**Supporting Information**

# Decoding Allosteric Communication Pathways in Cyclophilin A with a Comparative Analysis of Perturbed Conformational Ensembles

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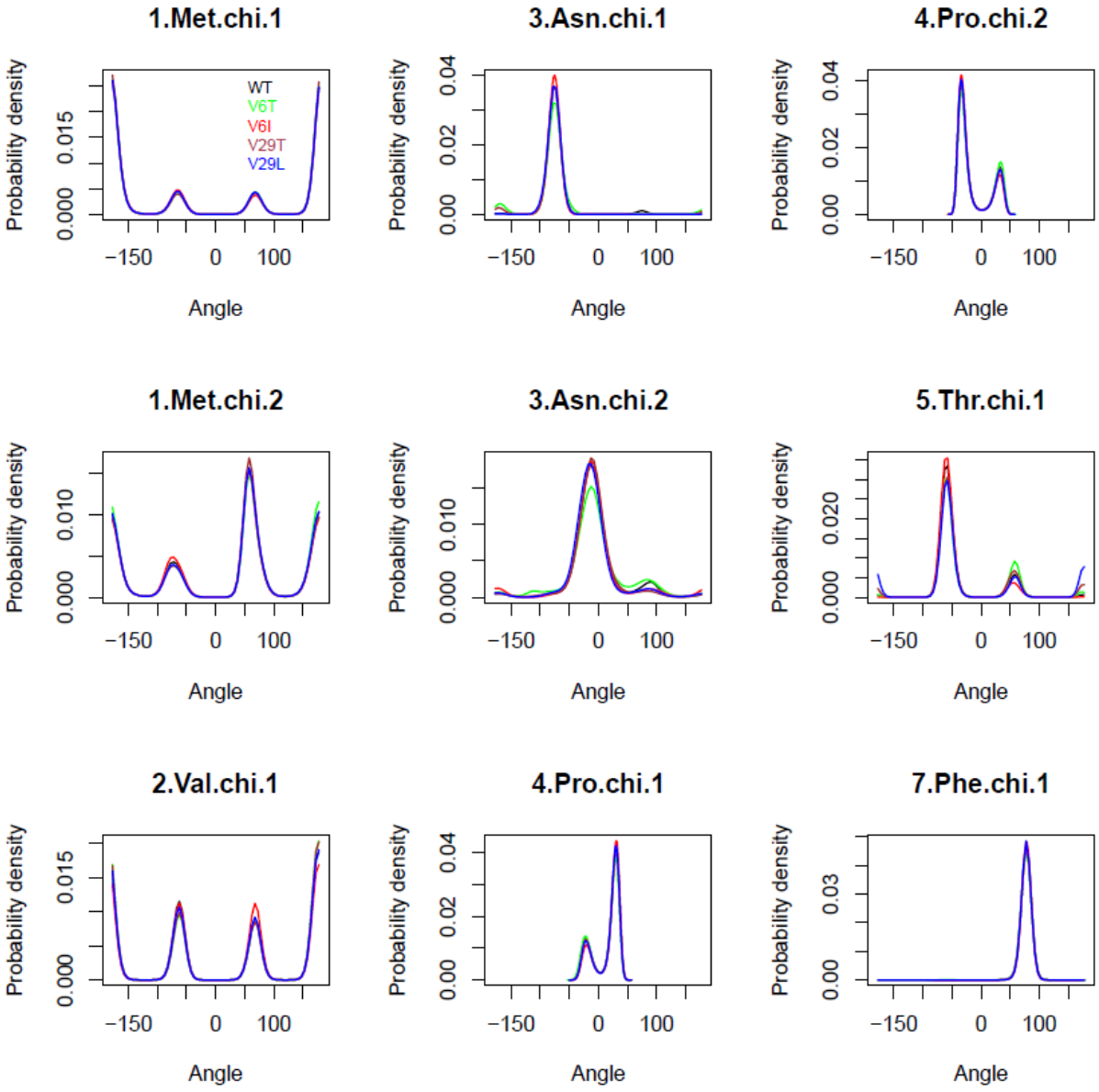
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4.Pro.chi.1
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Angle
WT
V6T
V6I
V29T
V29L
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0.000
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0.020
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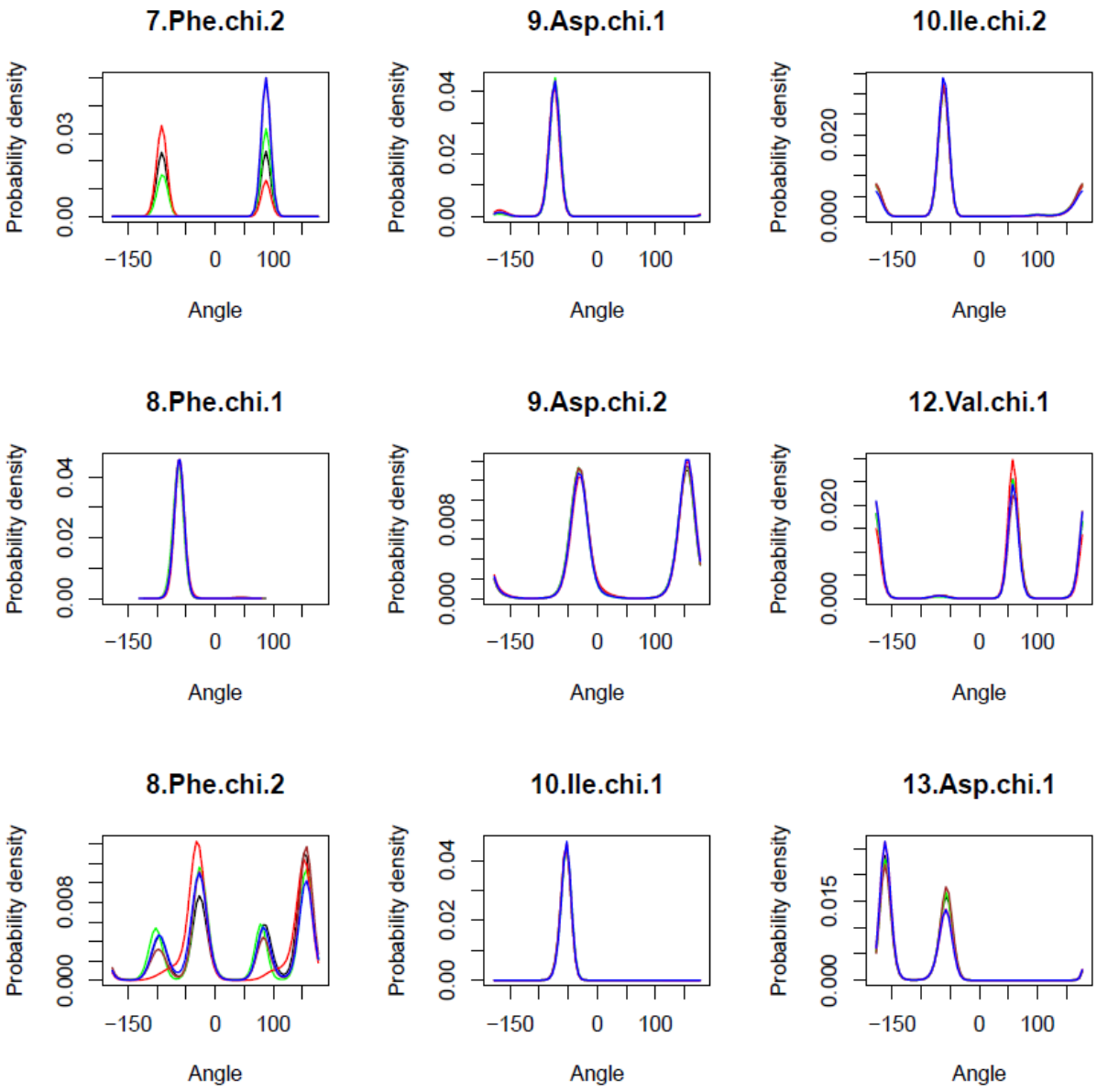
0.02
0.04
0.03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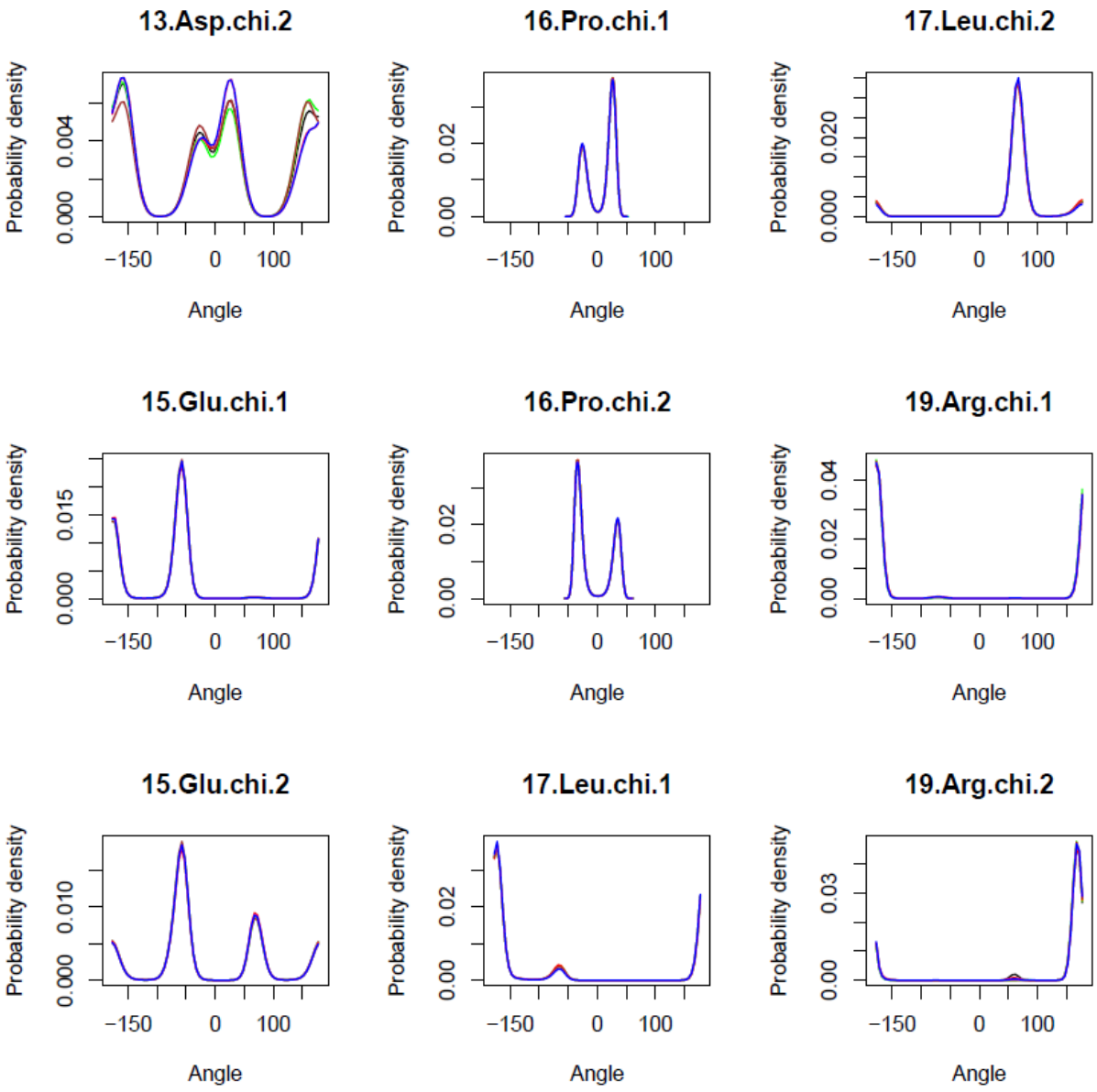
13.Asp.chi.1
Probability density
Angle
−150
0
100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16.Pro.chi.2
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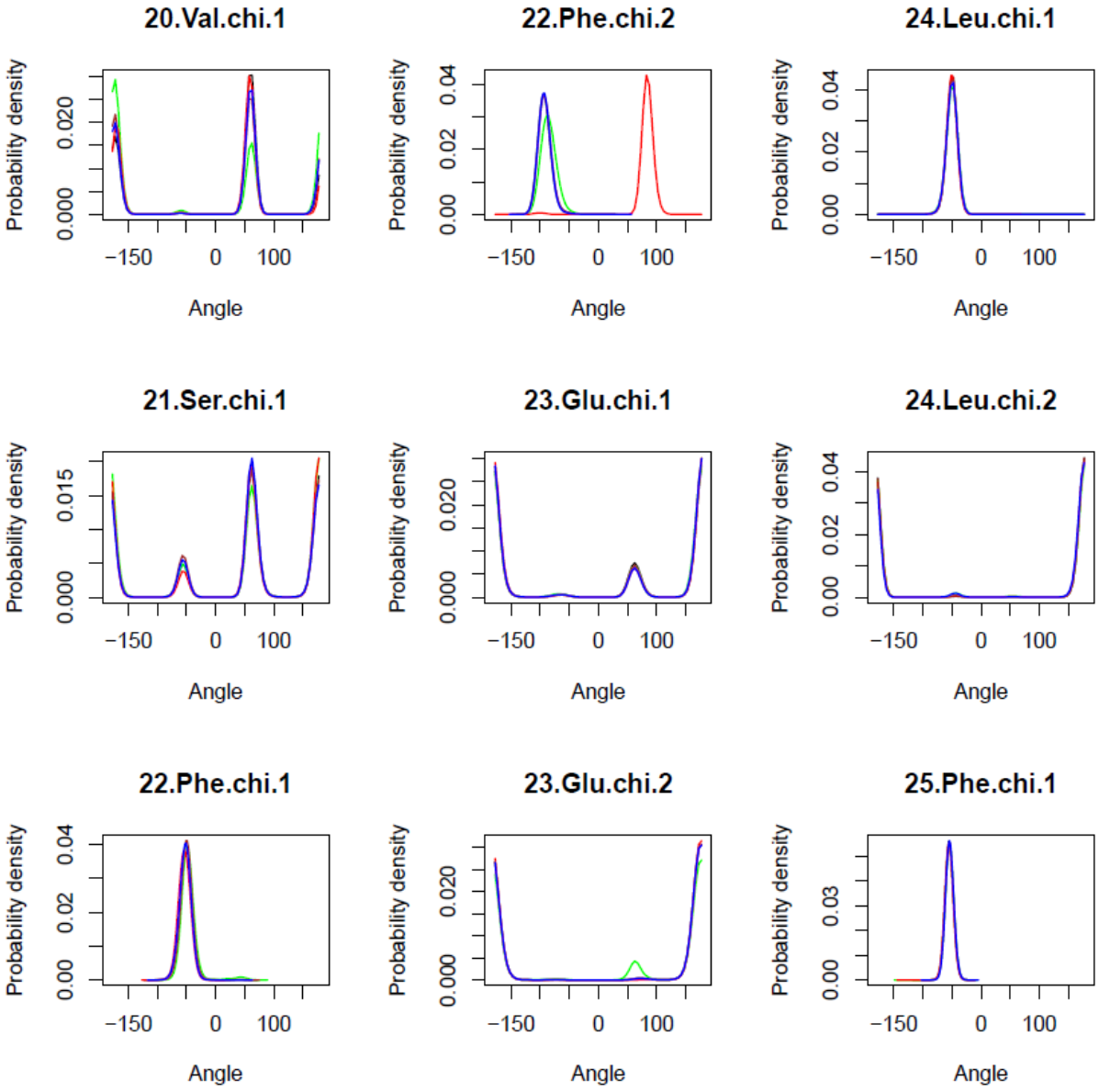
