

Development and application of a web-based integrated platform D3CARP for target prediction and virtual screening

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1. Introduction

2. New Methods for Protein Conformation Sampling

3. D3CARP for Target Prediction and Virtual Screening

4. Applications

Approaches for Target Prediction and Virtual Screening

Structure-Based:

Predicts how an active compound binds to a target protein. Software such as AutoDock, Glide, or DOCK simulates the binding interactions and ranks the predicted targets or screened compounds based on their docking scores.

Similarity-based:

A computational approach used to identify potential drug candidates by comparing their chemical similarity to known active compounds. This method relies on the principle that molecules with similar structures or properties are likely to exhibit similar biological activities.

Machine/Deep Learning Based:

Algorithms such as Support Vector Machines (SVMs), Neural Networks and Deep Learning can predict drug targets based on various features, including sequence data and biological interactions.

Questions

- **Should different conformations be considered for docking?**

Yes, but not included in most approaches (DFG-in vs DFG-out)

- **Should different binding sites be considered for docking?**

Yes, for example, allosteric sites

- **Is a platform with different approaches useful?**

Yes, for validation to increase reliability of the predictions

- **Is positive controls important for assessing results?**

Yes, same score but different activity (1nM vs 1mM)

1. Introduction

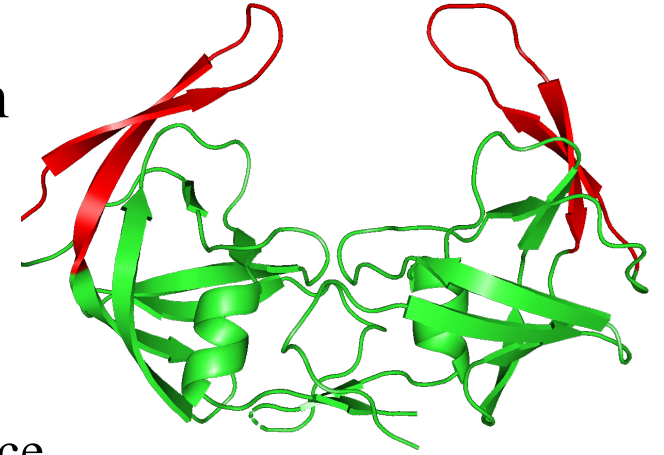
2. New Methods for Protein Conformation Sampling

3. D3CARP for Target Prediction and Virtual Screening

4. Applications

Protein conformation sampling is a challenge

- Protein adopts multiple conformations
- Conformation change is closely related to its biological function
- It is difficult to study the transition pathway experimentally
- Various simulation methods have been developed



Targeted MD

The free energy calculation is biased force dependent and its connection to function is unclear

Accelerated MD

REMD

The free energy calculation is time-consuming and computationally expensive

Metadynamics

Coarse Grained Method

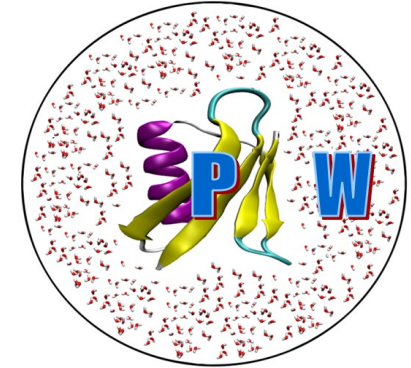
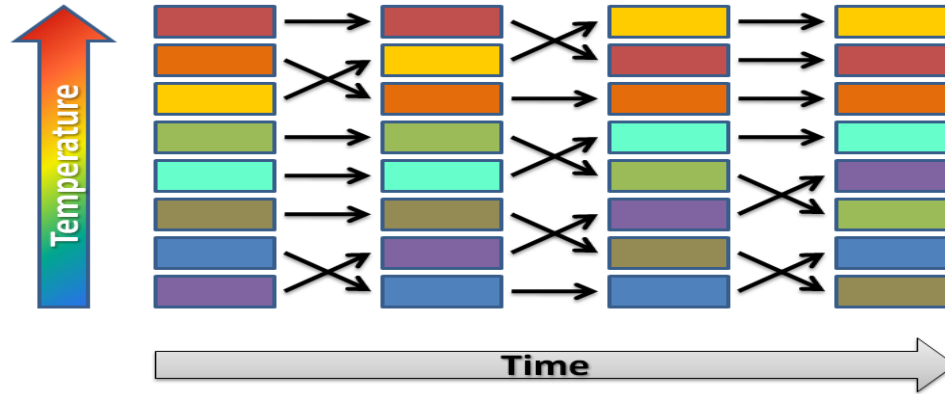
Can predict the transition pathway but can not provide the free energy information

Replica exchange molecular dynamics (REMD)

- **REMD is one of the well recognized MD methods for conformation sampling;**
- **It requires large computational resources**
 - Protein (214 aa) --- **80 replicas** --- 21.5 k RMB (3 k US\$)
 - Protein (856 aa) --- **~ 450 replicas** --- 3 m RMB (400 K US\$)

Therefore, highly efficient MD simulation methods are expected.

Conventional REMD



Replica (N_{replica}) required for REMD: $N_{\text{replica}} \propto \sqrt{n_{\text{freedom}}}$

Exchange criteria:

$$\omega(1 \leftrightarrow 2) = \min(1, \exp(\Delta\beta\Delta P))$$

System potential energy

$$P = P_{pp} + P_{pw} + P_{ww}$$

1. Improved REMD method: vsREMD

- The solvent atoms are not considered during replica exchange, the new exchange criteria could be

$$\omega(1 \leftrightarrow 2) = \min \left(1, \exp \left(\Delta\beta \Delta(P_{pp} + P_{pw}) \right) \right)$$

$$P = \boxed{(P_{pp} + P_{pw})} + P_{ww}$$

Exchange reference ← Velocity Scaling

Difference:

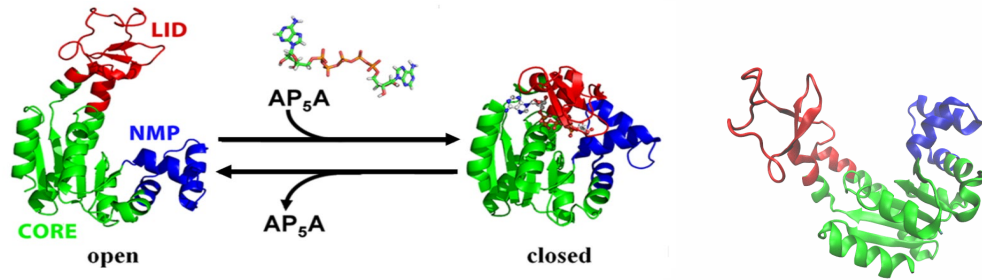
$$H = P_{ww}$$

- Velocity scaling (vsREMD):

$$\hat{v}^{(1 \rightarrow 2)} = v^{(2)} \sqrt{\frac{\hat{E}_{kin}^{(1)}}{E_{kin}^{(2)}}} = v^{(2)} \sqrt{\frac{E_{kin}^{(1)} - \Delta H}{E_{kin}^{(2)}}}$$
$$\hat{v}^{(2 \rightarrow 1)} = v^{(1)} \sqrt{\frac{\hat{E}_{kin}^{(2)}}{E_{kin}^{(1)}}} = v^{(1)} \sqrt{\frac{E_{kin}^{(2)} + \Delta H}{E_{kin}^{(1)}}}$$

Velocity Scaling REMD (vsREMD, developed based on GROMACS)

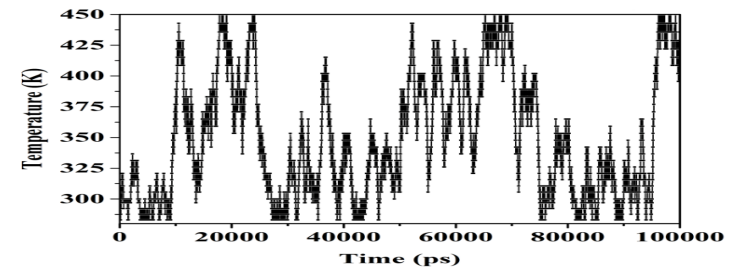
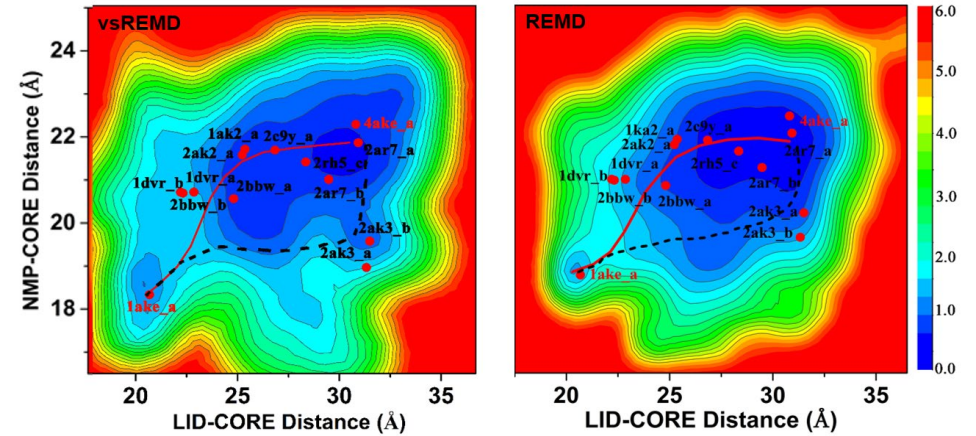
Testing vsREMD on Adenylate Kinase (AdK),



