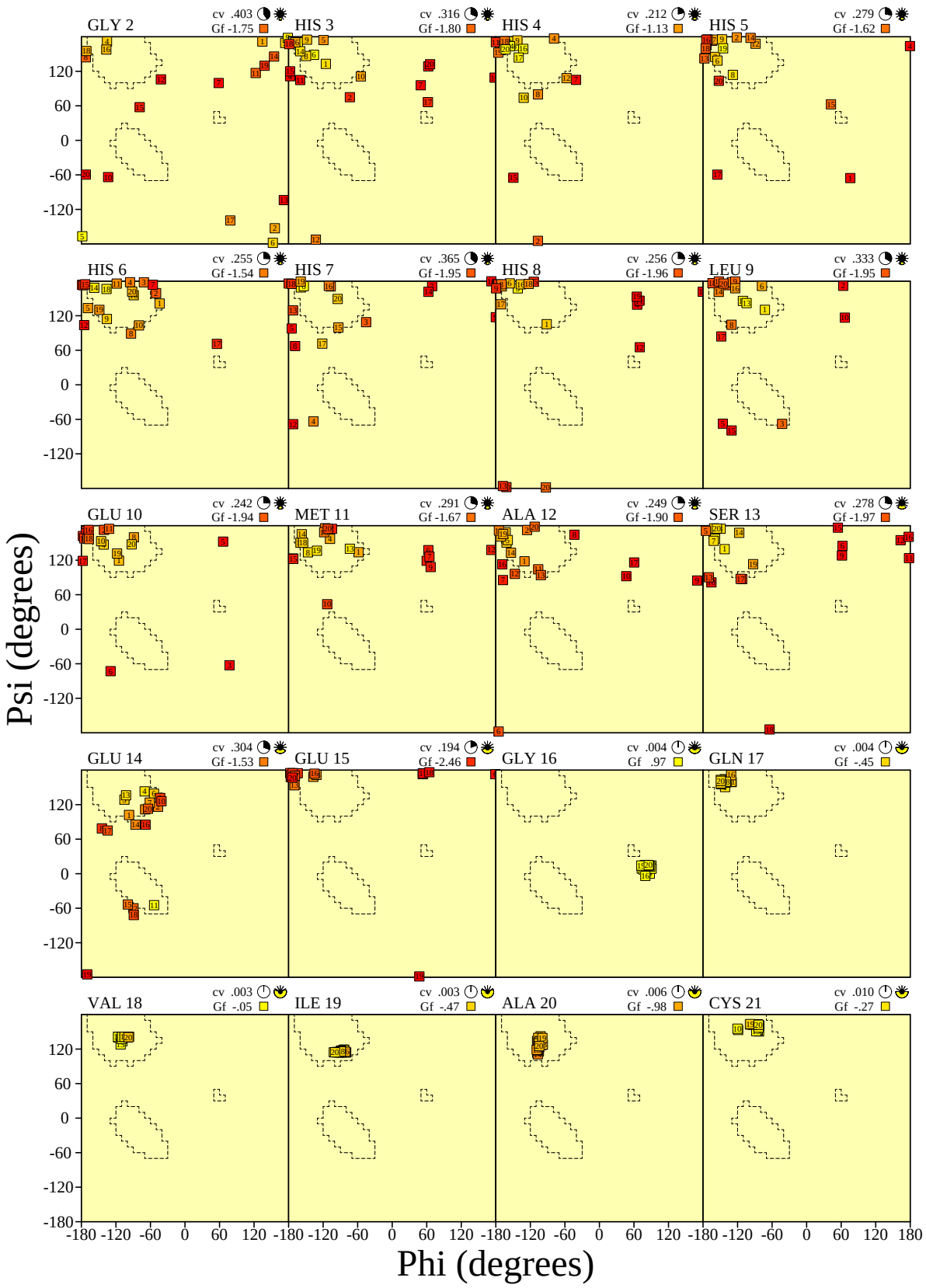
