

引用文献について

本ソフトウェアの使用時には、以下の文献を引用してください。

myPresto 全体及び Filling potential 法について

- 1) "The filling potential method: A method for estimating the free energy surface for protein-ligand docking", Yoshifumi Fukunishi, Yoshiaki Mikami, and Haruki Nakamura, *J. Phys. Chem. B.* (2003) 107, 13201-13210.

cosgene :Multicanonical MD について

- 2) "Determination of multicanonical weight based on a stochastic model of sampling dynamics", Jae Gill Kim, Yoshifumi Fukunishi, Akinori Kidera and Haruki Nakamura, *Physical Review E* (2003) 68, 021110.
- 3) "Multicanonical molecular dynamics algorithm employing adaptive force-biased iteration scheme", Jae Gil Kim, Yoshifumi Fukunishi, Haruki Nakamura, *Phys. Rev. E* 70, 057103 (2004).

Particle Mesh Ewald(PME)について

- 4) U.Essmann, L.Perera, M.L.Berkowitz, T.Darden, H.Lee and L.G.Pedersen. A smooth particle meth Ewald method. *J. Chem. Phys.* 103, 8577-8593(1995)

Accessible surface area (ASA)について

- 5) Kinjo, A. R., Kidera, A., Nakamura, H. & Nishikawa, K. Physicochemical evaluation of protein folds predicted by threading. *Eur Biophys J* 30, 1-10. (2001).

Fast Multipole Method (FMM)について

- 6) J. A. Board, Z. S. Hakura, W. D. Elliott, and W. T. Rankin. "Scalable variants of multipole-accelerated algorithms for molecular dynamics applications" In *Proceedings of the Seventh SIAM Conference on Parallel Processing for Scientific Computing*, February 1995.
- 7) W. T. Rankin, "Efficient Parallel Implementations of Multipole Based N-Body Algorithms." PhD thesis, Duke University, Department of Electrical and Computer Engineering, P.O.Box 90291, Durham, NC 27708-0291, April 1999.
- 8) W. T. Rankin, DPMTA –Distributed Parallel Multipole Tree Algorithm, Duke University, Durham, NC (2002).

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- 9) "Similarity among receptor pockets and among compounds: Analysis and application to in silico ligand screening", Y. Fukunishi, Y. Mikami, and H. Nakamura, *The Journal of Molecular Graphics and Modelling* 24 (2005) 34-45.

Multiple Target Screening (MTS)法について

- 10) "Multiple target screening method for robust and accurate in silico screening", Y. Fukunishi, Y. Mikami, S. Kubota, H. Nakamura, *Journal of Molecular Graphics and*

Modelling,25, 61-70 (2005).

- 11) "Noise reduction method for molecular interaction energy: application to in silico drug screening and in silico target protein screening", Y. Fukunishi, S. Kubota, H. Nakamura, Journal of Chemical Information and Modeling, 46, 2071-2084 (2006).
- 12) "Improvement of protein-compound docking scores by using amino-acid sequence similarities of proteins", Y. Fukunishi, H. Nakamura, Journal of chemical information and modeling, 48, 148-156 (2008)

Docking Score Index (DSI)法について

- 13) "Classification of chemical compounds by protein-compound docking for use in designing a focused library", Y. Fukunishi, Y. Mikami, K. Takedomi, M. Yamanouchi, H. Shima, H. Nakamura, Journal of Medicinal Chemistry, 49, 523-533 (2006).
- 14) "An efficient in silico screening method based on the protein-compound affinity matrix and its application to the design of a focused library for cytochrome P450 (CYP) ligands", Y. Fukunishi, S. Hojo, H. Nakamura, Journal of chemical information and modeling, 46, 2610-22 (2006).

Maximum Volume Overlap (MVO)法について

- 15) "Prediction of protein-ligand complex by docking software guided by other complex structures", Y. Fukunishi, H. Nakamura, Journal of Molecular Graphics and Modelling, 26 (2008) 1030-1033.