Two X-Ray ADK conformations: open (4AKE), closed (1AKE)

38% replica of REMD required for vsREMD

	副本	温度 (K)											
vsREMD	30	300.0	304.2	308.5	312.8	317.2	321.7	326.2	330.8	335.5	340.2	345.0	349.9
		354.8	359.8	364.9	370.0	375.2	380.5	385.8	391.3	396.8	402.4	408.0	413.8
		419.6	425.5	431.5	437.6	443.8	450.0						
REMD	80	300.0	301.5	303.1	304.6	306.2	307.8	309.4	311.0	312.6	314.2	315.8	317.4
		319.1	320.7	322.4	324.0	325.7	327.4	329.0	330.7	332.4	334.1	335.9	337.6
		339.3	341.1	342.8	344.6	346.4	348.2	349.9	351.7	353.6	355.4	357.2	359.0
		360.9	362.7	364.6	366.5	368.4	370.3	372.2	374.1	376.0	377.9	379.9	381.8
		383.8	385.8	387.7	389.9	391.8	393.8	395.8	397.8	399.9	402.0	404.0	406.1
		408.2	410.3	412.4	414.5	416.7	418.8	421.0	423.1	425.3	427.5	429.7	431.9
		434.1	436.4	438.6	440.9	443.1	445.4	447.7	450.0				



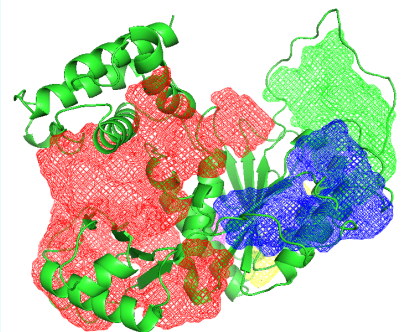
- Similar transition pathways and free energy landscapes are obtained by vsREMD and REMD;
- All the crystal structures are sampled in the area with low free energies.

Biophys J, 2020, **118**, 1009-1018.

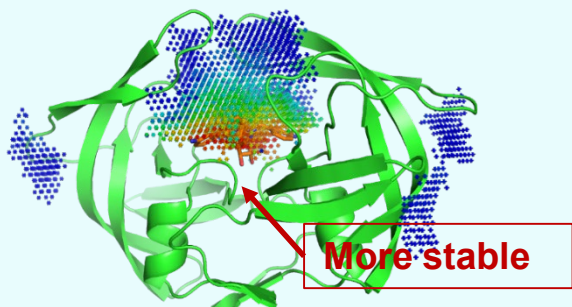
Challenge: it is hard to simulate the transition from DFG-in to DFG-out of kinase.

2. Quantitative Analysis Method for Pocket Dynamics Behavior: D3Pockets

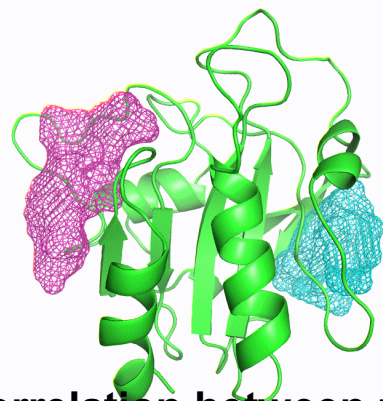
D3Pockets for quantitatively analyzing dynamic behavior



Drug binding pockets are constantly dynamic.

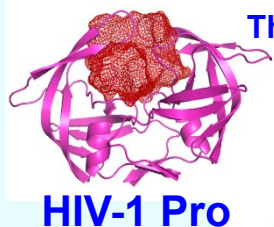


unstable → stable
Pocket Stability



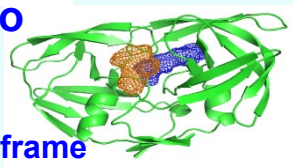
Correlation between pockets
Allosteric site?

The first frame

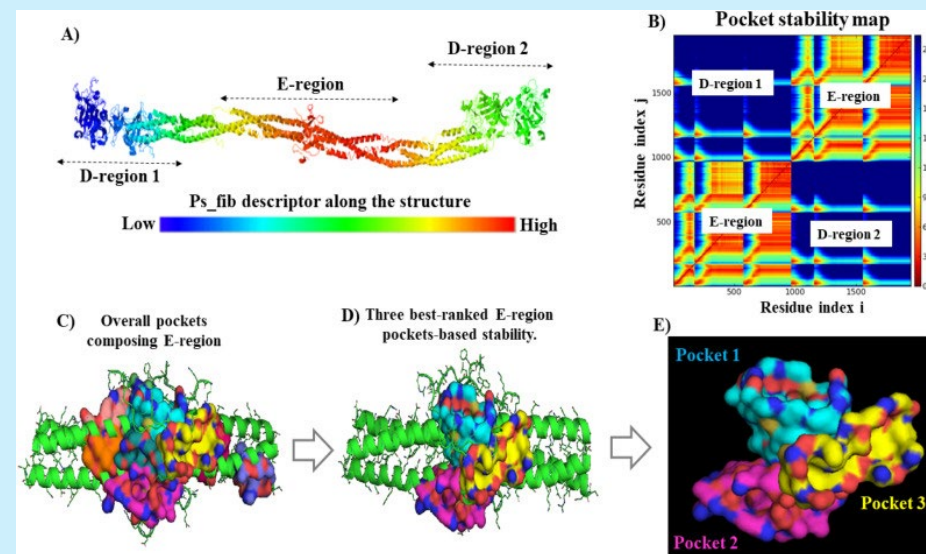


HIV-1 Pro

The 4305th frame



Pocket Continuity



Professor Rusoa *et. al* at the University of Santiago de Compostela in Spain used D3Pockets to compute the dynamic properties of pockets within the fibrinogen protein, which was employed to assess the biochemical correlations between significant regions of the protein. (*Journal of Molecular Liquids* 2021, 324)

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3. D3CARP: A Comprehensive Platform for Target Prediction and Virtual Screening

Target Structure Database Construction

PDBbind Database(v2020)



J Med Chem,
2005, 48: 4111-9.

■ Molecular Docking Software

AutoDock Vina (v1.2.0)

■ Pre-docking

- Docking score < -5 kcal/mol
- RMSD < 2 Å
- **9352 3D conformations of 1970 proteins with active ligands**

■ Output Results

- Docking scores, atomic efficiency, 2D/3D similarities, score ratio, disease information
- Positive control compounds and literature sources

Ligand Database Construction

BindingDB Database(2021.11.1)



Nucleic Acids Res,
2016, 44: D1045-53.

■ Ligand Database

- **1.01 million active compounds, 7362 targets associated with 2168 disease types**
- **2.19 million drug-target pairs**

■ Standard Dataset ($K_i/K_d/IC_{50}/EC_{50} < 10 \mu M$)

- 0.79 million ligands, 5901 targets
- 1.20 million drug-target pairs

■ Normalized Dataset ($K_i < 1 M$)

- 0.19 million ligands, 2568 targets
- 0.34 million drug-target pairs

- Standardized inhibition constant nK_i :
$$nK_i = \frac{lgK_i}{lgK_{i_{max}}}$$
- Inhibition constant K_i :
$$K_i = 10^{nK_i \times lgK_{i_{max}}}$$

Disease Database Construction

Therapeutic target database

Gene Name	EGFR
Target Type	Successful target
Disease	[+] 9 Target-related Diseases
1	Angina pectoris [ICD-11: BA40]
2	Breast cancer [ICD-11: 2C60-2C6Y]
3	Colorectal cancer [ICD-11: 2B91]
4	Diabetic foot ulcer [ICD-11: BD54]
5	Ischemia [ICD-11: 8B10-8B11]
6	Lung cancer [ICD-11: 2C25]
7	Renal cell carcinoma [ICD-11: 2C90]
8	Solid tumour/cancer [ICD-11: 2A00-2F9Z]
9	Unspecific body region injury [ICD-11: ND56]

Ref: *Nucleic Acids Res*, 2020, 48: D1031-D1041.

UniProtKB

Disease & Variants ¹	
Involvement in disease ¹	
Lung cancer (LNCR)	
3 Publications	
Note	The gene represented in this entry is involved in disease pathogenesis
Description	A common malignancy affecting tissues of the lung. The most common form of major histologic subtypes: squamous cell carcinoma, adenocarcinoma, and large cell carcinoma.
See also	MIM:211980 E
Inflammatory skin and bowel disease, neonatal, 2 (NISBD2)	
1 Publication	
Note	The disease is caused by variants affecting the gene represented in this entry
Description	A disorder characterized by inflammatory features with neonatal onset, involving erythema, psoriasiform erythroderma, with flares of erythema, scaling, and watery diarrhea that is exacerbated by intercurrent gastrointestinal infections. The disorder is autosomal recessive.