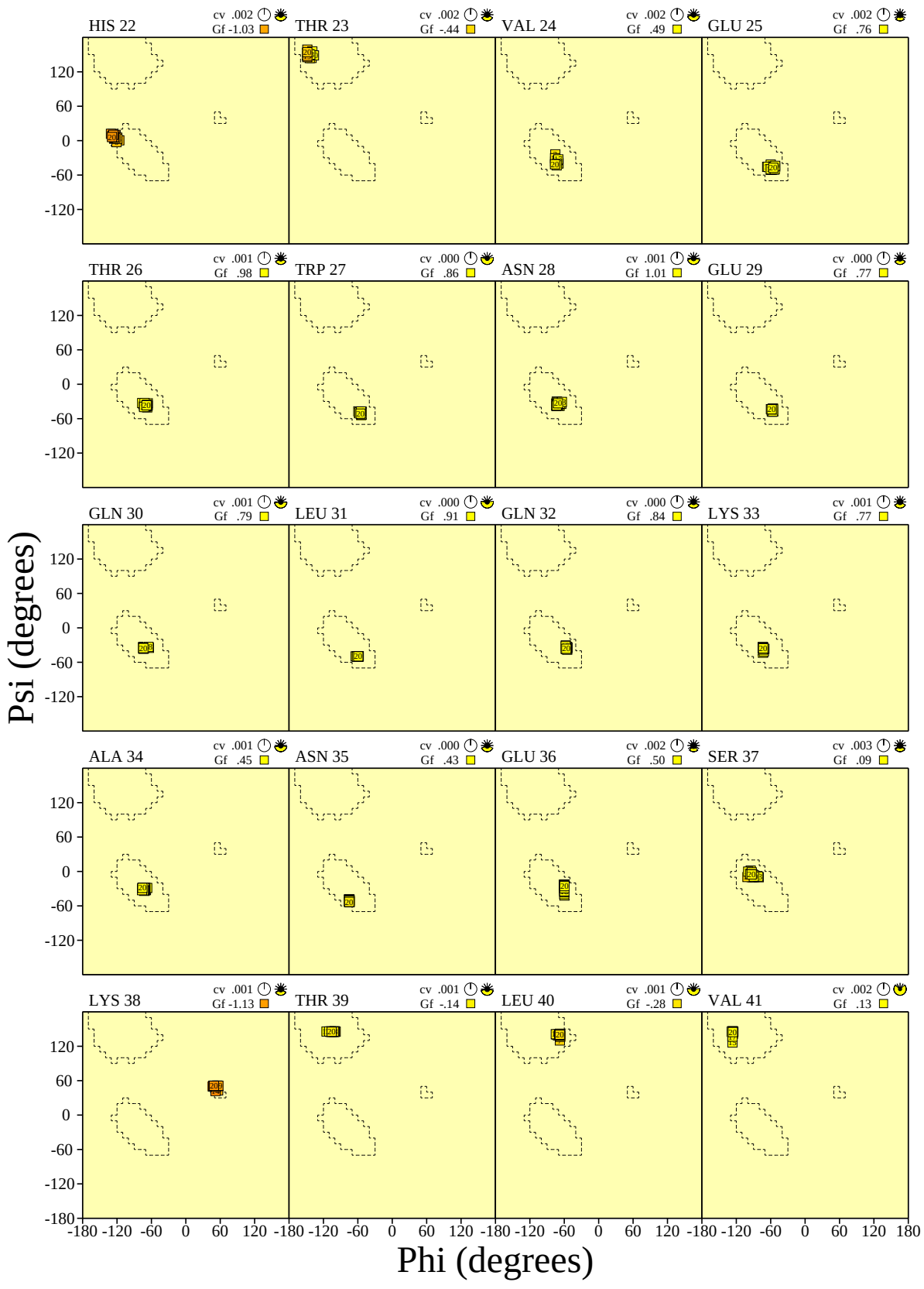
PROCHECK-NMR