15.Glu.chi.2
17.Leu.chi.1
19.Arg.chi.2
Probability density
Angle
−150
0
100
0.000
0.004
0.00
0.02
0.020
0.015
0.010
0.03
0.04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100
Angle
22.Phe.chi.2
Probability density
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0.02
0.04
−150
0
100
Angle
24.Leu.chi.1
Probability density
0.00
0.02
0.04
−150
0
100
Angle
21.Ser.chi.1
Probability density
0.000
0.015
−150
0
100
Angle
23.Glu.chi.1
Probability density
0.000
0.020
−150
0
100
Angle
24.Leu.chi.2
Probability density
0.00
0.02
0.04
−150
0
100
Angle
22.Phe.chi.1
Probability density
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0.02
0.04
−150
0
100
Angle
23.Glu.chi.2
Probability density
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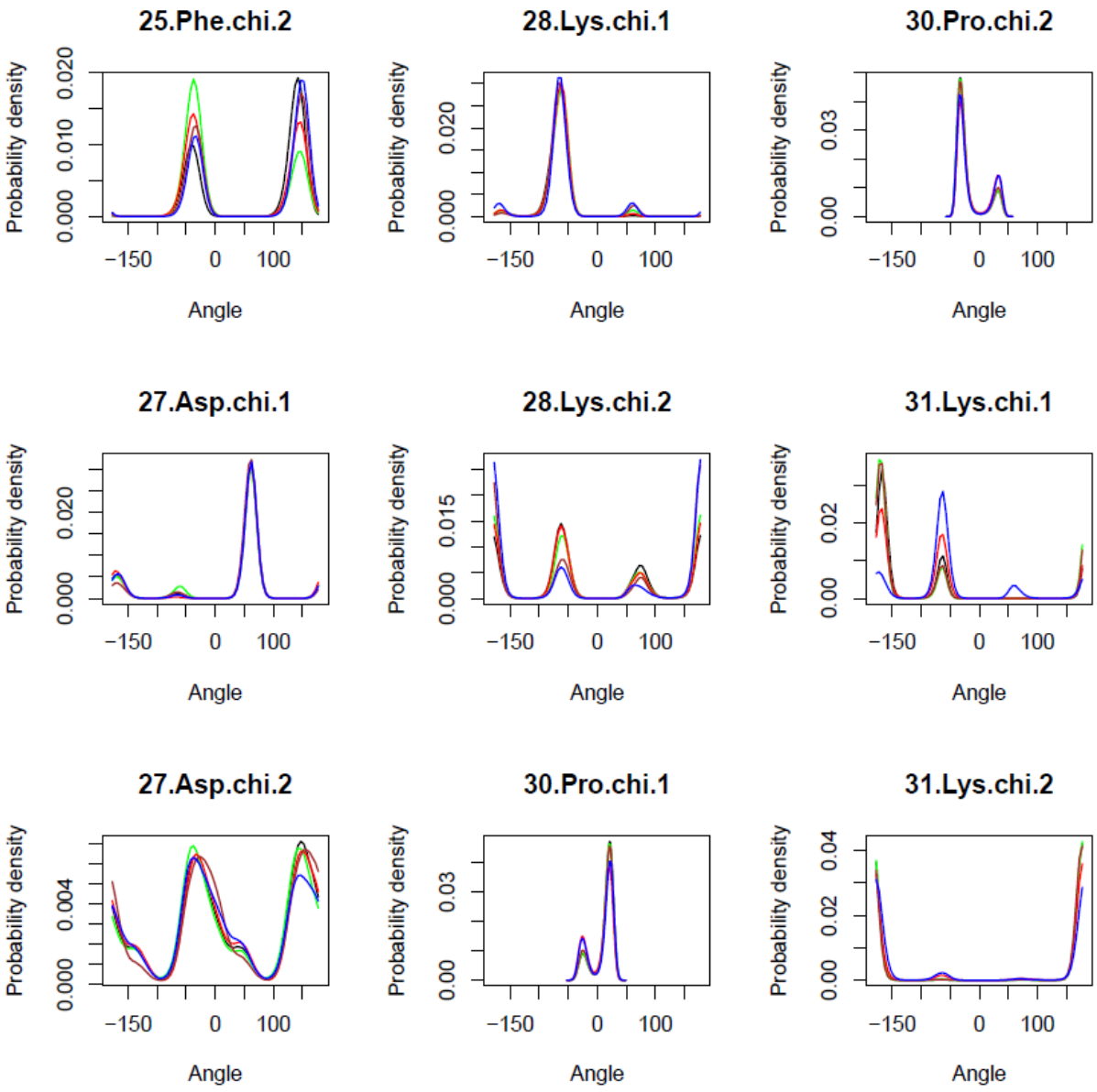
0.020
−150
0
100
Angle
25.Phe.chi.1
Probability density
0.00
0.03
−150
0
100
