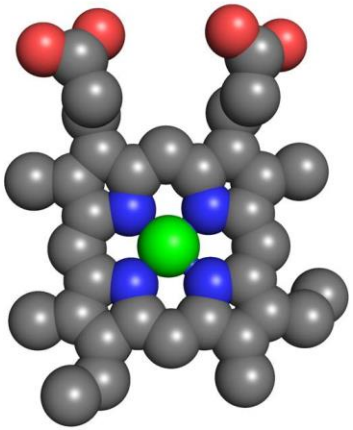
DNA



Esferas

- O modo de representação “esferas” (do inglês, *spheres*) indica os átomos em escala de acordo com o raio de van der Waals (*i.e.*, o raio da esfera aumenta em função do aumento do raio atômico.
- Esse modo de representação é também conhecido pela sigla “CPK”, que indica as iniciais dos pesquisadores Corey, Pauling e Koltun responsáveis pelo desenvolvimento do modelo físico no qual foi inspirado esse tipo de representação.

Micromolécula



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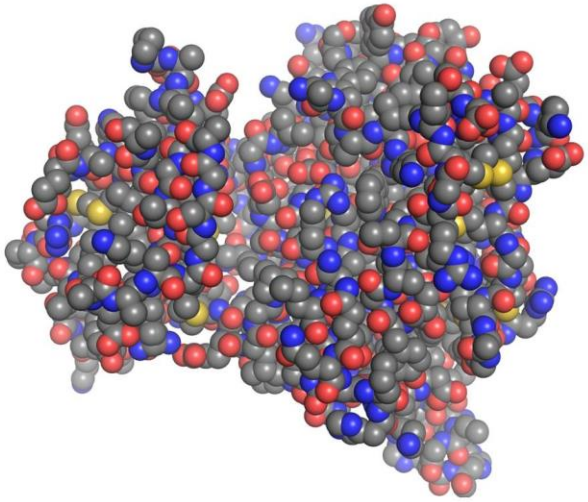
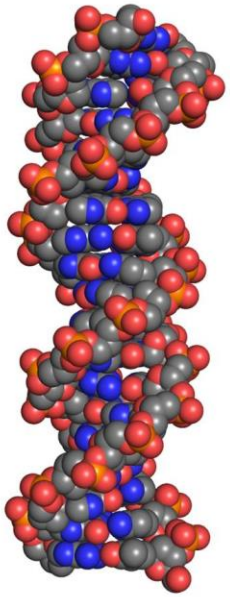


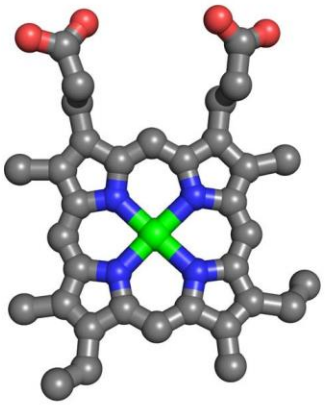
DNA



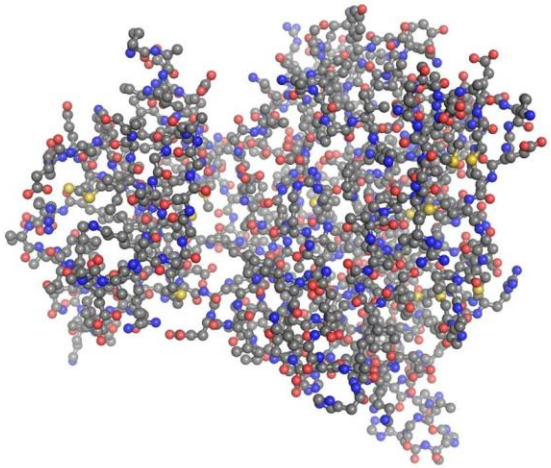
Esfera e bastões

- Um modo híbrido que combina os modos bastões e esferas e representa as ligações químicas como bastões e os átomos constituintes da molécula como esferas, porém sem utilizar a escala proporcional ao raio de van der Waals.
- O modo esfera e bastões é uma opção atrativa para diferenciar os átomos da micro e da macromoléculas em complexos do tipo ligante-proteína

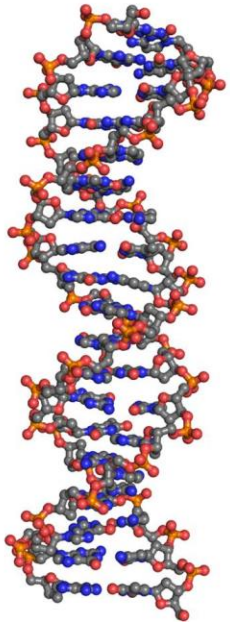
Micromolécula



Proteína



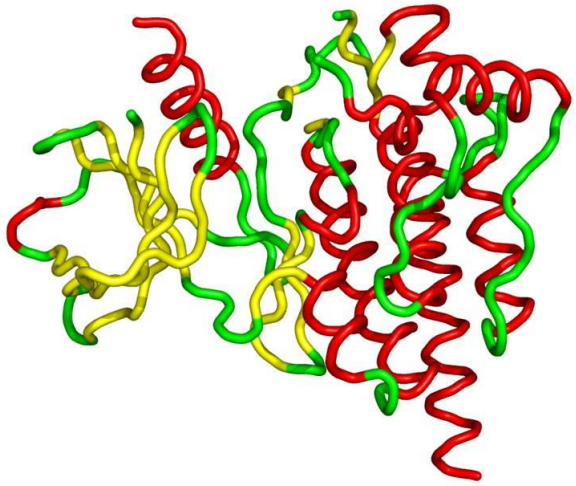
DNA



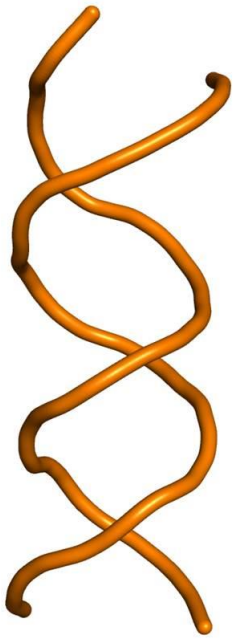
Traço da cadeia principal

- O modo “traço da cadeia principal” (do inglês, *ribbon*) é uma representação que considera apenas os átomos da cadeia principal (*e.g.*, carbonos α de cadeias polipeptídicas, átomos de fósforo de fitas de DNA ou RNA). Nesse modo de representação, átomos específicos consecutivos são conectados entre si através de segmentos de retas.

Proteína



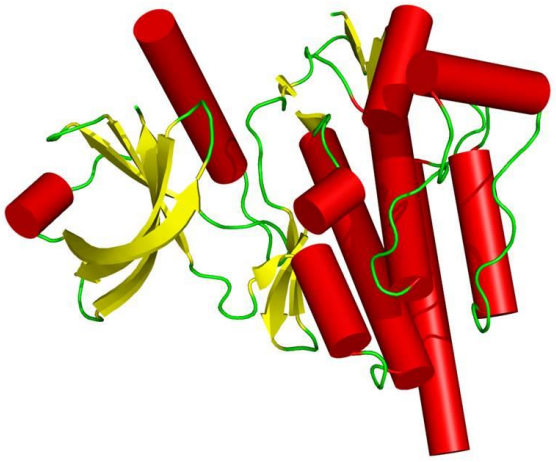
DNA

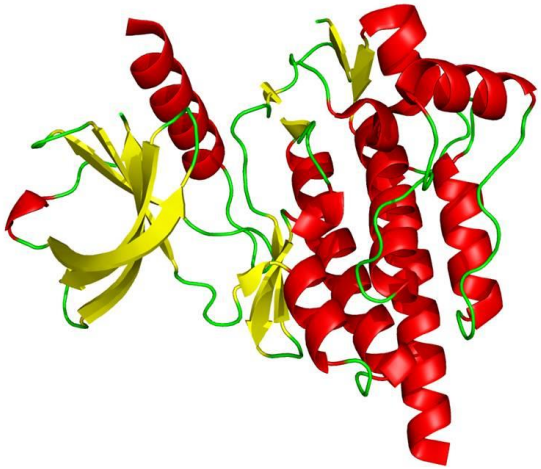


Cartoon

- Dentre os modos de representação de macromoléculas disponíveis, um dos mais populares e atrativos é o “cartoon”. Esse modo também é amplamente empregado em comparações estruturais entre proteínas homólogas e, adicionalmente, ilustra de maneira clara e elegante os elementos de estrutura secundária, tipos de enovelamento, direção da cadeia peptídica/fita de DNA ou RNA e domínios estruturais

Proteína





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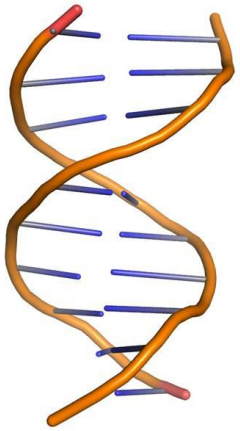
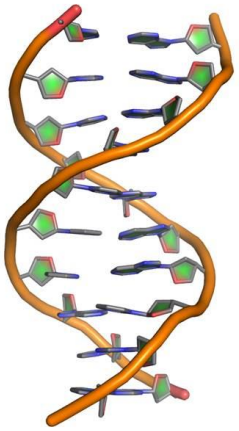
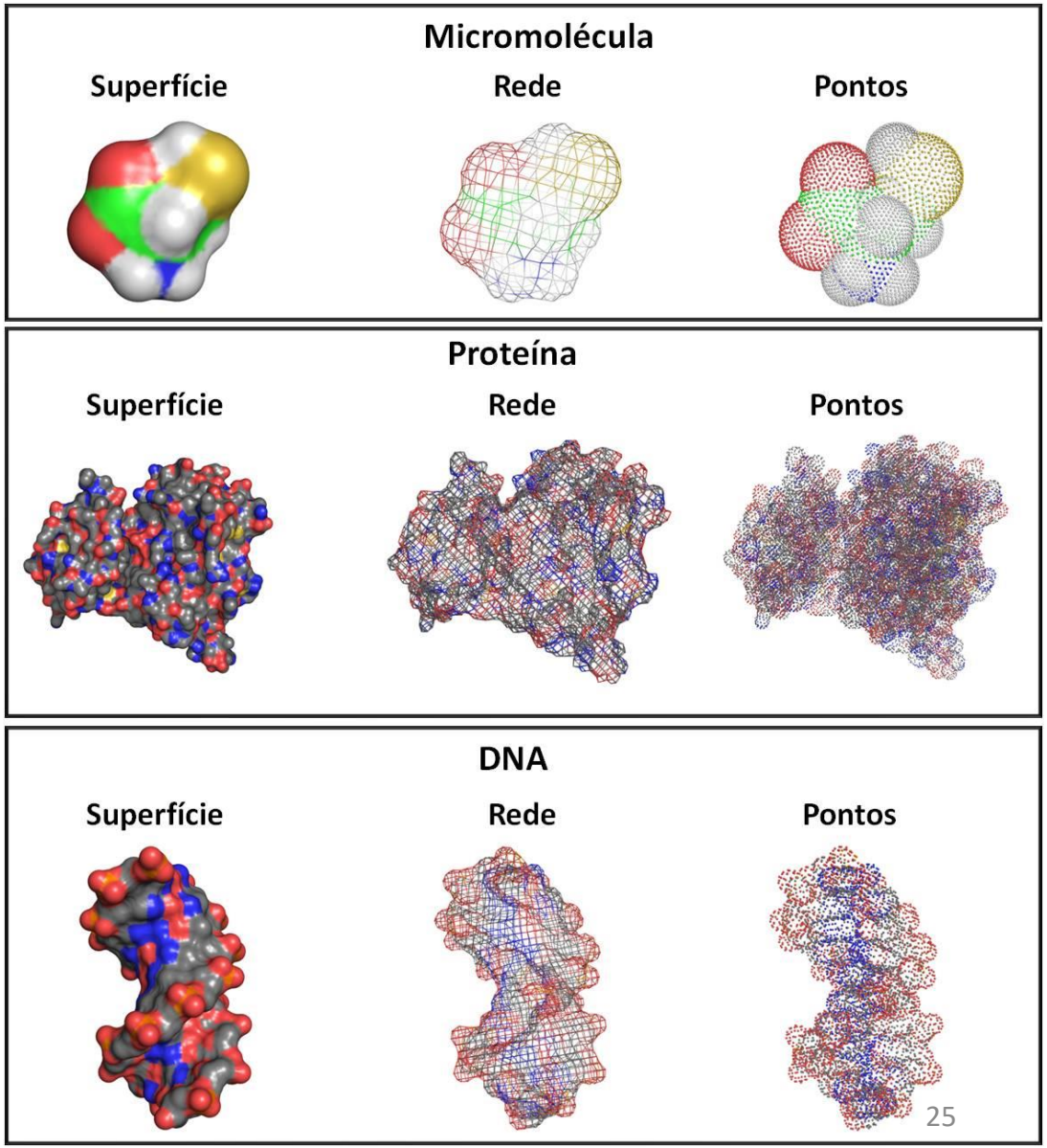


