Figure 1: Ramachandran plots for the 20 amino acid residues. Ramachandran maps represents the amino acid conformational preference of β-Bridge secondary structure (B). The dark red color marks the most densely occupied regions of the Ramachandran plot.
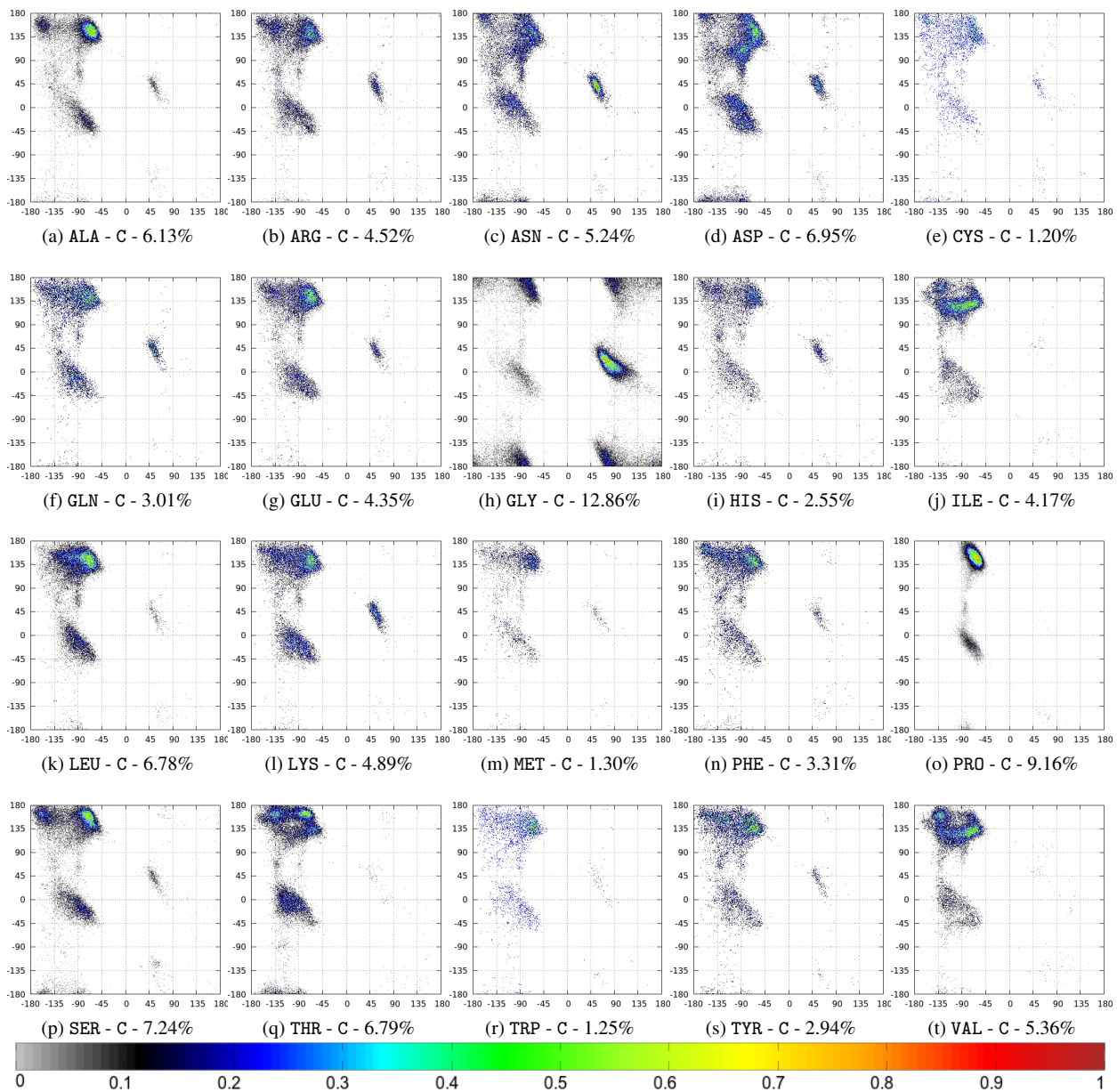
Figure 2: Ramachandran plots for the 20 amino acid residues. Ramachandran maps represents the amino acid conformational