Angle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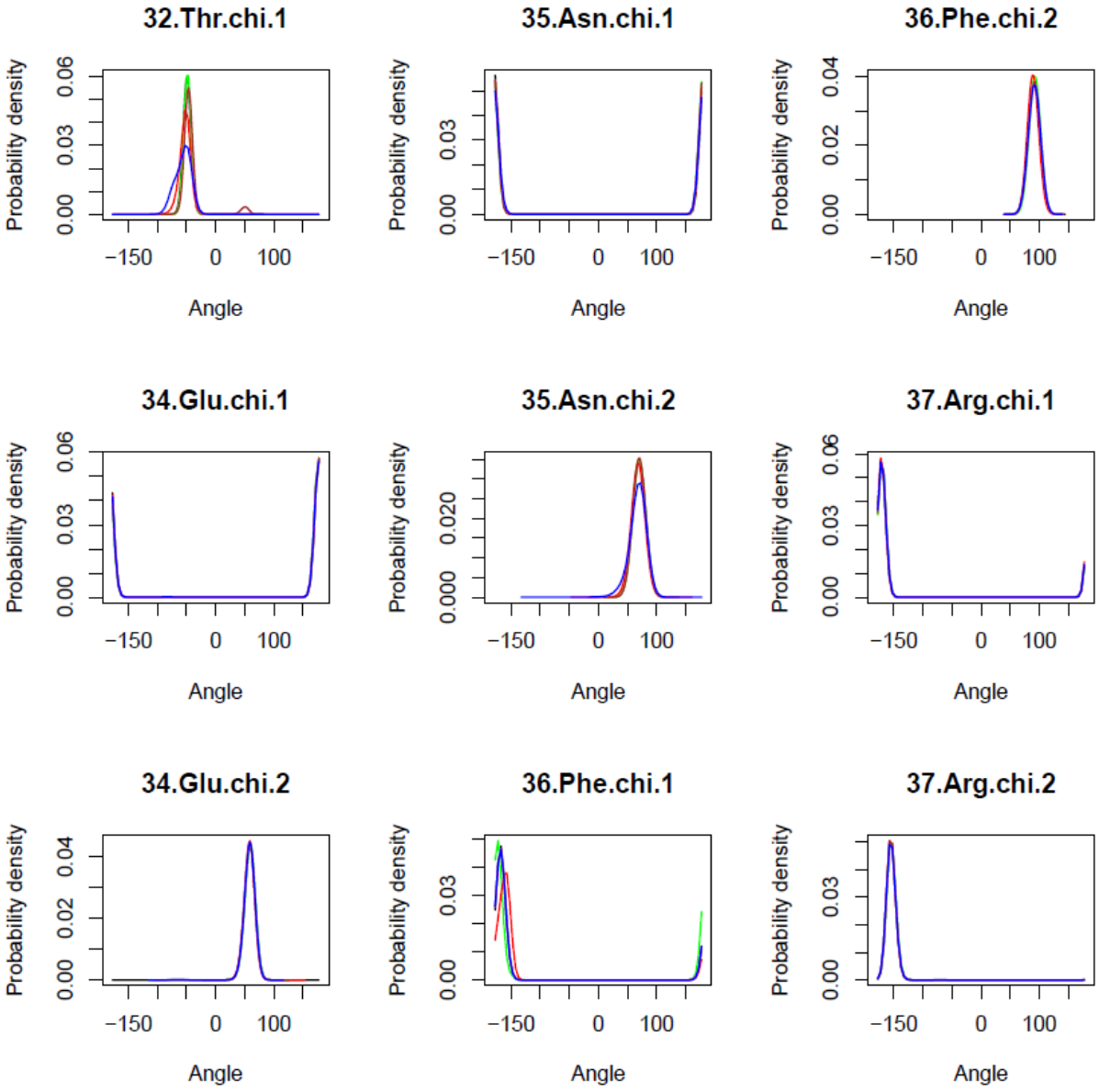
31.Lys.chi.2
Probability density
Angle
−150
0
100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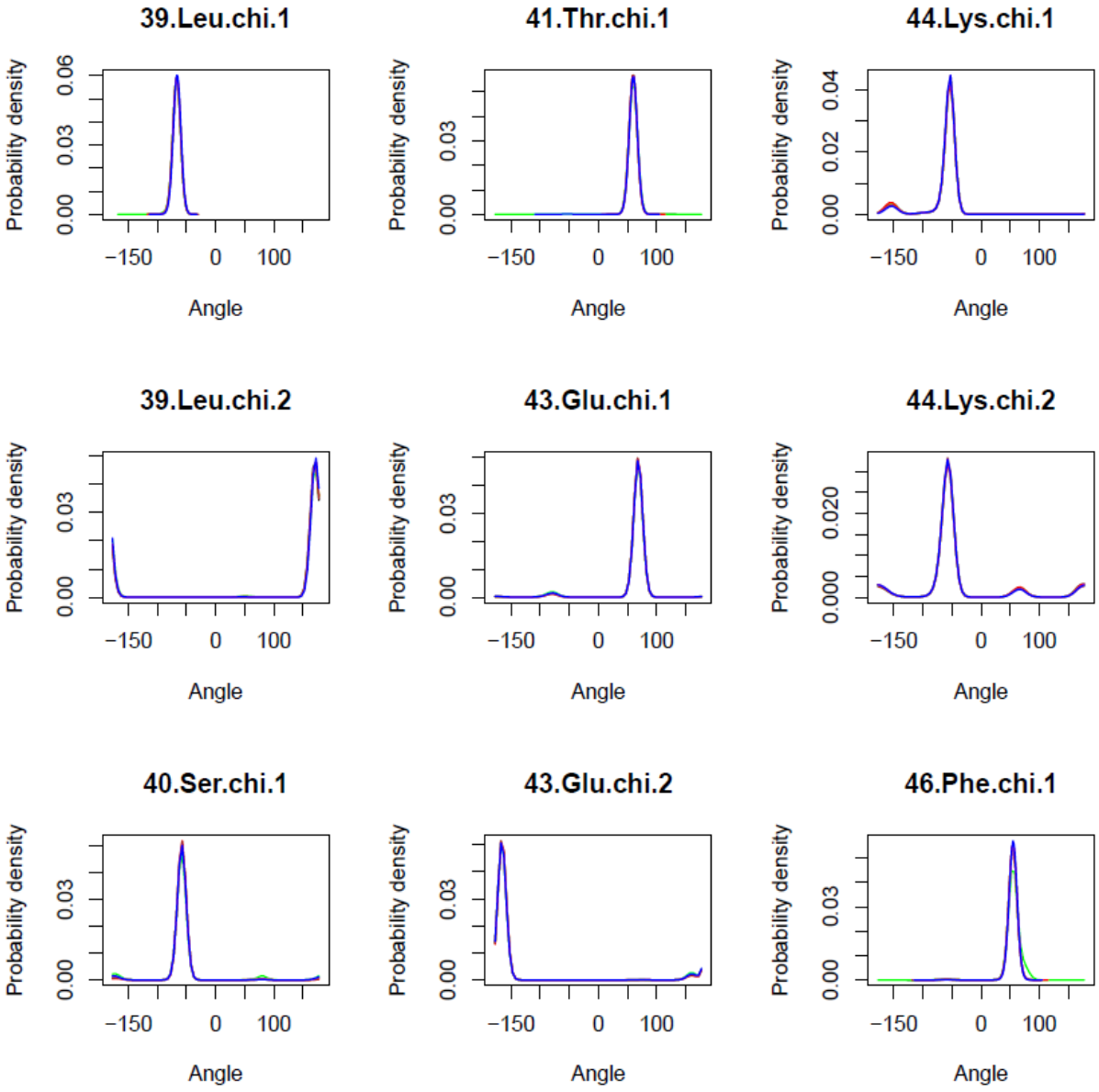
36.Phe.chi.1
37.Arg.chi.2
Probability density
Angle
−150
0
100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40.Ser.chi.1
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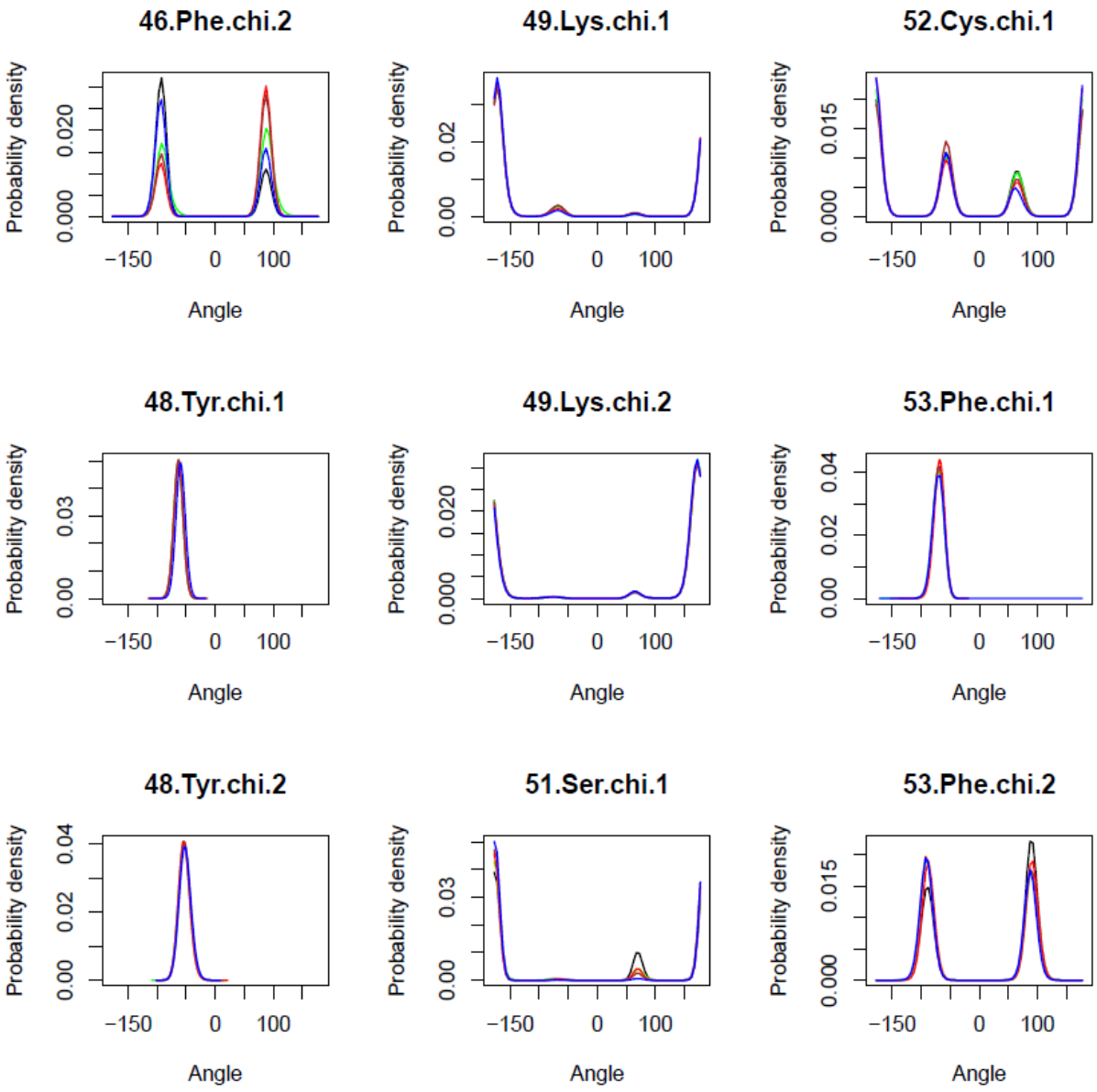
46.Phe.chi.1
Probability density
Angle
−150
0
100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48.Tyr.chi.1
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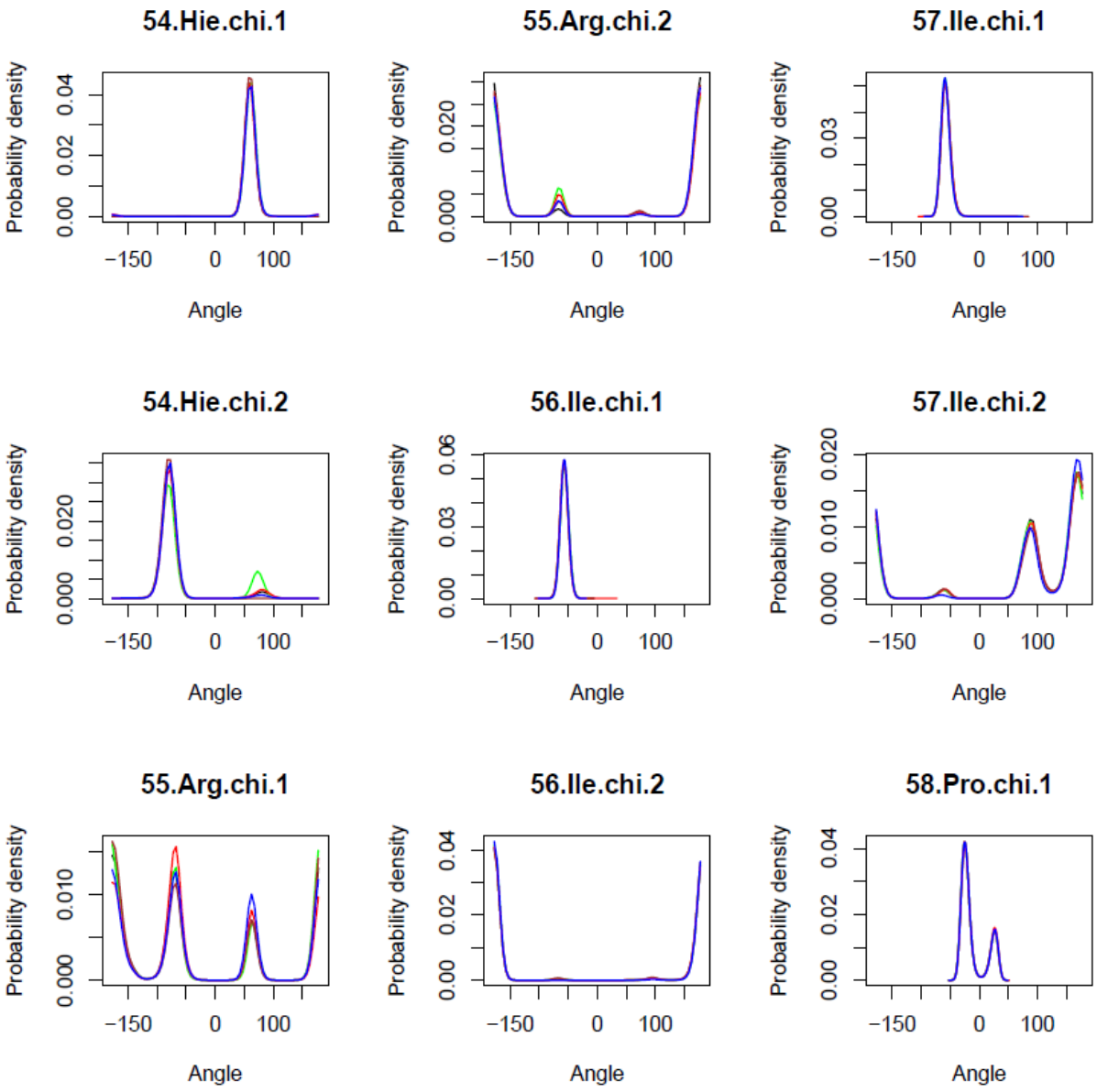
53.Phe.chi.2
Probability density
Angle
−150
0
100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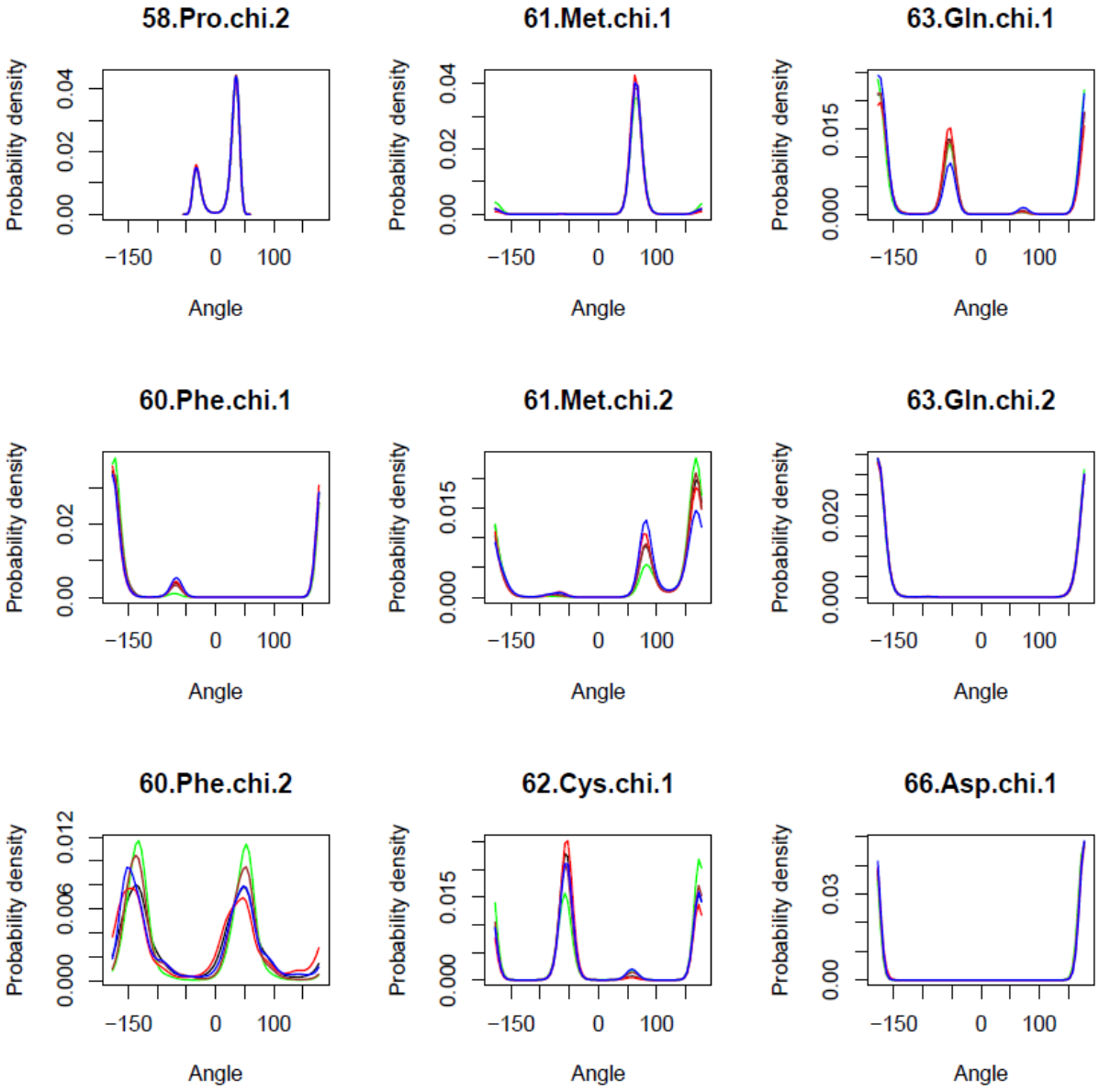
Probability density
Angle
−150
0
100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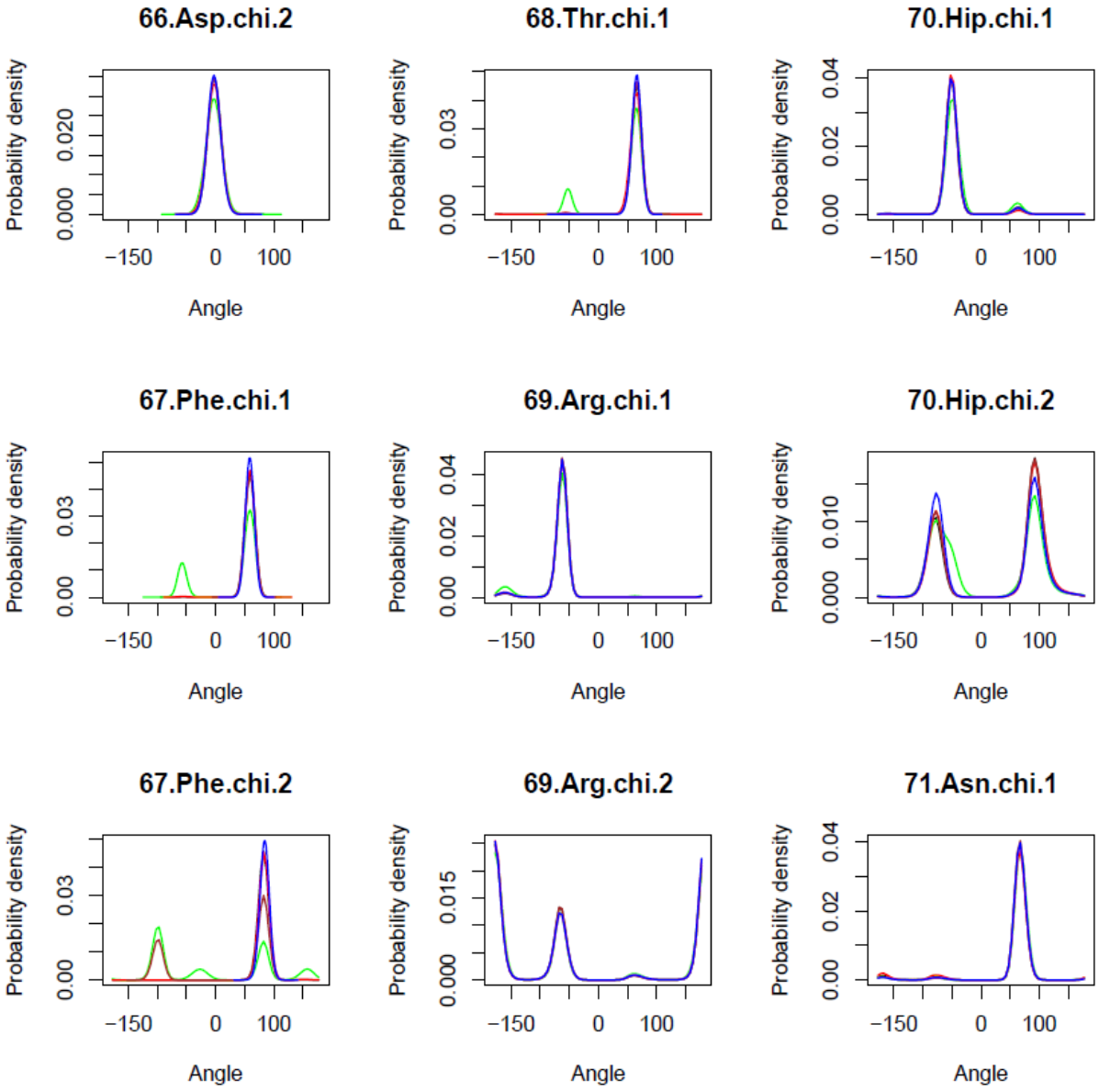
