



Central European Institute of Technology
BRNO | CZECH REPUBLIC



Vizualizace proteinů a ligandů

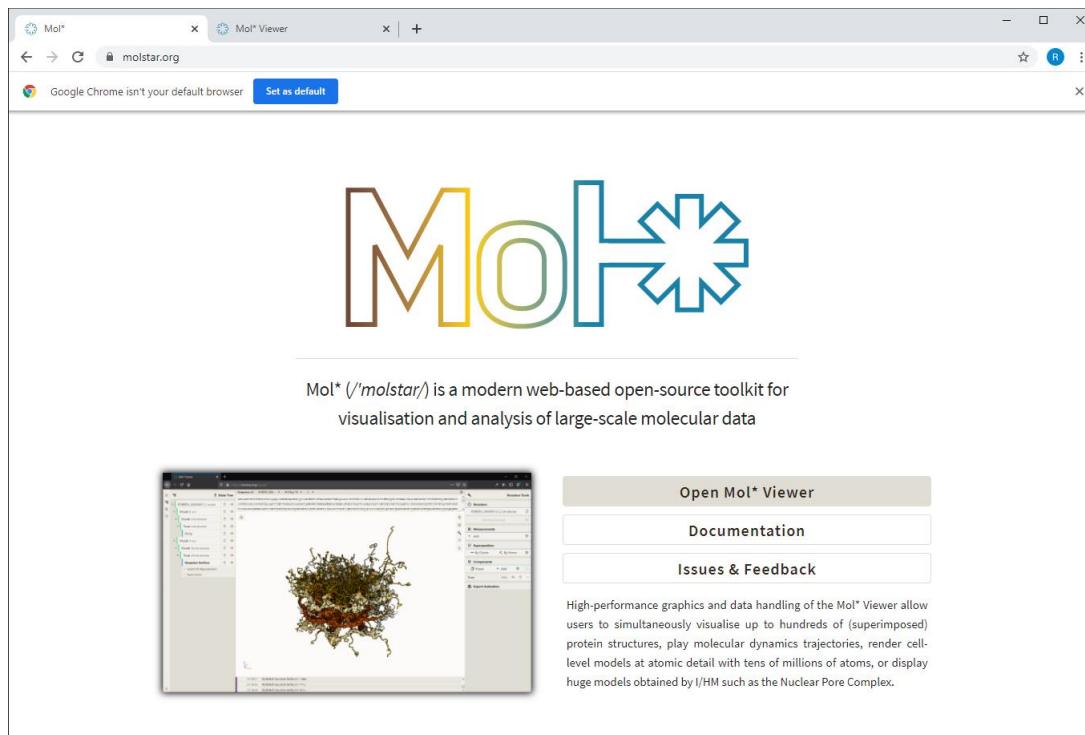


EUROPEAN UNION
EUROPEAN REGIONAL DEVELOPMENT FUND
INVESTING IN YOUR FUTURE



MolStar

- Webová aplikace pro vizualizaci proteinů a ligandů
- Zvládá i extrémně velké systémy
- Integrovaný v Protein Data Bank
- Využíjený u nás v Národním centru pro výzkum biomolekul, ve spolupráci s EMBL EBI a RCSB PDB
- <https://molstar.org/>



MolStar

Mol*

Mol* Viewer

Mol* Viewer

molstar.org/viewer/

Home

Sequence No structure available

Download Structure

Source PDB

PDB Id(s) 1tqn

Apply

Add Trajectory

Download Density

Download File

Open Files

Download

Load CellPack

Load Genome 3D (G3D)

Remote States

Nuclear Pore Complex

NPC-CIF

1RB8 Annotated Assembly

Zika+EM

Cytochromes Superposition

AS

ASX

ASX-1 Something

1

2

Structure Tools

Structure

Nothing Loaded

Nothing Focused

Measurements

Add

Components

Preset Add

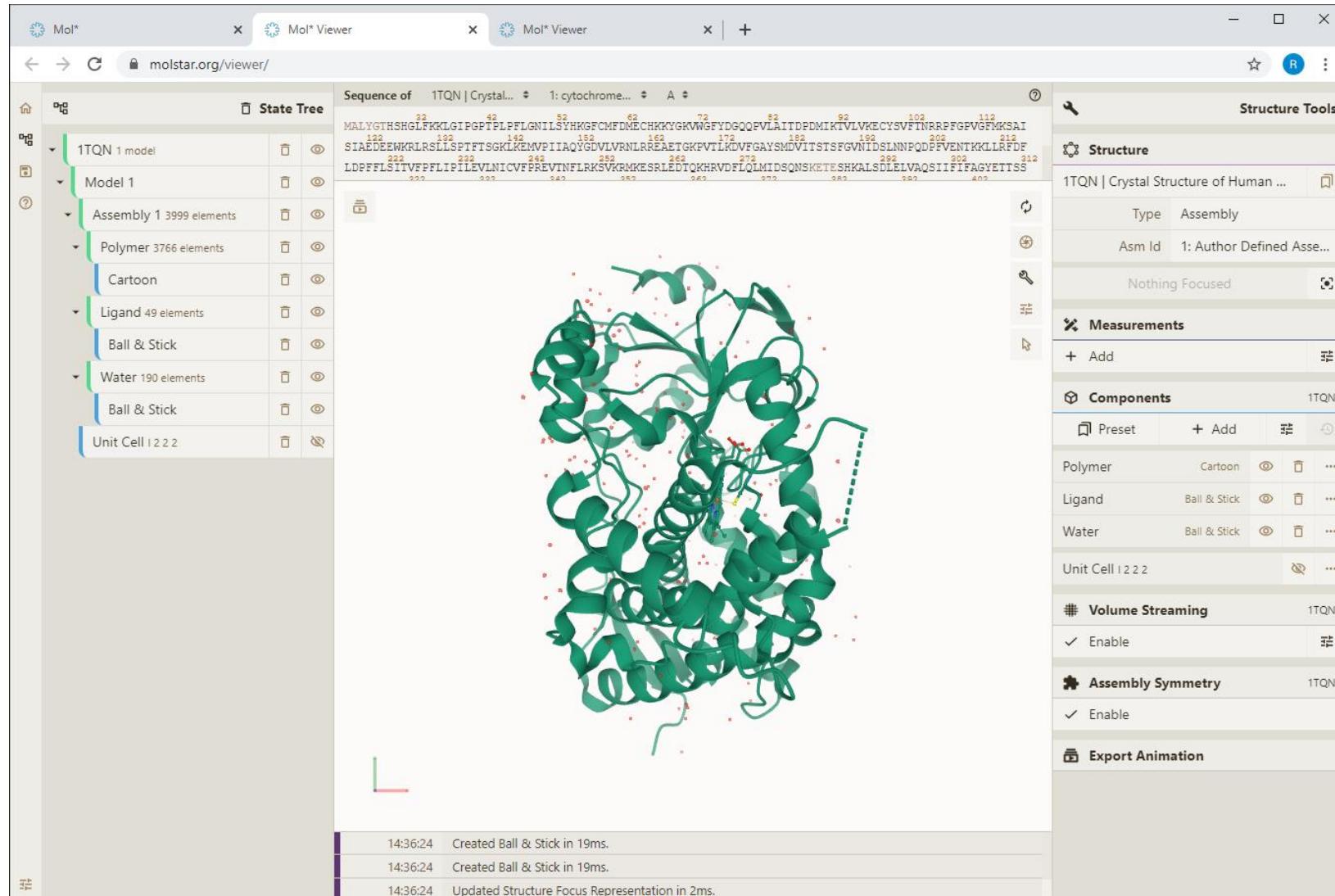
Export Animation

14:28:23 Mol* Plugin 1.2.7 [12/19/2020, 11:52:32 AM]

