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## Citing Zebra3D

If you find the Zebra3D+Mustguseal tool or its results useful please cite:

Timonina D., Sharapova Y., Švedas V., Suplatov D. (2021) Bioinformatic analysis of subfamilyspecific regions in 3D-structures of homologs to study functional diversity and conformational plasticity in protein superfamilies. Comput. Struct. Biotechnol. J., DOI: 10.1016/j.csbj.2021.02.005

Suplatov D.A., Kopylov K.E., Popova N.N., Voevodin V.V., Švedas V.K. (2018) Mustguseal: a Server for Multiple Structure-Guided Sequence Alignment of Protein Families. Bioinformatics, 34(9), 1583-1585. DOI: 10.1093/bioinformatics/btx831.

Please also cite the work of third-party contributors, whose programs and algorithms are currently implemented in the Zebra web-server:

The **PyMol** program is implemented to compile the binary PSE session with the annotated representative structure:

PyMol: A molecular visualization system. http://pymol.org/, Copyright (C) Schrodinger, LLC