Ensemble Ramachandran plots
ensemble_analyzed (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 Ramachandran plots
ensemble_analyzed (20 models)



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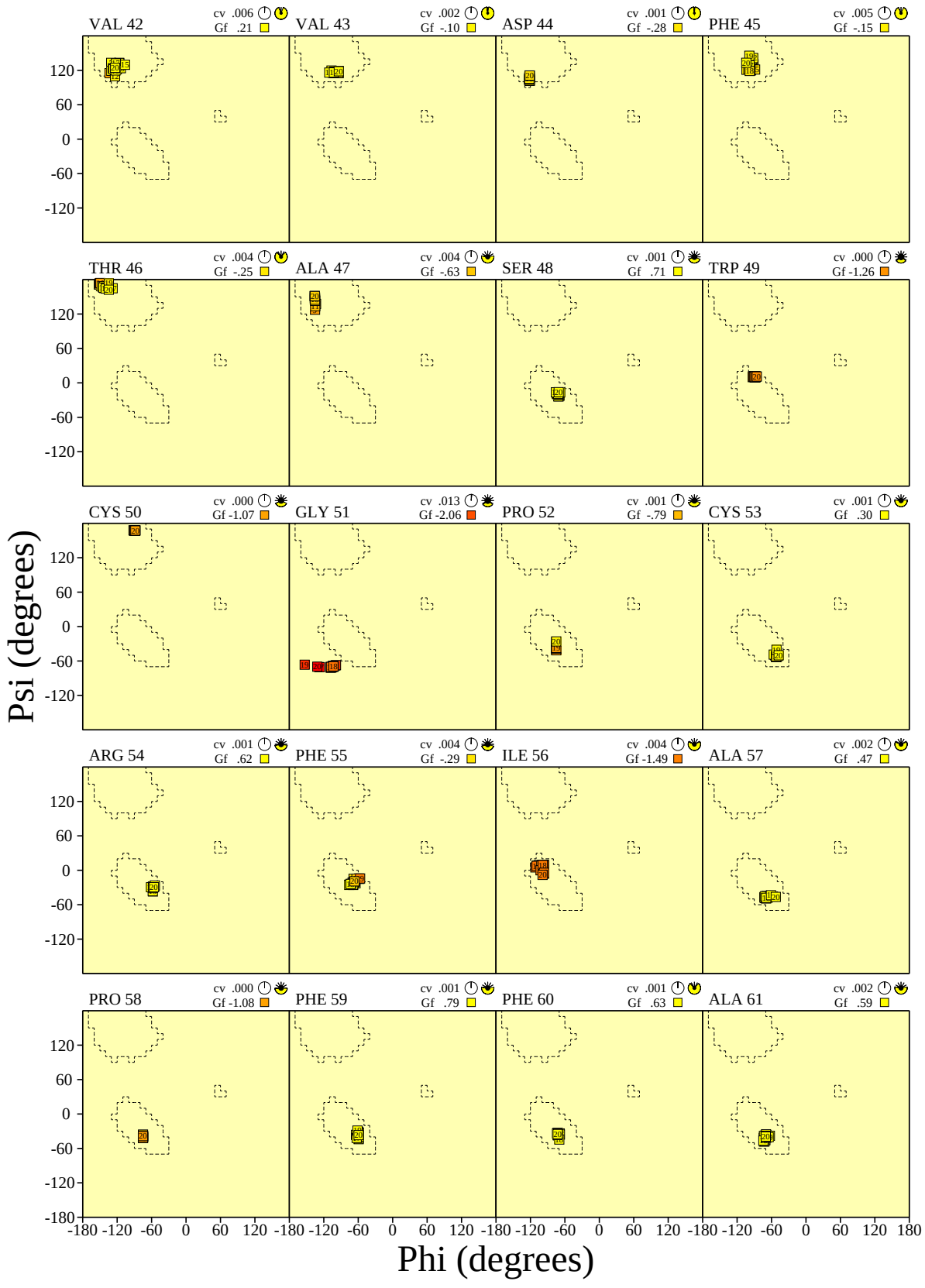
Gf = Average G-factor for the residue (the higher the value the more favourable the conformations) based on analysis of high-res. Xstal structures
Data points coloured according to G-factor: Favourable Unfavourable