60.Phe.chi.2
62.Cys.chi.1
66.Asp.chi.1
Probability density
Angle
−150
0
100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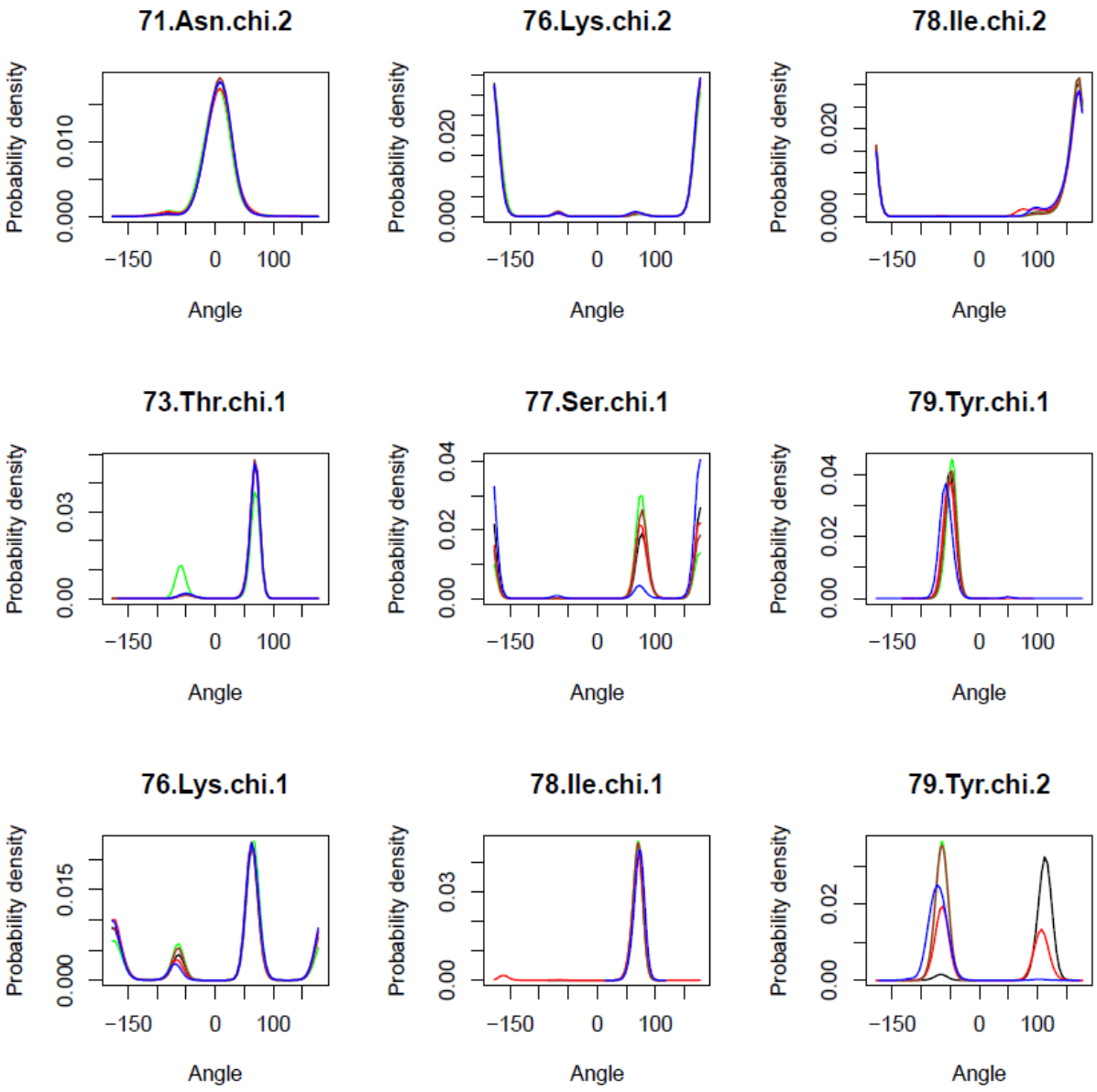
Probability density
Angle
−150
0
100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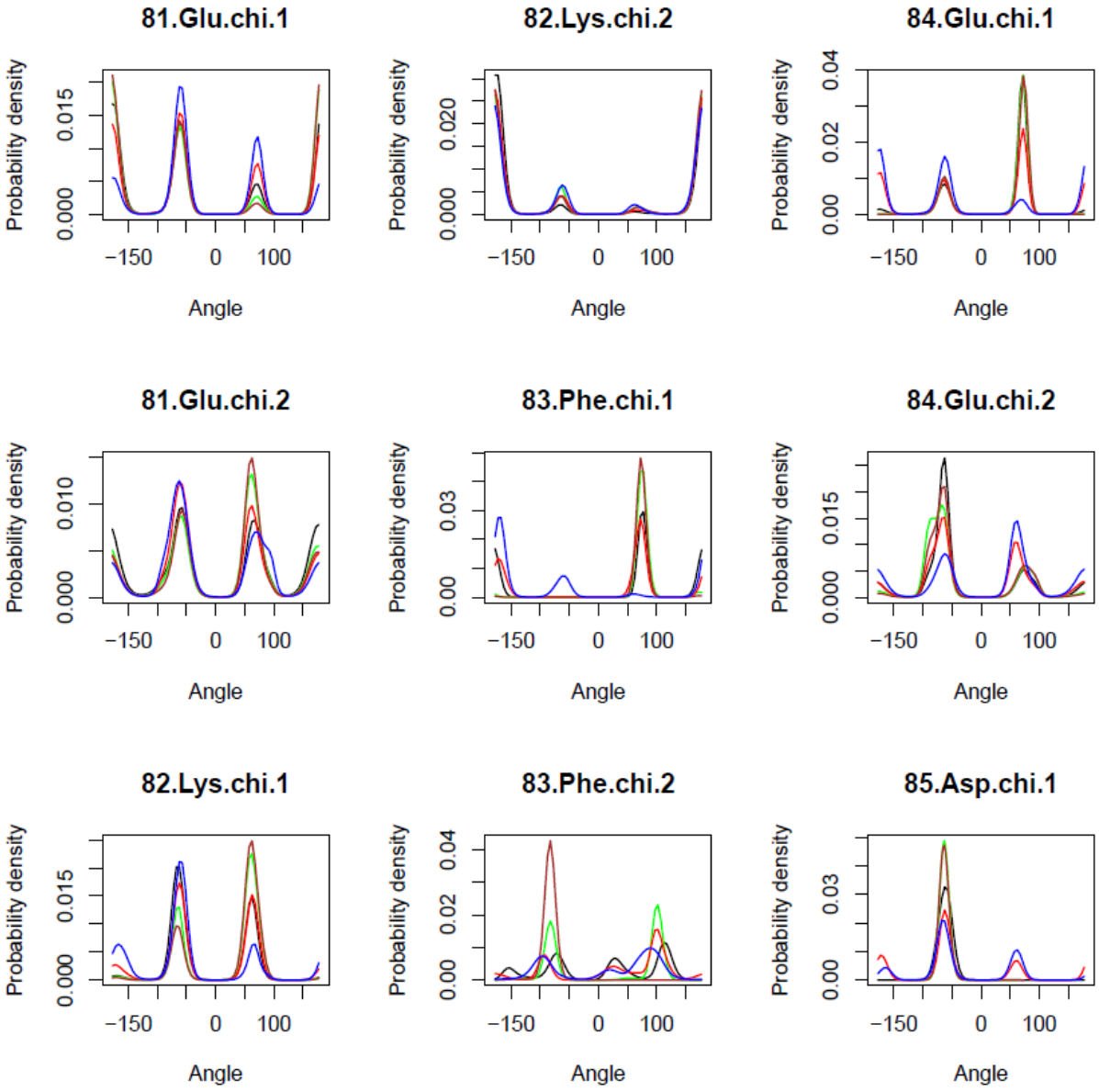
77.Ser.chi.1
79.Tyr.chi.1
76.Lys.chi.1
78.Ile.chi.1
79.Tyr.chi.2
Probability density
Angle
−150
0
100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0.015
−150
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Angle
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Probability density
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0.020
−150
0
100
Angle
84.Glu.chi.1
Probability density
0.00
0.02
0.04
−150
0
100
Angle
81.Glu.chi.2
Probability density
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0.010
−150
0
100
Angle
83.Phe.chi.1
Probability density
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0.03