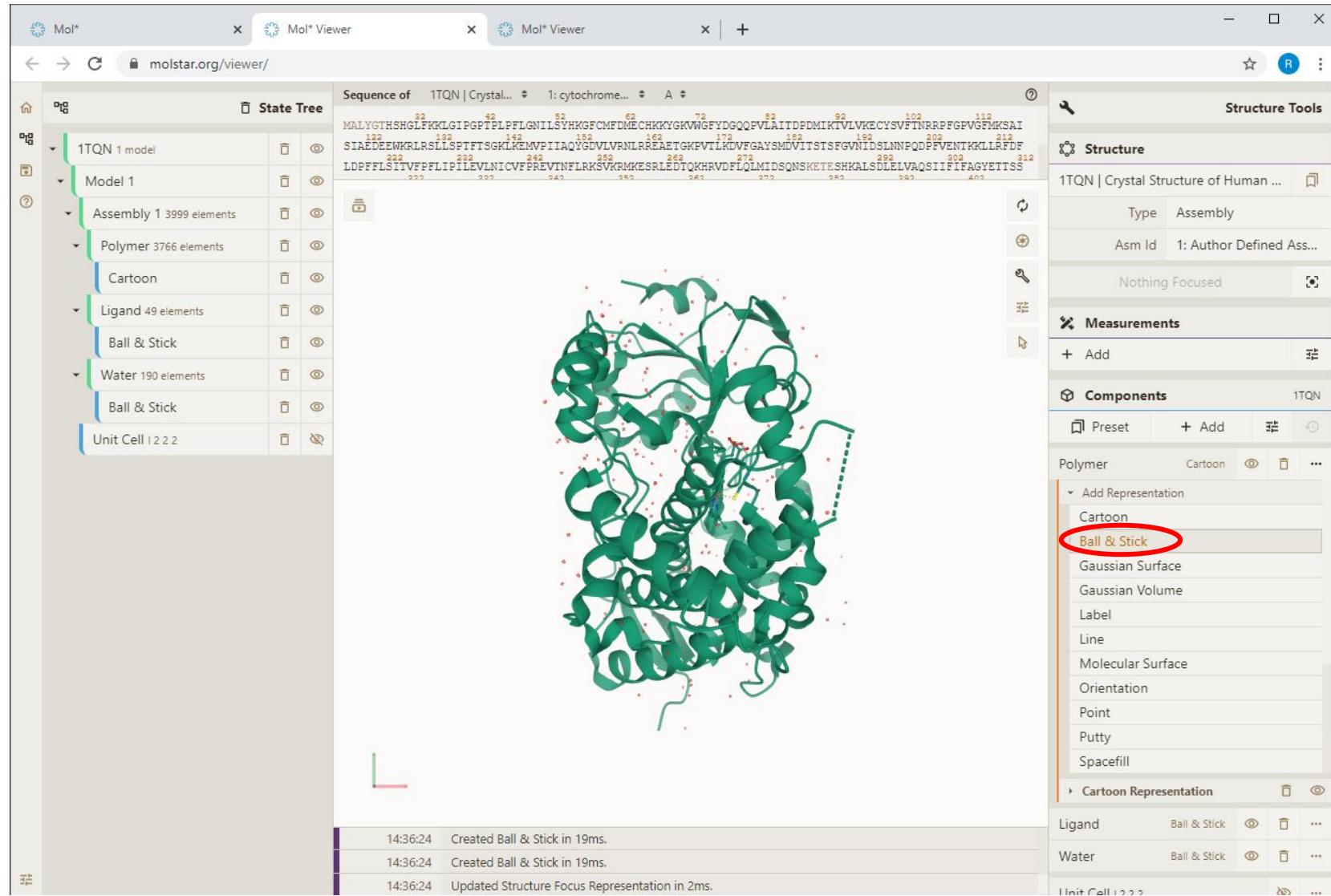
MolStar

Vizualizace 3D souřadic molekuly

Vizualizační model cartoon

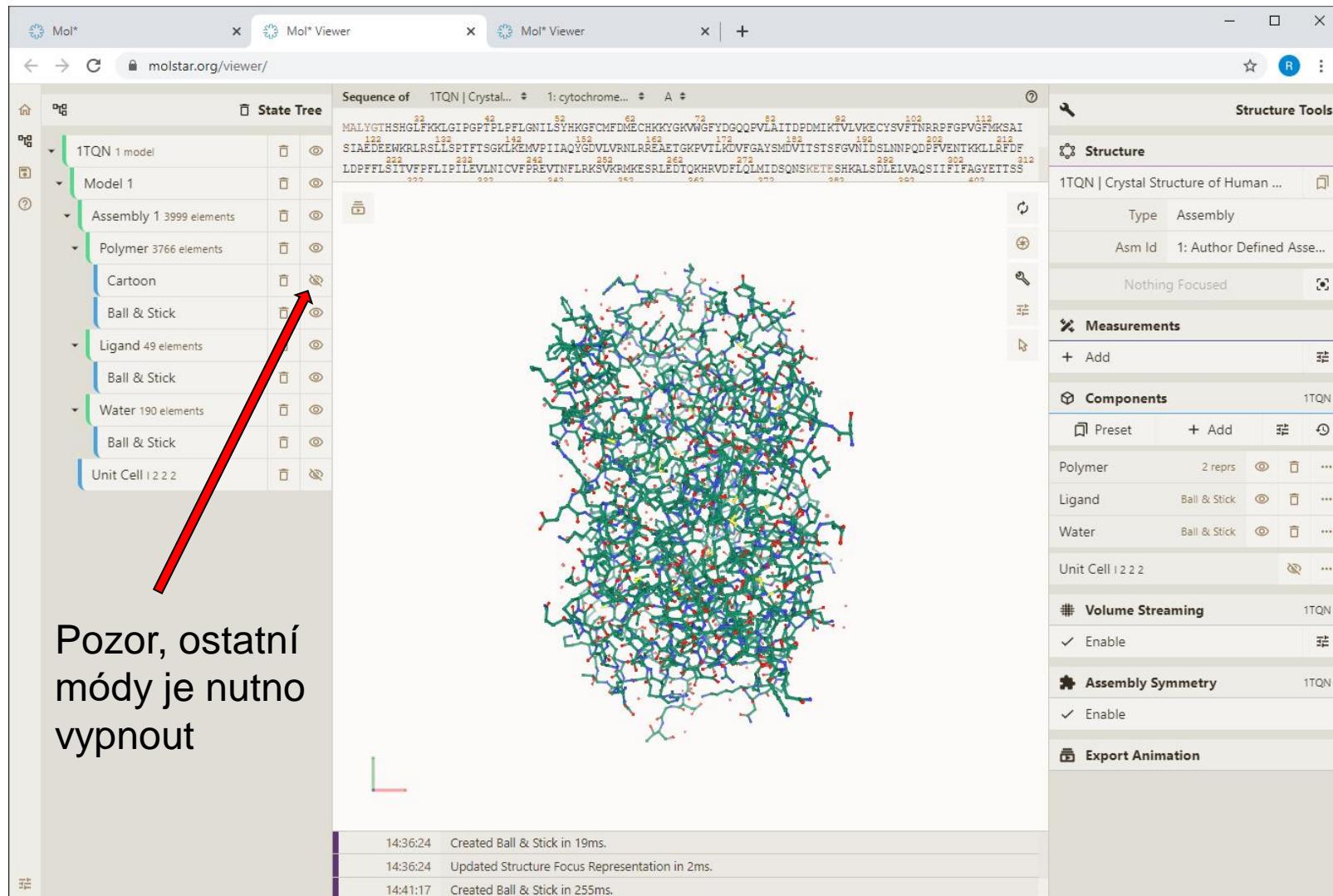


Vizualizace 3D souřadic molekuly Volba vizualizačních modelů



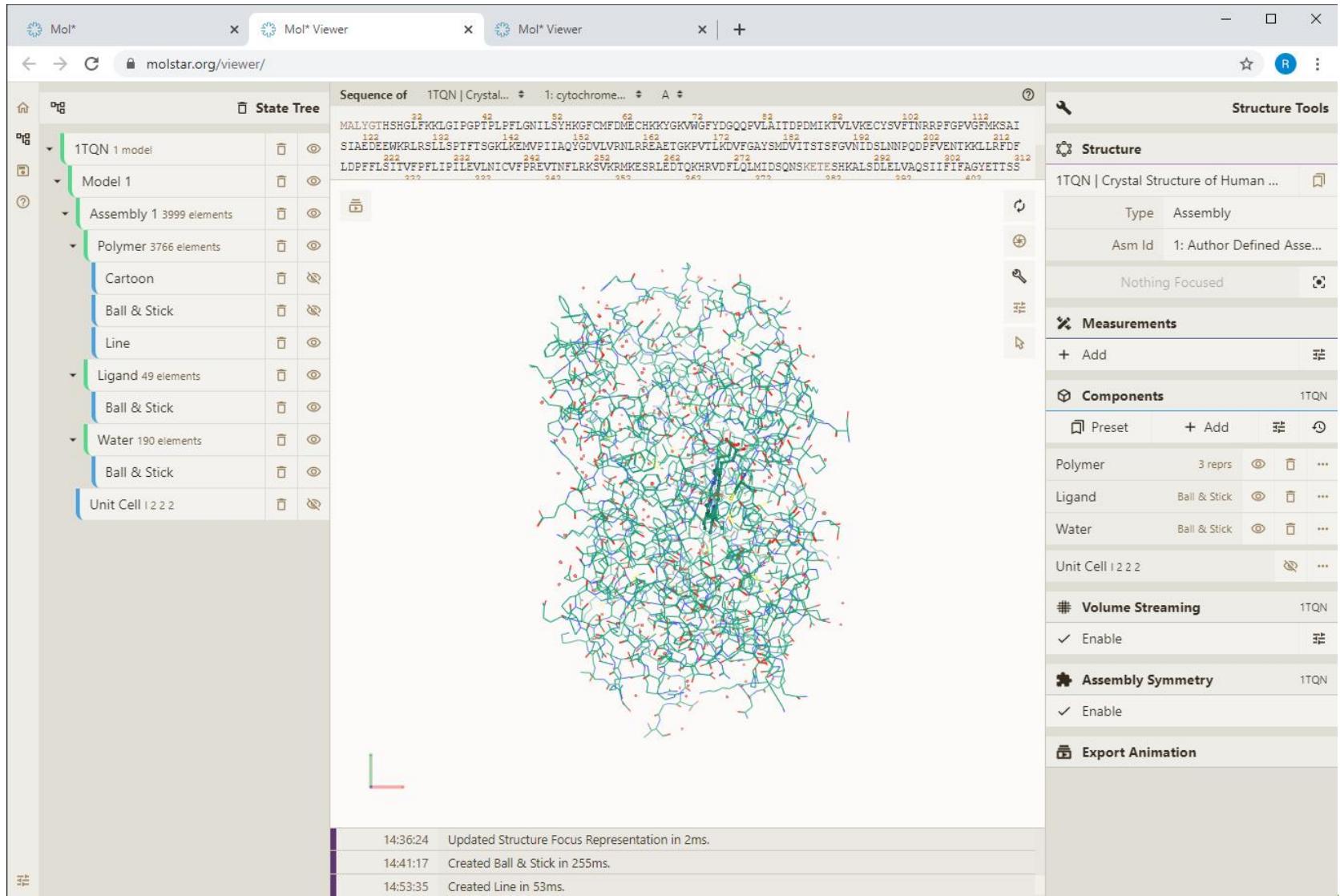
Vizualizace 3D souřadic molekuly

Vizualizační model Ball & Stick



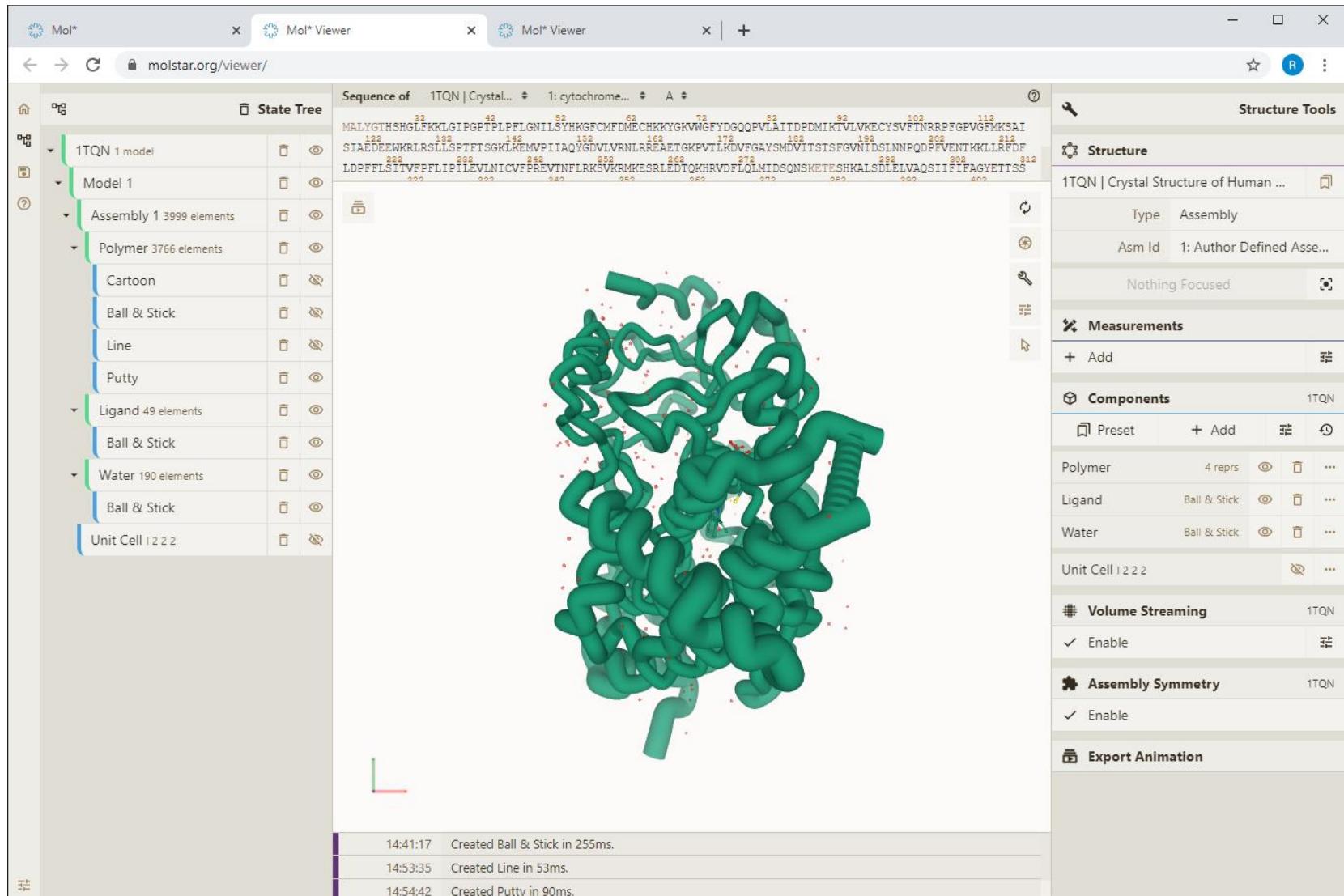
Vizualizace 3D souřadic molekuly

