

# Attempt to Treat Coronavirus Disease (COVID-19) with Electromagnetic Wave Irradiation

The effectiveness of a combination of frequency, intensity, etc., in the natural vibration of microwaves targeting the collapse of the most delicate part, the Heptad Repeat 2 (HR 2) region, in spike proteins of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is investigated. Based on the results, inactivation of the virus is attempted through the use of irradiating microwaves directed toward the infected site from outside the body.

by Ryoji Furui on Jun 7, 2021 @[www.ryoji.info](http://www.ryoji.info)

# 1. What is the HR2 region?

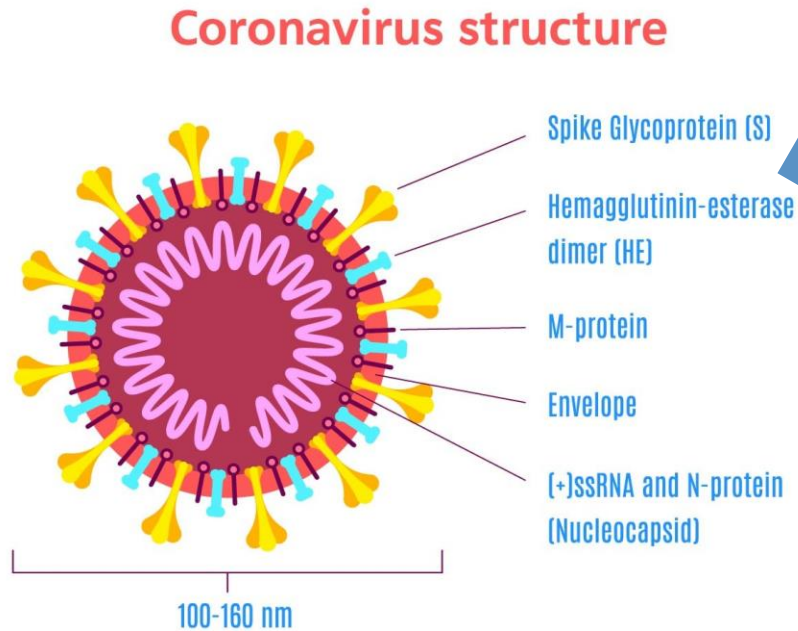


Fig. 1 Structure of coronavirus

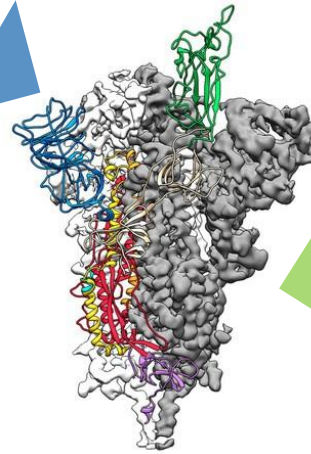


Fig. 2 Spike

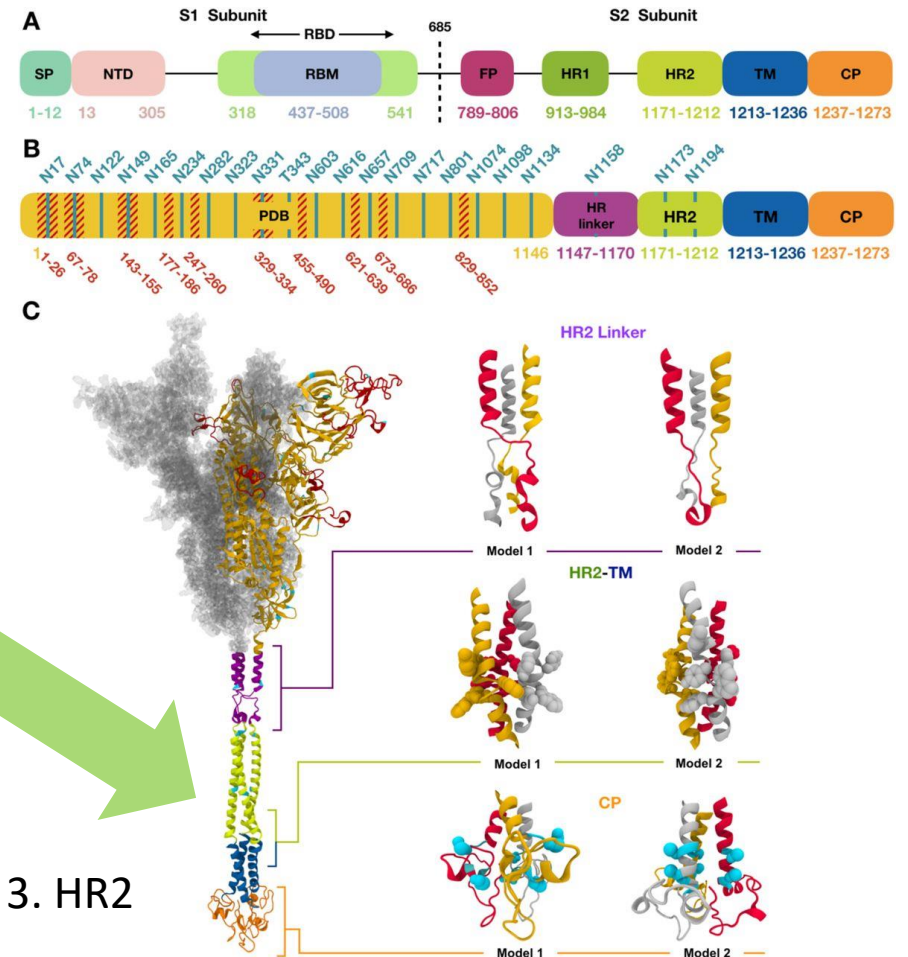


Fig 3. HR2

HR2 is a thin part at the root of the surface spike protein on SARS-CoV-2. It collapses when the temperature is raised from 25°C to 50°C ①. A similar collapse is attempted by using non-thermal effects, ② such as microwave irradiation. Assuming that the HR2 region is the most vulnerable part in the SARS-CoV-2 S protein, its alteration and division are targeted.