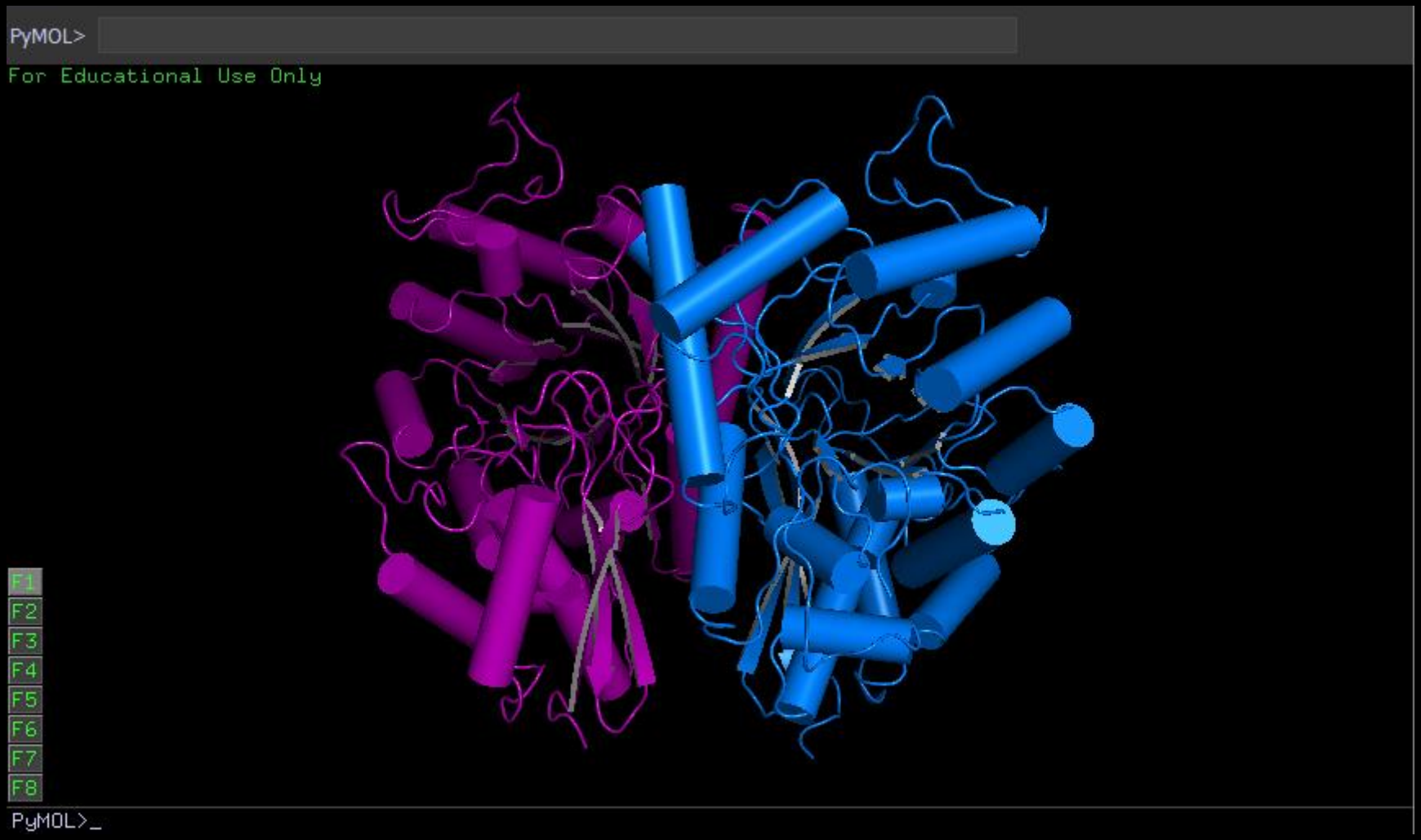


Superfície

O modo “superfície” (do inglês, *surface*) indica a superfície acessível ao solvente de micro e macromoléculas. Esse modo consiste no elemento gráfico de representação molecular mais complexo entre os atualmente disponíveis, pois o processo de renderização exige recursos computacionais avançados para que possa ser utilizado rotineiramente.



