Supporting Information

1. To identify the IRR ectodomain, western blot was used as described in the materials and methods. Western blot analysis showed that antibodies specifically bind to the isolated protein in all the fractions analyzed.

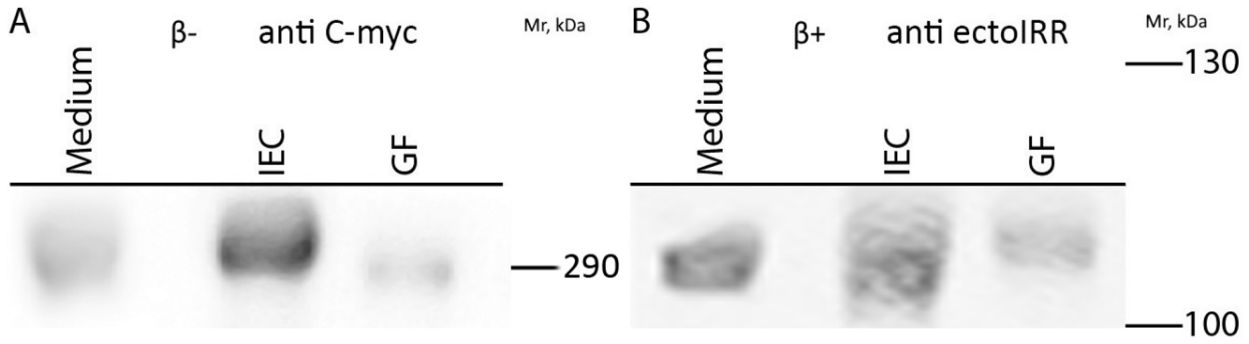

Figure SI 1. Western blot staining of samples containing the ectoIRR (A) blotted with antibodies against C-myc without β-mercaptoethanol (B) blotted with antibodies against ectoIRR with β-mercaptoethanol. Medium - culture medium, IEC - ion exchange chromatography fraction, GF-fraction after gel filtration. Mr, kDa – molecular weight marker.

2. Experimental small-angle X-ray scattering curves of the ectoIRR at pH 7.0 (1) and pH 9.0 (2) and comparison of *ab initio* shapes calculated by DAMMIN program.

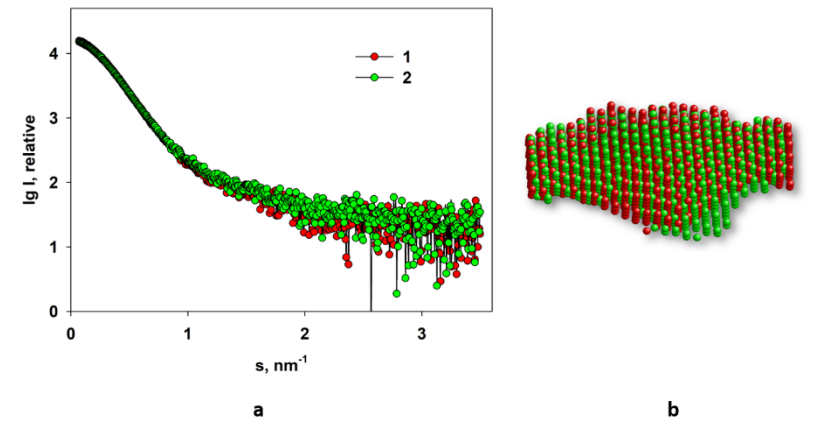

Figure SI 2. a: Comparison of the experimental small-angle X-ray scattering curves at pH 7.0 (1) and pH 9.0 (2); **b:** Superposition of the ab initio shapes reconstructed by the program DAMMIN at pH7 (red) and pH 9 (green), NSD = 0.5.

3. SDS-PAGE analysis of the pure protein under reducing conditions shows bands corresponding to the expected molecular masses of the separate, glycosylated α-chain (~110 kDa) and β-chain (~37 kDa) of ectoIRR. Under nonreducing conditions, the same analysis shows a single band at molecular mass corresponding to the intact, glycosylated ectoIRR homodimer (~290 kDa).