~ Defeat spike proteins that are important for infection, like "Ashiharai" (sweeping one's opponent's legs) in Judo!

## 2. Understanding the physical phenomena of temperature change in HR 2 and reproduction of results via non-thermal effects of electromagnetic waves

- Molecular motion of HR2 in water at 25°C, and above 50°C, is understood, and its collapse is simulated. At a water temperature of 38°C, the natural frequency that is the most effective for collapsing HR2 via non-thermal effects, such as microwaves irradiation, is derived. (In the calculation, the natural vibration of the total S2 subunit, including HR1, is considered.)
- To obtain the most suitable combination of parameters such as frequency, (minimum) strength, synthesis, modulation, irradiation time, direction, number of irradiations, and interval, simulation, and irradiation experiments are conducted.
- To obtain transmission of terahertz and strength of lower frequency waves, those waves can replace to microwave's modulation. Ultralow frequency waves can replace to sonic waves.
- Referencing the natural vibration ③ of the S1 subunit, the natural vibration of the total spike protein is obtained. An electromagnetic wave is generated by the synthesis or modulation, and the generated wave induces the resonance of the spike protein itself. Through these processes, the effect of the collapse can be enhanced.
- Effective targets potentially exist at other sites, such as the joint part of S1 and S2 subunits, apart from HR2.
- The effects on human tissues are also investigated. If the electromagnetic irradiation is effective for treatment, the irradiation instruments will be mass-produced.

