

سید شهریار عرب

دکتری بیوانفورماتیک

دانشیار
مدیر گروه بیوفیزیک
دانشکده علوم زیستی
دانشگاه تربیت مدرس

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تحصیلات:

- ۱۳۸۸: دکتری بیوانفورماتیک – دانشگاه تهران
مقایسه و پیشگویی ساختار سوم پروتئین براساس کمینه انرژی قطعات محلی
- ۱۳۷۹: کارشناسی ارشد بیوفیزیک – دانشگاه تربیت مدرس
پیشگویی سطح در دسترس پروتئین ها با استفاده از تئوری اطلاعات
- ۱۳۷۵: لیسانس زیست شناسی - علوم میکروبیولوژی – دانشگاه تهران

تجربیات مرتبط:

۱. دانشگاه تربیت مدرس
تهران
۱۳۸۹ - تا حال
عضو هیئت علمی (گروه بیوفیزیک)

۲. پژوهشگاه دانشهای بنیادی (IPM)
تهران ۱۳۹۹ - ۱۳۸۹
پژوهشگر غیر مقیم

۳. پژوهشگاه دانشهای بنیادی (IPM)

تهران ۱۳۹۹ - ۱۳۹۳
دستیار پژوهش - مدیر سرور لینوکس (گروه بیوانفورماتیک)

مهارت‌ها و توانایی‌ها:

طراحی پروتئین و پپتید:

Protein Modelling/Visualizing (Modeler, Nanome, Maestro, YASARA, Chimera, Discovery Studio, VMD, PyMol, ...)

Molecular Docking (Autodock, Vina, HADDOCK, ClusPro, MOE, Glide)

Molecular Dynamic simulation (GROMACS, NAMD)

برنامه نویسی:

C ++

Python

Perl

Matlab

دیتابیس:

Microsoft SQL Server

MySQL

سیستم عامل:

Linux

MacOS

Windows

عضویت‌های معتبر:

عضو هیئت مدیره و نایب رئیس انجمن بیوانفورماتیک ایران (۱۳۹۸ - ۱۳۹۵)

عضو هیئت مدیره انجمن بیوانفورماتیک ایران (۱۴۰۱-۱۳۹۸)

فعالیت‌های اجرایی:

مدیر گروه بیوفیزیک (از سال ۱۳۹۰)

دبیر علمی هفتمین کنفرانس بیوانفورماتیک ایران (دی ۱۳۹۶)

پتن:

1. Rismani, E., TeimooriToolabi, L., Karimipoor, M. & Arab, S. S. Peptides for targeting lrp6-overexpressed cells. US Patent App. 17/175,704 (2021).

گزیده مقالات:

