

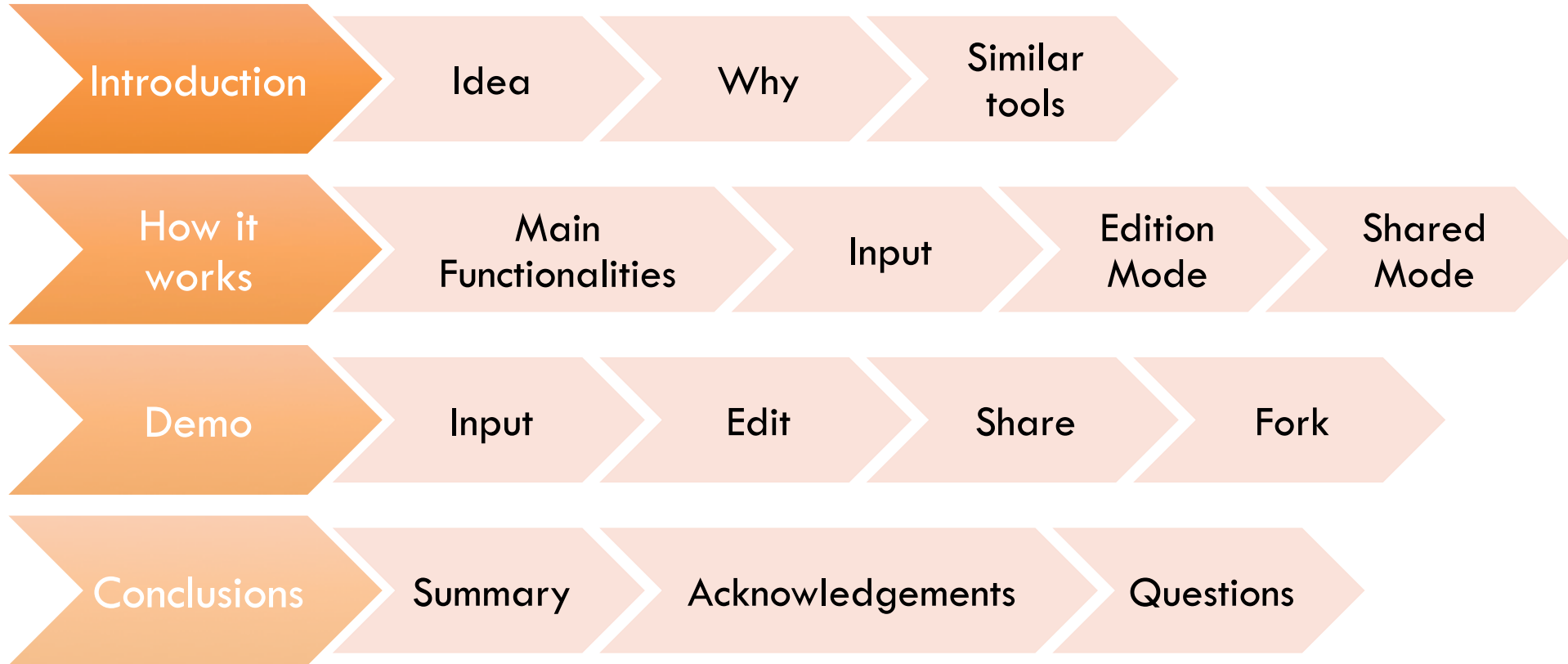
3dRS; a Web-Based Tool to Share Interactive Representations of 3D Biomolecular Structures and Molecular Dynamics Trajectories

BioExcel Webinar, 2021-10-26

Adam Hospital

adam.hospital@irbbarcelona.org

Index





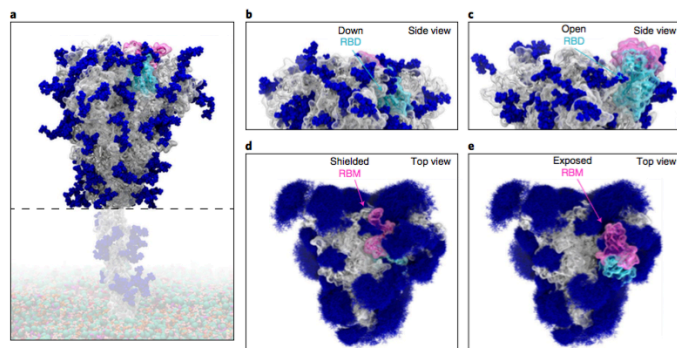


Fig. 1 | Glycosylated spike RBD 'down' and 'open' conformations. **a**, The SARS-CoV-2 spike head (grey) with glycans (dark blue) as simulated, with the stalk domain and membrane (not simulated here, but shown as transparent for completeness). RBD shown in cyan, RBM in pink. **b, c**, Side view of the RBD_{down} (shielded, **b**) and RBD_{open} (exposed, **c**). **d, e**, Top view of the RBM_{down} (shielded, **d**) and RBM_{open} (exposed, **e**). Composite image of glycans (dark blue lines) shows many overlapping snapshots of the glycans over the microsecond simulations.

trajectories provides an unbiased characterization of the system's time-dependent ensemble properties¹¹. The WE strategy therefore generates continuous pathways with unbiased dynamics, yielding the most direct, atomistic views for analysing the mechanism of functional transitions, including elucidation of transient states that are too fleeting to be captured by laboratory experiments. Furthermore, while the strategy requires a progress coordinate towards the target state, the definition of this target state need not be fixed in advance when applied under equilibrium conditions¹¹, enabling us to refine the definition of the target 'open' state of the spike protein on the basis of the probability distribution of protein conformations sampled by the simulation.

Our work characterizes a series of transition pathways of the spike opening, in agreement with conformations detected in the cryo-EM dataset by ManifoldEM²³, and identifies key residues, including a glycan at position N343, that participate in the opening mechanism. Our simulation findings are corroborated by biolayer interferometry (BLI) experiments, which show a reduction in the ability of the spike to interact with ACE2 after mutation of these key residues.

Results and discussion

WE simulations of spike opening. As mentioned above, simulations of the spike-opening process require an enhanced sampling strategy as the process occurs beyond the microsecond timescale (that is, the seconds timescale¹²). We therefore used the WE path-sampling strategy, which enabled the generation of continuous, atomistic pathways for the spike-opening process with unbiased dynamics (Fig. 2a–e and Supplementary Video 1); these pathways were hundreds of nanoseconds long, excluding the waiting times in the initial 'down' state. The protein model was based on the head region (residues 16 to 1,140) of the glycosylated SARS-CoV-2 spike from Casalino et al.⁸ (Fig. 1), which in turn was built on the cryo-EM structure of the three-RBD-down spike (Protein Data Bank (PDB) ID, 6VXX (ref. 7)). The entire simulation system, including explicit water and salt ions, reaches almost half a million atoms. We focused sampling along a two-dimensional progress coordinate to track RBD

opening; the difference in the centre of mass of the spike core to the RBD and the root-mean-square deviation of the RBD from the RBD_{down} state (Fig. 2f,g). On the San Diego Supercomputer Center (SDSC) Comet and Texas Advanced Computing Center (TACC) Longhorn supercomputers, 100 graphics processing units (GPUs) ran the WE simulations in parallel for over a month, generating over 130 μs of glycosylated spike trajectories and more than 200 TB of trajectory data. We simulated a total of 310 independent pathways, including 204 pathways from the RBD_{down} conformation (PDB ID, 6VXX (ref. 7)) to the RBD_{open} conformation (PDB ID, 6VSB (ref. 7)) and 106 pathways from the RBD_{down} to the RBD_{open} state, in which the RBD twists open beyond the 6VSB (ref. 7) cryo-EM structure. Remarkably, the RBD_{open} state that we sampled includes conformations that align closely with the ACE2-bound spike cryo-EM structure (PDB ID, 7A95 (ref. 9)) even though this structure was not a target state of our progress coordinate (Fig. 2f,g, Supplementary Video 1 and Supplementary Figs. 2 and 3). This result underscores the value of using (1) equilibrium WE simulations that do not require a fixed definition of the target state and (2) a two-dimensional progress coordinate that allows the simulations to sample unexpected conformational space along multiple degrees of freedom. The ACE2-bound spike conformation has also been sampled by the Folding@home-distributed computing project¹³, and RBD rotation has been detected in cryo-EM experiments⁸.

Comparison with spike conformations detected by ManifoldEM.

To validate our simulated RBD_{down} to RBD_{open} pathway, the ManifoldEM framework²³ was applied using the cryo-EM dataset of PDB 6VSB from McLellan and colleagues⁷. The ManifoldEM method allows characterization of conformational variations as obtained from a single-particle cryo-EM ensemble of a molecule in thermal equilibrium. Two conformational coordinates (that is, collective motion coordinates) CC1 and CC2 were discovered from this dataset, and observed from several exemplary projection directions (PDs) showing a (1) RBD_{down} to RBD_{up} pathway and (2) RBD outward opening pathway (Supplementary Fig. 4 and Supplementary Videos 2 and 3).