### 3. Examples of natural vibration synthesis to collapse the spike protein

- HR2 collapse by dual wave synthesis

Natural vibration of the total spike protein

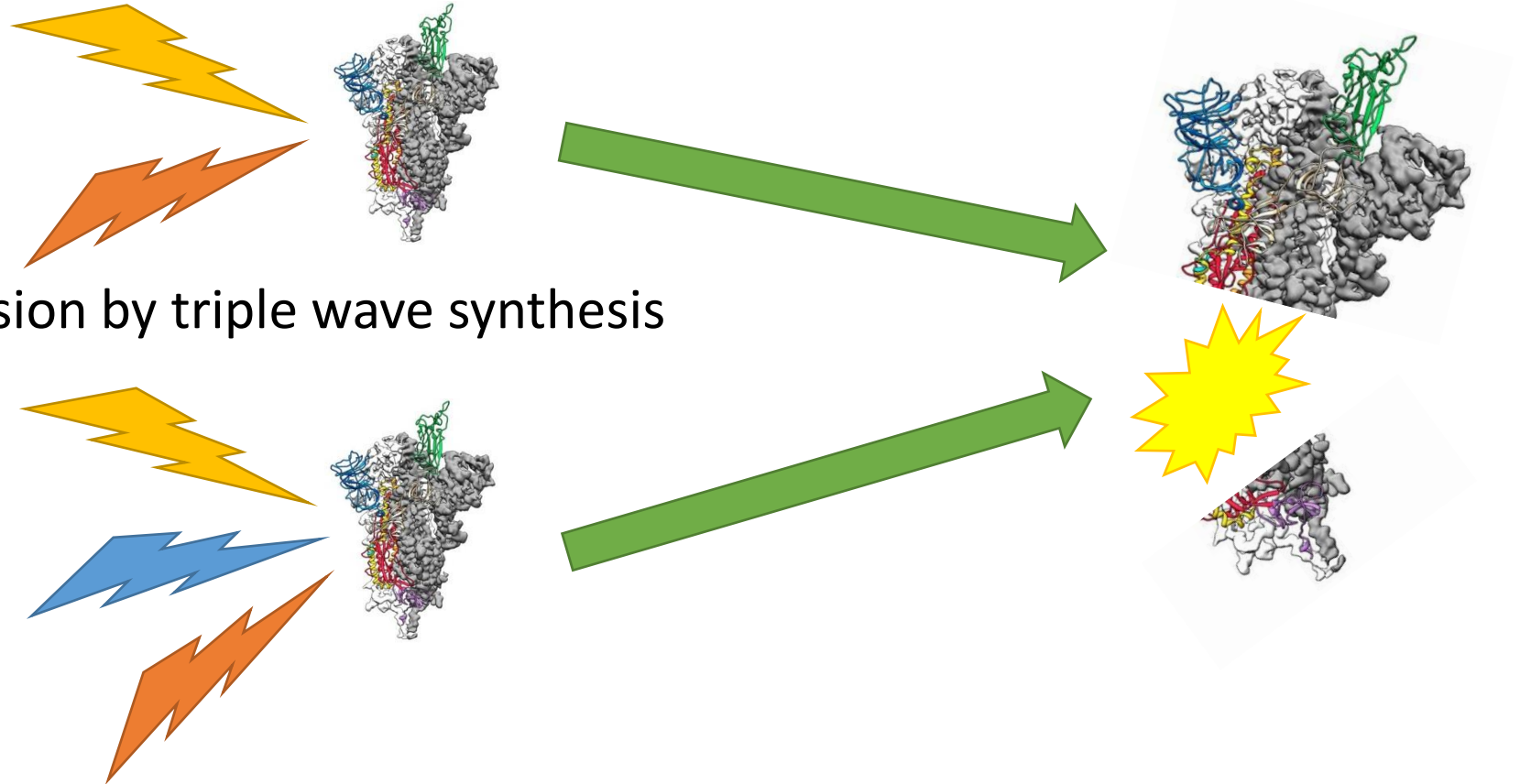
Natural vibration of HR2

- S1 and S2 subunit division by triple wave synthesis

Natural vibration of S1 subunit

Natural vibration of S1 and S2 subunits' joint

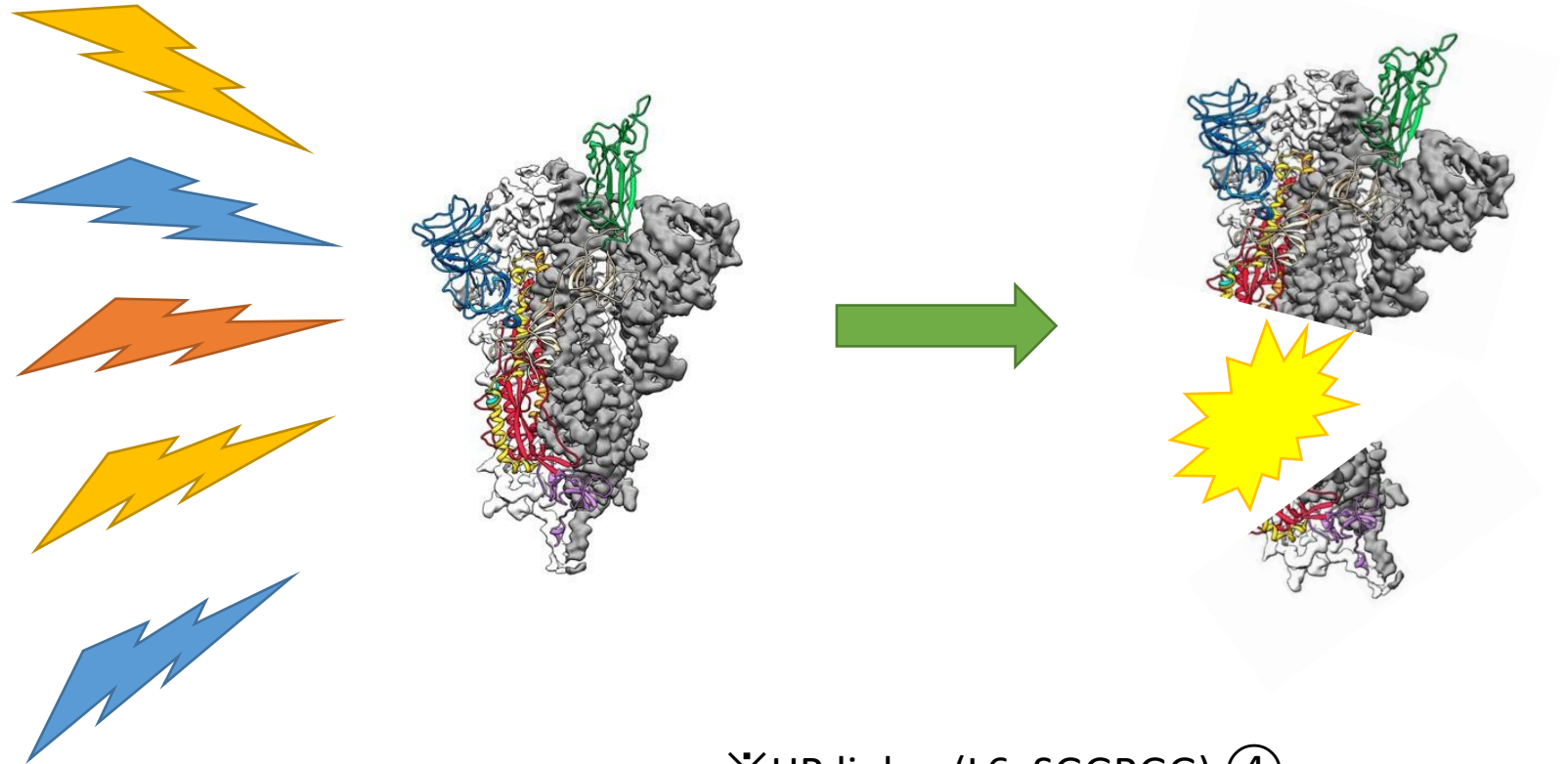
Natural vibration of S1 subunit



## 4. All-out attack by seven wave synthesis

Natural vibration of

- The total spike protein
- S1 subunit
- S1 and S2 subunits' joint
- S2 subunit
- HR1
- HR linker ✕
- HR2

