Structural Biology Group

HEAD:

Maria Górna*, PhD

GROUP MEMBERS:

Anna Antosiewicz, PhD; Maria Klimecka, PhD; Matthew Merski, PhD; Martyna Nowacka, PhD; Anna Trzemecka, PhD
PhD students: Daria Dawidziak, Matylda Izert, Natalia Karolak
MSc students: Mikołaj Kuska, Kamil Szostak, Patrycja Szybowska
BSc student: Piotr Twardowski

RESEARCH PROFILE:

Structural Biology, Biotechnology, Molecular Biology, Protein Crystallography, Protein purification, Protein Engineering, Protein-ligand interactions, Innate Immunity and Inflammation, Antiviral effectors, Antibiotics, Drug discovery

CURRENT RESEARCH ACTIVITIES:

We study the structure and function of proteins using structural biology methods such as protein crystallography and small angle X-ray scattering (SAXS), bioinformatics analysis and molecular dynamics simulations, as well as by functional assays both in vitro and in cell culture. We are especially interested in proteins for which little structural information is available, so that we can answer vital questions about the activity and function of these proteins. Some of our interests include proteins working on RNA, helical repeats, protein engineering and molecular diagnostics. We also use structural models of proteins to elucidate the molecular mechanisms underlying selected human diseases or to aid drug discovery. Through our findings and inventions, we would like to help combat infections or treat human inflammatory disorders.
Currently, our main research topics regard: (1) development of proteolysis-targeting compounds in bacterial systems that can lead to novel antibiotics (2) complexes of human antiviral effectors from the IFIT protein family and (3) mitochondrial post-transcriptional regulators from the FASTK protein family (3). These projects are related to studies of innate immune and inflammatory processes and developing

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anti-inflammatory or antimicrobial agents. We also engineer proteins for biotechnology applications and molecular diagnostics and we collaborate with the pharmaceutical industry.
More updates at https://gorna.uw.edu.pl

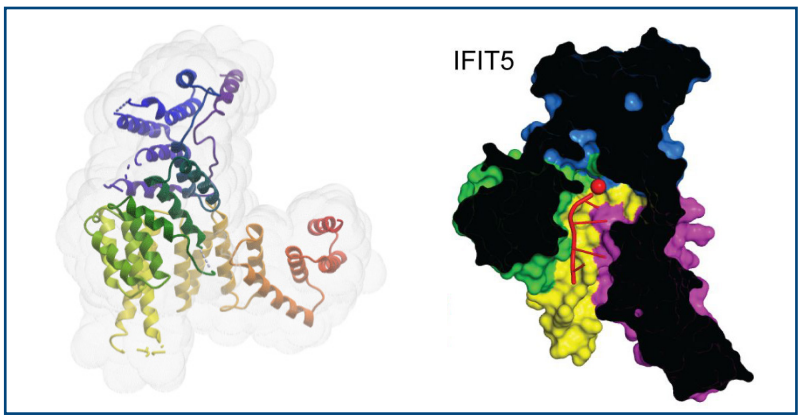

Fig. 1. Crystal structure of the human antiviral IFIT5 protein. Left, cartoon representation. Right, crosssection demonstrating that the dimensions of the pocket enable selectivity for single-stranded RNA [4].

SELECTED PUBLICATIONS:

1. M. Merski, K. Młynarczyk, J. Ludwiczak, J. Skrzeczkowski, S. Dunin-Horkawicz, M.W. Górna, Self-analysis of repeat proteins reveals evolutionarily conserved patterns, BMC Bioinformatics. 21 (2020) 179.
2. J. Kutner, I.G. Shabalin, D. Matelska, K.B. Handing, O. Gasiorowska, P. Sroka, M.W. Górna, K. Ginalski, K. Woźniak, W. Minor, Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies, Biochemistry. 57(6) (2018) 963-977.
3. K. Byrgazov, R. Kastner, M. Górna, G. Hoermann, M. Koenig, M. Ulreich, M. Benesch, V. Strenger, H. Lackner, W. Schwinger, P. Sovinz, O.A. Haas, M. van den Heuvel-Eibrink, C.M. Niemeyer, O. Hantschel, P. Valent, G. Superti-Furga, C. Urban, M.N. Dworzak, T. Lion, NDEL1-PDGFRB fusion gene in a myeloid malignancy with eosinophilia associated with resistance to tyrosine kinase inhibitors, Leukemia. 31(1) (2017) 237-40.
4. N. Dölker, M.W. Górna, L. Sutto, A.S. Torralba, G. Superti-Furga, F.L. Gervasio, The SH2 domain regulates c-Abl kinase activation by a cyclin-like mechanism and remodulation of the hinge motion, PLOS Comput Biol. 10(10) (2014) 1003863.
5. Y.M. Abbas, A. Pichlmair, M.W. Górna, G. Superti-Furga, B. Nagar, Structural basis for viral 5'-PPP-RNA recognition by human IFIT proteins, Nature. 494 (2013) 60-4.