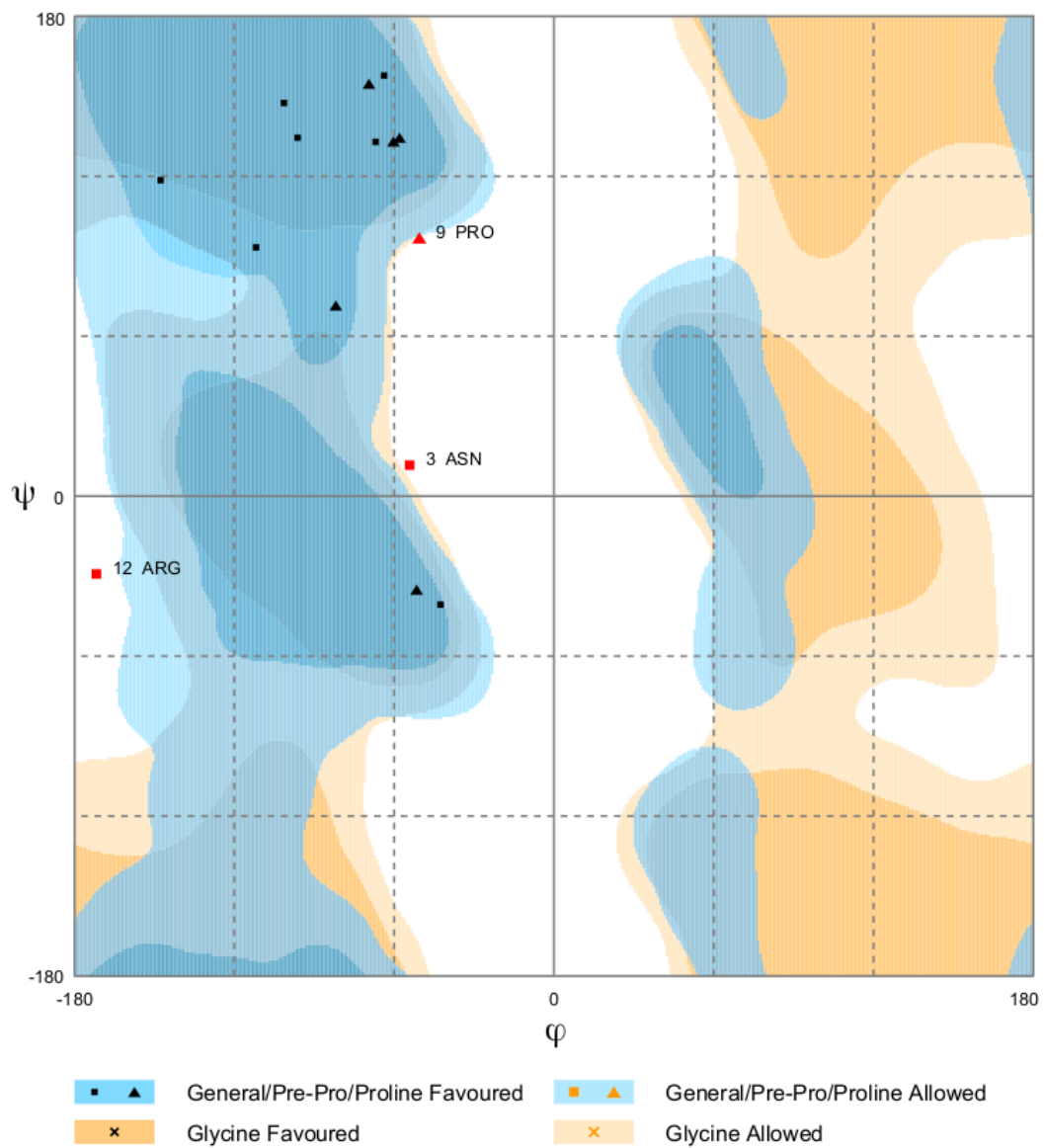
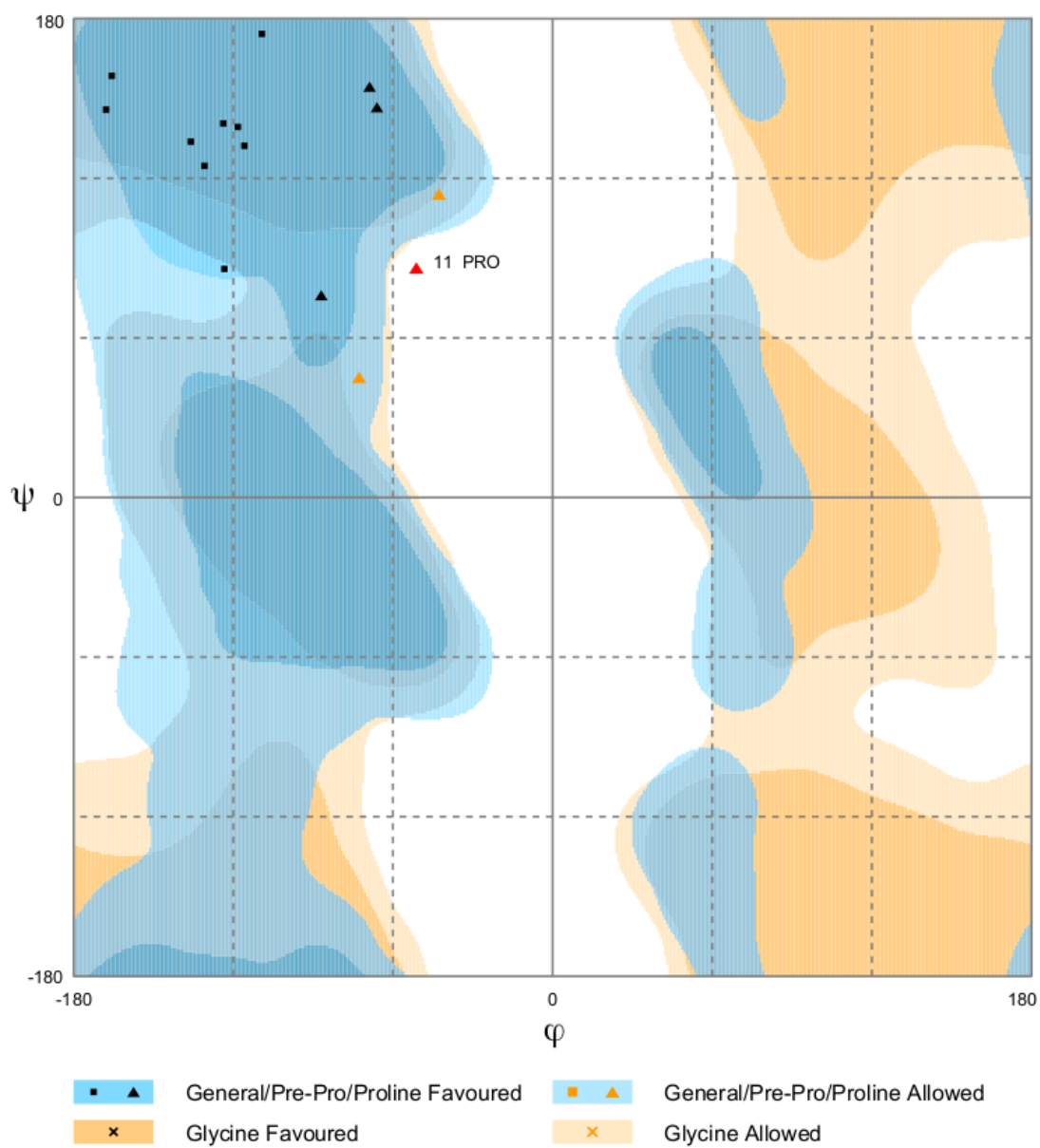


Apidaecin-IA



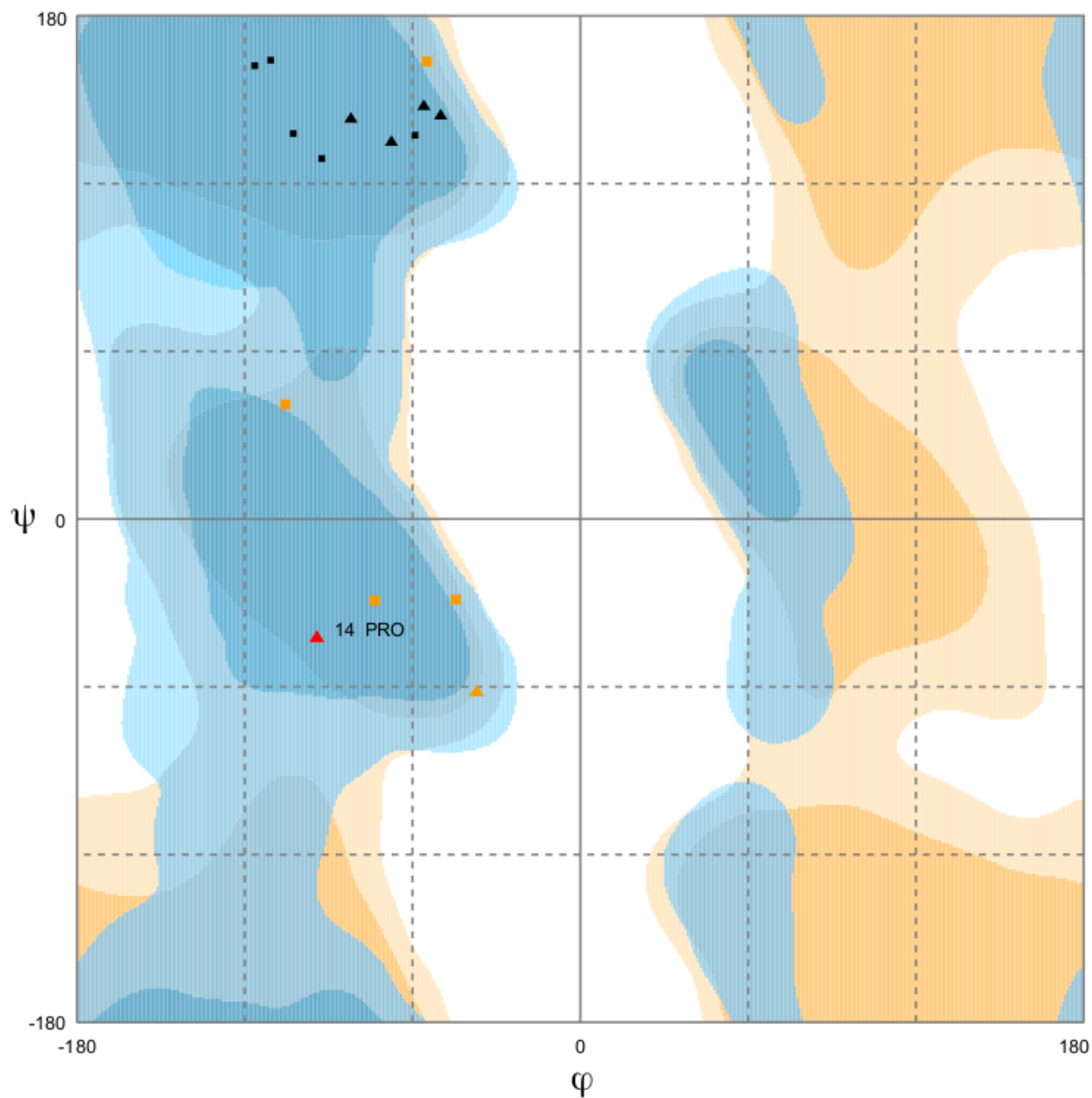
Number of residues in favoured region (~98.0% expected)	: 12 (80.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 3 (20.0%)

