

[s8a.m4.p7] An unusual carbohydrate binding site revealed by the structures of two *Maackia amurensis* lectins complexed with sialic acid-containing oligosaccharides. J. Lescar, A. Imberty, C. Gautier, R. Loris, L. Wyns, S. Percz. CERMAV-CNRS, Grenoble cedex 9 38041 France Vrije Universiteit Brussel, Paardenstraat 65, B-1640 Sint-Genesius-Rode Belgique.

Keywords: membrane proteins, receptors.

Seeds from the legume tree *Maackia amurensis* contain two lectins that can agglutinate different blood cell types. Their specificity toward sialylated oligosaccharides is unique among legume lectins: the leucoagglutinin preferentially binds to sialyllactosamine whereas the hemagglutinin displays higher affinity for a disialylated tetrasaccharide. The three-dimensional structure of the complex between *Maackia amurensis* leucoagglutinin and sialyllactose has been determined at 2.75 resolution using X-ray crystallography. The carbohydrate binding site consists of a deep cleft that accommodates the three carbohydrate residues of the sialyllactose. The central galactose sits in the primary binding site in an orientation that has not been observed previously in other legume lectins.

The complex between *Maackia amurensis* hemagglutinin and a disialylated tetrasaccharide could be modeled from the leucoagglutinin/sialyllactose crystal structure. The substitution of one tyrosine by an alanine residue is responsible for the difference in fine specificity between the two isolectins. Comparison with other legume lectins indicates that oligosaccharide specificity within this family is achieved by the recycling of structural loops in different combinations.

[s8a.m4.p8] Structural studies of the purple bacterial photosynthetic reaction centre. P.K. Fyfe, J.P. Ridge^{1,3}, K.E. McAuley^{2,4}, A. W. Roszak², R.J. Cogdell², N.W. Isaacs², M.R. Jones *Department of Biochemistry, School of Medical Sciences, University of Bristol, Bristol, BS8 1TD, U.K.* ¹*Department of Molecular Biology and Biotechnology, Krebs Institute, Firth Court, University of Sheffield, Western Bank, Sheffield, S10 2UH. U.K.* and ²*Department of Biochemistry and, Department of Chemistry, University of Glasgow, University Avenue, Glasgow, G12 8QQ, U.K.* *Current Addresses:* ³*Department of Microbiology, University of Queensland, St. Lucia, Brisbane, QLD 4072, Australia.* ⁴*Department of Chemistry, University of York, Heslington, York, YO10 5DD U.K.*

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Several crystal structures of the bacterial photosynthetic reaction centre from *Rhodospseudomonas viridis* and *Rhodobacter sphaeroides* are now available^{1,2}. The availability of these structures has greatly enhanced our understanding of how these integral membrane pigment:protein complexes function, and has allowed the rational design of site-directed mutants to probe structure/function relationships within the complex. X-ray crystallography is now also being applied to the mutant complexes themselves, with several crystal models revealing hitherto unexpected structural arrangements^{3,4,5}. This presentation will discuss the results of the recent study of two complexes. The first bears a mutation in the Q_A binding pocket, which does not exclude the quinone, but does allow its removal from and reconstitution back into the complex. The second strain carries the mutation H1.168I², which breaks the only hydrogen bond between the protein and the so-called "special pair" of bacteriochlorophylls. The structural impact of breaking this hydrogen bond will be discussed in the context of the pre-existing bank of spectroscopic data that exists for this mutant⁶. A short report will also be made on progress on the previously reported crystal structure of a mutant photosynthetic reaction centre with a bound cardiolipin molecule⁷.

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