

Curriculum Vitae

Sepideh Parvizpour

Personal Details:

Name: Sepideh Parvizpour
Sex: Female
Date of Birth: June 1977
Tel: +98 9144903414
Language Skill: Persian (native), Turkish (native), English (good)
Marital Status: Married
Nationality: Iranian
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Educational background:

PHD: 2012 –2015 – Bioscience, Universiti Teknologi Malaysia, Johor, Malaysia,
Thesis: “Cold adaptation study of glycosyl hydrolase enzymes via computational methods”
M.Sc.: 2010 to 2012, Biotechnology, Universiti Teknologi Malaysia, Johor, Malaysia,
Thesis: “Isolation and Molecular Identification of 3-Chloropropionic Acid Degrading Fungi”
B.Sc.: 1995 to 2000, Bioscience, Tabriz University, Tabriz, Iran,

Skills:

- Computational vaccine design,
- Computational drug design,
- Protein 3D model prediction,
- Molecular Dynamic simulation with GROMACS,
- Protein-protein interaction network,
- Protein–ligand docking,
- Protein cavity instruction and analysis.

Teaching Experiences:

2013-2014: Research Assistant, Faculty of Biosciences and Medical Engineering, UTM, Johor Bahru, Malaysia.
2016: System biology, Azarbaijan Shahid Madani University, Tabriz, Iran

Academic Awards:

- 2015, Best student Award, 55th UTM Convocation.
- 2012-2015, Awarded the International Doctoral Fellowship (IDF) From Universiti Teknologi Malaysia
- 2009, Best Paper Award for:
 - J. Razmara, S. Deris, S. Parvizpour, "Text-Based Protein Structure Modeling for Structure Comparison", Int. Conf. of Soft Computing and Pattern Recognition (SOCPAR), December 2009, Melacca, Malaysia.
- 2016, Gratitude letter from Congenital Muscle Disease International Registry (CMDIR-United States) for the research on Congenital Myopathy

Journal Papers:

- 1) **S. Parvizpour**, N Hussin, MS Shamsir, J. Razmara, "Psychrophilic enzymes: structural adaptation, pharmaceutical and industrial applications", *Applied Microbiology and Biotechnology*, 2021, Doi:10.1007/s00253-020-11074-0. **(Q1)**
- 2) M. Pourseif, **S. Parvizpour**, B. Jafari, J. Dehghani, B. Naghili, Y. Omid, "Prophylactic domain-based vaccine against SARS-CoV-2, causative agent of COVID-19 pandemic", *BioImpacts*. 2021, DOI:10.21203/rs.3.rs-32539/v1. **(Q1)**
- 3) **S. Parvizpour**, M. Pourseif, J. Razmara, Y. Omid, "Epitope-based vaccine design: a comprehensive overview of bioinformatics approaches", *Drug Discovery Today*, 2020, Doi:10.1016/j.drudis.2020.03.006. **(Q1)**
- 4) A. Moradi, M. Pourseif, B. Jafari, **S. Parvizpour**, Y. Omid, "Nanobody-based therapeutics against colorectal cancer: Precision therapies based on the personal mutanome profile and tumor neoantigens", *Pharmacological Research*, 2020, 156, Doi:10.1016/j.phrs.2020.104790. **(Q1)**
- 5) **S. Parvizpour**, J. Razmara, M. Pourseif, Y. Omid, "In silico design of a triple-negative breast cancer vaccine by targeting cancer testis antigens", *Bioimpacts*, 2019, 9(1), 45-56. **(Q1)**
- 6) **S. Parvizpour**, J. Razmara, Y. Omid, "Breast cancer vaccination comes to age: impacts of bioinformatics", *Bioimpacts*, 2018, 8(3), 223-235. **(Q1)**
- 7) E. Dalir, **S. Parvizpour**, B. Jafari, Y. Omid, Role of cellulose family in fibril organization of collagen for forming 3D cancer spheroids: in vitro and in silico approach, *Bioimpacts*, 2020, Doi: 10.34172/bi.2021.18. **(Q1)**
- 8) **S. Parvizpour**, A. F. Jomah, J. Razmara, "Structural and Functional Analysis of Mutated Human Pysin B30.2 Domain", *Current Proteomics*, 2019, 17(1), 1-8, DOI: 10.2174/1570164616666190628165835. **(Q3)**