Vizualizační model Line



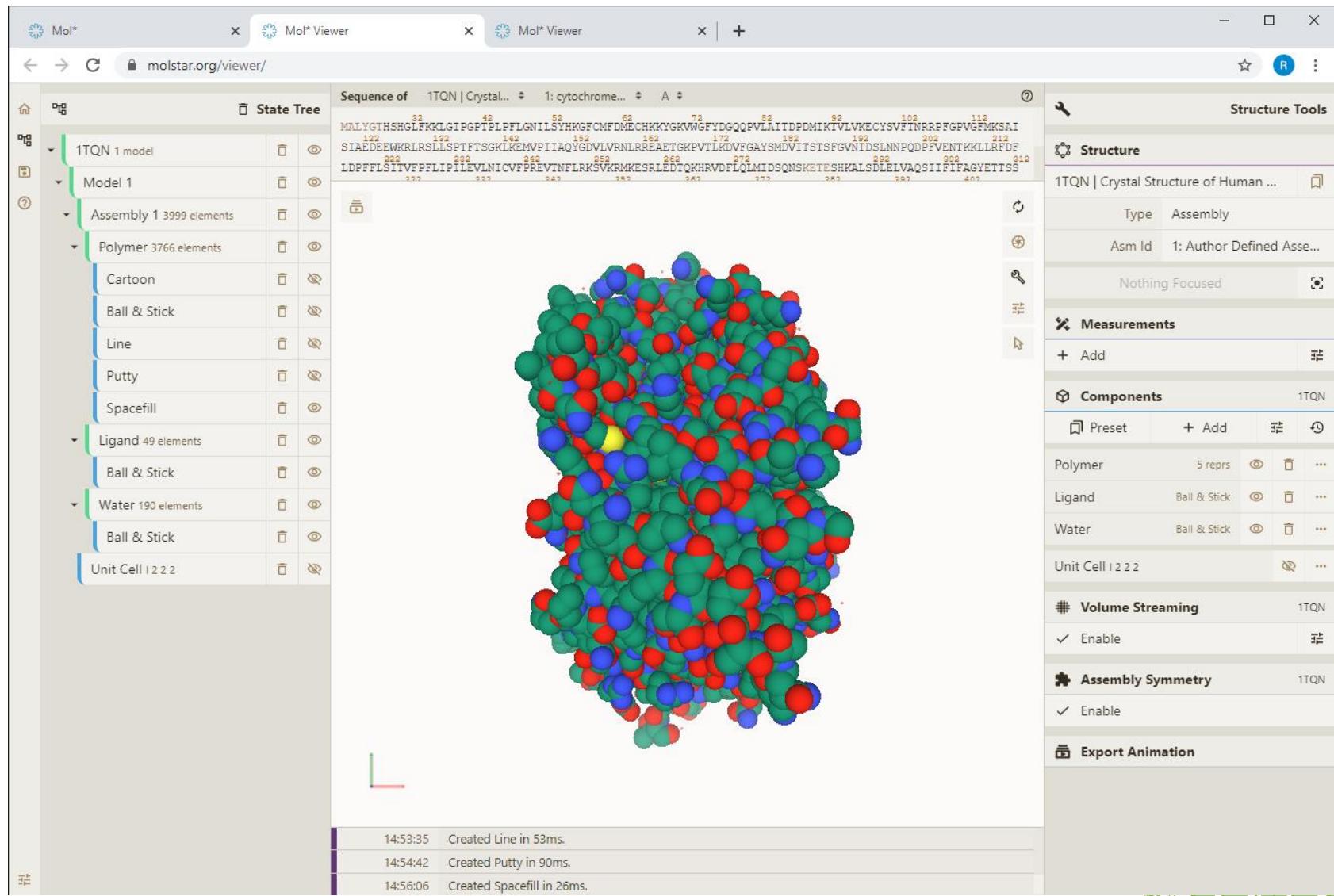
Vizualizace 3D souřadic molekuly

Vizualizační model Putty



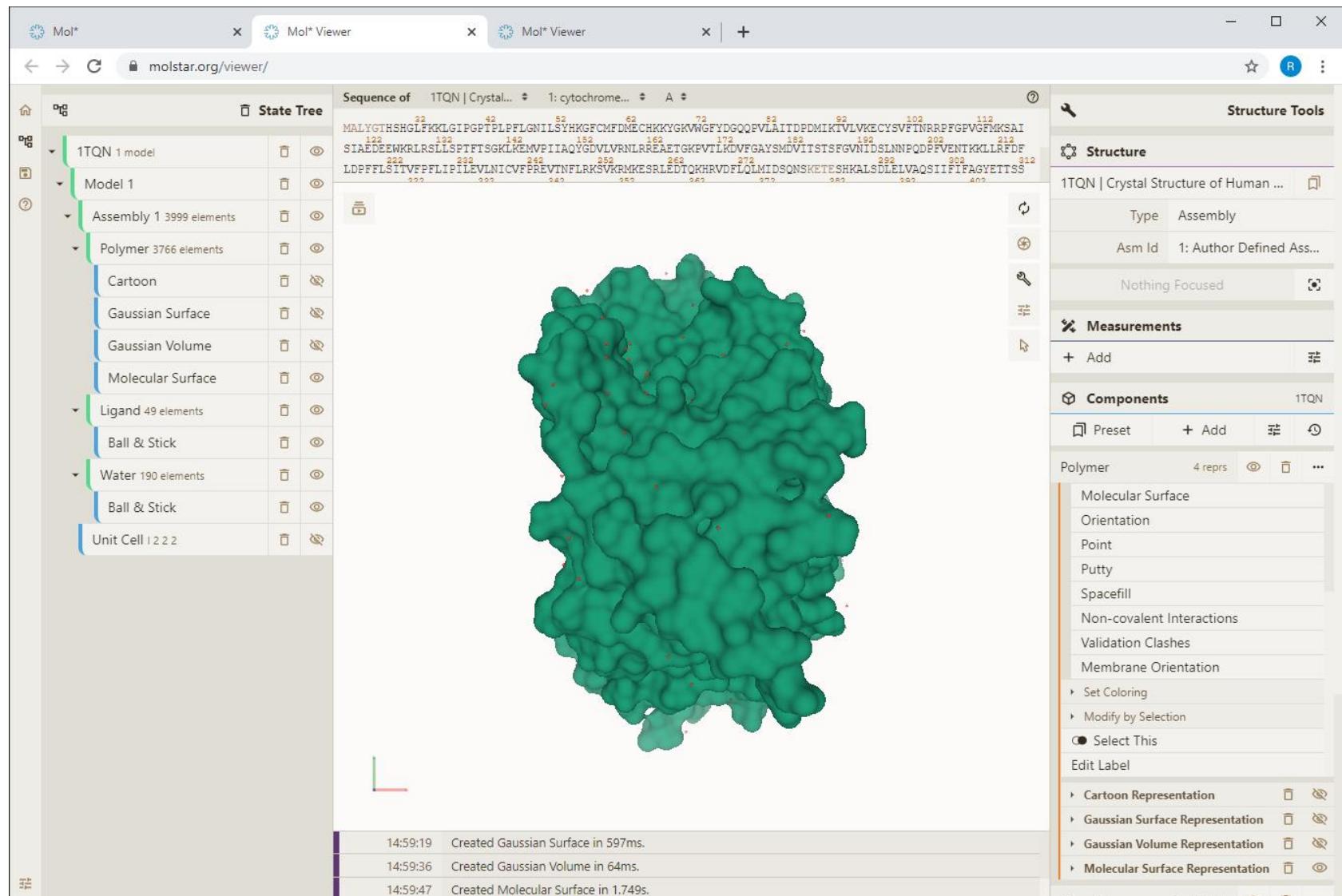
Vizualizace 3D souřadic molekuly

Vizualizační model Spacefil



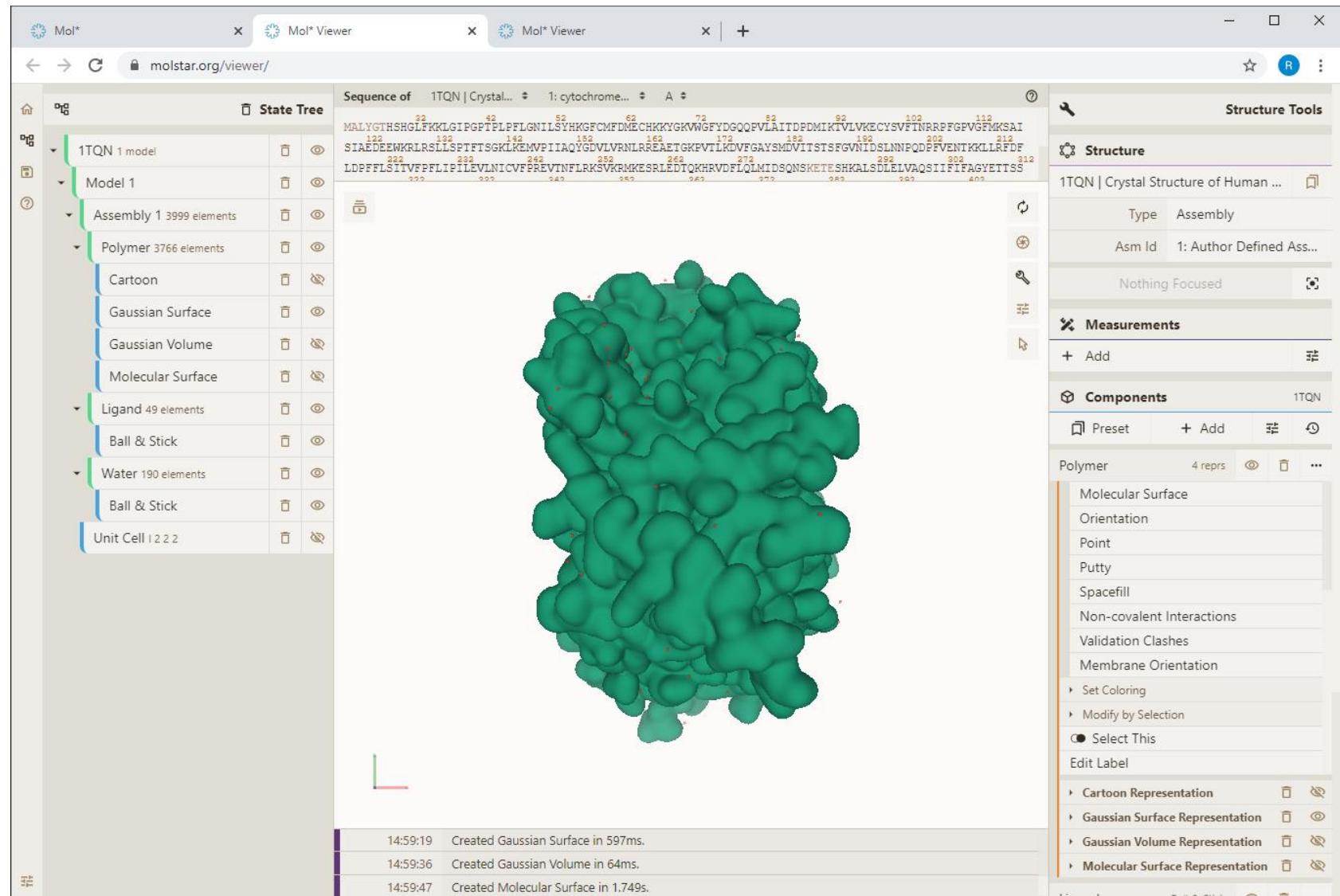
Vizualizace povrchu molekuly

Vizualizační model Molecular Surface



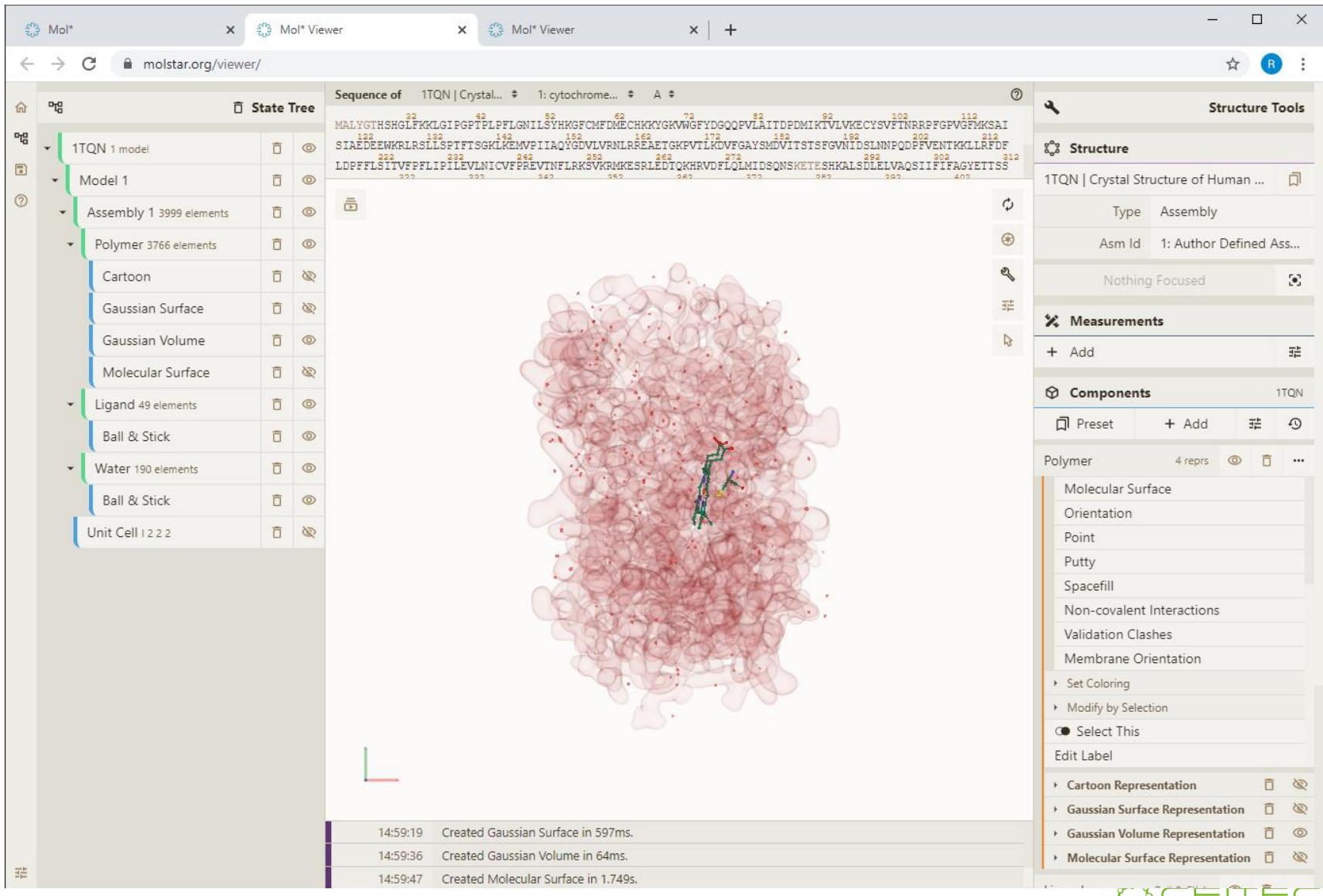
