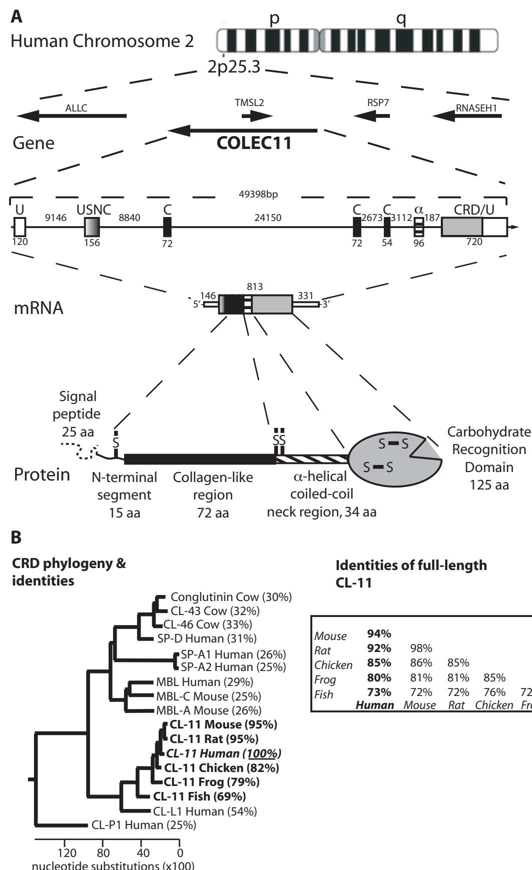
Supplemental Figure 1



	Human	Mouse	Rat	Chicken	Frog
Mouse	**94%**				
Rat	**92%**	98%			
Chicken	**85%**	86%	85%		
Frog	**80%**	81%	81%	85%	
Fish	**73%**	72%	72%	76%	72%

Supplemental Figure 1. A) The CL-11 gene and transcript. Genes are symbolized accordingly to HUGO: ALLC (allantoicase), COLEC11 (CL-11), TMS L (thymosin-like 2), RPS7 (ribosomal protein S7) and RNASEH1 (ribonuclease H1). Exons are designated U: 5'-untranslated sequence (exon 1); USNC: 5'-untranslated, signal peptide, N-terminal segment and collagen-like region (exon 2); C: collagen-like region (exon 3 – 5); α: alpha-helical neck region (exon 6) and CRD/U: carbohydrate recognition domain and 3'-untranslated sequence (exon 7). The sizes of exons, introns and mRNA are given in base pair and nucleotides, respectively. **B) CL-11 identities and phylogeny.** CL-11 amino acid sequences were predicted from the following Genbank depositions: AY358439, NM_027866, NM_001044665, NM_001007331, AAH56052, and Ensemble report ENSRNOP00000011290 - derived from the rat genome project. The phylogeny was based on amino acid sequence alignment of the carbohydrate recognition domains (CRD) of collectins, and actual CRD identities are given in parenthesis. Sequences were aligned by the Clustal W method using a Gonnet matrix and the tree was subsequently constructed by means of the likelihood of branching orders from an ancestral sequence and the neighbourhood joining method.