Apidaecin-IB



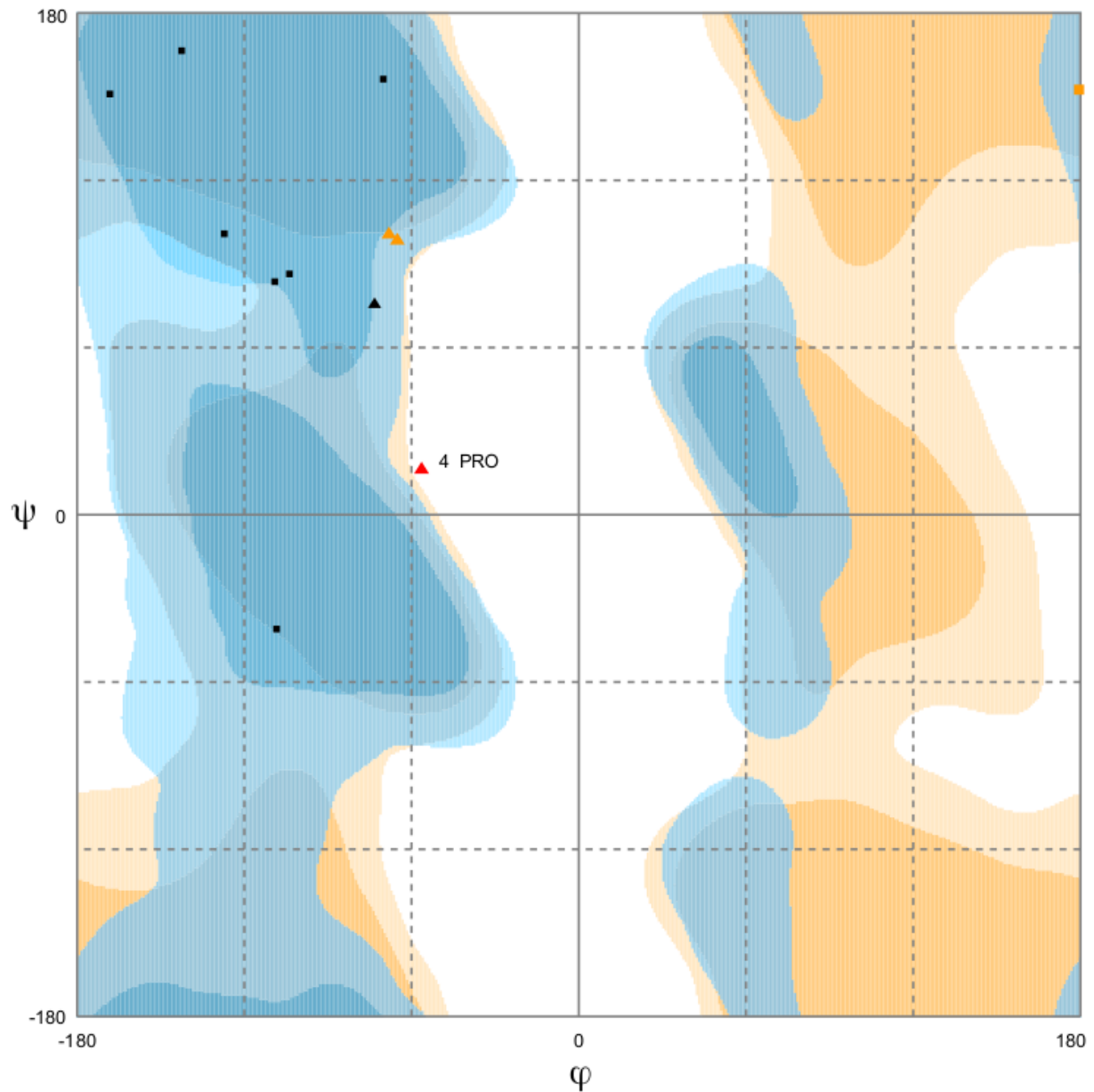
Number of residues in favoured region (~98.0% expected)	: 12 (80.0%)
Number of residues in allowed region (~2.0% expected)	: 2 (13.3%)
Number of residues in outlier region	: 1 (6.7%)

Apidaecin II



Number of residues in favoured region (~98.0% expected)	: 9 (60.0%)
Number of residues in allowed region (~2.0% expected)	: 5 (33.3%)
Number of residues in outlier region	: 1 (6.7%)

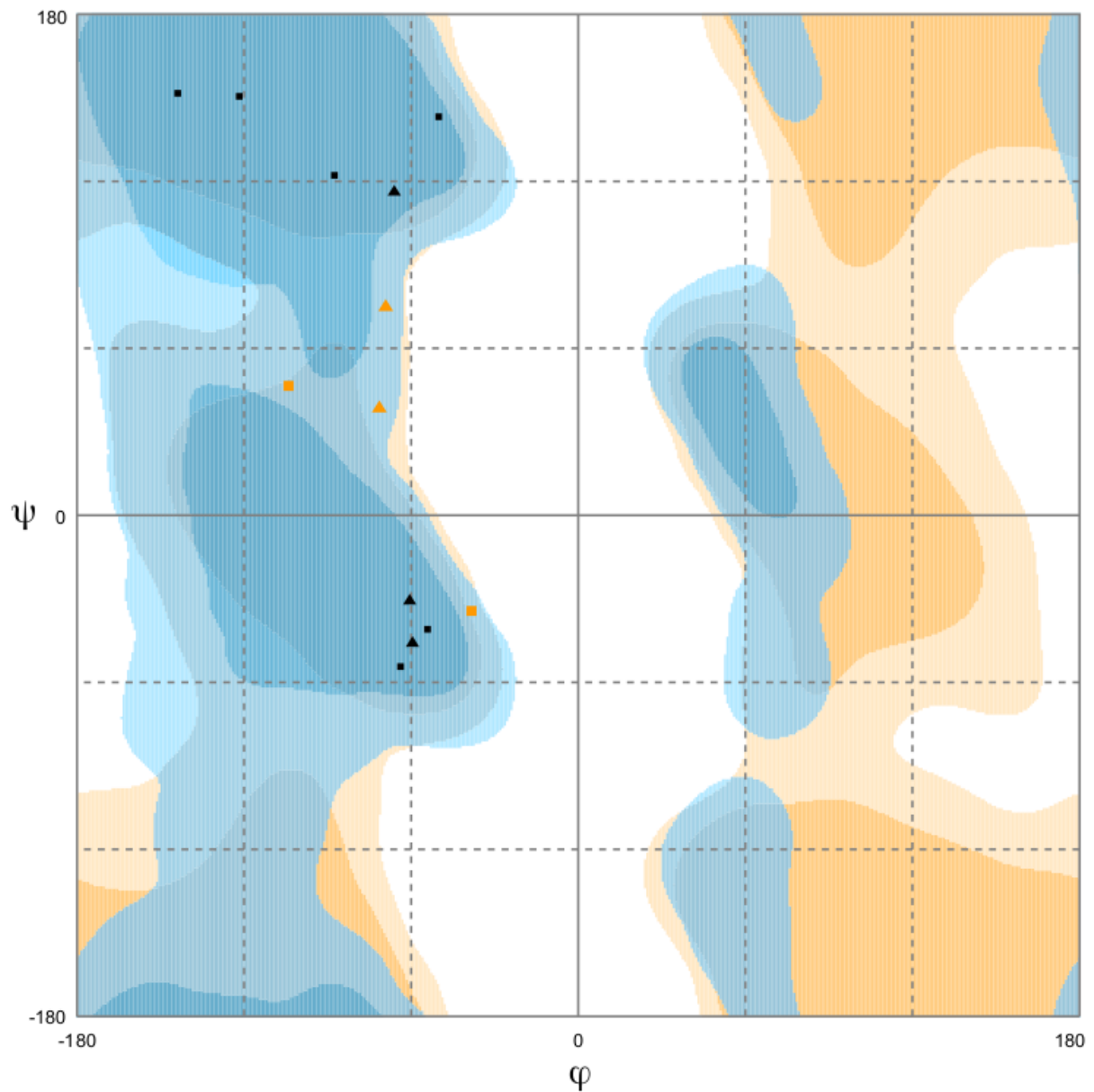
Metalnikowin IIA



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

Number of residues in favoured region (~98.0% expected)	: 8 (66.7%)
Number of residues in allowed region (~2.0% expected)	: 3 (25.0%)
Number of residues in outlier region	: 1 (8.3%)