−150
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Angle
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Probability density
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Angle
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Probability density
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Angle
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Probability density
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Angle
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Probability density
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0.03
−150
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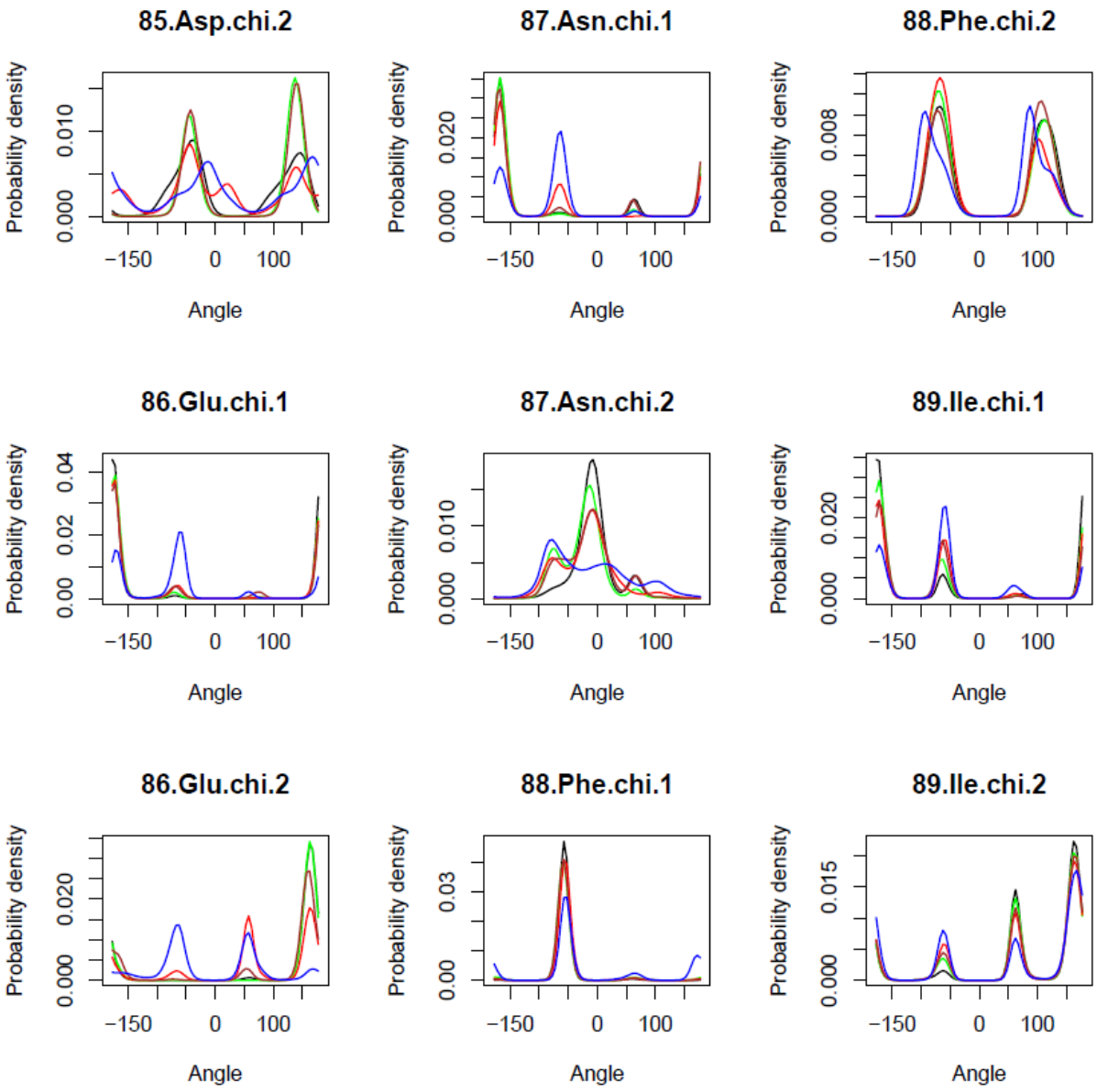
100
Angle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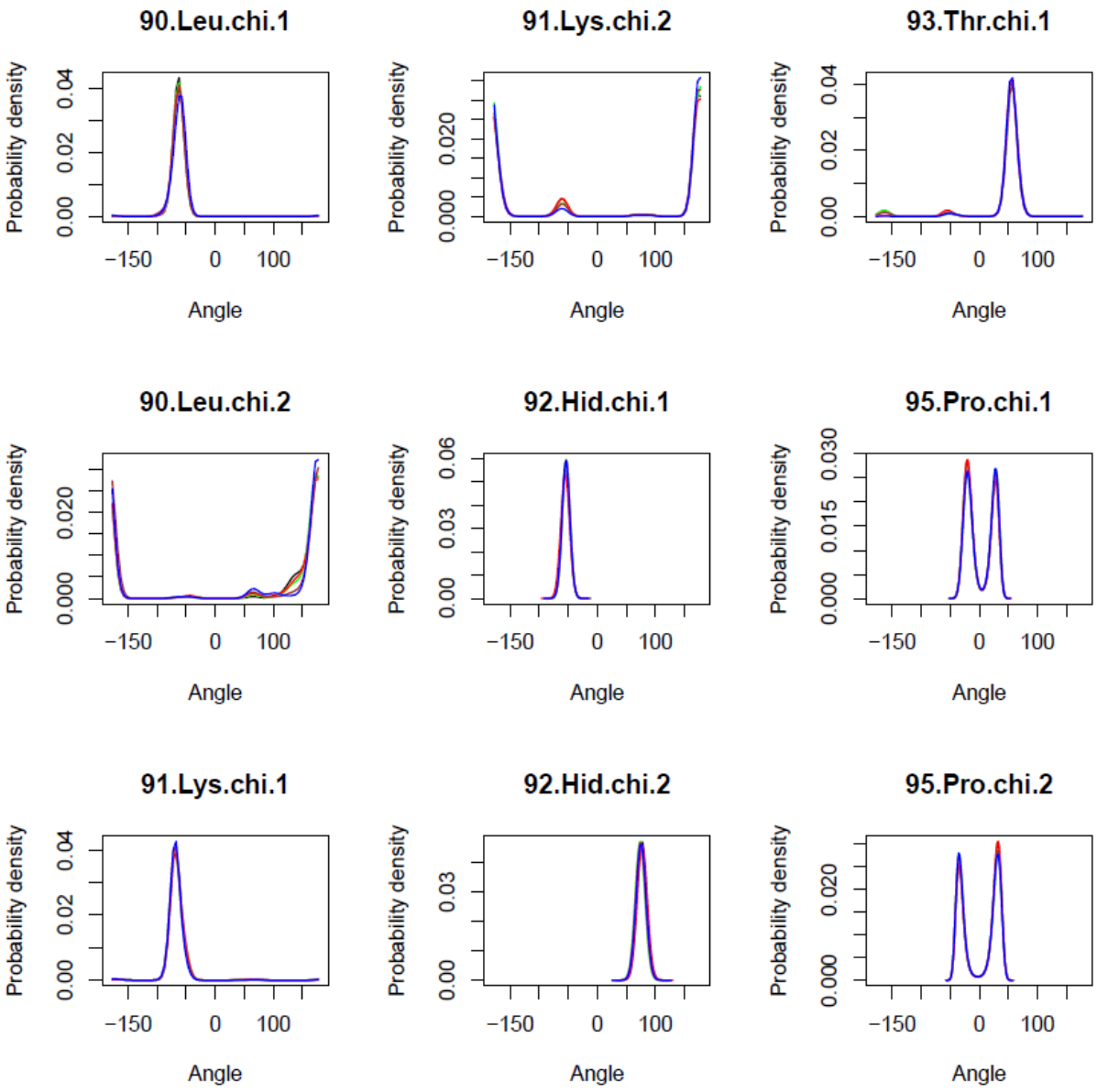
Probability density
Angle
−150
0
100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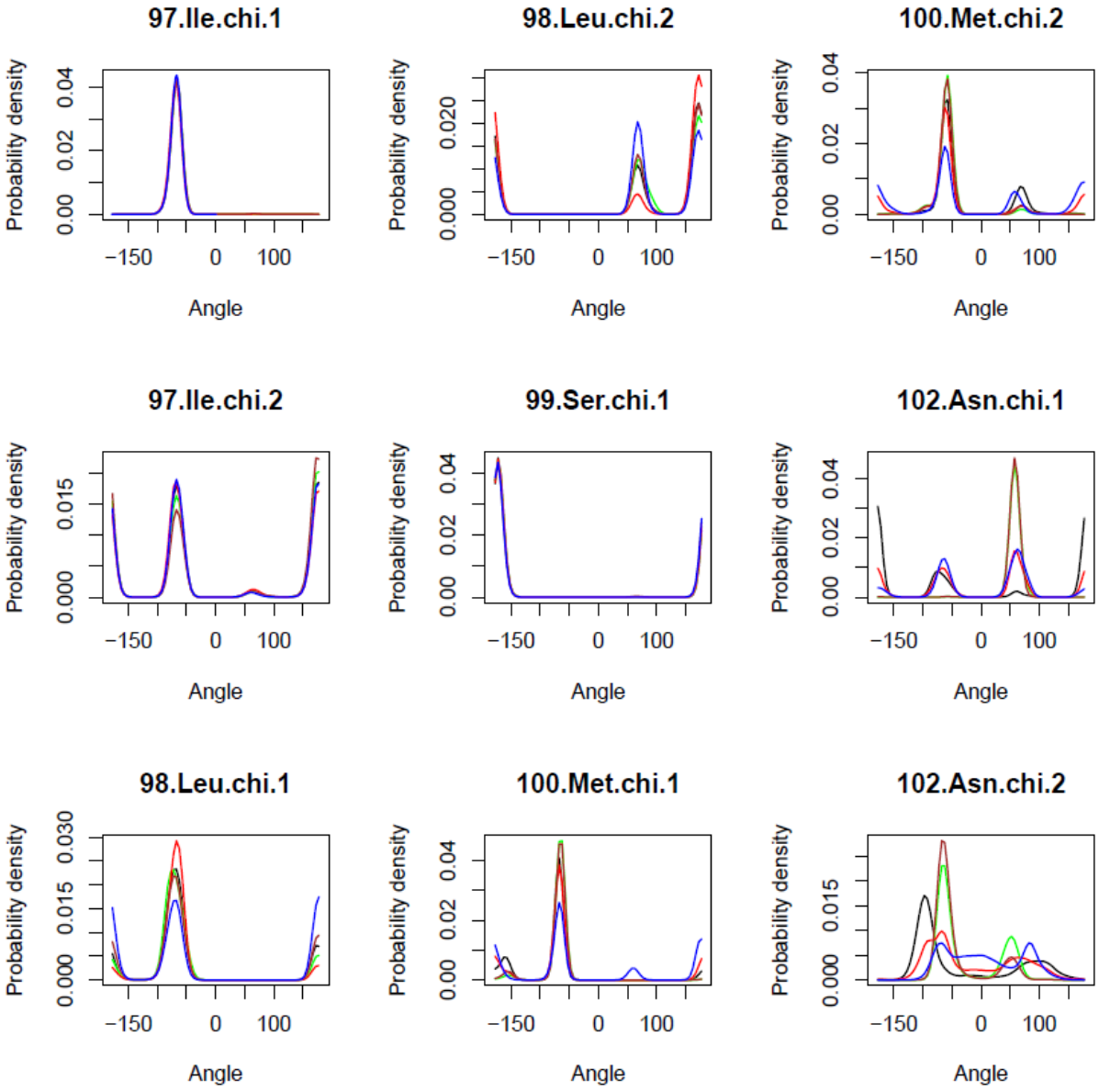