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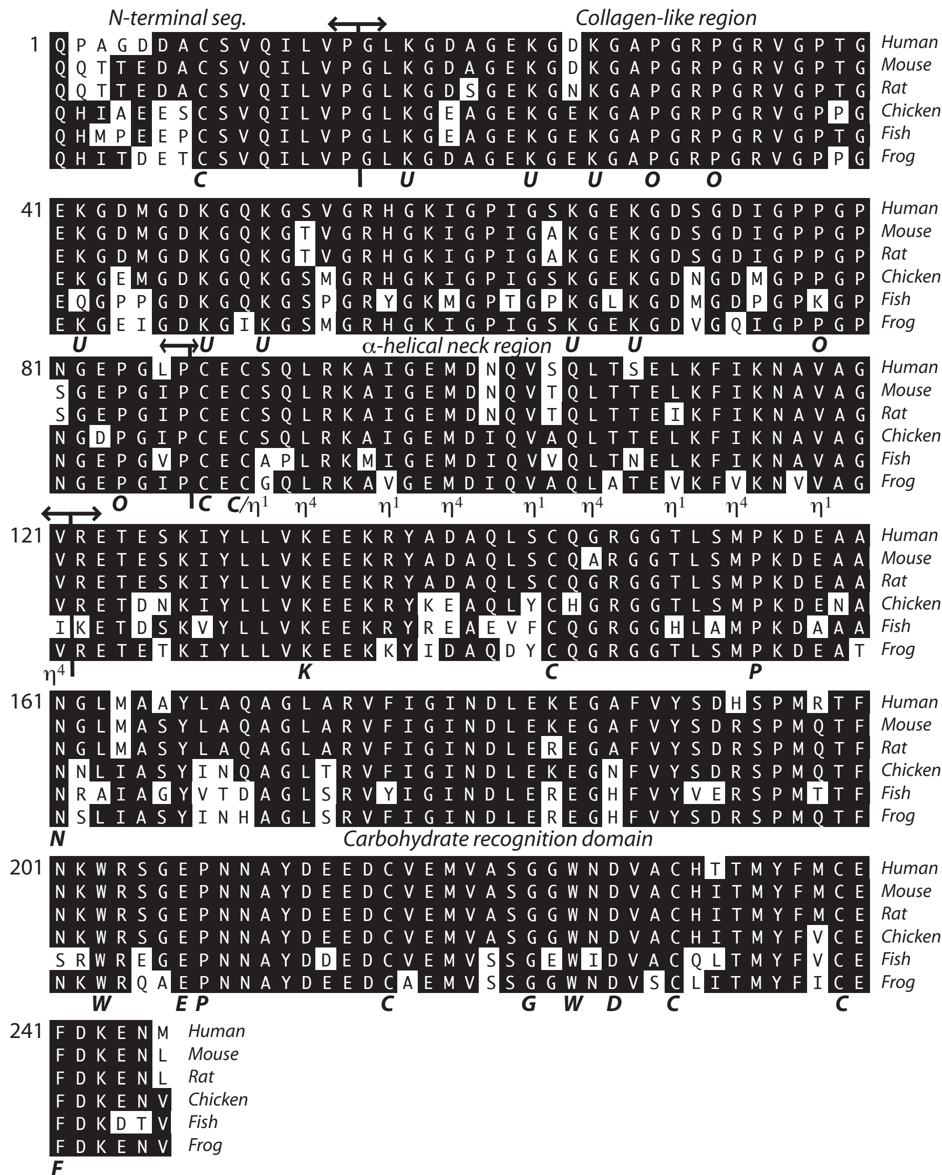
Supplemental Figure 2



Supplemental Figure 2. CL-11 identity among species. The amino acid sequences of CL-11 from human (*Homo sapiens*), mouse (*Mus musculus*), rat (*Rattus norvigecus*), chicken (*Galus galus*), fish (*Danio rerio)* and frog (*Xenopus tropicalis)* were aligned by means of Clustal W (Gonnet Matrix). Sequences were predicted from the following Genbank depositions: AY358439, NM_027866, NM_001044665, NM_001007331, AAH56052. Rat CL-11 was predicted from the ensemble report ENSRNOP00000011290 derived from the rat genome project and partial mRNA transcripts. Cysteine residues and the 14 conserved residues found in the carbohydrate recognition domain of all collectins are indicated by one-letter amino acid symbols. Potential hydroxyprolines and hydroxylysines are indicated by the letters, O and U, respectively. The conserved hydrophobic residues at position 1 and 4 in the heptad repeat of the alpha-helical coiled-coil neck region are indicated with the Greek letter ETA (η).

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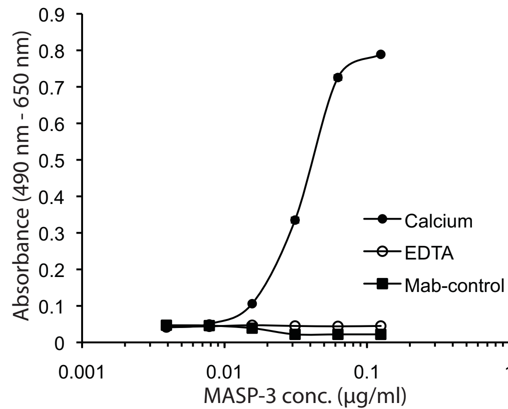
Supplemental figure 3