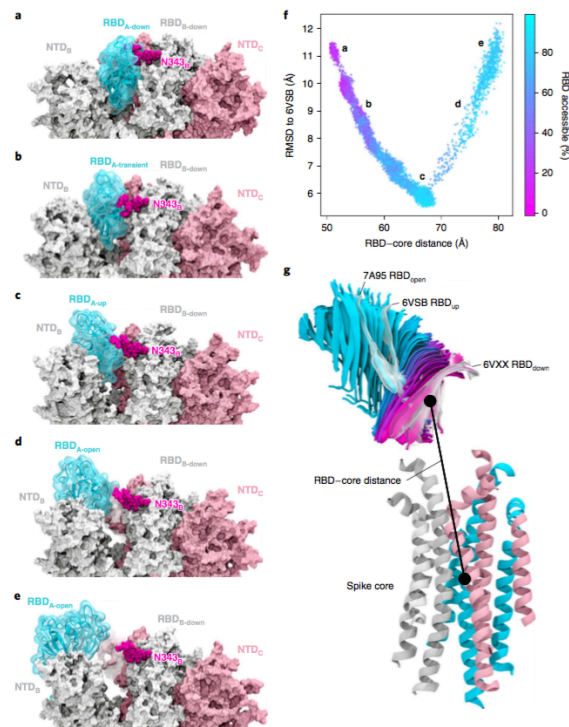


Fig. 2 | Atomically detailed pathways of spike opening. **a–e**, Snapshot configurations along the opening pathway with chain A shown in cyan, chain B in grey, chain C in pink and the glycan at position N343 in magenta. Each RBD and N-terminal domain (NTD) are subscripted with their chain ID (A, B or C). RBDs are also subscripted with their conformation from initial conformation with all three RBDs in the 'down' state (6VXX) (**a**), RBD, in a 'transient' state in between the 'down' and 'up' state (6VSB) (**b**), RBD, in the 'up' state (**c**), RBD, in the 'open' state (beyond 6VSB) (**d**) and RBD, in the furthest open state sampled (**e**). **f**, Scatter plot of data from the 310 continuous pathways with the C α -root-mean-square deviation (RMSD) of the RBD from the RBD_{down} state plotted against the RBD-core distance. Data points are coloured on 1 RBD_{open} state. The locations of the snapshots shown in **a–e** are labelled. The spike core is composed of three central helices per trimer, colour beta-sheets, and an overlay of snapshots from a continuous WE simulation cryo-EM structures are highlighted and labelled including the initial

These projections were next aligned to corresponding dimensional projections of coulomb potential maps generated from the WE simulation (Supplementary Fig. 2 and Supplementary Videos 2 and 3). Overall, there was very agreement between the ManifoldEM conformational coordinates and the WE trajectory, aside from two discrepancies. First, CC2 observed in the ManifoldEM included concerted opening of all three RBDs, while the WE focused sampling on the



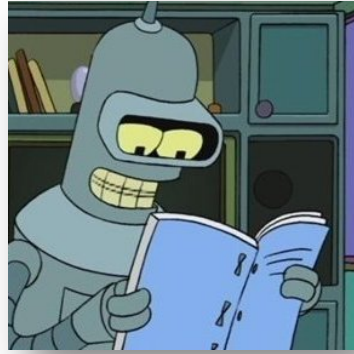
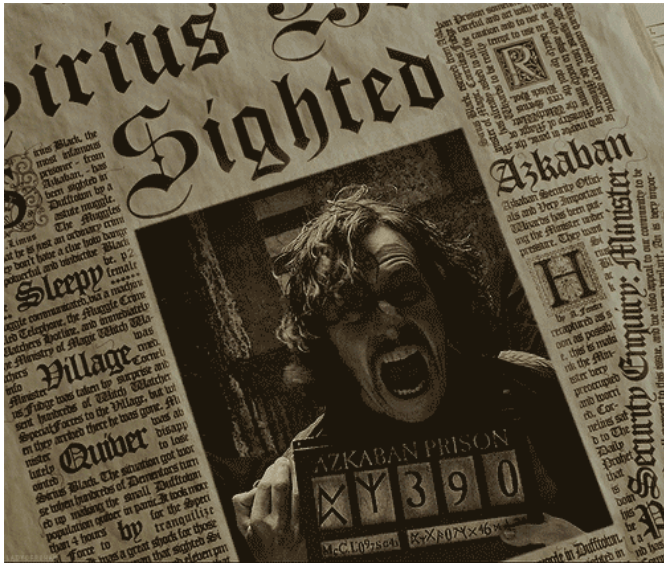
Article | Published: 19 August 2021

A glycan gate controls opening of the SARS-CoV-2 spike protein

Terra Sztain, Surl-Hee Ahn, Anthony T. Bogetti, Lorenzo Casalino, Jory A. Goldsmith, Evan Seitz, Ryan S. McCool, Fiona L. Kearns, Francisco Acosta-Reyes, Suvrajit Maji, Ghoncheh Mashayekhi, J. Andrew McCammon, Abbas Ourmazd, Joachim Frank, Jason S. McLellan, Lillian T. Chong & Rommie E. Amaro

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A glycan gate controls opening of the SARS-CoV-2 spike protein

[Terra Sztain](#), [Suri-Hee Ahn](#), [Anthony T. Bogetti](#), [Lorenzo Casalino](#), [Jory A. Goldsmith](#), [Evan Seitz](#), [Ryan S. McCool](#), [Fiona L. Kearns](#), [Francisco Acosta-Reyes](#), [Suvrajit Maji](#), [Ghoncheh Mashayekhi](#), [J. Andrew McCammon](#), [Abbas Ourmazd](#), [Joachim Frank](#), [Jason S. McLellan](#), [Lillian T. Chong](#) ✉ & [Rommie E. Amaro](#) ✉

[Nature Chemistry](#) **13**, 963–968 (2021) | [Cite this article](#)

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Abstract

1TRO

CRYSTAL STRUCTURE OF TRP REPRESSOR OPERATOR COMPLEX AT ATOMIC RESOLUTION

NOTE: Use your mouse to access Jsmol features and to drag, rotate, and zoom in and out of the structure. [Help](#)



Structure
Biological Assembly 1

Select Options

Style
Cartoon

Color
Secondary Structure

Surface
None

Surface options may take a long time to render, especially for larger structures

Scripting Options

Select a different viewer: JSmol (JavaScript)

Display Files Download Files

Structure Details

Structure
Biological Assembly 1

Select Options

Style
Cartoon

Color
Secondary Structure

Surface
None

Surface options may take a long time to render, especially for larger structures

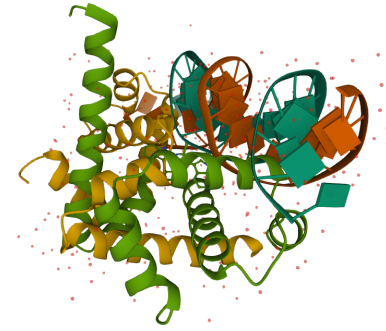


Select a different viewer: JSmol (JavaScript)

1TRO

CRYSTAL STRUCTURE OF TRP REPRESSOR OPERATOR COMPLEX AT ATOMIC RESOLUTION

Sequence of 1TRO | CRY... Chain 1: DNA (5'... A [auth] ...



Structure
1TRO | CRYSTAL STRUCTURE OF ...

Type Assembly

Asm Id 1: Author Defined Asse...

Dynamic Bonds Off

Nothing Focused

Measurements

Structure Motif Search

Components 1TRO

Preset + Add

Polymer Cartoon

Ligand Ball & Stick

Water Ball & Stick

Unit Cell P 1 2 1

Density

Assembly Symmetry

Export Animation

Mol*

Select a different viewer: Mol* (JavaScript)

Display Files Download Files

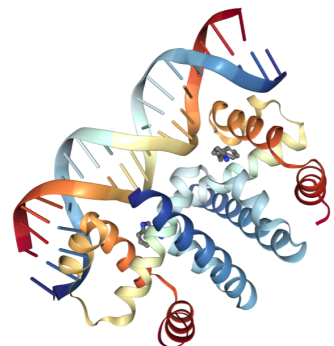


- ✧ *HTMol*
- ✧ *MolMil*
- ✧ *3DMol.js*
- ✧ *LiteMol*
- ✧ *Protein Viewer*
- ✧ ...

1TRO

CRYSTAL STRUCTURE OF TRP REPRESSOR OPERATOR COMPLEX AT ATOMIC RESOLUTION

Note: Use your mouse to drag, rotate, and zoom in and out of the structure. Mouse-over to identify atoms and bonds. [Mouse controls documentation.](#)



Structure View Electron Density Maps Ligand View

Structure View Documentation

Assembly Bioassembly 1

Model Model 1

Symmetry None

Style Cartoon

Color Rainbow

Ligand Ball & Stick

Quality Automatic

Water Ions

Hydrogens Clashes

Default Structure View

Spin Center Fullscreen Screenshot Perspective Camera White background Focus

Select a different viewer: NGL (WebGL)

Display Files Download Files

Structure View Electron Density Maps Ligand View

Structure View Documentation

Assembly Bioassembly 1

Model Model 1

Symmetry None

Style Cartoon

Color Rainbow

Ligand Ball & Stick

Quality Automatic

Water Ions

Hydrogens Clashes

Default Structure View



NGL is a WebGL based 3D viewer powered by MMTF.

Select a different viewer: NGL (WebGL)



Root Entity

- M 1TRO
- M Model 1 5373 atoms
- MC Complex
- G Sequence
- S All Residues 4749 atc
- V Cartoon
- G HET
- S Ligands 62 atoms
- V Balls and Sticks
- S Unbound Water 572 e
- V Balls and Sticks

Balls and Sticks

Selection

Name Optional name...

residuesByName('GLY', 'ALA')

