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**Galectin-3: is this member of a large family of multifunctional lectins
(already) a therapeutic target?**

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ABSTRACT

Introduction: The discoveries that sugars are a highly versatile platform to generate biochemical messages and that glycan-specific receptors (lectins) are a link between these signals and their bioactivity explain the interest in endogenous lectins such as galectins. Their analysis is a highly dynamic field. It is often referred to as being promising for innovative drug design.

Area covered: We present a primer to the concept of the sugar code by glycan-(ga) lectin recognition, followed by a survey on galectin-3 (considering common and distinct features within this family of multifunctional proteins expressed at various cellular sites and cell types). Finally, we discuss strategies capable of blocking (ga)lectin activity, with an eye on current challenges and inherent obstacles.

Expert opinion: The emerging broad profile of homeostatic and pathophysiological bioactivities stimulates further efforts to explore galectin (-3) functionality, alone and then in mixtures. Like thoroughly assessing the pros and cons of blocking approaches for a multifunctional protein active at different sites, identifying a clinical situation, in which the galectin is essential in the disease process, will be critical.

Keywords

adhesion; apoptosis; galectin-3 (Gal-3); glycans; glycoproteins; polysaccharides

Article Highlights

- Glycan-lectin recognition is an efficient and versatile means of cellular information transfer.
- Members of the galectin family are emerging as multifunctional effectors in diverse cell types and at various sites of cells and tissues.
- Galectin-3 has a unique modular architecture suited for context-dependent aggregation and also interactions with glycans and with proteins.
- *In vitro* and *in vivo* work in models gives reason to assume correlations between galectin expression and disease states.
- Various approaches offer potential for blocking pairing of galectins with counterreceptor(s).
- Multi-site activity of multifunctional effectors, likely in a network, poses attractive challenges on the way to define the status of galectin-3 as therapeutic target.

1 Introduction

Molecular selectivity underlies first the detection and then the characterization of the activity profile of a large superfamily of (glyco)proteins that are called lectins. This term originates from work on blood group typing. Precisely knowing the blood group status is essential to predict and to preclude incompatibility of transfusions, thus fatal outcomes. The observations that components of plant seed extracts agglutinated erythrocytes depending on the type of blood group of the donor, exactly as natural serum antibodies do, not only prompted to coin the technical name 'phytohaemagglutinin' but also „the word lectin from Latin *lectus*, the past principle of *legere* meaning to pick, choose or select“ [1]. It highlights that proteins different from immunoglobulins can distinguish between cell surface epitopes, *selecting* their binding partners.

The following discoveries that simple sugars competitively inhibited lectin-dependent haemagglutination, that ABH(0) histo-blood group determinants and other types of blood group systems are oligosaccharides and that plant agglutinins can also precipitate polysaccharides and glycoproteins in a carbohydrate-specific manner gave reason to connect the term 'lectin' with binding (receptor) capacity to carbohydrates (for review on the history of lectins, please see [2-4]). Since sugars have unsurpassed capacity to generate structural diversity in a minimum of size in oligomers [5], they are well-suited as a molecular alphabet to 'write' cellular signals, and this beyond the described phenotypic (signature-like) feature of erythrocytes. The known common abundance of glycoconjugates on cell surfaces with their high level of structural complexity (actually, glycans have indeed been called "complex carbohydrates" [6] or "complex heterosaccharides" [7]) and the fact that they "are much more complex, variegated and difficult to study than proteins or nucleic acids" [8] explain that the pace of progress in this field is necessarily slow in comparison. Presentation of elaborate structures at accessible positions, on surfaces and in the matrix [9,10], intimates that glycans are involved in information transfer. As the example of blood-group typing attests, they can be bioactive as ligands. Indeed, functional pairing of glycans with lectins as their receptors has become the tenet of the concept of the sugar code [11,12].

Fittingly, the toolbox for glycan synthesis and recognition is well equipped: a complex enzymatic machinery for glycan (ligand) assembly with many so-called glycogene products such as diverse families of glycosyltransferases and multiple folds for glycan recognition (by receptors), the currently accepted key characteristic for lectin classification, are at hand (for examples, please see [4,13-16]). In each category and case, the route via duplications and

ensuing sequence divergence in the coding and regulatory sections of the respective genes yielded groups of homologous proteins. They ensure fine-tuned signal ,writing' in the sugar language and ,translating' of these messages into widely diverse post-binding effects. The cyto- and histochemical application of plant and invertebrate lectins as laboratory tool to map the presence of cognate glycans substantiated the enormous potential of this class of receptors to pick certain epitopes of glycoconjugates from the cellular glycome [15,17].

The success of this work, too, contributed to direct attention to exploring the question on expression of lectins in vertebrates, especially in mammals. That a mammalian hepatic lectin proved to be responsible for rapid clearance of a glycoprotein (i.e. ceruloplasmin) from serum after loss of sialic acids from its N-glycans [18] and that a (β -)*ga*(lactose-binding)*lectin* from the electric eel (and from extracts of rat and chicken tissues and murine neuroblastoma cells) proved to be capable of bridging erythrocytes [19] established fundamental proof-of-principle evidence for the (patho)physiological relevance of this type of recognition [20,21]. 'Writing' glycan-encoded signals, being able to select and to 'read' distinct ,signals' (glycans) from the wide variety and ,translating' their messages into particular post-binding effects such as adhesion, cell-specific delivery (homing) or outside-in signaling are among the prerequisites to let „glycan functions pervade biology at all levels“ [22], questions on molecular mechanisms arising. „One incentive for asking such questions [on glycans and transmission of signals] is their immediate relevance to medicine, in areas such as protection against infectious disease agents and for targeting of drugs and enzymes to sites where they would best achieve their therapeutic effects“ [23]. In general terms, it appears that “glycans represent a largely untapped resource for biological discovery as well as unanticipated therapeutic opportunities” [24]. This aspect gives reason to explain interest in endogenous lectins, in our context in the family of the multifunctional galectins and its member classified as galectin-3 (Gal-3). The literature survey is based on routine monitoring of development of status of knowledge by Current Contents® combined with *Pubmed* searches and active research in the field for about 25 years or 35 years by the two authors.