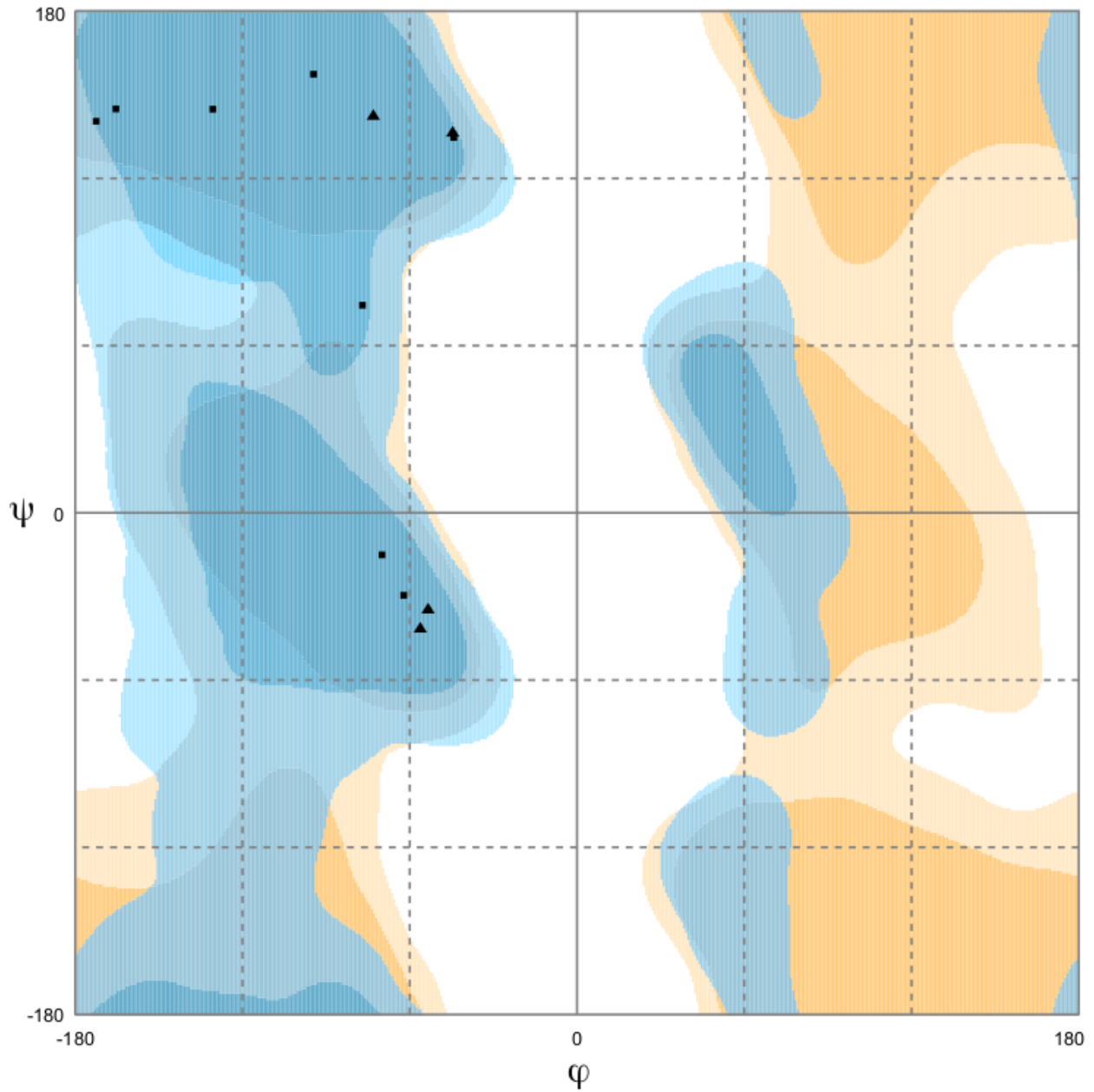
Metalnikowin III



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

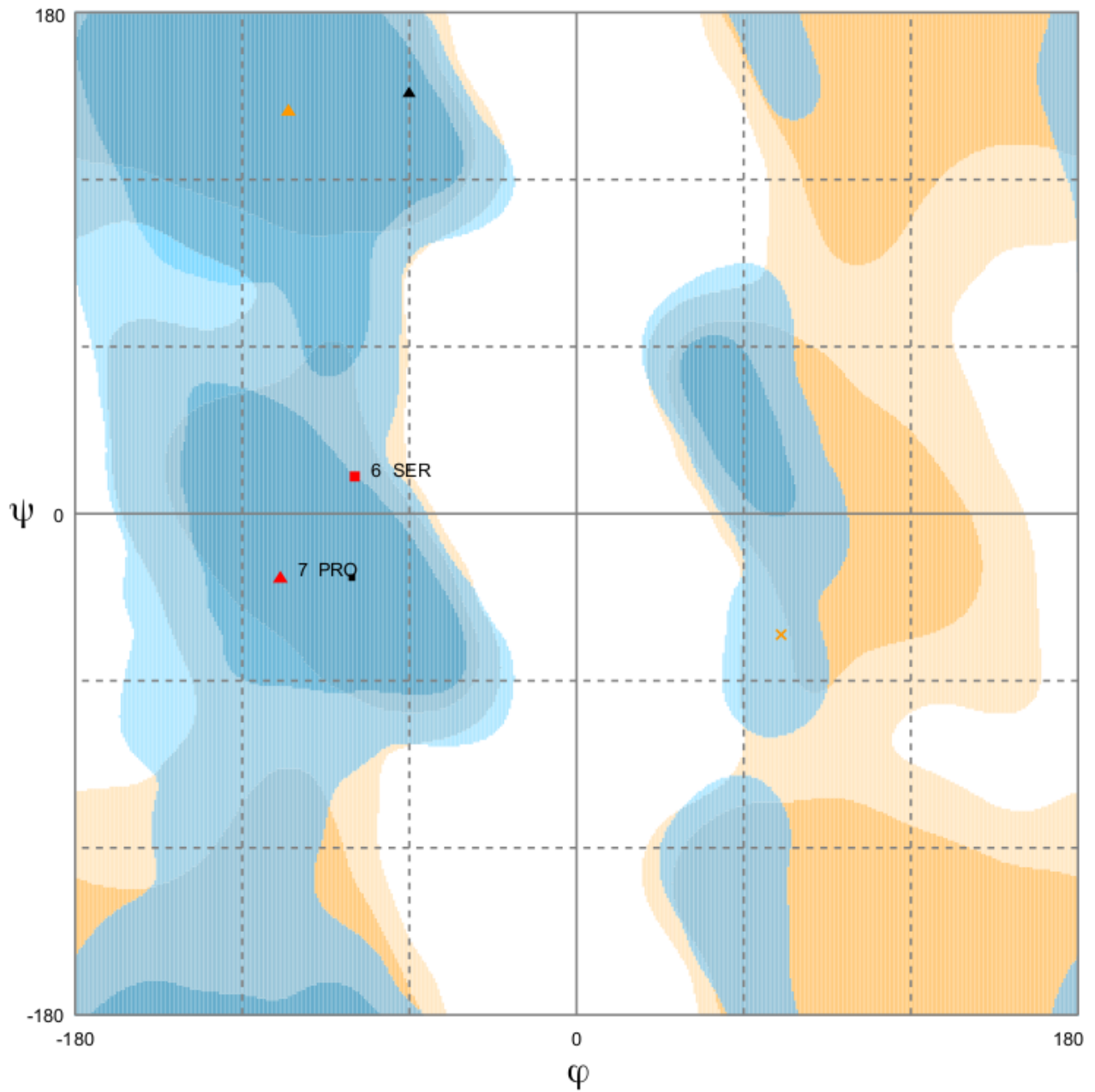
Number of residues in favoured region (~98.0% expected)	: 9 (69.2%)
Number of residues in allowed region (~2.0% expected)	: 4 (30.8%)
Number of residues in outlier region	: 0 (0.0%)

Astacidin 2



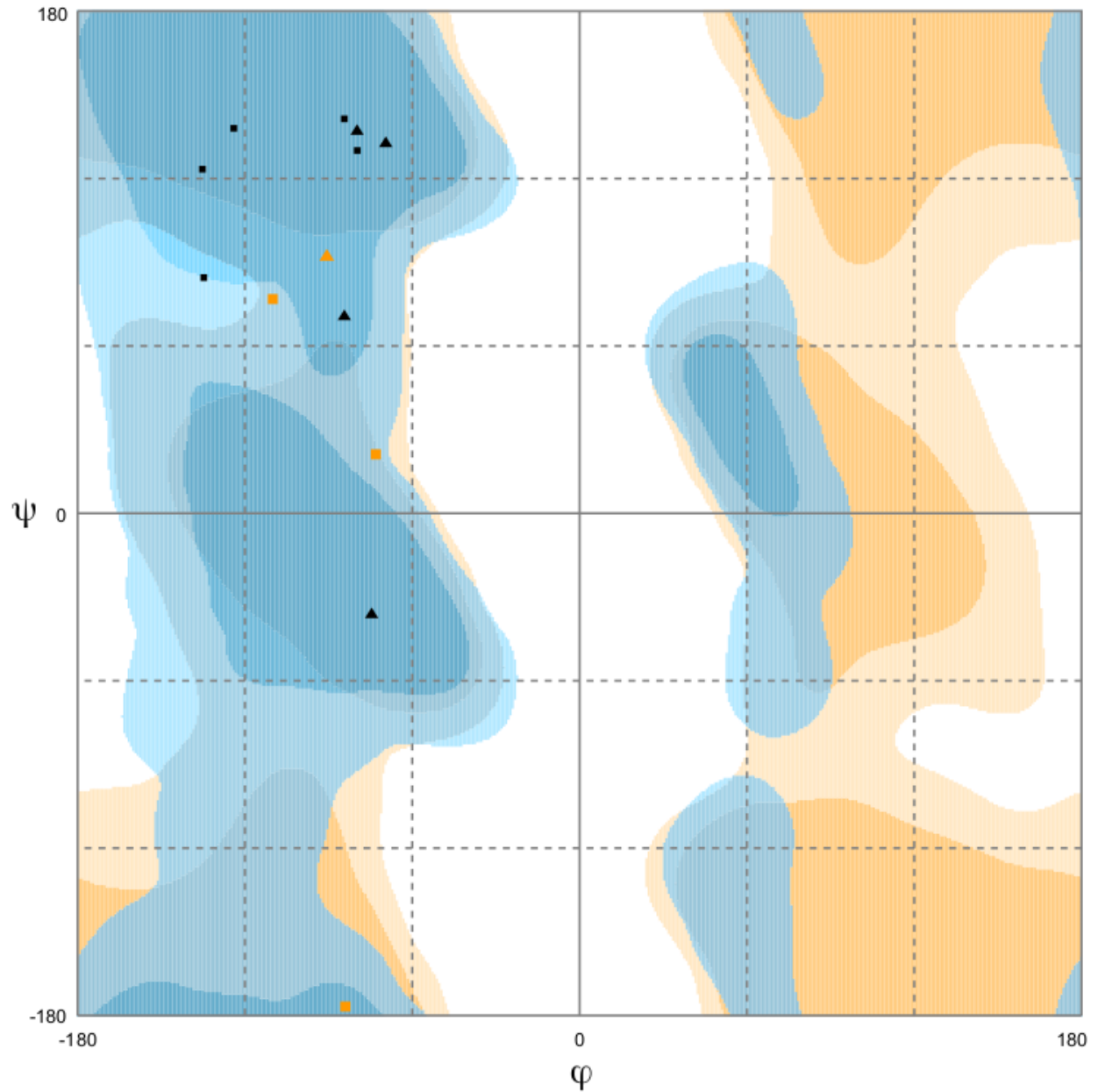
Number of residues in favoured region (~98.0% expected)	: 12 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

Bradykinin



Number of residues in favoured region (~98.0% expected)	: 2 (33.3%)
Number of residues in allowed region (~2.0% expected)	: 2 (33.3%)
Number of residues in outlier region	: 2 (33.3%)