Add

Labels

Kind Residue Full Id

Add

Particle Coloring

Update Visual

Type Balls and Sticks

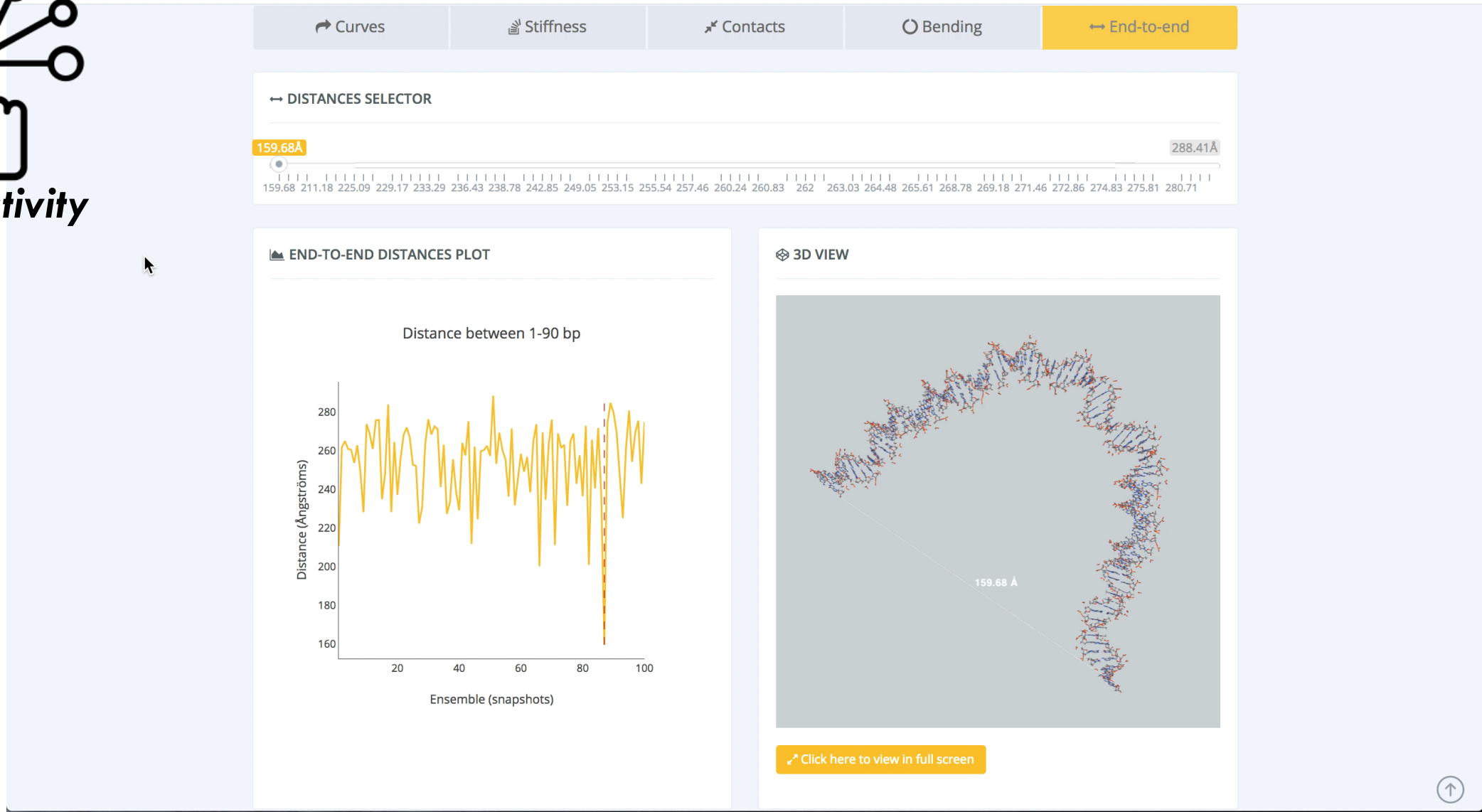
Coloring Element Symbol

LiteMol





Interactivity



What is Bandwidth?

* low bandwidth

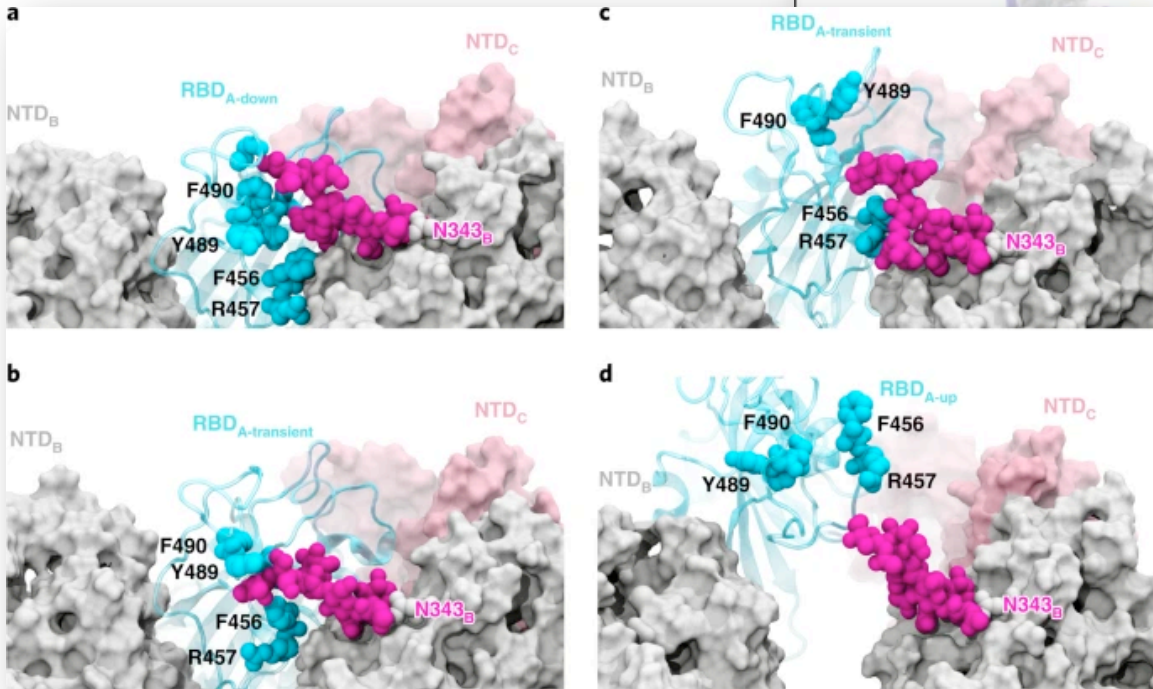
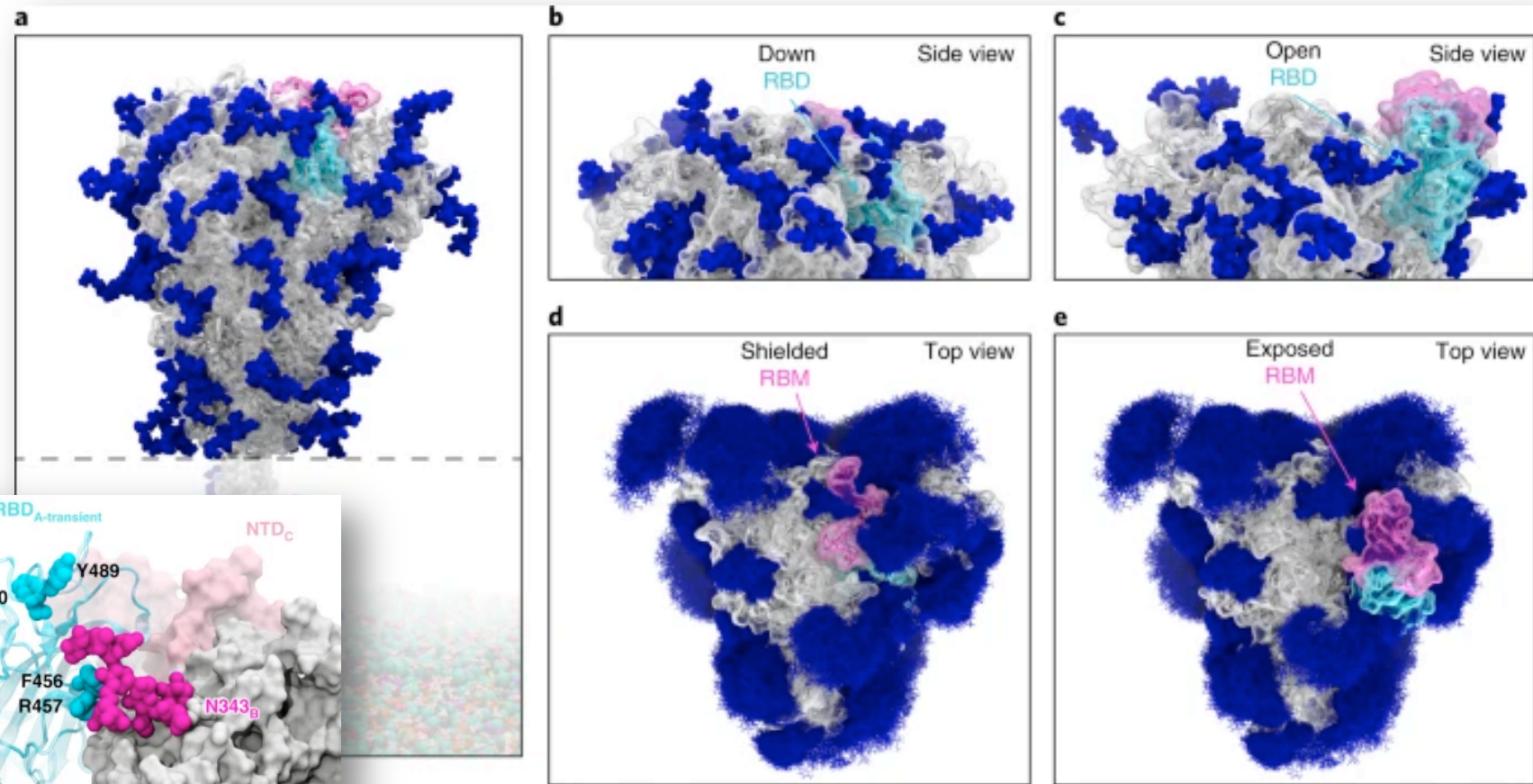
* high bandwidth

Lifewire



- ✓ WebGL tools
- ✓ Interactivity
- ✓ Network Bandwidths

Add Interactivity Add Movement?