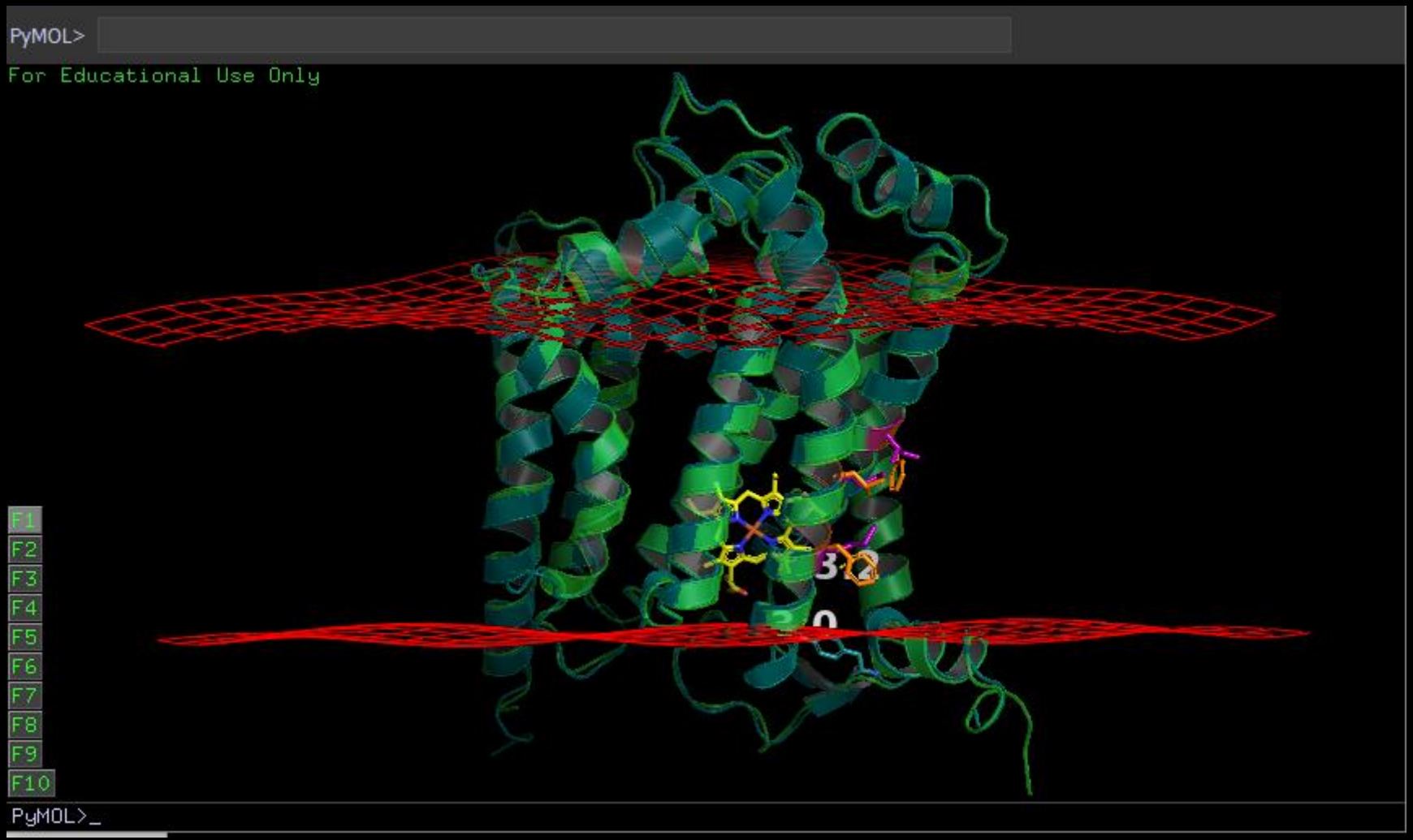
Exemplo 1 – enolase domínios



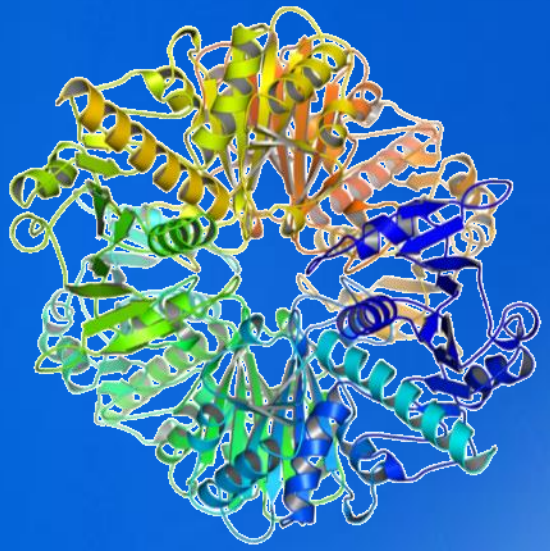
Exemplo 2 – enoloase-enoblock

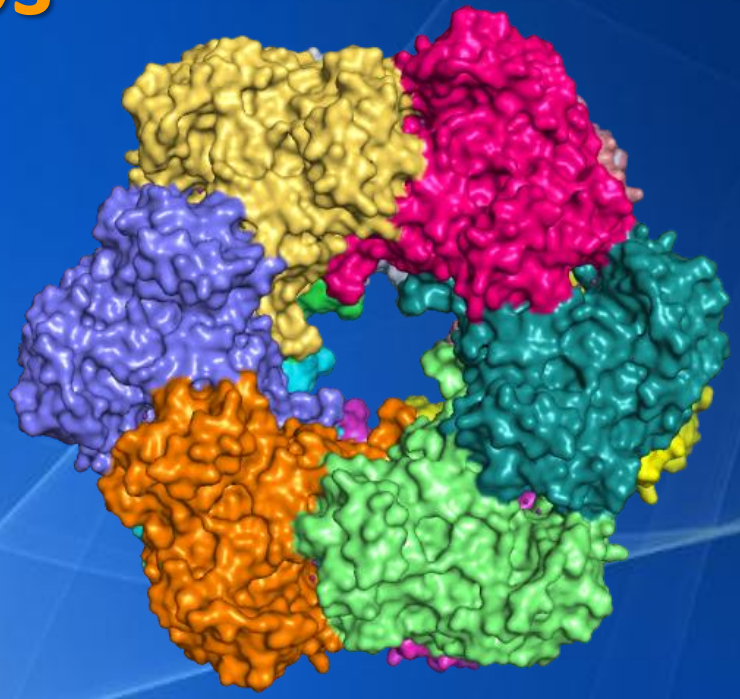
Exemplo 3 – Taq polimerase

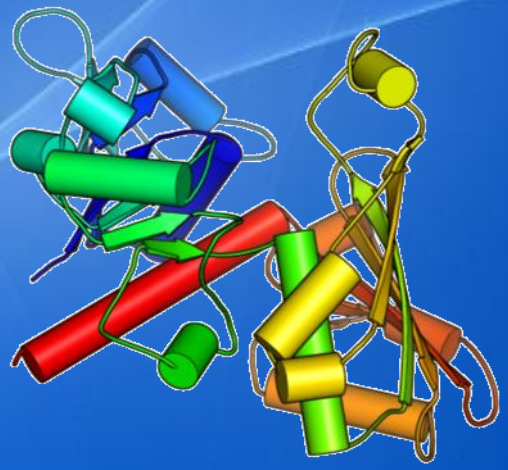
Exemplo 4 – Complexo bc1



Programas para Construção e Visualização de Modelos Moleculares







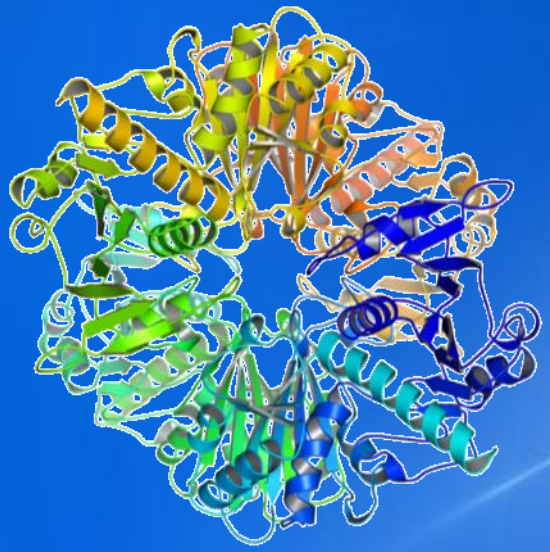
Programas

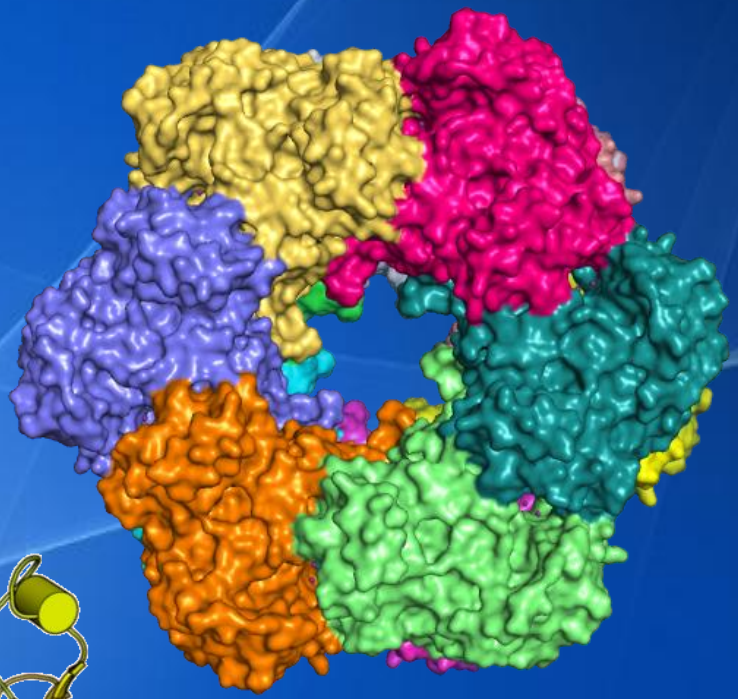
- Ferramentas de modelagem são desenvolvidas especificamente para a construção e/ou visualização de modelos moleculares
- Os programas são fundamentados na interpretação de dados experimentais, como os obtidos por cristalografia de raios X, e apresentam características apropriadas para a interpretação e representação dos mapas de densidade eletrônica.
- Em geral, os programas fornecem ao usuário ferramentas interativas para a manipulação de coordenadas atômicas e rotinas sofisticadas para a automação do processo de determinação estrutural.

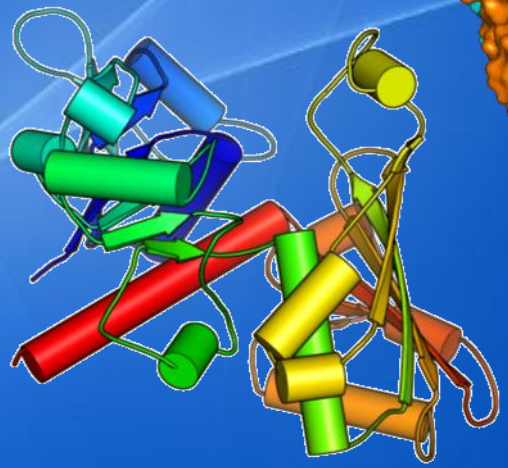
Programa

Nome	Disponível em	Aplicação	Plataforma
iMol	http://www.pirx.com/iMol/	Visualização e representação molecular	Mac
QuickPDB	http://www.rcsb.org/pdb/explore/quickPDB.do	Visualização e representação molecular	Web Linux, Mac, Windows
Rasmol	http://rasmol.org/	Visualização e representação molecular	Linux, Mac, Windows
Webmol	http://www.cmpharm.ucsf.edu/cgi-bin/webmol.pl	Visualização e representação molecular	Web
CCP4mg	http://www.ccp4.ac.uk/MG/	Visualização e representação molecular	Linux, Mac, Windows
Jmol	http://jmol.sourceforge.net/	Visualização e representação molecular	Web Linux, Mac, Windows
KiNG	http://kinemage.biochem.duke.edu/software/index.php	Visualização e representação molecular	Linux, Mac, Windows
MolScript	http://www.avatar.se/molscript/	Visualização e representação molecular	Linux
PyMOL	http://www.pymol.org	Visualização e representação molecular	Linux, Mac, Windows
Coot	http://lmb.bioch.ox.ac.uk/coot/	Visualização e construção de modelos	Linux, Mac, Windows
O	http://xray.bmc.uu.se/alwyn/TAJ/Home.html	Visualização e construção de modelos	Linux, Mac, Windows
Avogadro	http://avogadro.openmolecules.net/wiki/Main_Page	Visualização, análise e representação molecular	Linux, Mac, Windows
VMD	http://www.ks.uiuc.edu/Research/vmd/	Visualização, análise e representação molecular	Linux, Mac, Windows
Chimera	http://www.cgl.ucsf.edu/chimera/	Visualização, análise, modelagem e representação molecular	Linux, Mac, Windows
ICM	http://www.molsoft.com/icm_browser.html	Visualização, análise, modelagem, representação molecular	Linux, Mac, Windows
Yasara	http://www.yasara.org/	Visualização, análise, modelagem, representação molecular	Linux, Mac, Windows

“Belas e informativas” e “Não tão belas e não tão informativas” Figuras Publicadas (*Opinião Pessoal*)







"KISS principle"

Keep **I**t **S**imple, **S**tupid!

Keep **I**t **S**imple **S**ir

Keep **I**t **S**hort and **S**imple

Keep **I**t **S**uper **S**imple

Keep **I**t **S**imple and **S**incere

The KISS principle states that most ***systems work best if they are kept simple*** *rather than made complex, therefore, simplicity should be a key goal in design and* ***unnecessary complexity should be avoided****.*

http://en.wikipedia.org/wiki/KISS_principle

Figures - Exemples

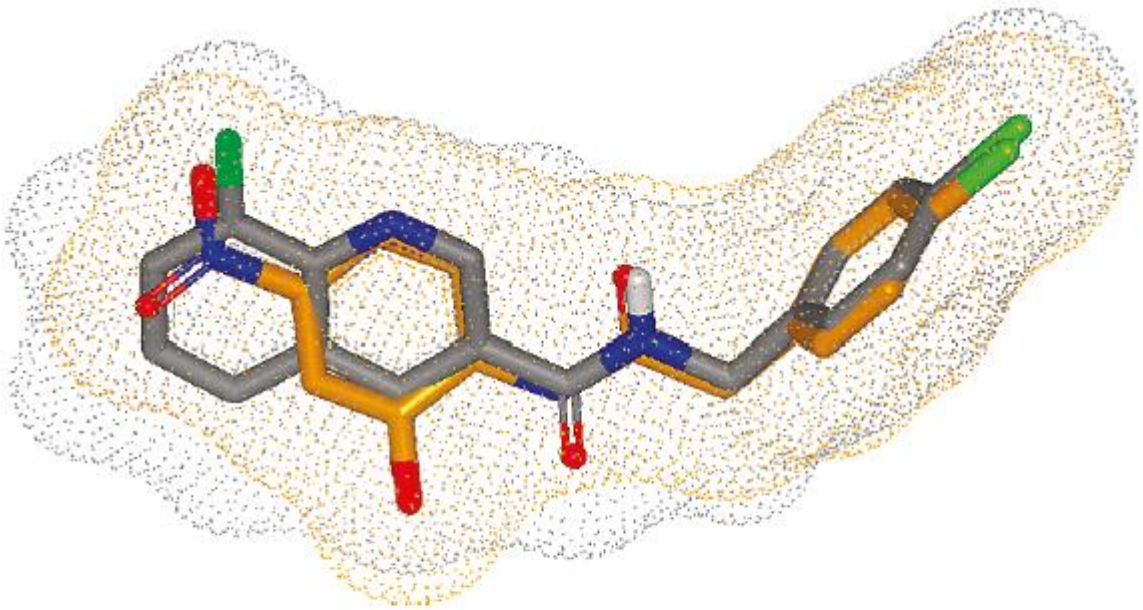


Figure 1. Compound **25** (orange carbons, orange surface) aligned to *N*-(4-chlorobenzyl)-8-fluoro-4-*oxo*-1,4-dihydroquinoline-3-carboxamide (gray carbons, blue surface), which was ranking top on the ROCS hitlist.