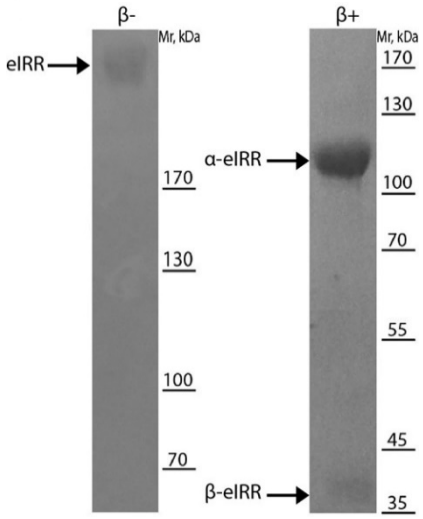

Figure SI 3. SDS-PAGE analysis of purified ectoIRR without (1) and with (2) addition of β-mercaptoethanol. The arrows indicate: IRR ectodomain (eIRR), α-subunit (α – eIRR) and β-subunit (β-eIRR) of the IRR ectodomain. Mr, kDa - molecular weight marker.

4. An attempt has been made to obtain only symmetrical open conformation by imposing the 2-fold symmetry axis between the dimer subunits, such that for each atom with the coordinates (X, Y, Z) in the first monomer a symmetry mate in the second monomer has the coordinates (-X, -Y, Z). Using the P2 symmetry constraint however yielded a worse fit to the experimental data with the χ^2 = 1.6 (Fig. SI 5).

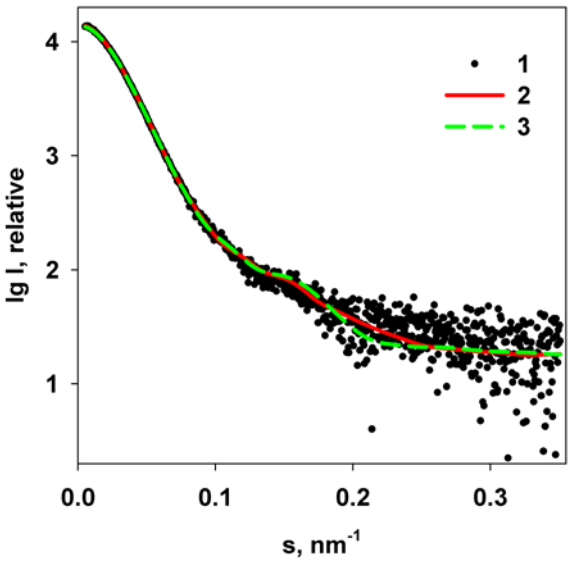

Figure S1 4. Comparison of rigid body modeling the dimeric ectoIRR structure with and without P2 symmetry: experimental scattering curve (1); scattering patterns computed from the CORAL model without imposing 2-fold symmetry axis between the monomers, χ^2 = 1.3 (2); scattering patterns computed from the CORAL model with P2 symmetry χ^2 = 1.6 (3).

5. In order to compare structures of ectoIRR and insulin receptor program CRYSOL was used to calculate scattering curve from a symmetrical head-to-tail crystal structure of insulin receptor (derived from the PDB entry: 4ZXB).

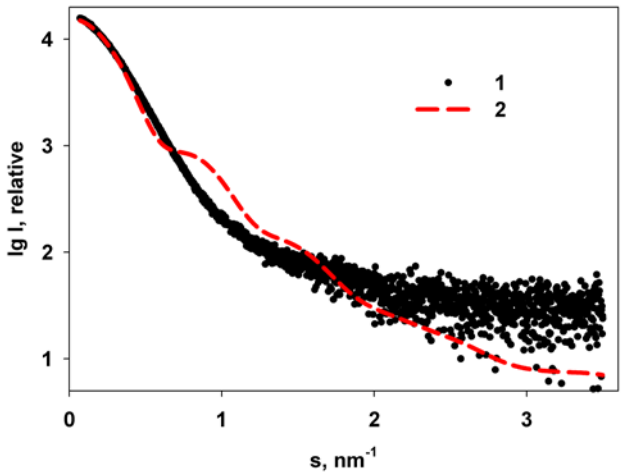

Figure SI 5. Comparison of scattering curves from the ectoIRR dimer (1) and calculated by program CRYSOL scattering from the crystal structure of insulin receptor ectodomain dimer derived from the PDB entry: 4ZXB (2).