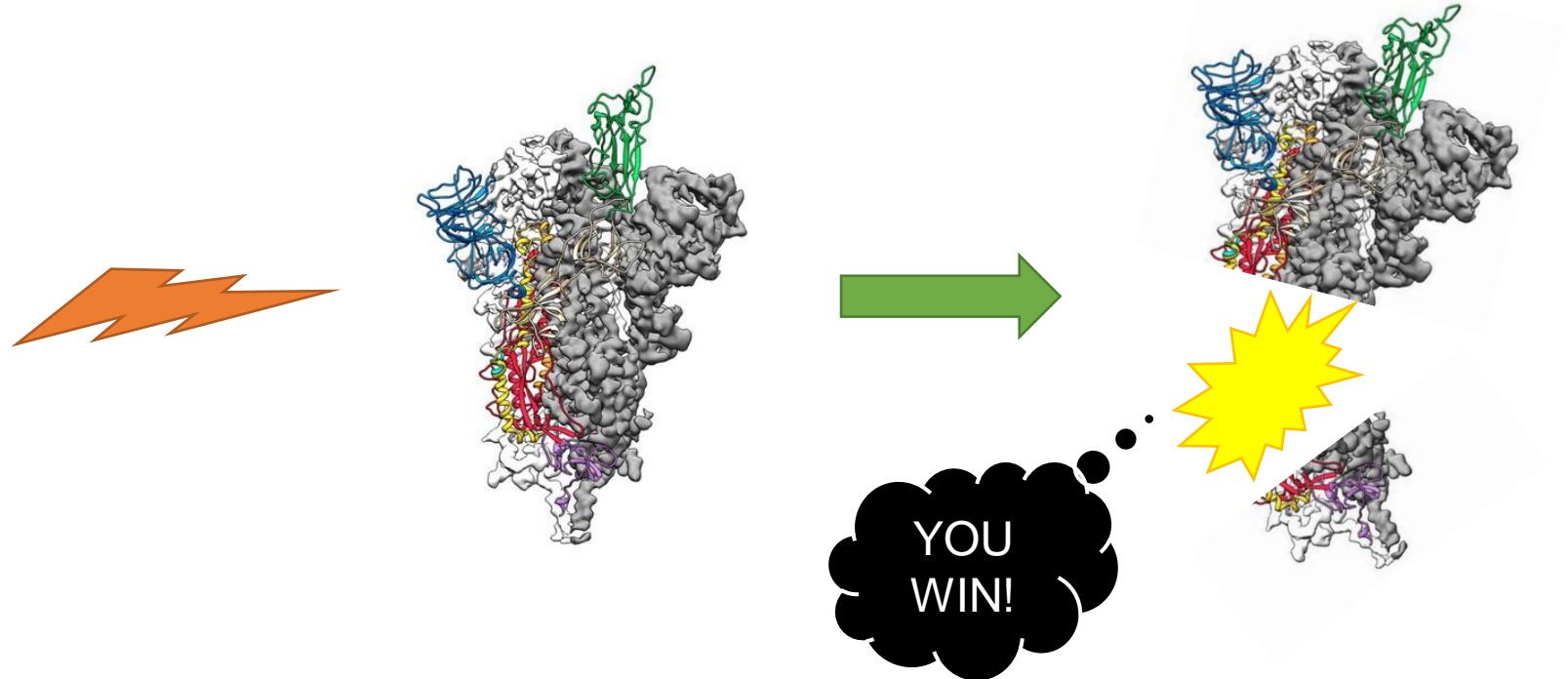


✕HR linker (L6, SGGRGG) ④

## 5. RBD alteration<sup>⑤</sup> by single frequency lasers

- RBD alteration by resonante with natural vibration of RBD fluctuations of open and closed states

Natural vibration of RBD  
fluctuations of open and  
closed states

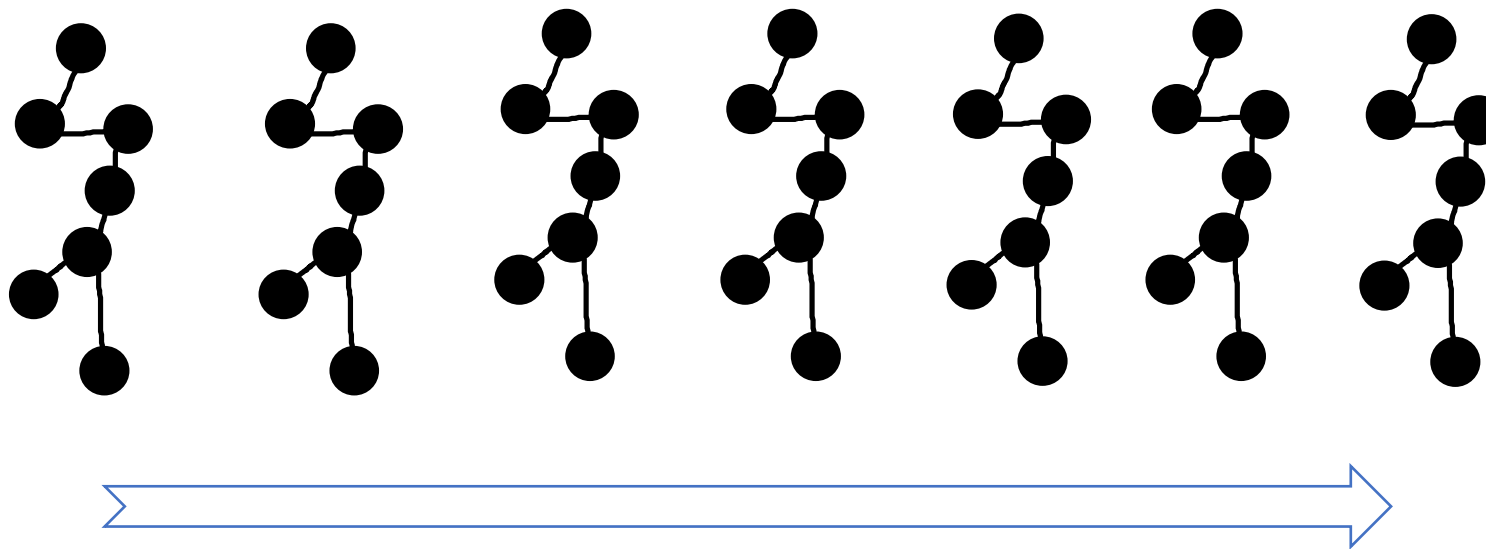


## 6.a. Simple detection of natural vibrations by combining molecular dynamics (MD) and pulsed 2450 MHz microwaves

- The velocity, magnetic field intensity, and thermal energy of low-level 2450 MHz microwaves are small enough to ignore.
- Therefore, only the electric field intensity (EFI), generated by pulse modulation, can be added to MD.
- If a 1 MHz pulse is combined with MD, the calculation of MD is repeated once- for 0.5  $\mu$ s with relevant EFI and another 0.5  $\mu$ s with null EFI.
- If the target molecule has 1 MHz natural vibration, partially or as a whole, repeating this calculation for a certain period of time would generate vibrations.
- A molecule with higher-order structure tends to have a low frequency of natural vibration.
- Sweeping frequency would turn out all natural vibrations of the molecule, but each range of EFI would be narrow and different. Therefore, the sweeping frequency of a single EFI will not turn out all vibrations at once.