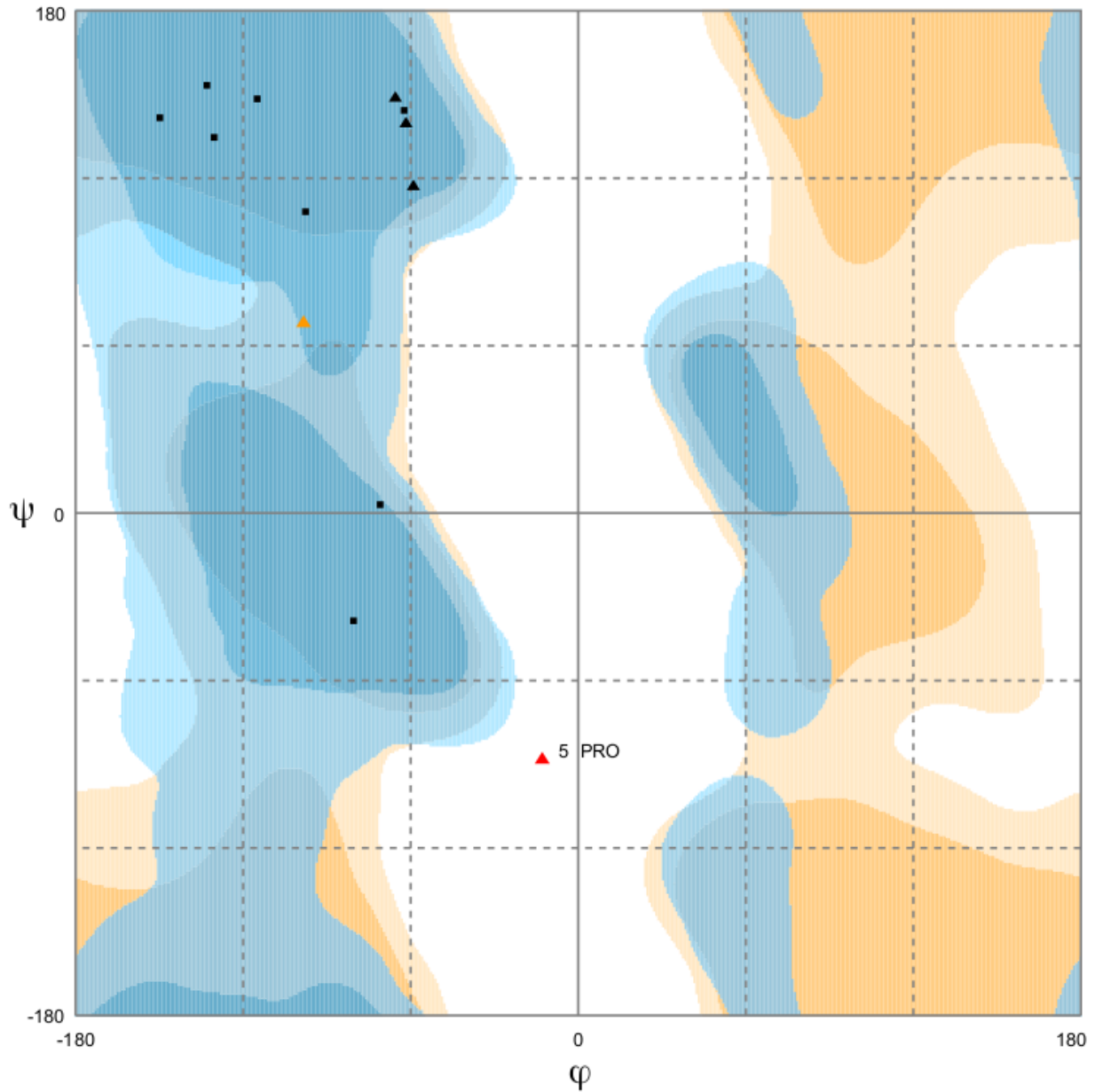
Formaecin 1



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

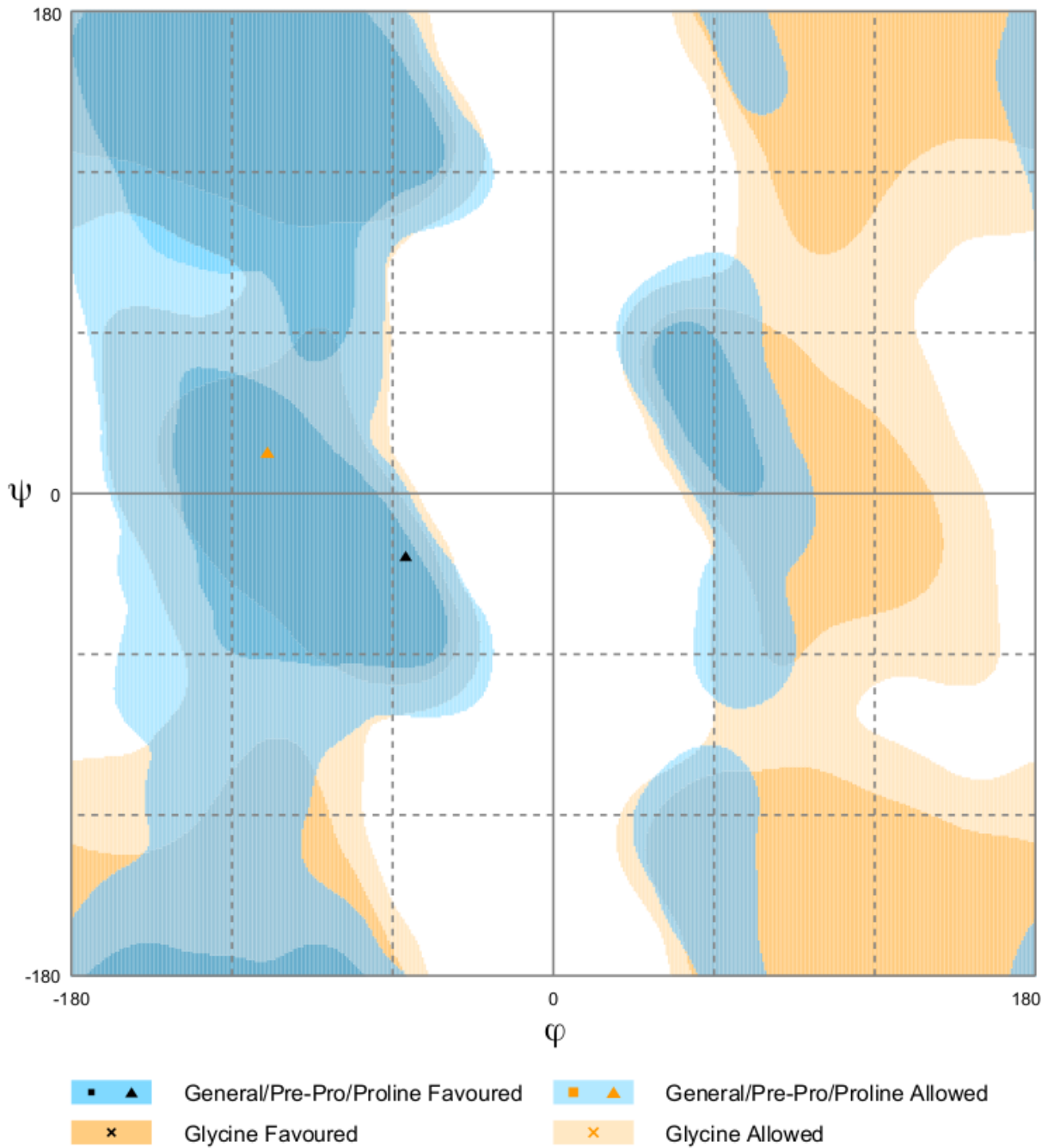
Number of residues in favoured region (~98.0% expected)	: 9 (69.2%)
Number of residues in allowed region (~2.0% expected)	: 4 (30.8%)
Number of residues in outlier region	: 0 (0.0%)

Formaecin 2



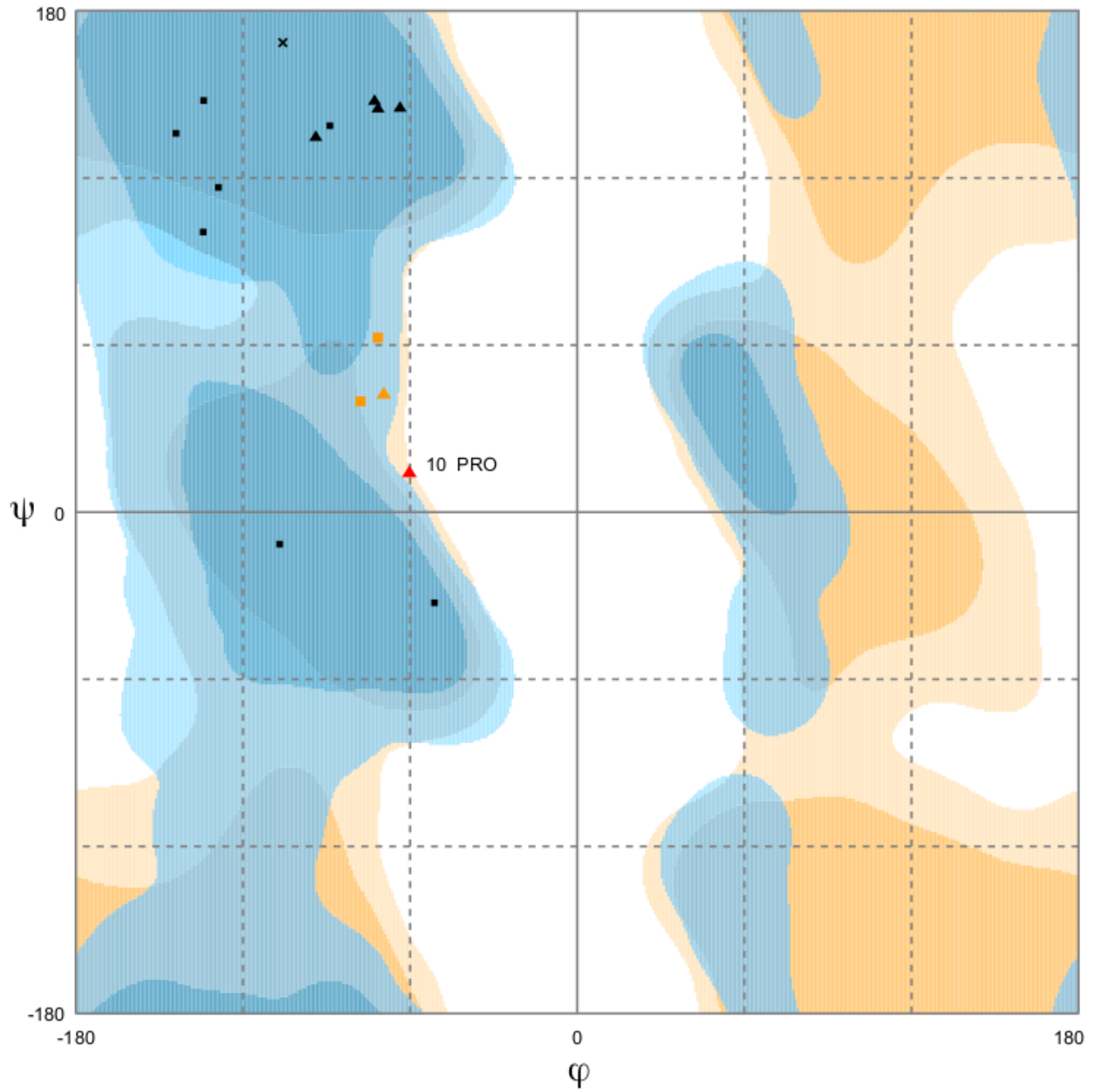
Number of residues in favoured region (~98.0% expected)	: 11 (84.6%)
Number of residues in allowed region (~2.0% expected)	: 1 (7.7%)
Number of residues in outlier region	: 1 (7.7%)

RLID 12.1



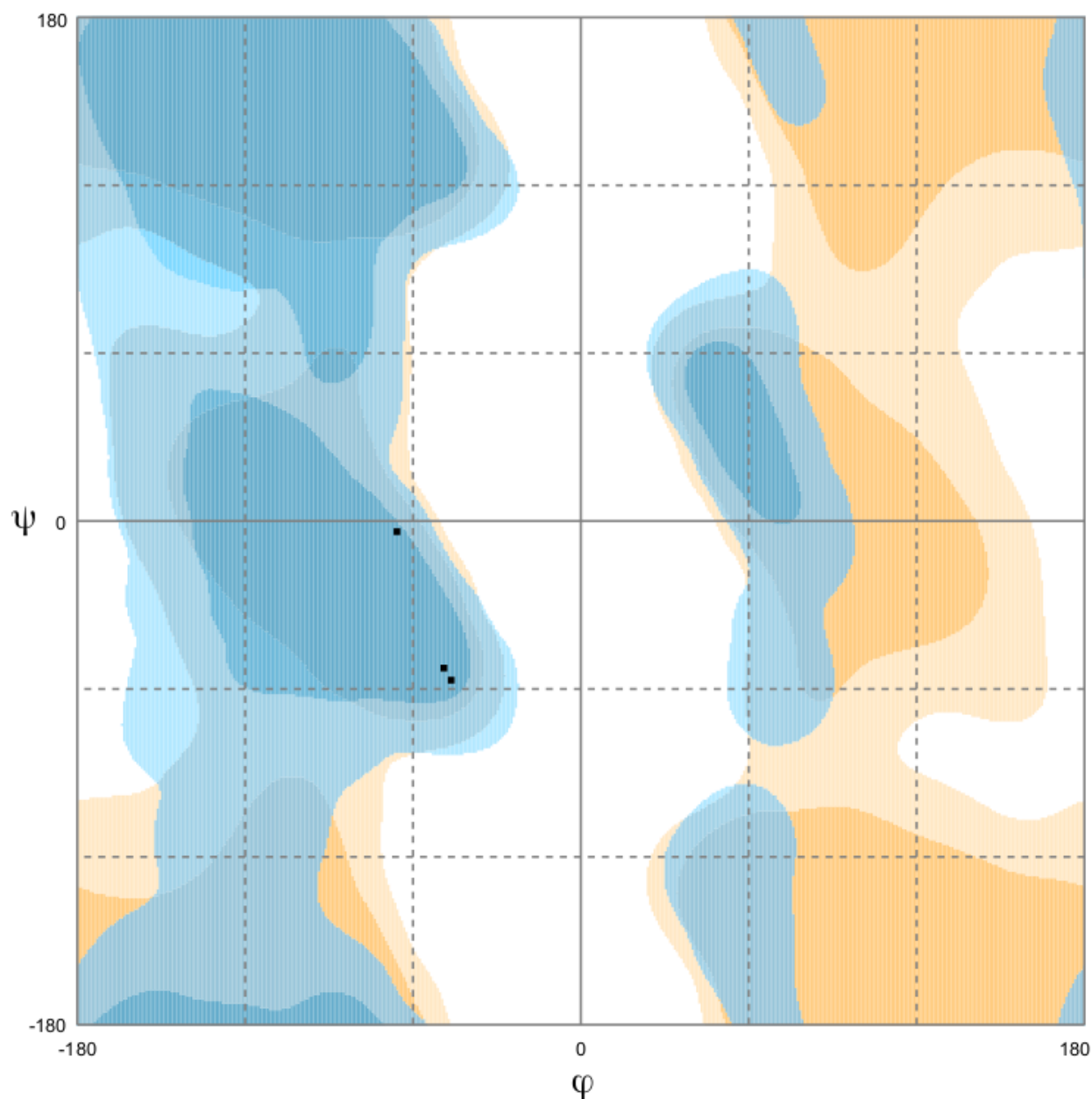
Number of residues in favoured region (~98.0% expected)	: 1 (50.0%)
Number of residues in allowed region (~2.0% expected)	: 1 (50.0%)
Number of residues in outlier region	: 0 (0.0%)