95.Pro.chi.2
Probability density
Angle
−150
0
100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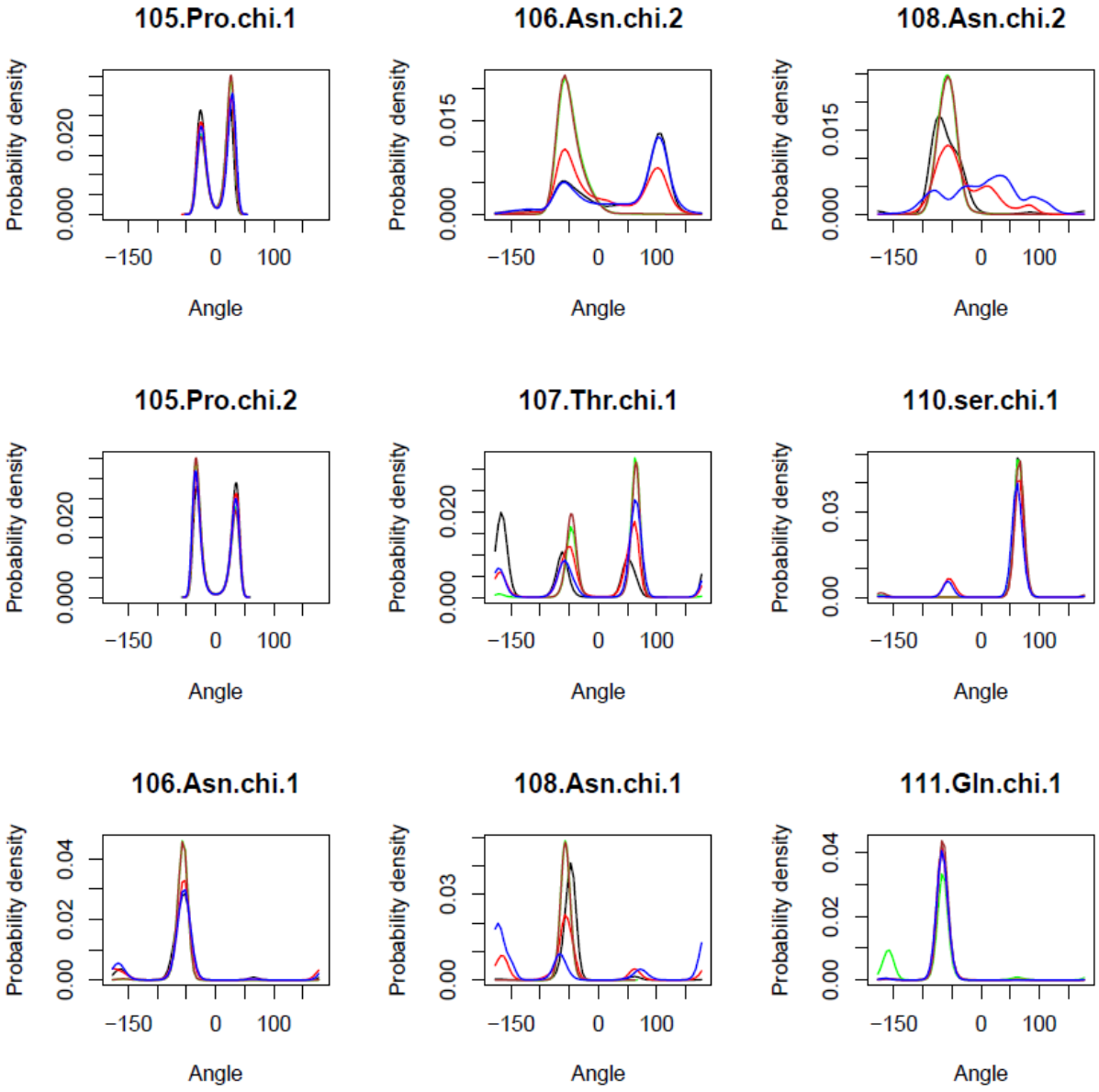
102.Asn.chi.2
Probability density
Angle
−150
0
100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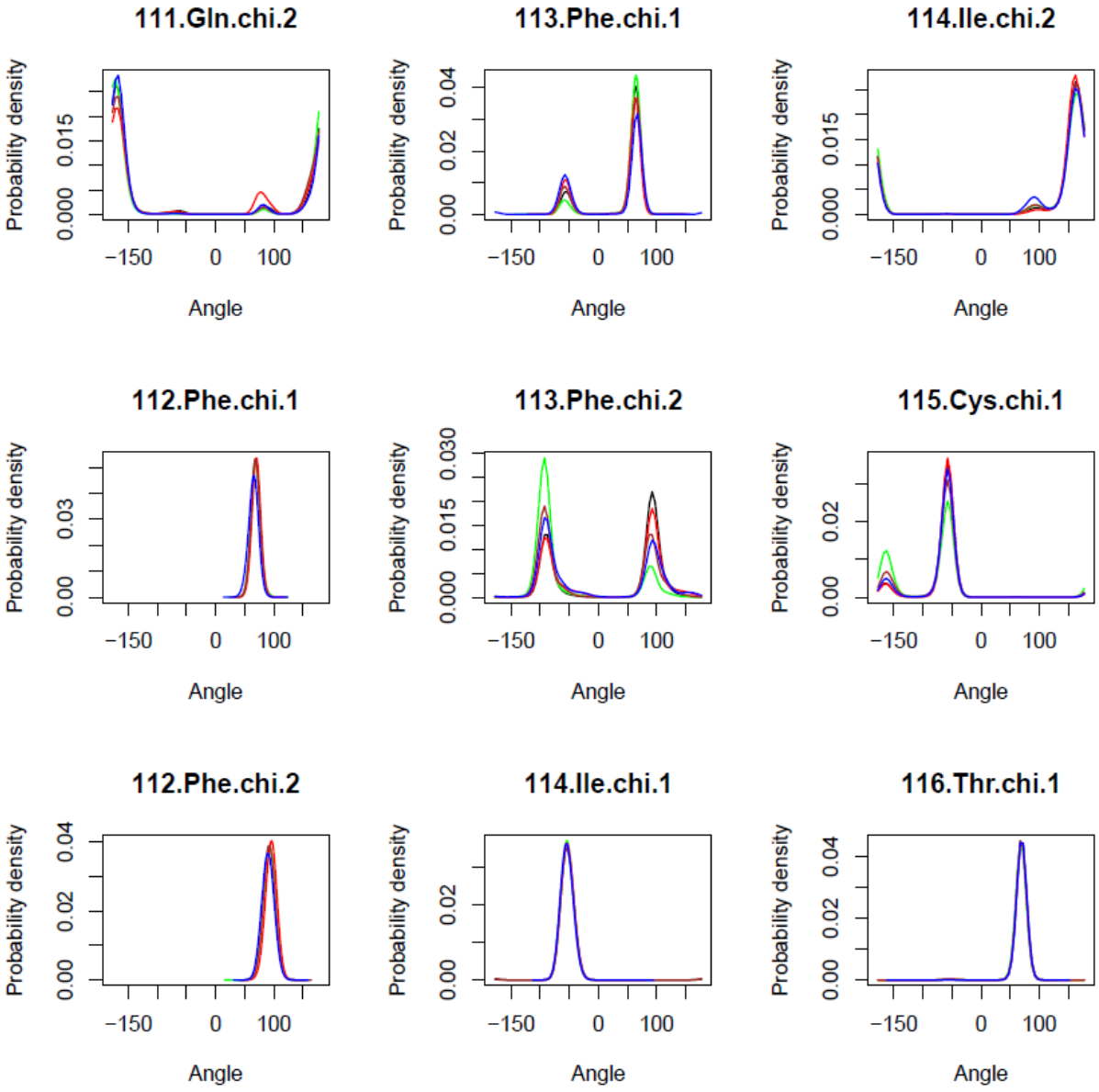
Probability density
Angle
−150
0
100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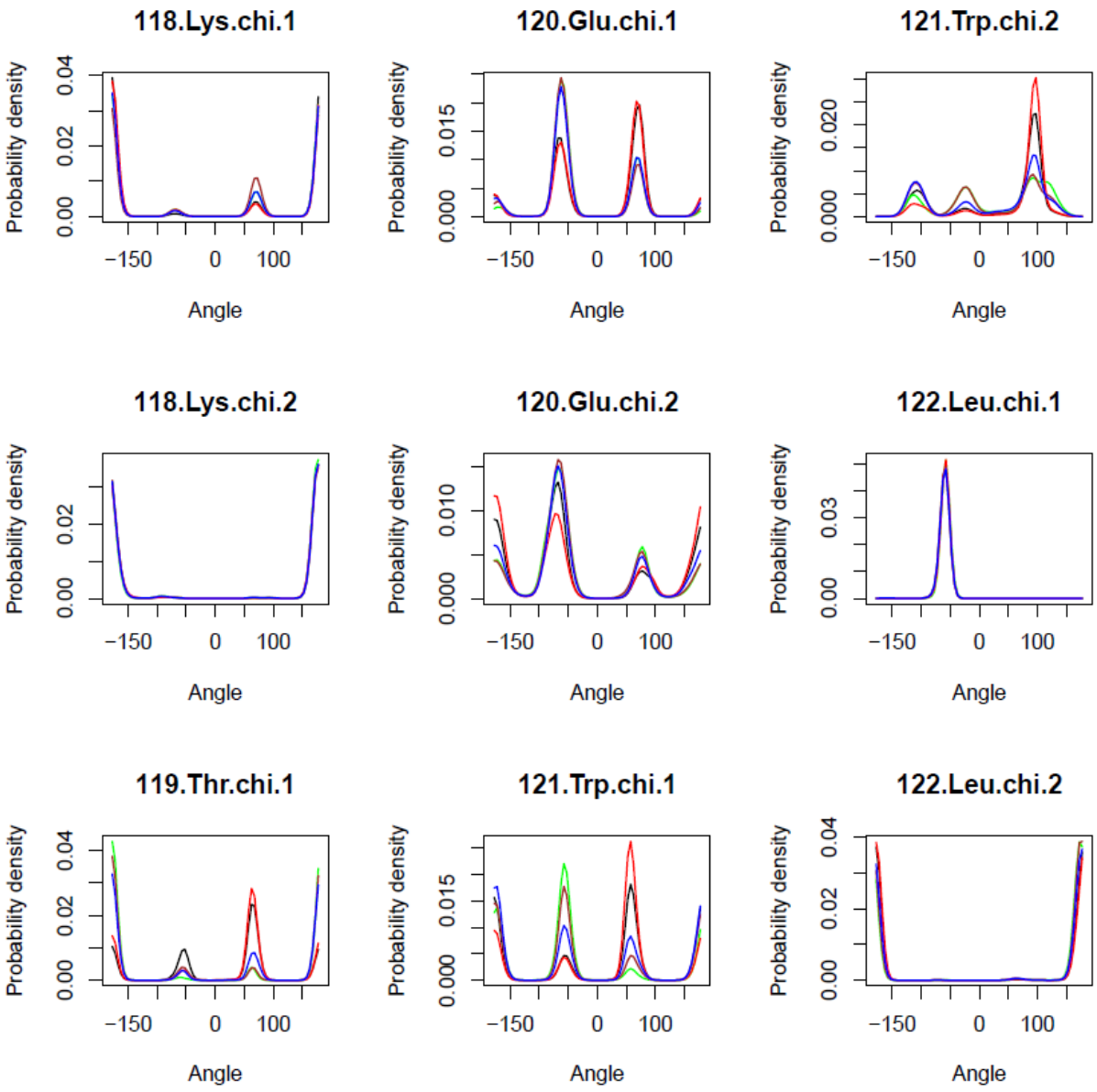
Probability density
Angle
−150
0
100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121.Trp.chi.1
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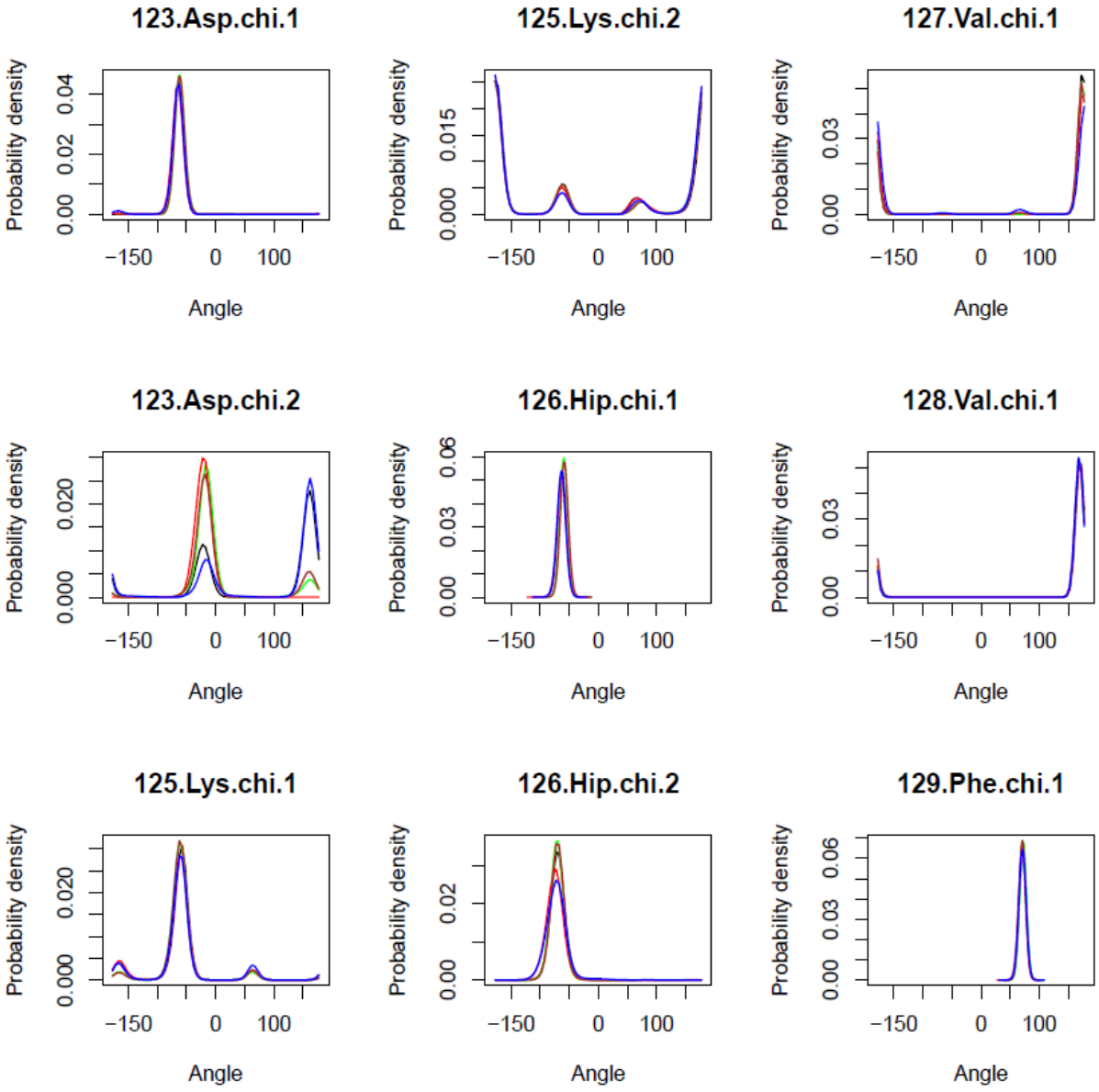
Probability density
Angle
−150
0
100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Probability density
Angle
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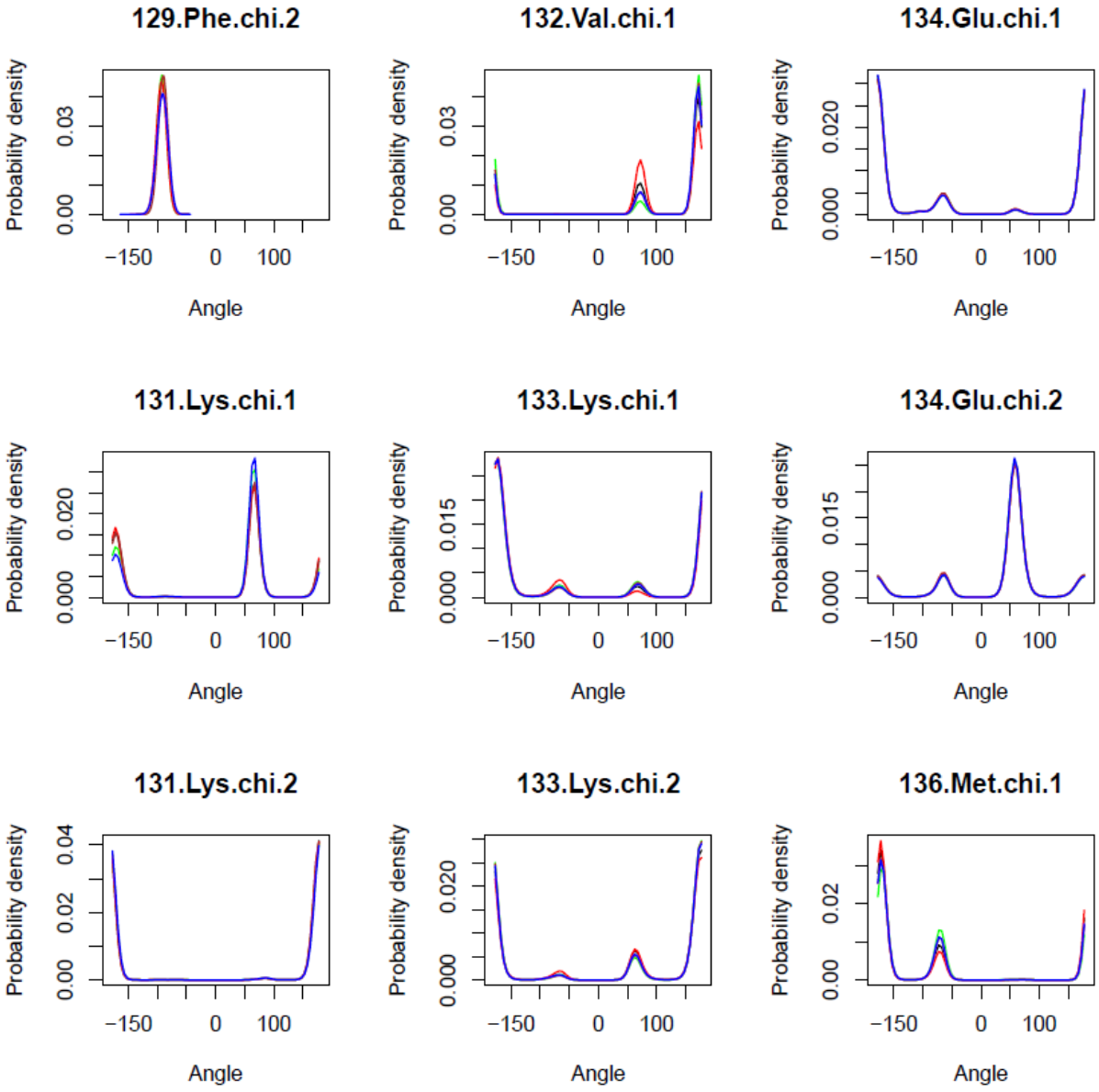
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Probability density