Sztain, T., Ahn, SH., Bogetti, A.T. et al. A glycan gate controls opening of the SARS-CoV-2 spike protein. *Nat. Chem.* 13, 963–968 (2021). <https://doi.org/10.1038/s41557-021-00758-3>



***Future?* Present
Journals**

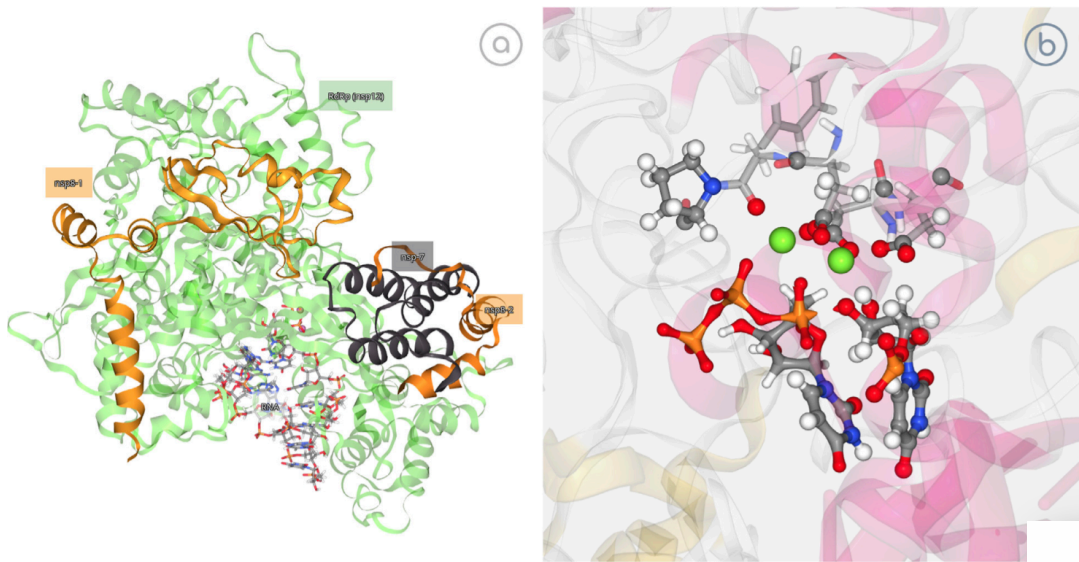


FIGURE 5 | SARS-CoV-2 RNA-Dependent RNA Polymerase (RdRp) study. **(A)** Interactive representation of RdRp bound to its essential co-factors nsp7 and nsp8; <https://mmb.irbbarcelona.org/3dRS/s/7Rn2Ka>; **(B)** Exploring the ability of RdRp to incorporate a natural triphosphate into a nascent RNA; <https://mmb.irbbarcelona.org/3dRS/s/TKf8yA>.

<https://mmb.irbbarcelona.org/3dRS/help/integration>

SARS-CoV-2 RNA-dependent RNA polymerase nsp12 (RdRp) bound to its essential co-factors, nsp7 and nsp8 +

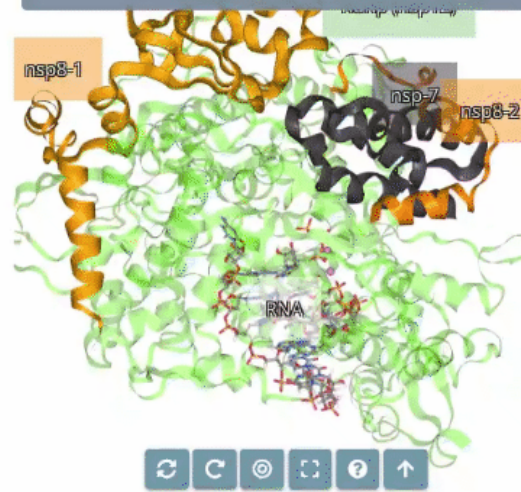


Fig.5a.- SARS-CoV-2 RNA-Dependent RNA Polymerase (RdRp) study: interactive representation of RdRp bound to its essential co-factors nsp7 and nsp8

RNA-Dependent RNA Polymerase from SARS-COV-2; Mechanism of reaction and inhibition by remdesivir +

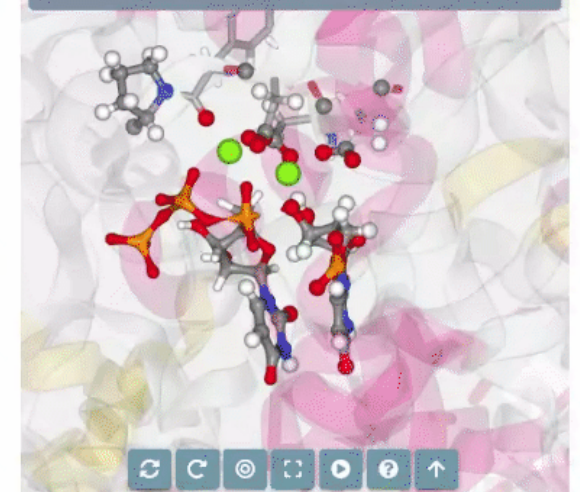
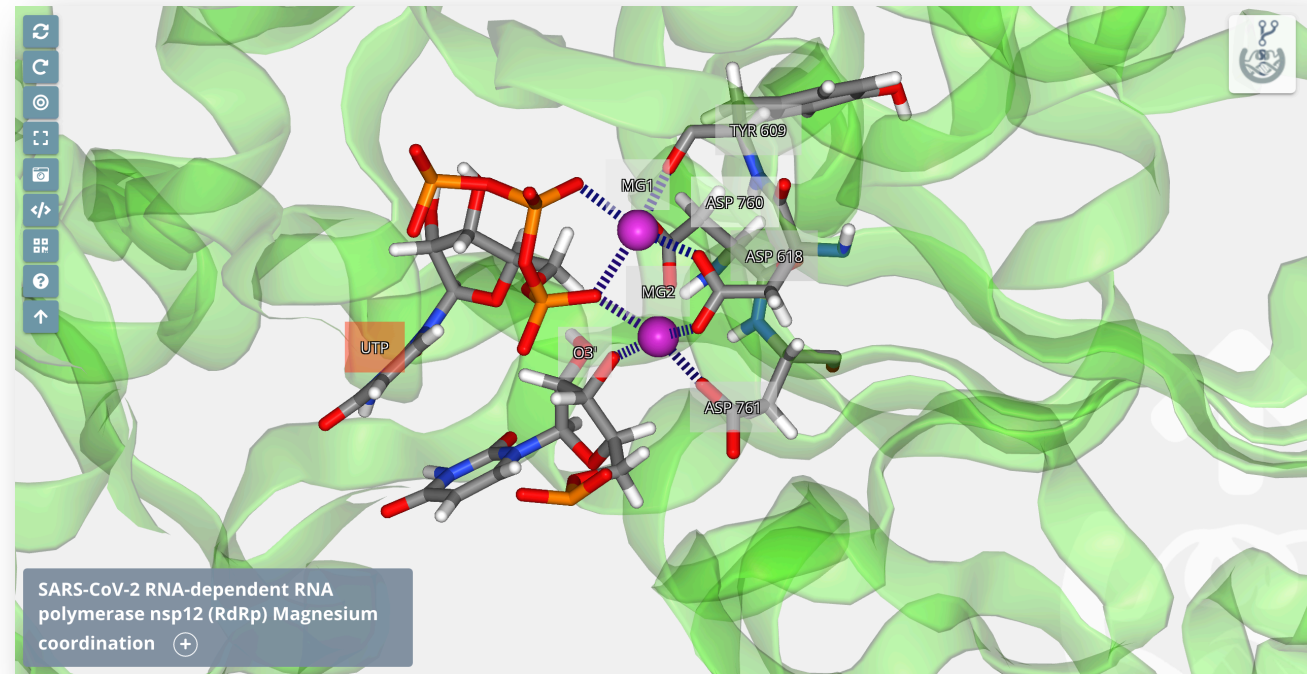


Fig.5b.- SARS-CoV-2 RNA-Dependent RNA Polymerase (RdRp) study: exploring the ability of RdRp to incorporate a natural triphosphate into a nascent RNA

Introduction: Why?



- **Live Figures**
- **Internal meetings** - same room
- **Collaborative projects**
- not in the same room
(e.g. BioExcel CoE partners)
- **Presentations** - show + share



<https://mmb.irbbarcelona.org/3dRS/s/TVVSQ2>

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All atoms

2D Cartoon Dynamically generated for selected residues. Nodes can be dragged or clicked.

Sequences and Annotations

Summary Details

Annotations: All Conserved Domains ClinVar Functional Sites Custom 3D Domains SNPs Interactions Disulfide Bonds Cross-Linkages

Show All Chains

Proteins:

Annotations of 1TUP_A: PROTEIN (P53 TUMOR SUPPRESSOR) (Gene: TP53) Add Track

Protein 1TUP_A + domain: P53 180 Res 1TUP_A 312 P53 180 Residues

Annotations of 1TUP_B: PROTEIN (P53 TUMOR SUPPRESSOR) (Gene: TP53) Add Track

Protein 1TUP_B + domain: P53 180 Res 1TUP_B 312 P53 180 Residues

Annotations of 1TUP_C: PROTEIN (P53 TUMOR SUPPRESSOR) (Gene: TP53) Add Track

Protein 1TUP_C + domain: P53 180 Res 1TUP_C 312 P53 180 Residues

Nucleotides:

Web3DMol 1MBS

Representation

Main Structure

- Hide
- Dot
- Line
- Backbone
- Tube
- Cartoon
- Cartoon Variants
- Stick
- Sphere
- Het Structure
- Hide
- Dot
- Line
- Stick
- Ball & Rod
- Sphere

Chain A

1	2	3	4	5	6	7	8	9	0	
0	G	L	S	D	G	E	W	H	L	V
1	L	N	V	W	G	K	V	E	T	D
2	L	A	G	H	G	Q	E	V	L	I
3	R	L	F	K	S	H	P	E	T	L
4	E	K	F	D	K	F	K	H	L	K
5	S	E	D	D	M	R	R	S	E	D
6	L	R	K	H	G	N	T	V	L	T
7	A	L	G	G	I	L	K	K	K	G
8	H	H	E	A	E	L	K	P	L	A
9	Q	S	H	A	T	K	H	K	I	P
10	I	K	Y	L	E	F	I	S	E	A
11	I	I	H	V	L	H	S	K	H	P
12	A	E	F	G	A	D	A	Q	A	A
13	M	K	K	A	L	E	L	F	R	N
14	D	I	A	A	K	Y	K	E	L	G
15	F	H	G							

