Supporting Information

Curvature and Torsion of Protein Main Chain as Local Order Parameters of Protein Unfolding

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Figure S1-S3: Free-energy landscapes $\Delta G_i(\gamma_i,\theta_i)$ for i=2,...,60 at T=280K. The unit of the color bar is RT. On each plot the green dots represent the (γ_i,θ_i) positions of the experimental structures (PDB ID: 2L6Q). White circles encompass native areas defined by $\Delta G_i(\gamma_i,\theta_i) < 4RT$. For most values of i, simulated native areas contain the experimental values and expand slightly around them, validating the free-energy landscape definition and the MD data. Ends of the chain make exceptions because they are disordered parts of the protein.

Figure S4-S6: Free-energy landscapes $\Delta G_i(\gamma_i,\theta_i)$ for i=2,…,60 at T=355K. The unit of the color bar is RT. On each plot the green dots represent the (γ_i,θ_i) positions of the experimental structures (PDB ID: 2L6Q). White circles encompass native areas defined by $\Delta G_i(\gamma_i,\theta_i) < 4RT$ at T=280K. At 355K, gpW is globally unfolded, which is manifested by exploration of nearly all possible values of (γ_i,θ_i), i.e., $-180° < \gamma < 180°$ and $60° < \theta < 130°$ (restriction on θ reflects steric effects).

Figure S7: Local nativeness f_i (T) for i=2,...,60 at three different temperatures: T=280K, T=355K and T=380K computed for the cut-off $H=4RT$.

Figures S8-S10: NMR signals for i=2,...,60, $\langle\Delta\delta_i\rangle(T) = \langle\delta_i\rangle(T) - \langle\delta_i\rangle\,(280K)$. The color bar unit is ppm. Black dots are the experimental values from Ref. [14]. Errorbars are $\langle\Delta\delta_i\rangle \pm \sigma(\langle\Delta\delta_i\rangle)$ signals computed from MD simulations with ShiftX2. For each value of i, average and standard deviation were computed using δ timeseries, restricted to frames where (γ_i,θ_i) is native (green) or non-native (red). Solid black curve is the average of $\langle\Delta\delta_i\rangle$ using all snapshots of each MD trajectory at the given temperature. Simulated values agree qualitatively with the experimental data, except for i=19, 30, 46, and 55-60 (C-terminal part of gpW). Deviations from experiment is caused by lack of a slow global increase of $\langle\delta_i(T)\rangle$, whose amplitude is lower than 1 ppm.

Figures S11-S13: $\delta(\gamma_i,\theta_i)$ landscape of Cα_i at T=355K for i=2..60, showing the average value in MD simulation, restricted to frames with expected value of (γ_i,θ_i). The color bar unit is ppm. Highest values are generally reached when (γ_i,θ_i) is in the α-helix area, enhancing coupling effects in the backbone. Then δ_i globally decreases as θ_i increases. Lowest relative values in the landscapes correspond to non-structured conformations or β-strand area. When backbone angles vary, chemical shift values take heterogenous values, confirming the sensitivity of NMR to structural changes at the scale of the backbone.

Figure S14-S15: Free-energy landscapes of residues in the surroundings of *i*=44: *j*=40-43 (Fig. S14), *j*=48-51 (Fig. S15). The color bar unit is RT. Top landscapes were computed from the full 355K MD trajectory (750000 snapshots). Bottom landscapes were computed by selecting only frames where $|\Delta\delta_{44}|$<0.5 ppm (about 60000-70000 snapshots). For all the values of *j*, the free-energy landscapes of the restricted trajectories resemble the landscapes computed from the entire duration of the MD trajectories, though they were built from much fewer snapshots. Some small regions of the free-energy landscapes are missing in the restricted case compared to the unrestricted calculation, like γ_j=-75°, θ_j=90° in the case of *j*=41-42. The behaviour of these residues is less modified than the neighbouring residues *j*=44-47, but they still feature small differences in the calculation done from the restricted MD trajectory compared to the calculation performed from the full MD trajectory.