## 6.b. Simple detection of natural vibrations by combining molecular dynamics (MD) and pulsed 2450 MHz microwaves

- Prepare 10- $\mu$ s MD record\* of target molecule in 38 °C water.
- Use a molecule with 7 mass points as a model.



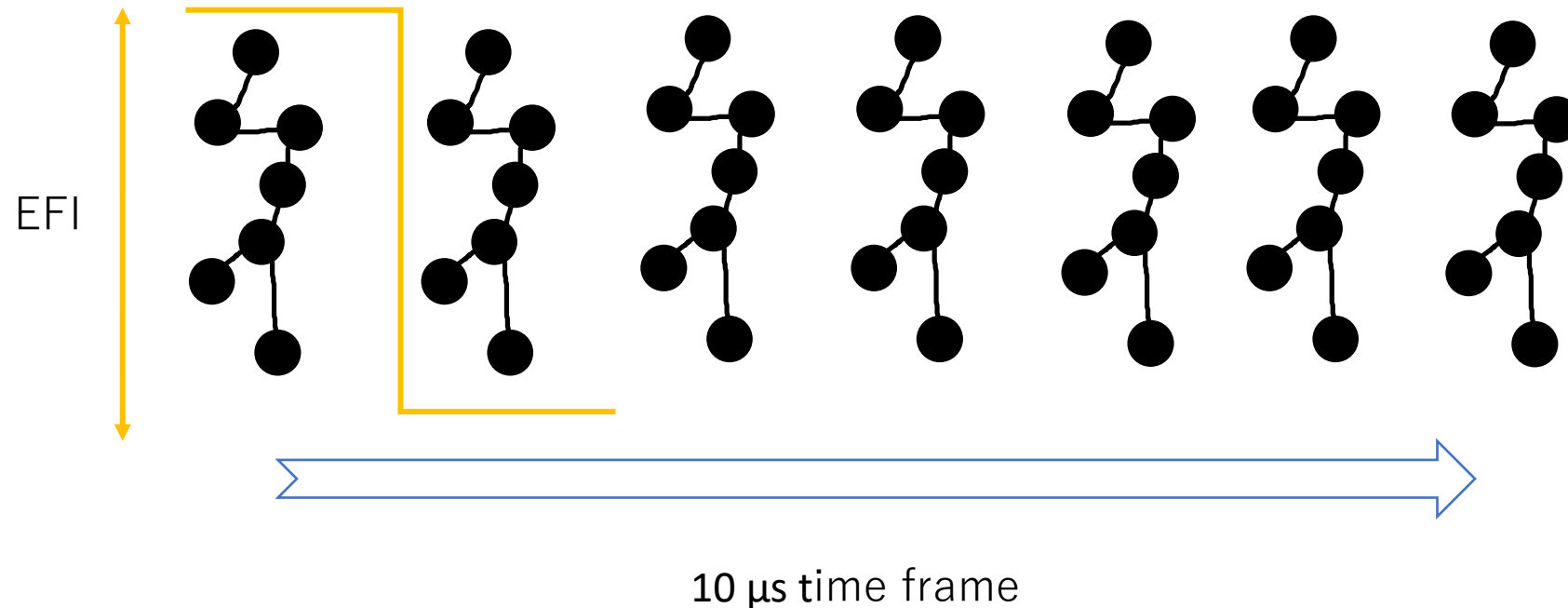
10  $\mu$ s time frame

\*RBD part of 10- $\mu$ s record: Komatsu, Teruhisa S., et al. "COVID-19 related trajectory data of 10 microseconds all atom molecular dynamics simulation of SARS-CoV-2 dimeric main protease." *Mendeley Data* 10 (2020). (<https://data.mendeley.com/datasets/vpps4vhryg/2>).