POLYVIEW-3D

Tutorial : FAQ : Statistics : Gallery : Credits

ABOUT The Annotations

ACE2 - Angiotensin-converting enzyme 2 - Homo sapiens - Q9BYF1

100 200 300 400

100 200 300 400

- Domains & sites
- Molecule processing
- PTM
- Sequence information
- Structural features
- Topology
- Mutagenesis
- Domain families
- Disordered regions
- Interacting residues
- Residue accessibility

Our web services

SABLE MINNOU SPPIDER POLYVIEW-2D POLYVIEW-3D POLYVIEW-MM PGP CINTENY

3dRS: Sharing Biomolecular Representations



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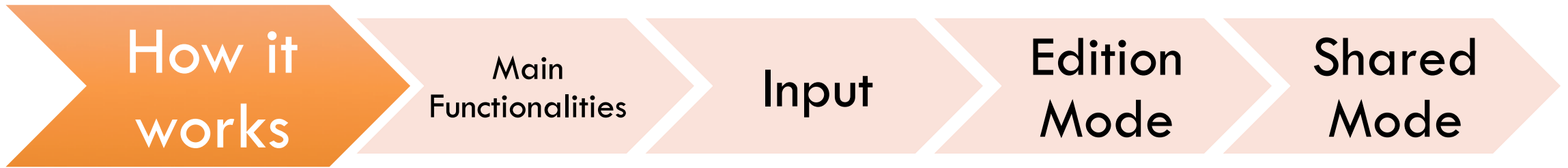
3-dimensional structure Representation Sharing

i Welcome to 3dRS



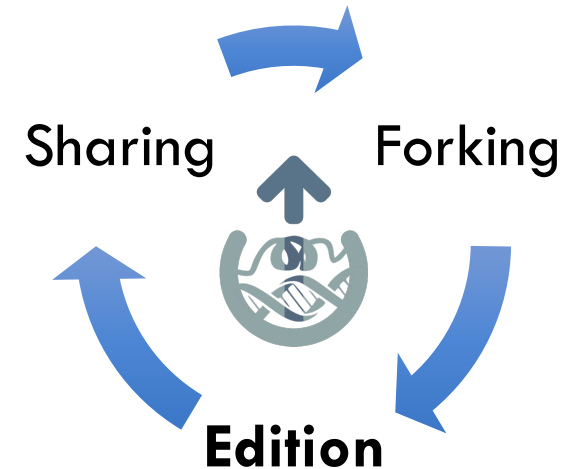
The **3-dimensional structure Representation Sharing (3dRS)** web application has been built with the aim of **sharing visualizations of 3D biological structures** through the web. In these visualizations, users will be able to draw several representations with different selections of the structure(s) previously **uploaded to the application**.

Our **philosophy for this project** is to make it accessible to everybody, so there is no private area and once a project is shared **everybody with the link can access it** with no restrictions.



3dRS: Main functionalities

- **Easy generation of 3D/4D biomolecular representations**
 - Single Page Application (SPA) Web-based Graphical user interface (GUI)
 - Seamless user experience, mimicking a native, standalone program (no reloads or saving buttons)
 - VMD-like selections + representations
- **Molecular Dynamics Trajectories** (using MDSrv)
- **Multiple structure representation**
- **Persistent URL to share the biomolecular representation**
(e.g. <https://mmb.irbbarcelona.org/3dRS/s/TVVSQ2>)
- **Representation Forking** (GitHub-like)





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Launch new 3dRS project

Please start uploading one or more structure files from your computer or with a Protein Data Bank ID and the structure will be automatically uploaded to our server:

Launch from PDB

Upload your own structure

Please click or drag and drop files, only **PDB** and **GRO** files accepted:

+ Select

Upload

× Cancel

EASY

Click **Select button** above or drag and drop files to here to upload.

Sequence

Chain X

1 PXISRORLTKYTMADLVYALRXFDENCDTLKEILVTVNCDDDDYFNKKDWDYFVENPDI LR VYAN GERV RQALLKTVQFCAMRNAGIVGLTLDNQDLNG
 111 121 131 141 151 161 171 181 191 201
 211 221 231 241 251 261 271 281 291 301
 311 321 331 341 351 361 371 381 391 401
 FNKDFYDFAVSKGFFKEGSSVELKXFFAQDGNAAISDYDYRYNLP T MCD I ROLL F VVEVVDKYFDCYDGGC INANQIVNNLDKSAGFPFNKWKARLYY

QMMM_REACTIVE_PATH_RDRP_SARS_COV2.MOD2.REF | Model 1 | Chain X | ASP (aspartic acid) 406

TRAJECTORY

Trajectory settings

Range 1 - 547

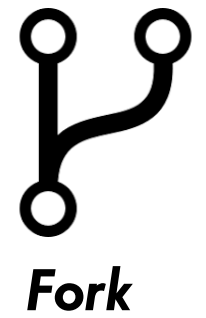
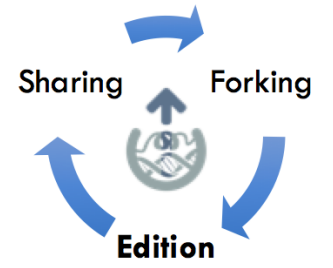
Step 7

Interpolation Spline

Timeout 13

Autoplay

Bounce / rock disabled



HNF-3/FORK Head DNA-Recognition Motif

Importance of arginine residues in the DNA-recognition binding of Hepatocyte Nuclear Factor-3 (HNF-3). Arginine residues are catching the DNA phosphate groups, and the interactions are maintained along the whole simulation (50ns). PDB code 1VTN. Trajectory taken from the BigNASim database, MD code NAFlex_FOXA3_crystal_rep5.

Sequence

Chain X

1 PXISRQLTKYTMADLVYALRXFDENCDTLKEILVTYNCDDDDYFNKKDWYDFVENPDI LR VYAN GERV RQALLKTVQFCAMRNAGIVGLTLDNQDLNG
 111 121 131 141 151 161 171 181 191 201
 211 221 231 241 251 261 271 281 291 301
 311 321 331 341 351 361 371 381 391 401
 411 421 431 441 451 461 471 481 491 501
 FNKDFYDFAVSKGFFKEGSSVELKXFFAQDGNAAISDYDYRYNLP T MCD I ROLL FVVEVVDKYFDCYDGGC INANQIVNNLDKSA GPF PFKWGKARLYY

QMMM_REACTIVE_PATH_RDRP_SARS_COV2.MOD2.REF | Model 1 | Chain X | ASP (aspartic acid) 406

TRAJECTORY

360

Trajectory settings

Range 1 - 547

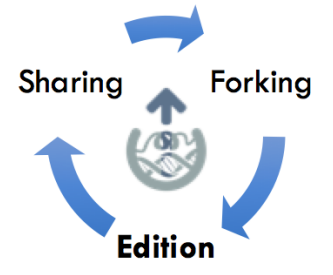
Step 7 Interpolation Spline

Timeout 13

Loop Autoplay

Bounce / rock disabled

Share



Shared Mode
Persistent Link

Edition Mode

Fork

HNF-3/FORK Head DNA-Recognition Motif

Importance of arginine residues in the DNA-recognition binding of Hepatocyte Nuclear Factor-3 (HNF-3).

Arginine residues are catching the DNA phosphate groups, and the interactions are maintained along the whole simulation (50ns).

PDB code 1V7N

Trajectory taken from the BigMDsim database, MD code NAFlex_FDXA3_crystal_rep5



VMD-like: Selections + Representations

VMD 1.9.2 OpenGL Display

Graphical Representations

Selected Molecule: 0: md.pdb

Create Rep Delete Rep

Style	Color	Selection
VDW	ResName	resid 1 3
Surf	ColorID 2	resid 600
CPK	Name	resid 600
VDW	ResName	resid 3 8
VDW	ColorID 2	resid 22

Selected Atoms: resid 1

Draw style: Selections | Trajectory | Periodic

Coloring Method: ColorID 3 | Material: Opaque

Drawing Method: VDW | Default

VMD Main

ID	T	A	D	F	Molecule	Atoms	Frames	Vol
0	T	A	D	F	md.pdb	12512	1	0

0 | zoom | Loop | step 1 | speed

3dRS: Selections + Representations

Representation

Select representation
Receptor Binding Dom... ▾

Select molecular representation
Line ▾

Select color scheme
Secondary structure ▾

Select opacity
100

Create new representation
Insert new name +

Selection

STRUCTURES
6XKL ▾

MODELS / CHAINS
Models
Chains

MOLECULES
Sequence
Chain A

```
27      37      47  
AYTNSFTRGVYYPDKVFRSSVLHSTQDLF  
57      67      77  
LPFFSNVTWFH      FDNPVL  
87      97      107  
PFNDGVYFAST      NIIRGWIFGTTLDSK  
117      127      137  
TQSLIVNNATNVVIKVFCEQFCNDPFL  
G      147      157      167  
      EFRVYSSANNCTFEY  
VSQPFL      177      187      197  
      KNLREFVFKNIDG
```

Heteroatoms
Ions
Waters

3dRS: Selections + Representations

The image displays the 3dRS interface in Edition Mode. A central 3D protein structure is shown, colored in yellow, pink, and white. Red arrows point from the 'Tools' panel to the structure, from the 'Stage Panel' to the structure, and from the structure to the 'Sharing' icon. A 'Representation' panel is open on the left, and a 'STRUCTURES' panel is open on the right. The 'Representation' panel includes options for 'Select representation' (Receptor Binding Dom...), 'Select molecular representation' (Line), 'Select color scheme' (Secondary structure), and 'Select opacity' (100). The 'STRUCTURES' panel shows the structure ID '6XKL', 'MODELS / CHAINS' (Models, Chains), and 'MOLECULES' (Sequence for Chain A). The sequence for Chain A is:

```
27      37      47  
AYTNSFTRGVYYPDKVFRSSVLHSTQDLF  
57      67      77  
LPFFSNVTWFH      FDNPVL  
87      97      107  
PFNDGVYFAST      NIIRGWIFGTTLDSK  
117     127     137  
TQSLIVNNTATNVVIKVFCEQFCNDPFL  
G      147     157     167  
      EFRVYSSANNCTFEY  
VSQPFL 177     187     197  
      KNLREFVFKNIDG
```