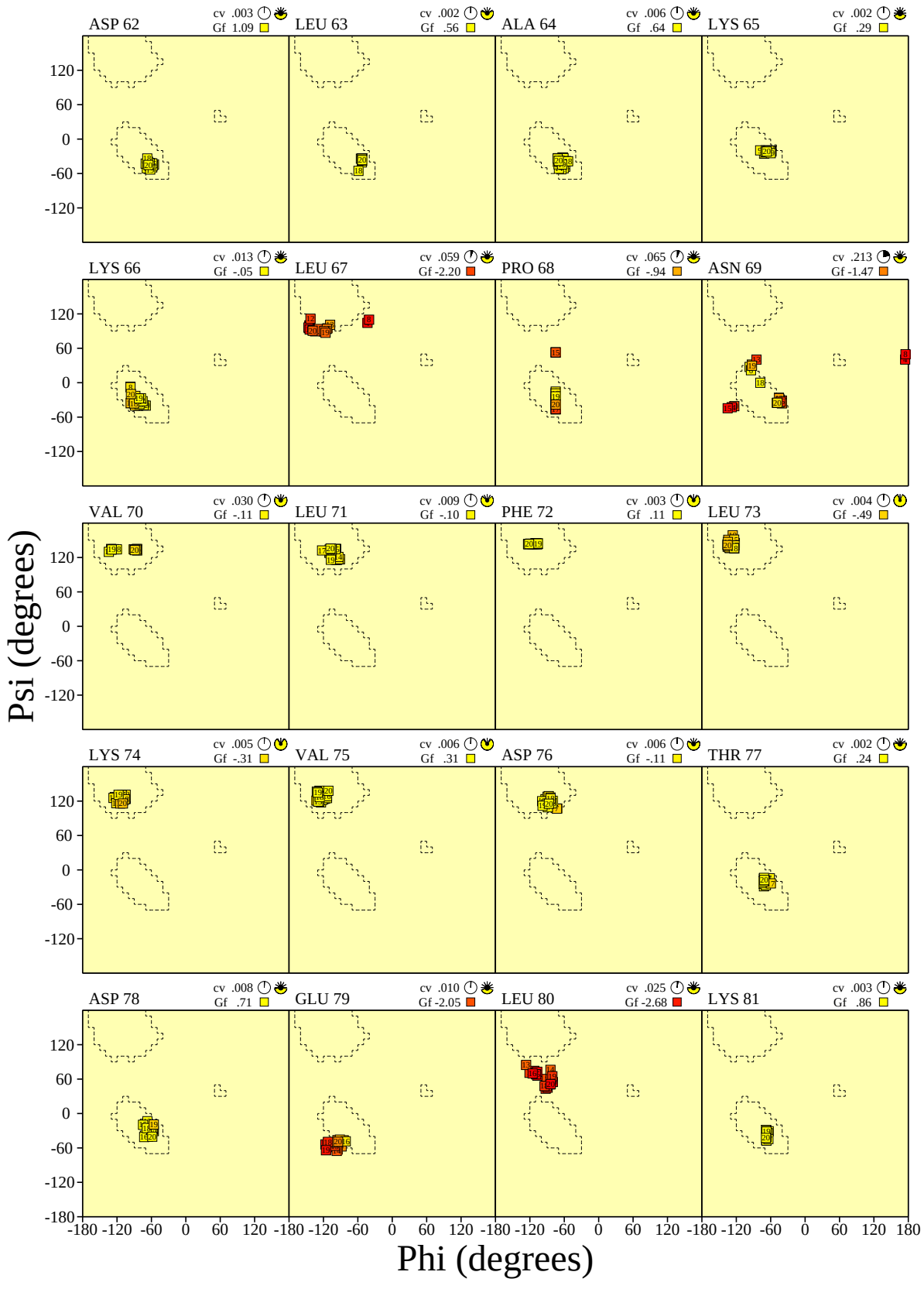
Ensemble Ramachandran plots
ensemble_analyzed (20 models)