PP30



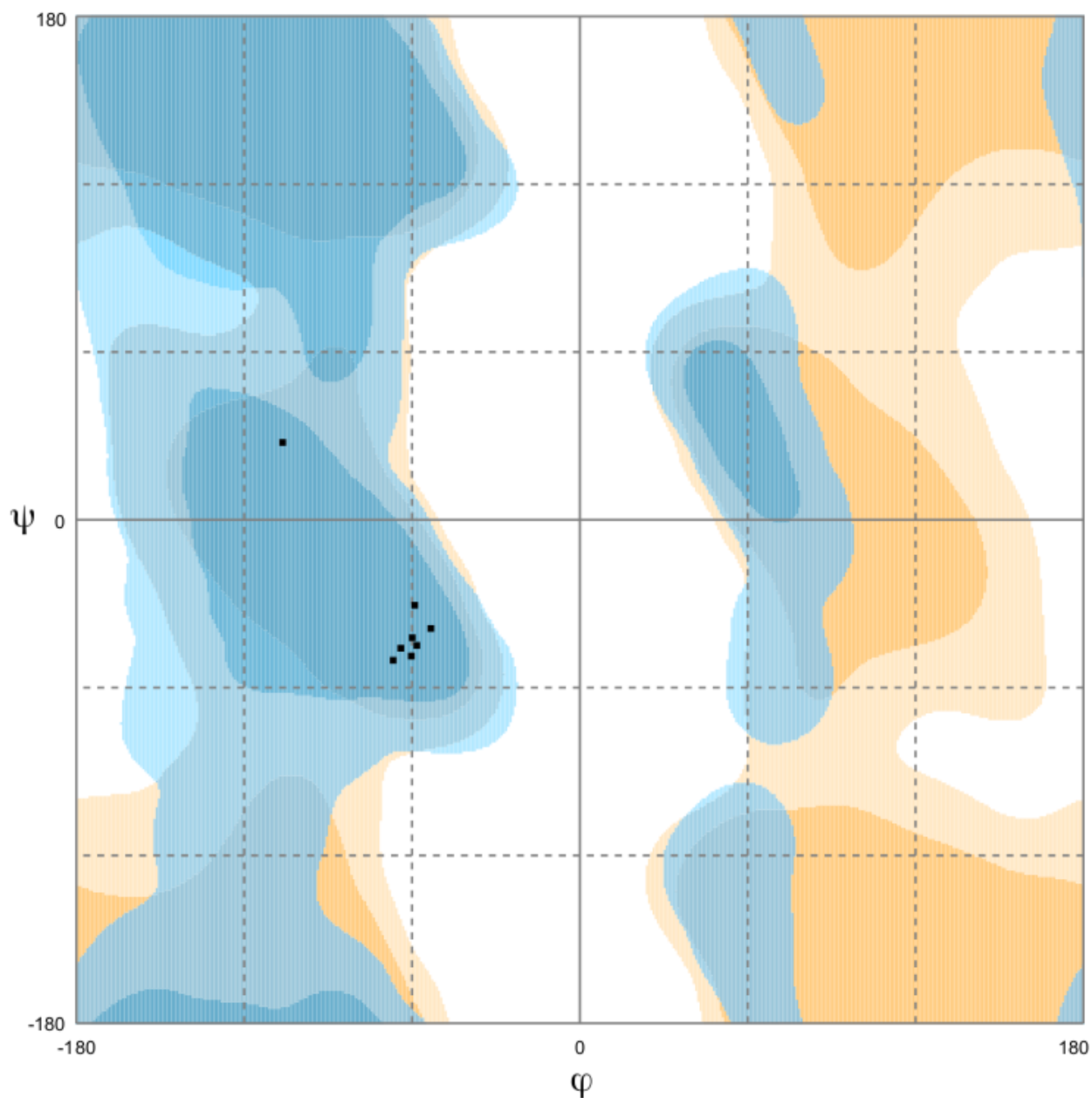
Number of residues in favoured region (~98.0% expected)	: 12 (75.0%)
Number of residues in allowed region (~2.0% expected)	: 3 (18.8%)
Number of residues in outlier region	: 1 (6.2%)

Combi-1



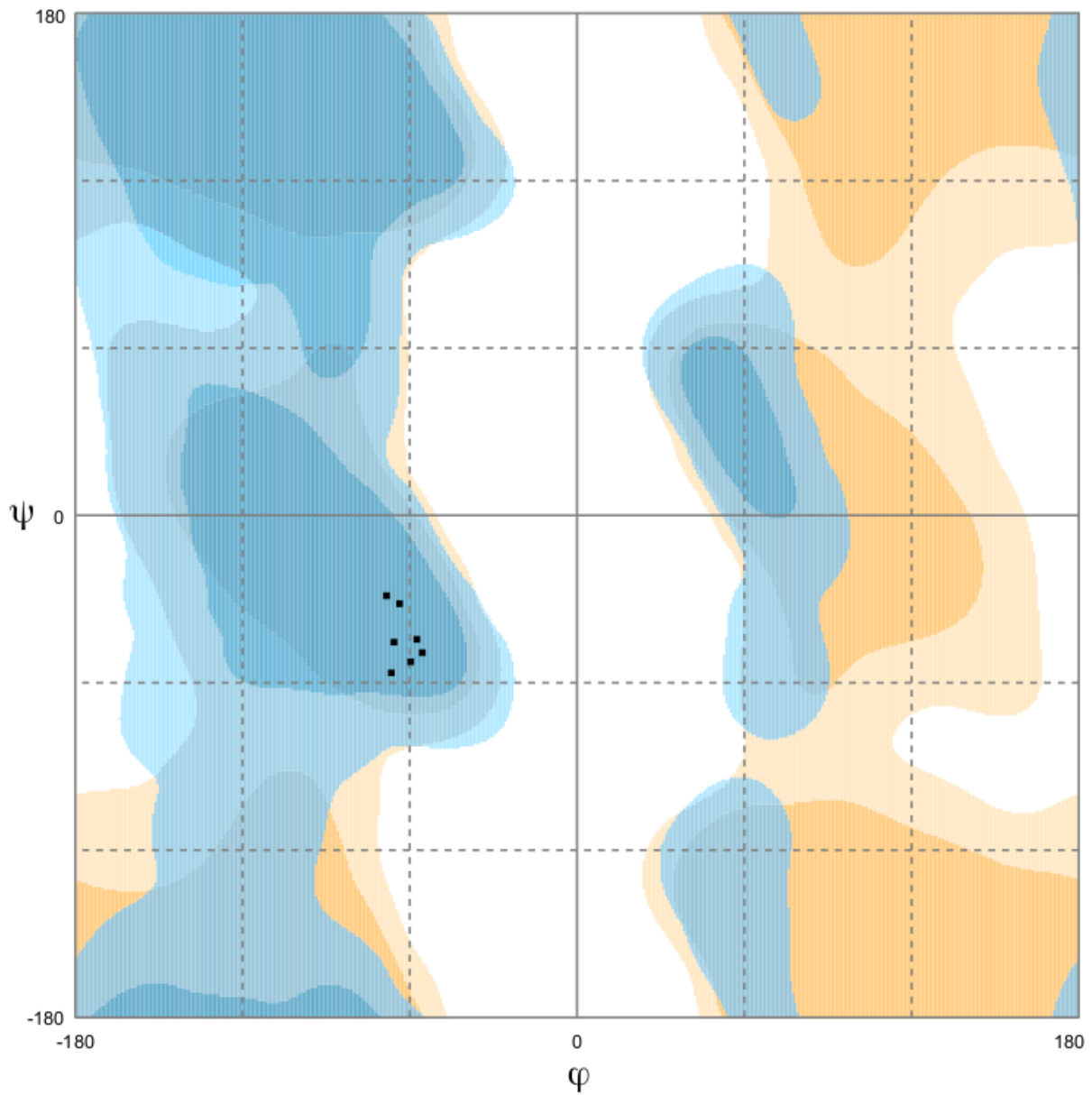
Number of residues in favoured region (~98.0% expected)	: 3 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

Inverso-CysHHC10 synthetic



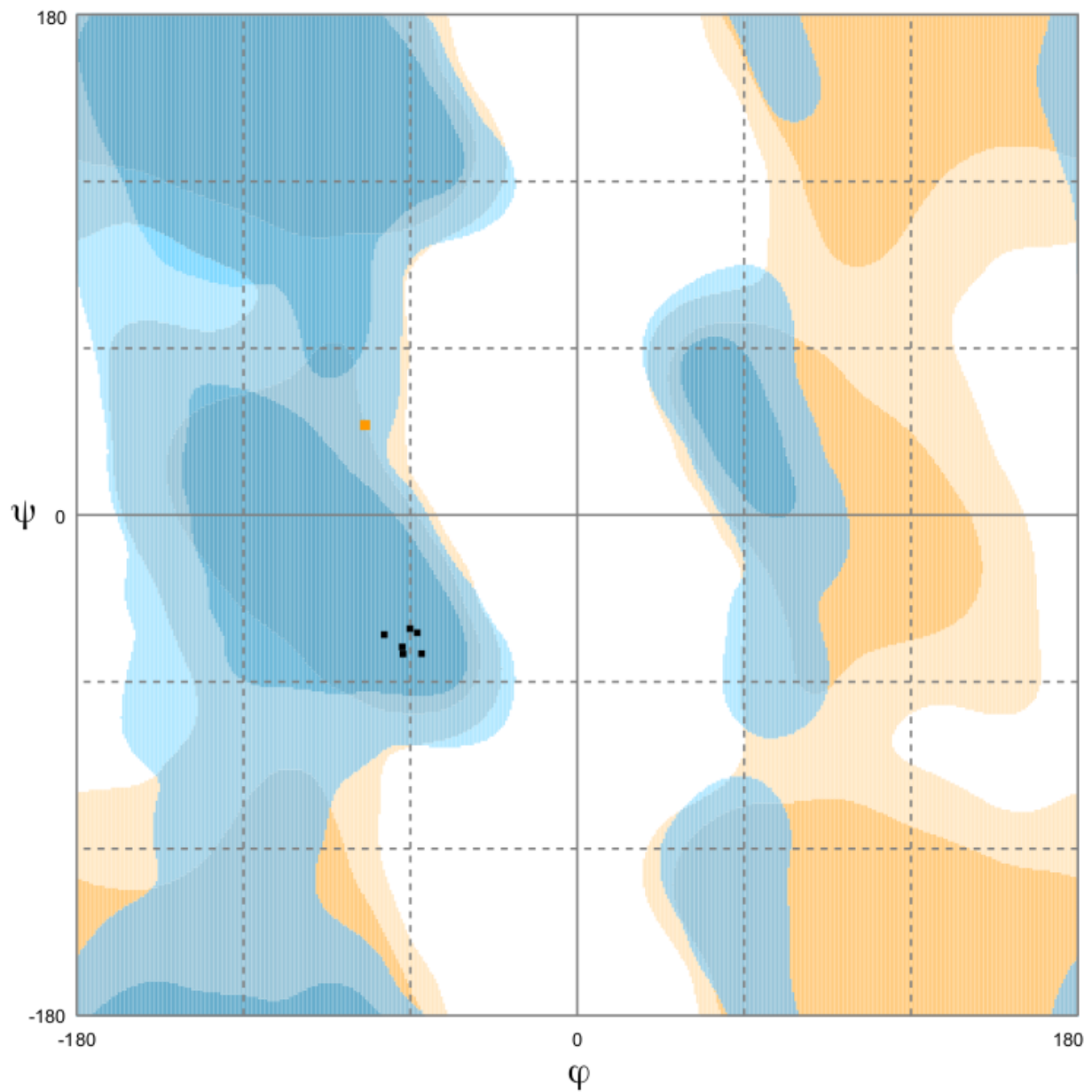
Number of residues in favoured region (~98.0% expected)	: 8 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet110



Number of residues in favoured region (~98.0% expected)	: 7 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