J. Med. Chem. **2009**, 52, 4257–4265

Figures - Exemples

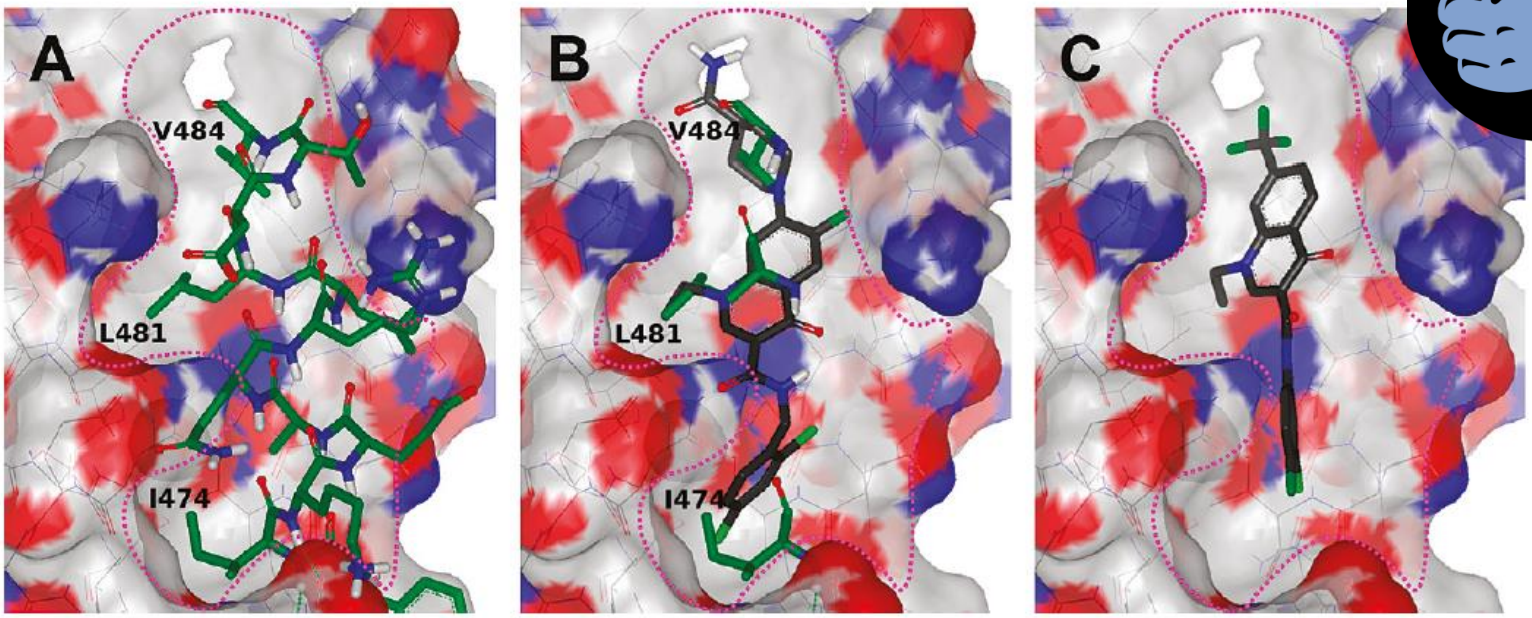


Figure 5. (A) Essential hydrophobic interactions between HR2 (green) and HR1 (surface). The binding of the HR2 amino acids I474, L481, and V484 into hydrophobic sites in the binding pocket of HR1 (pink dashes) is required for NiV fusion. (B) Structural overlay of the predicted binding mode of inhibitor **19** and the binding mode of HR2 in the NiV F-protein crystal structure (PDB 1WP7). The side chains of inhibitor **19** provide bioisosteric replacements of the HR2 amino acids (green) essential for HR1−HR2 binding. (C) Predicted binding mode of inhibitor **15**. Because of the tight binding of the trifluormethyl residue to the upper hydrophobic site (V484), the lower hydrophobic site (I474) cannot be addressed.

J. Med. Chem. **2009**, 52, 4257–4265

Figures - Exemples

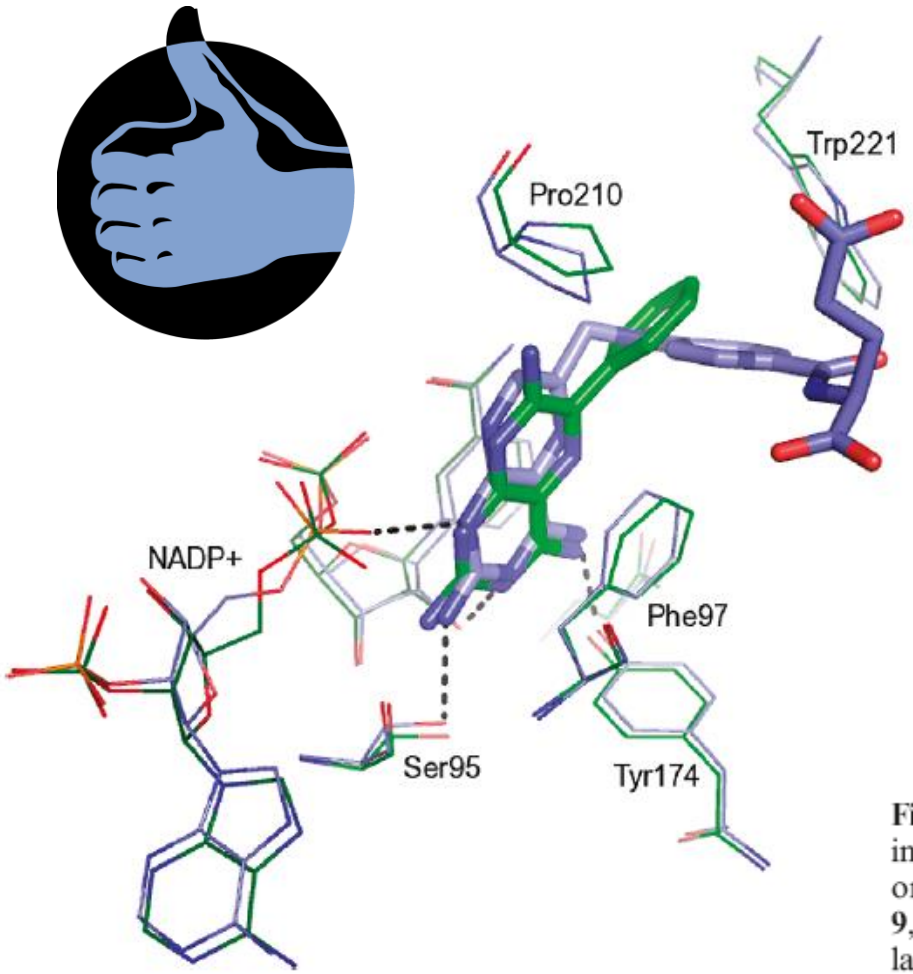


Figure 2. Ligands and binding site residues of *Tb*PTR1-methotrexate complex (2C7V, blue carbon atoms) superimposed with those from the triamterene complex (green carbon atoms).

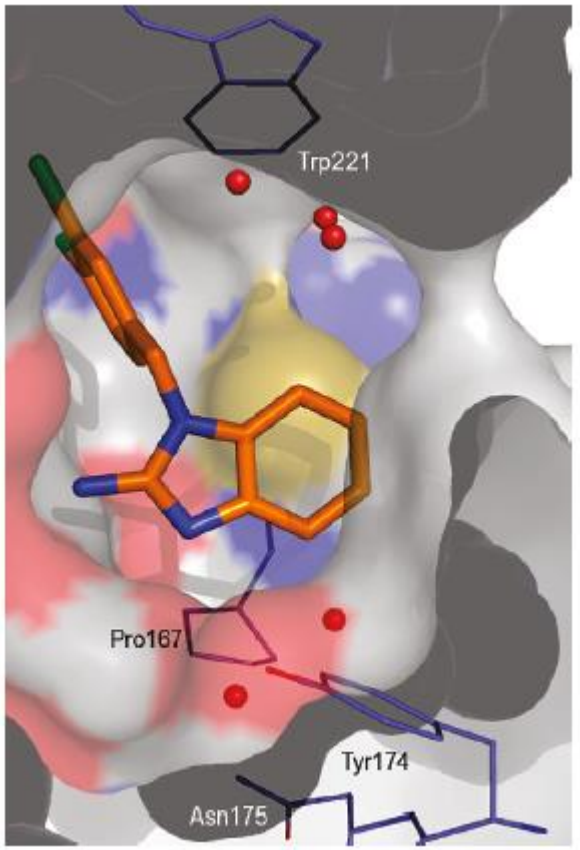


Figure 8. Cut-away view of solvent accessible surface of the binding pocket of PTR1·**9**. Two hydrophobic pockets filled with ordered water molecules are close the aminobenzimidazole core of **9**, a smaller pocket bordered by Pro167, Tyr174, and Asn175, and a larger one toward Trp221.

J. Med. Chem. **2009**, 52, 4454–4465

Figures - Exemples

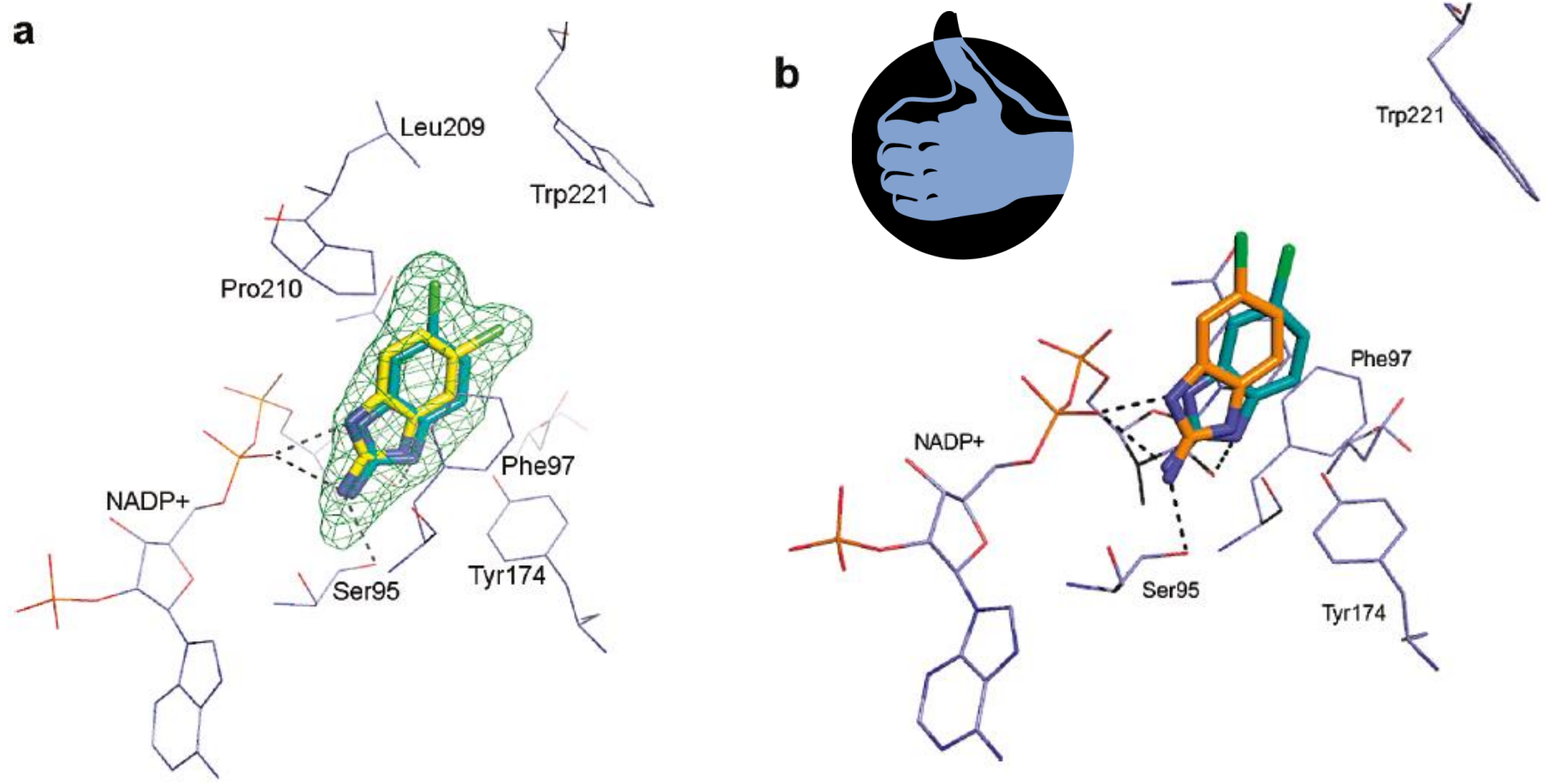


Figure 4. (a) View in the binding site of PTR1 3 4 together with Fo-Fc omit map (contoured on 2.0σ), which was calculated by omitting the ligand from the final model. The ligand adopts two distinct binding modes. In the major confirmation (green carbon atoms), the chloro-substituent packs against Leu209 and Pro210, whereas in the minor conformation (yellow carbon atoms), the chloro atom sits in the open cavity of the active site. (b) Modeled binding mode of 4 (orange carbon atoms) superimposed with the dominant binding mode determined crystallographically (green carbon atoms).