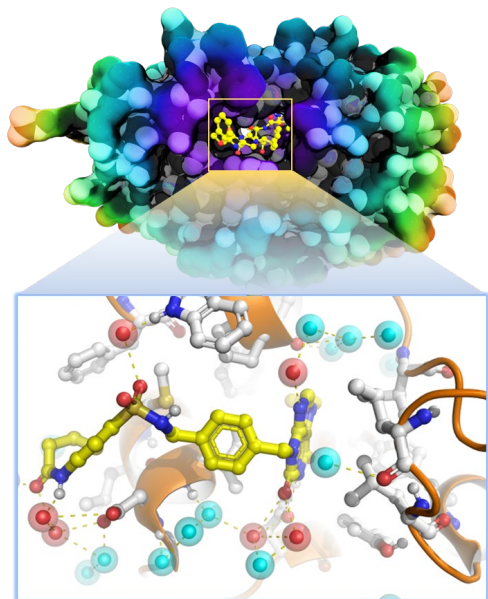
Ref: *Nucleic Acids Res*, 2021, 49: D480-D489.

3. D3CARP: A Comprehensive Platform for Target Prediction and Virtual Screening

Docking-Based

(Multi-conformation and binding sites)

9352 docking models for 1970 proteins

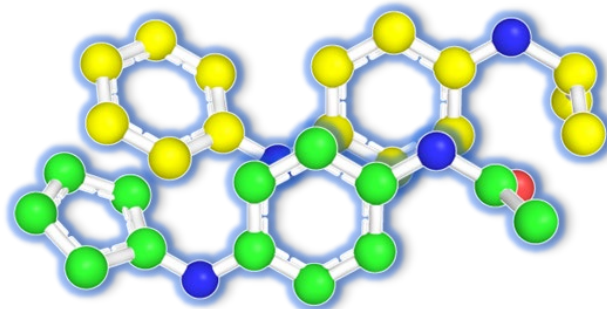


- **Molecular Docking Software**
AutoDock Vina (v1.2.0)
- **Format Conversion**
MGLTools program
- **Grid Box**
Ligand-based extension 5 Å

Ligand-Based

(Similarity search)

2.19 million drug-target pairs



2D Similarity

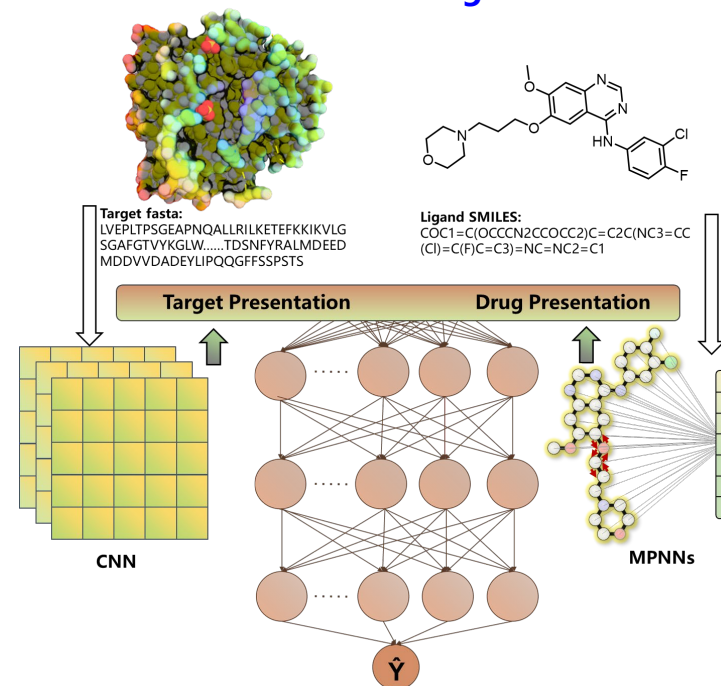
- Software: Open Babel
- Molecular fingerprint: FP2, FP4, MACCS

3D Similarity

- Conformation generation: RDKit
- Software: LS-align
 - Rigid-LS-align
 - Flexi-LS-align

Deep Learning Based

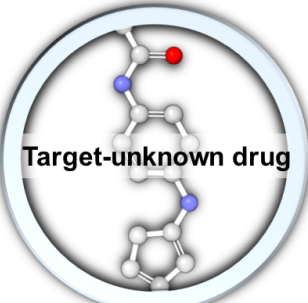
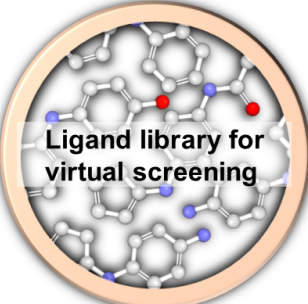
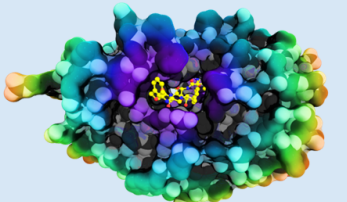



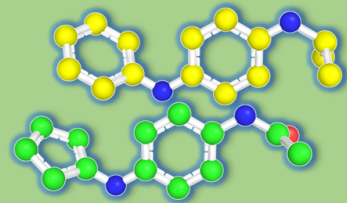
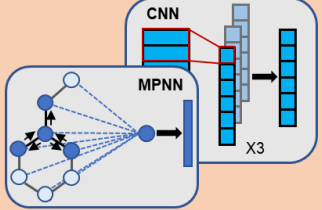
Classification and regression models



- Compound: MPNN
- Target protein: CNN
- Classification model: MPNN-CNN
- Regression model: MPNN-CNN-R
- Partition Dataset partition: 98:1:1

3. D3CARP: A Comprehensive Platform for Target Prediction and Virtual Screening

Input and Output

INPUT	METHOD	OUTPUT	
		Target Prediction	Virtual Screening
 <p>Target-unknown drug</p> <p>or</p>  <p>Ligand library for virtual screening</p> <p>Ligand Format: mol2, mol, sdf, or smi</p>	 <p>Molecular Docking</p>	<ul style="list-style-type: none"> ■ Target Name ■ Docking Score ■ Atom Efficiency ■ Ratio Value ■ 2D and 3D Similarity ■ Docking Score (positive control) ■ Atom Efficiency (positive control) ■ Potency(positive control) ■ Diseases 	 <p>Predicted DTIs</p>   <p>Screened hits</p>
	 <p>Ligand Similarity Search</p>	<ul style="list-style-type: none"> ■ Similar Ligand ■ Similarity ■ Target Name ■ K_i (nM) ■ IC_{50} (nM) ■ K_d (nM) ■ EC_{50} (nM) ■ Literature ■ Diseases 	
	 <p>Deep Learning</p>	<ul style="list-style-type: none"> ■ Target Name ■ Binding possibility ■ Binding strength ■ Predicted K_i (nM) ■ Strongest Ligand Potency (nM) ■ Diseases 	

Platform Features

- **Multiple Drug Design Approaches**
Docking, ligand similarity and DL
- **Ensemble Docking**
Multi-target conformations, 9000+
- **Positive Controls as References**
for 7000+ targets
- **Diverse Disease Types**
Conduct computational research on specific disease targets (2000+ disease)
- **Cross-Validation of Prediction Results**
- **Wide Range of Application Scenarios**
Target prediction, virtual screening, drug-target interaction mechanism, molecular scaffold novelty assessment, etc.

Free Application Website D3CARP: <https://www.d3pharma.com/D3CARP/index.php>

D3CARP-similar platform for COVID-19

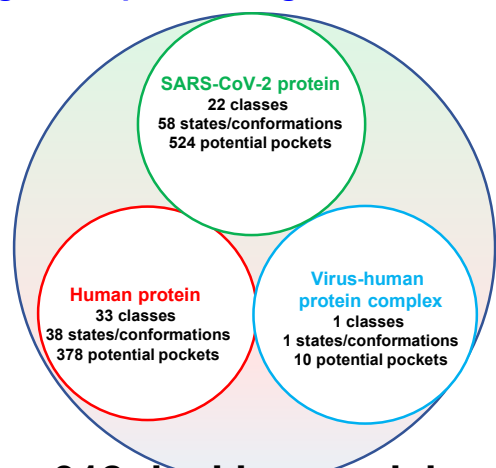
4. D3Targets: a Multi-Target and Multi-Conformation based Docking Platform for COVID-19



Research background

Challenges:

- Unclear Targets for many reported "effective drugs"
- Urgent Need for New Drug Development Against Specific Targets



912 docking models for 56 proteins

Functions:

- Prediction of the target for active compounds
- Multi-target, multi-conformation, multi-site-Based Drug Virtual Screening

Online server

<https://www.d3pharma.com/D3Targets-2019-nCoV/D3Docking/index.php>

Usage

Currently, there are 0 waiting jobs in queue... It takes 2-3 hours in average for a job.

Step 1. To set job title
Job Title:

Step 2. To upload ligand file (.sdf or .mol2)
Molecule File:
Sample File 1
File: The three-dimensional molecular structure file(sdf file or mol2 file).