Vizualizace povrchu molekuly

Vizualizační model Gaussian Surface

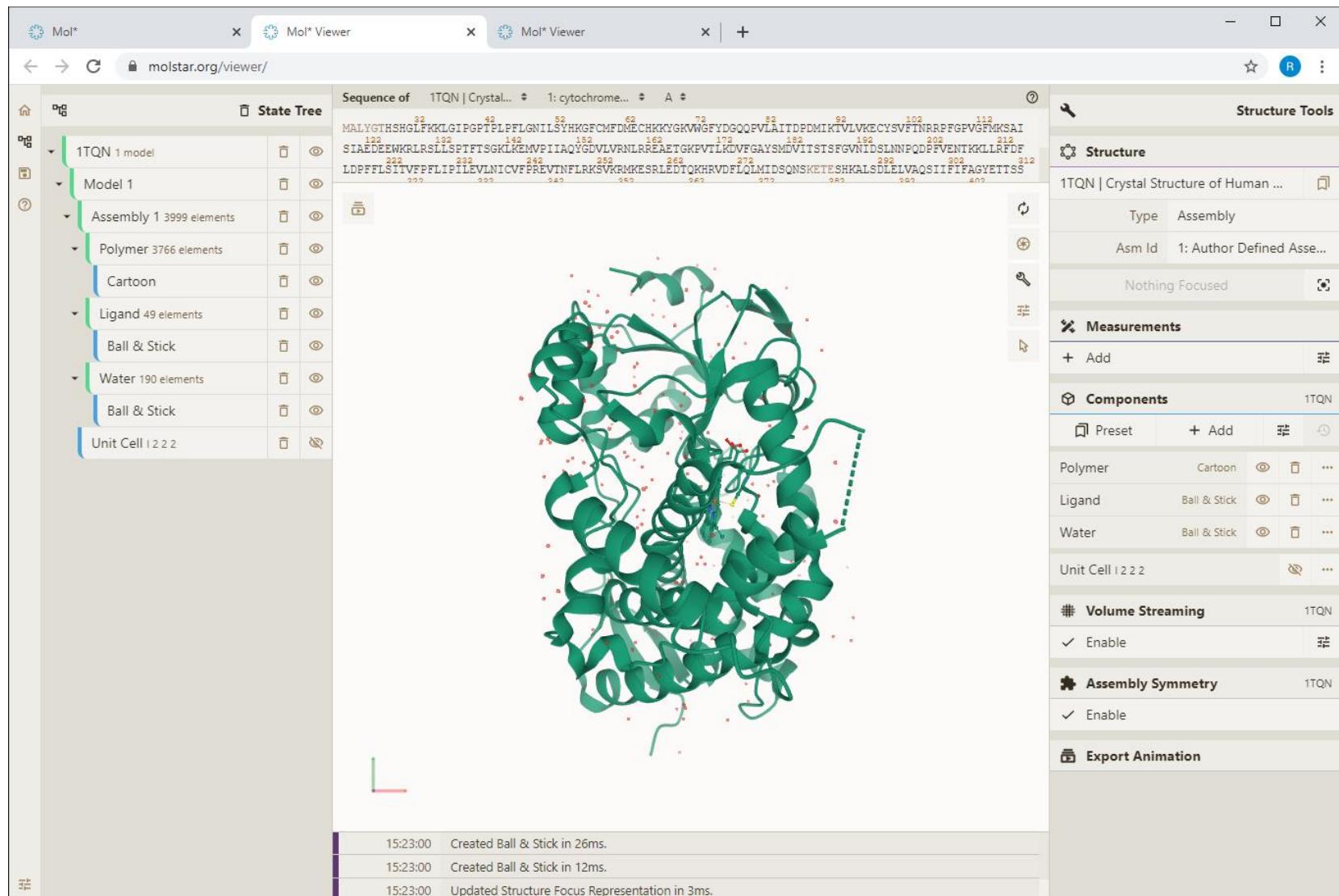


Vizualizace povrchu molekuly

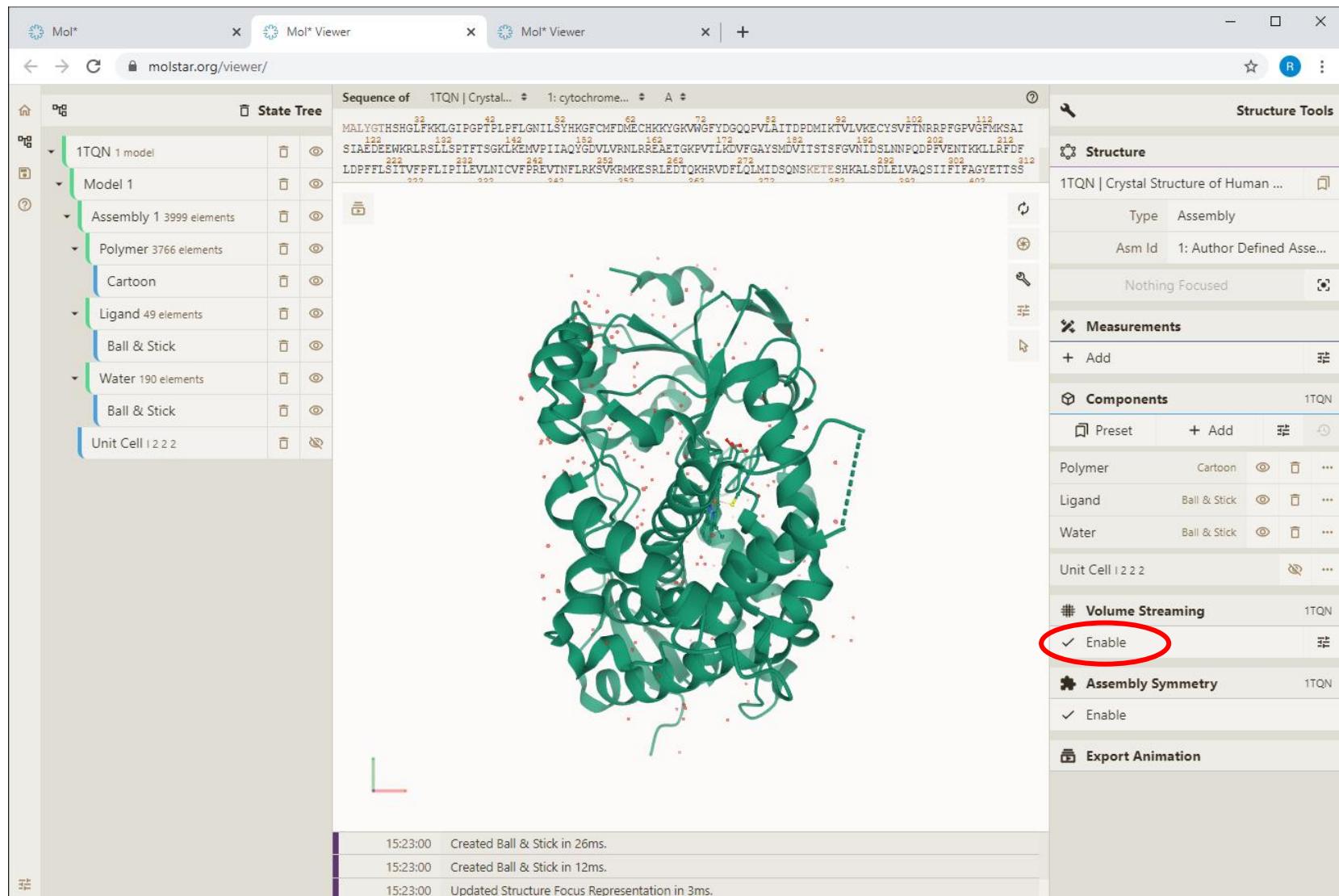
Vizualizační model Gaussian Volume



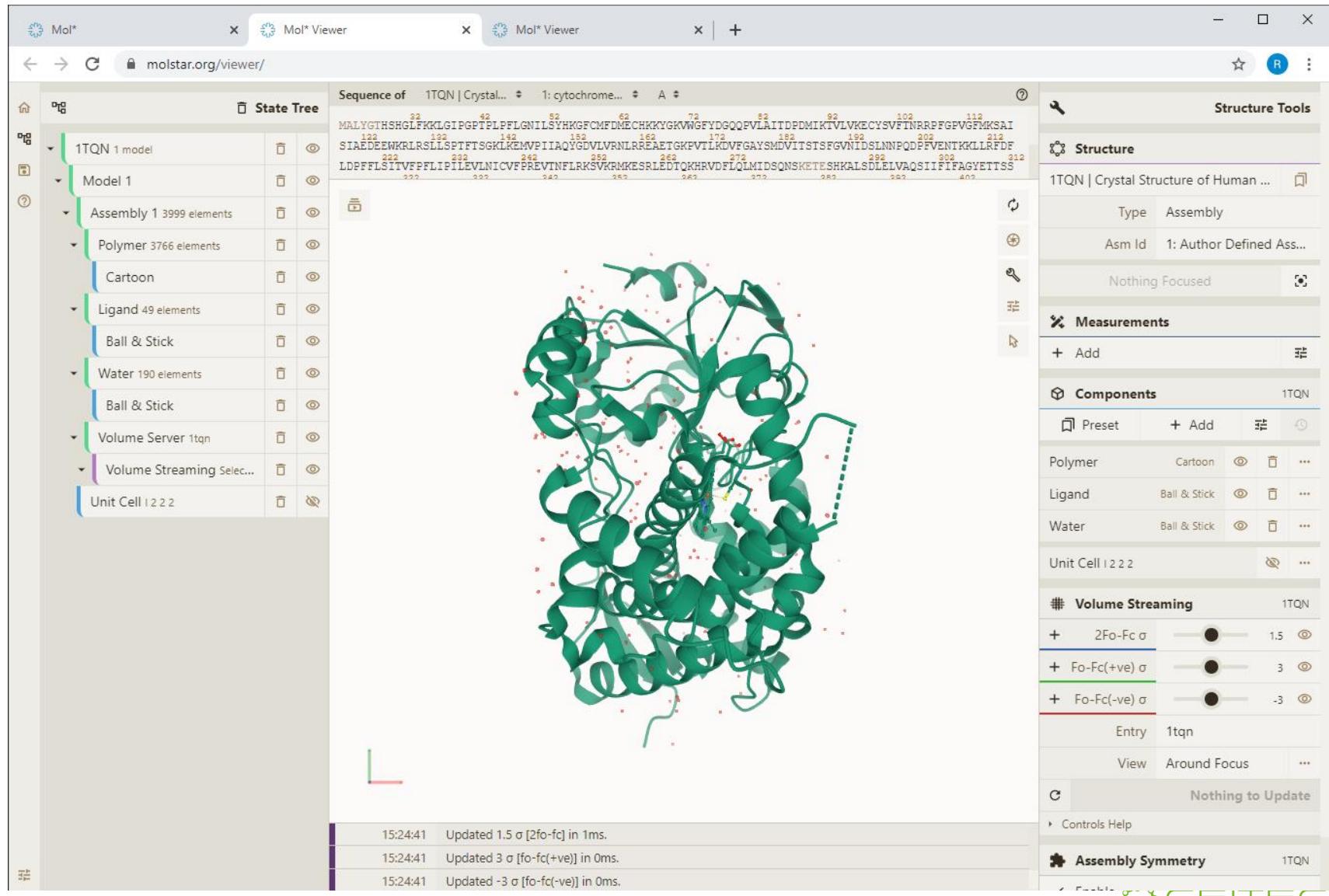
Vizualizace experimentálních dat Elektronová hustota



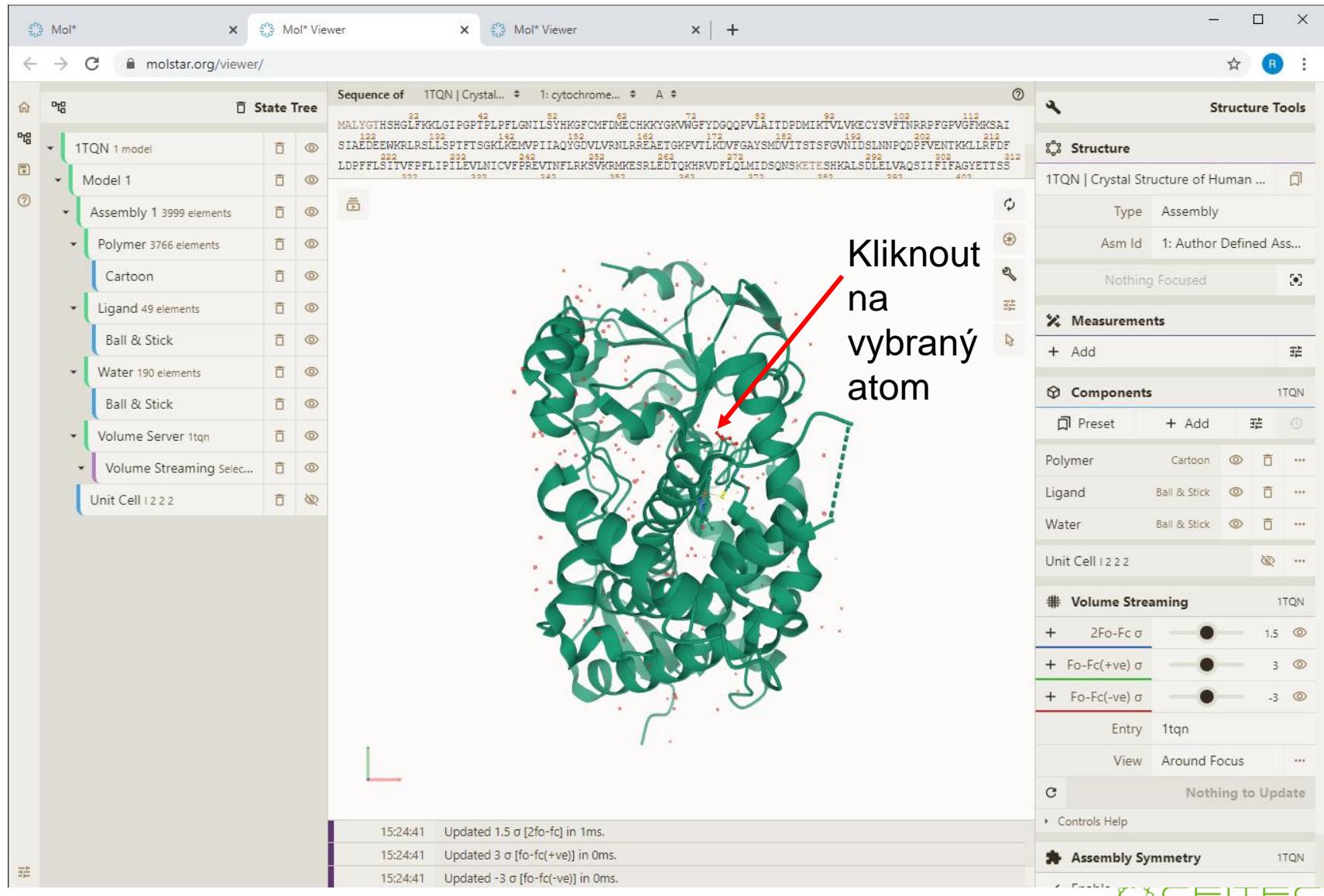
Vizualizace experimentálních dat Elektronová hustota