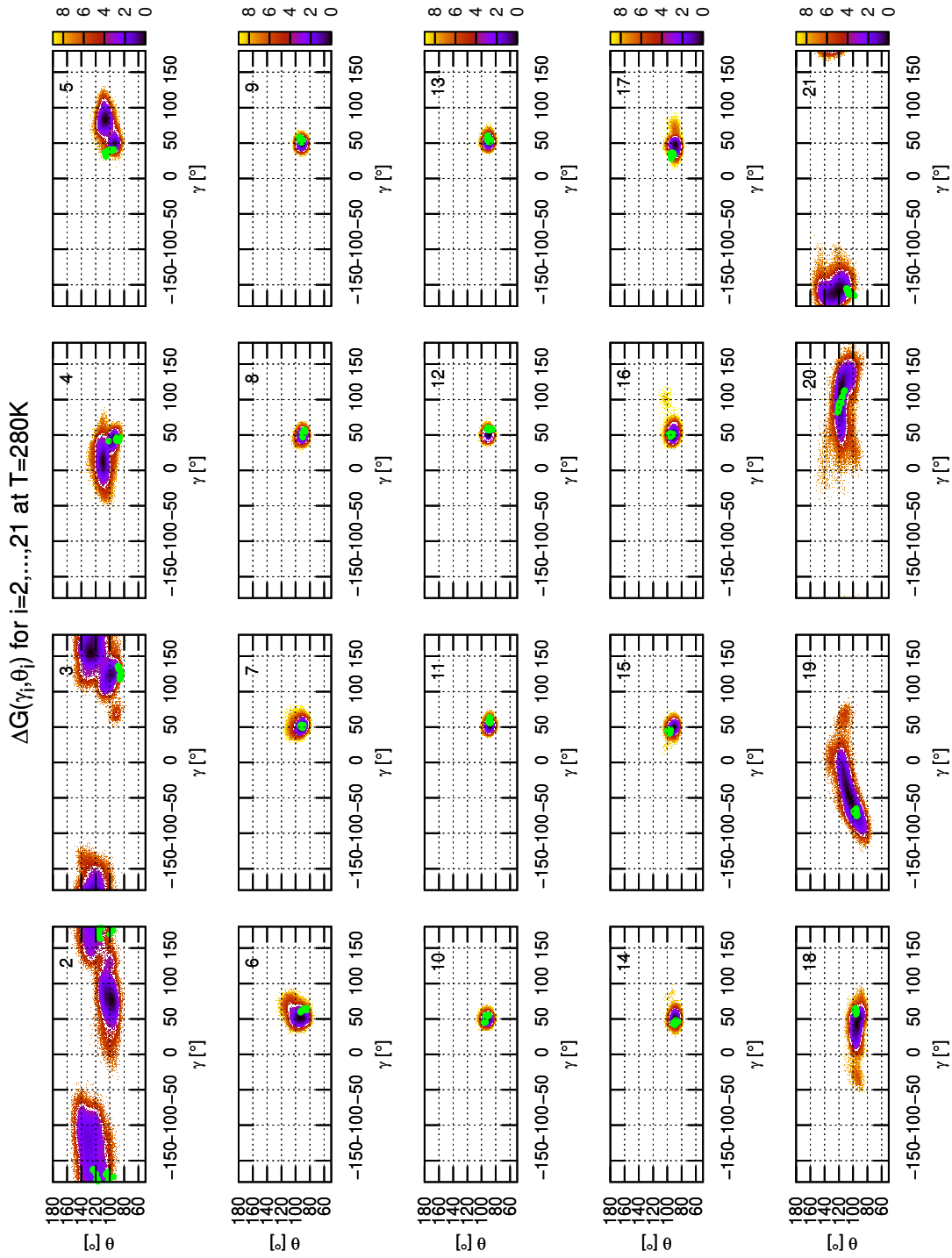

Figure S1

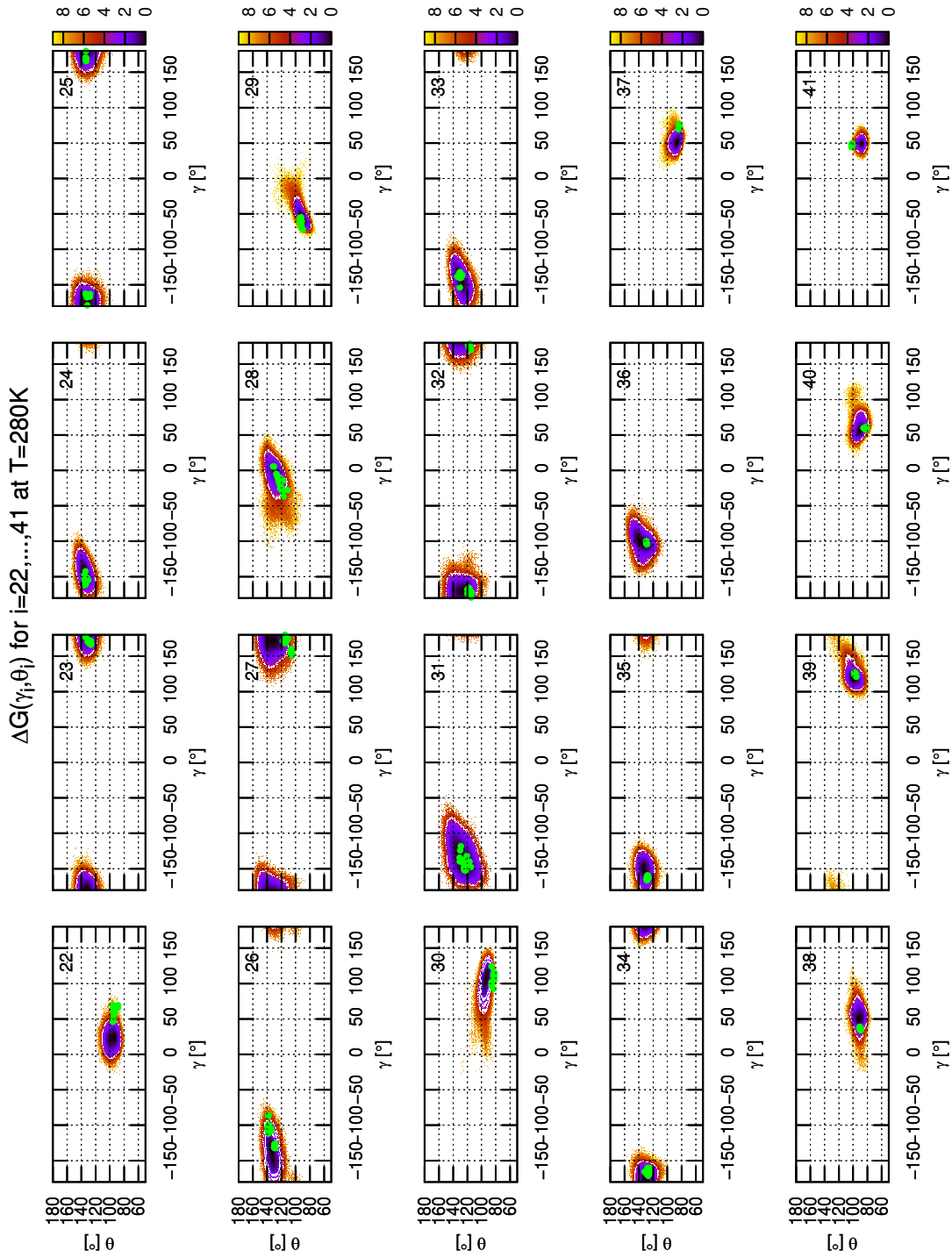
ΔG(γi,θi) for i=22,...,41 at T=280K
θ [°]
γ [°]
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41