preference of Coil secondary structure (`C`). The dark red color marks the most densely occupied regions of the Ramachandran plot.
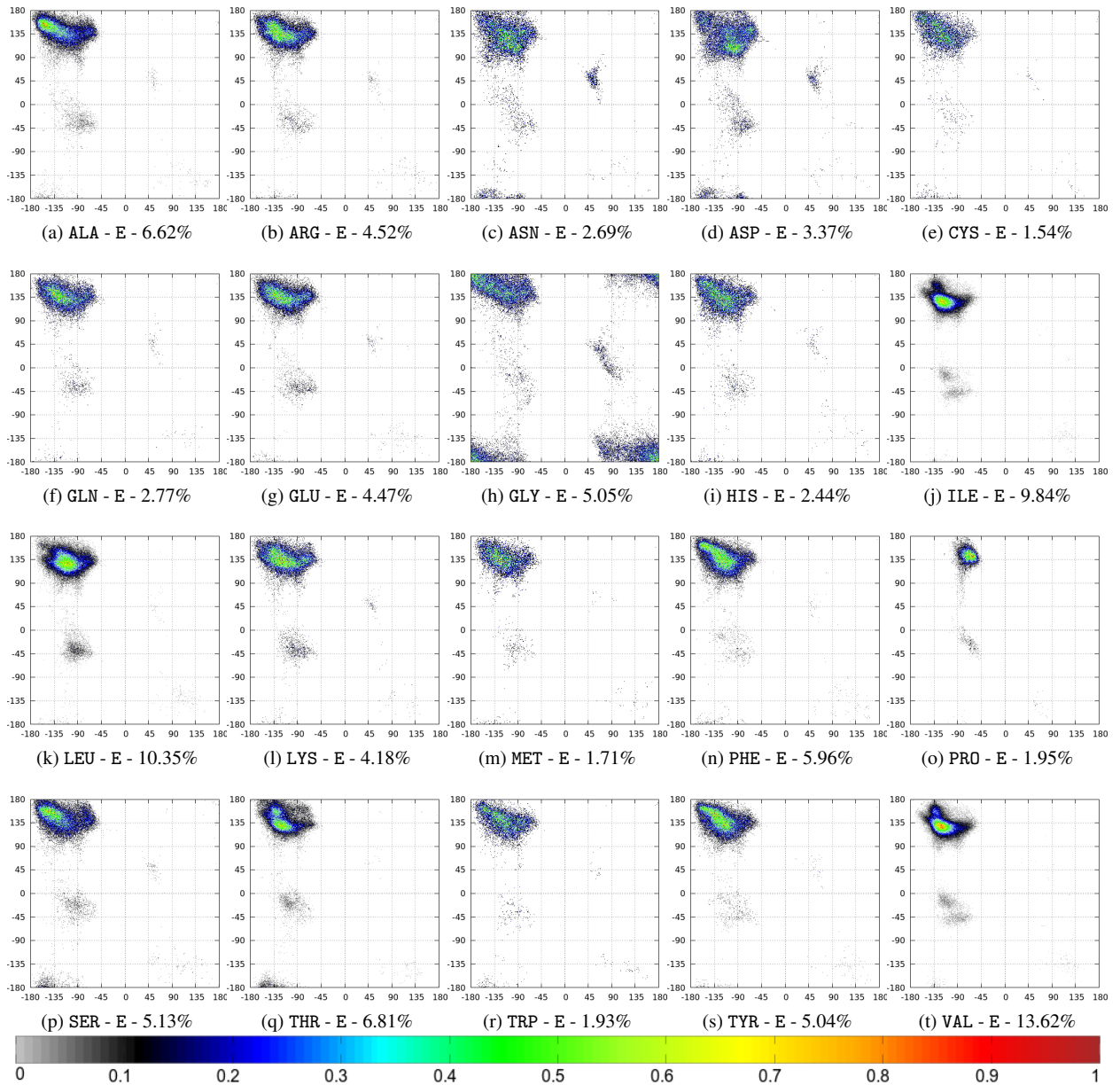
Figure 3: Ramachandran plots for the 20 amino acid residues. Ramachandran maps represents the amino acid conformational preference of β-sheet secondary structure (E). The dark red color marks the most densely occupied regions of the Ramachandran plot.