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

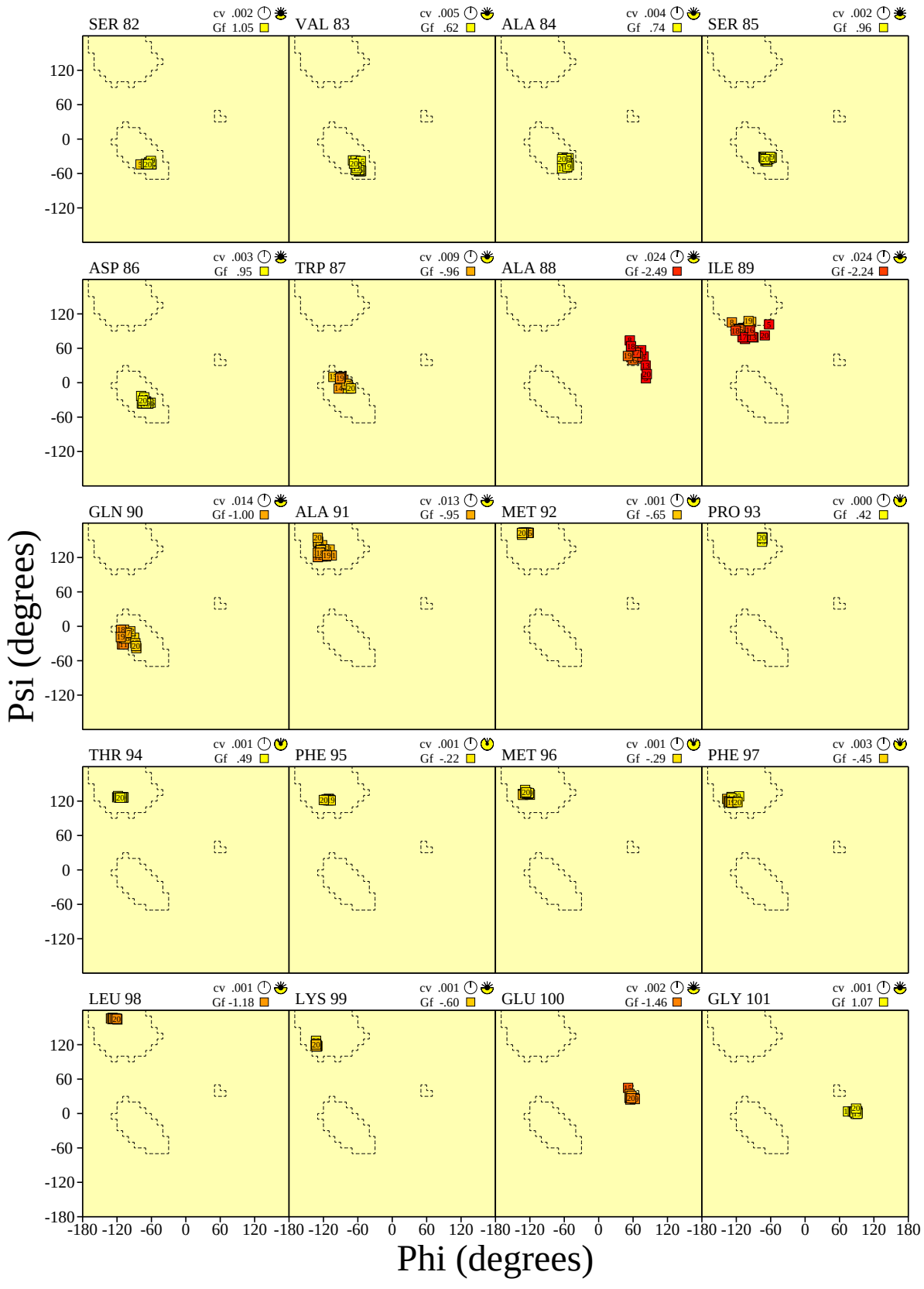
ensemble_analyzed_06.ps

Ensemble Ramachandran plots
ensemble_analyzed (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 Ramachandran plots
ensemble_analyzed (20 models)