J. Med. Chem. **2009**, 52, 4454–4465

Figures - Exemples

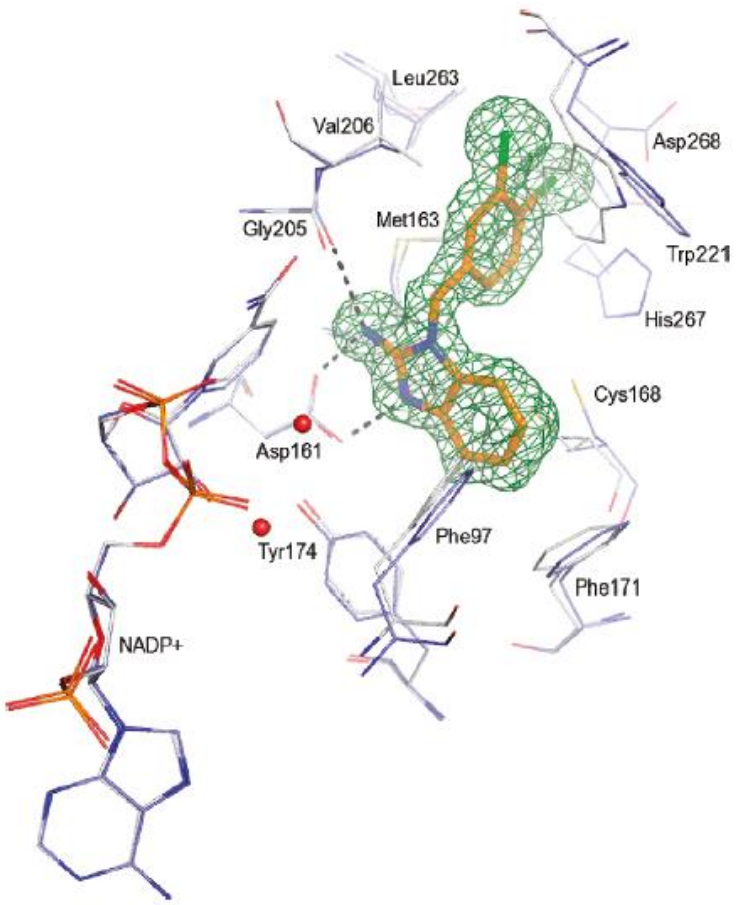


Figure 6. Crystallographically determined binding mode of **9** (orange carbon atoms for ligand and blue carbon atoms for protein) superimposed with the receptor conformation used for docking calculations (gray carbon atoms) together with F_o-F_c omit map (contoured on 2.0σ), which was calculated by omitting the ligand from the final model. To accommodate the ligand in the binding site, the side chain of Trp221 rotated by 10° and the sulfur atom of Cys168 shifted by 2 Å.

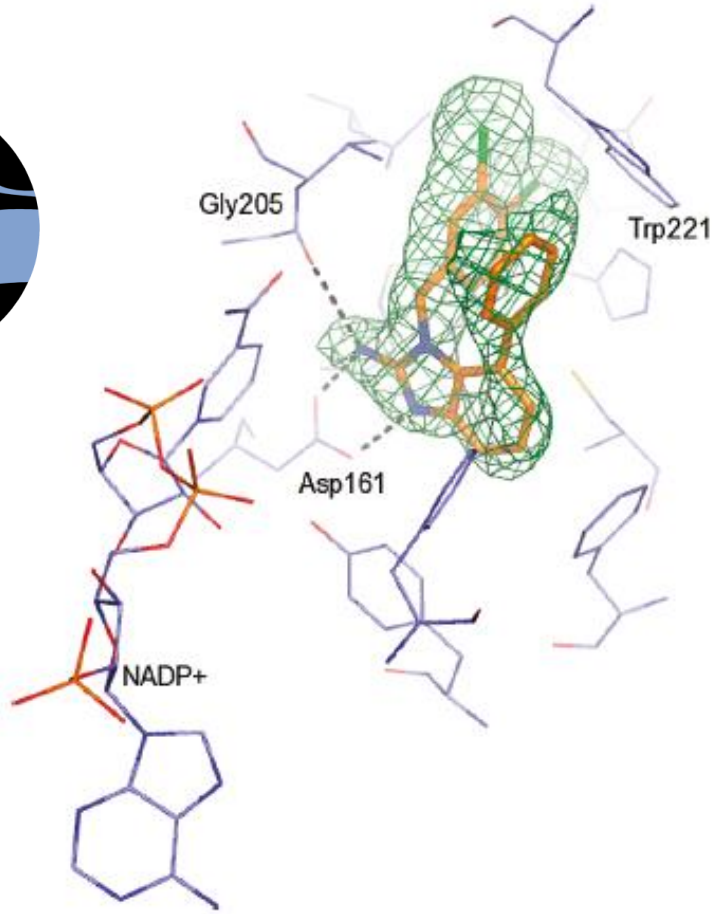


Figure 9. Crystallographically determined binding mode of **12** together with F_o-F_c omit map (contoured on 2.0σ), which was calculated by omitting the ligand from the final model. The phenyl group of the ligand forms an edge–face interaction with Trp221.

J. Med. Chem. **2009**, 52, 4454–4465

Figures - Exemples

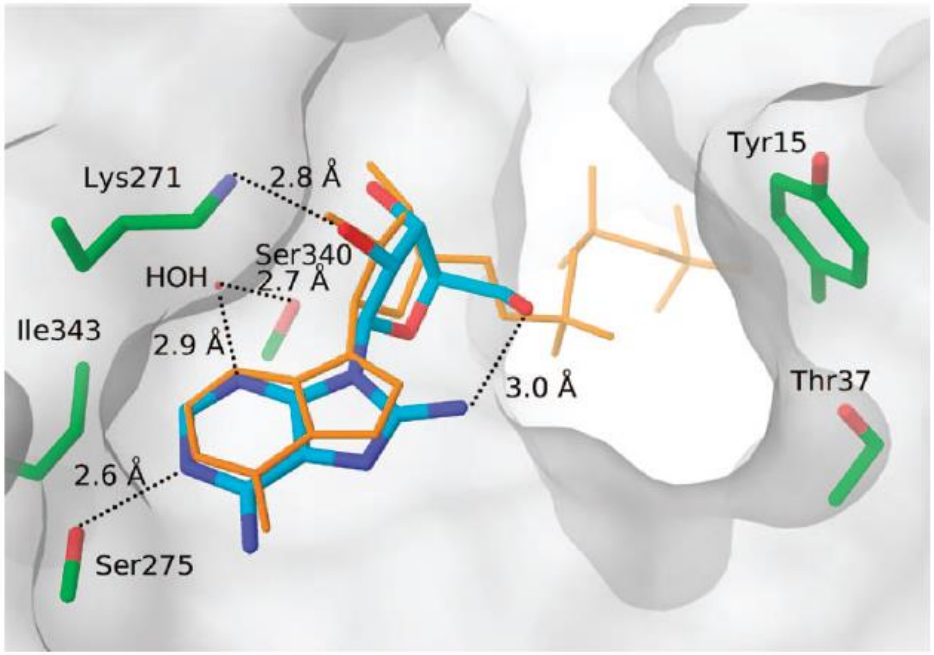


Figure 1. X-ray crystal structure of **4** (blue)/HSC70/BAG-1 (green) superimposed with ATP (**1**, orange), from an X-ray crystal structure of ATP (**1**)/HSC70/BAG-1.

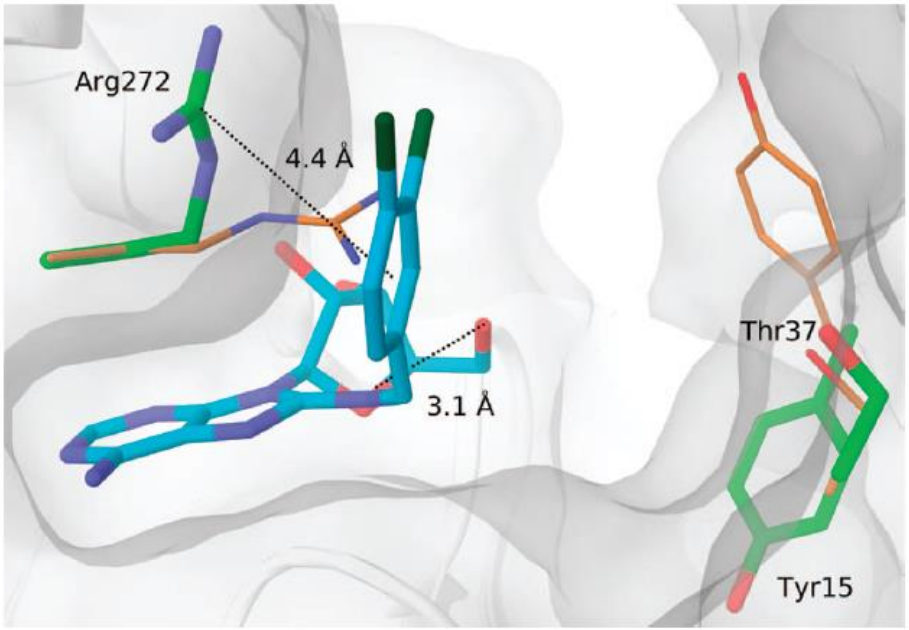


Figure 2. X-ray crystal structure of compound **7** (blue) in complex with HSC70/BAG-1 (green) showing π-stacking between the ligand and Arg272. Alternate conformers of Tyr15 and Arg272 from the X-ray structure of compound **4**/HSC70/BAG-1 are shown in orange.

J. Med. Chem. ***2009,*** *52, 1510–1513*

Figures - Exemples

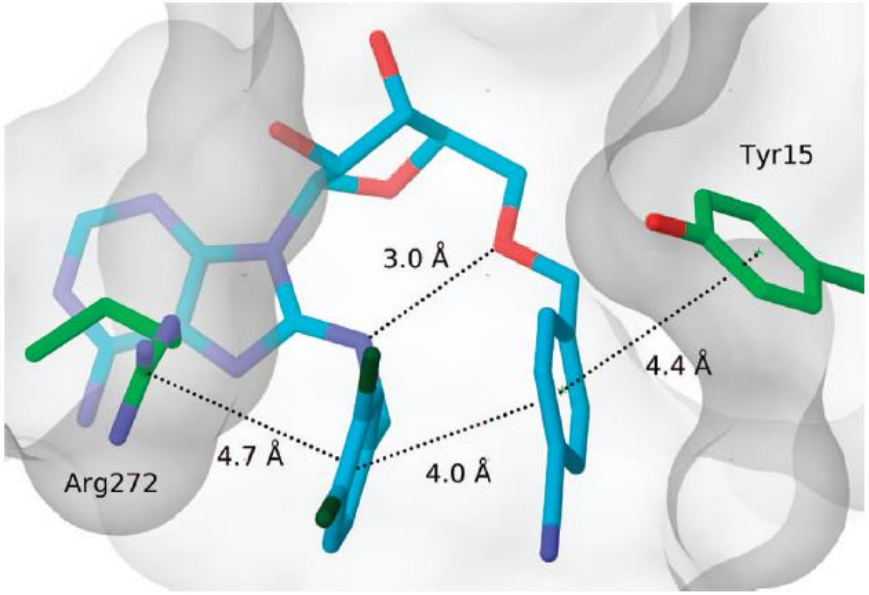


Figure 3. Inter- and intramolecular π-stacking interactions in the X-ray crystal structure of compound **12**/HSC70/BAG-1 in addition to the intramolecular H-bond between the 8-NH and 5-CH_2O of **12**.