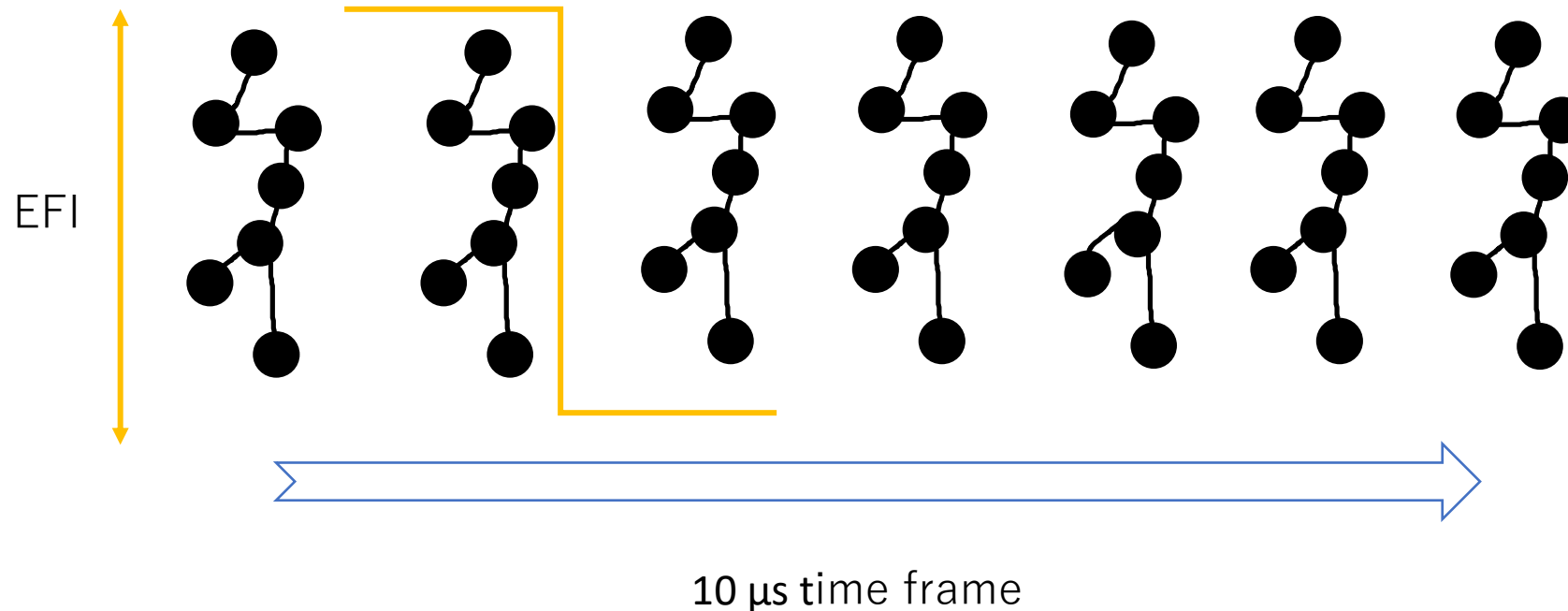
## 6.c. Simple detection of natural vibrations by combining molecular dynamics (MD) and pulsed 2450 MHz microwaves

- Calculate MD after 1  $\mu\text{s}$  of 1 MHz pulse combination; start from 0 s.
- Check the difference between MD after pulse combination and original MD (no pulse combined) after every 1  $\mu\text{s}$  for each mass point.



## 6.d. Simple detection of natural vibrations by combining molecular dynamics (MD) and pulsed 2450 MHz microwaves

- Repeat the last two steps with as many starting points as possible, such as 0.5  $\mu\text{s}$ , 1  $\mu\text{s}$ , 1.5  $\mu\text{s}$ ...
- Add all differences between original and pulse-combined MD (after 1  $\mu\text{s}$ ) for each mass point and find the average difference for each mass point.



#### 6.d. Simple detection of natural vibrations by combining molecular dynamics (MD) and pulsed 2450 MHz microwaves

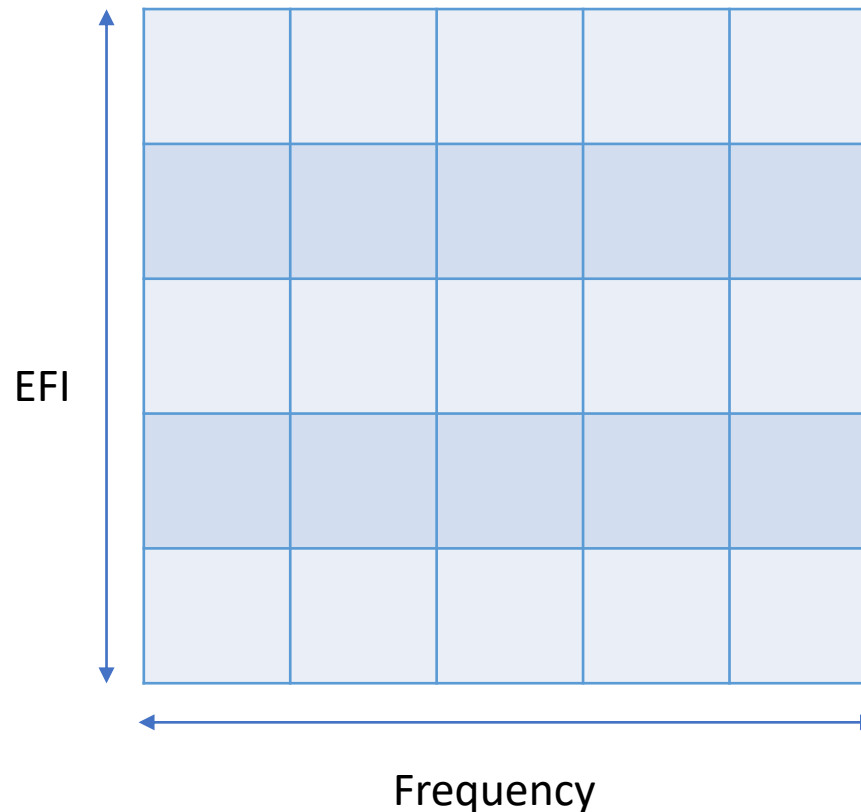
- Check a certain range of frequency and EFI and find the largest difference in MD as a peak at some point.
- This would likely be the natural vibration of the target molecule!
- If the molecule vibrates, check it further with longer period ( $>1\mu\text{s}$ ) of mixing.

## 7.a. An example of how to find a natural vibration on a decentralized computing system

- Calculate MD of the target molecule and prepare slots (can be NFT tokens) divided by frequency and EFI.