2. Galectin-3: its detection and characterization

This galectin has independently been detected by immunological and biochemical lines of research. With the intention to generate specific reagents for immunocyto- and histochemical applications and for functional assays, cells or subcellular fractions have been and still are used as antigen to raise monoclonal antibodies. Panel testing of the resulting hybridoma clones can then lead to interesting products. This was the case in a project on characterizing

phenotypic divergence of mononuclear phagocytes by antibodies, especially stages of activation of peritoneal exudate phagocytes after injection of known elicitors into (C57BL/6) mice, especially thioglycollate. When rat spleen cells were immunized to nuclei-free extracts of cell preparations that had been depleted of previously identified antigens by monoclonal antibody immunoabsorbents, a new macrophage (Mac) antigen was defined: supernatants of the hybridoma clones M3/31 and M3/38 precipitated a 32 kDa protein from extracts of activated murine peritoneal macrophages, called the Mac-2 antigen [25,26]. By the way, the Mac-1 antigen that was first identified by this approach is a subunit of an integrin now known as CD11b (the α_M -integrin subunit, also called CR3) [27,28].

Independently, by using extracts of the murine B16-F1 melanoma cell line for immunization, a monoclonal antibody (clone 5D7) was obtained that blocked haemagglutination by cell extracts, bound to bands at 34 kDa (called L-34) and 68 kDa of purified agglutinin, showed cross-reactivity to β -galactoside-binding lectins from electric eel and adult chicken muscle and localized antigen on the surface and in the cytoplasm of murine (B16-F1 and K-1735 melanoma; UV-2237 fibrosarcoma) and human (Hs939 melanoma; SK-DZ neuroblastoma; HeLa-53 carcinoma) tumor cells [29].

The second approach to detecting the galectin took advantage of its selective binding property for β -galactosides. Inspired by the pioneering purification of electrolectin, the galectin from the electric eel [19] (which turned out to be the first galectin [30]), affinity chromatography with resins presenting β -galactosides (the two glycoproteins asialofetuin and immunoglobulin E (IgE) or lactose) was performed with extracts of different sources. A protein of a molecular weight between 31-35 kDa was found in eluted fractions, from extracts of fibroblasts (3T3 and SL66 cells, called carbohydrate-binding protein (CBP) 35) [31], of murine or human tumors [32,33], of *Xenopus* oocytes after *in vitro* translation directed by injected mRNA of rat basophilic leukemia cells (binding IgE, thus called ϵ BP [34] and of rat lung (RL-29) [35]. Antibodies against purified protein revealed a broad profile of tissue expression in normal and tumor cells [36-38], also adding nuclear staining (apparently correlated to state of proliferation in 3T3 fibroblasts) to the sites of intracellular localization *in vitro* [39]. Biochemical and immunological comparisons as well as cloning and sequencing of the cDNAs converged to reveal that the Mac-2 (and 5D7) antigen, CBP35 (CBP30 in baby hamster kidney cells or RL-29) and ϵ BP are all homologues of a particular gene present in mammals, i.e. the gene coding for a protein of a growing family of tissue lectins, referred to as galectin (for review, please see [40]).

This special protein's structure is composed of three types of modules (Figure 1). Its sequence starts with an N-terminal section containing two sites for serine phosphorylation, followed by a Tyr-, Pro- and Gly-rich non-triple helical collagen-like repeat region of nine amino acids per unit (these two parts comprise the N-terminal tail (NT)) and the carbohydrate recognition domain (CRD) (Figure 1). Its trimodular design explains the term chimera-type galectin, in relation to the mono- and homodimeric (proto type) and linker-connected heterodimeric (tandem-repeat type) members of the galectin family (Figure 1) [41-43].

As common properties, these proteins share the β -sandwich fold and the contact profile to the canonical ligand lactose via hydrogen bonding and C-H/ π interactions. Key amino acid residues that form the conserved sequence signature with a central Trp residue (furnishing the π -electrons for contact to the three C-H sites on the B-face of D-galactose), are illustrated for CRDs of vertebrate galectins in Figure 2 (for further informations on crystallographic structures, please see [44]). Moreover, they all have no signal sequence so that galectins are secreted by not yet completely elucidated non-conventional routes [45]. As effectors, they are known to be multifunctional, active in intracellular compartments, on the cell surface and extracellularly, and opposite effects on cells (for example blocking or mediating adhesion or proliferation) depending on cell type, concentration and context are known [43,46-49]. In the words of K.-i. Kasai, "the same galectin species seems to participate in development, differentiation, morphogenesis, immunity, apoptosis, metastasis of malignant cells etc.... The biological function of galectins should vary from site to site, and from time to time.... The "one galectin – one phenomenon" relationship does not exist and the lack of specific and principal roles is the nature of the galectin family" [50]. In the classification system of the galectin family by numbers, the protein detected by the approaches given above was given the name Gal-3.

The structurally distinctive feature of Gal-3 with its unique trimodular design accounts for differences in the biological behavior. Among galectins, it opens the way toward special versatility in aggregate formation. Monomeric in solution, this galectin can form cross-linked complexes with glycoconjugate counterreceptors of characteristic topological order. They are different from lattices formed by a proto-type galectin, as revealed by precipitation and negative stain electron microscopy using a nonavalent glycoprotein (asialofetuin with its three complex-type N-glycans) and synthetic glycoclusters [51]. The combination of the collagen-like repeat section with the CRD, both capable to mediate self-aggregation (for recent literature surveys, please see [52,53]), underlies the difference relative to homodimeric Gal-1 that is solely built by one type of module, i.e. the CRD (Figure 1). As suggested for hamster

Gal-3 by applying NMR-spectroscopical analysis of full-length protein and fragments thereof as well as electron microscopical monitoring of Gal-3 preparations, “oligomerization of substratum-adsorbed galectin-3, through N- and C-terminal domain interactions, could be relevant to the positive cooperativity observed in binding of the lectin to immobilized multiglycosylated proteins such as laminin” [54]. Of note, the nature of the ligand is assumed to affect the aggregation process in a special manner [52,55-57]. On the atomic level, crystallographic mapping of intermolecular CRD contacts has recently become available (Figure 3) [53].

