S100B belongs to the highly conserved S100 family, a subclass of the EF-hand $Ca^{2+}$-binding proteins, constituted by 21 known members implicated in intracellular and extracellular regulatory activity[1]. It has been demonstrated that the binding of S100B and the C-terminal domain of p53, a well known tumor-suppressor protein, prevents p53 phosphorylation and tetramerization, blocking its anticancer activity [2]. This inhibitory activity has been related with S100B overexpression in some malignant tumors. This interaction between an anphypatic α-helix on a protein and a hydrophobic cleft on its partner is similar to other therapeutically relevant interactions suggesting the possibility to design small molecules inhibitors of protein-protein interaction. Few inhibitors have been identified so far by using a NMR-based screening [3,4]. Our objective is the identification of small molecules able to block the protein-protein interaction between S100B and p53, through the SAR by NMR approach, successfully developed and applied by Fesik and coworkers [5]. The biophysical screening was preceded from a computational screening aimed to filter fragments to be screened in the following assays. Siena Biotech's fragment collection was used for a virtual screening campaign based on docking and pharmacohore approaches, leading to the selection of 280 molecules. NMR-based screening (WaterLOGSY) was performed in order to identify interacting fragments and $^{15}N$-HSQC analysis confirmed the interaction of the strongest binders. Co-crystallization trials have been set up for one of the most active molecules. Crystals of protein-ligand complexes grow in few days and the analysis of diffraction data provides good-quality electron density maps at about 1.9 Å resolution. The binding site of the fragment has been clearly identified and corresponds to p53 binding site, as it was previously determined by the above mentioned NMR experiments. Structure-based library design has started in order to increase the potency of the fragments, through fragment evolution. Crystallization trials to obtain binary complexes of S100B with all the identified fragments are still on going.

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**Keywords: structure and function of protein; NMR spectroscopic investigations; X-ray structure determination**

## FA4-MS09-P09

**Electronic Structure of $[RuCl_3(indazole)_2NO]$.** Jozef Kožíšek[a], Marek Fronc[a], Marin Breza[a], Katharina Schiessl[b], Vladimir B. Arion[b]. [a]*Department of Physical Chemictry, Slovak Technical University, Radlinského 9, SK-812 37 Bratislava, Slovak Republic.* [b]*Institute of Inorganic Chemistry, University of Vienna, Währingerstr. 42, A-1090 Vienna, Austria.*
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The development of metallopharmaceuticals is a frontier area in bioinorganic chemistry where both the Ru(II) and Ru(III) coordination compounds play an important role [1]. We have synthesized a novel ruthenium nitrosyl compound, $[RuCl_3(indazole)_2NO]$ and studied its geometric and electronic structure.
An experimental data set (GEMINI R diffractometer, 100K, 47 runs, 147 740 diffractions, resolution 0.54Å) was measured. Data reduction was done by CrysAlis171.33.31 and an average redundancy of 12.8 gives $R_{int}$ of 0.045.
After the multipole refinement the topological analysis was performed using XD package. Theoretical calculation was done using CRYSTAL06 and TOPOND software.
Comparison of experimental and theoretical results will be disscussed.
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## FA4-MS09-P10

**Analysis of Organic Molecular Compounds and Pharmaceuticals from Their X-Ray Powder Diffraction Patterns.** Pauline Martinetto[a], Michel Anne[a], Pierre Bordet[a], Julie Linol[b], Gérard Coquerel[b], Eric Dooryhée[a], Pierre Terech[c]. [a]*Institut Néel, CNRS-UJF, Grenoble, France.* [b]*IMR, Université de Rouen, Mont Saint Aignan, France.* [c]*INAC, CEA, Grenoble, France.*
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Pharmaceutical developers are more and more concerned by solid form of drugs because it dictates their properties, including stability, hygroscopicity, dissolution rate, solubility, and bioavaibility. These solids can be molecular crystals (often prepared as polycrystalline powders) or noncrystalline solids (less stable but often with desirable pharmaceuticals properties, such as faster dissolution rates). In the recent years, advances in methodology have enabled to characterize both solid forms using only X-ray powder diffraction data. We have already reported structural studies carried out on a special steroid derivative molecule (STNH) which exhibits spectacular properties of an efficient organogelator of saturated alkanes [1]. Here, the crystallographic behavior of different xerogel forms are now observed ex- and in-situ using laboratory and synchrotron X-ray powder diffraction together with conventional and global optimization methods. We also present the study carried out on the molecular compound (±) modafinil, known to crystallise in five pure polymorphic forms [2, 3]. Under high energy milling, a new phase is obtained, which is a defective phase likely related to the original forms I and III. We are currently studying the total scattering signal