3dRS: Selections + Representations

STRUCTURES

2VXX

MODELS / CHAINS

Models

Chains

A B C D

MOLECULES

Sequence

Chain A

5	15	25
ALPRQAFGEMADTVILLEKATTPICEGM		
35	45	55
NRLASFQALYLQYQKHHFVVEGAEFYPL		
65	75	85
HQFFQDCYEQVQDQDHVHALGERLNLGGVP		
95	105	115
VAGFQQLAALCCFTPEPEGAFNCRQLSN		
125	135	145
DLQAEQAIIGVLRQQATQAESLGDRTAY		
155	165	175
LYDQILLKTEERAYHIGHFLANDSLKV		

Heteroatoms

Ions

Waters

STRUCTURES

1XKK

MOLECULES

Custom selection

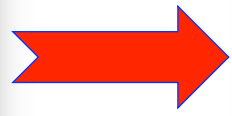
Add custom selection

FMM

Distance-based selection

Distance: 5

Whole residue(s)



Select representation

Nucleosome

Select molecular representation

Line

Select color scheme

Secondary structure

Select opacity

100

Create new representation

Insert new name



How it works – Edition Mode

3dRS: Representations

Select representation
Nucleosome

Label settings ?
Nucleosome Label

25

Select molecular representation
Line

Select color scheme
Secondary structure

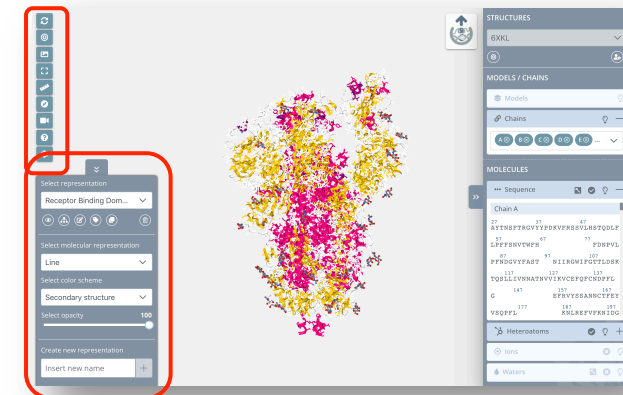
Select opacity
100

Create new representation
Insert new name

- ❖ **Hide Representation**
- ❖ **Edit Representation Name**
- ❖ **Clone Representation**
- ❖ **Open Label Settings**

- **Backbone**
- **Ball & Stick**
- **Cartoon**
- **Hyperball**
- **Licorice**
- **Line**
- **Ribbon**
- **Rope**
- **Spacefill**
- **Surface**
- **Trace**
- **Tube**

- **Atom index**
- **B-factor**
- **Chain**
- **Element**
- **Hydrophobicity**
- **Random**
- **Residue index**
- **Residue name**
- **Secondary Structure**
- **Uniform**
- **Model**



- Reload
- Center
- Background
- Full screen
- Superposition
- Measurements
- Navigation mode
- Camera type
- Help
- Project settings

3dRS: Trajectories

The screenshot shows the left sidebar of the 3dRS interface. It is divided into four main sections: STRUCTURES (with a dropdown for '1KX5'), MODELS / CHAINS (with 'Models' and 'Chains' buttons), MOLECULES (with 'Sequence', 'Heteroatoms', 'Ions', and 'Waters' buttons), and TRAJECTORY (with an 'Add Trajectory' button). The TRAJECTORY section is highlighted with a red rounded rectangle.

Powered by...
nglviewer/mdsrv
MD trajectory server

This screenshot shows a 3D molecular model of a protein-ligand complex in the center. To the right is the sidebar with 'STRUCTURES' (showing '1KX5'), 'MODELS / CHAINS' (showing 'Models' and 'Chains'), and 'MOLECULES' (showing 'Chain A' and a sequence list). A red rounded rectangle highlights the right sidebar.

The 'Upload Trajectory' dialog box contains the text: 'Please click or drag and drop files, only XTC, DCD, TRR, BINPOS and NETCDF files accepted:'. Below this text are three buttons: '+ Select', 'Upload', and 'Cancel'. A message below the buttons says: 'Click **Select** button above or drag and drop files to here to upload.'

500 MB maximum size

The 'Trajectory settings' dialog box includes the following controls:

- Range:** A slider set to '1 - 151'.
- Step:** A dropdown menu set to '1'.
- Interpolation:** A dropdown menu set to 'Spline'.
- Timeout:** A slider set to '17'.
- Loop:** A toggle switch that is currently off.
- Autoplay:** A toggle switch that is currently off.
- Bounce / rock disabled:** A toggle switch that is currently off.

3dRS: Sharing



Sharing

STRUCTURES
6XKL

Share representation

Share representation

Share project

For sharing it, **you just need to copy and share the address below:**

Copy <https://mmb.irbbarcelona.org/3dRS/s/E1gpTw> Open

Embed project

For embed it as a widget, **you just need to copy the HTML code below** and paste it into your website:

```
<iframe width="500" height="500" src="https://mmb.irbbarcelona.org/3dRS/e/E1gpTw" title="3dRS" frameborder="0" allowfullscreen></iframe>
```

Copy

QR code

Below you can find a **QR code for sharing the new generated address:**

Close

Sequence

Chain X

1 PXISRORLTKYTMADLVYALRFXFDEGNCDTLKEILVTVNCDDDDYFNKKDWDYFVNPDI LRVYANLGERVROALLKTVQFCAMRNAGIVGLTLDNQDLNG
 111 121 131 141 151 161 171 181 191
 211 221 231 241 251 261 271 281 291 301
 311 321 331 341 351 361 371 381 391 401
 411 421 431 441 451 461 471 481 491 501
 FNKDFYDFAVSKGFFKEGSSVELKXFFAQDGNAAISDYDYRYNLP T MCD I ROLL F VVEVVDKYFDCYDGGC INANQIVNNLDKSAGFPFNKWKARLYY

QMMM_REACTIVE_PATH_RDRP_SARS_COV2.MOD2.REF | Model 1 | Chain X | ASP (aspartic acid) 406

TRAJECTORY

Trajectory settings

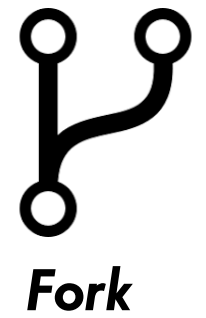
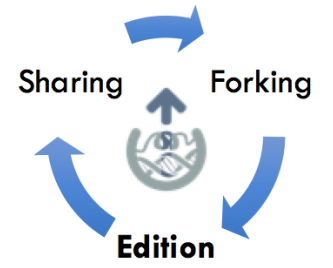
Range 1 - 547

Step 7 Interpolation Spline

Timeout 13

Loop Autoplay

Bounce / rock disabled



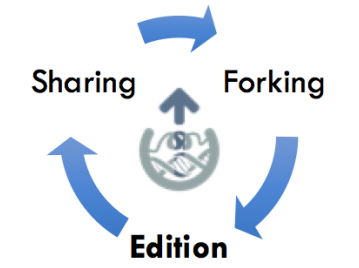
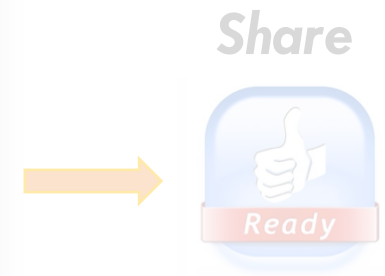
HNF-3/FORK Head DNA-Recognition Motif

Importance of arginine residues in the DNA-recognition binding of Hepatocyte Nuclear Factor-3 (HNF-3). Arginine residues are catching the DNA phosphate groups, and the interactions are maintained along the whole simulation (50ns). PDB code 1VTN. Trajectory taken from the BigNASim database, MD code NAFlex_FOXA3_crystal_rep5.

Sequence Editor: Chain X
 PXISRORLTKYTMADLVYALRXFDENCDTLKEILVYNYNCDDDYFNKKDWYDFVENPDI LRVYANLGERVROAL LKTVOFCAMRNAGIVGLTLDNQDLNG
 NHYDFGDF LOTTTPGSGVPPVSDSYSLNPILTLTRALTAESXVDTLTKPKYIKWDLKDYDFTEERLKLFDRYFKYWDOTYXPNCVCLDDRCILXCA
 NFNVL FSTVFPPTSFGPLVRKIFVDGVPFVVSTGYXFRELGVVXNQDVLXSSRLSFKELLYAADPAMXAASGNLLLDKRTTCFSAALTMNVAFOTVKPGN
 FNKDFYDFAVSKGFFKEGSSVELKXFFAODGNAAISDYDYRYNLPNCDIRQLLVVEVVDKYFDCYDGGCINANOVI VNNLDKSAGFPFNKWKARLYY

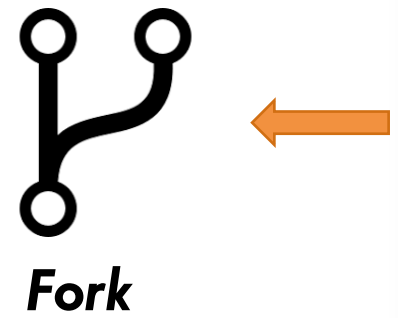
MOLECULES: Sequence, Heteroatoms, Ions, Waters

TRAJECTORY: Trajectory settings (Range: 1-547, Step: 7, Interpolation: Spline, Timeout: 13, Autoplay: on)