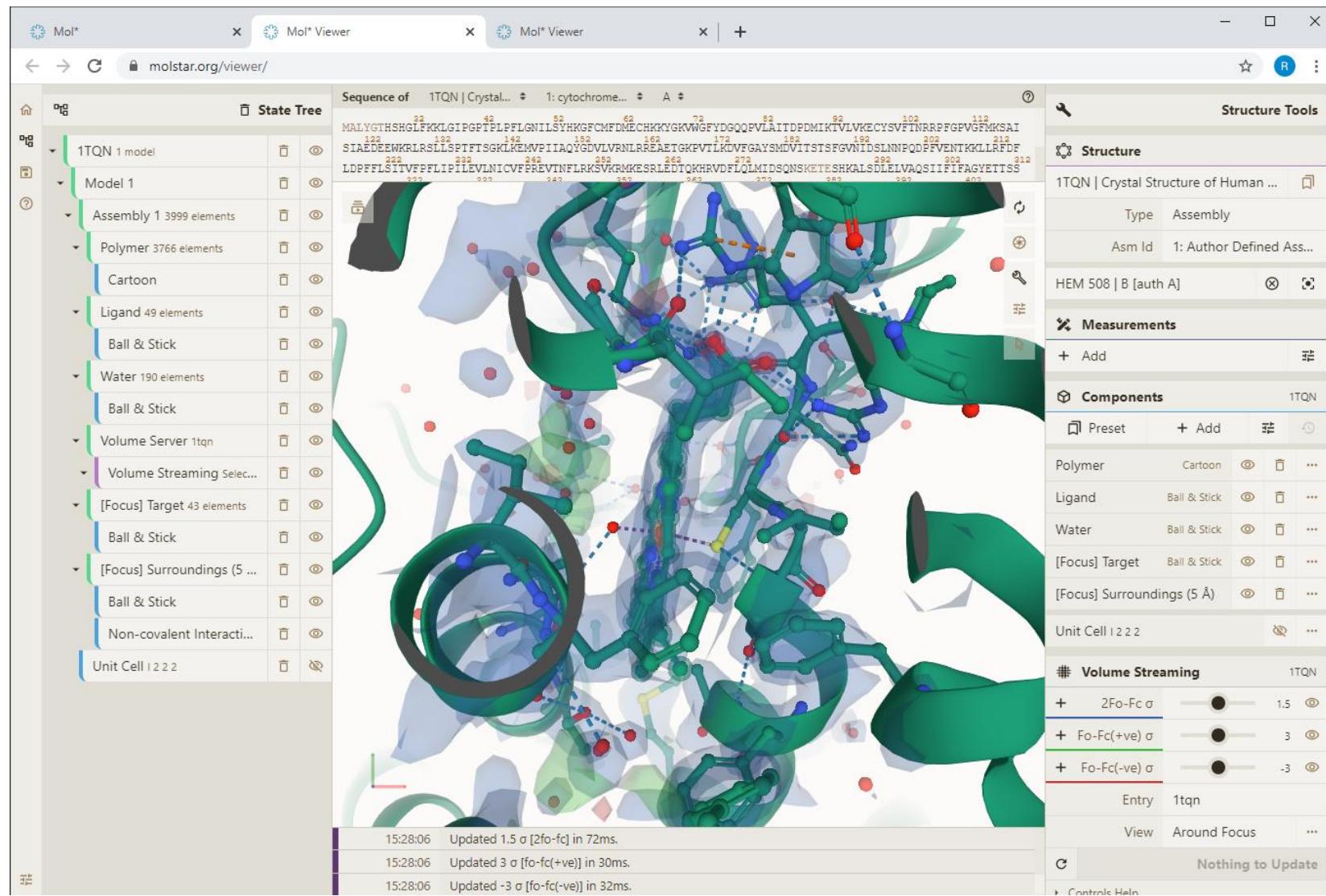
Vizualizace experimentálních dat Elektronová hustota



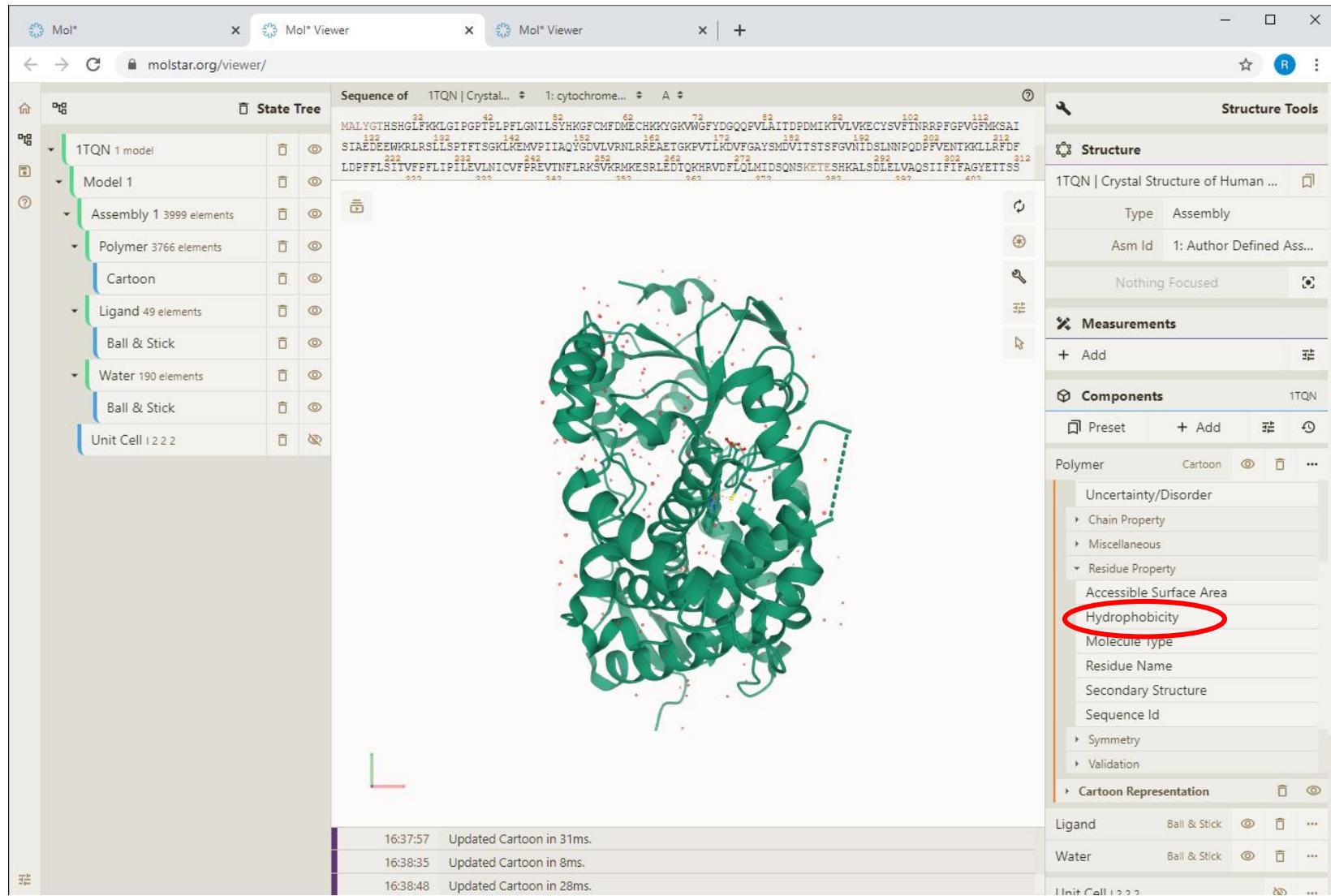
Vizualizace experimentálních dat Elektronová hustota



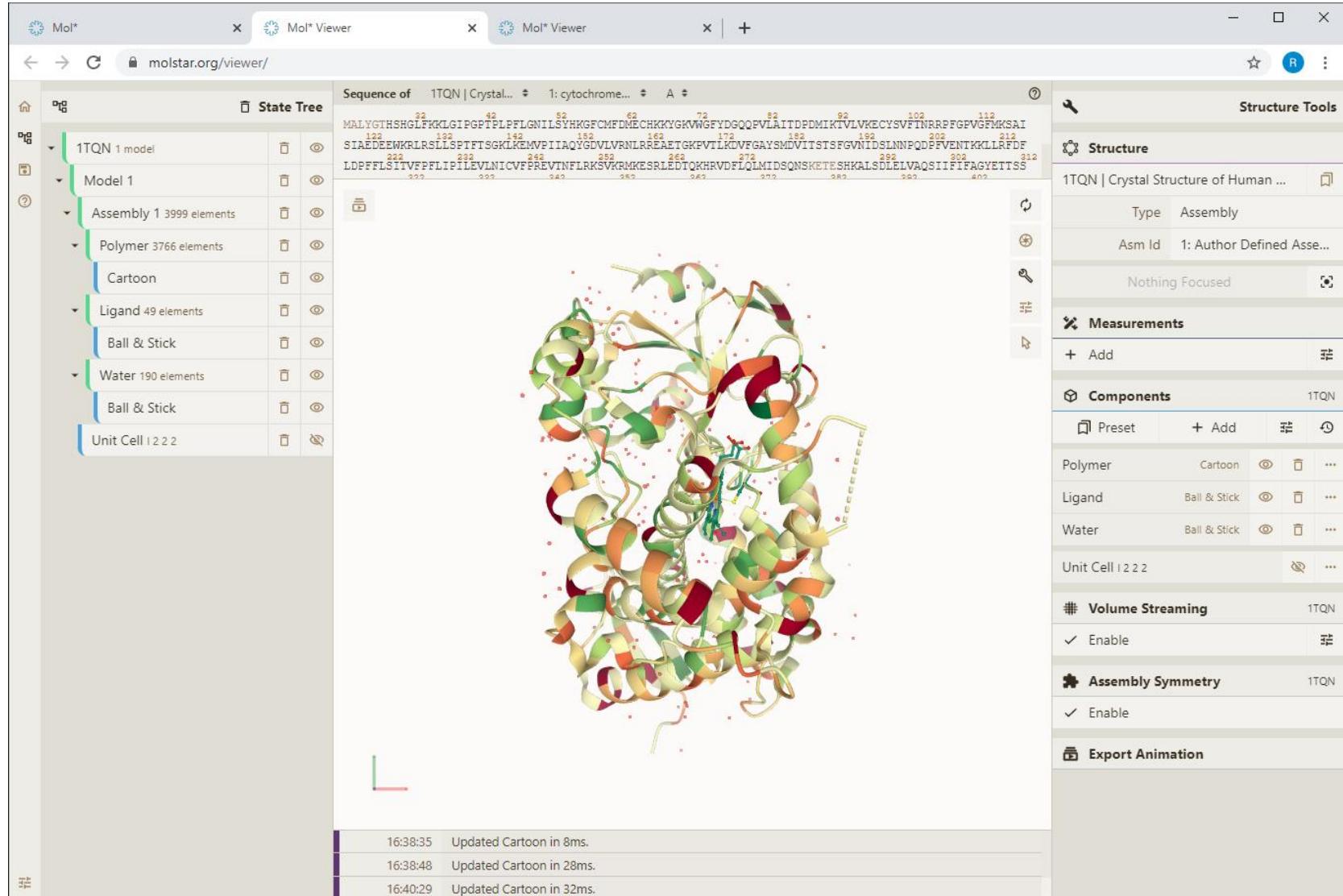
Vizualizace experimentálních dat Elektronová hustota



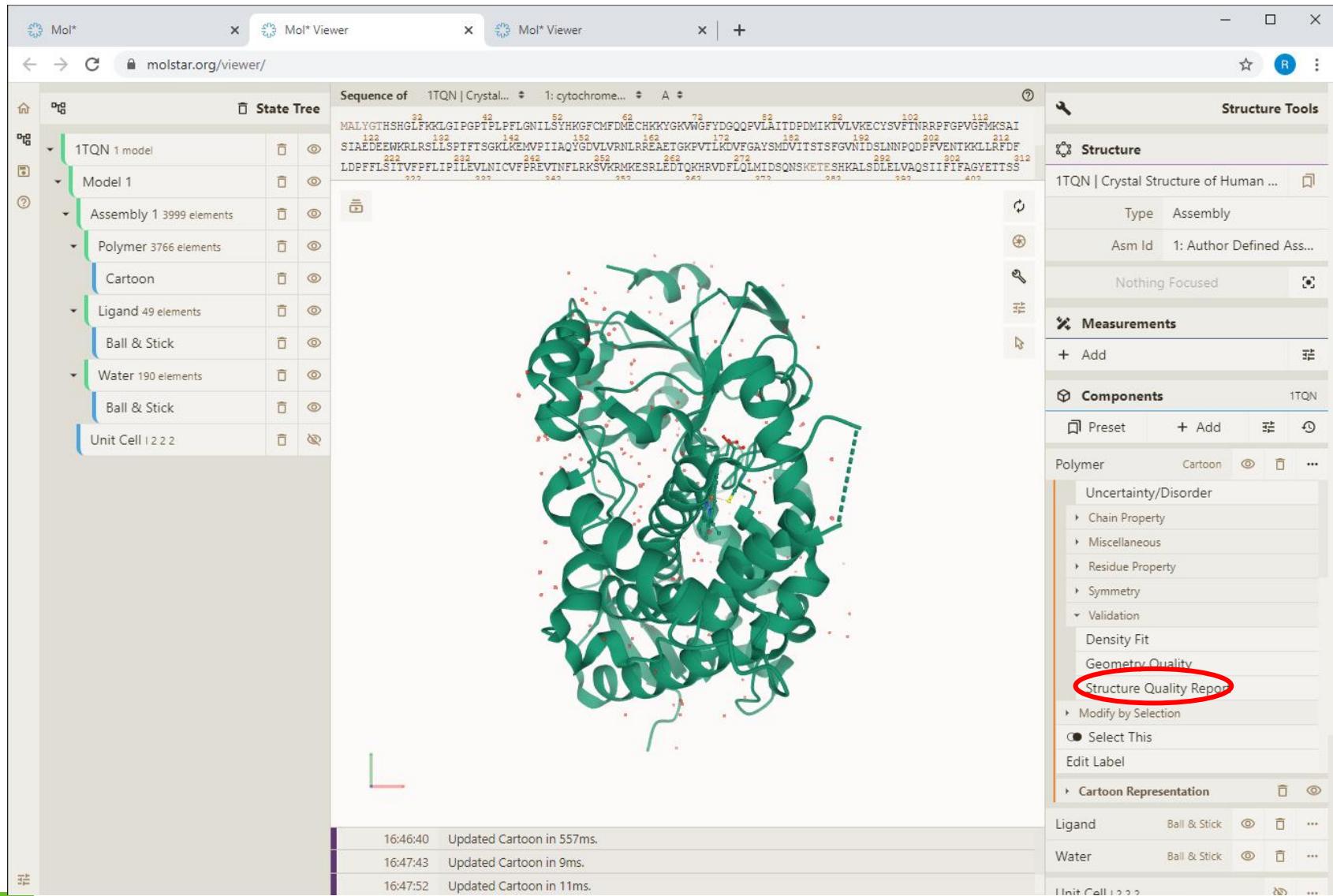
Vizualizace anotací Obarvení podle vlastnosti