In comparison to the CRD, the enormous flexibility of the NT with its collagen-like repeats is precluding to reach the same level of structural analysis. The physiological truncation of this section by proteases, especially matrix metalloproteinases, that modulates Gal-3's bioactivity, as shown e.g. in breast cancer cells [58] or neutrophils [59], has inspired design of Gal-3 variants by stepwise deletion of sequence repeats. This approach is instrumental to explore the significance of number of tandem repeats and to reduce extent of flexibility [60]. Indeed, first crystallographic information on a part of the NT has become available by using a variant generated this way (Figure 4) [53]. Of interest in this context, the CRD, too, has inherent spatial flexibility. When binding the ligand lactose, its accommodation, is associated with an increase in conformational entropy of the protein without any structural changes, a substantial contribution to the thermodynamics and a caveat to solely base drug-design efforts on static X-ray structures [61].

In further structural terms, the nature of galectins as homologous proteins (for a phylogenetic tree of this family, please see [62]) with conservation of the signature sequence and its presentation in the binding site, as shown in Figure 2, let it expect that their binding profiles to glycans are rather similar, *cum grano salis*. Assumed similarity is for example reflected in the compilation of respective results obtained by frontal affinity chromatography [63]. Substitutions of the canonical N-acetyllactosamine (LacNAc) core to build blood group ABH(0) epitopes therefore are favorable to increase affinity not only for human Gal-3, as initially detected by inhibition assays using glycans to interfere with galectin-asialofetuin (immobilized on Sepharose beads) interaction [64], but also for the tandem-repeat-type galectins-4, -8 and -9 [63]. That occurrence of ‘cross-reactivity’ for glycans among galectins is naturally common is further exemplified for tandem-repeat-type galectins-4 and -9. They interact with a Gal-3-binding TF-disaccharide-presenting glycopeptide at low nM-affinity [65], as 3'-sulfated lactose is a contact site for glycodendrimersome bridging for these galectins [66]. Adding an example for proto-type proteins, galectins-2 and -7 bridge

nanoparticles with the parasitic signature disaccharide LacdiNAc (GalNAc β 1,4GlcNAc), a contact point first reported for Gal-3 and assumed to be specific due to the reported lack of binding by Gal-1 [67,68]. Such case studies advise rigorous comprehensive panel testing prior to claiming inter-galectin specificity.

On the level of the natural glycoconjugate counterreceptors, multivalency of glycoproteins, clustering in microdomains and the evidence for a gradient of decreasing affinity constants upon loading with galectin make “fractional high-affinity binding” and thus “supramolecular assemblies” already at low galectin concentrations possible that “can trigger cell surface signal transduction mechanism” [69]. To do so, the galectin selects few binding partners for building aggregates, and this – as far as we know at this moment – depending on cell type (for a compilation of glycoconjugate counterreceptors, please see Table 1). Of note, the level of expression of the protein as scaffold for glycans and the structure of the glycan part, especially the status of α 2,6-sialylation of N-glycans, are effective regulators of extent of galectin binding. In addition, “a majority of Gal-3’s intracellular interactions occur via protein-protein interactions” [70]: respective binding partners are also presented in Table 1. Except for the case of Gal-3–B cell lymphoma 2 (Bcl-2) recognition that appears to involve the NWGR motif also essential for lactose binding and thus is impaired by presence of the cognate sugar [71,72], the atomic details on Gal-3–protein interactions await structural characterization.

In summary, whereas the analysis of the structure and binding properties to glycans of the CRD of Gal-3 revealed (expectable) similarities, the trimodular design is unique (Figure 1). The currently described panel of counterreceptors, given in Table 1, substantiates the validity of the assumption for a selective process, as implied by the term ‘lectin’. The current status of insight into this galectin’s functional profile invites to deliberate pros and cons of considering Gal-3 as a therapeutic target.

4. Gal-3: a therapeutic target?

In principle, three fundamental points deserve attention to answer this question:

1. As already noted above, galectins are multifunctional, and the literature provides ample evidence to encourage further investigations. Thus, with focus on tumor biology, “it is increasingly recognized that galectin-3 is an important regulator of a broad range of cancer cell activities and plays important roles in cancer cell growth, transformation, apoptosis, angiogenesis, adhesion, invasion and metastasis. Such a divergent influence of galectin-3 on cancer activities derives from its multiple inter-

and sub-cellular localizations where it interacts with a range of different binding partners” [73]. A recent study on negative correlation between Gal-3 presence and β_3 -integrin expression, pointing to nuclear events on the level of the promoter, in murine melanoma metastasis concluded that “it is possible that even a single molecule can affect several different processes of cancer cell biology in a context-dependent manner” [74]. Due to its wide range of expression, adding to its multifunctionality, short- and long-term consequences of any kind of targeting Gal-3 systemically will definitely need to be examined thoroughly.

2. Evidence for an involvement of Gal-3 in pathogenesis is often derived from work with mouse models deficient in galectin expression, as exemplified by the following statement: “based on these data [on galectin-3 null mice], it appears that galectin-3 protein is implicated in the development of fibrosis resulting from inflammatory or toxic insults, thereby establishing a rationale to antagonize its function to treat fibrosis” [75]. Experience with such a model in tumor biology taught a salient lesson deserving to be noticed: the (apparently unexpected) lack of impact of absence of Gal-3 in mouse models genetically programmed to develop cancer “could possibly be explained by the fact that adaptive mechanisms arise” [76]. Such alterations as response to a knock-out may not only be instrumental for maintaining homeostasis, as documented *in vivo* upon creating a deficiency in N-glycan branching, a factor relevant for binding of tissue lectins [77-79]. They may also cause not readily predictable outcomes, calling for cautious interpretation. Of course, and nearly needless to say, general extrapolation from mice to man, too, is less than straightforward. Looking at the equipment with lectins between species on the genome level, pronounced differences of not yet fully understood consequences have been detected, for example in the case of a C-type lectin (DC-SIGN, CD209) with eight genetic homologs in mice and no clear ortholog of the human protein [80], and also the genetic background can affect characteristics of the loss-of-function phenotype, as discussed for Gal-1 [81].
3. While exploring the expression of the members of the family of galectins step by step and performing functional analysis on each protein, the emerging aim is to elucidate the possibility for interplay between galectins. Fittingly, initial comprehensive network analysis for galectins by immunohistochemistry revealed expression profiles with overlaps and differences [82]. Galectins may therefore influence each other’s activities when being co-expressed, and this context dependently in different manners.