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Angle
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Probability density
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Angle
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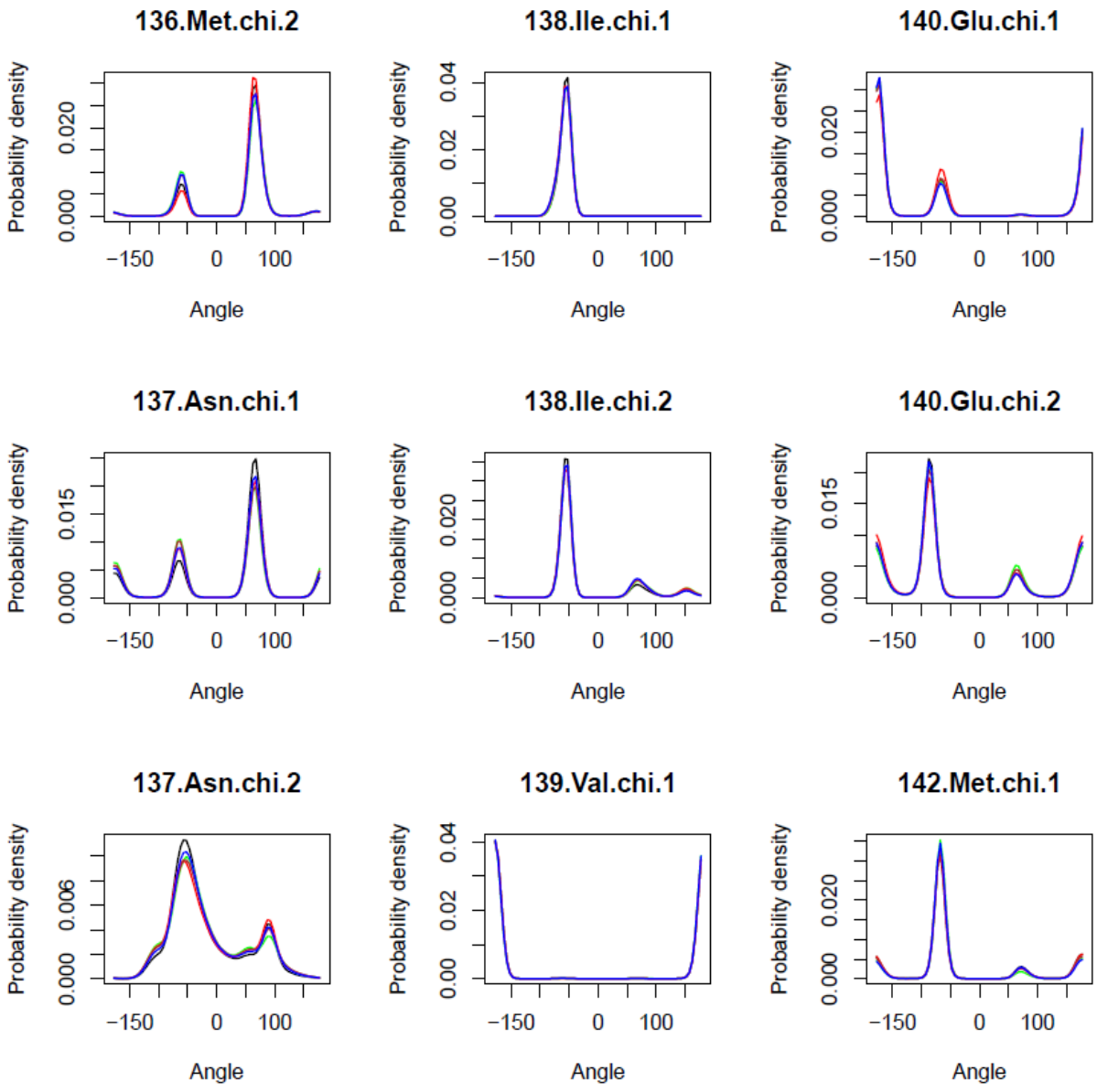
Angle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Angle
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Angle
137.Asn.chi.1
Probability density
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Angle
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Angle
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Angle
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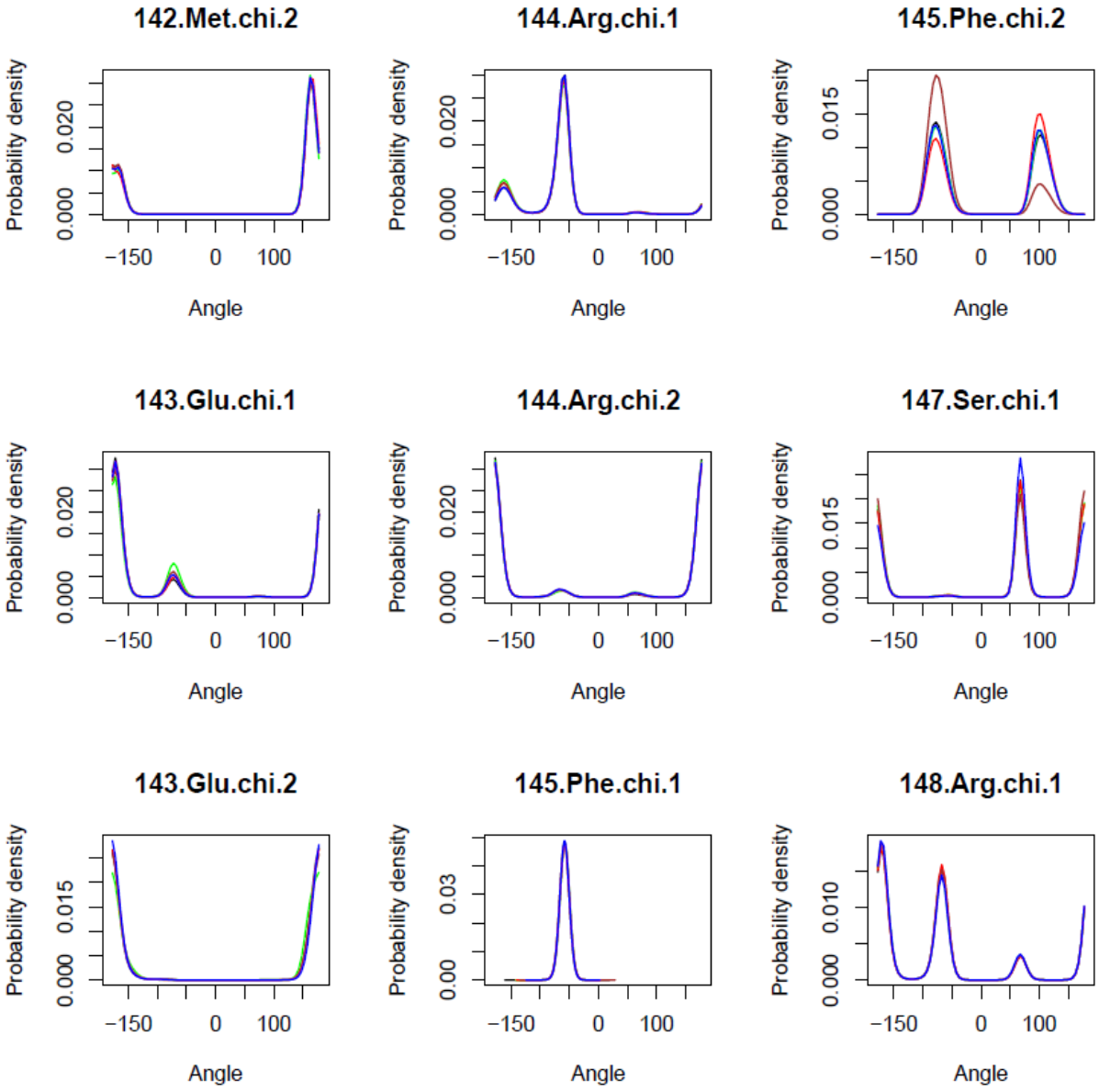
Angle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Angle
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0.000
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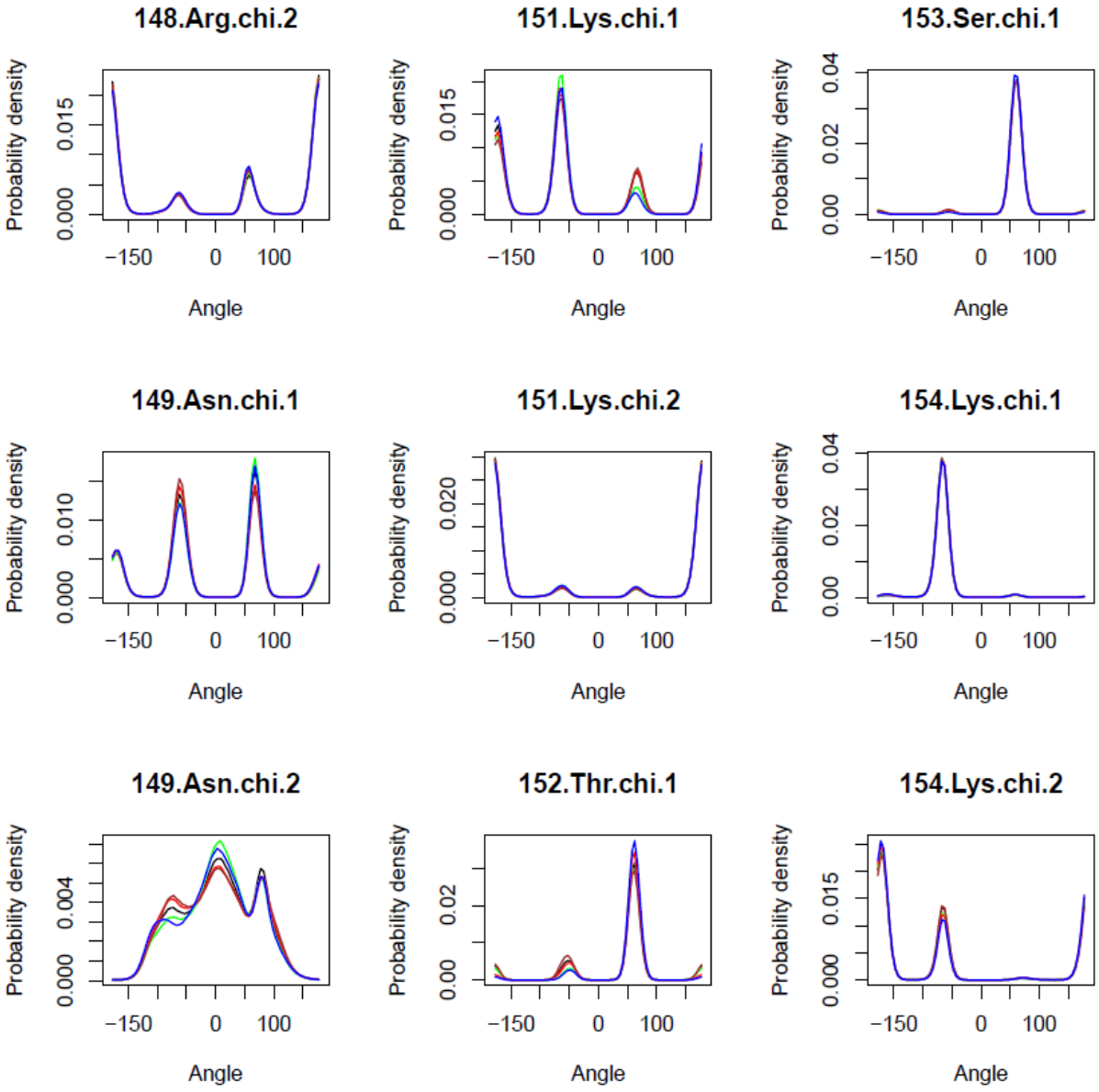