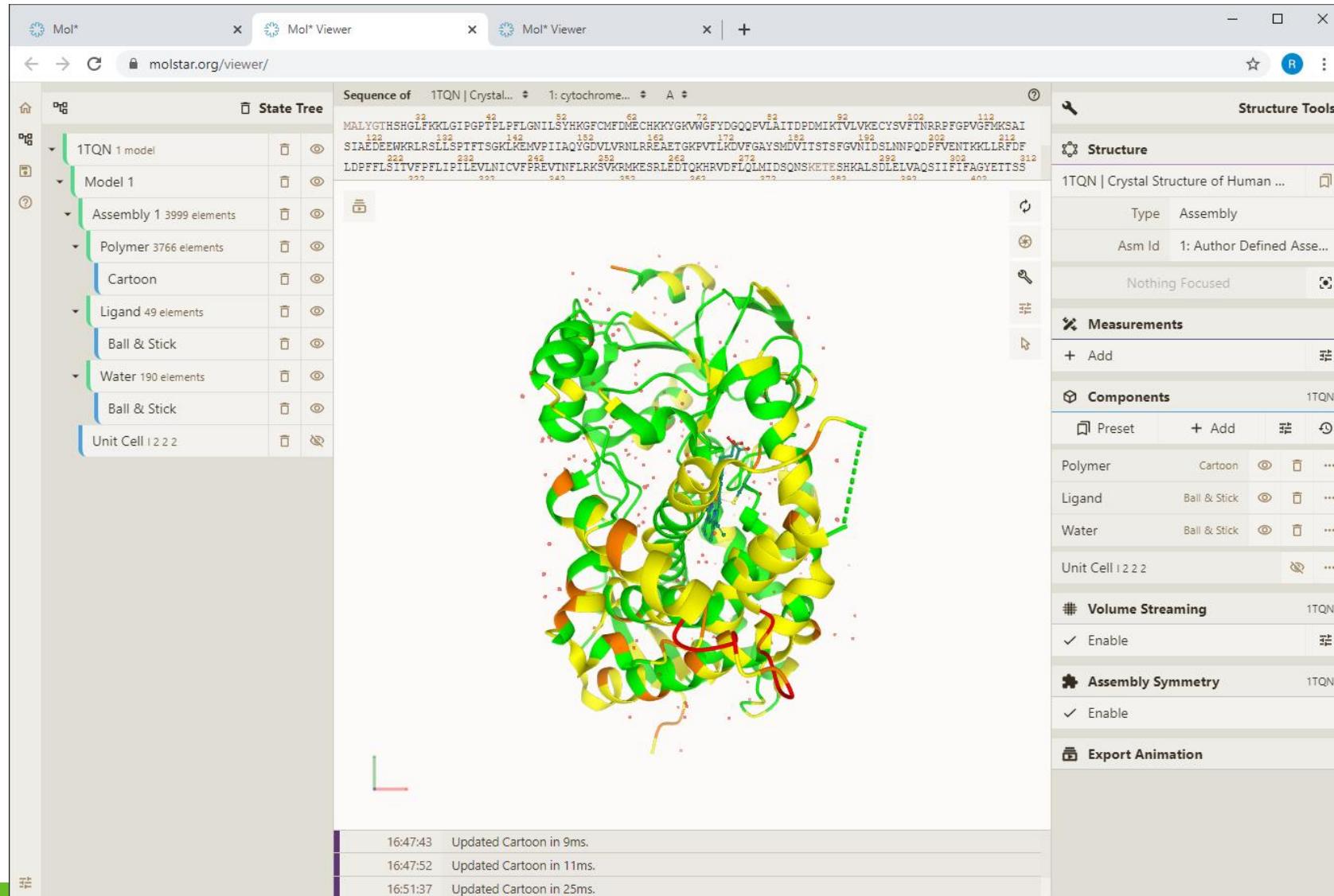
Vizualizace anotací Obarvení podle vlastností - hydrofobicitá



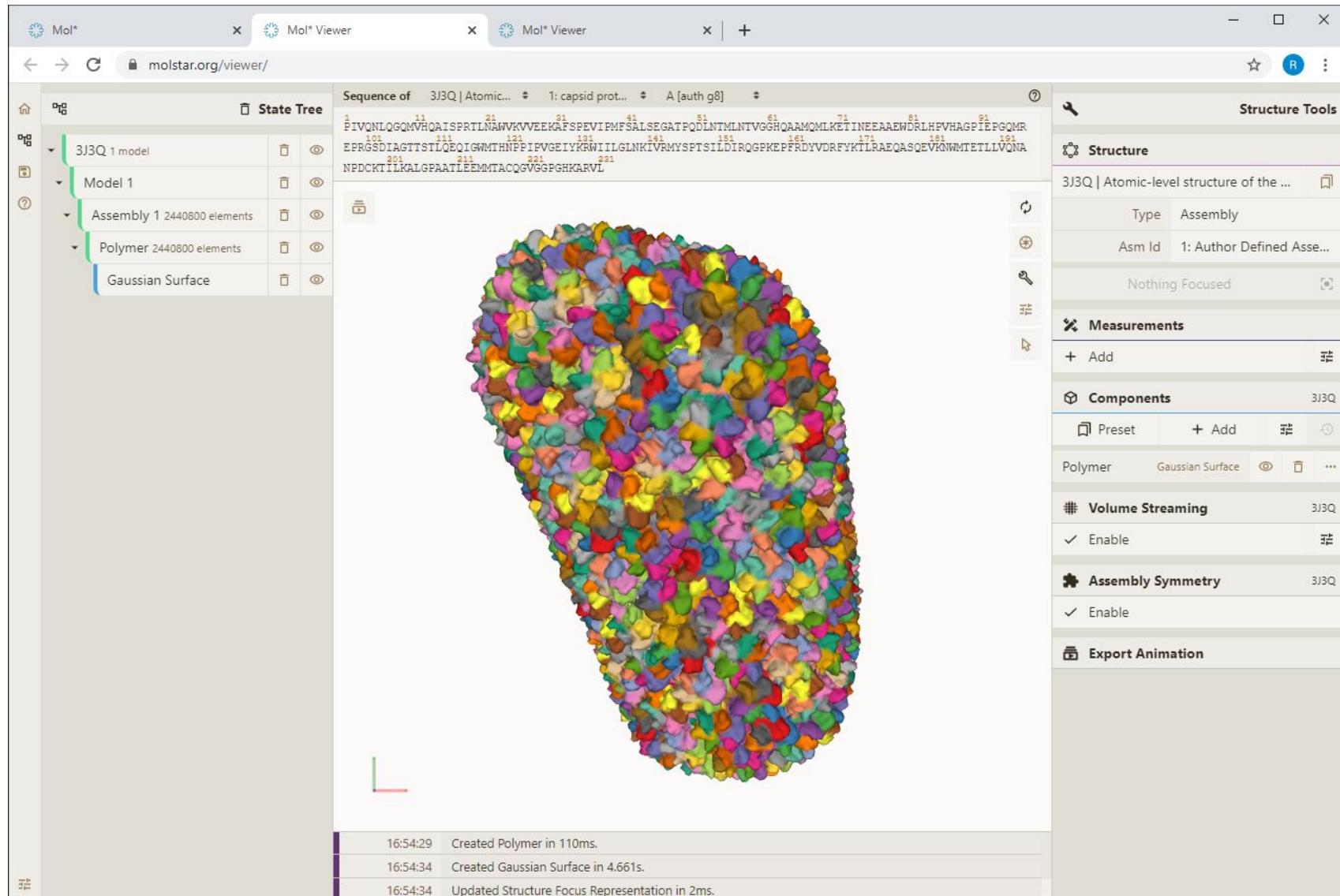
Vizualizace anotací Obarvení podle vlastností – kvalita



Vizualizace anotací Obarvení podle vlastností - kvalita



Vizualizace proteinových assemblies



Měření

Mol* Mol* Mol* molstar.org/viewer/ mol* Mol* Mol* Structure Tools

Sequence of 1TQN | Crystal... 1: cytochrome... A

MALYGTHSHGLFKKLGI³²PGPTPLPFLGNILS⁴²YHKGFCMFDMECHKKYGKVWGFYDGQQPVLAITDPDMIKTVLVKECYSVFTNRRPFGEVGFMKSAI⁵²SIAEDEEWKRLRSLLSP¹²²TSGKLKEMVPIA¹³²QYGDVLVRNLRREAETGKPVTILKDFVGAYSMDVITSTSFGVNIDS¹⁴²LNNPQDPFVENTK¹⁵²KKLRLRDF¹⁶²LDPFFLSITVFPFLIPILEV²²²LNICVF²³²PREVNTL²⁴²RKS²⁵²VRMKESLED²⁶²TQKH²⁷²RVD²⁸²FQLM²⁹²DSQNS³⁰²KETESH³¹²HALSD³²²ELVAQ³³²SIIIF³⁴²FAGYET³⁵²SS

Residue

Assembly 1 3999 elements

Model 1

1TQN | Crystal Structure of Human ...

Type Assembly

Asm Id 1: Author Defined Asse...

Nothing Focused

1 Chain + 1 Residue Selected

Measurements

+ Add

Distances

2.92 Å | HEM 508 — CYS ...

Components

Preset + Add

Polymer Cartoon

Ligand Ball & Stick

Water Ball & Stick

Unit Cell 1 2 2 2

Volume Streaming

Enable

Assembly Symmetry

Enable

Export Animation

2.92 Å

1:20:48 Created Ball & Stick in 23ms.

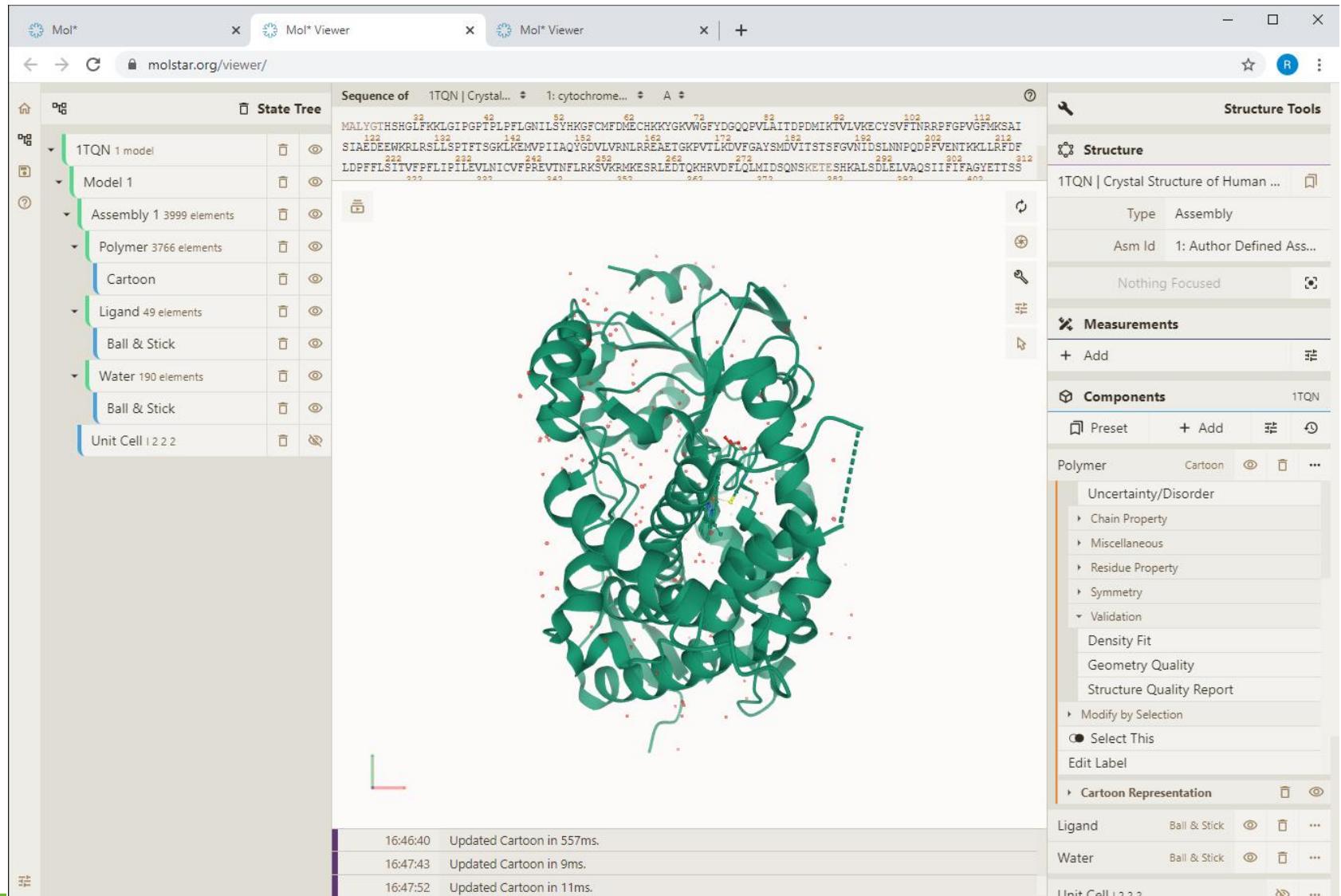
1:20:48 Created Ball & Stick in 11ms.