Figure S2

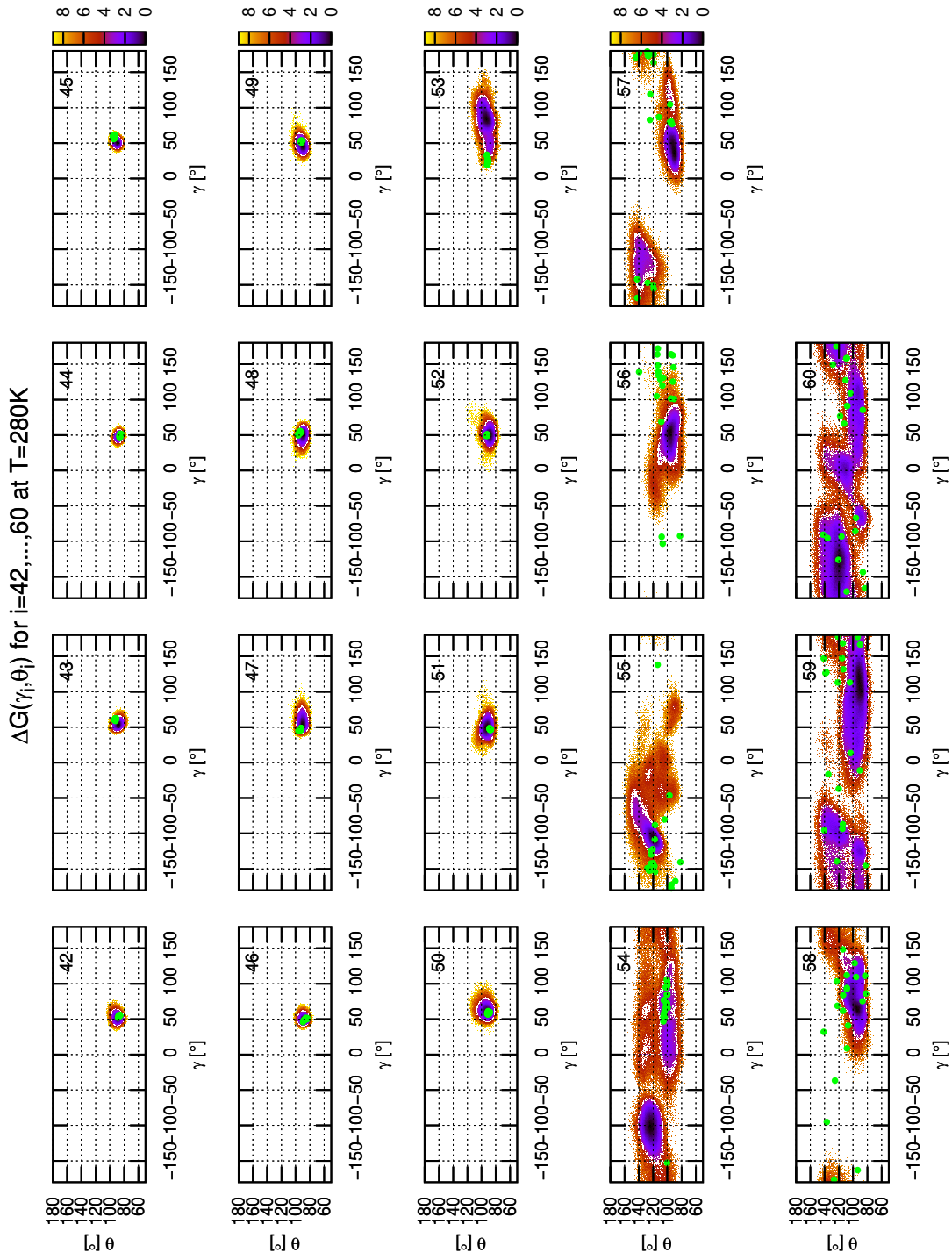

Figure S3

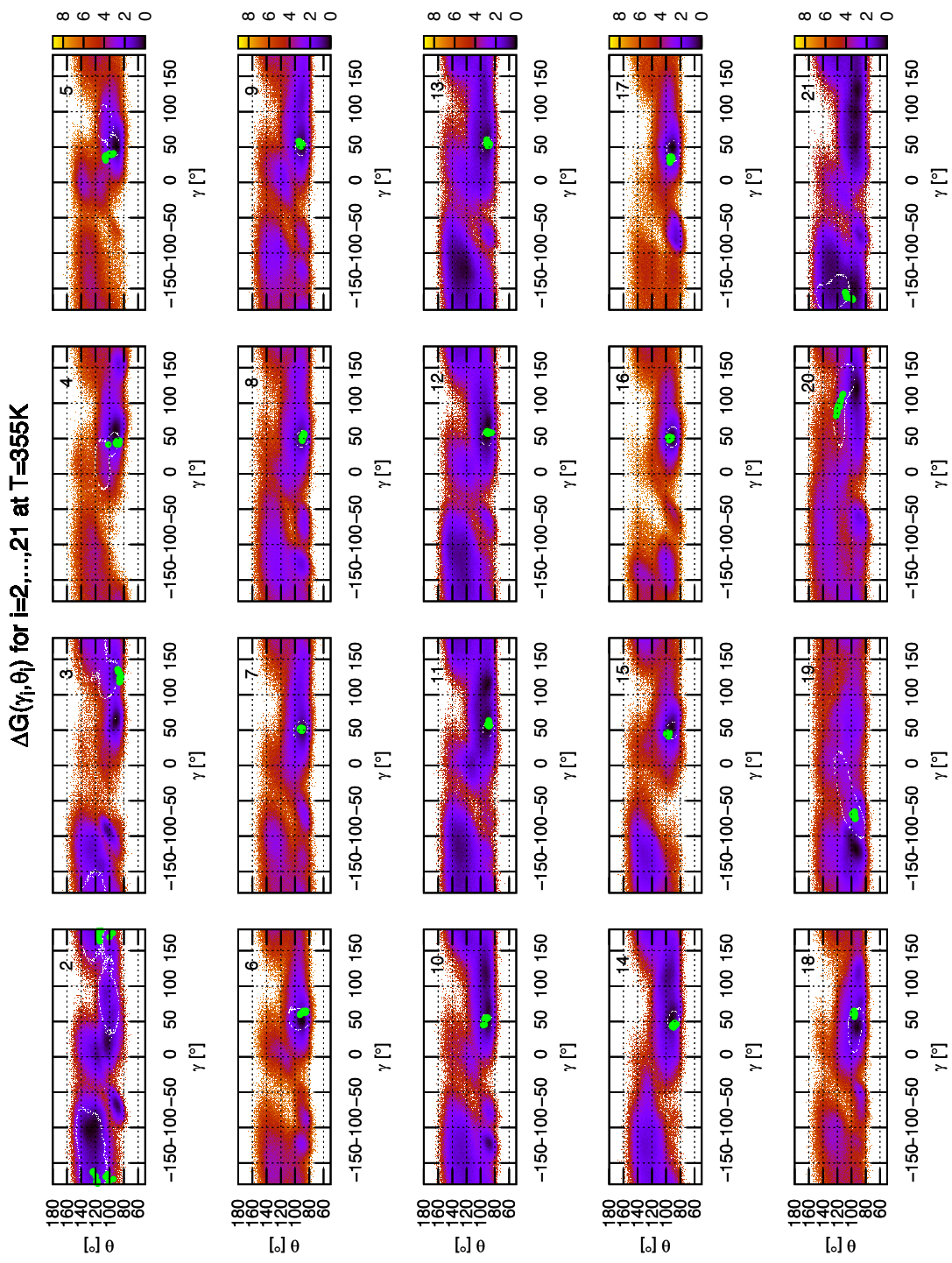

Figure S4

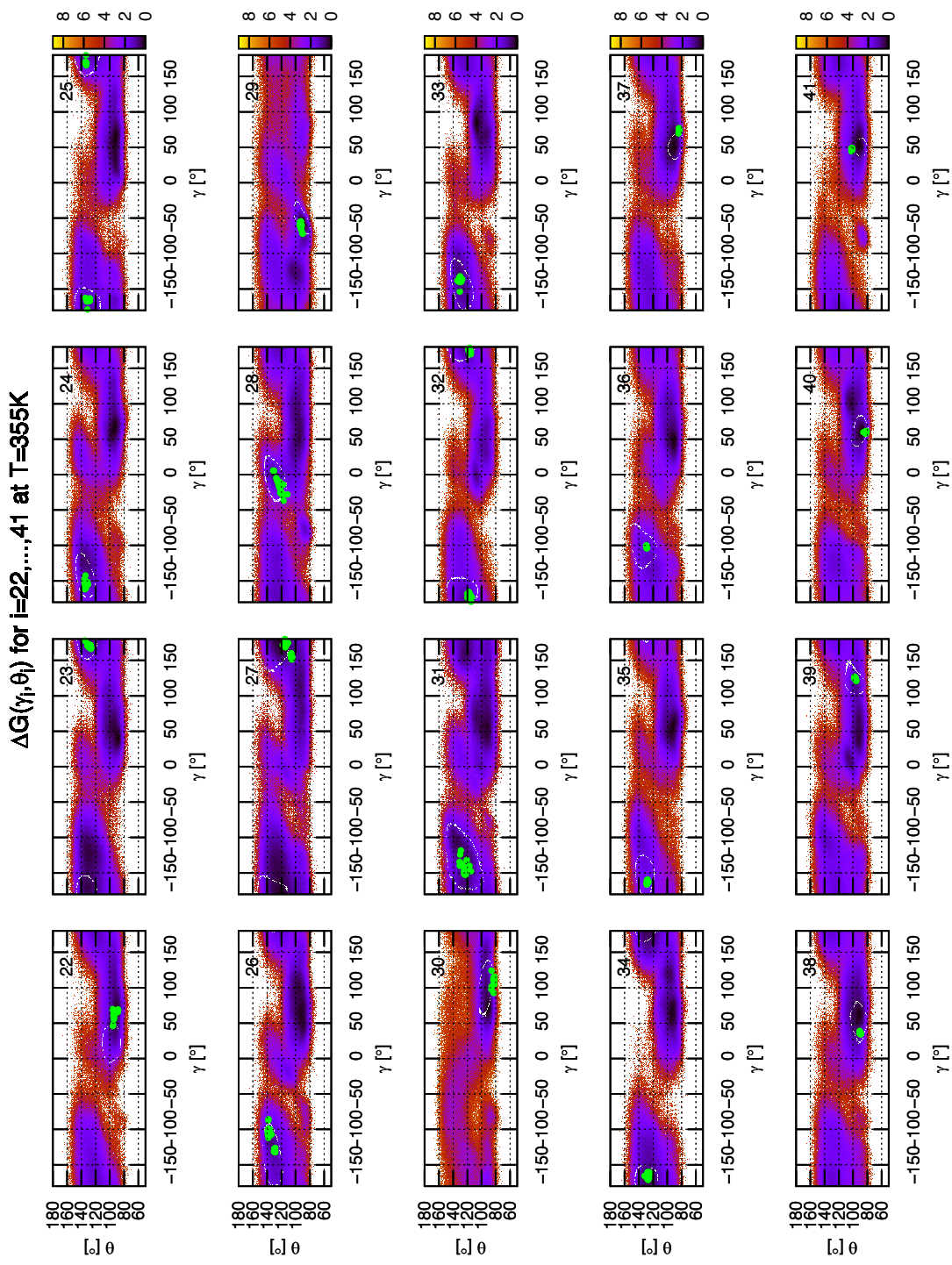

Figure S5

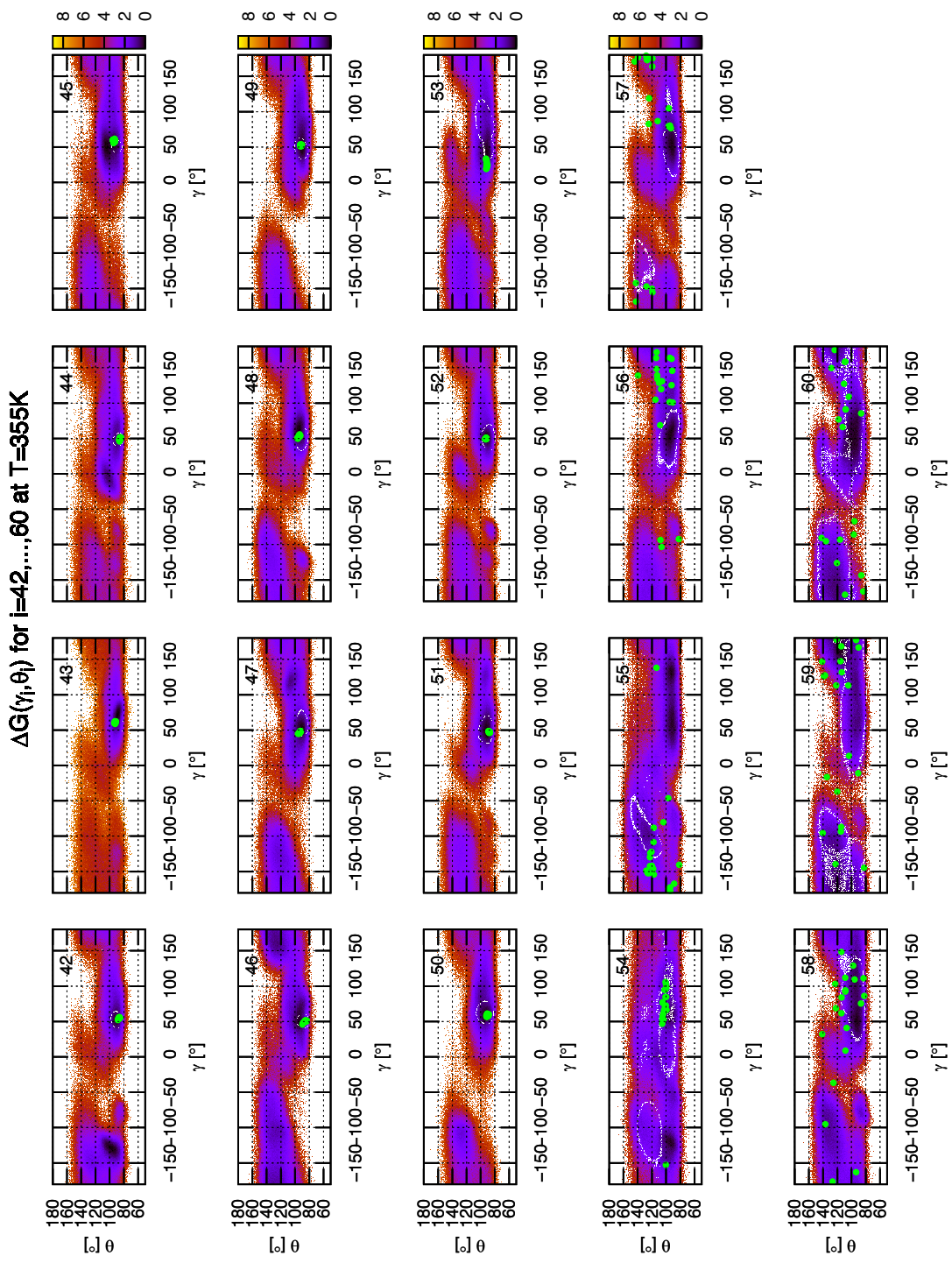
ΔG(γi,θj) for i=42,...,60 at T=355K