Upload the ligand file

Score: **Output docking scores, rankings, and pocket locations for each protein**

Rank	Target Full Name	State	Score	ProteinID	Pocket	Organ
1	RNA-dependent RNA polymerase	+RNA & +Mg	-12.95	QHD43415.1	Pocket1	SARS-CoV-2
2	Eukaryotic initiation factor 4A-I		-11.88	P60842	Pocket2	human
3	Dihydroorotate dehydrogenase		-11.54	Q02127	Pocket1	human
4	ORF1ab polyprotein 4393-5324 RNA-dependent RNA polymerase	+Mg	-11.37	QHD43415.1	Pocket1	SARS-CoV-2
5	cGMP-specific 3',5'-cyclic phosphodiesterase		-10.35	O76074	Pocket1	human PDB 9
6	Spike protein	Open	-10.28	QHD43416.1	Pocket8	SARS-CoV-2 PDB 1
7	ADP ribose phosphatase	Dimer	-10.15	QHD43415.1	Pocket2	SARS-CoV-2 PDB 2
8	ADP ribose phosphatase	Monomer	-10.1	QHD43415.1	Pocket1	SARS-CoV-2 PDB 2



ORIGINAL ARTICLE

D3Targets-2019-nCoV: a webserver for predicting drug targets and for multi-target and multi-site based virtual screening against COVID-19

Yulong Shi^{1,2,3,4}, Xinben Zhang^{1,2}, Kaijie Mu^{1,2,3,4}, Cheng Peng^{1,2,3,4}, Zhengdan Zhu^{1,2,3,4}, Xiaoyu Wang^{1,2}, Yanqing Yang^{1,2}, Zhijian Xu^{1,2,3,4}, Weiliang Zhu^{1,2,3,4}

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³Nano Science and Technology Institute, University of Science and Technology of China, Sichou 215123, China

Received 1 March 2020; received in revised form 23 March 2020; accepted 25 March 2020

KEY WORDS

COVID-19; SARS-CoV-2; Target prediction; Multi-conformation; Multi-site; Docking; D3Targets-2019-nCoV

Abstract: A highly effective medicine is urgently required to cure coronavirus disease 2019 (COVID-19). For the purpose, we developed a molecular docking based webserver, namely D3Targets-2019-nCoV, with two functions, one is for predicting drug targets for drugs or active compounds observed from clinic or in vitro/in vivo studies, the other is for identifying lead compounds against potential drug targets via docking. This server has its unique features, (1) the potential target proteins and their different conformations involving in the whole process from virus infection to replication and release were included as many as possible; (2) all the potential ligand-binding sites with volume larger than 200 Å³ on a protein structure were identified for docking; (3) correlation information among some conformations or binding sites was annotated; (4) it is easy to be updated, and is accessible freely to public (<https://www.d3pharma.com/D3Targets-2019-nCoV/index.php>). Currently, the webserver contains 42 proteins [20 severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) encoded proteins and 22 human proteins involved in virus infection, replication and release] with 69 different conformations/structures and 557 potential ligand-binding pockets in total. With 6 examples, we demonstrated that the webserver

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[†]These authors made equal contributions to this work.

Peer review under the responsibility of Chinese Pharmaceutical Association and Institute of Materia Medica, Chinese Academy of Medical Sciences.

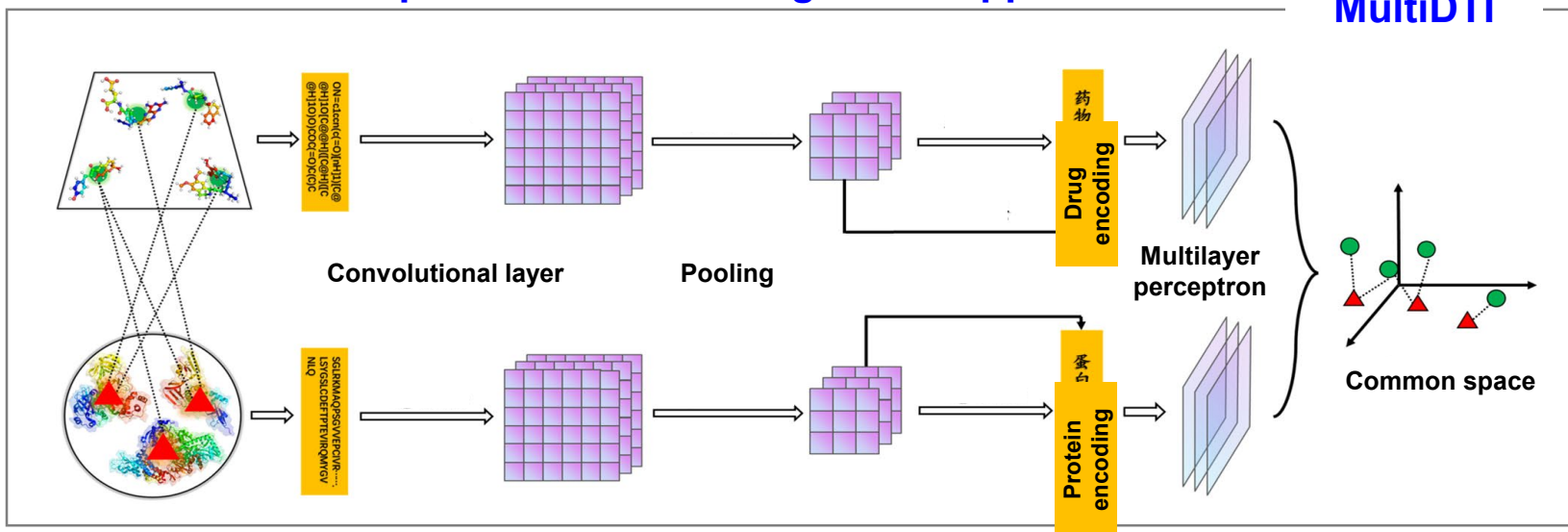


The article was recognized as the high-impact outstanding paper of APSB 2020.

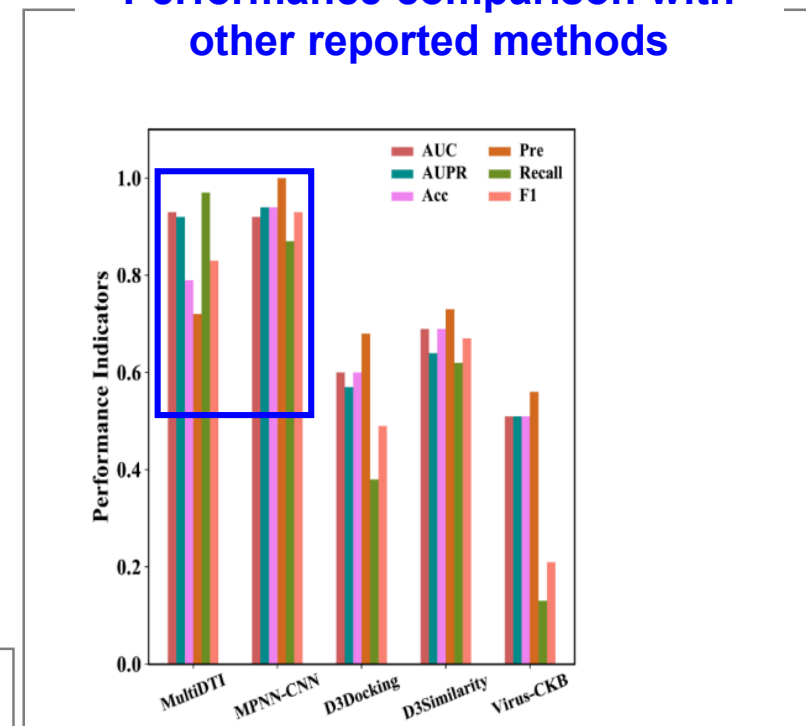
Acta Pharm Sin B, 2020, IF: 11.4

5. D3AI-CoV: An AI-Based Platform for COVID-19 Target Prediction and Virtual Screening

Multi-modal representation learning based approach

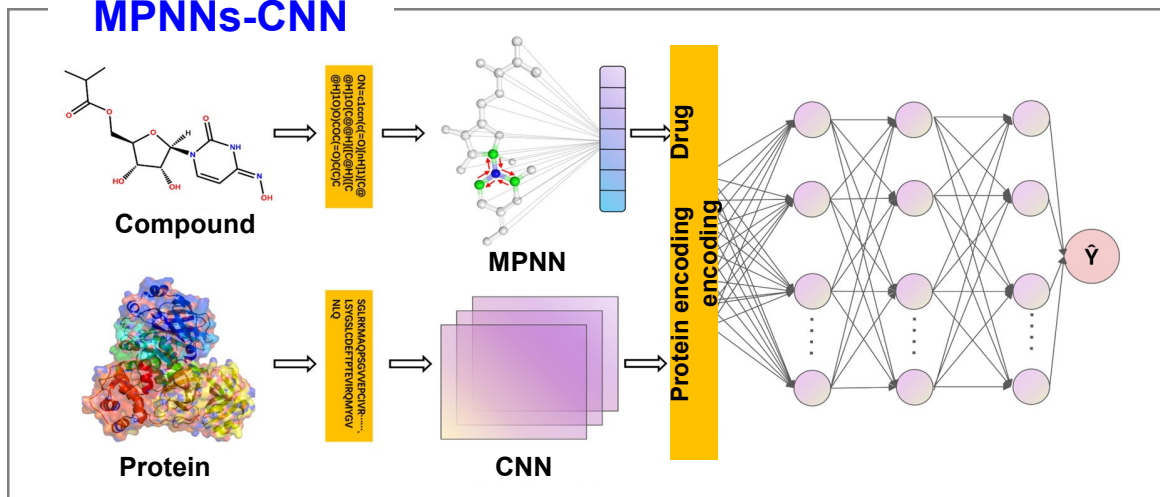


Performance comparison with other reported methods



Message Passing Neural Network/Convolutional Neural Network/Regression

MPNNs-CNN



MPNNs-CNN-R

- Normalization of Activity Data.
 $score = 2 - \lg(activity)$
- MPNNs-CNN-R was used to explore the relationship between molecular targets and activity.

