Experimental report for ESRF Expt. MX-1495, proposer Clemens Grimm, University of Wuerzburg, Beamline ID14-4

Overview

Galectin-1, a prominent member of animal lectins, is overexpressed in malignant tissues and involved in numerous types of cancer.^{1, 2, 3} The protein exhibits characteristic carbohydrate-recognition domains on opposite sites of the homodimeric structure and interacts selectively with β -galactosides (like lactose and *N*-Acetyllactosamine) of glycoconjugates on cell surfaces. These interactions introduce biomolecular processes as cell proliferation, apoptosis and tumor progression.

The binding constants of natural carbohydrates are low and range in the micromolar.^{4, 5} This fact demonstrates the urgent need for the identification and development of highly affine and selective ligands. Our work presents a rational approach for the design of novel Galectin-1 ligands and aims at introducing binding partners as potential lead structure for therapeutical drug development.

To realize this intent natural (lactose and *N*-Acetyllactosamine) with an artificial bioorthogonal function in variable positions of the carbohydrate structure were docked with the crystal structure of Galectin-1.⁵ Promising candidates (**1** and **2**) were synthesized in our lab and cocrystallized with Galectin-1. The structure elucidation of these complexes will allow us to identify amino acids that are located adjacent to the carbohydrate binding domain. To address these amino acids and generate a highly affine binding partner the adequate functional group is inserted in a following step as an azide by the Sharpless-Huisgen-Meldal "click reaction".^{6,7}



Evaluation and results

After testing a variety of differently soaked or co-crystallized crystals, we were able to collect several datasets that allowed clear identification of density for bound *N*-Acetyllactosamine as well as ligand (1) and ligand (2) (see Fig. 1 and Table 1 for data collection and refinement statistics). We are currently preparing a variety of click-reaction products to create ligands with increased affinity for Gal1.

Table1: Data collection and refinement statistics of the 6S complex crystal

Data Collection	
Beamline	ID14-4
Wavelength (Å)	0.9792
Space group	P212121
Cell dimensions	
a, b, c (Å)	43.2, 58.2, 111.3
No. molecules in asymmetric unit	2
Resolution (Å)	55-1.3
Rsym (%)	9.7
Mean $I/\sigma(I)$	19.2
Completeness (%)	96.5
Refinement	0.174 / 0.010
K / Rfree	0.1/4/0.212
RMS deviations	
Bond lengths (Å)	0.012
Bond angles (°)	1.520
Ramachandran	
Favoured, Allowed, Outliers [%]	98.3, 1.8, 0.0

Fig. 1: Ligand (2) bound to the Gal1 dimer. Model density for the ligand contoured at 0.9 σ .



References

- (1) Thijssen, V.; Poirier, F.; Baum, L. G.; Griffioen, A. W. Blood 2007, 110, 2819.
- (2) Rabinovich, G. A.; Toscano, M. A. Nat. Rev. Immunol. 2009, 9, 338-352.
- (3) Vasta, G. R. Nat. Rev. Microbiol. 2009, 7, 424-438.
- (4) Camby, I.; Le Mercier, M.; Lefranc, F.; Kiss, R. Glycobiolgy 2006, 16, 137R.
- (5) Lopez-Lucendo, M. F.; Solis, D.; André, S.; Hirabayashi, J.; Kasai, K.; Kaltner, H.; Gabius, H. J.; Romero, A. J. Mol. Biol. 2004, 343, 957.
- (6) Rostovsev, V. V.; Green, L. G.; Fokin, V. V.; Sharpless, K. B. Angew. Chem. Int. Ed. 2002, 41, 2596.
- (7) Tornoe, C. W.; Christensen, C.; Meldal, M. J. Org. Chem. 2002, 67, 3057.