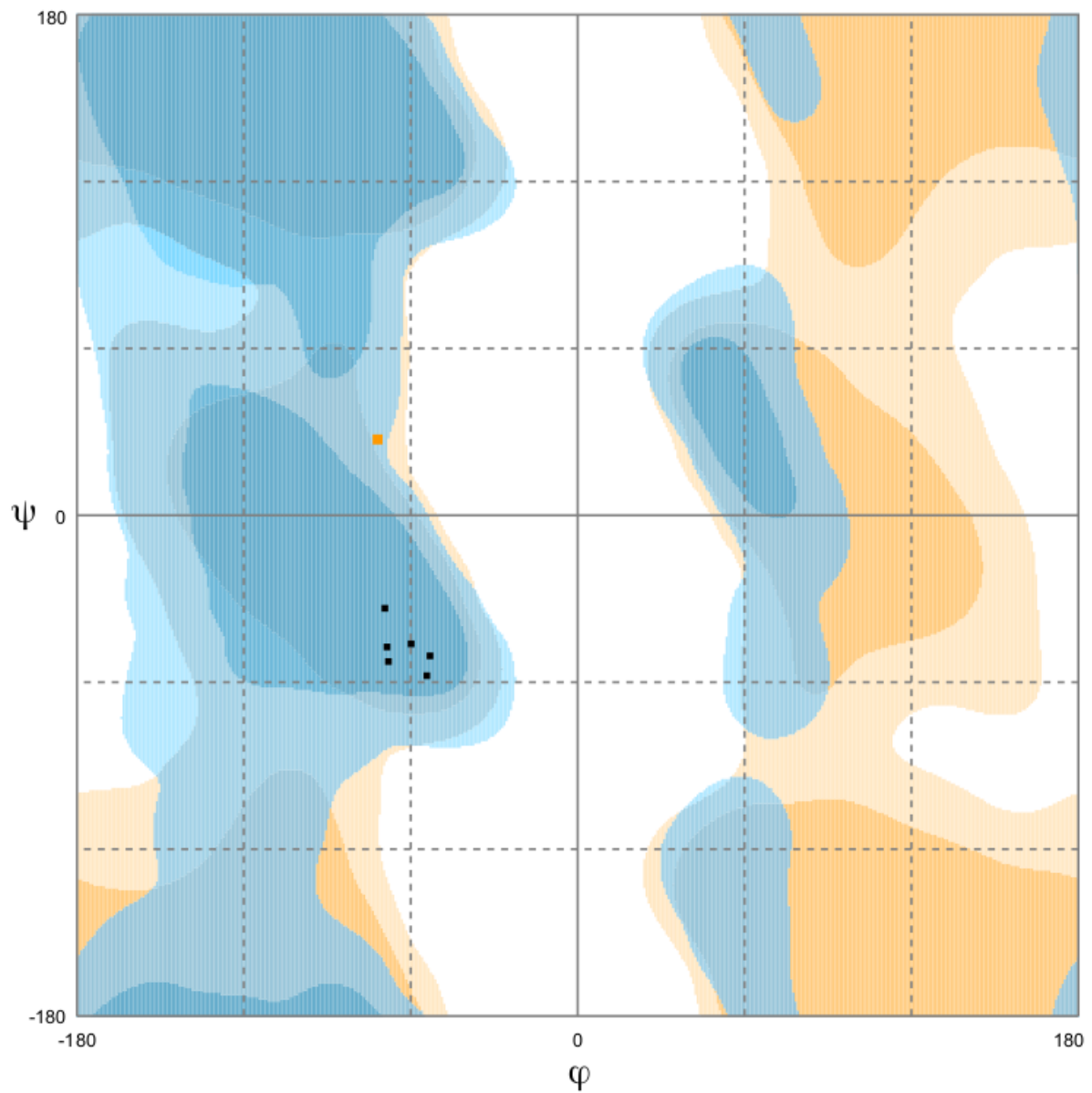
Tet112



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

Number of residues in favoured region (~98.0% expected)	: 6 (85.7%)
Number of residues in allowed region (~2.0% expected)	: 1 (14.3%)
Number of residues in outlier region	: 0 (0.0%)

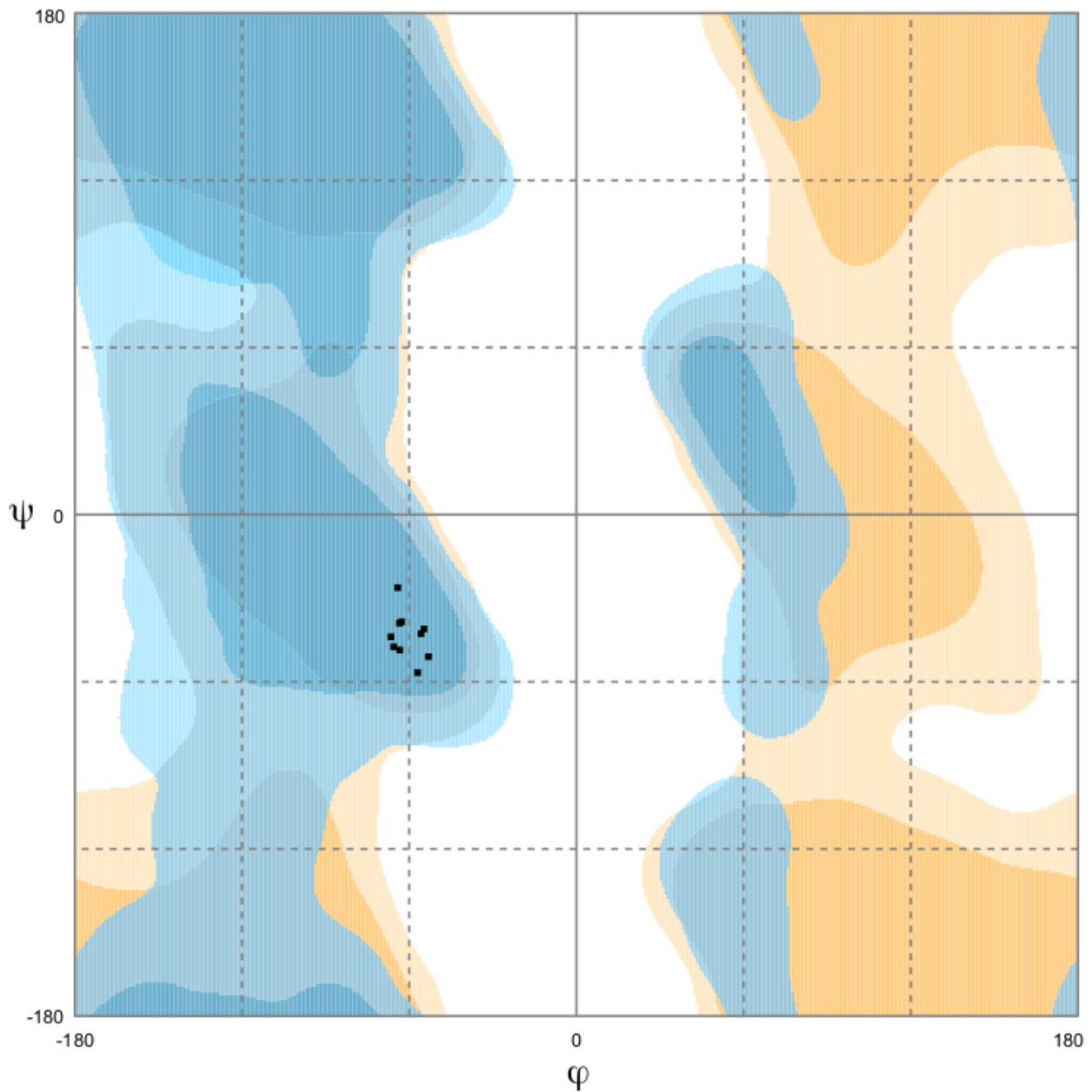
Tet127



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

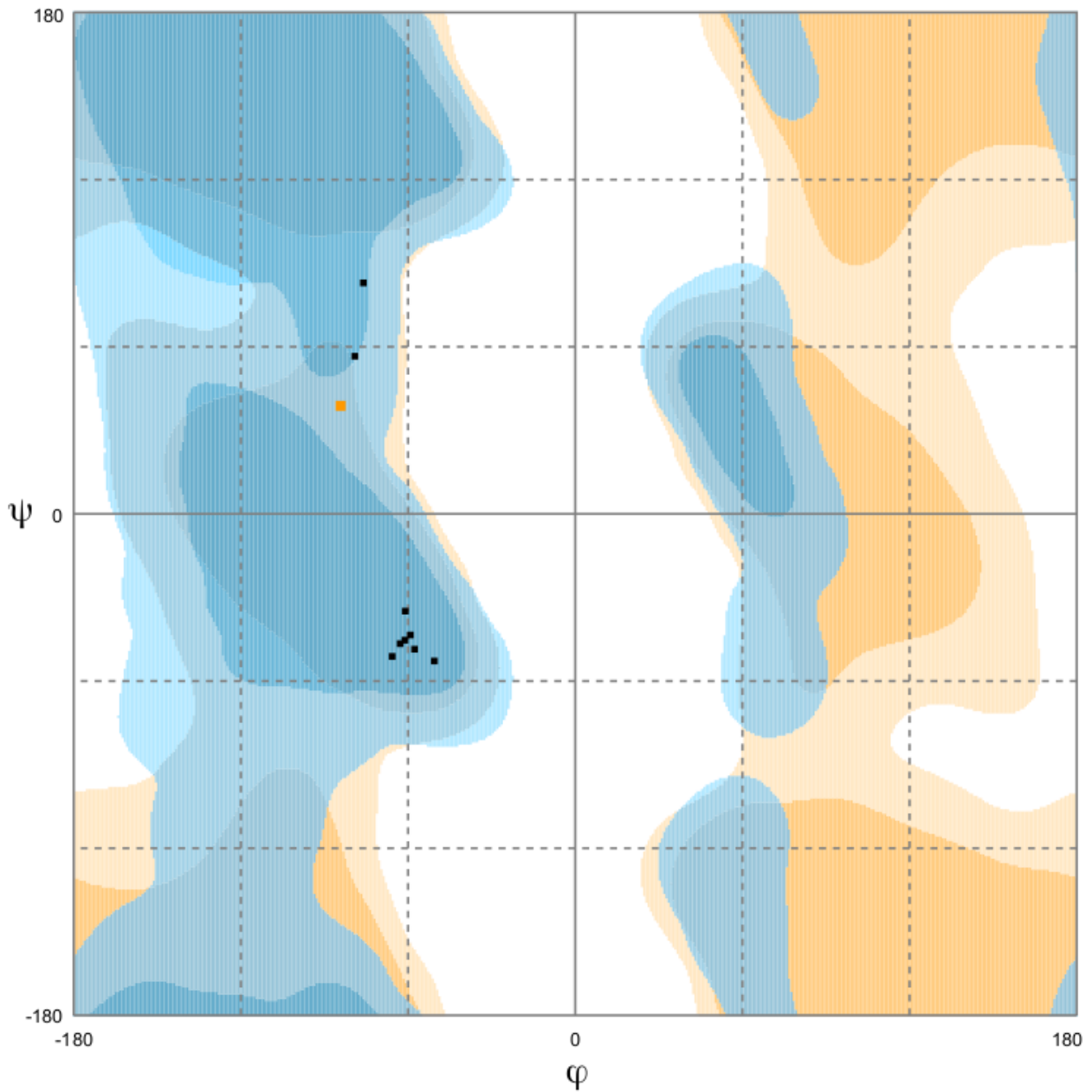
Number of residues in favoured region (~98.0% expected)	: 6 (85.7%)
Number of residues in allowed region (~2.0% expected)	: 1 (14.3%)
Number of residues in outlier region	: 0 (0.0%)

Tet033



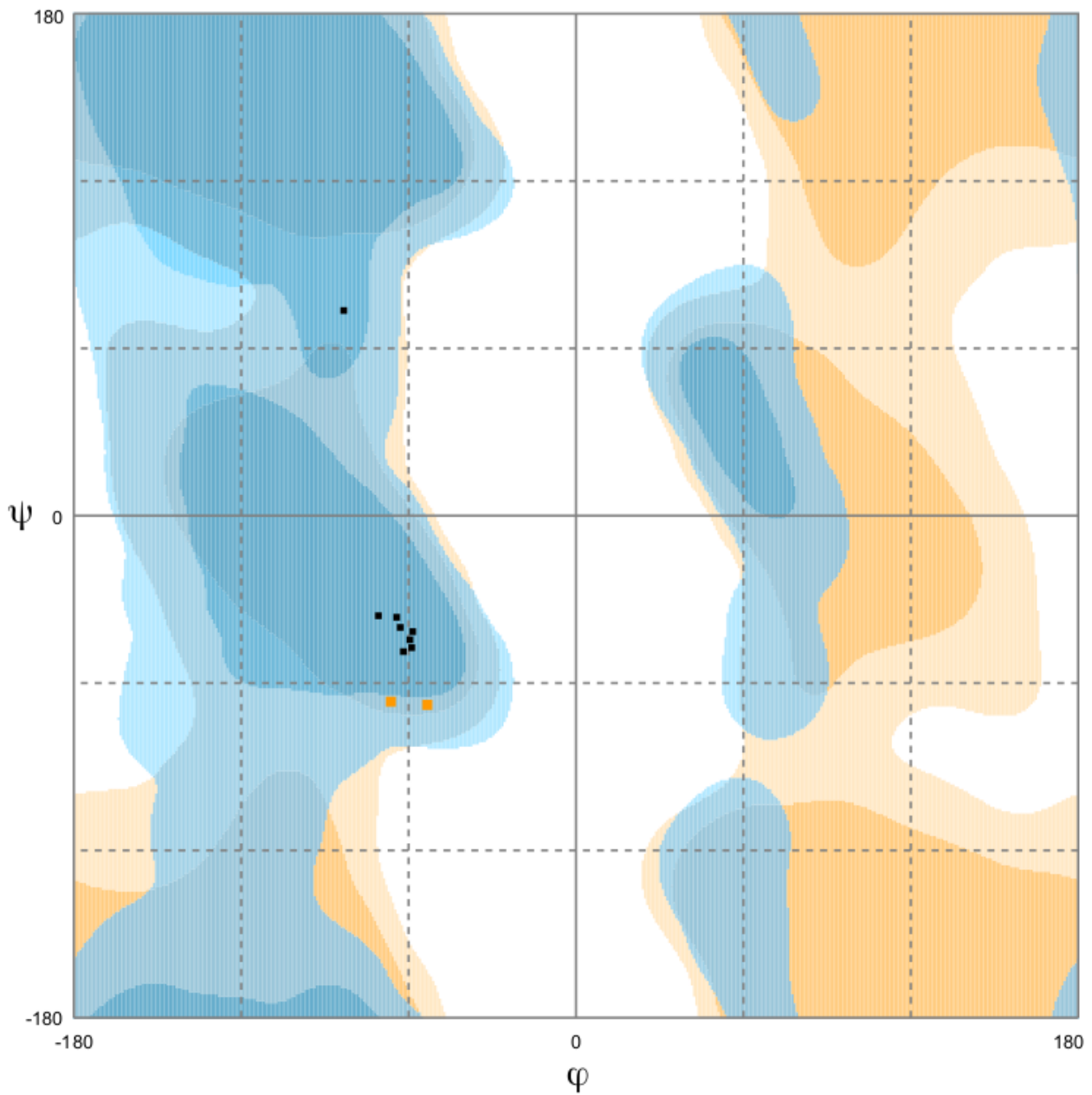
Number of residues in favoured region (~98.0% expected)	: 10 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet091