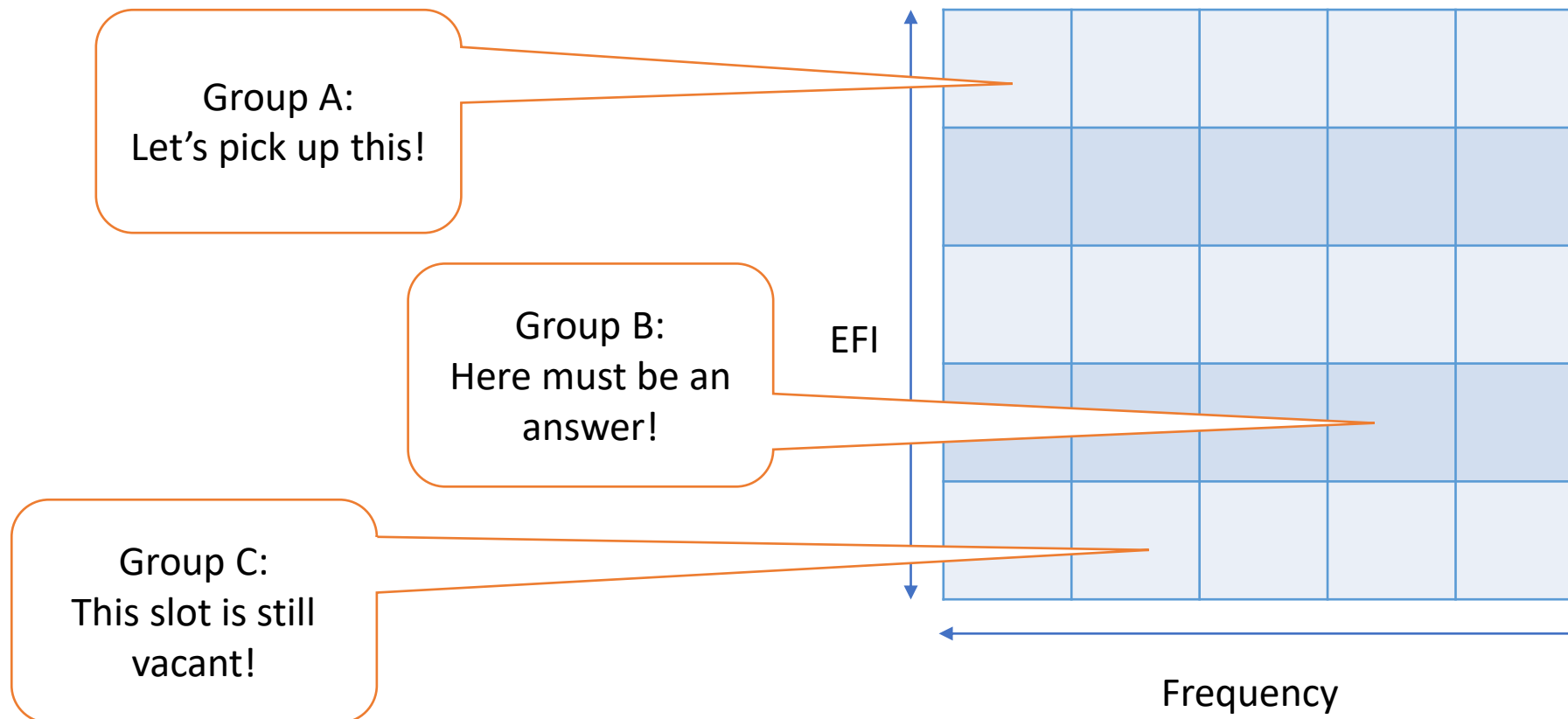


Let's find the natural vibration of HR linker!



## 7.b. An example of how to find a natural vibration on a decentralized computing system

- Each group selects a unique slot to compute.



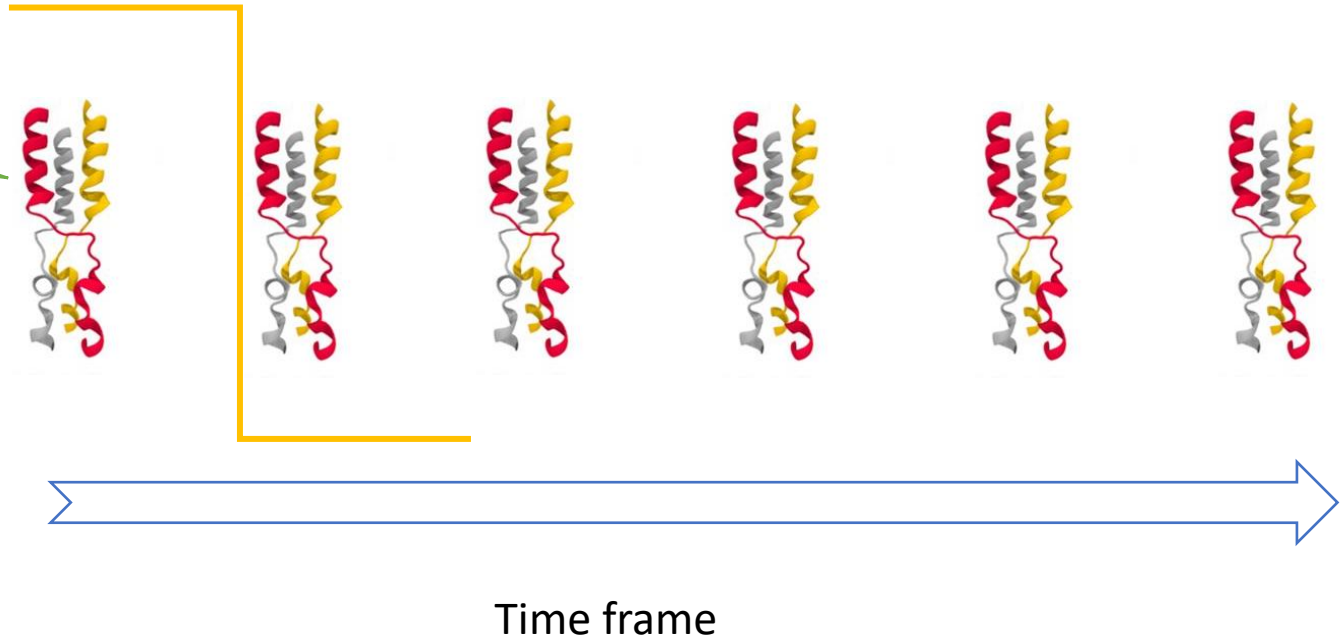
## 7.c. An example of how to find a natural vibration on a decentralized computing system