 **Shared Mode**
Persistent Link

 **Edition Mode**



HNF-3/FORK Head DNA-Recognition Motif

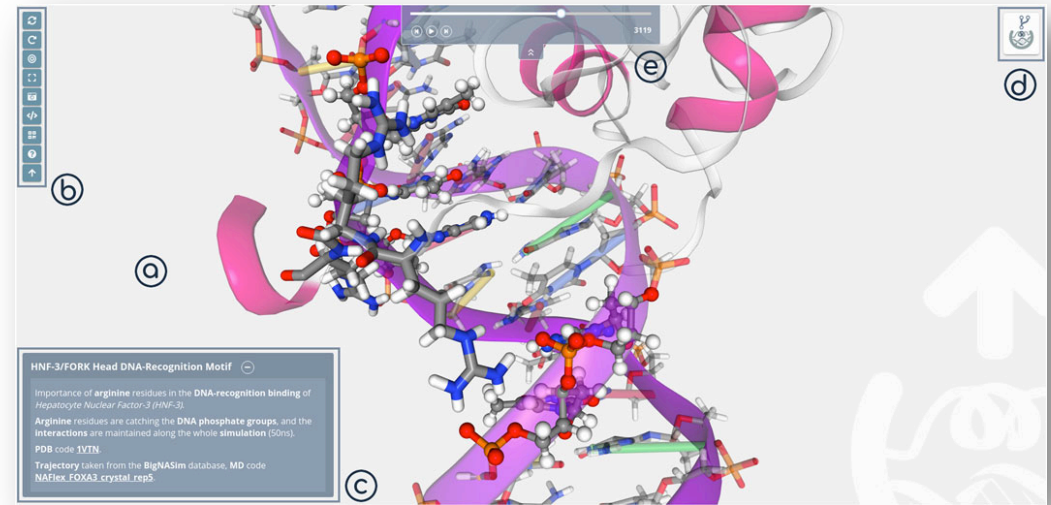
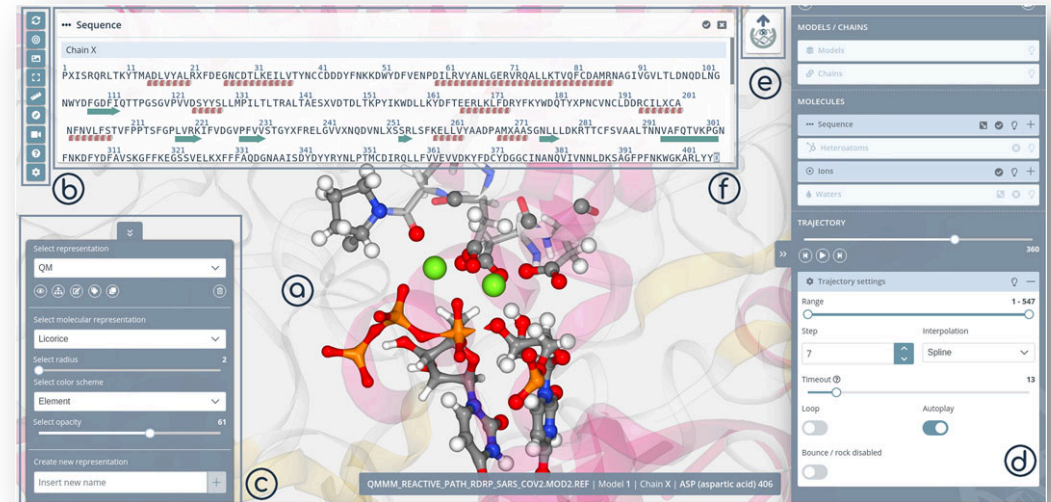
Importance of **arginine** residues in the **DNA-recognition** binding of Hepatocyte Nuclear Factor-3 (*HNF-3*).
Arginine residues are catching the **DNA phosphate groups**, and the **interactions** are maintained along the whole **simulation** (50ns).
 PDB code **1VTN**.
 Trajectory taken from the BigNASim database, MD code **NAFlex_FOXA3_crystal_rep5**.

Main differences between Edition and Shared Mode

- No modification
 - Selection / representation
 - Labels / Measurements
 - Background color / Perspective

- Zoom / Rotation
- Atom-Residue information

- Figure Caption
- Trajectory Player
- Specific Tools
- Forking process



Trajectory Player

Tools

(b)

Trajectory Player

3119

(e)

(d)

Fork

Tools

(a)

Figure Caption

Stage Panel



HNF-3/FORK Head DNA-Recognition Motif

Importance of **arginine** residues in the **DNA-recognition binding** of *Hepatocyte Nuclear Factor-3 (HNF-3)*.

Arginine residues are catching the **DNA phosphate groups**, and the **interactions** are maintained along the whole **simulation (50ns)**.

PDB code **1VTN**.

Trajectory taken from the **BigNASim** database, MD code **NAFlex FOXA3 crystal rep5**.

(c)



Launch Project

Home > Launch

Launch new 3dRS project

Please start uploading one or more structure files from your computer or with a Protein Data Bank ID and the structure will be automatically uploaded to our server:

Launch from PDB Upload your own structure

Please type the PDB ID(s) you want to use and a list of options will be shown:

Insert here the PDB ID(s)

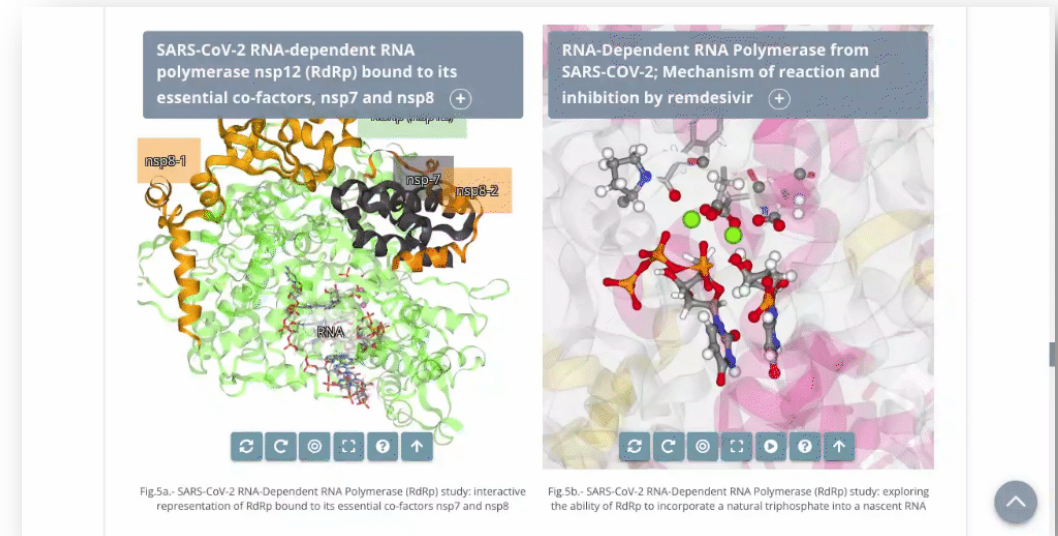
✓ Submit

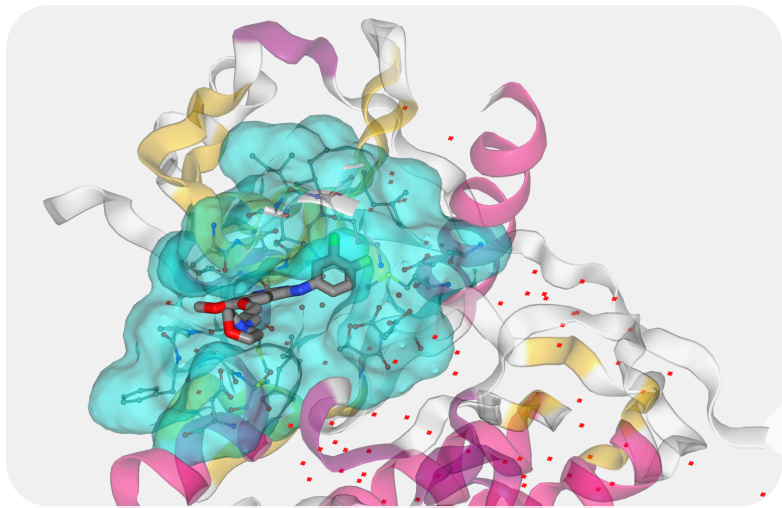


Summary

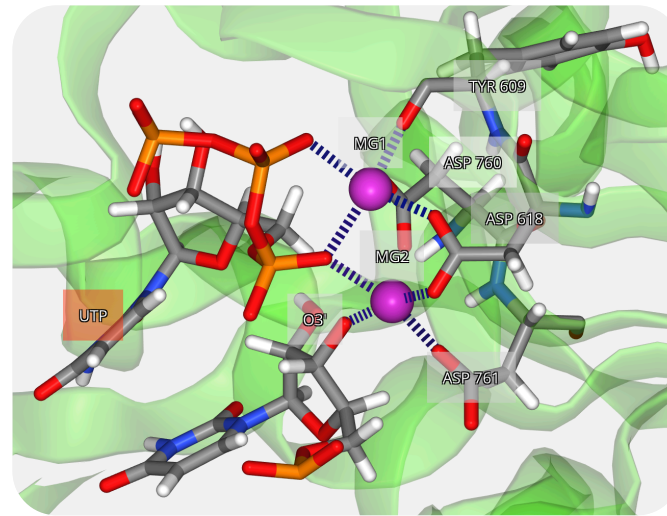
EASY

- **Generation** and **sharing** of **living, interactive, 3D/4D custom representations**
 - SPA designed web page (*VueJS, MongoDB*)
 - **VMD-like** Selections and Representations
 - **NGL** to efficiently show 3D macromolecular representations
 - **MDsrv** to efficiently stream MD data