- 9) **S. Parvizpour**, J. Razmara, S. Shahir, “Temperature adaptation analysis of a psychrophilic mannanase through structural, functional and molecular dynamics simulation”, *Molecular Simulation*, 2018, 44(15). (Q2)
- 10) M. Pourseif, G. Moghaddam, B. Naghili, N. Saeedi, **S. Parvizpour**, A. Nematollahi, Y. Omid, “A novel in silico minigene vaccine based on CD4+ T-helper and B-cell epitopes of EG95 isolates for vaccination against cystic echinococcosis”, *Computational Biology and Chemistry*, 2018, 72, 150–163. (Q2)
- 11) F. S. Mohajer, **S. Parvizpour**, J. Razmara and S. Shamsir, “The two mutations of actin–myosin interface and their effect on the dynamics, structures, and functions of skeletal muscle actin”, *Journal of Biomolecular Structure and Dynamics*, 2018, DOI: 10.1080/07391102.2018.1427630. (Q2)
- 12) A Adamu, S. Shamsir, R. A. Wahab, **S. Parvizpour** and F. Huyop, “Multi-template homology based structural model of L-2-haloacid dehalogenase (DehL) from *Rhizobium* sp. RC1”, *Journal of Biomolecular Structure and Dynamics*. 2016, 35:15, 3285-3296, DOI: 10.1080/07391102.2016.1254115. (Q2)
- 13) F. S. Mohajer, **S. Parvizpour**, J. Razmara, M. Khoshkhooy, S. Shahir, “Structural, Functional and Molecular Dynamics Analysis of the Native and Mutated Actin to Study its Effect on Congenital Myopathy”, *Journal of Biomolecular Structure and Dynamics*. 2016, DOI: 10.1080/07391102.2016.1190299. (Q2)
- 14) **S. Parvizpour**, J. Razmara, S. Shahir, R. Illias, A. M. A. Murad, “The role of alternative salt bridges in cold adaptation of a novel psychrophilic laminarinase”, *Journal of Biomolecular Structure and Dynamics*. 2016, DOI: 10.1080/07391102.2016.1191043. (Q2)
- 15) S. Mohammadi, **S. Parvizpour**, J. Razmara, F. D. Abu Bakar, R. Illias, N. M. Mahadi, A. M. Abdul Murad, “Structure Prediction of a Novel Exo-b-1,3-Glucanase: Insights into the Cold Adaptation of Psychrophilic Yeast *Glaciozyma antarctica* PI12”, *Interdisciplinary Science: Computational Life Science*, 2016, DOI 10.1007/s12539-016-0180-9. (Q3).
- 16) **S. Parvizpour**, J. Razmara, A. F. Jomah, R. Illias, S. Shahir, “Structural prediction of a novel laminarinase from the psychrophilic *Glaciozyma antarctica* PI12 and its temperature adaptation analysis”, *Journal of Molecular Modeling*, 21(3):2617. DOI: 10.1007/s00894-015-2617-1. (Q3)
- 17) **S. Parvizpour**, J. Razmara, A. M. Ramli, R. Illias, S. Shahir, “Structural and functional analysis of a novel psychrophilic β -mannanase from *Glaciozyma antarctica* PI12”, *Journal of Computer-Aided Molecular Design*, 2014, 28:685-698. (Q1).
- 18) J. Razmara, S. Fotoohi, **S. Parvizpour**, “Flexible protein structure alignment based on topology string alignment of secondary structure”, *Int. Journal of e-Education, e-Business, e-Management, and e-Learning*, August 2013, DOI: 10.7763/IJEEEE.

- 19) J. Razmara, S. Deris, **S. Parvizpour**, “A Context Evaluation Approach for Protein Structure Comparison using Cross Entropy over n-gram Modeling”, *Computers in Biology and Medicine*, 2013, 43 (10): 1614–1621. **(Q2)**.
- 20) J. Razmara, S. Deris, R. Illias, **S. Parvizpour**, “Artificial signal peptide prediction by a hidden Markov model to improve protein secretion via *Lactococcus lactis* bacteria”, *Bioinformation*, 2013, 9(7): 345-348.
- 21) J. Razmara, S. Deris, **S. Parvizpour**, “TS-AMIR: A Topology String Alignment Method for Intensive Rapid Protein Structure Comparison”, *Algorithms for Molecular Biology* 2012, 7(4).(impact factor : 2.8) .**(Q1)**
- 22) J. Razmara, S. Deris, **S. Parvizpour**, “A rapid protein structure alignment algorithm based on a text modeling technique”, *Bioinformation*, 2011, 6(9): 344-347.
- 23) **S. Parvizpour**, F. Huyop, “Molecular identification and biodegradation of 3-Chloropropionic Acid (3CP) by filamentous fungi-*Mucor* and *Trichoderma* species isolated from UTM agricultural land”, *Malaysian Journal of Microbiology*, 2012. **(Q4)**

* **Quartiles were extracted from scimago web site (www.scimago.com)**

Submitted Journal papers:

Conference Papers:

- 1) S. Parvizpour, S. Shamsir, Structural and functional analysis of a novel psychrophilic α -glucosidase from *Glaciozyma antarctica* PI12, 5th International Graduate Conference on Engineering, Science and Humanity, 2014.
- 2) J. Razmara, S. Parvizpour, “A Method For Multiple Structural Alignment Of Proteins Using Text Modeling Techniques”, 7th Int. Conf. on Adv. Computer Theory and Eng., August 2014, Singapore.
- 3) J. Razmara, S. Fotoohi, S. Parvizpour, “Flexible protein structure alignment based on topology string alignment of secondary structure”, *Int. Journal of e-Education, e-Business, e-Management, and e-Learning*, August 2013, DOI: 10.7763/IJEEEE.
- 4) J. Razmara, S. Deris, S. Parvizpour, “Protein Structure Modeling in Two-Level Topology Strings for Structure Comparison”, *Signal-Image Technology and Internet-Based Systems Conference*, December 2010, Kuala Lumpur, Malaysia.
- 5) J. Razmara, S. Deris, R.M. Illias, “Structural Alignment of Biomolecules by Text Modeling Techniques”, *WSEAS International Conference on APPLICATIONS of COMPUTER ENGINEERING*, March 2010, Penang, Malaysia.
- 6) J. Razmara, S. Deris, S. Parvizpour, “Text-Based Protein Structure Modeling for Structure Comparison”, *International Conference of Soft Computing and Pattern Recognition (SOCPAR)*, December 2009, Melacca, Malaysia.

Book Chapters:

- 1) Sepideh Parvizpour, Mohamed Faraj Edbeib and Fahrul Huyop, “Molecular Identification of filamentous fungi that able to grow on 3-chloropropionic acid as a carbon source” in Chapter 6 of “Advances in Bioinformatics”, 2017.