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Ph.D. of Bioinformatics

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Educational background:

2010: Ph.D. in Bioinformatics at University of Tehran
      Thesis: "Comparison and Prediction of protein 3D structure based on local fragment minimum energy".

2000: Master of Science in Biophysics (Tarbiat-Modarres University)
      Thesis: "Prediction of Protein Surface Accessibility using Information Theory".

1997: Bachelor of Science in Microbiology (University of Tehran).

Relevant Experiences:

1. **Tarbiat Modares University**
   Tehran
   2011 – up to now
   Academic Board (Biophysics Department)

2. **Institute for Research in Fundamental Sciences (IPM)**
   Tehran
   2010 – 2020
   Nonresident researcher (School of Biological Sciences)

3. **Institute for Research in Fundamental Sciences (IPM)**
   Tehran
   Oct 2004 – 2010
   Research assistant & Linux Server Administrator (Bioinformatics Group)

Skills and Abilities:

Protein and Peptide Design:
    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)

Programming:
    C ++
    Python
    Perl
    Matlab

Database:
    Microsoft SQL Server
    MySQL

OS:
    Linux
    MacOS
    Windows

Prestigious memberships:
    Vice President of the Iranian Bioinformatics Association (2016 - 2019)
    Member of the Board of the Iranian Bioinformatics Association (2016 - up to now)

Executive activities:
    Head of biophysics department (for 8 years from 2010 up to now)
    Scientific Secretary of the 7th Iranian Bioinformatics Conference (Jan 2018)

Current Projects:

    Designing a biosensor to detect spike protein based on Aequorin
    Designing a plant resistant protein against TMV (Tobacco Mosaic Virus)

    EasyModel: A web-based graphical interface for Modeller
    ApInAPDB: Apoptosis-Inducing Anticancer Peptides Database
    HomoRNA: Solving RNA Design Problem Based on Homology Modelling

Patent:

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

Publications:

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. Ahmadieh 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, Sadeghizadeh 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 $\alpha_v\beta_3$ 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-- μplasmin 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.
20. Jangholi A, Ashrafi-Kooshk MR, Arab SS, Karima S, Poorebrahim M, Ghadami SA, Moosavi-Movahedi AA, Khodarahmi R: **Can any "non-specific charge modification within microtubule binding domains of Tau" be a prerequisite of the protein amyloid aggregation? An in vitro study on the 1N4R isoform**. *Int J Biol Macromol* 2018, **109**.
21. Rismani E, Rahimi H, Arab SS, Azadmanesh K, Karimipoor M, Teimoori-Toolabi L: **Computationally Design of Inhibitory Peptides Against Wnt Signaling Pathway: In Silico Insight on Complex of DKK1 and LRP6**. *Int J Pept Res Ther* 2018, **24**.
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 IFNβ in EAE model of multiple sclerosis**. *Prog Neuro-Psychopharmacology 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.

26. Nakhaee N, Asad S, Khajeh K, Arab SS, Amoozegar MA: **Improving the thermal stability of azoreductase from Halomonas elongata by introducing a disulfide bond via site-directed mutagenesis**. *Biotechnol Appl Biochem* 2018, **65**:883–891.

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**.

28. Jabbari S, Dabirmanesh B, Arab SS, Amanlou M, Daneshjou S, Gholami S, Khajeh K: **A novel enzyme based SPR-biosensor to detect bromocriptine as an ergoline derivative drug**. *Sensors Actuators, B Chem* 2017, **240**.

29. Mohandesi N, Haghbeen K, Ranaei O, Arab SS, Hassani S: **Catalytic efficiency and thermostability improvement of Suc2 invertase through rational site-directed mutagenesis**. *Enzyme Microb Technol* 2017, **96**.

30. Dehnavi E, Fathi-Roudsari M, Mirzaie S, Arab SS, Ranaei Siadat SO, Khajeh K: **Engineering disulfide bonds in Selenomonas ruminantium β-xylosidase by experimental and computational methods**. *Int J Biol Macromol* 2017, **95**.