θ [°]
γ [°]
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Figure S6

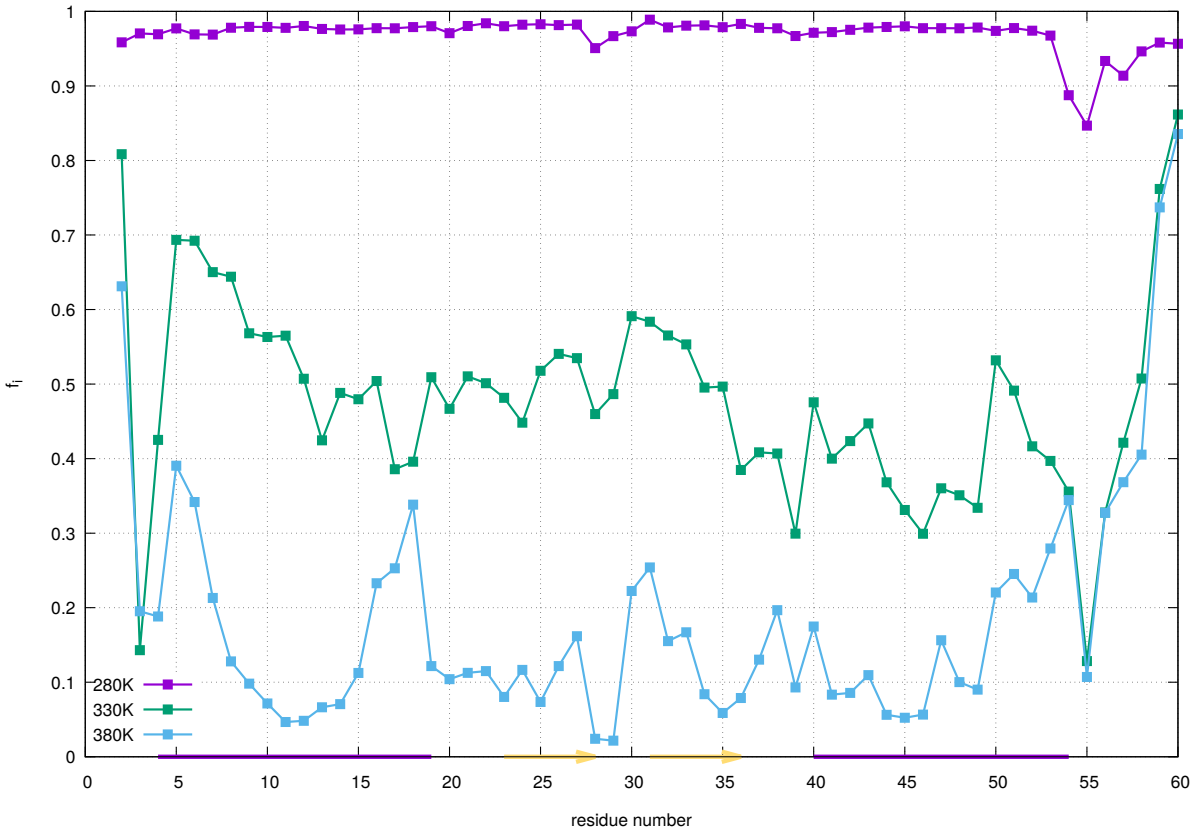
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
f_i
280K
330K
380K
0
5
10
15
20
25
30
35
40
45
50
55
60
residue number