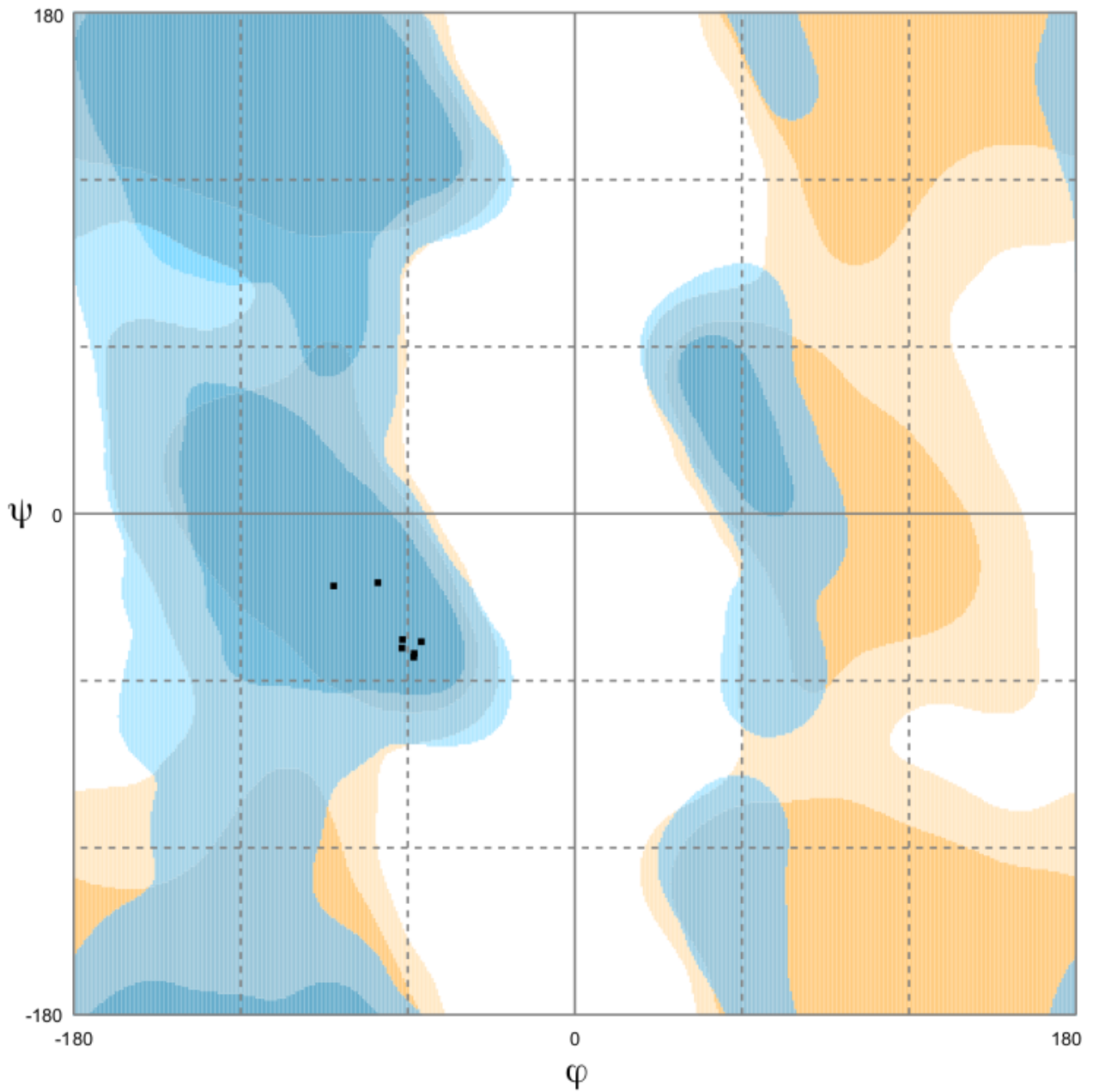
Number of residues in favoured region (~98.0% expected)	: 9 (90.0%)
Number of residues in allowed region (~2.0% expected)	: 1 (10.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet032



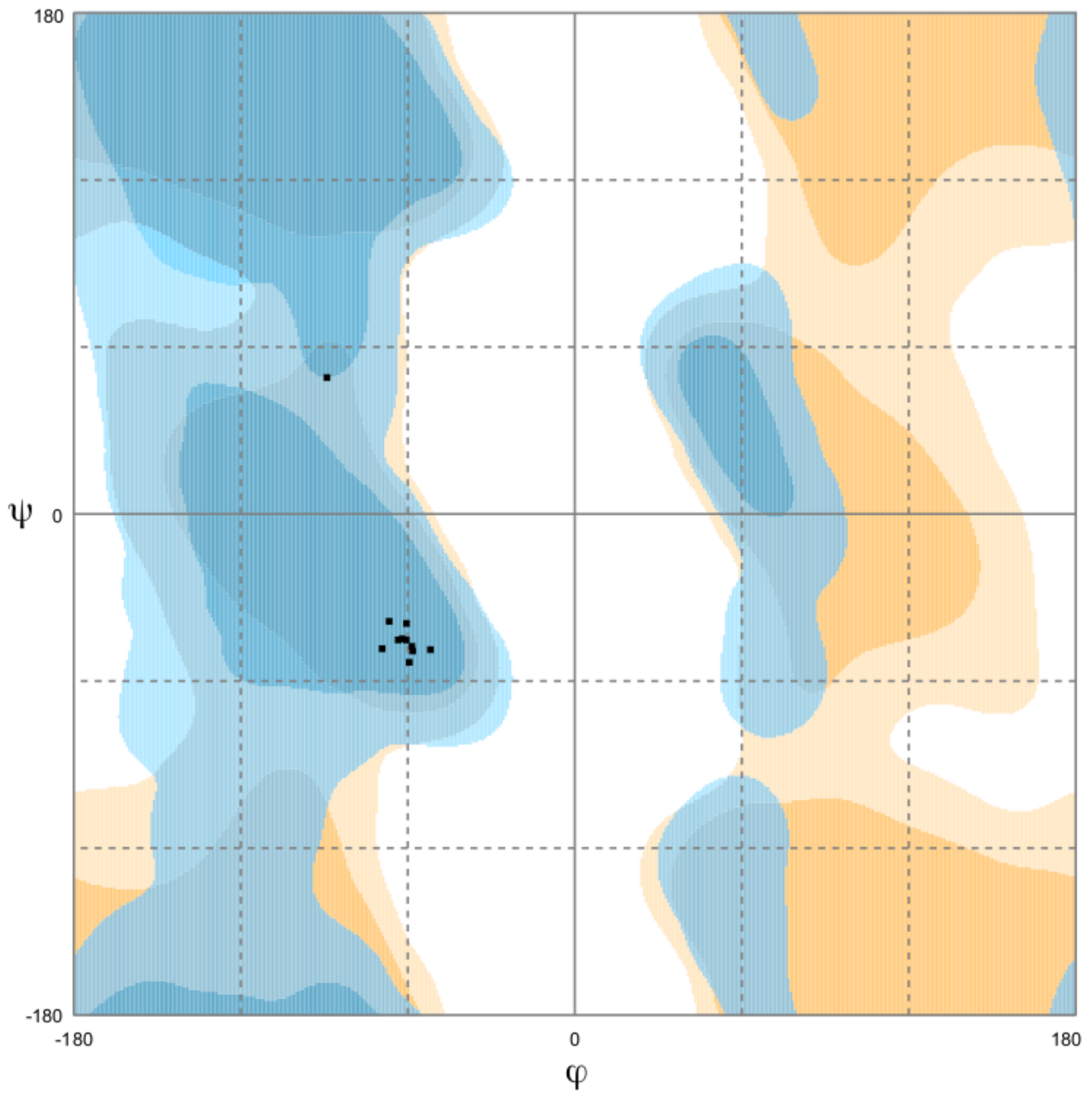
Number of residues in favoured region (~98.0% expected)	: 8 (80.0%)
Number of residues in allowed region (~2.0% expected)	: 2 (20.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet124



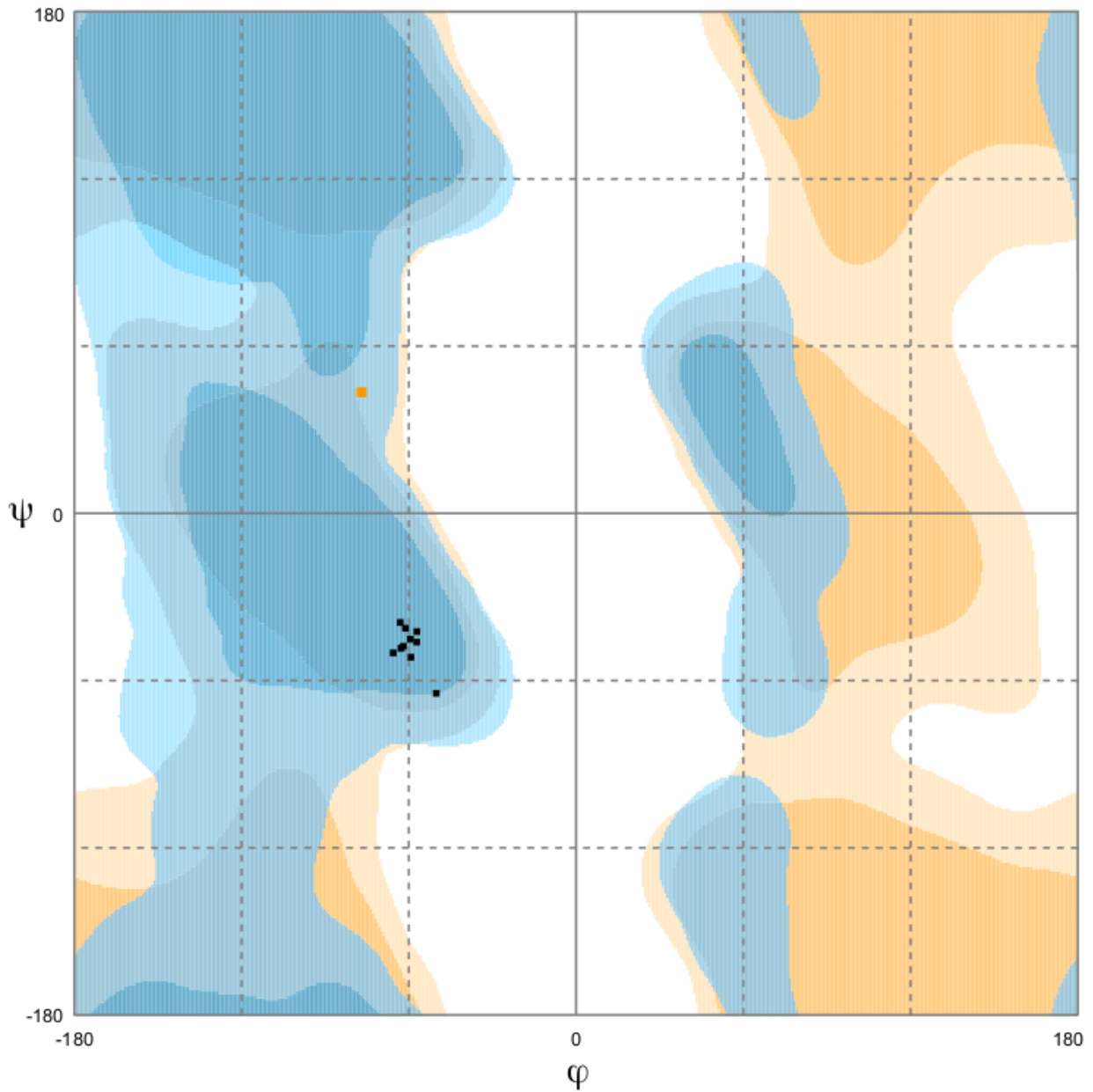
Number of residues in favoured region (~98.0% expected)	: 7 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet092