(a) ALA - G - 9.56%   (b) ARG - G - 5.13%   (c) ASN - G - 4.36%   (d) ASP - G - 7.73%   (e) CYS - G - 1.10%

(f) GLN - G - 3.92%   (g) GLU - G - 8.86%   (h) GLY - G - 5.44%   (i) HIS - G - 2.59%   (j) ILE - G - 3.20%

(k) LEU - G - 9.42%   (l) LYS - G - 5.59%   (m) MET - G - 1.59%   (n) PHE - G - 4.43%   (o) PRO - G - 6.48%

(p) SER - G - 7.03%   (q) THR - G - 3.97%   (r) TRP - G - 2.08%   (s) TYR - G - 4.11%   (t) VAL - G - 3.43%
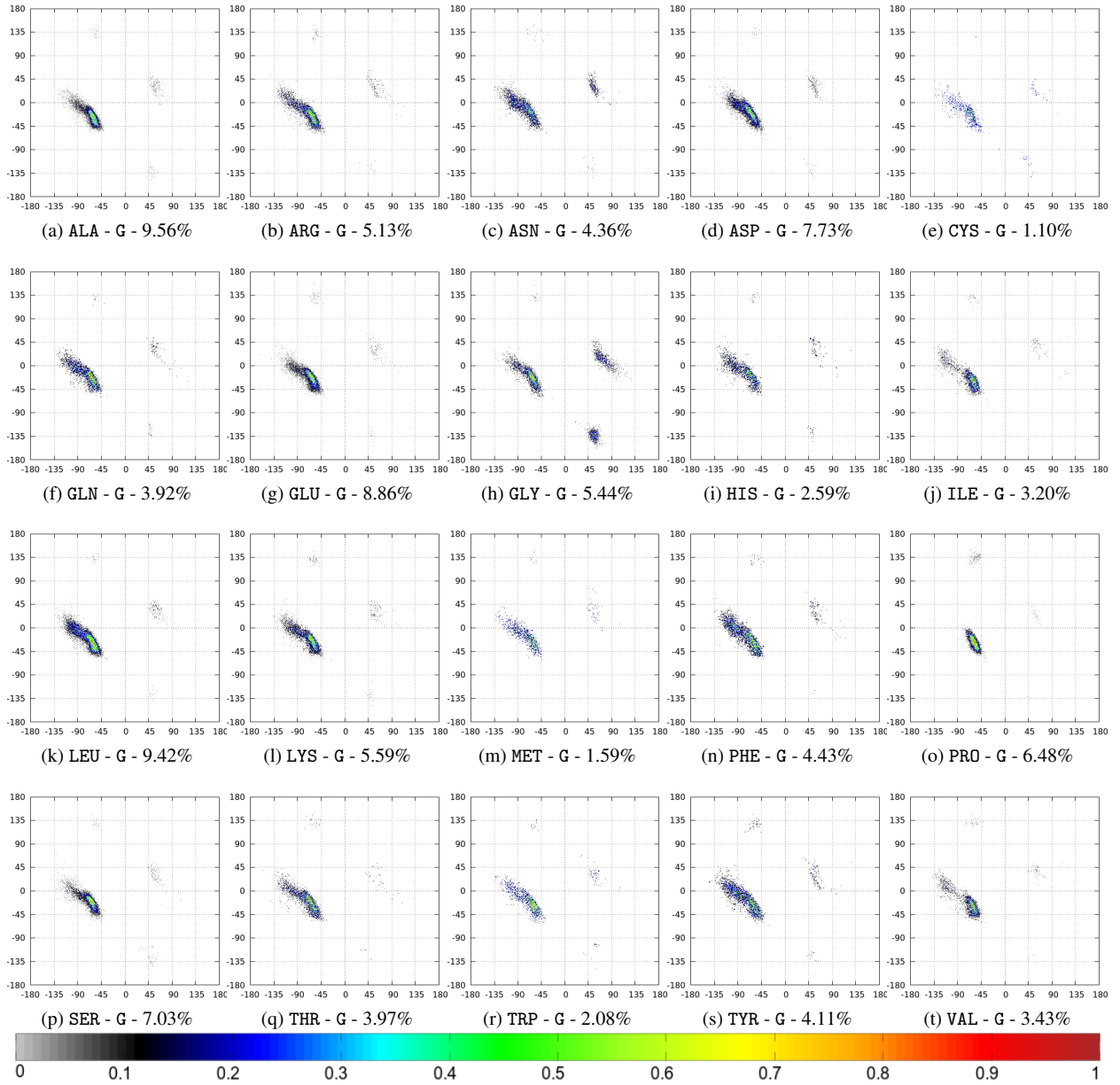