In fact, pilot studies have disclosed that i) Gal-3 acts as an antagonist of Gal-1 in growth regulation [83,84], ii) it can trigger apoptosis in primary activated T cells in contrast to Gal-1, which in neutrophils yet both induce phosphatidylserine exposure [85] and iii) it can cooperate with Gal-1 and -8 in osteoarthritis pathogenesis [86]. These initial insights into versatility of functional interplay offer opportunities and challenges.

In addition to these issues, any targeting approach will need to take similarities among the members of this mammalian family in protein structure and in ligand binding, here also for other types of lectins with affinity to LacNAc and its derivatives, into consideration. As listed in the following paragraph, several approaches are in principle capable to interfere with Gal-3 activities:

1. The available monoclonal antibodies, especially with epitope recognition in the tail, appear to allow blocking of extracellular Gal-3. Of note, presence of autoantibodies against Gal-3 in human serum [87] should be taken into account when analyzing data on Gal-3 obtained with clinical samples, as is also the case for galectin presence in serum and cellular microenvironments.
2. Small molecule inhibitors, especially derivatized lactose or thiodigalactoside, and natural polysaccharides such as processed citrus pectin are possible means to interfere with carbohydrate-dependent binding, (most probably) mostly extracellularly, as antibodies can do. Their target selectivity and specificity as well as potential to trigger effects via off-target binding is currently under dispute for polysaccharides [88,89]. Design of glycoclusters suited to distinguish of different modular architecture (shown in Figure 1), in analogy to work on the hepatic asialoglycoprotein receptor that established the concept of the glycoside cluster effect [90], has potential to exploit difference in protein architecture (Gal-3 vs Gal-1; [91]).
3. As a means to downregulate Gal-3 presence globally, also in nuclei and cytoplasm, siRNA offers the potential to switch off production after cell-type-specific delivery. Rigorous controls for off-target effects, determination of extent of achievable silencing and analysis on occurrence of any “adaptive mechanisms” are mandatory.
4. Viewed from the counterreceptor side, Gal-3-driven pathogenesis could ideally be slowed by manipulations on glycan (or cognate protein; for examples, please see bottom part of Table 1) accessibility or presence. Masking of Gal-3-binding

glycans, using as platform for amendments Gal-3-derived ligand-binding peptides [92], or downregulating distinct counterreceptors (cognate glycosylation and/or its protein scaffold; cognate proteins) are means to lower output of Gal-3-dependent signaling.

5. An emerging strategy is to direct Gal-3-dependent signaling *in situ* into a favorable direction by letting a Gal-3 variant with a new type of architecture act as competitor and elicitor. Proof of principle to this concept has recently been obtained by demonstrating an engineered Gal-3 homodimer that exhibits anti-proliferative activity for human neuroblastoma (SK-N-MC) cells so that endogenous (chimera-type) Gal-3 is more than simply neutralized [68].

Summarizing its effects, this variant should compete with the wild-type protein for binding to counterreceptors (neutralization) and initiate different (at best opposite) post-binding signaling (elicitor activity) due to changes in the topology of formed lattices. Obviously, such variants can prove very useful in delineating the relationship between galectin architecture and lattice structure.

In essence, a series of hurdles has to be cleared to reach the aim to define Gal-3 as a therapeutic target, as outlined in the first part of this section. When this has successfully been done, then work on an approach to evaluate the possibility for blocking may follow. In the case of a multifunctional protein acting at many sites and this likely in a network, this is not a trivial task.

5. Conclusion

Guided by the assumptions that “complex carbohydrate-containing molecules may function in synaptic recognition and transmission through establishment of cell-cell contacts and possibly as mediators of communication between the surface and the interior of the cell” and – “in line with these ideas” – and that therefore presence of “protein capable of interacting with saccharides” is expectable, the first galectin had been detected by its β -galactoside-inhibitable bridging of trypsin-treated rabbit erythrocytes and purified by affinity chromatography [19]. This work was the starting point for discovering a family of proteins that share affinity to the canonical ligand lactose and the β -sandwich fold. They are present in many types of cells, on the cellular level intracellularly and after non-conventional secretion in the medium or bound to the cell surface and in the matrix. Structurally, their modular design guides to classify vertebrate galectins into the three classifications presented in Figure 1. The common CRD has the expectable similarity among members of the family illustrated in Figure 2.

On the level of their cellular binding partners, galectins appear to be highly selective for certain binding partners. Faced with the large variety of cellular glycoconjugates, they engage in functional pairing with few distinct counterreceptors. Their suitability to associate to galectin(s) is dynamically regulated (levels of protein or sphingolipid presence and of cognate glycosylation). In addition, peptide motifs satisfy criteria for recognition (for examples, please see Table 1).

Since the discovery of galectins, special attention has been given to the investigation of galectins-1 and -3. In addition to further broadening our knowledge on these two proteins and to systematically filling gaps by studying all family members, the investigation of their activity profiles in mixtures, mimicking the *in vivo* situation, is an emerging challenge. Since simple extrapolations from *in vitro* models to the *in vivo* situation and from mouse models to man are not valid, progress toward defining clinical situation(s) as candidates for considering galectin-based interventions is expected to be slow, as has been observed in the case of the selectins. In this field, the recent testing of a small molecule inhibitor and a humanized anti-P-selectin monoclonal antibody revealed potential in reducing time or rate of sickle cell-related vaso-occlusive pain crises [93-95]. *Mutatis mutandis*, and selectins have a much narrower functionality profile as cell adhesion molecules than galectins, problems and considerations how to proceed are similar: “given the inherent risks in extrapolating data from animal models to humans, careful selection of clinical targets and proper trial design will be essential for further progress” [93].

