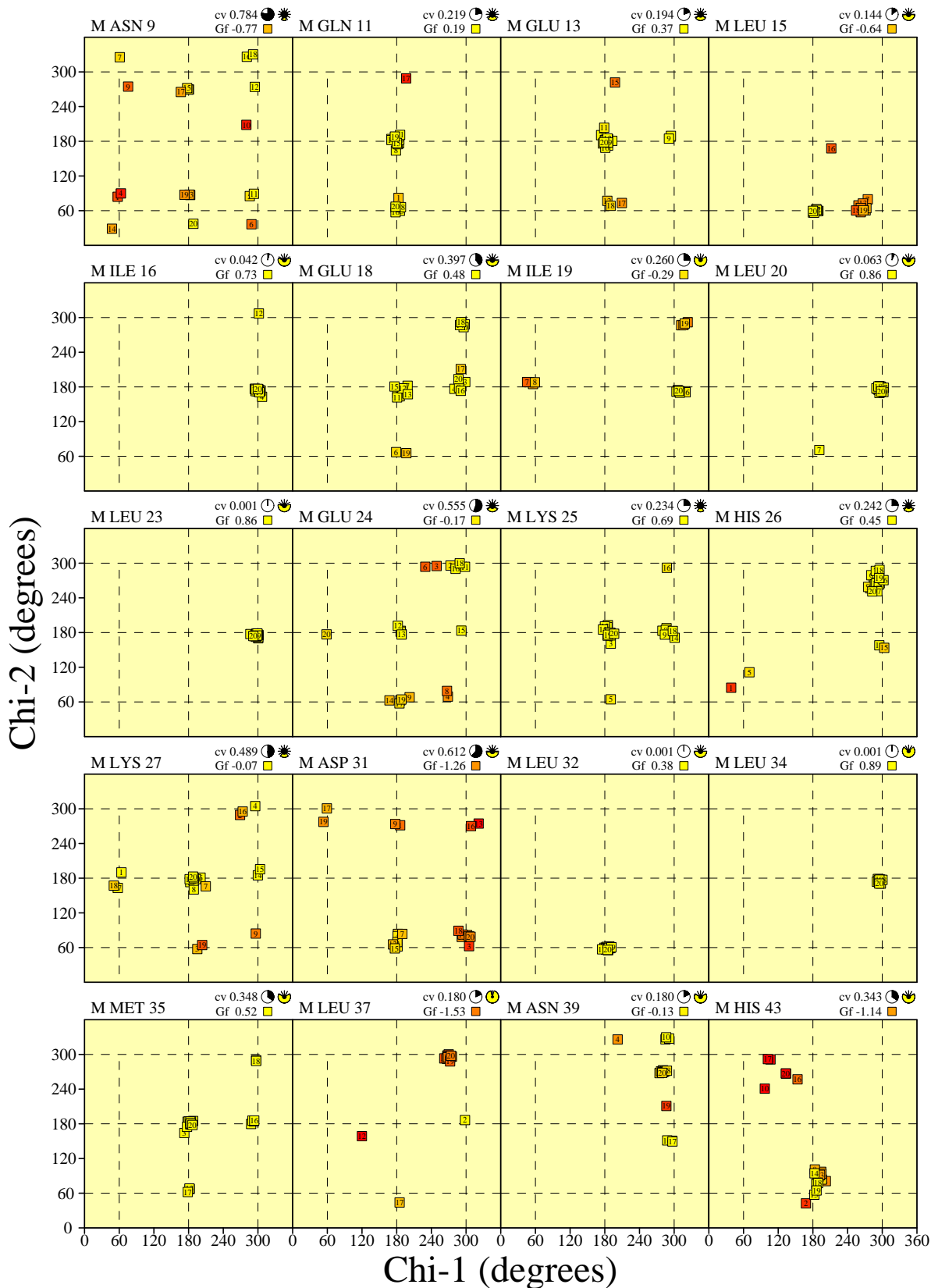


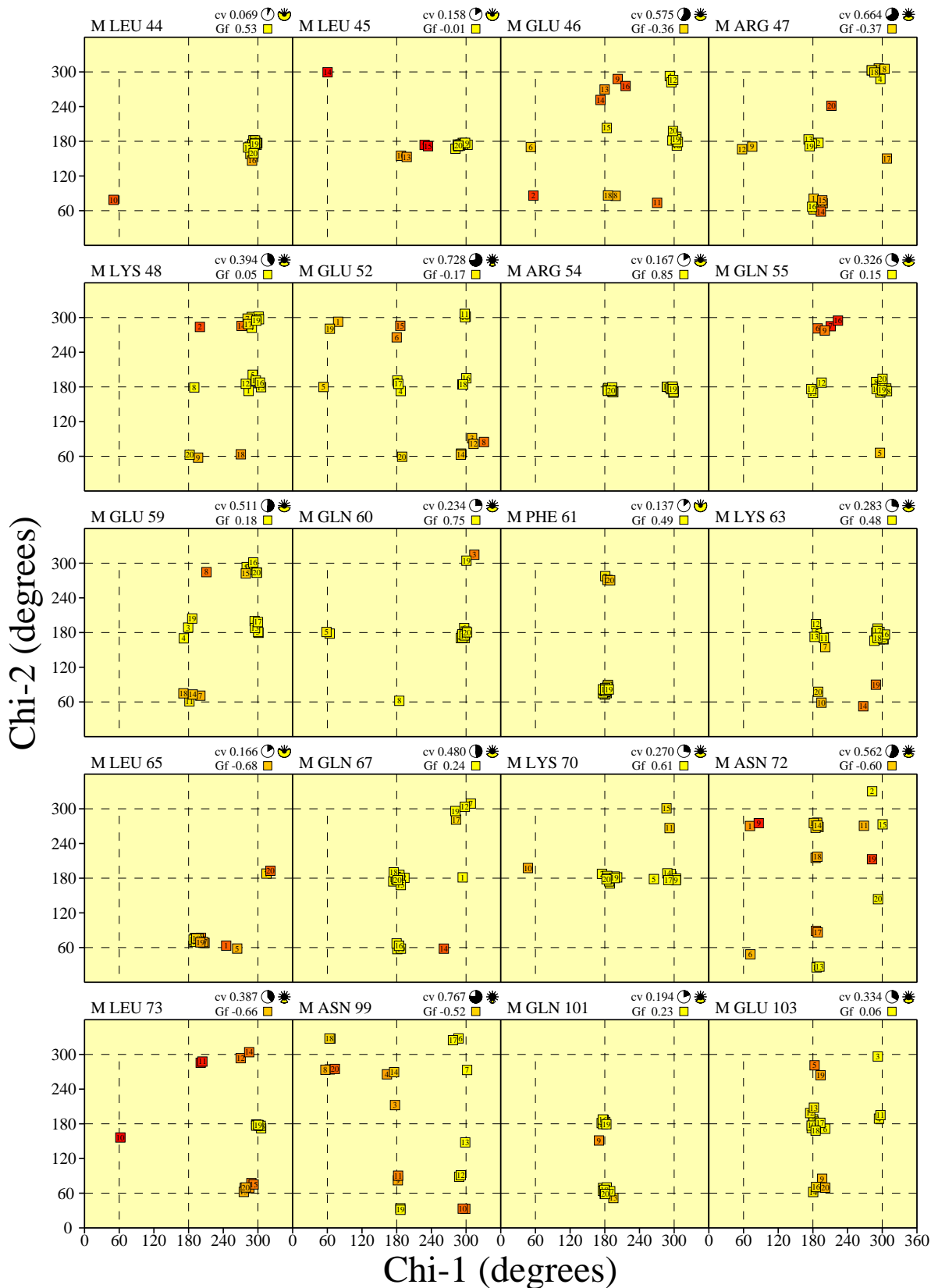
Ensemble chi1-chi2 plots

SOR77_NMR_em_bcr3 (20 models)**



cv = Circular Variance (low values signify high clustering of the data points). ☀ Accessible 🌙 Buried
 Gf = Average G-factor for the residue (the higher the value the more favourable the conformations) based on analysis of high-res. Xstal structures
 Data points coloured according to G-factor: 🟡 Favourable 🔴 Unfavourable