31. Yousefi F, Ataei F, Arab SS, Hosseinkhani S: **Increase of Bacillus badius Phenylalanine dehydrogenase specificity towards phenylalanine substrate by site-directed mutagenesis**. *Arch Biochem Biophys* 2017, **635**.

32. Jangholi A, Ashrafi-Kooshk MR, Arab SS, Riazi G, Mokhtari F, Poorebrahim M, Mahdiuni H, Kurganov BI, Moosavi-Movahedi AA, Khodarahmi R: **Appraisal of role of the polyanionic inducer length on amyloid formation by 412-residue 1N4R Tau protein: A comparative study**. *Arch Biochem Biophys* 2016, **609**.

33. Niknam N, Khakzad H, Arab SS, Naderi-Manesh H: **PDB2Graph: A toolbox for identifying critical amino acids map in proteins based on graph theory**. *Comput Biol Med* 2016, **72**.

34. Siah M, Farzaei MH, Ashrafi-Kooshk MR, Adibi H, Arab SS, Rashidi MR, Khodarahmi R: **Inhibition of Guinea pig aldehyde oxidase activity by different flavonoid compounds: An in vitro study**. *Bioorg Chem* 2016, **64**.

35. Movahedi M, Zare-Mirakabad F, Arab SS: **Evaluating the accuracy of protein design using native secondary sub-structures**. *BMC Bioinformatics* 2016, **17**.

36. Hesampour A, Siadat SER, Malboobi MA, Mohandesi N, Arab SS, Ghahremanpour MM: **Enhancement of Thermostability and Kinetic Efficiency of Aspergillus niger PhyA Phytase by Site-Directed Mutagenesis**. *Appl Biochem Biotechnol* 2015, **175**.

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**.

38. Jalili M, Salehzadeh-Yazdi A, Asgari Y, Arab SS, Yaghmaie M, Ghavamzadeh A, Alimoghaddam K: **CentiServer: A comprehensive resource, web-based application and R package for centrality analysis**. *PLoS One* 2015, **10**.

39. Ghavamipour F, Shahangian SS, Sajedi RH, Arab SS, Mansouri K, Aghamaali MR: **Development of a highly-potent anti-angiogenic VEGF8-109 heterodimer by directed blocking of its VEGFR-2 binding site**. *FEBS J* 2014, **281**:4479–4494.

40. Neyshabur B, Khadem A, Hashemifar S, Arab SS: **NETAL: A new graph-based method for global alignment of protein-protein interaction networks**. *Bioinformatics* 2013, **29**.

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**.

43. Ghahremanpour MM, Arab SS, Aghazadeh SB, Zhang J, van der Spoel D: **MemBuilder: a web-based graphical interface to build heterogeneously mixed membrane bilayers for the GROMACS biomolecular simulation program**. *Bioinformatics* 2013, **30**:439–441.

44. Arab S, Sadeghi M, Eslahchi C, Pezeshk H, Sheari A: **A pairwise residue contact area-based mean force potential for discrimination of native protein structure**. *BMC Bioinformatics* 2010, **11**.

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.

46. Eslahchi C, Pezeshk H, Sadeghi M, Massoud Rahimi A, Maboudi Afkham H, Arab S: **STON: A novel method for protein three-dimensional structure comparison**. *Comput Biol Med* 2009, **39**.

47. Sheari A, Kargar M, Katanforoush A, Arab S, Sadeghi M, Pezeshk H, Eslahchi C, Marashi S-A: **A tale of two symmetrical tails: Structural and functional characteristics of palindromes in proteins**. *BMC Bioinformatics* 2008, **9**.

48. Zarei R, Arab S, Sadeghi M: **A method for protein accessibility prediction based on residue types and conformational states**. *Comput Biol Chem* 2007, **31**.

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**.

50. Naderi-Manesh H, Sadeghi M, Arab S, Moosavi Movahedi AA: **Prediction of protein surface accessibility with information theory**. *Proteins Struct Funct Genet* 2001, **42**.