6. Expert opinion

Research on galectins is a highly fertile field that is contributing exciting lines of evidence to substantiate the validity of the concept of the sugar code. Having started with the analysis of individual members of the family, an emerging topic of research is the network monitoring. The growing awareness of the possibility of local co-presence sets the stage for the discovery of functional interplay even including antagonism.

Of equal importance, it is becoming apparent that availability of counterreceptors for galectin(s) is intimately controlled to gain specific effects at distinct places and time points. The galectins' ability to recognize β -galactosides or glycosaminoglycans or sphingolipids (from 3'-O-sulfated galactose to oligosaccharides) enables their broad-scale involvement in the flow of biological information in (patho)physiological processes. The amazingly fine-tuned coordination of glycosylation (i.e. sialylation via throttling sialic acid biosynthesis) with galectin, and counterreceptor (i.e. $\alpha_5\beta_1$ -integrin) expression by a tumor suppressor, i.e.

p16^{INK4a}, to facilitate susceptibility of pancreatic carcinoma (Capan-1) cells to anoikis induction by Gal-1 *in vitro* [96] is one of several examples pointing to potential for (patho)physiological significance, if these changes will be documented to occur *in vivo*. Essentially, the indicated cross-talk between galectins (and probably other types of lectins) as well as between galectins and the glycosylation/glycoconjugate profile needs to be resolved, then set into relation to distinct disease processes *in vitro* and *in vivo*. Multifunctionality and multi-site expression of the galectins, their likely interplay at sites of co-expression and the emerging-noted variability of counterreceptors on the levels of glycan and scaffold structures among cell types including dynamic regulatory mechanisms (up- and downregulation of *de novo* synthesis and enzymatic remodeling of glycans) make galectins demanding but fascinating study objects. Admittedly, a clinical impact is rather likely not just around the corner.

In general, it is not uncommon that, as encountered as factor to explain the low success rate in phase III randomized clinical trials (RCTs for cancer), “investigators consistently make overly-optimistic assumptions regarding treatment benefits when designing RCTs” [97]. Following a 4-step validation procedure patiently and perseveringly can help decrease likelihood of disappointments [98]. The status of clinical testing in galectin-related phase I/II trials has recently been reviewed with the conclusion that “some of these strategies will be more successful than others” [99]. As stated in connection with the just mentioned assessment of failure rate in RCTs in oncology, “although our goals may initially be lofty, they eventually meet reality” [100]. In this spirit, the aim of reaching an understanding of context-dependent functionality of these multi-purpose effectors alone and in the natural network, and this in models of reasonable translatability, will most likely keep us busy for time to come.

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List of abbreviations

CBP, carbohydrate-binding protein; CRD, carbohydrate recognition domain; Gal, (β -) ga(lactoside-binding)lectin = galectin; IgE/G, immunoglobulin E/G; Mac, macrophage; NT, N-terminal tail (of Gal-3); RCT, randomized clinical trial

Figure 1. Modular architecture of vertebrate galectins. The canonical carbohydrate recognition domain (CRD) is presented in three versions in vertebrates: a hybrid with collagen-like repeats (nine in man) and an N-terminal peptide with two sites of serine phosphorylation (top), a non-covalently associated homodimer (center) and a linker-connected dimer of two different domains (bottom).

Figure 2. Illustration of the structural homology and the canonical contact pattern in ligand binding based on the signature sequence of galectins. a: galectin-1 (Gal-1) (PDB code: 1GZW), b: Gal-2 (5DG2), c: Gal-3 (4LBN), d: Gal-4N (5DUW), e, f: Gal-4C with 3'-sulfated lactose (4YM2) or lacto-N-neotetraose (4YL7) as ligand, g: Gal-7 (4XBQ), h: Gal-8N (3AP9), i, j: Gal-9N with the Forssman pentasaccharide (2EAL) or the N-acetyllactosamine (LacNAc) dimer (DiLacNAc) (2ZHK) as ligand, k: Gal-9C (3NV2) and l: the chicken *galectin-related inter-fiber protein* (C-GRIFIN) (5NLD).

Figure 3. Crystal structure of a variant of human Gal-3 with CRD, collagen-like tandem repeats VII-IX (in purple) and the N-terminal section (in green; please see Figure 1 for modular design of Gal-3) in ribbon (left) and in surface presentation (right); for details, please see [53].

Figure 4. Illustration of CRD-CRD interactions in the case of the crystallized truncated Gal-3 version shown in Figure 3. Three tetramers face each other, each subunit colored. The highlighted central area is given below, showing regions involved in cross-contacts for each subunit (left) and a snapshot showing residues involved in cross-contacts between CRDs and lactose (right); for details, please see [53].