Figure S7

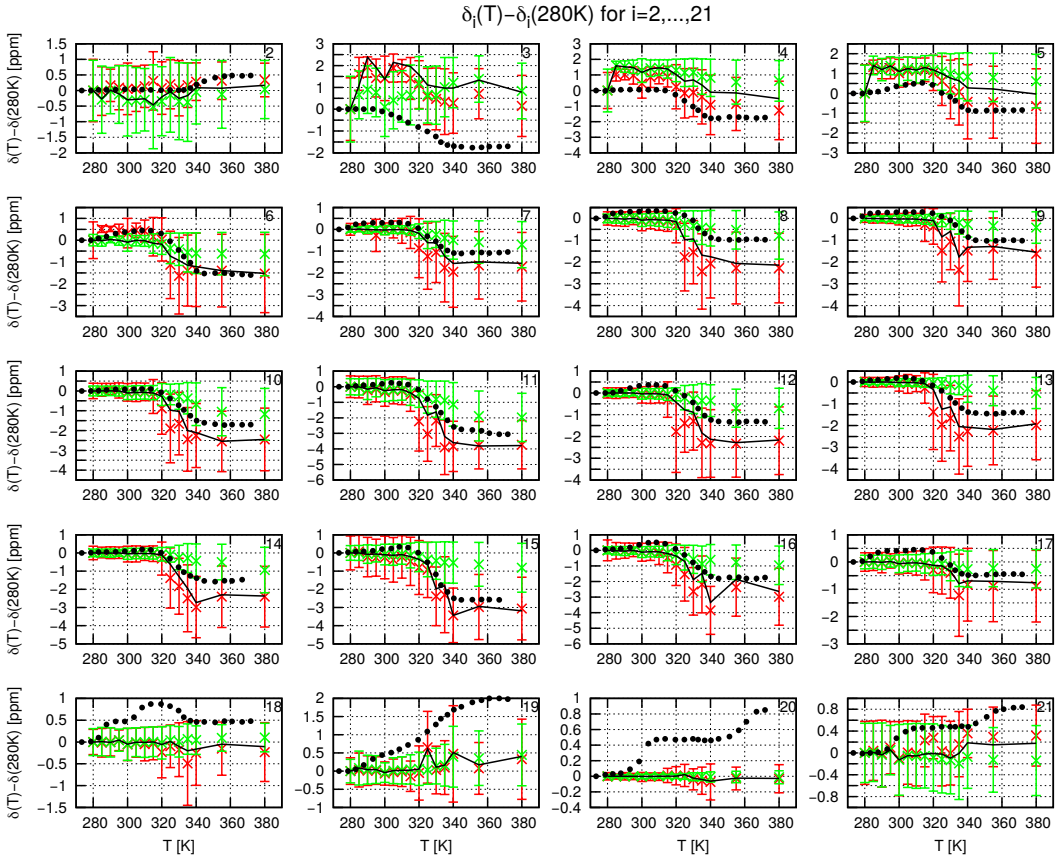

Figure S8

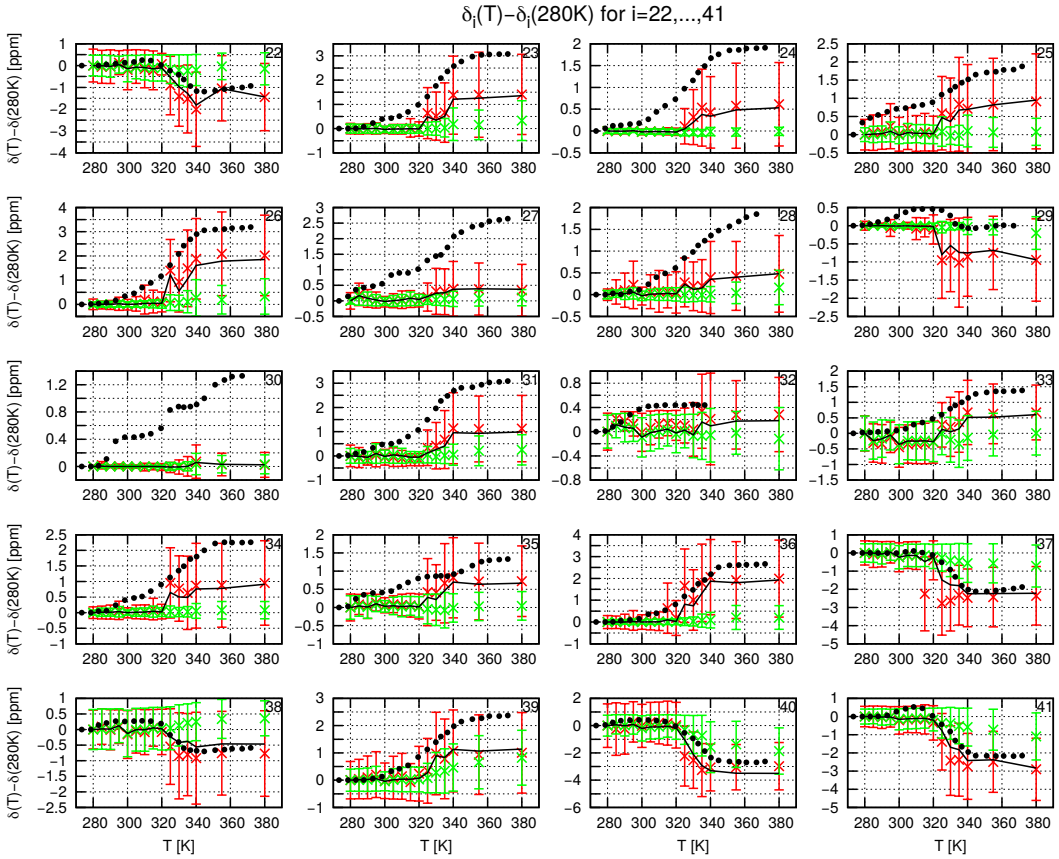

Figure S9

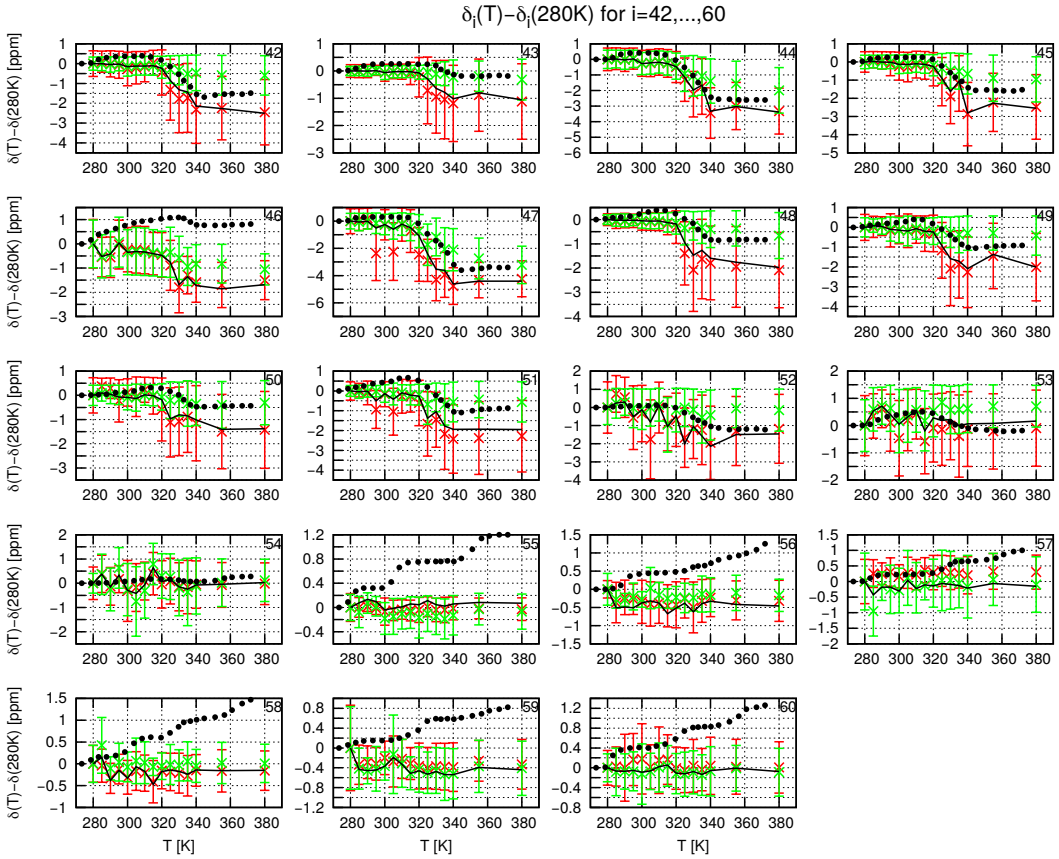

Figure S10

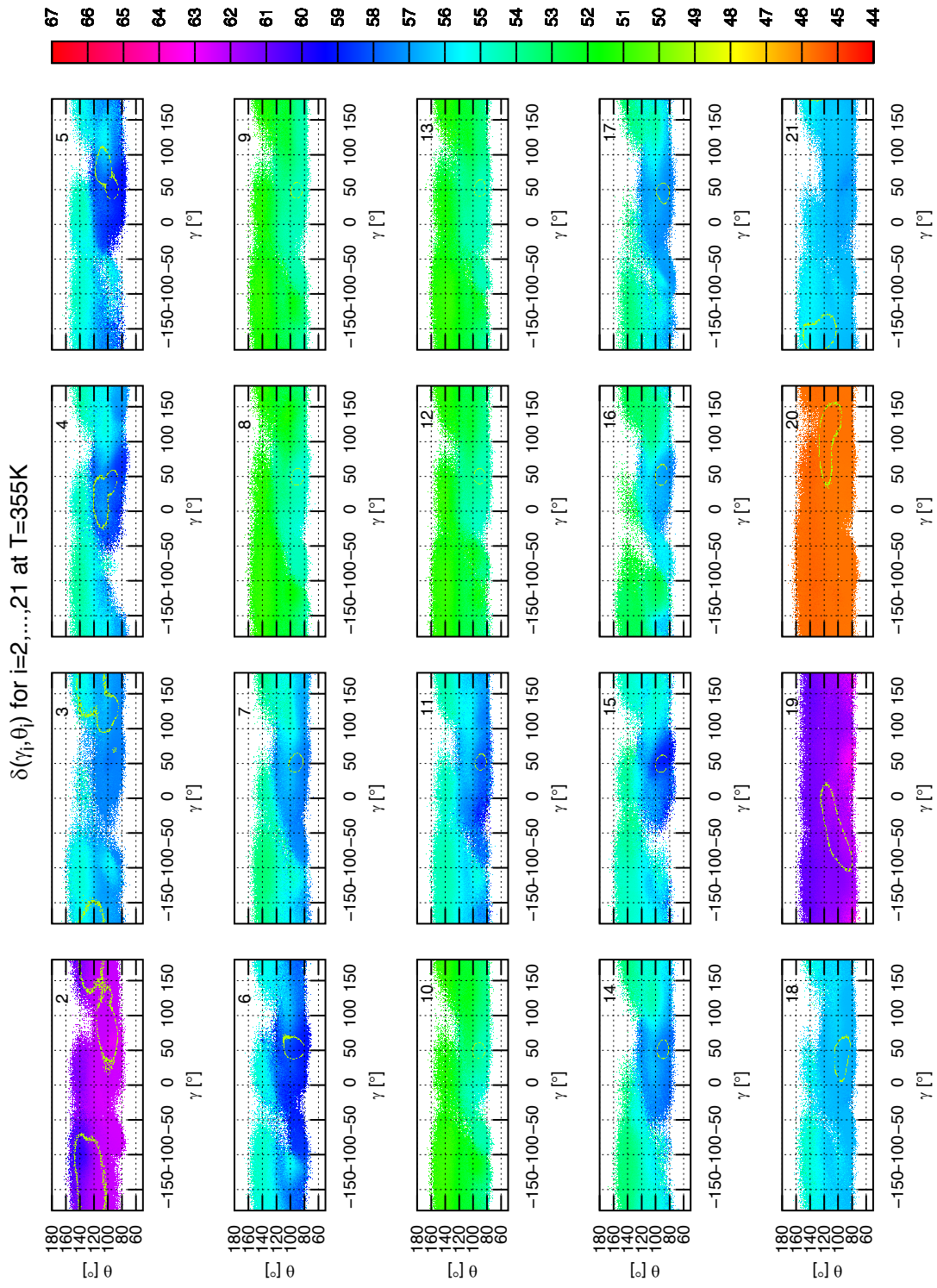
δ(γi,θi) for i=2,...,21 at T=355K
67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44
θ [°]
γ [°]
−150 −100 −50 0 50 100 150
180 160 140 120 100 80 60
2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21