- Each group begins parallel computing on the blockchain.

O.K! We have loaded  
our slot on Dapp.  
Let's start!

It is lucky to reuse  
our resting mining  
machine!

Proof of history is  
the fastest way to  
parallel  
computing?



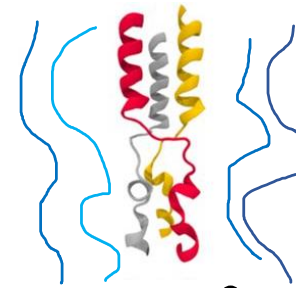
## 7.d. An example of how to find a natural vibration on a decentralized computing system

- Finally, one of the groups detects the natural vibration along with its frequency!

Hey! It is vibrating  
with pulsed EM!

Yes! We made it!!!

Let's report that we  
detected it!



Congratulations!  
You may get a reward  
from WHO?

## 8. Discussion

- There is a high possibility that the energy of irradiation achieved at 50°C is not harmful to human tissues.
- Microwave irradiation at the appropriate frequency can be applied to treatments involving inactivation of other viruses or bacteria and the exhaust of heavy metals from human body.

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# References

- ① Yanhui Xu, Jieqing Zhu, Yiwei Liu, Zhiyong Lou, Fang Yuan, Yueyong Liu, David K. Cole, Ling Ni, Nan Su, Lan Qin, Xu Li, Zhihong Bai, John I. Bell, Hai Pang, Po Tien, George F. Gao, and Zihao Rao. (2004). Characterization of the Heptad Repeat Regions, HR1 and HR2, and Design of a Fusion Core Structure Model of the Spike Protein from Severe Acute Respiratory Syndrome (SARS) Coronavirus. *Biochemistry* 2004, 43, 44, 14064–14071.  
<https://pubs.acs.org/doi/pdf/10.1021/bi049101q>
  - ② Junichi Nishizawa. (2004). Target Molecule Manipulating Device And Target Molecule Manipulating Method. Patent Application No. 2004-154603 (J-PlatPat).  
<https://www.j-platpat.inpit.go.jp/c1800/PU/JP-2004-154603/169055F155461115F7E14D5393C14042E0D1A0091DE7B4AB36E0C23DD879F2EF/10/en>
  - ③ Yiwen Hu, Markus J. Buehler. (2020). Comparative Analysis of Nanomechanical Features of Coronavirus Spike Proteins and Correlation with Lethality and Infection Rate. *Matter* 4, 265–275.  
<http://dx.doi.org/10.1016/j.matt.2020.10.032>
  - ④ Shuai Xia, Meiqin Liu, Chao Wang, Wei Xu, Qiaoshuai Lan, Siliang Feng, Feifei Qi, Linlin Bao, Lanying Du, Shuwen Liu, Chuan Qin, Fei Sun, Zhengli Shi, Yun Zhu, Shibo Jiang & Lu Lu, (2020), Inhibition of SARS-CoV-2 (previously 2019-nCoV) infection by a highly potent pan-coronavirus fusion inhibitor targeting its spike protein that harbors a high capacity to mediate membrane fusion, *Cell Research* volume 30, pages343–355(2020).  
<https://www.nature.com/articles/s41422-020-0305-x>
  - ⑤ Takaharu Mori, Jaewoon Jung, Chigusa Kobayashi, Hisham M. Dokainish, Suyong Re, Yuji Sugita. (2021). Elucidation of interactions regulating conformational stability and dynamics of SARS-CoV-2 S-protein. *Biophysical Journal* VOLUME 120, ISSUE 6, P1060-1071.  
<https://doi.org/10.1016/j.bpj.2021.01.012>
- Fig. 1 • DECTRIS. Science in the time of corona.  
<https://www.dectris.com/landing-pages/science-in-the-time-of-corona>
- Fig. 2 • Marc G Airhart. (2020). Breakthrough in Coronavirus Research Results in New Map to Support Vaccine Design. The University of Texas.  
<https://cns.utexas.edu/news/breakthrough-in-coronavirus-research-results-in-new-map-to-support-vaccine-design>
- Fig. 3 • Hyeonuk Woo, Sang-Jun Park, Yeol Kyo Choi, Taeyong Park, Maham Tanveer, Yiwei Cao, Nathan R. Kern, Jumin Lee, Min Sun Yeom, Tristan I. Croll, Chaok Seok, Wonpil Im. (2020). Developing a Fully-glycosylated Full-length SARS-CoV-2 Spike Protein Model in a Viral Membrane. *J. Phys. Chem. B* 2020, 124, 33, 7128–7137.  
<https://doi.org/10.1021/acs.jpcc.0c04553>