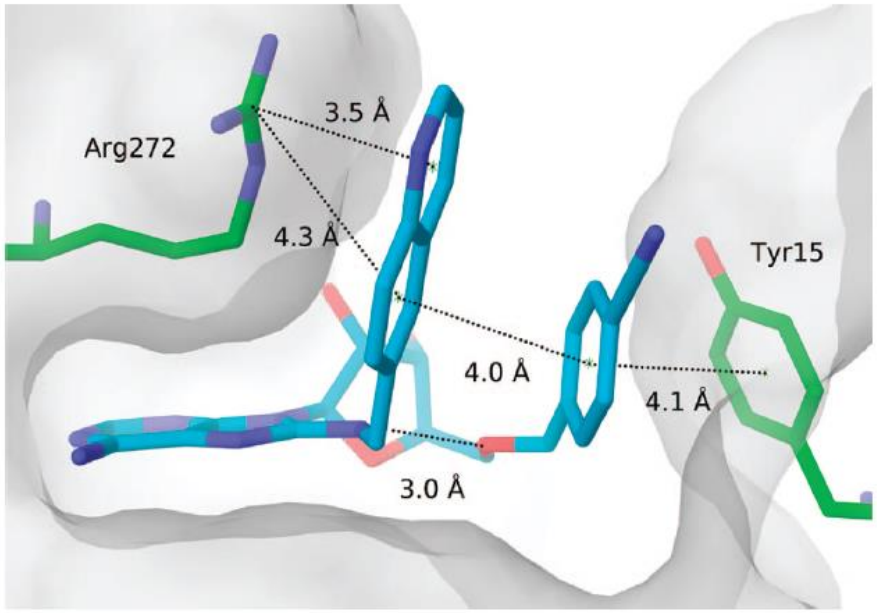


Figure 4. Improved π-stacking in the X-ray structure of compound **15**/HSC70/BAG-1.

J. Med. Chem. ***2009,*** *52, 1510–1513*

Figures - Exemples

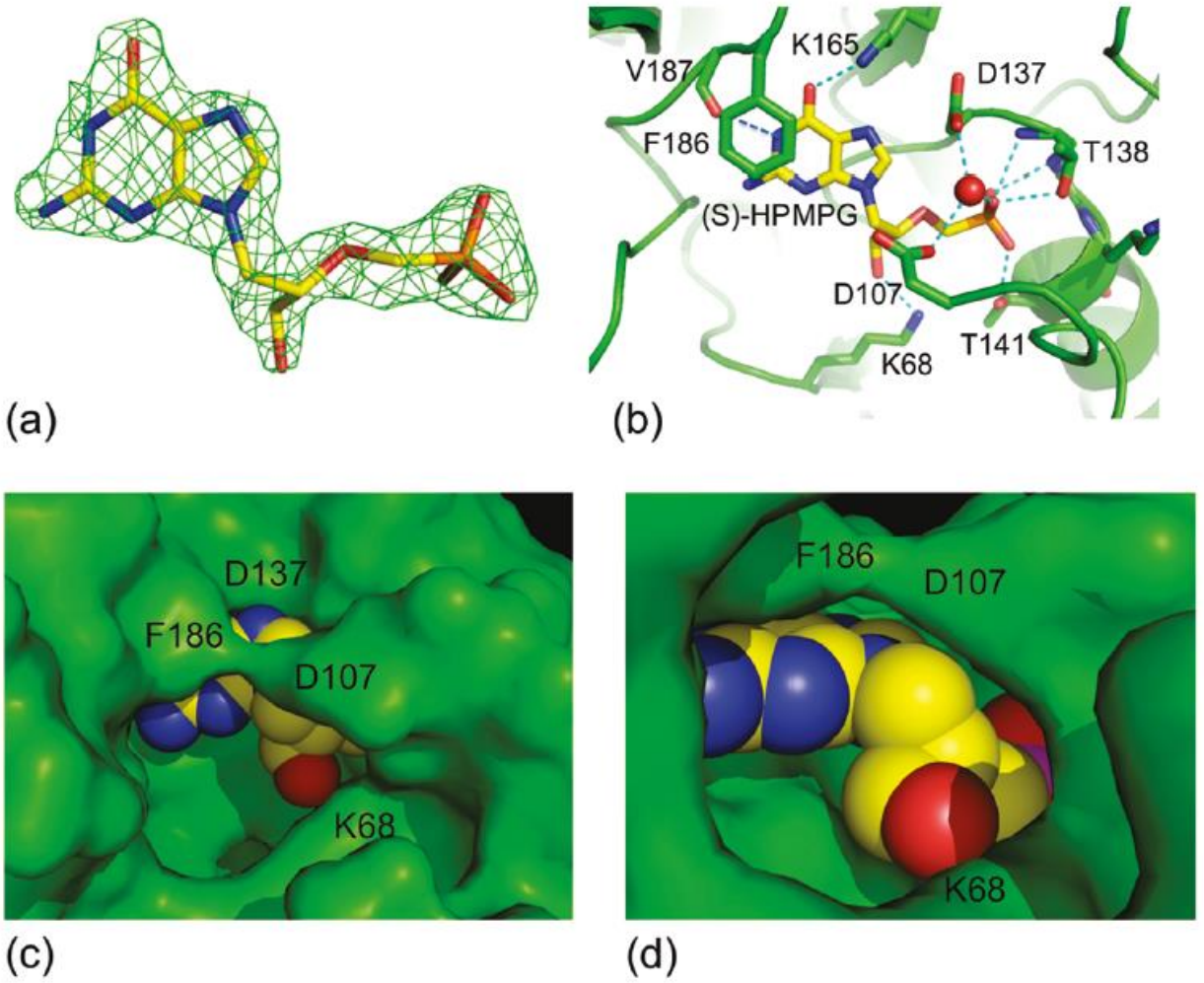


Figure 3. (a) The 2Fo - Fc electron density for (S)-HPMPG in complex with human HGPRT (subunit A) contoured at 1.5 σ. (b) The specific interactions of (S)-HPMPG with human HGPRT active site residues and the large mobile loop. (c,d) Two views of the Connolly surface of human HGPRT showing the location of (S)-HPMPG (drawn as solid spheres)

J. Med. Chem. **2009**, 52, 4391–4399

Figures - Exemples

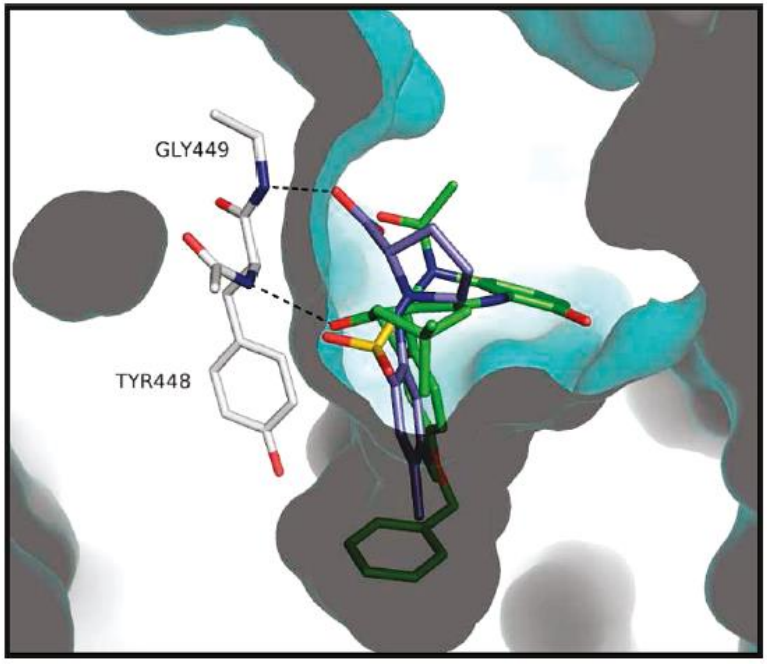


Figure 2. Overlay of the 2.75 Å resolution crystal structure of BZD (*R*)-**1b** (green, by atom) bound to HCV NS5B (white, by atom) with that of proline sulfonamide **3** (purple, by atom), indicating the common hydrogen bond with Tyr448:N and the additional hydrogen bond of **3** with Gly449:N.

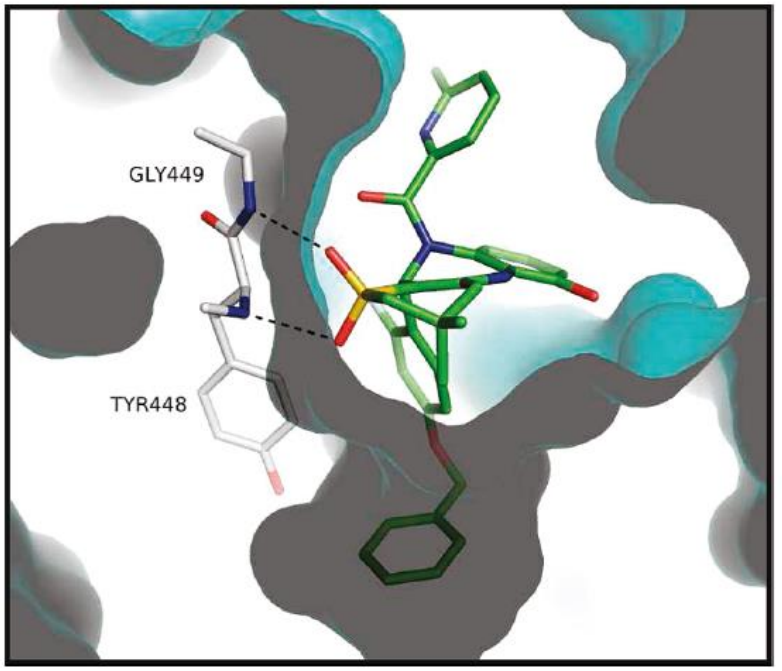


Figure 3. The 2.4 Å resolution crystal structure of (*S*)-**4c** bound to HCV NS5B polymerase.

J. Med. Chem. **2009**, 52, 4099–4102

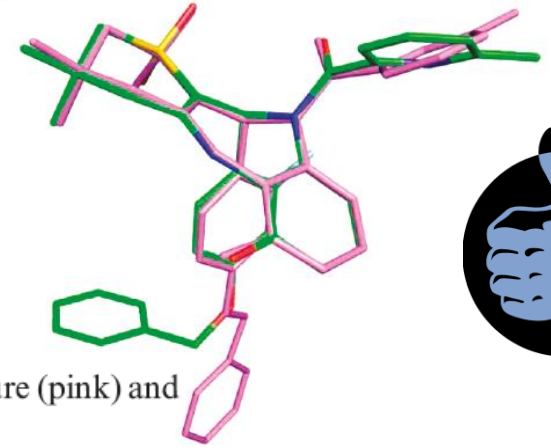


Figure 4. Overlay of the small molecule crystal structure (pink) and the NS5B-bound structure (color by atom) of (*S*)-**4c**.