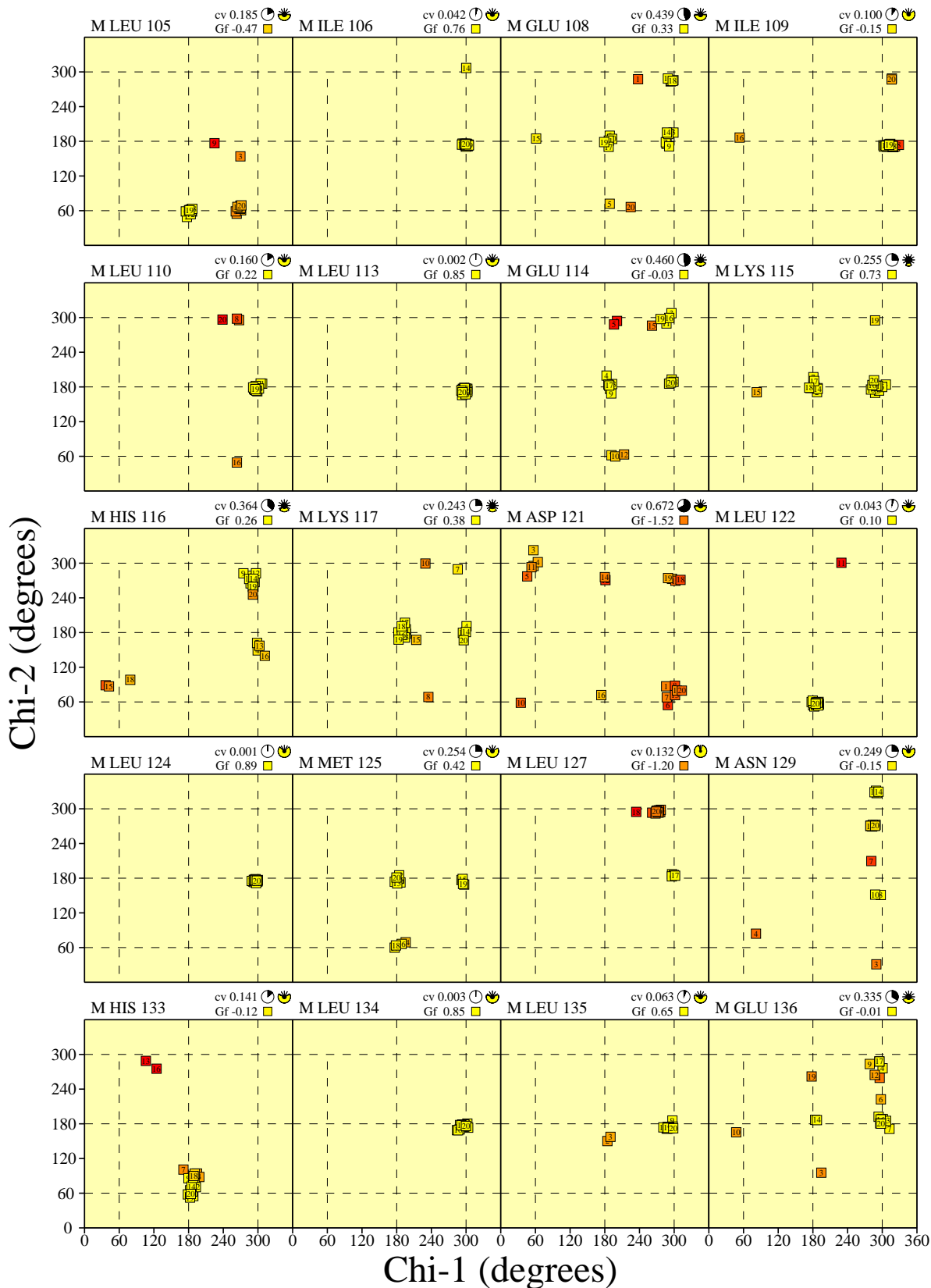
Ensemble chi1-chi2 plots SOR77_NMR_em_bcr3 (20 models)**



cv = Circular Variance (low values signify high clustering of the data points). * Accessible ◻ Buried
 Gf = Average G-factor for the residue (the higher the value the more favourable the conformations) based on analysis of high-res. Xstal structures
 Data points coloured according to G-factor: ◻ Favourable ◻ Unfavourable