Figure 4: Ramachandran plots for the 20 amino acid residues. Ramachandran maps represents the amino acid conformational preference of 3_{10}-helix secondary structure (G). The dark red color marks the most densely occupied regions of the Ramachandran plot.
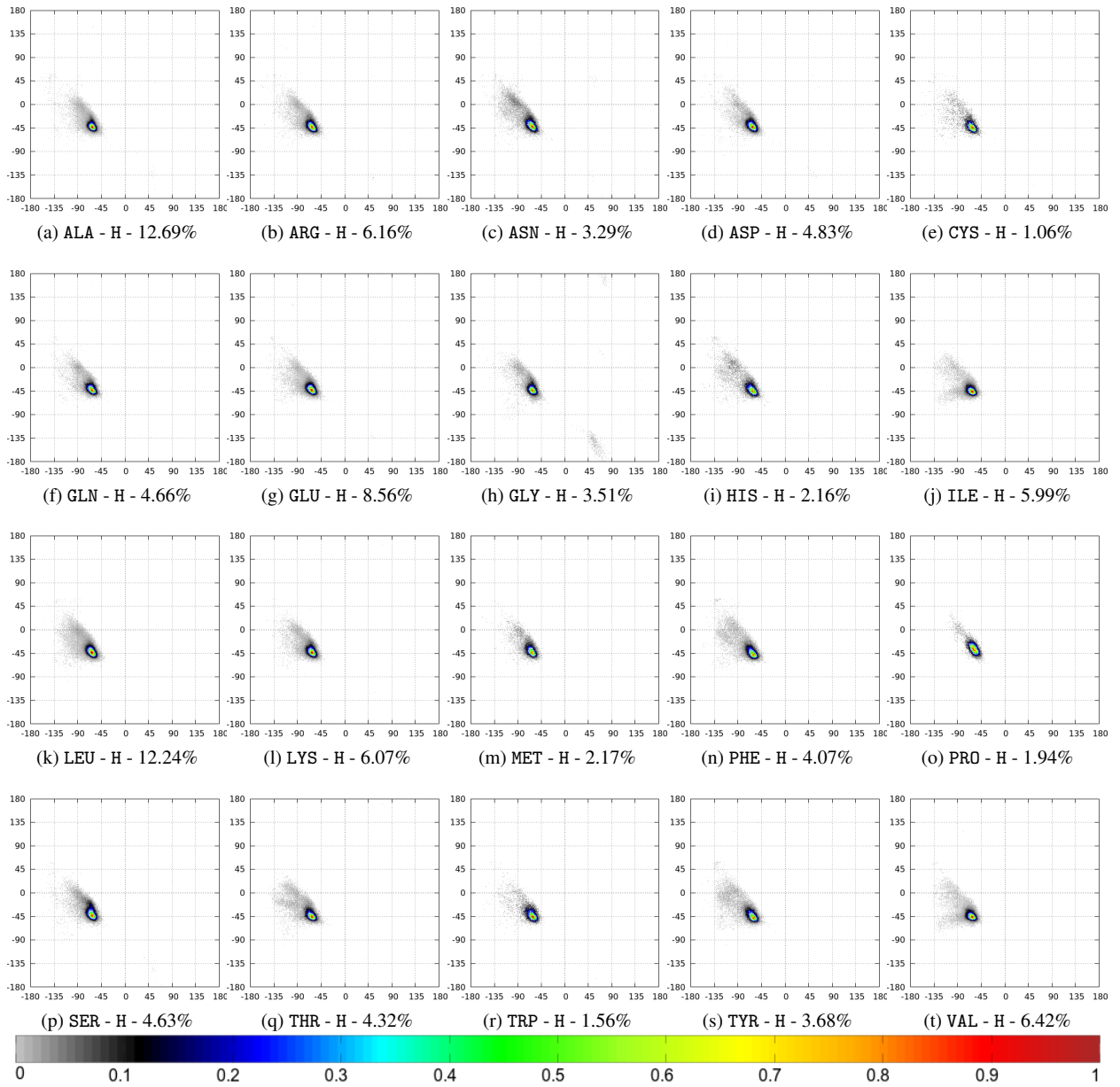
Figure 5: Ramachandran plots for the 20 amino acid residues. Ramachandran maps represents the amino acid conformational preference of α-helix secondary structure (H). The dark red color marks the most densely occupied regions of the Ramachandran plot.