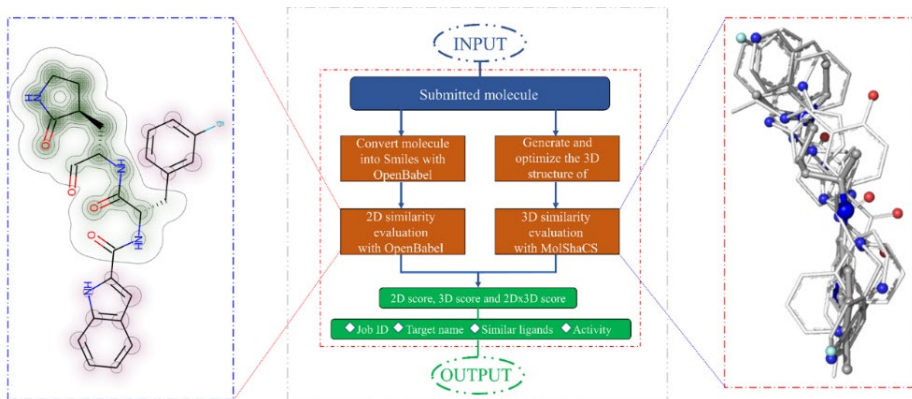
- The First Web Application Platform Applying Deep Learning Models for COVID-19 Target Prediction.
- The First AI-based Regression Model for COVID-19 Virtual Screening.

6. D3Similarity: Target Prediction and Virtual Screening Method Based on Ligand Similarity

Database Construction (in 178 Research Papers)

- 7 Pathogenic Coronaviruses
- 32 Target Proteins
- 604 Active Compounds

Similarity Comparison and Search (Open Babel, RDKit, MolShaCS)

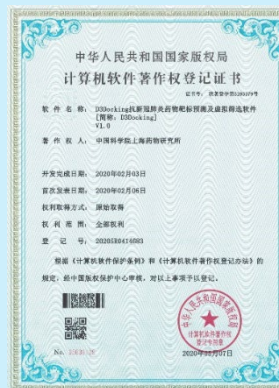


Briefings in Bioinformatics, 2021, IF=11.622

Online server

<http://www.d3pharma.com/D3Targets-2019-nCoV/D3Similarity/index.php>

D3Targets-2019-nCoV Global Visitor Distribution



- **>3 Million Pageviews, from Over 60 Countries and Regions Worldwide.**
- **The peak task queue reached 355.**
- **D3Docking was used to study the affinity of bioactive compounds in the Huoshiluo formula with SARS-CoV-2-related proteins by Chen et..**
(*Ann Palliat Med*, 2021)
- **Researchers from Peking University utilized D3Similarity to evaluate the novelty of their newly discovered main protease inhibitors.**
(*Brief. in Bioinf.*, 2021)

1. Introduction

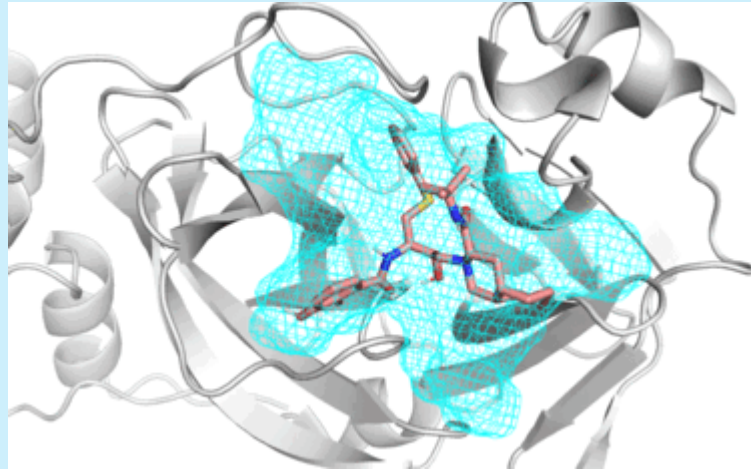
2. New Methods for Protein Conformation Sampling

3. D3CARP for Target Prediction and Virtual Screening

4. Applications

7. Repurposing nelfinavir as a drug against SARS-CoV-2

Nelfinavir was predicted to be 3CL^{pro} inhibitor



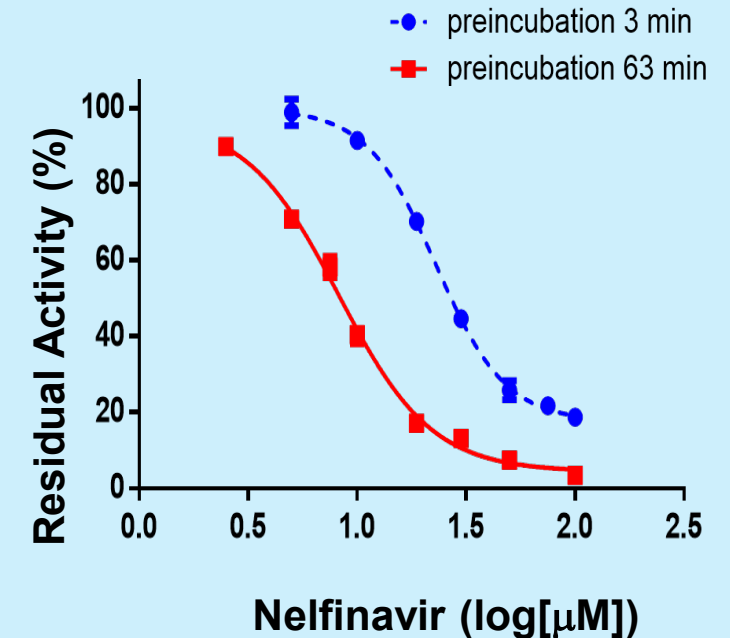
Molecular dynamics simulation

Sequence with 98% similarity to SARS-CoV-1

	nelfinavir	Pitavastatin	Perampanel	praziquantel
Docking Score	-9.18	-8.06	-8.63	-7.38
3D Similarity	70.2%	68.1%	66.9%	65.8%
$\Delta G(\text{MM/GBSA})^*$	-24.69 ± 0.52	-12.70 ± 0.38	-14.98 ± 0.34	-6.51 ± 0.21
$\Delta G(\text{SIE method})^*$	-9.42 ± 0.04	-7.53 ± 0.04	-7.55 ± 0.03	-6.39 ± 0.04

Nelfinavir was predicted to be a potential inhibitor of 2019-nCov main protease by an integrative approach combining homology modelling, molecular docking and binding free energy calculation *bioRxiv* 2020. 1. 27

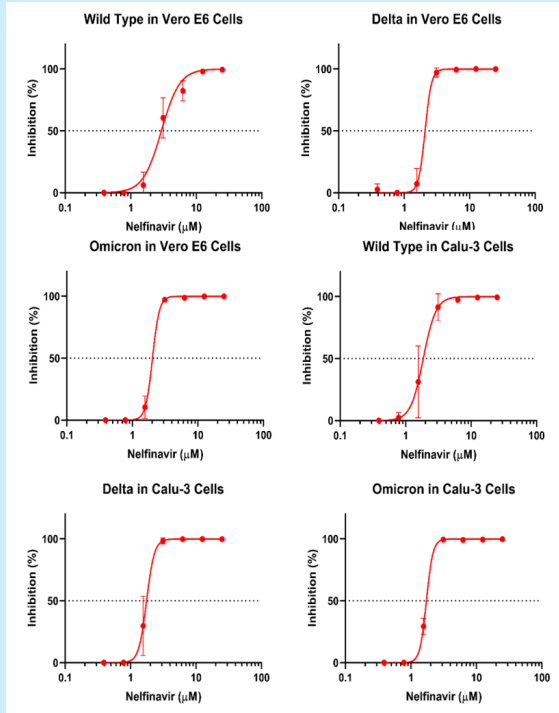
Activity at 3CL^{pro} level



IC₅₀ values of $23.04 \pm 1.02 \mu\text{M}$ (3-min incubation) and $8.26 \pm 1.04 \mu\text{M}$ (63-min incubation)

Repurposing nelfinavir as a drug against SARS-CoV-2

Bioassay at cellular level



In vitro inhibition of nelfinavir against wild type, Delta, Omicron SARS-CoV-2 in Vero E6 and Calu-3 cells.