Ensemble chi1-chi2 plots

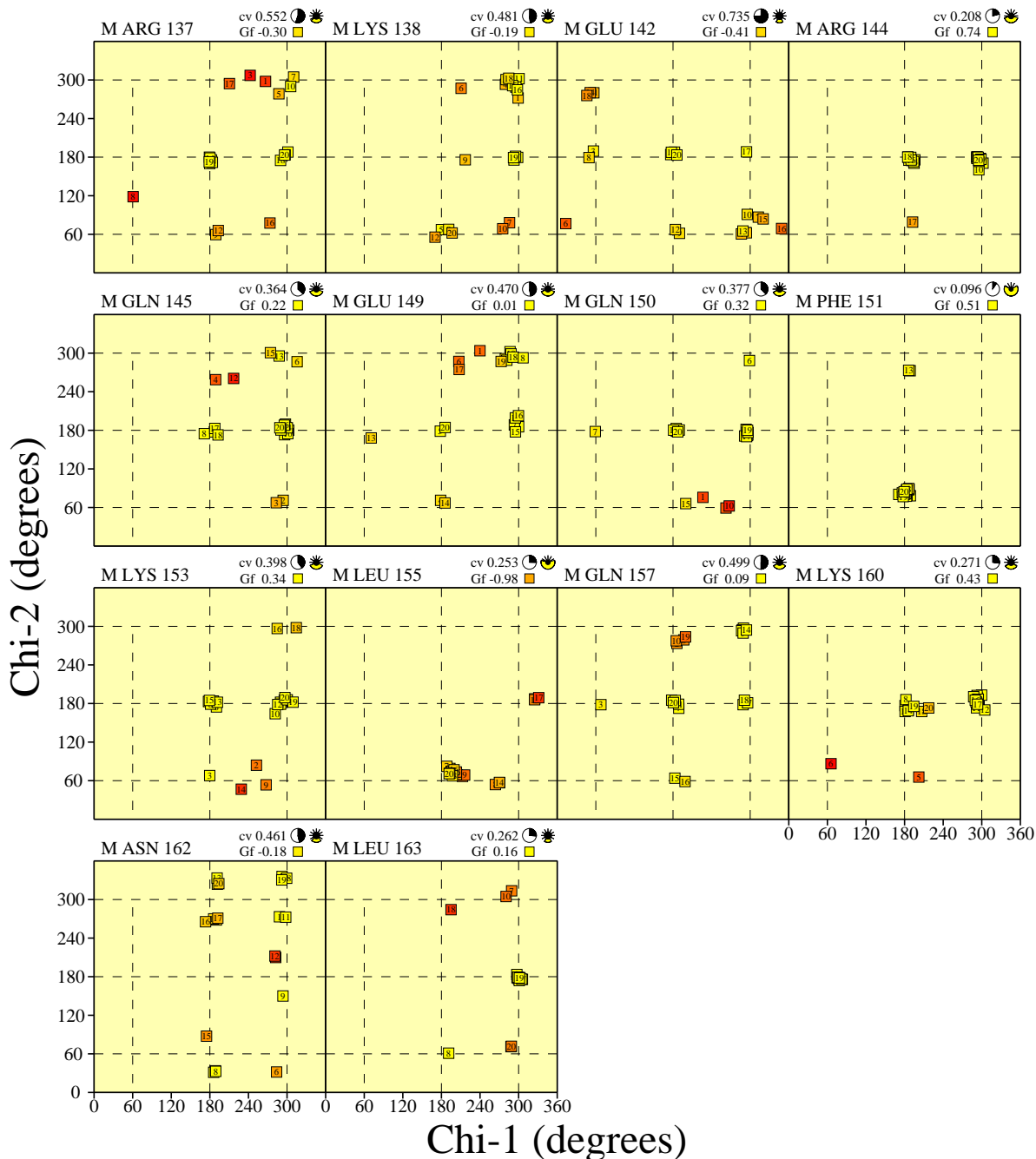
SOR77_NMR_em_bcr3 (20 models)**



cv = Circular Variance (low values signify high clustering of the data points). * Accessible ☺ Buried
 Gf = Average G-factor for the residue (the higher the value the more favourable the conformations) based on analysis of high-res. Xstal structures
 Data points coloured according to G-factor: Favourable Unfavourable

Ensemble chi1-chi2 plots

SOR77_NMR_em_bcr3 (20 models)**



cv = Circular Variance (low values signify high clustering of the data points). ☀ Accessible 🌙 Buried
 Gf = Average G-factor for the residue (the higher the value the more favourable the conformations) based on analysis of high-res. Xstal structures
 Data points coloured according to G-factor: Favourable Unfavourable