

## Irina Tuszyńska

### LISTA PUBLIKACJI z dnia 31 października 2012

#### Publikacje w czasopismach

1. Sulej A, Tuszyńska I, Skowronek KJ, Nowotny M, Bujnicki JM, 2012, **Sequence-specific cleavage of the RNA strand in DNA-RNA hybrids by the fusion of ribonuclease H with a zinc finger**, Nucleic Acids Res, Dec 1;40(22):11563-70.
2. Cruz JA, Blanchet MF, Boniecki M, Bujnicki JM, Chen SJ, Cao S, Das R, Ding F, Dokholyan NV, Flores SC, Huang L, Lavender CA, Lisi V, Major F, Mikołajczak K, Patel DJ, Philips A, Puton T, SantaLucia J, Sijenyi F, Hermann T, Rother K, Rother M, Serganov A, Skorupski M, Soltyssinski T, Sripakdeevong P, Tuszyńska I, Weeks KM, Waldsch C, Wildauer M, Leontis NB, Westhof E, 2012, **RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction**, RNA, Apr;18(4):610-25.
3. Fislage M, Roovers M, Tuszyńska I, Bujnicki JM, Droogmans L, Versées W, 2012, **Crystal structures of the tRNA:m2G6 methyltransferase Trm14/TrmN from two domains of life**, Nucleic Acids Res, Jun 1;40(11):5149-5161.
4. Puton T, Kozlowski L, Tuszyńska I, Rother K, Bujnicki JM, 2011, **Computational methods for prediction of protein-RNA interactions**, J Struct Biol, Sep;179(3):261-8.
5. Tuszyńska I, Bujnicki JM, 2011, **DARS-RNP and QUASI-RNP: New statistical potentials for protein-RNA docking**, BMC Bioinformatics, Aug 18;12(1):348
6. Gajda MJ, Tuszyńska I, Kaczor M, Bakulina AY, Bujnicki JM, 2010, **FILTREST3D: discrimination of structural models using restraints from experimental data**, Bioinformatics, Dec 1;26(23):2986-7.  
*Gajda MJ i Tuszyńska I – dzielone pierwsze autorstwo*
7. Tuszyńska I, Bujnicki JM, 2010, **Predicting atomic details of the unfolding pathway for YibK, a knotted protein from the SPOUT superfamily**. J Biomol Struct Dyn; Feb;27(4):511-520.
8. Kennaway CK J, Obarska-Kosinska A, White JK, Tuszyńska I, Cooper LP, Bujnicki JM, Trinick J, Dryden DTF, 2009, **The structure of M.EcoKI Type I DNA methyltransferase with a DNA mimic antirestriction protein**. Nucleic Acids Res, Feb;37(3):762-70.
9. Pietal M, Tuszyńska I, Bujnicki JM, 2007, **PROTMAP2D: visualization, comparison, and analysis of 2D maps of protein structure**. Bioinformatics , 23(11):1429-1430.

10. Gabant G, Auxilien S, Tuszyńska I, Locard M, Gajda MJ, Chaussinand G, Fernandez B, Dedieu A, Grosjean H, Golinelli-Pimpaneau B, Bujnicki JM, Armengaud J., 2006, **THUMP from archaeal tRNA:m<sup>2</sup>G10 methyltransferase, a genuine autonomously folding domain.** Nucleic Acids Res, May 10;34(9):2483-94.