Figures - Exemples

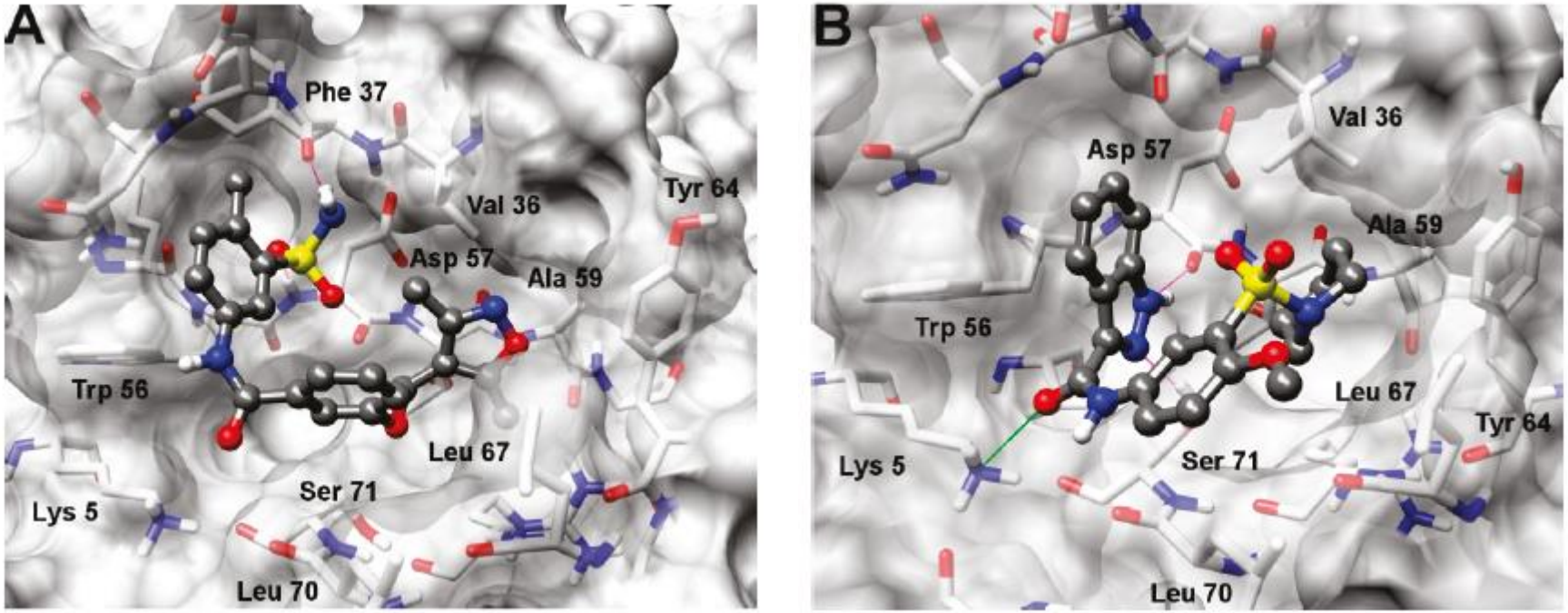


Figure 4. Predicted binding modes for **4** (A) and **5** (B). True hydrogen bonds are represented as magenta lines, while hydrogen interactions are depicted as green lines.

J. Med. Chem. **2009**, 52, 4087–4090

Figures - Exemples

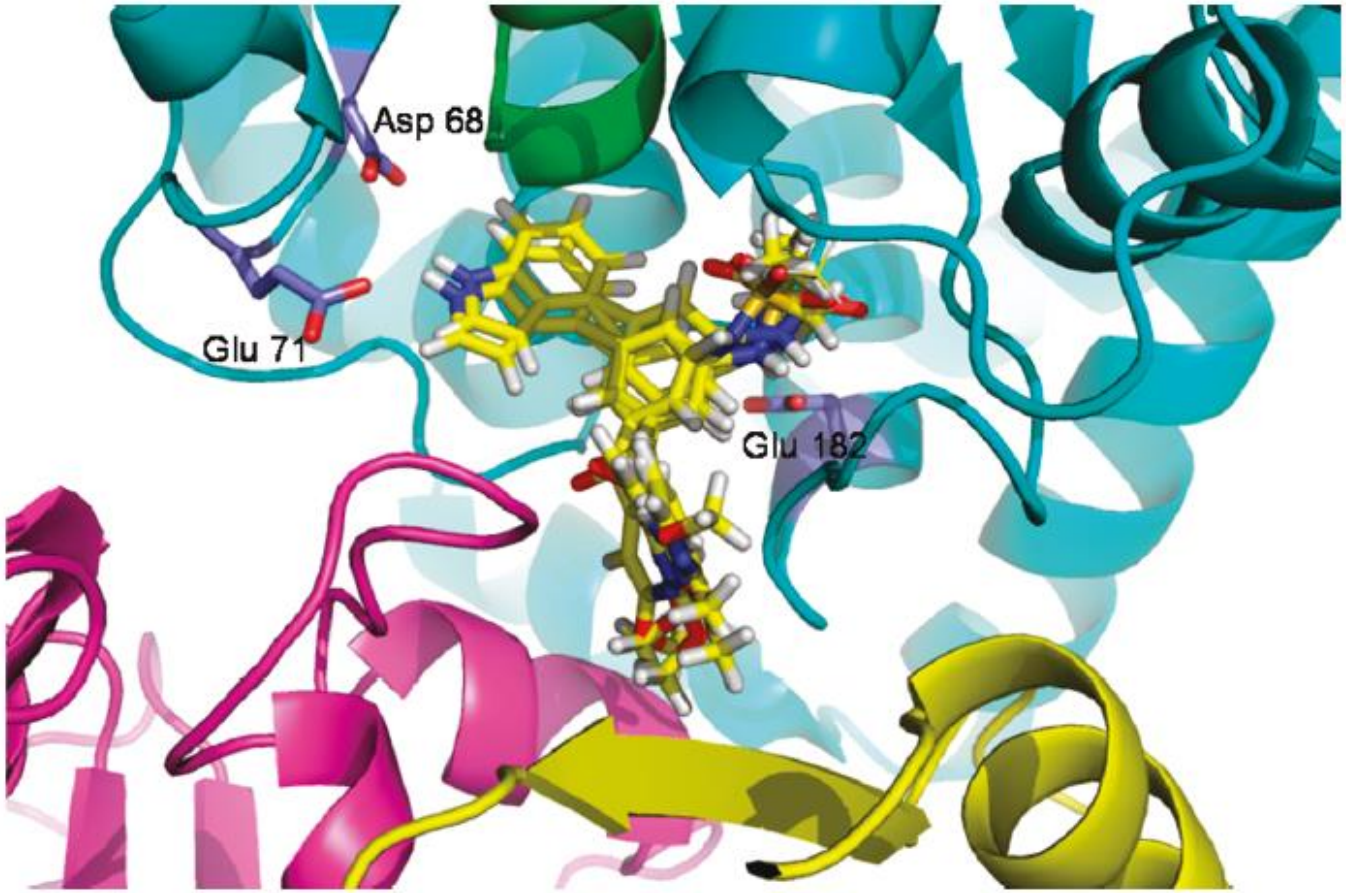


Figure 3. Distribution of molecule poses of **58** from molecule builds. Image was generated with the program PyMol.

J. Med. Chem. **2011**, 54, 179–200

Figures - Exemples

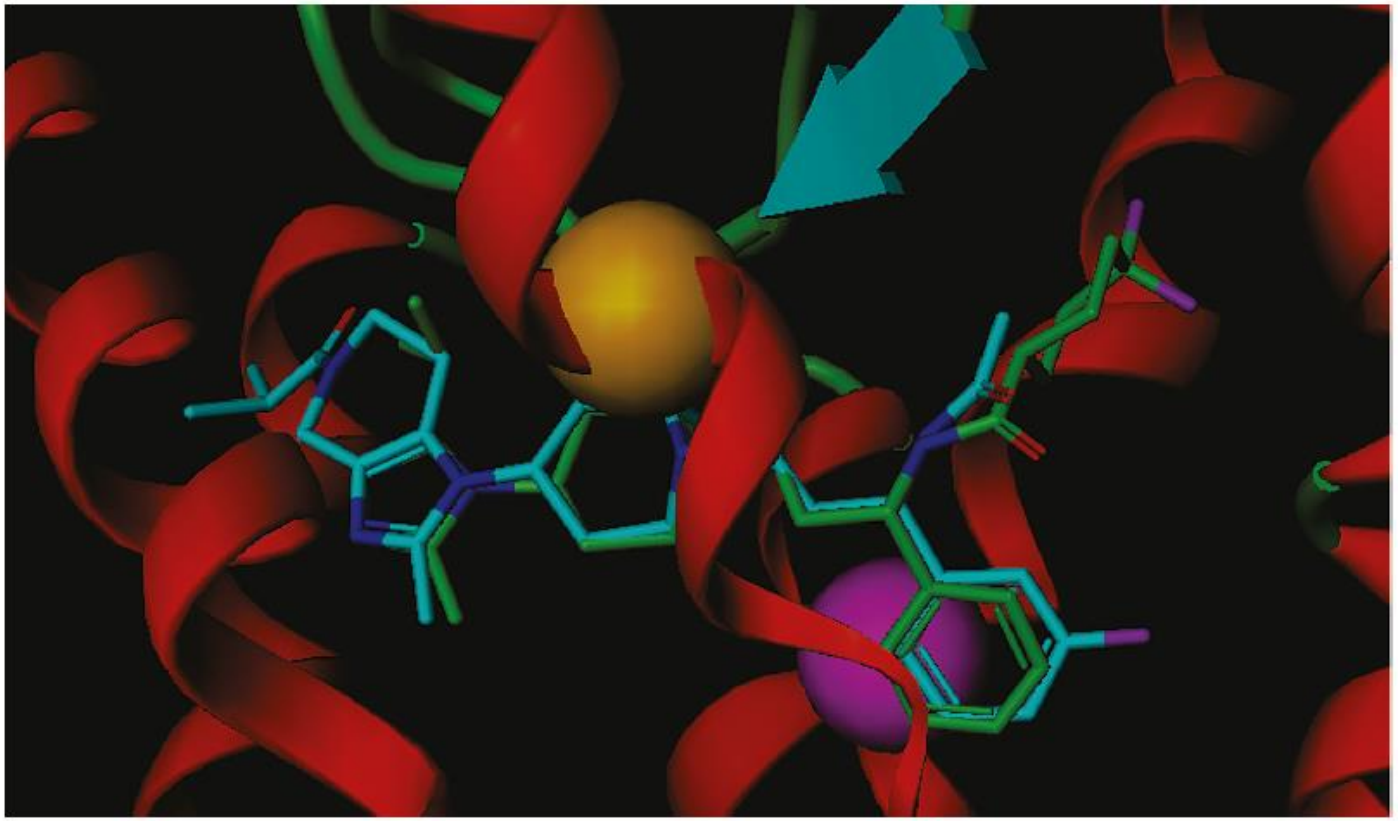


Figure 2. Docking of **1** (green) and **41f** (cyan) into a model of CCR5. E283 is indicated in orange, and Y108 is shown in magenta.