1:20:48 Updated Structure Focus Representation in 2ms.

23

CEITEC

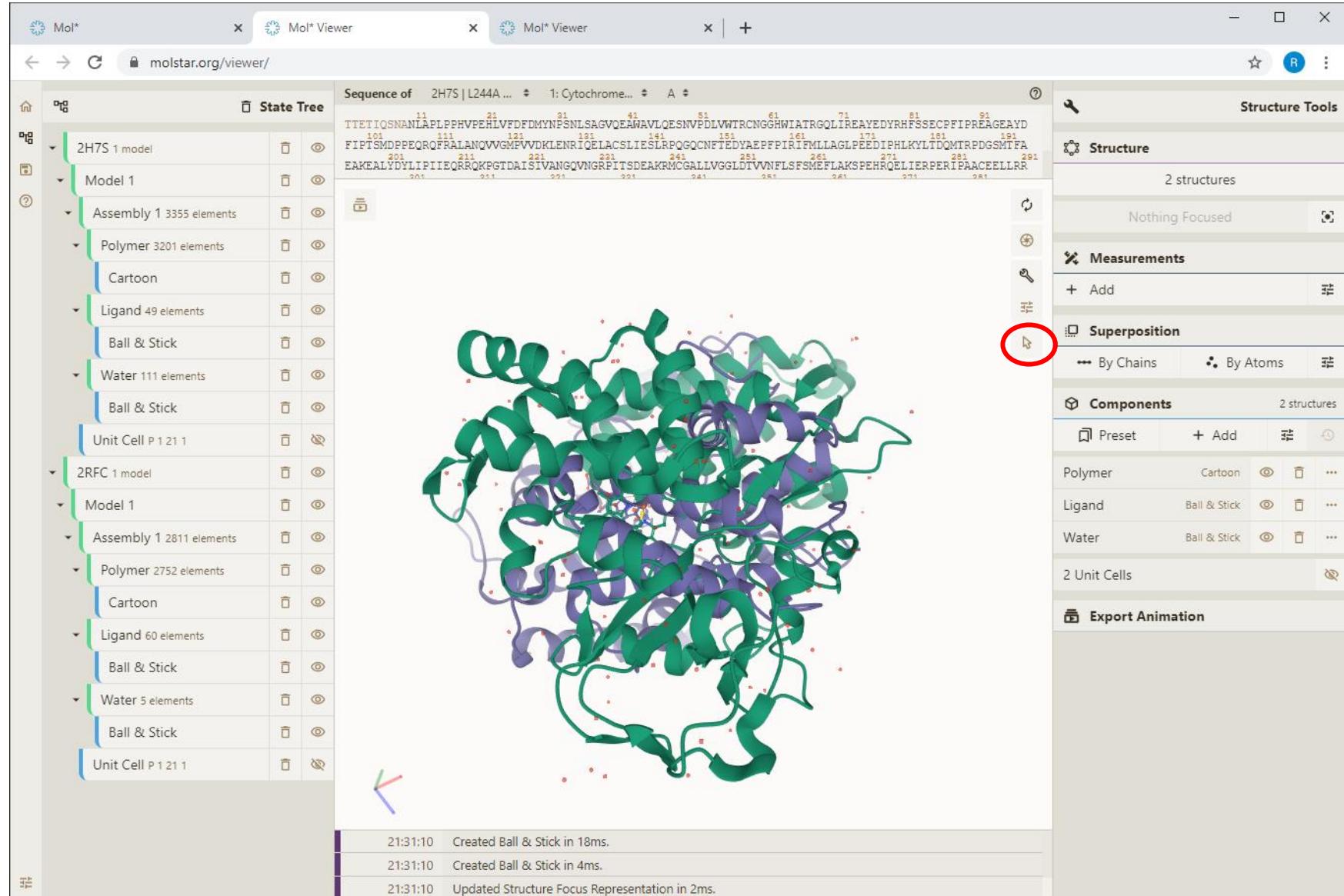
Vizualizace anotací Obarvení podle vlastností - hydrofobicitá



Přikládání struktur

The screenshot shows the Mol* software interface with three tabs open: Mol*, Mol* Viewer, and Mol* Viewer. The central panel displays the Mol* Viewer with the message "Sequence No structure available". The left sidebar contains a "Download Structure" section where "PDB Id(s)" 2h7s 2rfc are highlighted with a red oval. The bottom status bar shows the time 21:28:55 and the Mol* Plugin version 1.2.7 [12/19/2020, 11:52:32 AM]. The right sidebar is titled "Structure Tools" and includes sections for "Structure", "Measurements", "Components", and "Export Animation".

Příkladání struktur



Příkladání struktur

Mol* Mol* Viewer Mol* Viewer

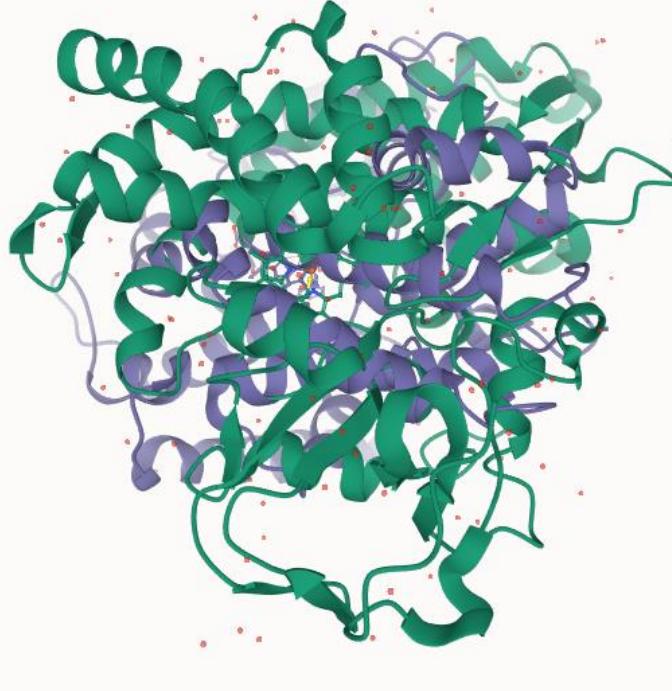
molstar.org/viewer/ Sequence of 2H7S | L244A ... 1: Cytochrome... A ?

State Tree

2H7S 1 model

- Model 1
- Assembly 1 3355 elements
 - Polymer 3201 elements
 - Cartoon
 - Ball & Stick
 - Ligand 49 elements
 - Cartoon
 - Ball & Stick
 - Water 111 elements
 - Ball & Stick
 - Unit Cell P 1 21 1
- 2RFC 1 model
- Model 1
- Assembly 1 2811 elements
 - Polymer 2752 elements
 - Cartoon
 - Ball & Stick
 - Ligand 60 elements
 - Cartoon
 - Ball & Stick
 - Water 5 elements
 - Ball & Stick
 - Unit Cell P 1 21 1

Residue 



Structure Tools

Structure 2 structures Nothing Focused

Measurements

+ Add

Superposition By Chains By Atoms

Components Preset + Add 2 structures

Polymer Cartoon

Ligand Ball & Stick

Water Ball & Stick

2 Unit Cells

Export Animation

21:31:10 Created Ball & Stick in 18ms.
21:31:10 Created Ball & Stick in 4ms.
21:31:10 Updated Structure Focus Representation in 2ms.

Příkladání struktur

Mol* Mol* Viewer Mol* Viewer molstar.org/viewer/ + Structure Tools

Sequence of 2H7S | L244A ... 1: Cytochrome... A ?

TTETIQSNANLAPLPPHPVPERHLVFDMDYNPNSNLNSAGVQEAWVLQESNVPDLVWTRCNHHWIATRGQLIREAYEDYRHFSSECPEPFIPREAGEAYD
FIFISMDPPEQRQFRALANQVVGMEVVDKLENRIGELACSLIESLRPQQCNCNTIEDVAEPFFPIRIFMLIAGLPEEDIPHLYKLTDQMTRPDGSMIFAE
EAKEALYDYLIPILIEQRRQPKPTDAISIVANGVNQNGRFITSDEAKRMCGALLIVGGLDITVNNFLSFSMELFLAKSPHEHQELIERPERIACELLRA

Residue Add/Union Selection All

Polymer/Carbohydrate Entities

Ligand/Non-standard Residue

Type

Structure Property (circled in red)

Bond Property

Residue Property

Manipulate Selection

Amino Acid

Nucleic Base

Element Symbol

Structure Tools

Structure 2 structures Nothing Focused

Measurements

Add

Superposition By Chains By Atoms

Components Preset Add 2 structures

Polymer Cartoon

Ligand Ball & Stick

Water Ball & Stick

2 Unit Cells

Export Animation

21:31:10 Created Ball & Stick in 18ms.

21:31:10 Created Ball & Stick in 4ms.

21:31:10 Updated Structure Focus Representation in 2ms.

The screenshot shows the Mol* viewer interface with the URL 'molstar.org/viewer/'. On the left, a tree view lists models and their components: '2H7S 1 model' contains 'Model 1', 'Assembly 1 3355 elements' (including 'Polymer 3201 elements', 'Cartoon', 'Ligand 49 elements', 'Ball & Stick', 'Water 111 elements', 'Ball & Stick', 'Unit Cell P 1 21 1'); '2RFC 1 model' contains 'Model 1', 'Assembly 1 2611 elements' (including 'Polymer 2752 elements', 'Cartoon', 'Ligand 60 elements', 'Ball & Stick', 'Water 5 elements', 'Ball & Stick', 'Unit Cell P 1 21 1'). The main area displays a 3D ribbon model of a protein. To the right, the 'Structure Tools' panel is open, showing tabs for 'Structure' (selected), 'Measurements', 'Superposition', 'Components', and 'Export Animation'. In the 'Structure' tab, it says '2 structures' and 'Nothing Focused'. The 'Structure' sub-tab shows options like 'Add/Union Selection' with 'All' selected, and a dropdown menu for 'Type' where 'Structure Property' is circled in red. The 'Components' tab lists 'Polymer' (Cartoon), 'Ligand' (Ball & Stick), 'Water' (Ball & Stick), and '2 Unit Cells'. The bottom status bar shows log messages about ball stick creation and structure focus updates.

Přikládání struktur

Mol* Mol* Viewer Mol* Viewer

molstar.org/viewer/ molstar.org/viewer/ molstar.org/viewer/ +

Sequence of 2H7S | L244A ... 1: Cytochrome... A

State Tree

2H7S 1 model

- Model 1
 - Assembly 1 3355 elements
 - Polymer 3201 elements
 - Cartoon
 - Ligand 49 elements
 - Ball & Stick
 - Water 111 elements
 - Ball & Stick
- Unit Cell P 1 21 1

2RF1 1 model

- Model 1
 - Assembly 1 2811 elements
 - Polymer 2752 elements
 - Cartoon
 - Ligand 60 elements
 - Ball & Stick
 - Water 5 elements
 - Ball & Stick
- Unit Cell P 1 21 1

Residue Add/Union Selection

All

- Polymer/Carbohydrate Entities
- Ligand/Non-standard Residue
- Type
- Structure Property
 - Trace
 - Backbone**
 - Sidechain
 - Sidechain with Trace
 - Helix
 - Beta Strand/Sheet
- Bond Property