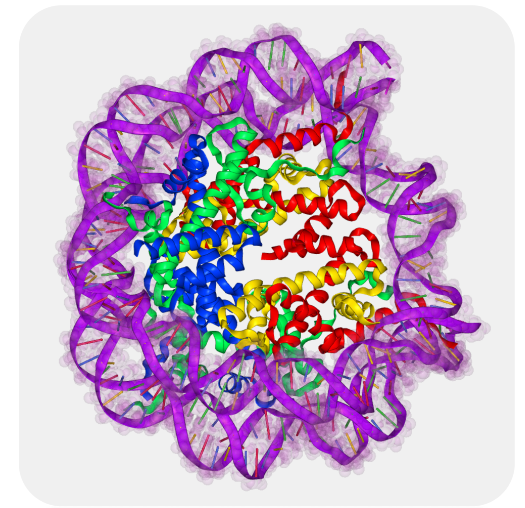




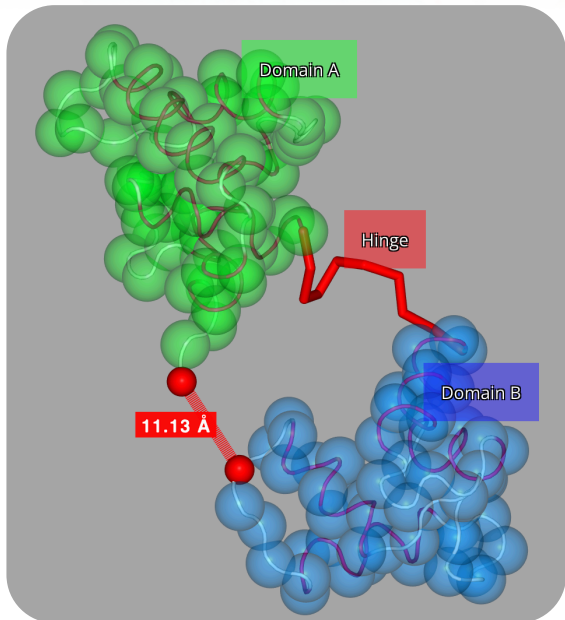
EGFR kinase domain complexed with gefitinib



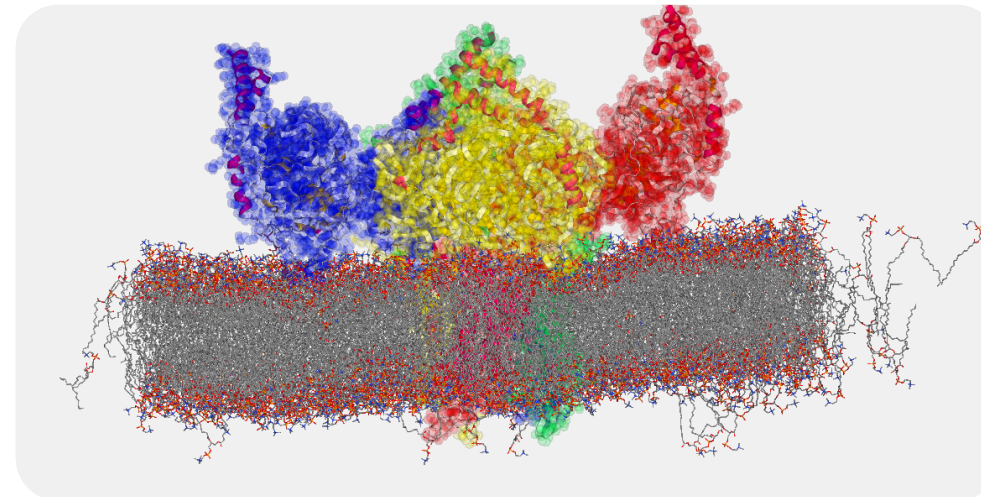
SARS-CoV-2 polymerase Magnesium coordination



Nucleosome Core Particle



**Conformational Changes
(Calcium Saturated
Cardiac Troponin C)**



**G Protein-Gated
K⁺ Ion Channel**

<https://mmb.irbbarcelona.org/3dRS/gallery>



latest

Introduction

Launch project

Edit representation

Share representation

Changelog

Read the Docs

v: latest

» 3dRS documentation

Edit on GitHub

docs passing

<https://3drs-documentation.readthedocs.io/>

3dRS documentation



Brief description

Documentation for the web application **3-dimensional structure Representation Sharing (3dRS)**. This application has been built with the aim of **sharing visualizations of 3D biological structures** through the web. In these visualizations, users will be able to draw several representations with different selections of the structure(s) previously **uploaded to the application**.

Our **philosophy for this project** is to make it accessible to everybody, so there is no private area and once a project is shared



Share representation

Sharing instructions

If your project is ready for sharing, **please follow the next steps:**

1) First off, **take a look to the project draft**. It will show you the project the same way the final users will see it. Take into account that **this address shouldn't be shared**, because until you **generate a shared project**, the current one will be **expirable**.

[View draft](#)

2) Be sure that you agree with the **fork permissions** for this project. You can allow or not other users to **fork this project** once it is shared:

Fork enabled

3) Allow or not to **make this project public** and **available to other users** throughout the home page:

Project is private

4) Finally, clicking the button below **the shared project will be you want**, but once a project is shared, the subsequent update projects.

[Share project](#)



Last projects

List with the last projects developed by our users:

Name	Date	Link
EGFR kinase domain comple...	02/08/2021 15:19:00	Open
AppA BLUF domain	02/08/2021 09:35:44	Open
SARS-CoV-2 glycosylated S...	30/07/2021 09:32:23	Open
Nucleosome core Particle,...	30/07/2021 08:40:34	Open
G protein-gated inward re...	29/07/2021 17:14:10	Open

Acknowledgments



Prof. Modesto Orozco

RESEARCH GROUP
**Molecular Modelling and
Bioinformatics**
Mechanisms of Disease



Genís Bayarri

Questions

TECHNOLOGY AND CODE article

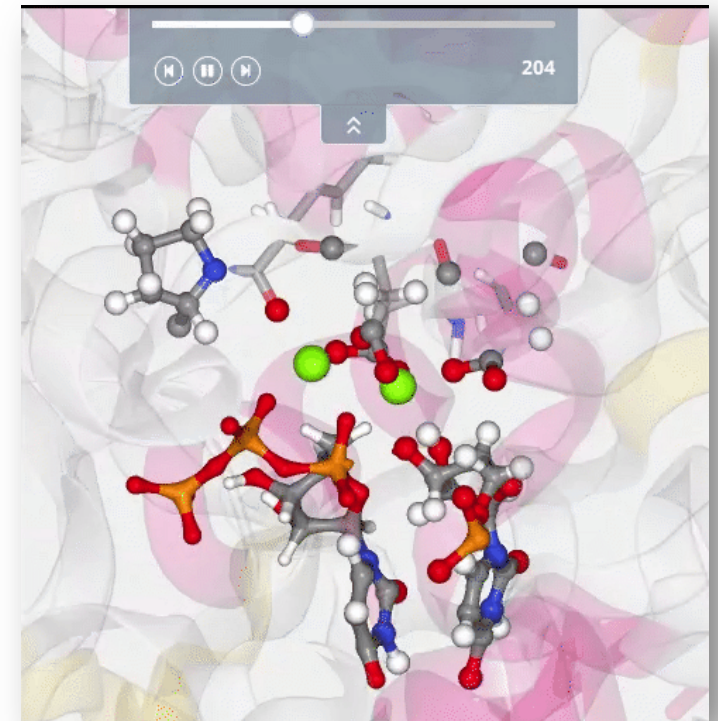
Front. Mol. Biosci., 13 August 2021 | <https://doi.org/10.3389/fmolb.2021.726232>

3dRS, a Web-Based Tool to Share Interactive Representations of 3D Biomolecular Structures and Molecular Dynamics Trajectories

 **Genís Bayarri**¹,  **Adam Hospital**^{1*} and  **Modesto Orozco**^{1,2*}

¹Institute for Research in Biomedicine (IRB Barcelona), The Barcelona Institute of Science and Technology (BIST), Barcelona, Spain

²Departament de Bioquímica i Biomedicina, Facultat de Biologia, Universitat de Barcelona, Barcelona, Spain



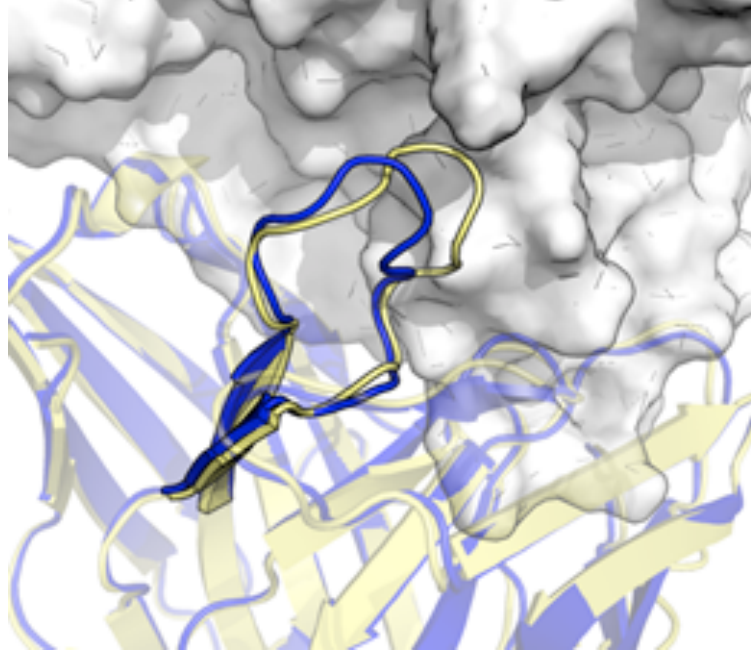
Audience Q&A session

- Please use the Q&A function at the bottom of **Zoom** application



- If you can't use your microphone, write **no micro** and we will read the question for you
- Any other questions or points to discuss after the live webinar? Join the discussions at <http://ask.bioexcel.eu>.

Next BioExcel webinar



Webinar: Computationally designing therapeutic antibodies - combining immune repertoire data and structural information.
(2021-11-09)

By Charlotte Deane

3dRS infrastructure scheme