ChemRxiv, 30 Mar 2020

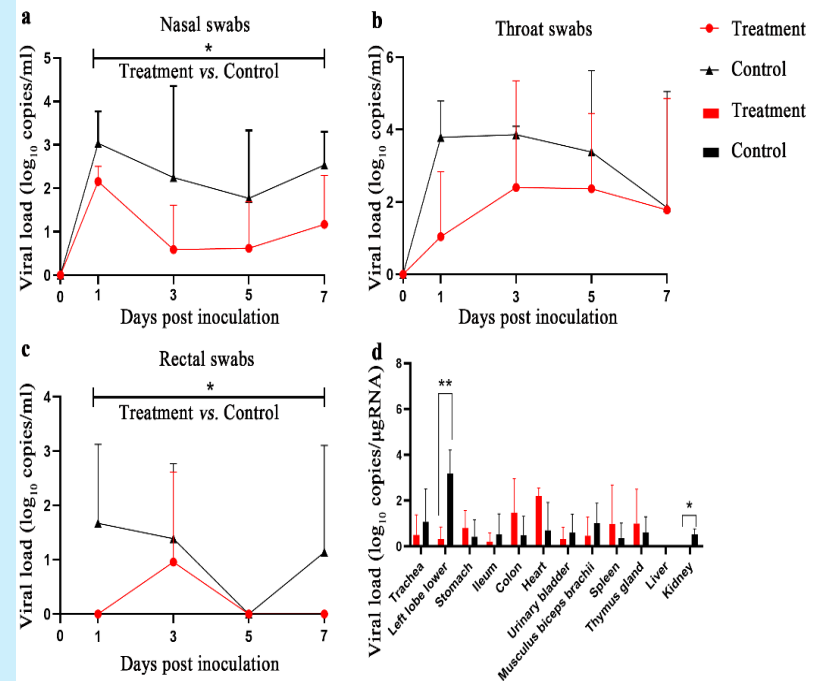
<https://doi.org/10.26434/chemrxiv.12039888.v1>

Inhibit SARS-CoV-2 in Vero E6

(EC₅₀=2.89 μM)

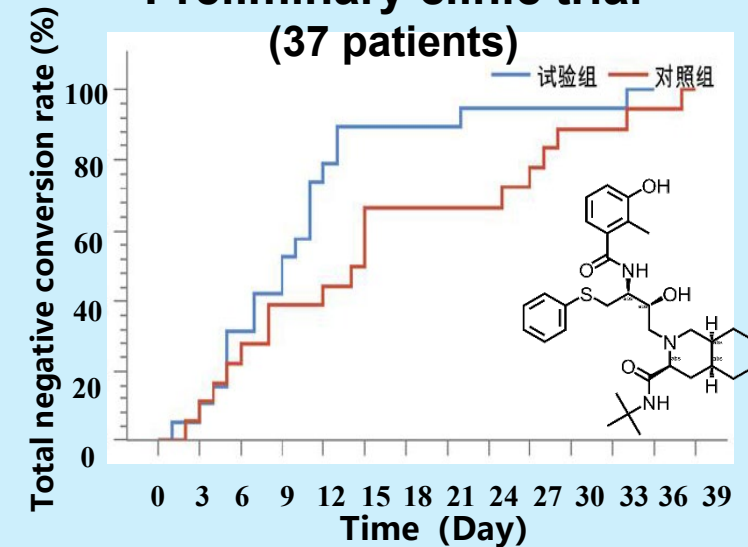
(Remdesivir: ~2 μM)

Preventive benefits in rhesus macaques



- Significantly reduced virus loads in the lungs and kidneys;
- Significantly reduced virus loads in the nasal and anal swabs;
- Virus shedding was not reduced by remdesivir. (ref.: *Nature* 2020, 585, 273)

Preliminary clinic trial (37 patients)



Shorten the duration of viral shedding by 5.5 days (9.0 vs. 14.5 days, $P = 0.055$) and the duration of fever time by 3.8 days (2.8 vs. 6.6 days, $P = 0.014$)

Signal Transduction and Targeted Therapy www.nature.com/sigtrans

ARTICLE OPEN

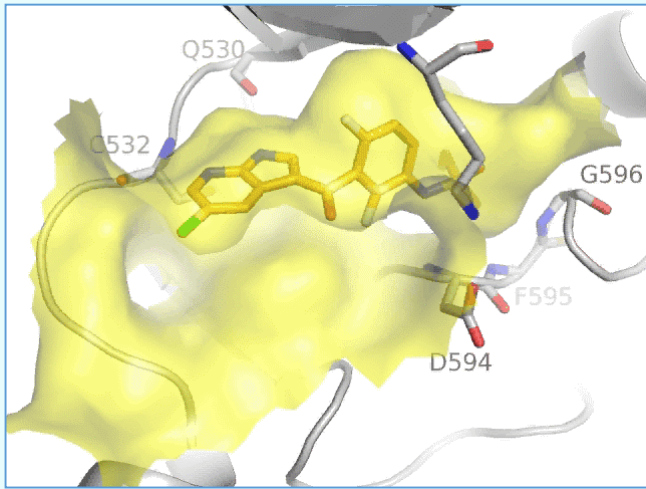
Preventive and therapeutic benefits of nelfinavir in rhesus macaques and human beings infected with SARS-CoV-2

Zhijian Xu^{1,2,3}, Danrong Shi⁴, Jian-Bao Han⁵, Yun Ling⁶, Xiangrui Jiang^{1,3}, Xiangyun Lu⁴, Chuan Li^{1,3}, Likun Gong^{1,3,7}, Guangbo Ge⁸, Yan Zhang^{1,3}, Yi Zang^{1,3}, Tian-Zhang Song^{9,9}, Xiao-Li Feng¹, Ren-Rong Tian^{1,9}, Jia Ji¹, Miaojin Zhu¹, Nanping Wu¹, Chunhui Wu^{1,3}, Zhen Wang^{1,3}, Yechun Xu^{1,2,3}, Cheng Peng^{1,2,3}, Min Zheng¹, Junling Yang^{1,2}, Feifei Du^{1,2}, Junliang Wu^{1,3,7}, Peipei Wang^{1,3}, Jingshan Shen^{1,3,10}, Jianliang Zhang^{6,10}, Yong-Tang Zheng^{6,9,10}, Hangping Yao^{6,10,10} and Weiliang Zhu^{2,3,10}

Effective drugs with broad spectrum safety profile to all people are highly expected to combat COVID-19 caused by SARS-CoV-2. Here we report that nelfinavir, an FDA approved drug for the treatment of HIV infection, is effective against SARS-CoV-2 and COVID-19. Preincubation of nelfinavir could inhibit the activity of the main protease of the SARS-CoV-2 (IC₅₀ = 826 μM), while its antiviral activity in Vero E6 cells against a clinical isolate of SARS-CoV-2 was determined to be 2.93 μM (EC₅₀). In comparison with vehicle-treated controls, nelfinavir treatment significantly reduced viral loads in nasal and rectal swabs, shortened the duration of viral replication in the lungs by nearly three orders of magnitude. A prospective clinical study with 37 enrolled treatment-naïve patients at Shanghai Public Health Clinical Center, which were randomized (1:1) to nelfinavir and control groups, showed that the nelfinavir treatment could shorten the duration of viral shedding by 5.5 days (9.0 vs. 14.5 days, $P = 0.055$) and the duration of fever

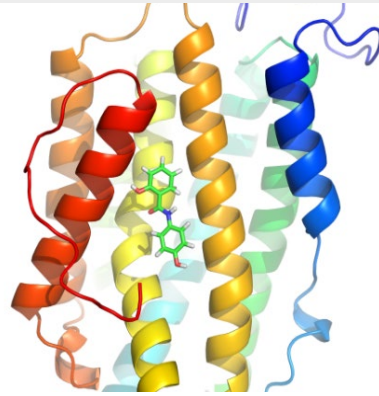
Signal Transduction Target Ther 2023

8. Repurposing Osalmide as a drug against multiple myeloma (MM)



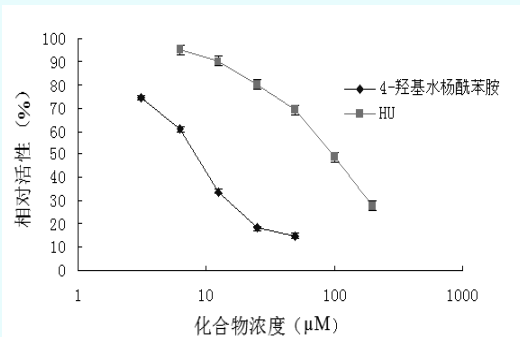
Molecular docking for ribonucleotide reductase RR