0.03
0.010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Probability density
Angle
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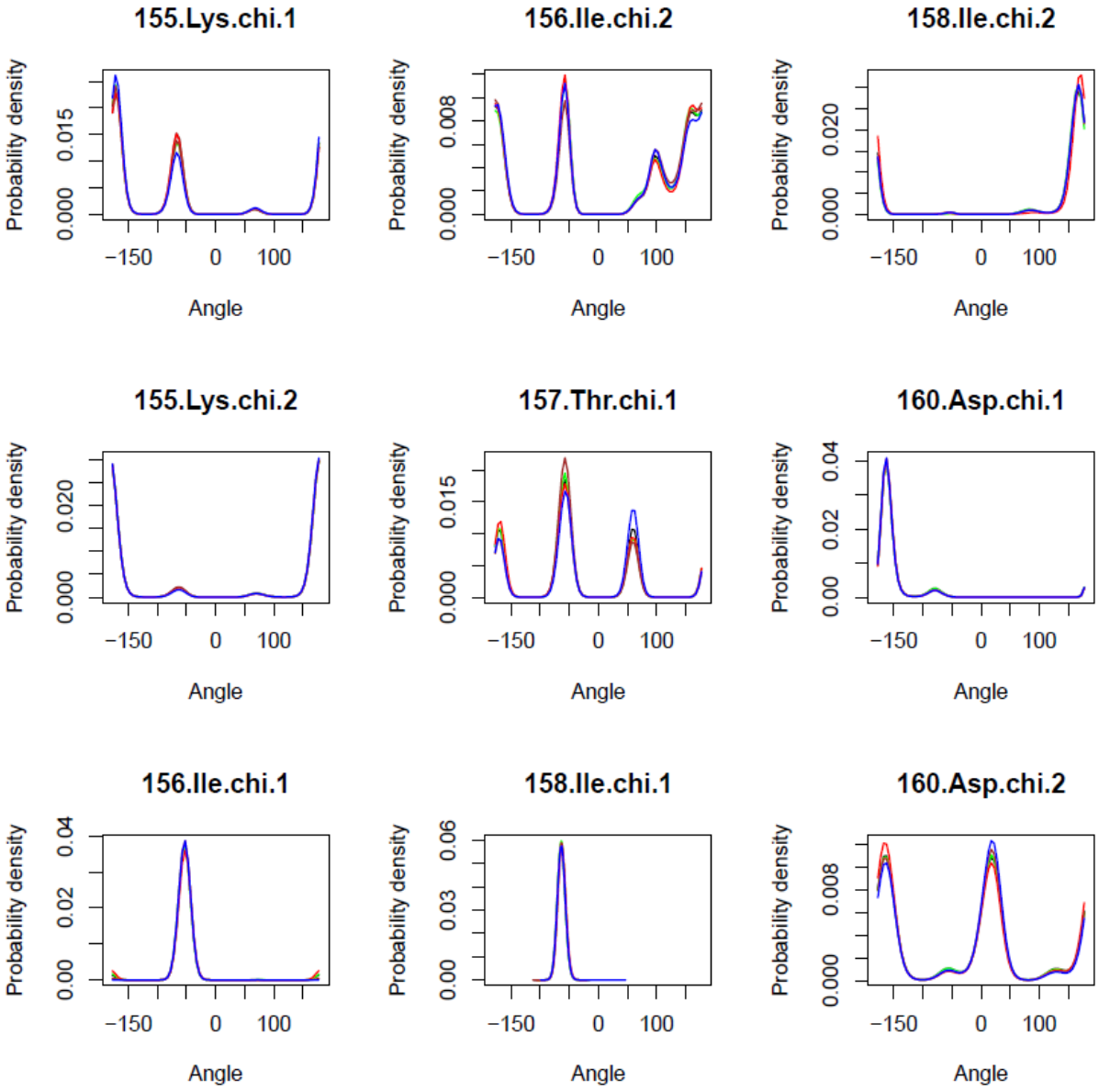
0
100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158.Ile.chi.1
160.Asp.chi.2
Probability density
Angle
−150
0
100

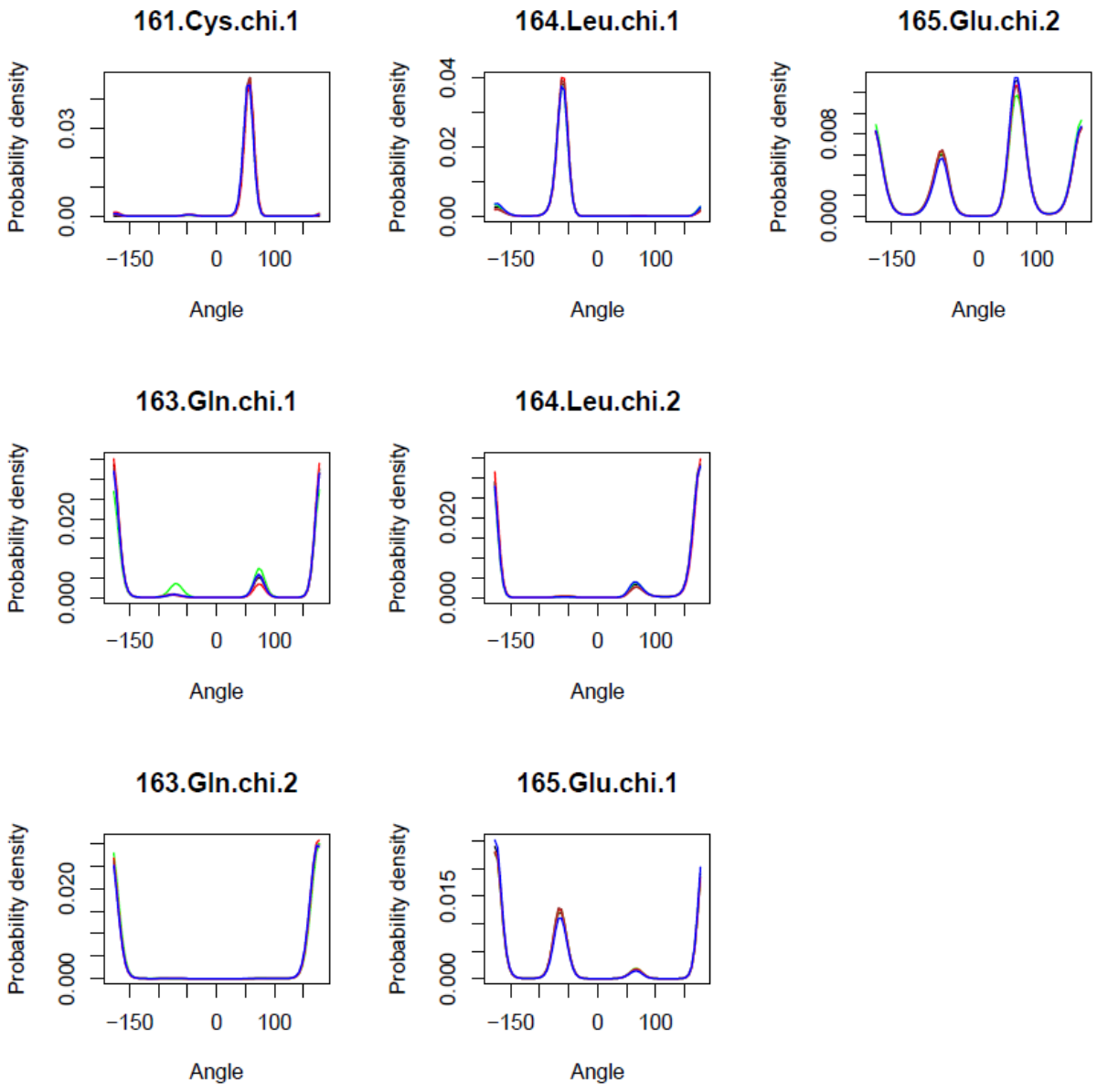


**Figure S1. Probability density distributions of the side chain torsional angles of all CypA residues except for glycines and alanines.** Depicted are the χ torsion angles derived from the five simulations performed: wild-type (black), V6I (red), V6T (green), V29L (blue), and V29T (brown). Each panel shows an angle of a specific residue.

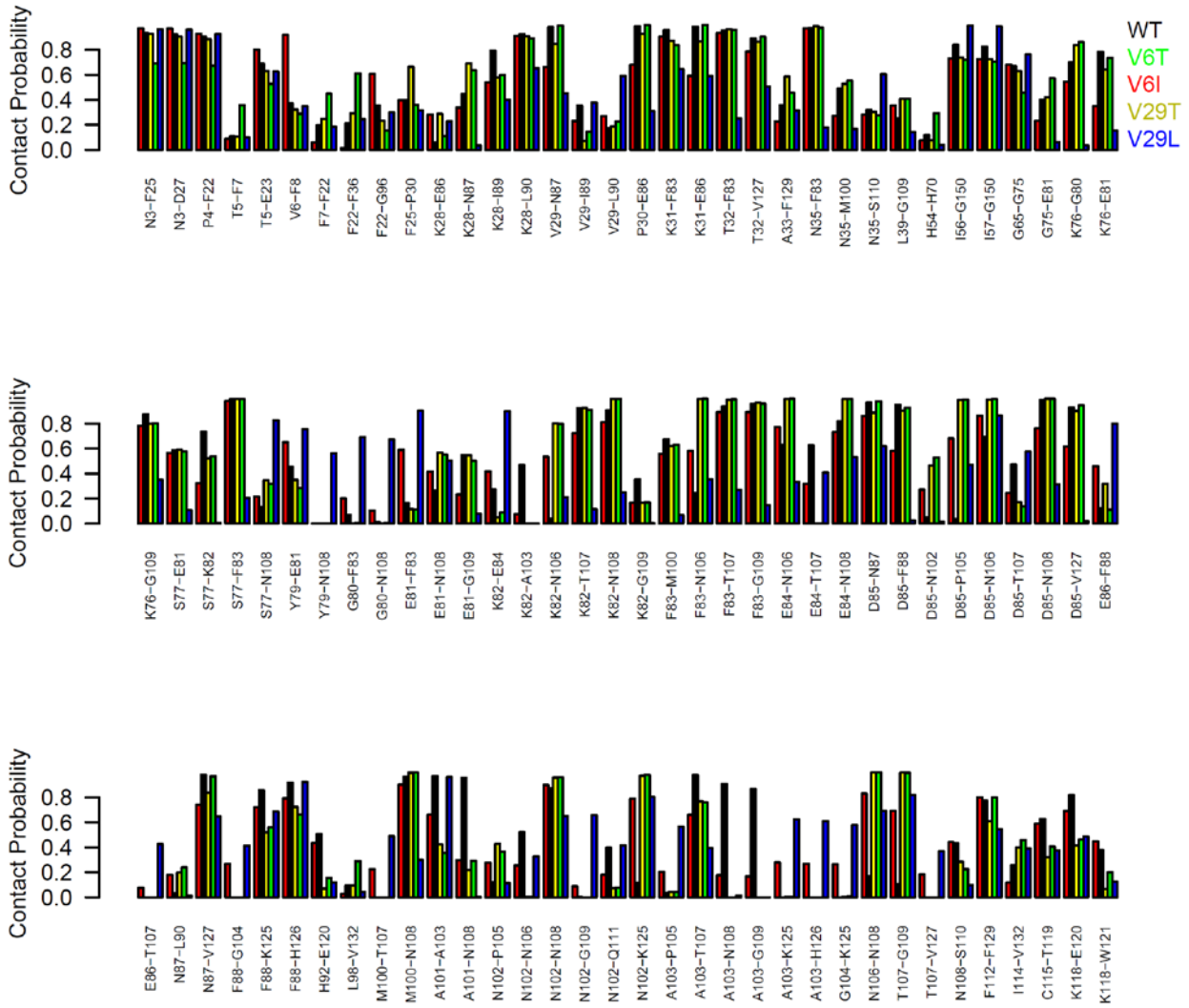


**Figure S2. Formation probabilities of all dynamic contacts during simulations.** Wild-type (black), V6I (red), V6T (green), V29L (blue), and V29T (yellow).