Figure S11

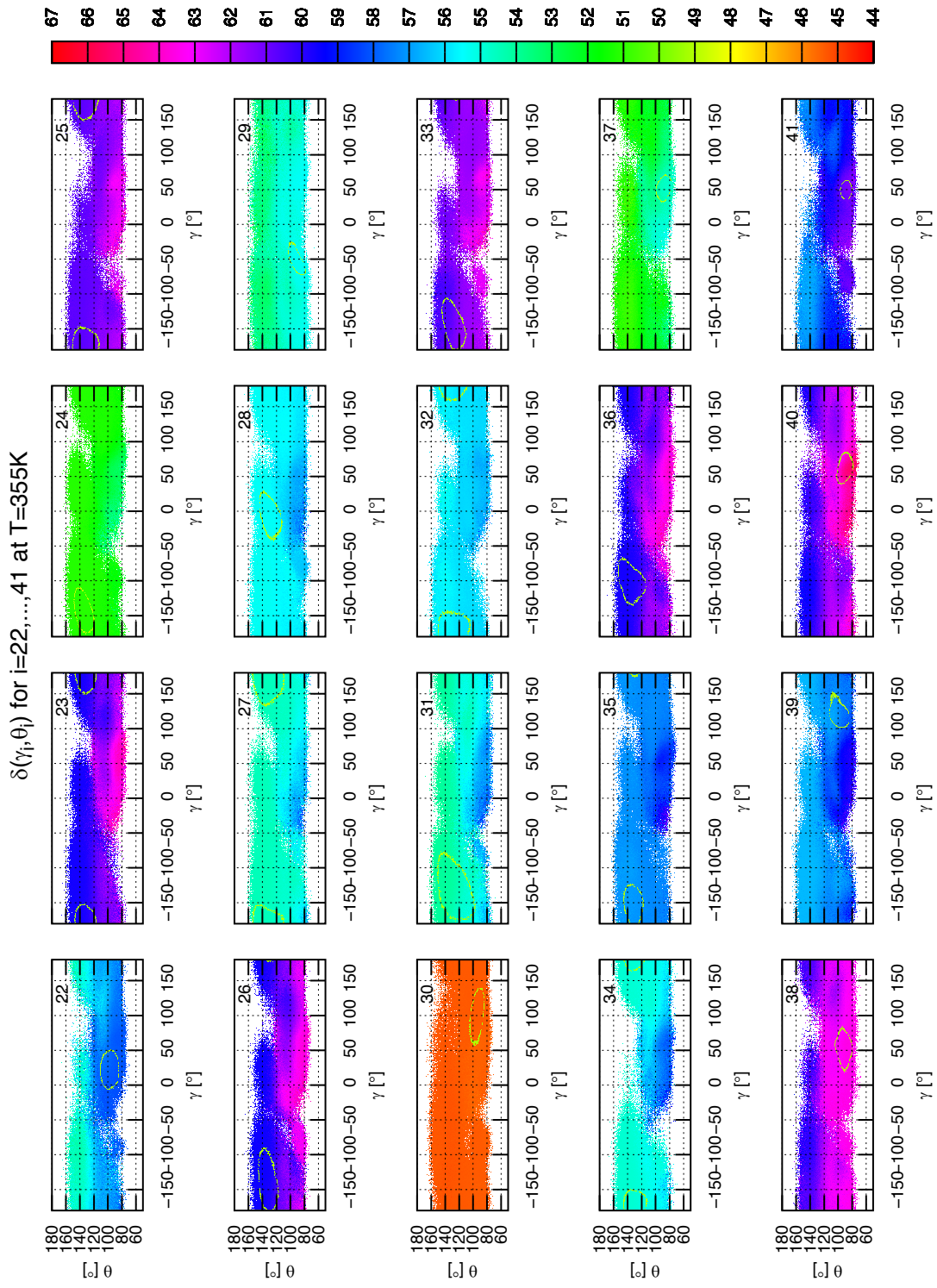
δ(γi,θi) for i=22,...,41 at T=355K
67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44
22 23 24 25
26 27 28 29
30 31 32 33
34 35 36 37
38 39 40 41
θ [°]
γ [°]
180 160 140 120 100 80 60
−150 −100 −50 0 50 100 150

Figure S12

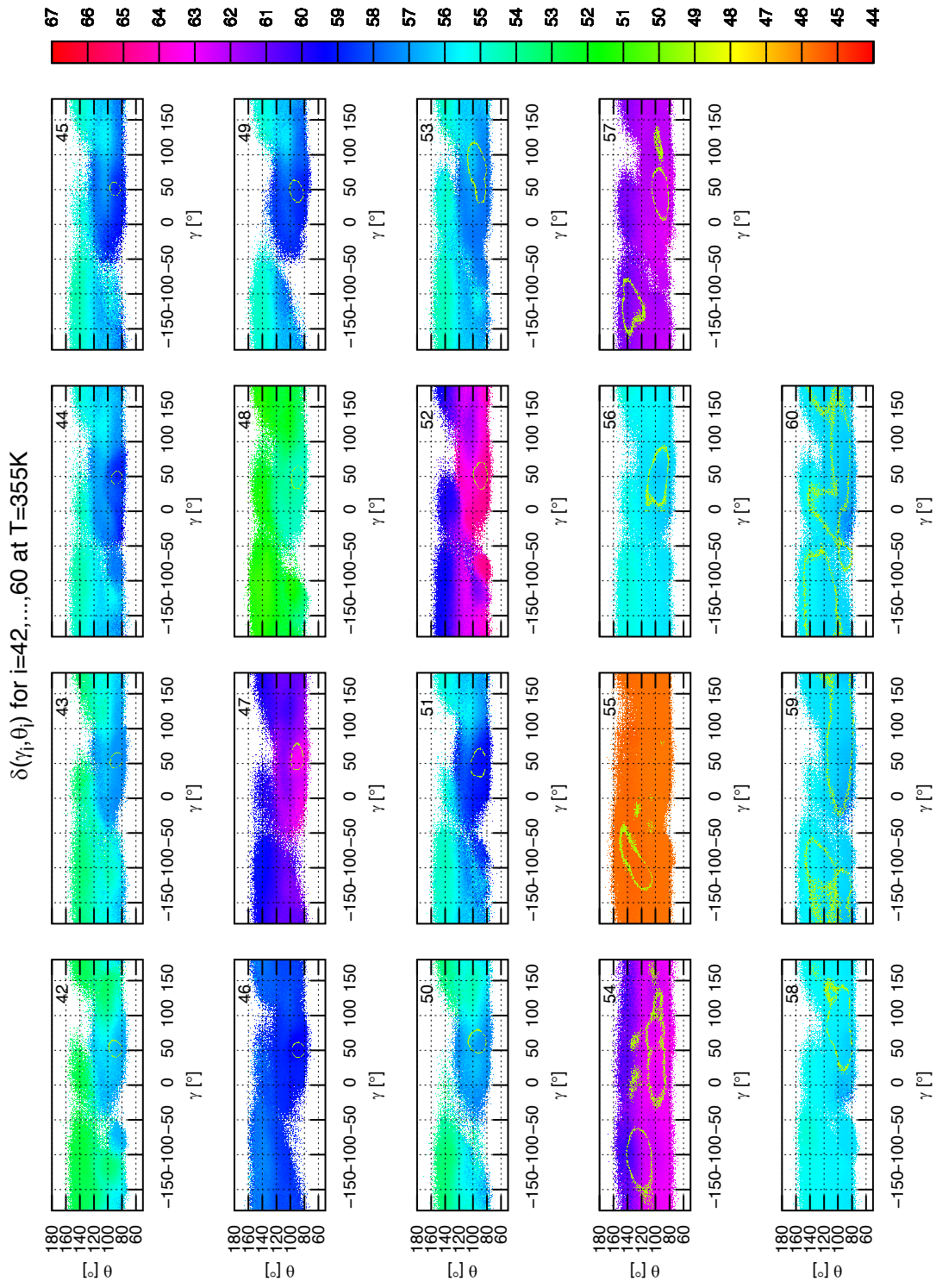
δ(γi,θi) for i=42,...,60 at T=355K
67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44
42 43 44 45
46 47 48 49
50 51 52 53
54 55 56 57
58 59 60
θ [°]
γ [°]
−150 −100 −50 0 50 100 150
180 160 140 120 100 80 60

