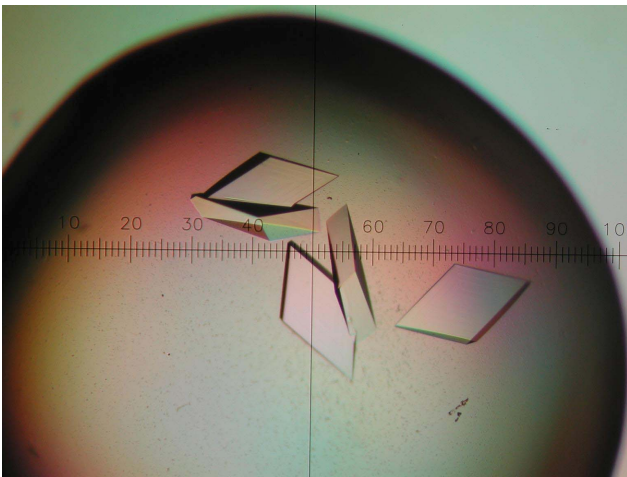


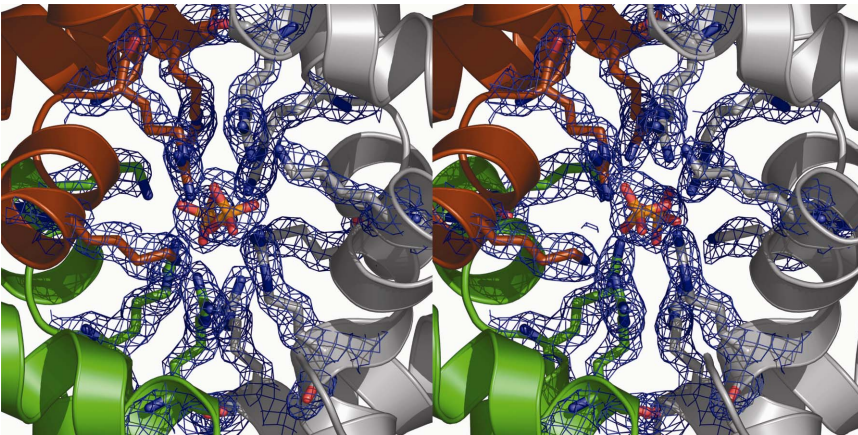
Supplementary Gene-Bank accessions for sequences in main article figure 2

Aligned sequences correspond to the following Gene-Bank accessions. *Ustilago maydis* (Um) Arc1p, XP_400509.1, GluRS, XP_402397.1; *Schizosaccharomyces pombe* (Sc) Arc1p, NP_594656.1, GluRS, NP_593483.1; *Yarrowia lipolytica* (Yl) Arc1p, XP_503499.1, GluRS, XP_504508.1; *Debaryomyces hansenii* (Dh) Arc1p, XP_456881.1, GluRS, XP_461343.1; *Candida albicans* (Ca) Arc1p, XP_713255.1, GluRS, XP_720349.1; *Kluyveromyces lactis* (Kl) Arc1p, XP_455553.1, GluRS, XP_451028.1; *Ashbya gossypii* (Ag) Arc1p, NP_985516.1, GluRS, NP_985811.1; *Saccharomyces cerevisiae* (Sc) Arc1p, X95481, GluRS: P46655.

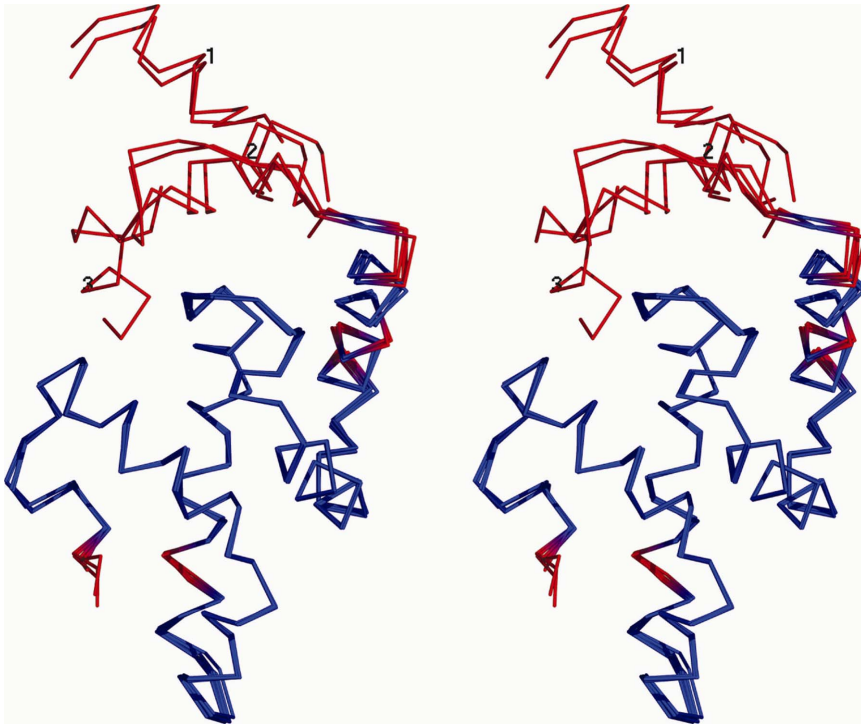
Supplementary figures



Supplementary Fig. 1. Photograph of typical GluRS_1-207 crystals (maximum 350 μm in length).



Supplementary Fig. 2. Two sulfates in the center of each tetramer are coordinated by four arginine and two lysine side chains each. 2Fo-Fc electron density for the sulfates and coordinating residues has been contoured at 1.5σ .



Supplementary Fig. 3. Conformationally flexible (red) and invariant (blue) parts in Arc1p-N. Stereo view of five monomers each representing a cluster of conformers shown as C^α-traces and superimposed on their invariant parts. Due to the 20-fold NCS, the structure of Arc1p-N lends itself to an analysis of conformationally flexible and invariant parts. Manual inspection of the structure suggests that the conformation of the 20 monomers is very similar from residue 23 onwards, but the N-terminal 22 residues adopt three significantly different conformations (main article fig. 3*b*). Detailed analysis of the conformational variance among the 20 monomers by automated error-scaled difference distance matrix analysis as implemented in *ESMET* (Schneider, 2000, 2002, 2004) reveals conformationally invariant and flexible regions of Arc1p-N and identifies the flexible segments as residues 3-22, 24-25, 32, 34, 38, 81-82 and 120-122. While the alternative conformation is obvious (main article Fig. 3*b* and this figure) for residues 3-22, the variations in the other segments are more subtle. In the case of residues 120-122 it appears to be due to conformational freedom that naturally occurs at the very C-terminus of the protein. In the case of the remaining segments it may be due to slight distortions resulting from crystal packing as the involvement of these residues in inter-chain crystal contacts differs among the 20 monomers.