(a) ALA - T - 6.86% (b) ARG - T - 4.19% (c) ASN - T - 7.02% (d) ASP - T - 9.39% (e) CYS - T - 1.26%

(f) GLN - T - 3.04% (g) GLU - T - 5.44% (h) GLY - T - 13.71% (i) HIS - T - 2.73% (j) ILE - T - 2.76%

(k) LEU - T - 5.47% (l) LYS - T - 4.85% (m) MET - T - 1.09% (n) PHE - T - 3.19% (o) PRO - T - 8.24%

(p) SER - T - 6.95% (q) THR - T - 5.47% (r) TRP - T - 1.30% (s) TYR - T - 3.11% (t) VAL - T - 3.95%
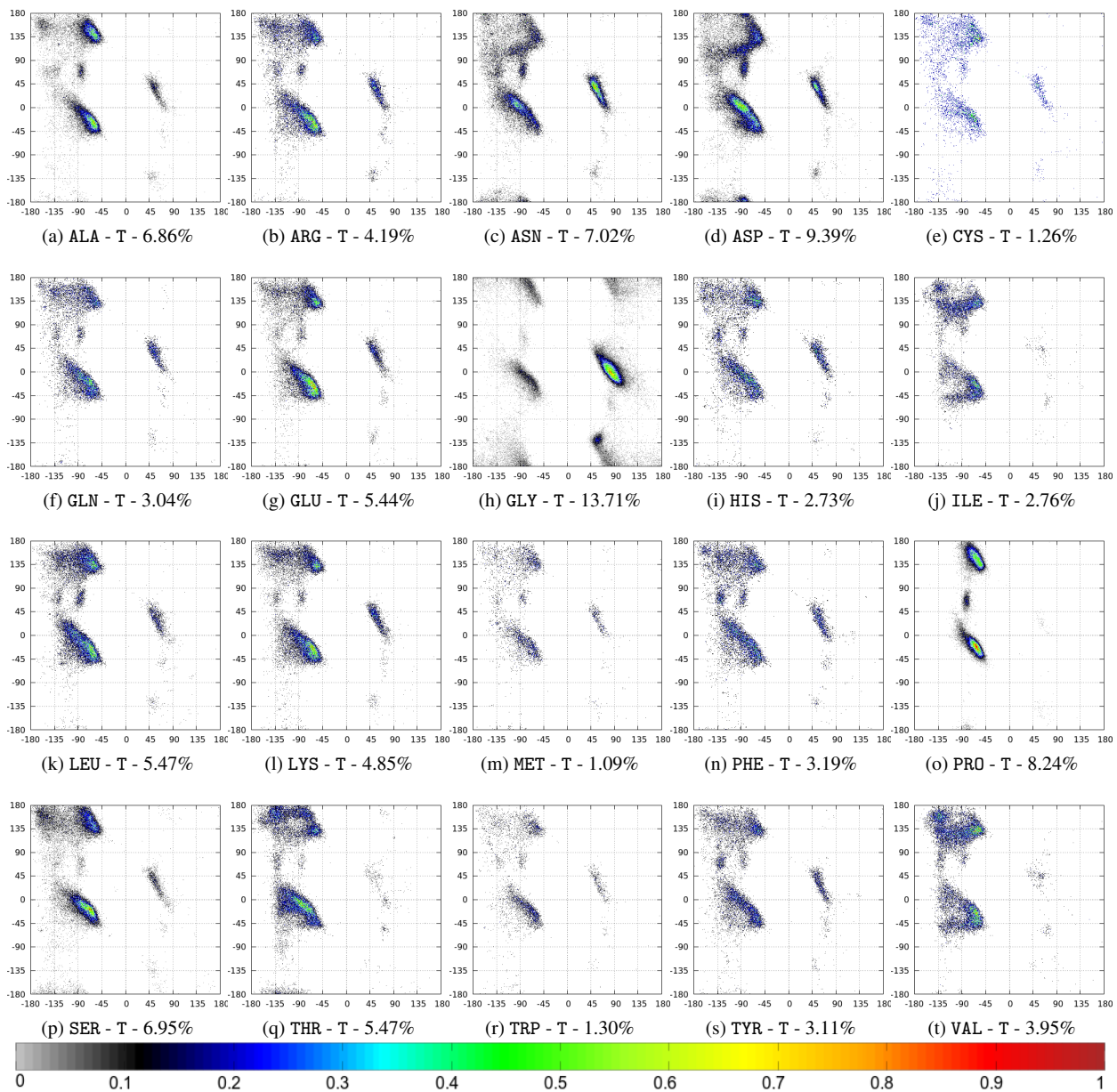
Figure 6: Ramachandran plots for the 20 amino acid residues. Ramachandran maps represents the amino acid conformational preference of Turn secondary structure (T). The dark red color marks the most densely occupied regions of the Ramachandran plot.

6