Table 1. Compilation of documented counterreceptors (glycan part of cellular glycoconjugates, proteins) of mammalian galectin-3

type of ligand	galectin-3
glycan	CD6, CD7, CD11b of CD11b/CD18 (Mac-1 antigen, CR3), CD13 (aminopeptidase N), CD32, CD43, CD44, CD45, CD66a,b, CD71, CD95, CD98, CD146 (MCAM, MUC18), CD147, CD166 (ALCAM), CEA, colon cancer mucin, corneal mucin (MUC16), pancreas cancer mucin-4 and MUC1-D (N-glycan at Asn36), cubilin, C4.4A (member of Ly6 family), mDectin-1/2, desmoglein-2, epidermal growth factor receptor, glycoform of IgE, haptoglobin β -subunit (after desialylation), hensin (DMBT-1), insulin receptor, insulin-like growth factor-1 receptor, β_1 -integrin (CD29), $\alpha_4/\alpha_5/\beta_1$ - and $\alpha_v\beta_3$ -integrins, interferon- γ , keratan sulfate, LI-cadherin, laminin, lamp-1/-2, lubricin, Mac-2-binding protein, Mac-3, MAG, MP20 (tetraspanin), Na^+/K^+ -ATPase, NG2 proteoglycan, NKp30, TCR complex, tenascin, tissue plasminogen activator, SIGN-R1, Toll-like receptor-4, transforming growth factor- β receptor, vascular cell adhesion molecule-1, vascular endothelial growth factor receptor 2, von Willebrand factor, ganglioside GM1
protein	AGE products, Alix/AIP-1, ATP synthase b-subunit, axin, bax, bcl-2, β -catenin, Cys/His-rich protein, Gemin4, glycogen synthase kinase-3 β , hnRNP A2B1, hnRNP Q, mSufu, Mer receptor tyrosine kinase, myosin-2A, NLRP3 (NOD-like receptor family, pyrin domain containing 3, cryoporin), non-receptor tyrosine kinases c-Abl and Arg, nucleoporin Nup98, nucling, oncogenic K-Ras, OCA-B, pCIP, PIAS1, synexin (annexin VII), Tsg101, TTF-1, tripartite motif protein (TRIM) 16 (and also 5 α , 6, 17, 20, 22, 23 and 49)