Osalmide for cholecystitis

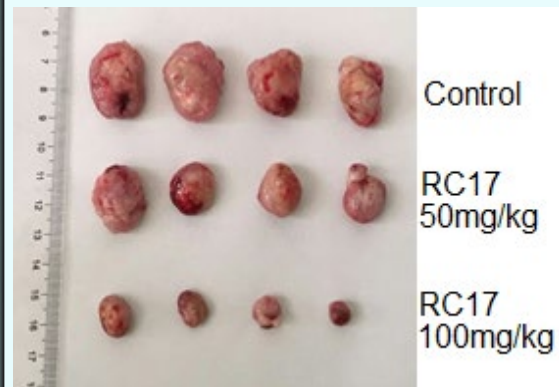


Docked structure of osalmide-RR complex

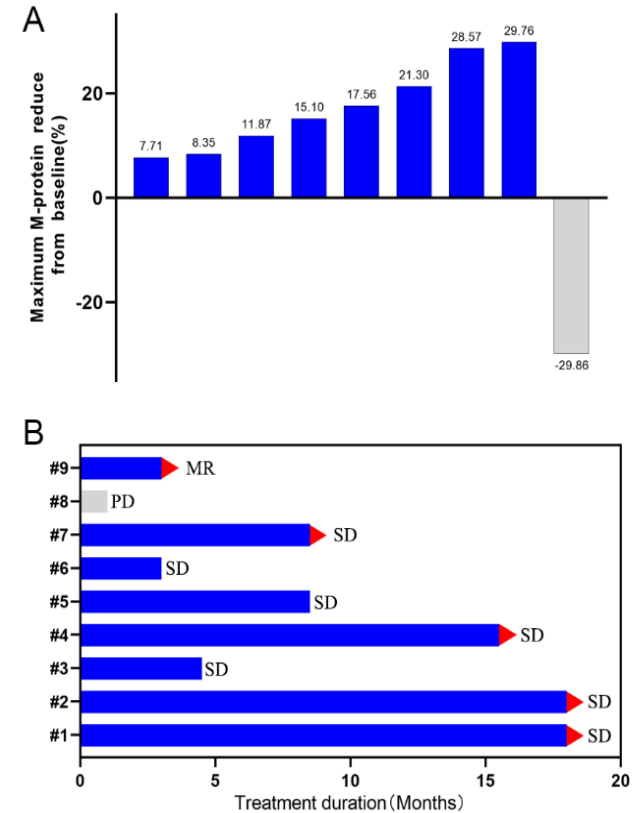
New application?



Much stronger than HU

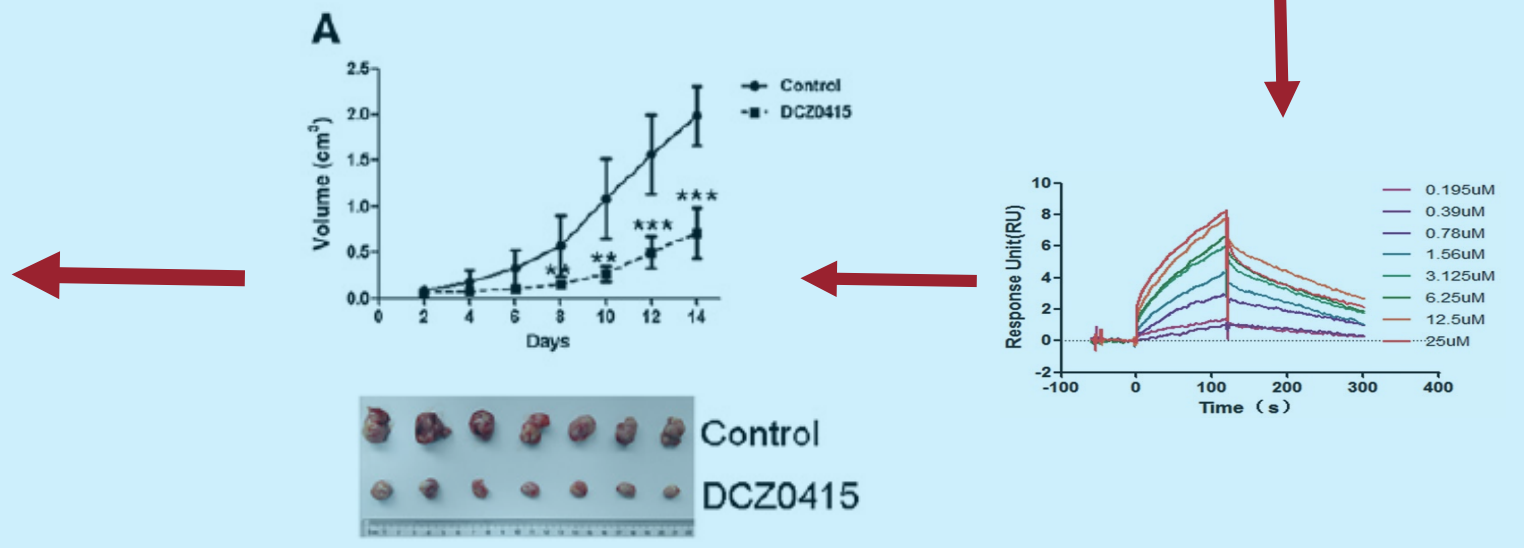
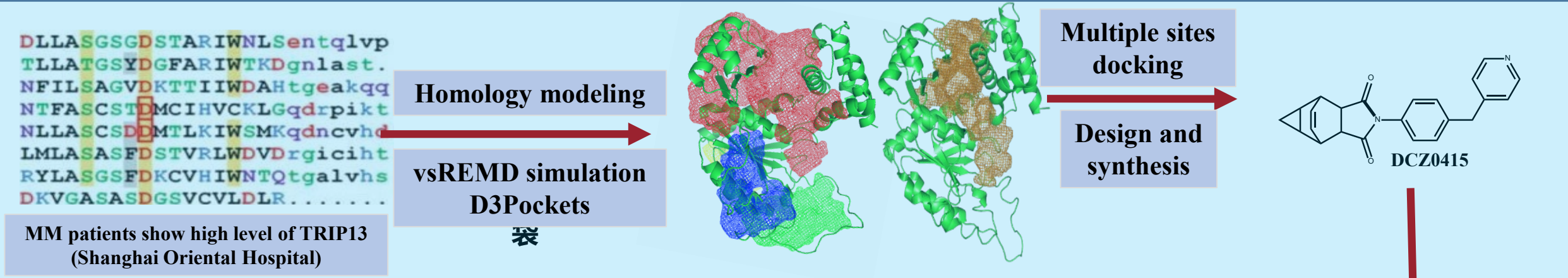


In vivo activity on mouse model



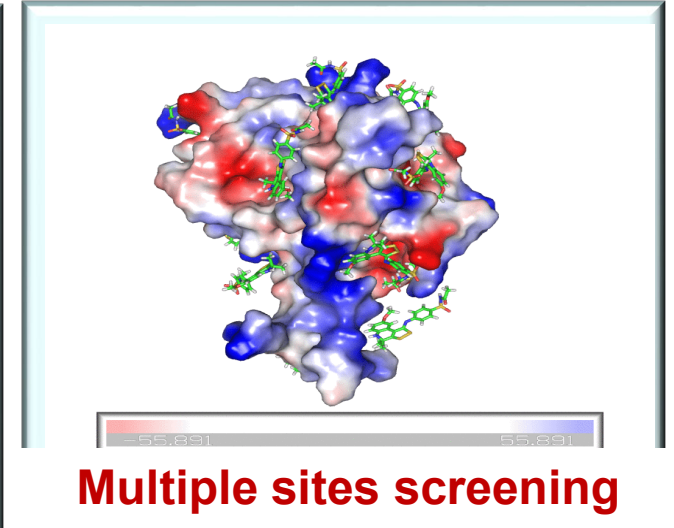
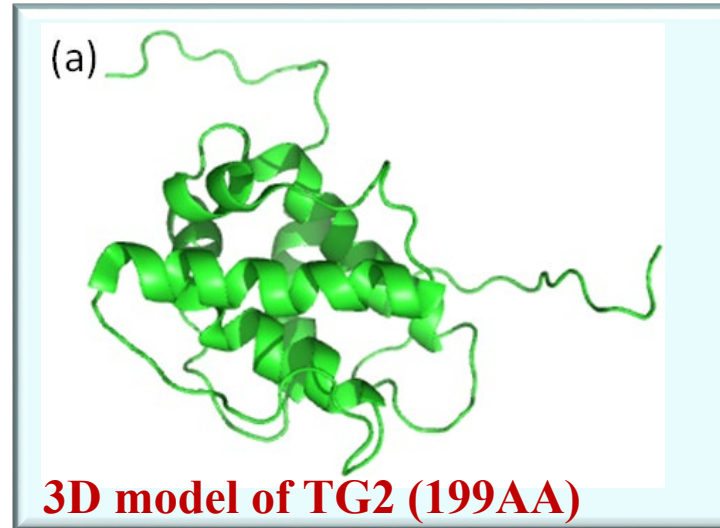
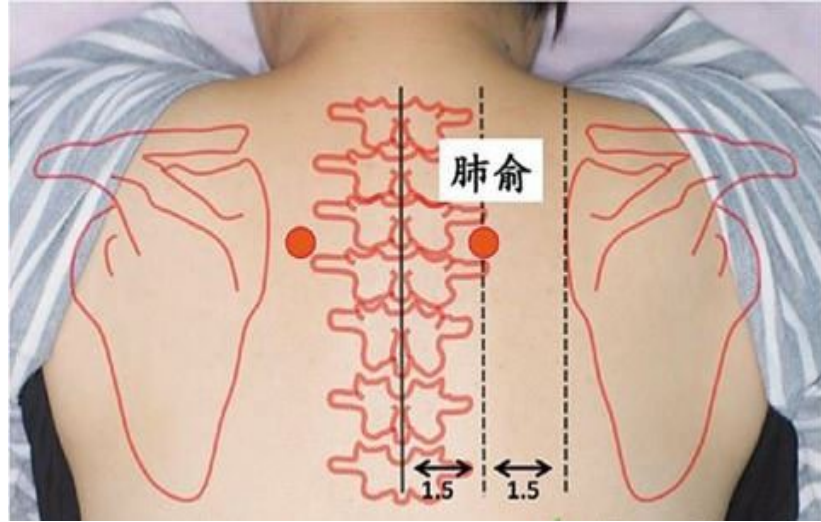
Clinic study of osalmide on MM (SD: stable disease)
 (A) The maximum change from baseline in the level of M-protein after HDS treatment. (B) Swim-lane plot show the treatment response and duration for 9 MM patients after HDS treatment. Arrows: still ongoing at the time of study closure. *J. Biomed. Sci.* **2022**, *29*, 32