Supplemental Figure 3. Interaction between recombinant CL-11 and MASP-3. Recombinant MASP-3 was produced in CHO cells similar with the production of CL-11 described in materials and method section. Maxisorb ELISA plates were coated with mannan (10 μg/ml), blocked and incubated o/n with at fixed concentration of CL-11 (1μg/ml) in either TBS/Ca or TBS/EDTA. Wells were washed in buffer with TBS/Ca and dilutions of MASP-3 in TBS/Ca were incubated for 3 hours. Well were washed in TBS/Ca and immobilized MASP-3 was detected with biotinylated anti-MASP-1/3 antibody (8B3) as described in materials and method section. A biotinylated-isotype-matched control antibody (anti-mSP-D) was in separate TBS/Ca samples included (Mab-nonsense) to validate unspecific binding.

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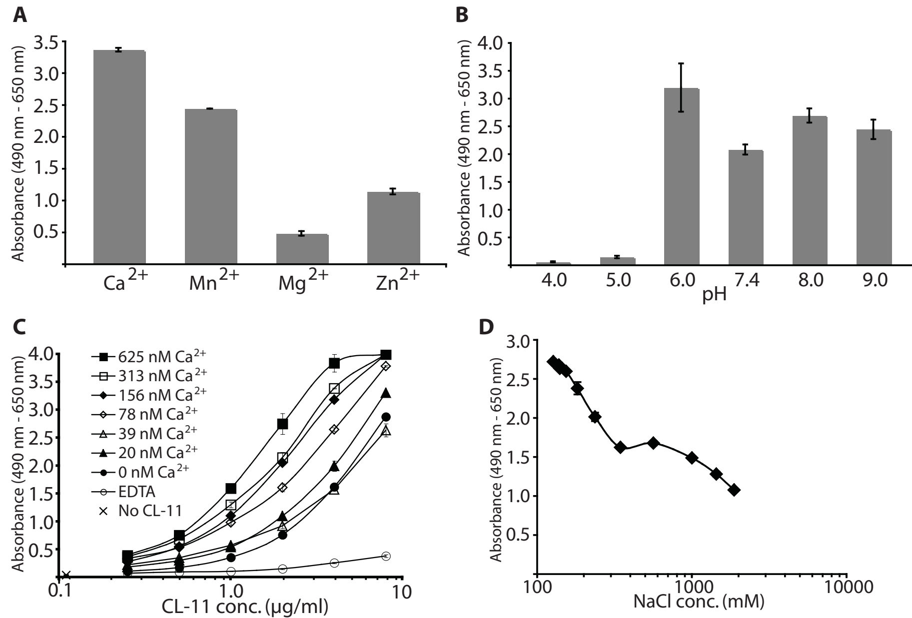
Supplemental Figure 4



Supplemental Figure 4. Characteristics of lectin activity. The binding of human CL-11 to solid phase bound mannan was characterised with respect to the dependency on different cations (**A**), pH (**B**), calcium concentrations (**C**), and ionic strength (**D**). Microtiter plates were coated with mannan (5 μg/ml) or mannose-BSA (2 μg/ml) as described above. Dilutions of untagged human CL-11 prepared in various buffers were incubated, and detected as above by means of biotinylated polyclonal rabbit-anti-CL-11. The dependency on calcium concentrations was analyzed by inclusion of varying $CaCl_2$ concentrations in the TBS/Tw/Ca buffer (1 mg HSA per ml) used for the dilution of CL-11. The dependency of divalent cations was analyzed using 5 mM of either $CaCl_2$, $MnCl_2$, $MgCl_2$, or $ZnCl_2$, in the TBS/Tw buffer (1 mg HSA per ml) used for the dilution of recombinant CL-11. The dependency of ionic strength was analyzed by including varying concentration of NaCl in TBS/Tw/Ca buffer (1 mg HSA per ml) used for dilutions of CL-11. The dependency of pH was analysed by using physiological saline buffers buffered by either 10 mM 2-(N-morpholino)ethanesulfonic acid (pH 4.0 - 5.5) or 10 mM Tris (pH 6.0 – 9.5) adjusted in pH using HCl or NaOH. The buffers included 1 mM $CaCl_2$, 0.01% Tween and 1 mg of HSA per ml. Washes and subsequent incubations were performed using TBS/Tw/Ca, pH 7.4.

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