J. Med. Chem. **2011**, 54, 67–77

Figures - Exemples

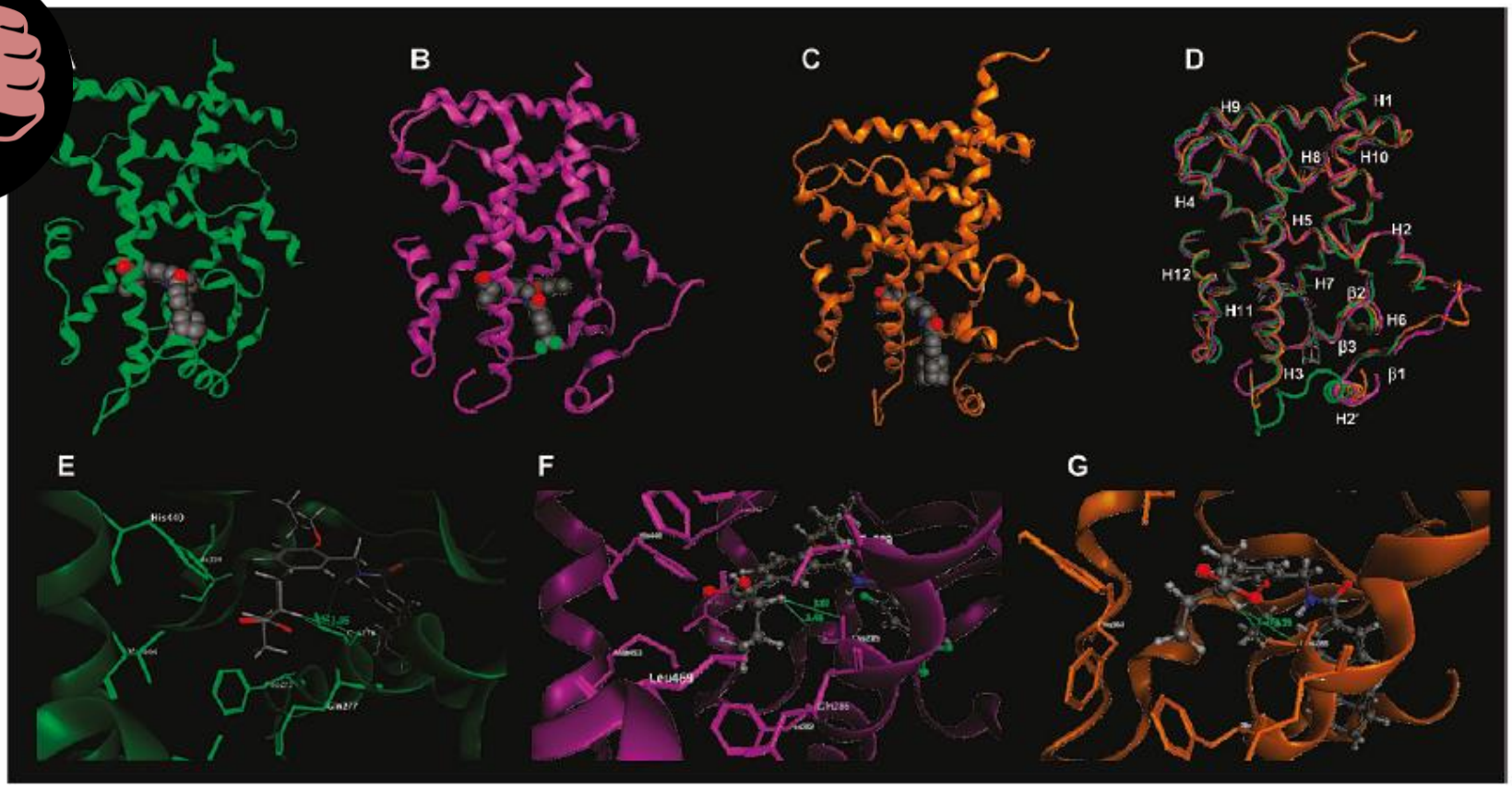


Figure 5. (A–C) Crystal structures of PPARs LBD–TIPP complexes. (A) PPARα LBD–(*S*)-**6** complex; (B) PPARδ LBD–(*S*)-**5** complex; (C) PPARγ LBD–(*S*)-**6** complex. Proteins are represented as ribbon models and the ligands are depicted as space-filling models, with F, C, N, and O atoms in aqua, gray, blue, and red, respectively. (D) Superposition of the main chains of each PPARs LBD. The numbering of the second structure is also depicted. (E–G) Zoomed view of the ligand-binding mode of PPARs LBD–TIPP complexes. (E) PPARα LBD–(*S*)-**6** complex; (F) PPARδ LBD–(*S*)-**5** complex; (G) PPARγ LBD–(*S*)-**6** complex. Proteins are represented as ribbon models and the ligands are depicted as cylinder models, with F, C, N, and O atoms in aqua, gray, blue, and red, respectively.

J. Med. Chem. **2011**, 54, 331–341

Figures - Exemples

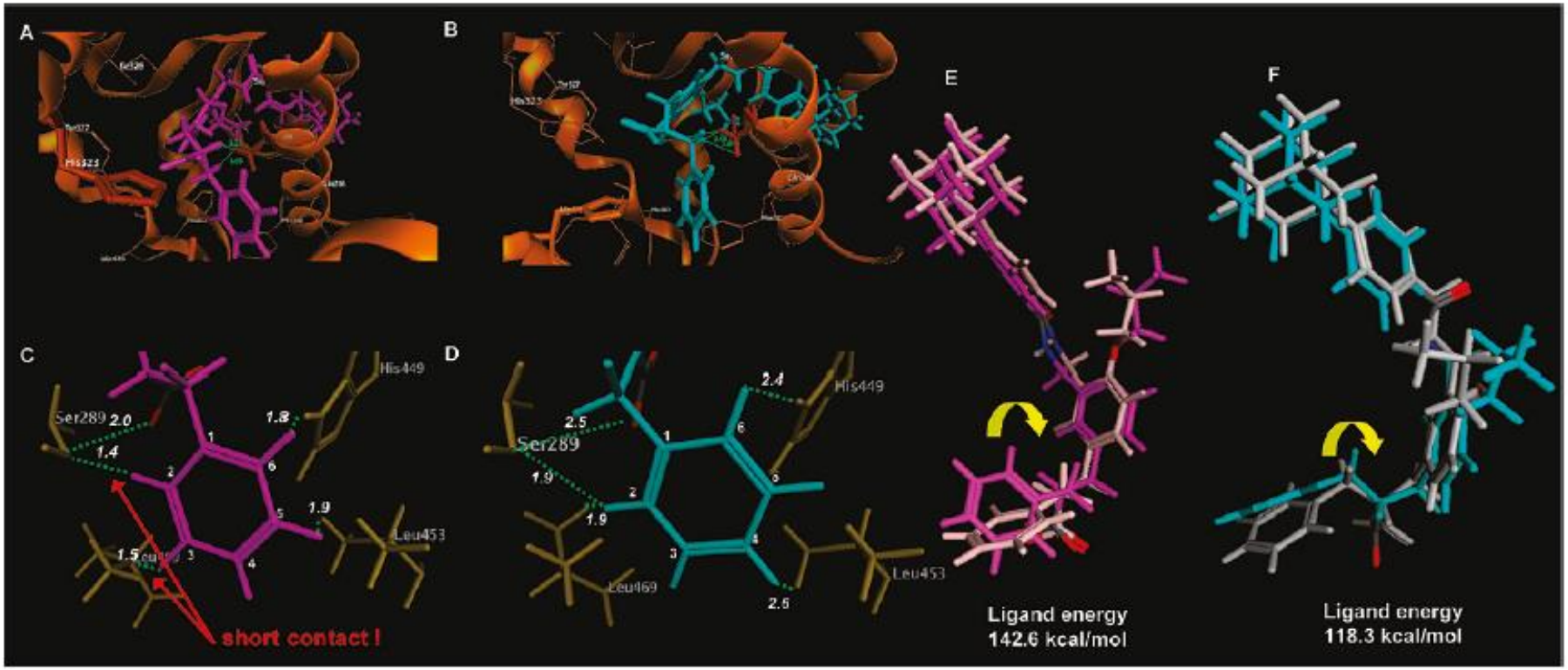


Figure 5. (A−C) Crystal structures of PPARs LBD−TIPP complexes. (A) PPARα LBD−(*S*)-**6** complex; (B) PPARδ LBD−(*S*)-**5** complex; (C) PPARγ LBD−(*S*)-**6** complex. Proteins are represented as ribbon models and the ligands are depicted as space-filling models, with F, C, N, and O atoms in aqua, gray, blue, and red, respectively. (D) Superposition of the main chains of each PPARs LBD. The numbering of the second structure is also depicted. (E−G) Zoomed view of the ligand-binding mode of PPARs LBD−TIPP complexes. (E) PPARα LBD−(*S*)-**6** complex; (F) PPARδ LBD−(*S*)-**5** complex; (G) PPARγ LBD−(*S*)-**6** complex. Proteins are represented as ribbon models and the ligands are depicted as cylinder models, with F, C, N, and O atoms in aqua, gray, blue, and red, respectively.

J. Med. Chem. **2011**, 54, 331–341

Figures - Exemples

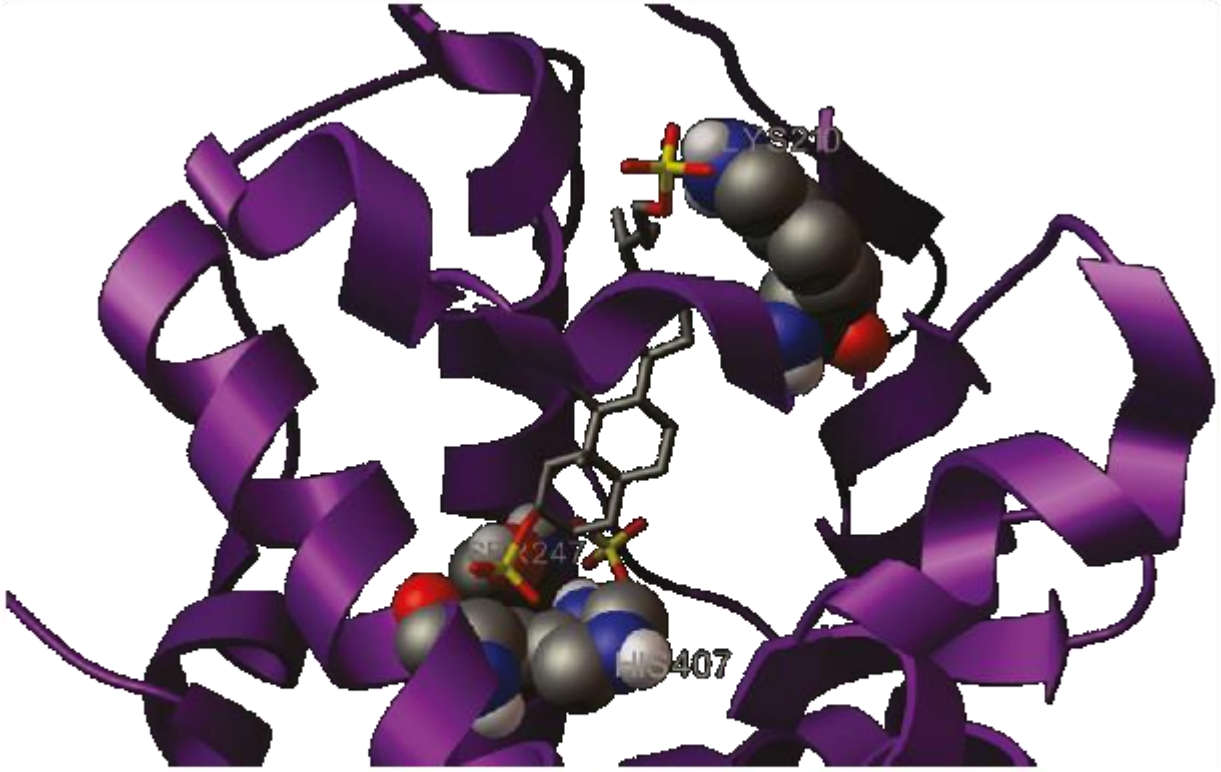


Figure 5. Docked model of **1** bound to PXR model (PDB code: 1M13, displayed as purple ribbon); **1** is displayed as sticks colored by atom type, while His407, Ser247, and Lys210 are depicted as atom type colored CPK models.

J. Med. Chem. **2011**, 54, 331–341

Tarefa

- Cada grupo deverá pesquisar a literatura e trazer para a próxima aula:
  - 1 exemplo de figura de proteína que vocês consideram uma **boa figura**
  - 1 exemplo de figura de proteína que vocês consideram uma **figura ruim**
- Em ambos os casos incluir nos slides:
  - Qual(is) o(s) tipo(s) de representação(ões) utilizada(s)
  - Qual(is) a(s) referência(s)