9. The first inhibitor of TRIP13



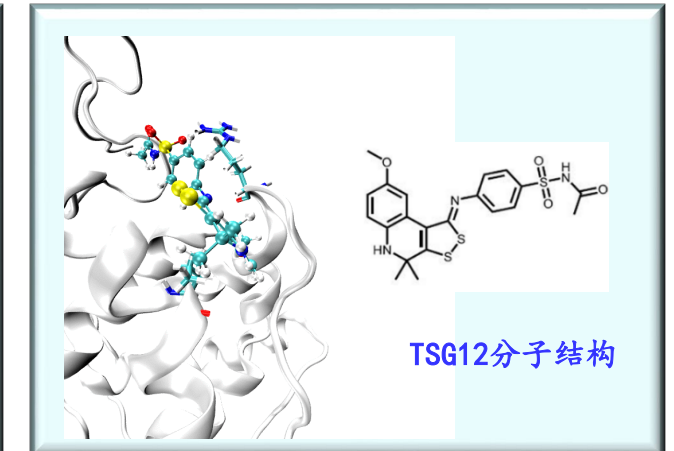
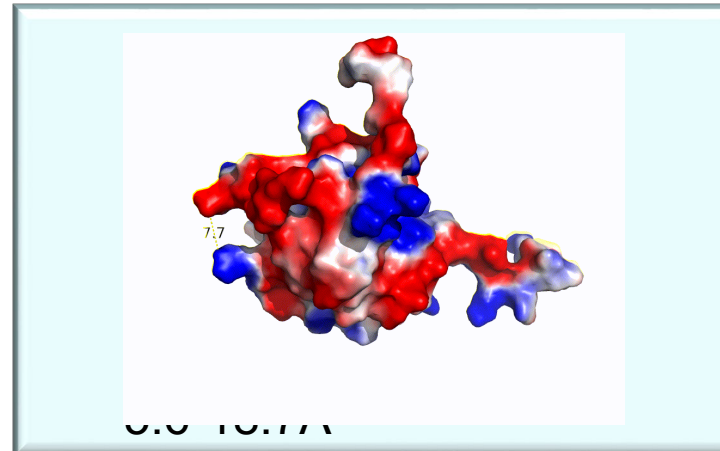
Cancer Res. 2020, 80(3), 536 (IF=9.7)

10. Discovering the first agonist of TG2

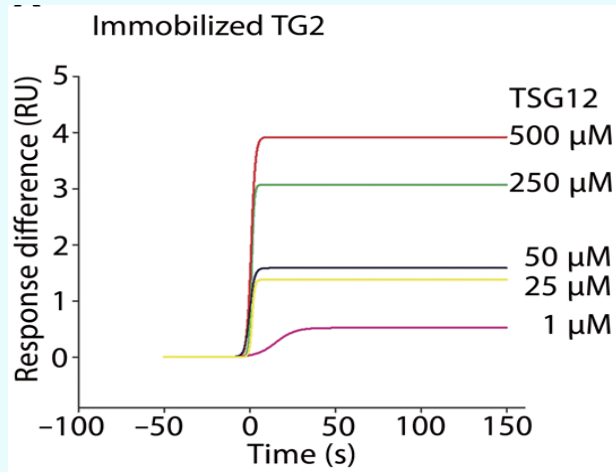


Asthma $\xrightarrow[\text{Collaborator}]{\text{Acupuncture}}$ TG2 pathway activated

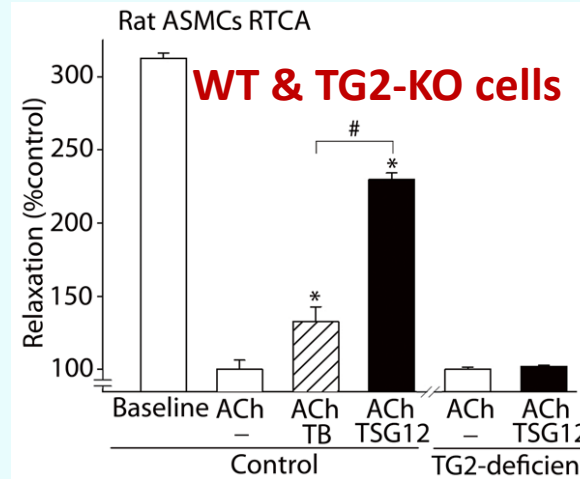
TG2 agonist as anti-asthma drugs?



10. Discovering the first agonist of TG2

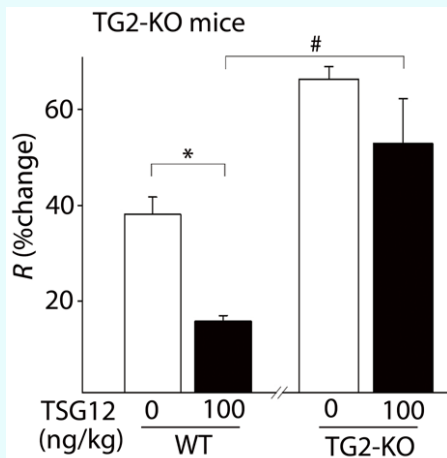


TG2-TSG12 binding (Biacore)

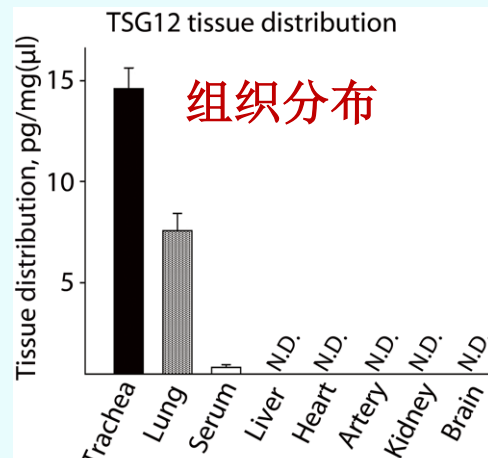


At airway smooth muscle cell (ASMC) level

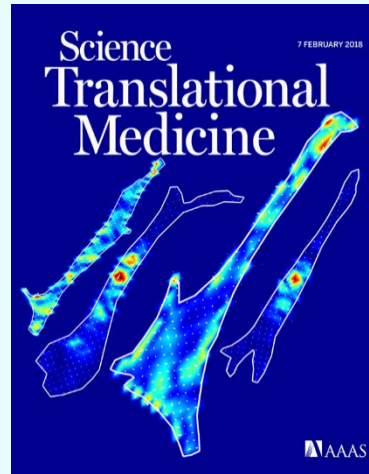
- One of the "Top 10 Academic Advances in Traditional Chinese Medicine in 2020"
- *Nature* cited it as a model of modernization research in traditional Chinese medicine (special issue of "Focus on Traditional Chinese Medicine" 2021,)



WT & TG2-KO mice
Aerosol administration



Tissue distribution



Sci. Trans. Med., 2018, 10
Cover article



Patents

Research Team

1. Group members

- 3 Professors
- 1 Associate
- 1 Senior technician
- 1 Technician

2. Ongoing Projects Chaired

- 1 National key R&D project
- 1 National Excellent Young Scientists Fund
- 4 NSFC projects
- 6 Other projects

3. Research fields: Drug design and innovative drug development

- Development of new methods and theories for drug design
- Discovery and optimization of lead compounds
- Drug repurposing
- Traditional Chinese medicine and natural products based new drugs

4. Research methods

- Quantum Mechanics
- Molecular Dynamics
- Statistical Mechanics
- Deep Learning



**Thank you for your
attention!**