Figure S13

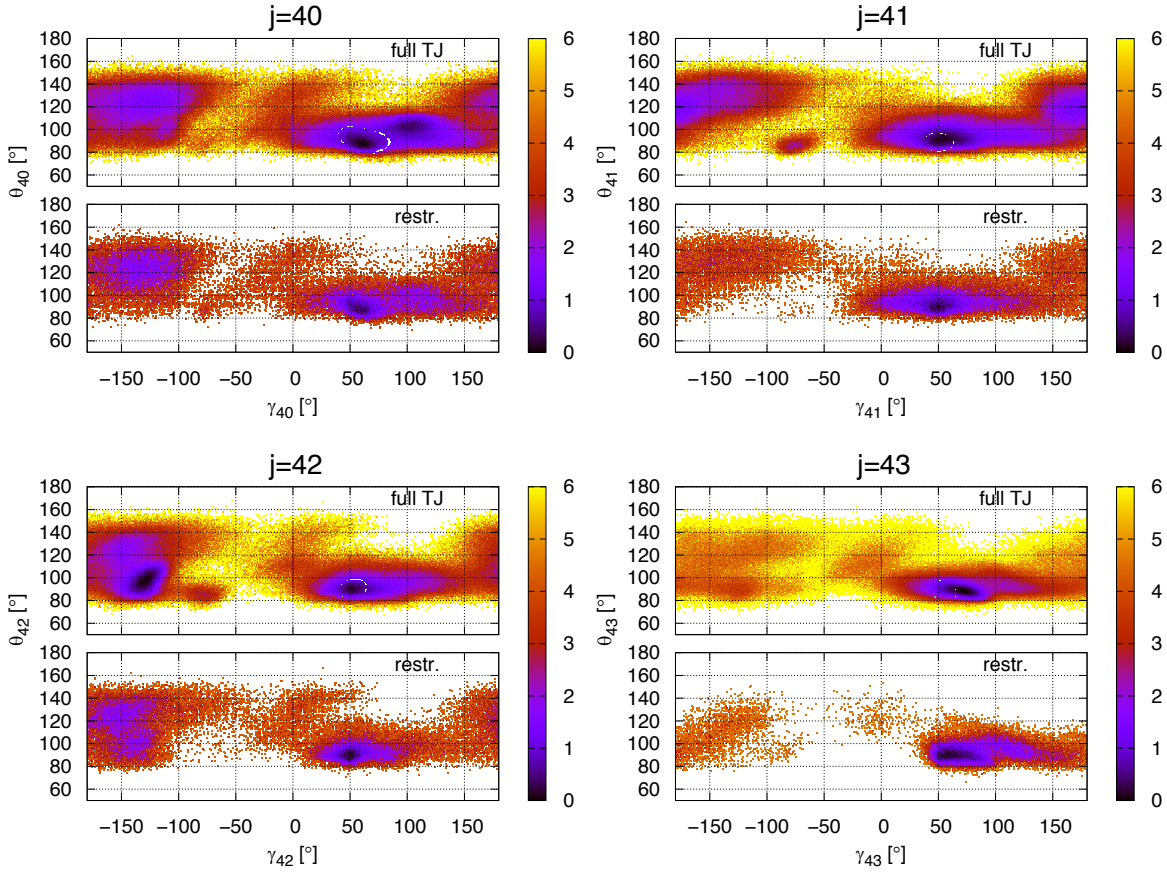

Figure S14

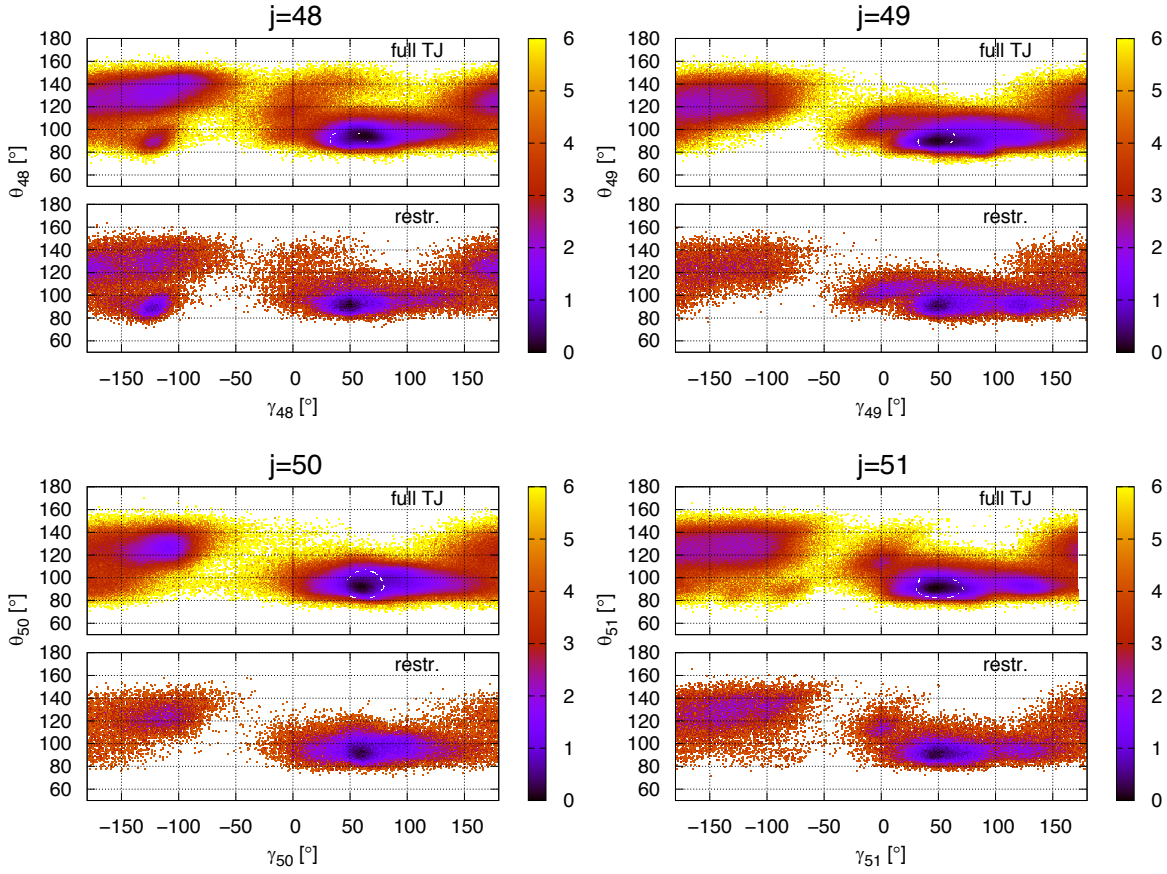
j=48
j=49
j=50
j=51
full TJ
restr.
θ48 [°]
θ49 [°]
θ50 [°]
θ51 [°]
γ48 [°]
γ49 [°]
γ50 [°]
γ51 [°]
180
160
140
120
100
80
60
−150 −100 −50 0 50 100 150
0 1 2 3 4 5 6

Figure S15