1. Akbarimotlagh M, Arab SS, Palukaitis P, Shams-bakhsh M: **In silico investigation of symptom development model based on coat protein interactions of two cucumber mosaic virus strains.** *Physiol Mol Plant Pathol* 2022, **118**:101811.
2. Rostami N, Choupani E, Hernandez Y, Arab SS, Jazayeri SM, Gomari MM: **SARS-CoV-2 spike evolutionary behaviors; simulation of N501Y mutation outcomes in terms of immunogenicity and structural characteristic.** *J Cell Biochem* 2021,
3. Salehi Z, Keramatipour M, Talebi S, Arab SS, Moghadasi AN, Sahraian MA, Izad M: **Exome sequencing reveals novel rare variants in Iranian familial multiple sclerosis: The importance of POLD2 in the disease pathogenesis.** *Genomics* 2021, **113**:2645–2655.
4. Ahmadi H, Latifi-navid H, Soheili Z-S, Sadeghi M, Samiei S, Pirmardan ER, Taghizadeh S, Arab S, Tajbakhsh S, Zakeri F: **sFLT01-anti-ANG2: a Novel Potent Inhibitor as a Next-generation Anti-angiogenic Molecule.** *Invest Ophthalmol Vis Sci* 2021, **62**:225.
5. Mahmoudi Gomari M, Rostami N, Omidi-Ardali H, Arab SS: **Insight into molecular characteristics of SARS-CoV-2 spike protein following D614G point mutation, a molecular dynamics study.** *J Biomol Struct Dyn* 2021,
6. Moradi M, Hosseinkhani S, Arab SS, Khammari A: **Effects of Linker Flexibility and Conformational Changes of IP3 Receptor on Split Luciferase Complementation Assay.** *Iran J Biotechnol* 2020, **18**:106–114.
7. Fahimian G, Zahiri J, Arab SS, Sajedi RH: **RepCOOL: computational drug repositioning via integrating heterogeneous biological networks.** *J Transl Med* 2020, **18**:375.
8. Pirooznia N, Abdi K, Beiki D, Emami F, Arab SS, Sabzevari O, Soltani-Gooshkhaneh S: **177Lu-labeled cyclic RGD peptide as an imaging and targeted radionuclide therapeutic agent in non-small cell lung cancer: Biological evaluation and preclinical study.** *Bioorg Chem* 2020, **102**:104100.
9. Khammari A, Arab SS, Ejtehadi MR: **The hot sites of α -synuclein in amyloid fibril formation.** *Sci Rep* 2020, **10**:1–14.
10. Rahimzadeh M, Sadeghzadeh M, Najafi F, Arab SS, Pourhosseini PS: **Application of a novel pH-responsive gemini surfactant for delivery of curcumin molecules.** *Mater Res Express* 2020, **7**.
11. Modiri S, Kasra Kermanshahi R, Soudi MR, Arab SS, Khammari A, Cousineau B, Vali H, Zahiri HS, Noghabi KA: **Multifunctional Acidocin 4356 Combats Pseudomonas aeruginosa through Membrane Perturbation and Virulence Attenuation: Experimental Results Confirm Molecular Dynamics Simulation.** *Appl Environ Microbiol* 2020, **86**:e00367-20.
12. Pirooznia N, Abdi K, Beiki D, Emami F, Arab SS, Sabzevari O, Pakdin-Parizi Z, Geramifar P: **Radiosynthesis, Biological Evaluation, and Preclinical Study of a ^{68}Ga -Labeled Cyclic RGD Peptide as an Early Diagnostic Agent for Overexpressed α/β_3 Integrin Receptors in Non-Small-Cell Lung Cancer.** *Contrast Media & Mol Imaging* 2020, **2020**:8421657.
13. Sepehri S, Arab SS, Behmanesh M, Sajedi RH: **Directed blocking of TGF- β receptor i binding site using tailored peptide segments to inhibit its signaling pathway.** *Iran J Biotechnol* 2020, **18**:79–89.
14. Yazdani R, Shams-Bakhsh M, Hassani-Mehraban A, Arab SS, Thelen N, Thiry M, Crommen J, Fillet M, Jacobs N, Brans A: **Production and characterization of virus-like particles of grapevine fanleaf virus presenting L2 epitope of human papillomavirus minor capsid protein.** *BMC Biotechnol* 2019, **19**:1–12.
15. Abdolvahab MH, Venselaar H, Fazeli A, Arab SS, Behmanesh M: **Point Mutation Approach to Reduce Antigenicity of Interferon Beta.** *Int J Pept Res Ther* 2019,
16. Kazemi F, Arab SS, Mohajel N, Keramati M, Niknam N, Aslani MM, Roohvand F: **Computational simulations assessment of mutations impact on streptokinase (SK) from a group G streptococci with enhanced activity—insights into the functional roles of structural dynamics flexibility of SK and stabilization of SK–uplasmin catalytic co.** *J Biomol Struct Dyn* 2019, **37**:1944–1955.
17. Fozoungari F, Dalimi AH, Arab SS, Behmanesh M: **Role of Mutation in Sb (V)-As (V) Reductase Enzyme of Leishmania tropica Isolates Resistant to Glucantim in Iran.** *Pathobiol Res* 2019, **22**:63–68.
18. Khorsand B, Khammari A, Shirvanizadeh N, Zahiri J, Arab SS: **OligoCOOL: A mobile application for nucleotide sequence analysis.** *Biochem Mol Biol Educ* 2019, **47**:201–206.
19. Yazdani R, Arab SS, Hassani-Mehraban A, Shams-Bakhsh M: **Solubilization and Refolding of Inclusion Body of Grapevine fanleaf virus-coat Protein Produced in *E. coli*.** *J Agric Biotechnol* 2019, **11**:151–167.
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22. Poorebrahim M, Asghari M, Abazari MF, Askari H, Sadeghi S, Taheri-Kafrani A, Nasr-Esfahani MH, Ghoraeian P, Aleagha MN, Arab SS, et al.: **Immunomodulatory effects of a rationally designed peptide mimetic of human IFN β in EAE model of multiple sclerosis.** *Prog Neuro-Psychopharmacol Biol Psychiatry* 2018, **82**.
23. Aliebrahimi S, Kouhsari SM, Ostad SN, Arab SS, Karami L: **Identification of phytochemicals targeting c-Met kinase domain using consensus docking and molecular dynamics simulation studies.** *Cell Biochem Biophys* 2018, **76**:135–145.
24. Shirvanizadeh N, Vriend G, Arab SS: **Loop modelling 1.0.** *J Mol Graph Model* 2018, **84**:64–68.
25. Aliebrahimi S, Kouhsari SM, Arab SS, Shadboorestan A, Ostad SN: **Phytochemicals, withaferin A and**

- carnosol, overcome pancreatic cancer stem cells as c-Met inhibitors.** *Biomed Pharmacother* 2018, **106**:1527–1536.
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27. Rezaeian N, Shirvanizadeh N, Mohammadi S, Nikkhah M, Arab SS: **The inhibitory effects of biomimetically designed peptides on α -synuclein aggregation.** *Arch Biochem Biophys* 2017, **634**.
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35. Movahedi M, Zare-Mirakabad F, Arab SS: **Evaluating the accuracy of protein design using native secondary sub-structures.** *BMC Bioinformatics* 2016, **17**.
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37. Salehi M, Nikkhah M, Ghasemi A, Arab SS: **Mitochondrial membrane disruption by aggregation products of ALS-causing superoxide dismutase-1 mutants.** *Int J Biol Macromol* 2015, **75**.
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41. Arab SS, Gharamaleki MP, Pashandi Z, Mobasseri R: **Putracer: A novel method for identification of continuous-domains in multi-domain proteins.** *J Bioinform Comput Biol* 2013, **11**.
42. Pirooznia N, Hasannia S, Arab SS, Lotfi AS, Ghanei M, Shali A: **The design of a new truncated and engineered alpha1-antitrypsin based on theoretical studies: An antiprotease therapeutics for pulmonary diseases.** *Theor Biol Med Model* 2013, **10**.
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45. Ayati M, Taheri G, Arab S, Wong L, Eslahchi C: **Overcoming drug resistance by co-targeting.** In *Proceedings - 2010 IEEE International Conference on Bioinformatics and Biomedicine, BIBM 2010*. . 2010.
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49. Sadeghi M, Parto S, Arab S, Ranjbar B: **Prediction of protein secondary structure based on residue pair types and conformational states using dynamic programming algorithm.** *FEBS Lett* 2005, **579**.
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