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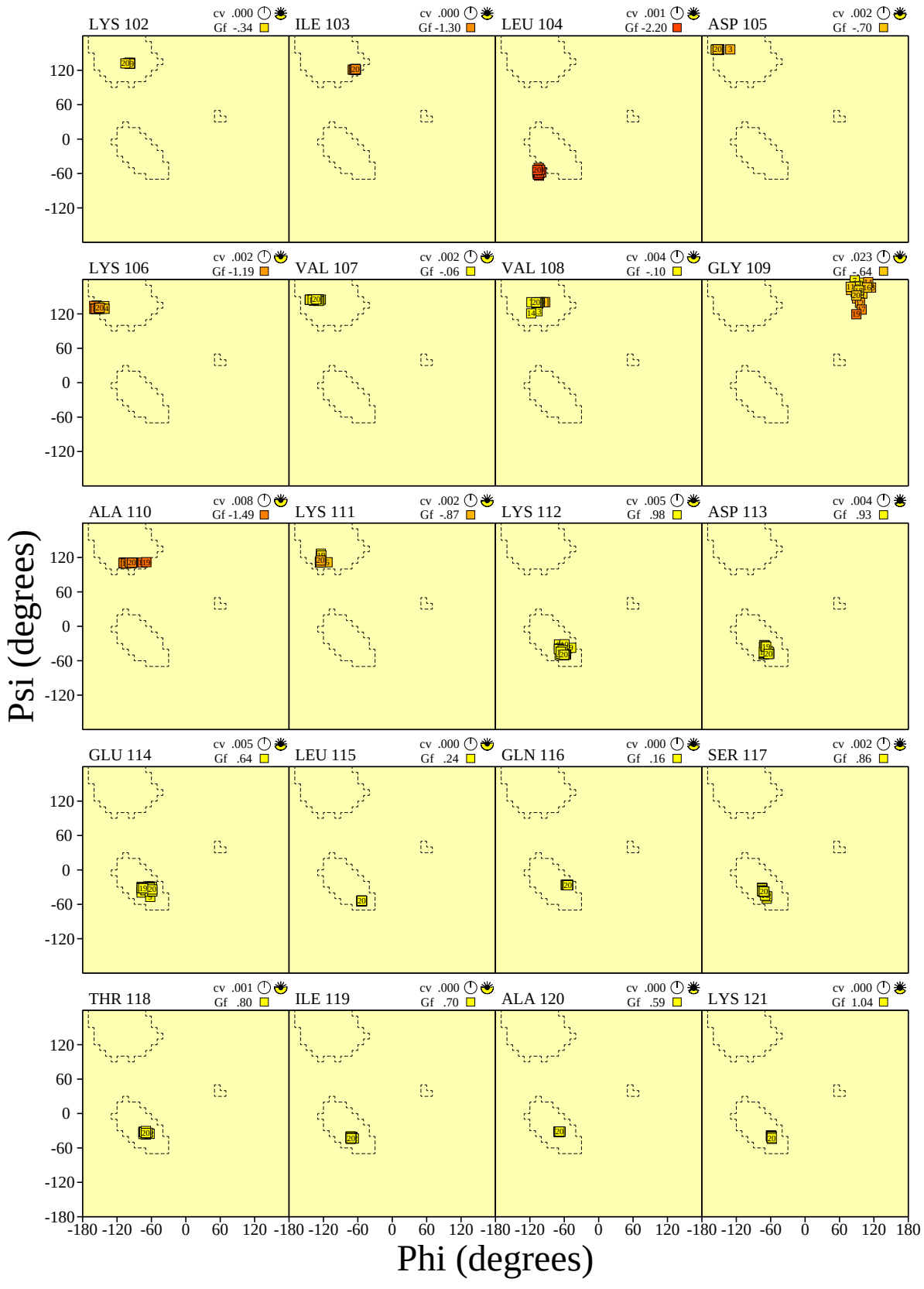
Gf = Average G-factor for the residue (the higher the value the more favourable the conformations) based on analysis of high-res. Xstal structures
Data points coloured according to G-factor: Favourable Unfavourable

PROCHECK-NMR

Ensemble Ramachandran plots
ensemble_analyzed (20 models)



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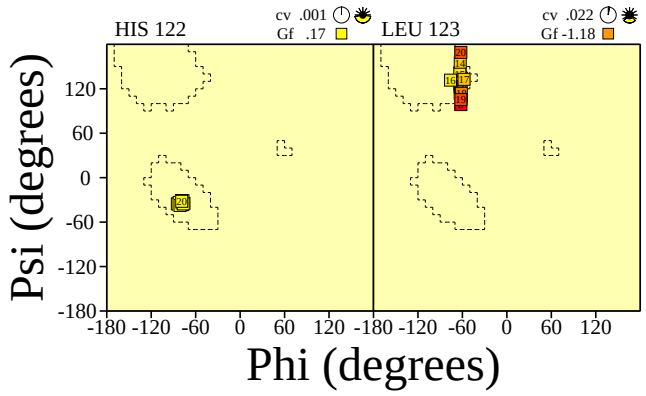
Gf = Average G-factor for the residue (the higher the value the more favourable the conformations) based on analysis of high-res. Xstal structures
Data points coloured according to G-factor: Favourable Unfavourable

Ensemble Ramachandran plots
ensemble_analyzed (20 models)



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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