Structure Tools

Structure

Measurements

Superposition

Components

Presets

2 structures

Nothing Focused

Backbone

Sidechain

Sidechain with Trace

Helix

Beta Strand/Sheet

Bond Property

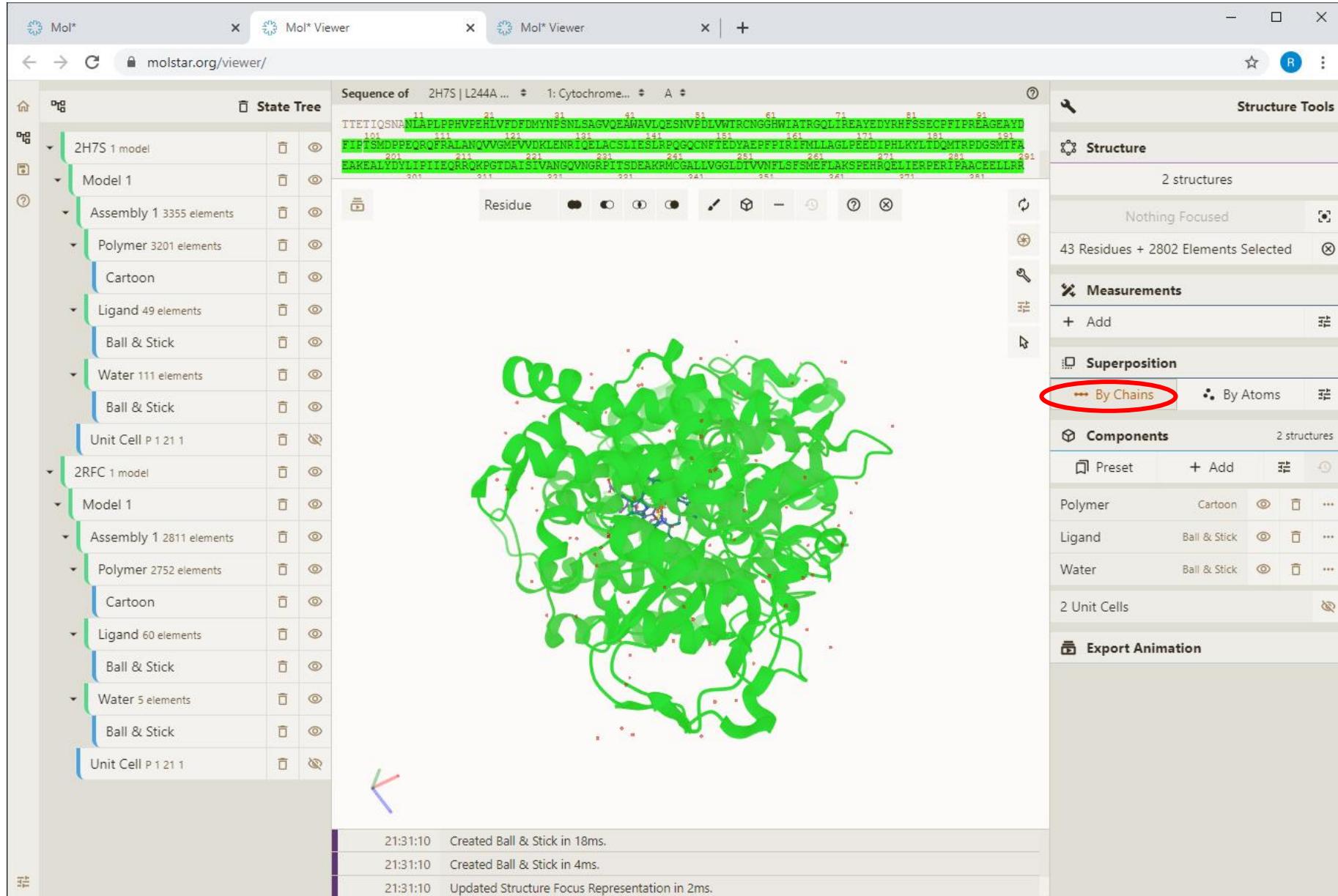
2 Unit Cells

Export Animation

21:31:10 Created Ball & Stick in 18ms.
21:31:10 Created Ball & Stick in 4ms.
21:31:10 Updated Structure Focus Representation in 2ms.

The screenshot shows the Mol* viewer interface with three tabs open. The central tab displays a protein structure (2H7S) in cartoon representation, overlaid with a green backbone trace. A context menu is open over the structure, with the 'Backbone' option highlighted. The left sidebar shows the 'State Tree' with two main models: '2H7S 1 model' and '2RF1 1 model'. The right sidebar contains various analysis tools like 'Structure Tools', 'Measurements', and 'Components'. A log at the bottom indicates recent operations: creating ball-and-stick models and updating the structure focus representation.

Přikládání struktur



Příkladání struktur

Mol* Mol* Viewer Mol* Viewer

molstar.org/viewer/ State Tree Sequence of 2H7S | L244A ... 1: Cytochrome... A

2H7S 1 model Model 1 Assembly 1 3355 elements Polymer 3201 elements Cartoon Ligand 49 elements Ball & Stick Water 111 elements Ball & Stick Unit Cell P 1 21 1 2RFC 1 model Model 1 Assembly 1 2811 elements Polymer 2752 elements Cartoon Ligand 60 elements Ball & Stick Water 5 elements Ball & Stick Unit Cell P 1 21 1

TTETIQSNA 11 NIAPLPEPHVVF 21 LIVDFDIDMYNPSNL 31 SAGVOEAWAVLQESNV 41 PDLIVWTRCN 51 GHWIA 61 TRGOLIRE 71 AVEVDYRHFSSECBF 81 P 91

PIPSM 101 DPEPORQFRALAN 111 QVGMPVVKLENR 121 IELACSLIESLR 131 POGOCNF 141 TDEVAEEFP 151 PIRIFPMLIAGL 161 PEPDIPH 171 KLYLTDOMTRPDGSM 181 TFA 191

EAKAEALYDV 201 LILIEQR 211 RQKPGTDA 221 8 231 VANGQVN 241 GRPITS 251 DEAK 261 KRCGALL 271 VGNFLS 281 EPLAKSP 291 FERQL 301 PERIPAA 311 CELLER 321 331 341 351 361 371 381 391

Residue

Structure Tools Structure Measurements Superposition Components Export Animation

2 structures Nothing Focused 43 Residues + 2802 Elements Selected

Superpose

25 Residues + 1521 Elements | A | 2H7S
18 Residues + 1281 Elements | A | 2RFC

2 structures Preset Add

Polymer Cartoon

Ligand Ball & Stick

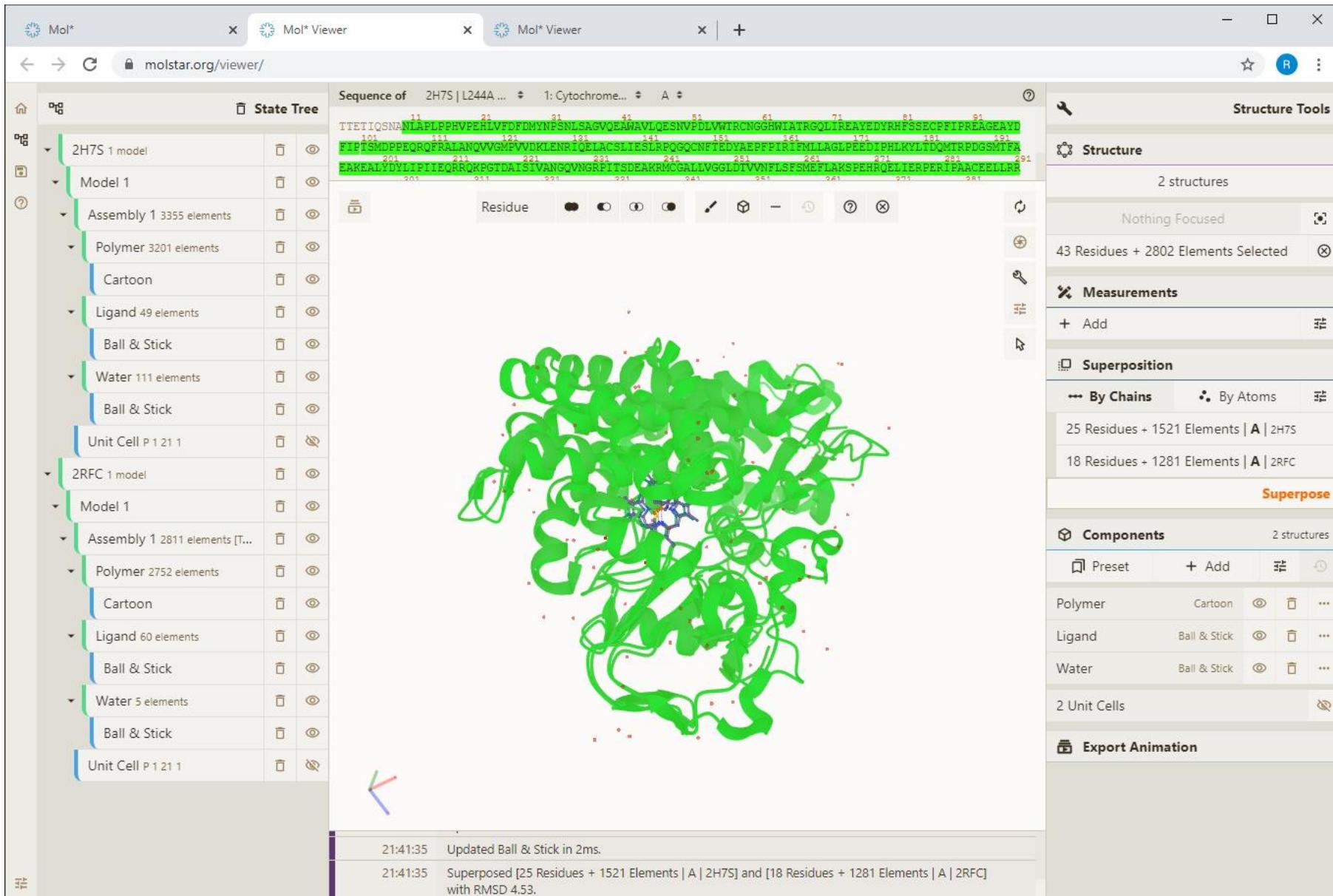
Water Ball & Stick

2 Unit Cells

Created Ball & Stick in 18ms.
Created Ball & Stick in 4ms.
Updated Structure Focus Representation in 2ms.

21:31:10 Created Ball & Stick in 18ms.
21:31:10 Created Ball & Stick in 4ms.
21:31:10 Updated Structure Focus Representation in 2ms.

Příkladání struktur



Příkladání struktur

Mol* Mol* Viewer Mol* Viewer

molstar.org/viewer/ State Tree Sequence of 2H7S | L244A ... 1: Cytochrome... A

2H7S 1 model Model 1 Assembly 1 3355 elements Polymer 3201 elements Cartoon Ligand 49 elements Ball & Stick Water 111 elements Ball & Stick Unit Cell P 1 21 1 2RFC 1 model Model 1 Assembly 1 2811 elements [T... Polymer 2752 elements Cartoon Ligand 60 elements Ball & Stick Water 5 elements Ball & Stick Unit Cell P 1 21 1

Residue

TTETIQS... 11 21 31 41 51 61 71 81 91
101 111 121 131 141 151 161 171 181 191
FIPITSMDP... 201 211 221 231 241 251 261 271 281 291
EAKEALYDYLPIIEQRQRQKEGTDAISIVANGQVNGRPITSDEAKRMC... 201 211 221 231 241 251 261 271 281 291

Structure Tools Structure Measurements Superposition Components Export Animation

Nothing Focused

Cytochrome P450-cam 2H7S | Model 1 | Instance ASM_1 | A | ARG 290

21:41:35 Updated Ball & Stick in 2ms.
21:41:35 Superposed [25 Residues + 1521 Elements | A | 2H7S] and [18 Residues + 1281 Elements | A | 2RFC] with RMSD 4.53.

The screenshot shows the Mol* viewer interface with three tabs open. The central tab displays the sequence alignment between two models, 2H7S and 2RFC, with residues numbered 1 to 291. The main workspace shows a 3D ribbon model of the protein structure, colored by component (Polymer in green, Ligand in blue, Water in red). The right panel contains various tools for structure analysis, including 'Structure Tools' for superposition and 'Components' for selecting different parts of the model. A message at the bottom indicates a recent update to the ball-and-stick representation and a successful superposition of the two models with a RMSD of 4.53.

2DProts: Integration of AlphaFoldDB

The screenshot shows a web browser window displaying the AlphaFold Protein Structure Database. The URL in the address bar is <https://alphafold.ebi.ac.uk>. The page features a dark blue header with the EMBL-EBI logo and navigation links for Home, About, FAQs, and Downloads. Below the header, the main title "AlphaFold Protein Structure Database" is prominently displayed in large white text against a blue background with faint protein structure graphics. A sub-header below the main title reads "Developed by DeepMind and EMBL-EBI". At the bottom, there is a search bar with the placeholder "Search for protein, gene, UniProt accession or organism", a "BETA" button, and a "Search" button. Below the search bar, examples of search terms are listed: "Free fatty acid receptor 2", "At1g58602", "Q5VSL9", "E. coli", and "Help: AlphaFold DB search help". A link for "Feedback on structure: Contact DeepMind" is also present.

2DProts: Integration of AlphaFoldDB

The screenshot shows a web browser window for the AlphaFold Protein Structure Database at <https://alphafold.ebi.ac.uk>. The page has a dark blue header with the EMBL-EBI logo and navigation links for Home, About, FAQs, and Downloads. A large central text box states: "AlphaFold DB provides open access to over 200 million protein structure predictions to accelerate scientific research." Below this, it says "Developed by DeepMind and EMBL-EBI". At the bottom is a search bar with examples like "Free fatty acid receptor 2" and "At1g58602".

AlphaFold Protein Structure Database

Home About FAQs Downloads

AlphaFold DB provides open access to over 200 million protein structure predictions to accelerate scientific research.

Developed by DeepMind and EMBL-EBI

Search for protein, gene, UniProt accession or organism

BETA Search

Examples: Free fatty acid receptor 2 At1g58602 Q5VSL9 E. coli Help: AlphaFold DB search help

Feedback on structure: Contact DeepMind

Příkladání struktur – PDB a AlphaFold

Pairwise Structure Alignment

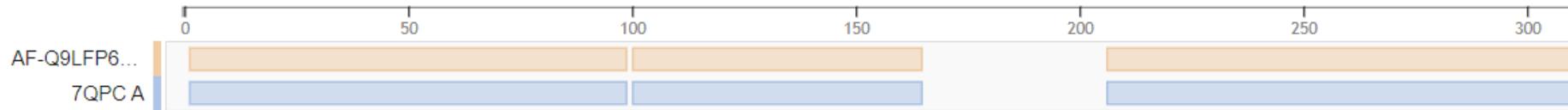
Help

- ▶ Compare Protein Structures

Entry ID	Chain ID	Description	Organism	Sequence Length	Modeled Residues
AF-Q9LFP6-F1	A	N/A	N/A	367	367
7QPC	A	Auxin efflux carrier component 8	Arabidopsis thaliana	376	327

SEQUENCE ALIGNMENT

SCORES



<https://www.rcsb.org/alignment/>

Přiklání struktur – PDB a AlphaFold