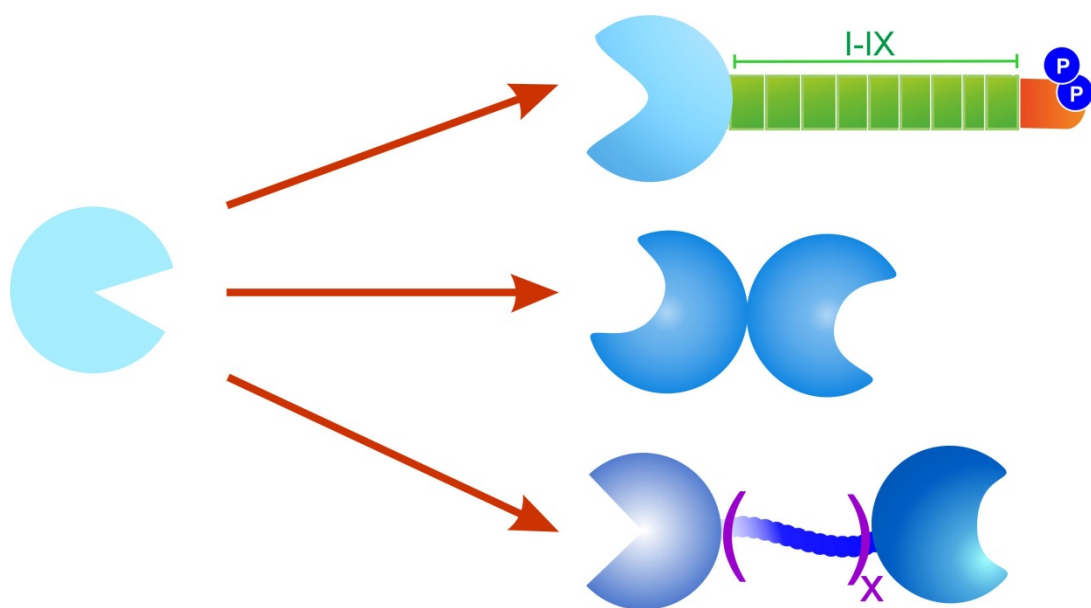


Figure1

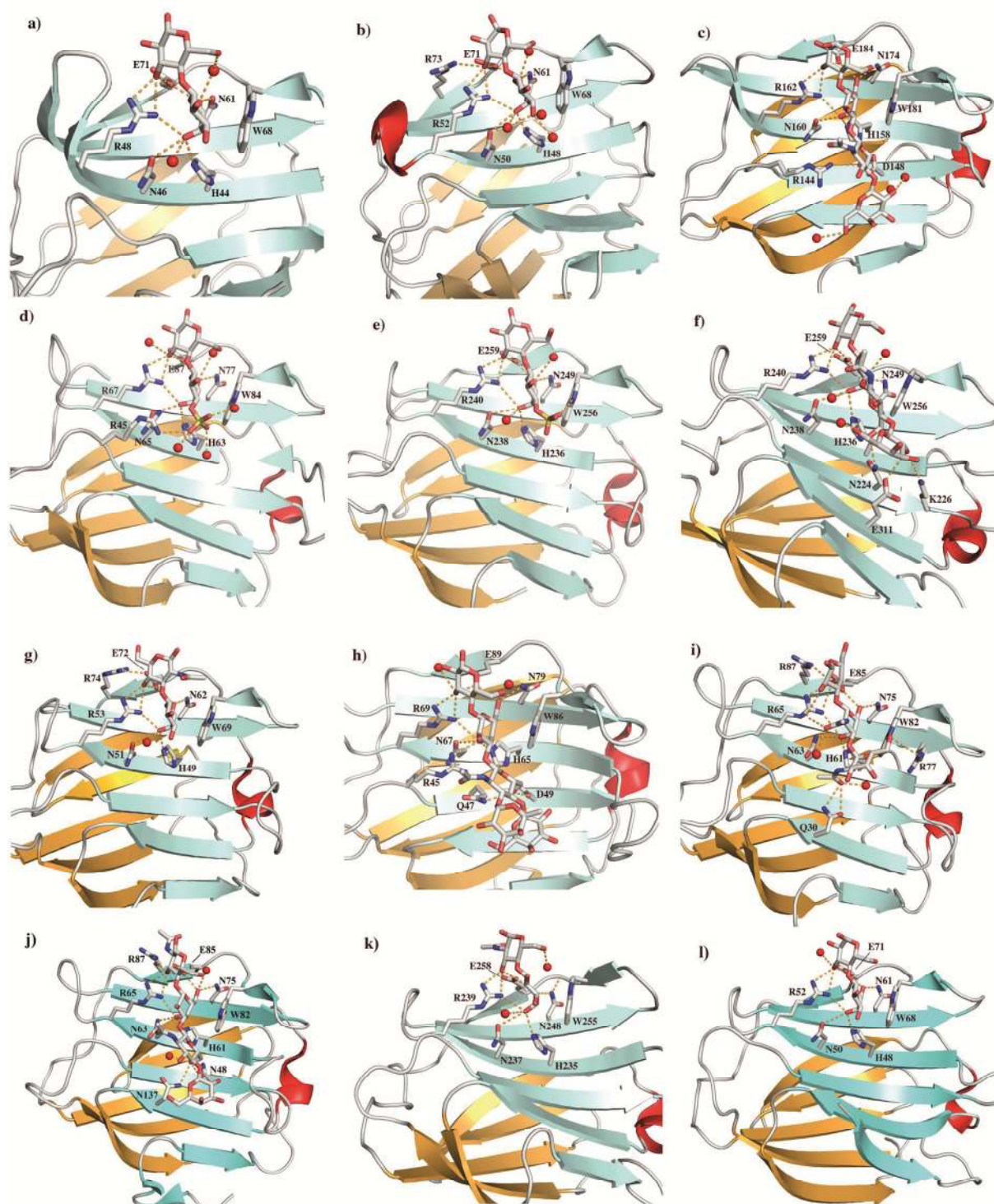


Figure2

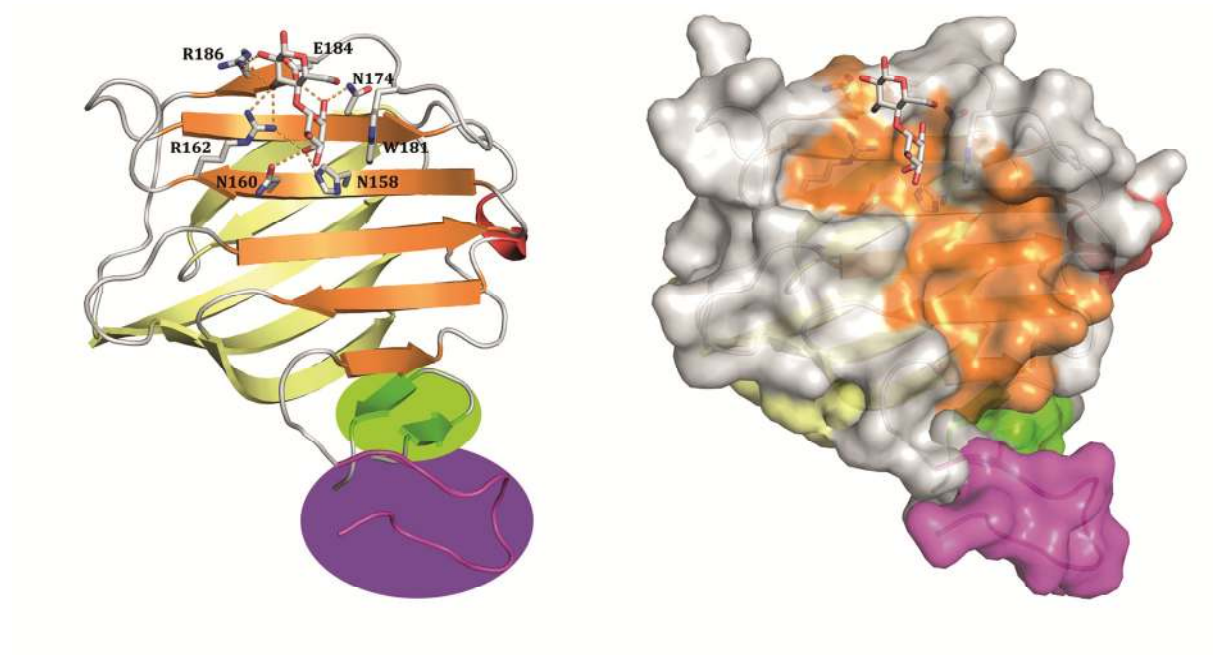


Figure3

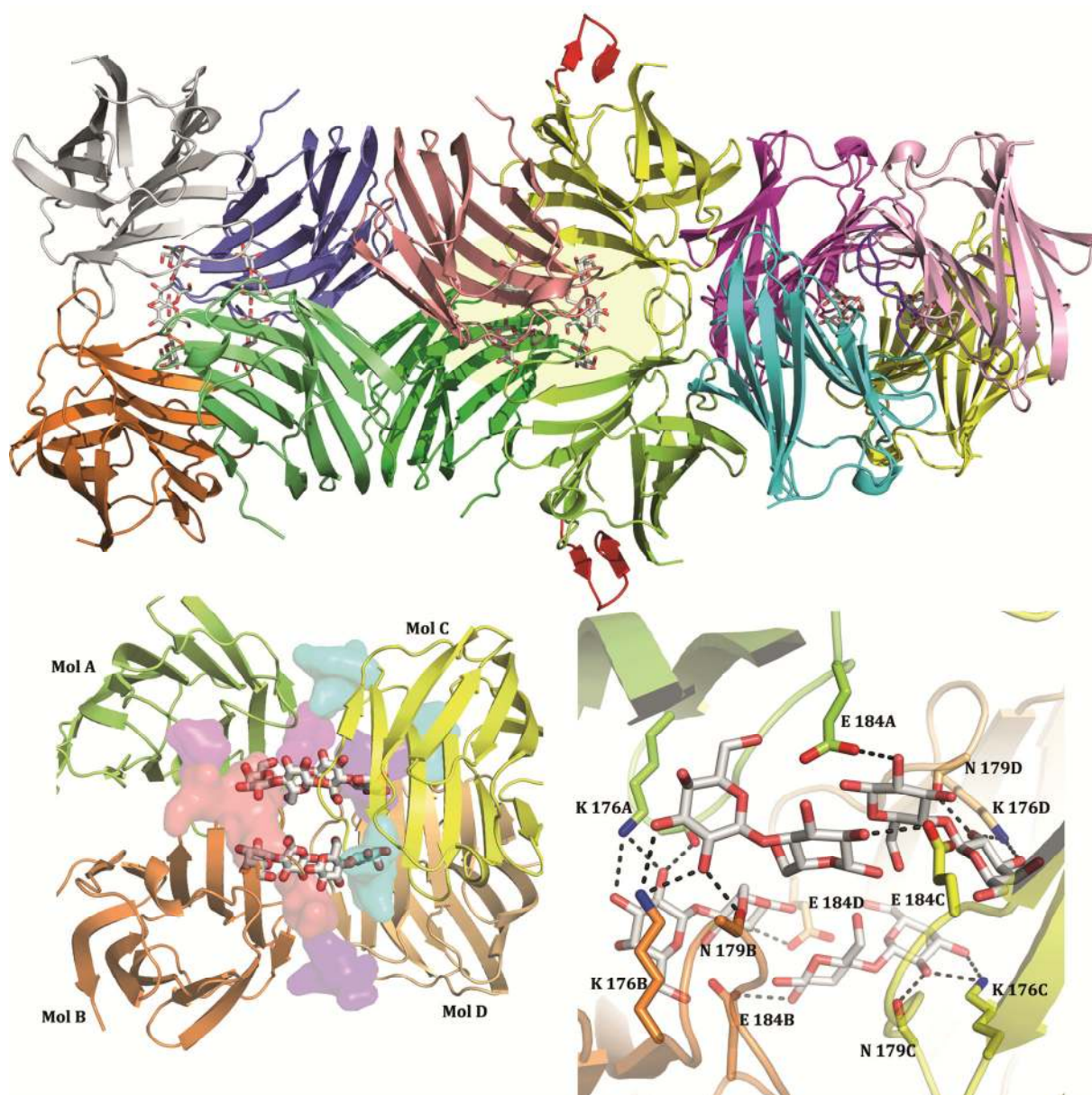
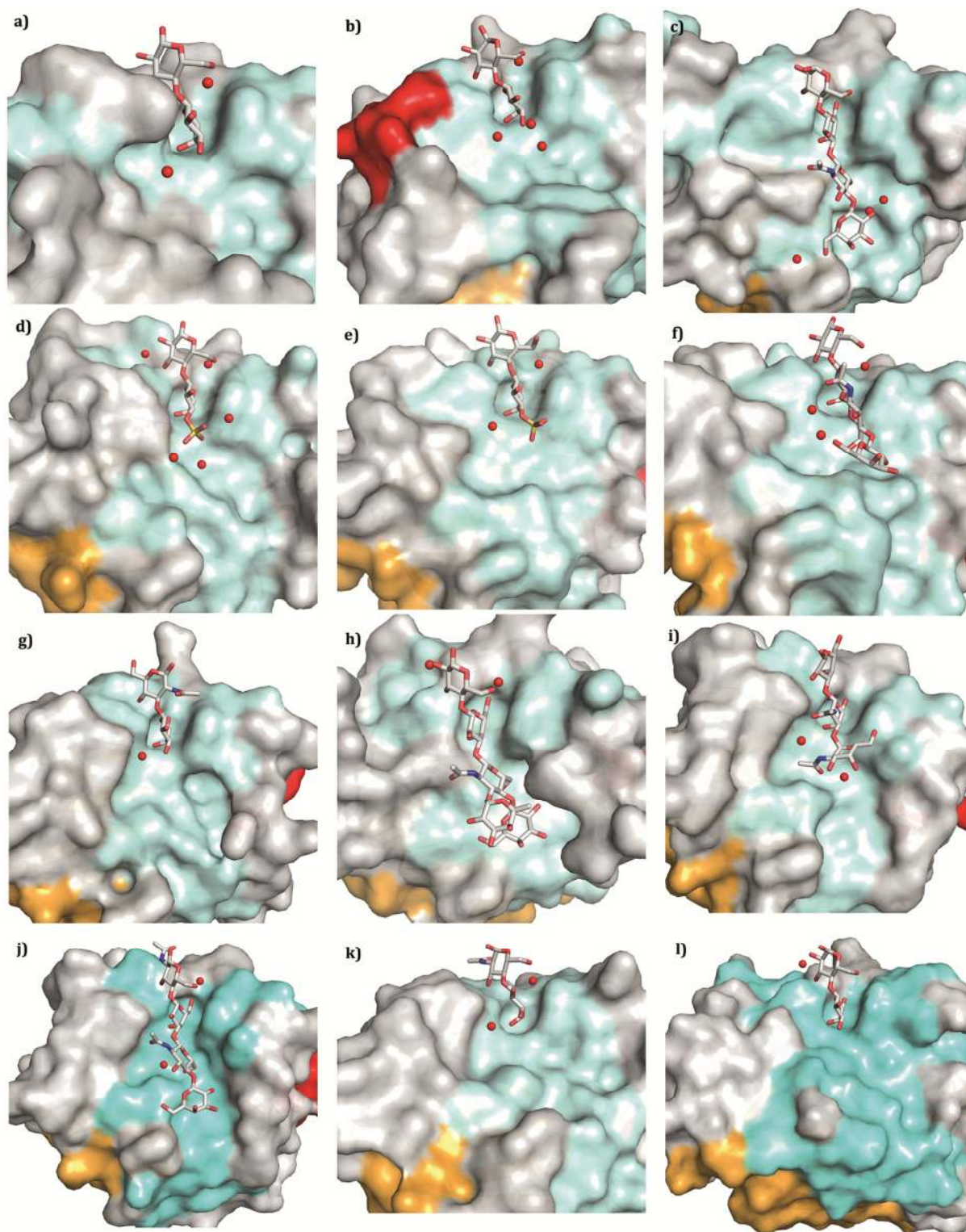


Figure4



Supplementary Figure S1. Illustration of protein surface of the panel of galectins given in Figure 1 (for details on the nature of galectin in each case, please see legend of that figure).