Number of residues in favoured region (~98.0% expected)	: 11 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

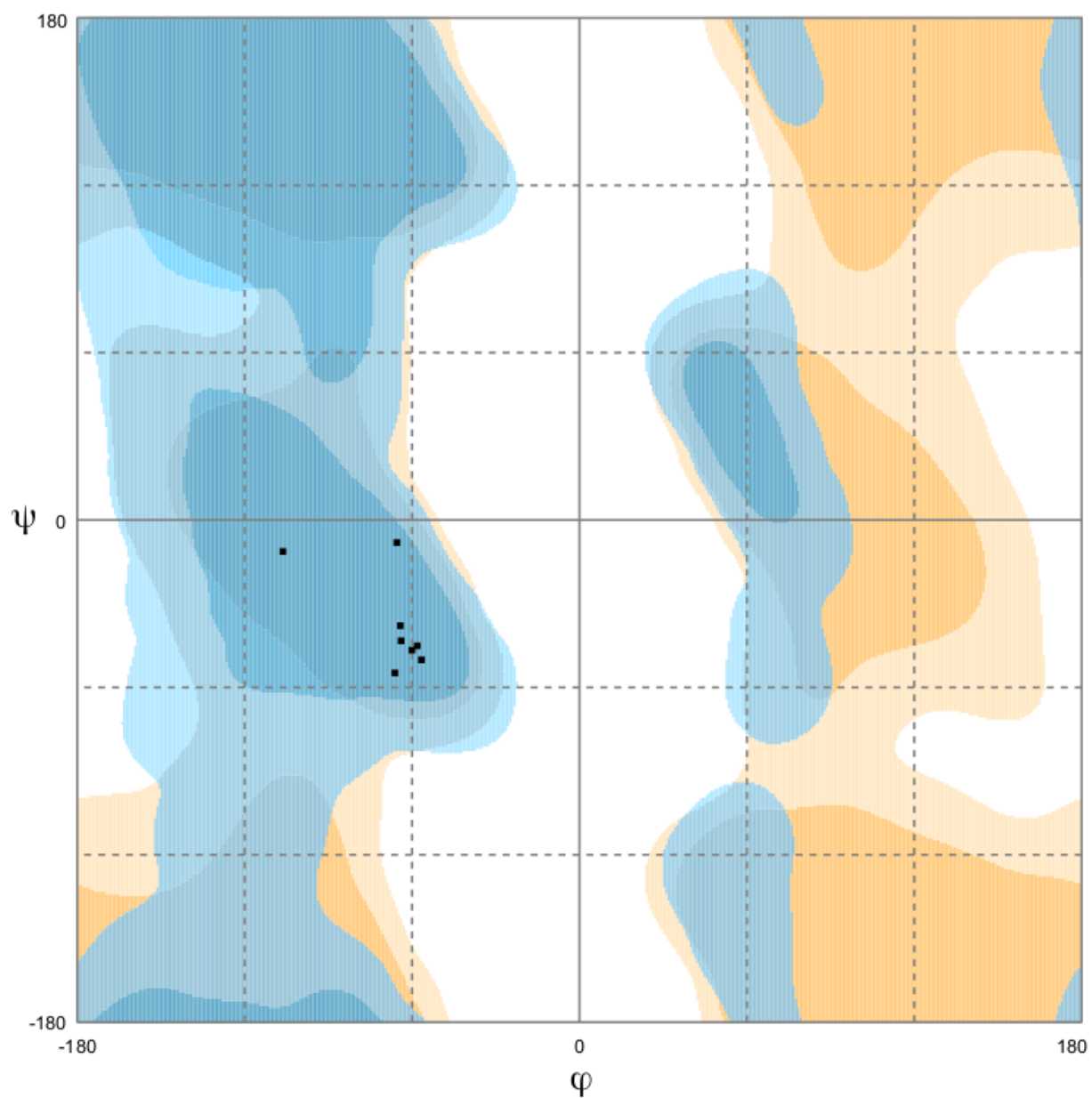
Tet099



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

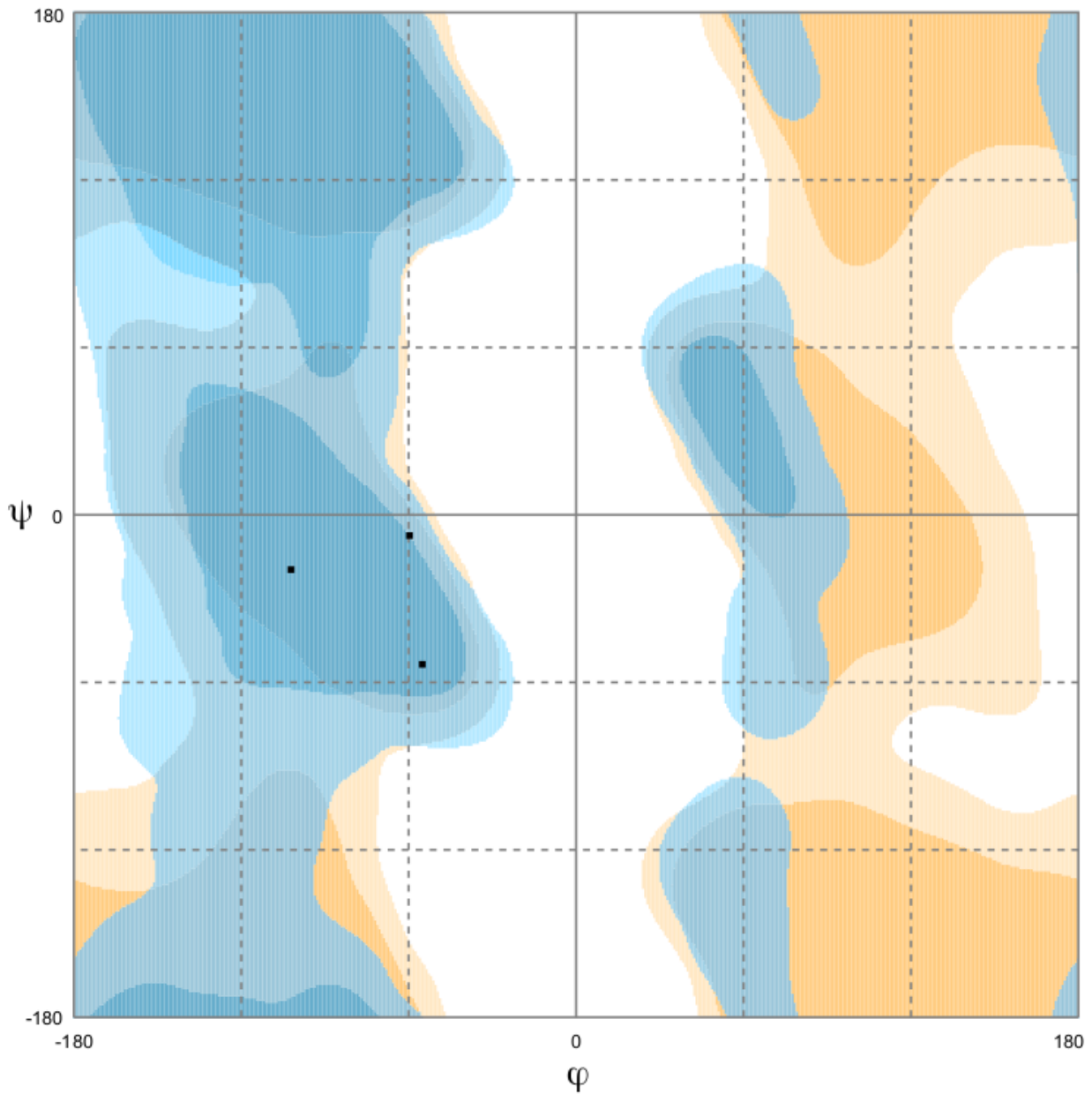
Number of residues in favoured region (~98.0% expected)	: 10 (90.9%)
Number of residues in allowed region (~2.0% expected)	: 1 (9.1%)
Number of residues in outlier region	: 0 (0.0%)

Tet213



Number of residues in favoured region (~98.0% expected)	: 8 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

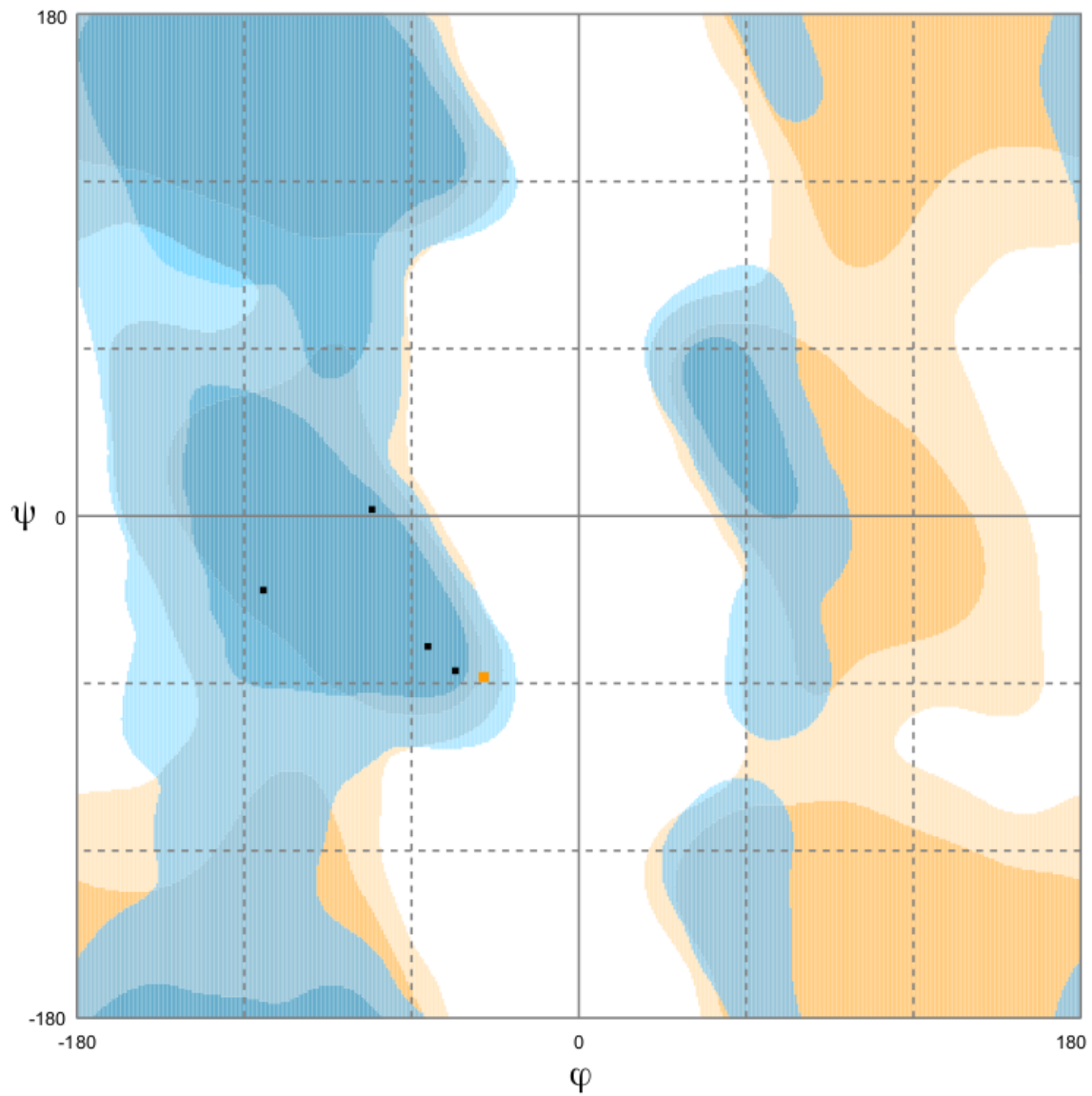
PAF26



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

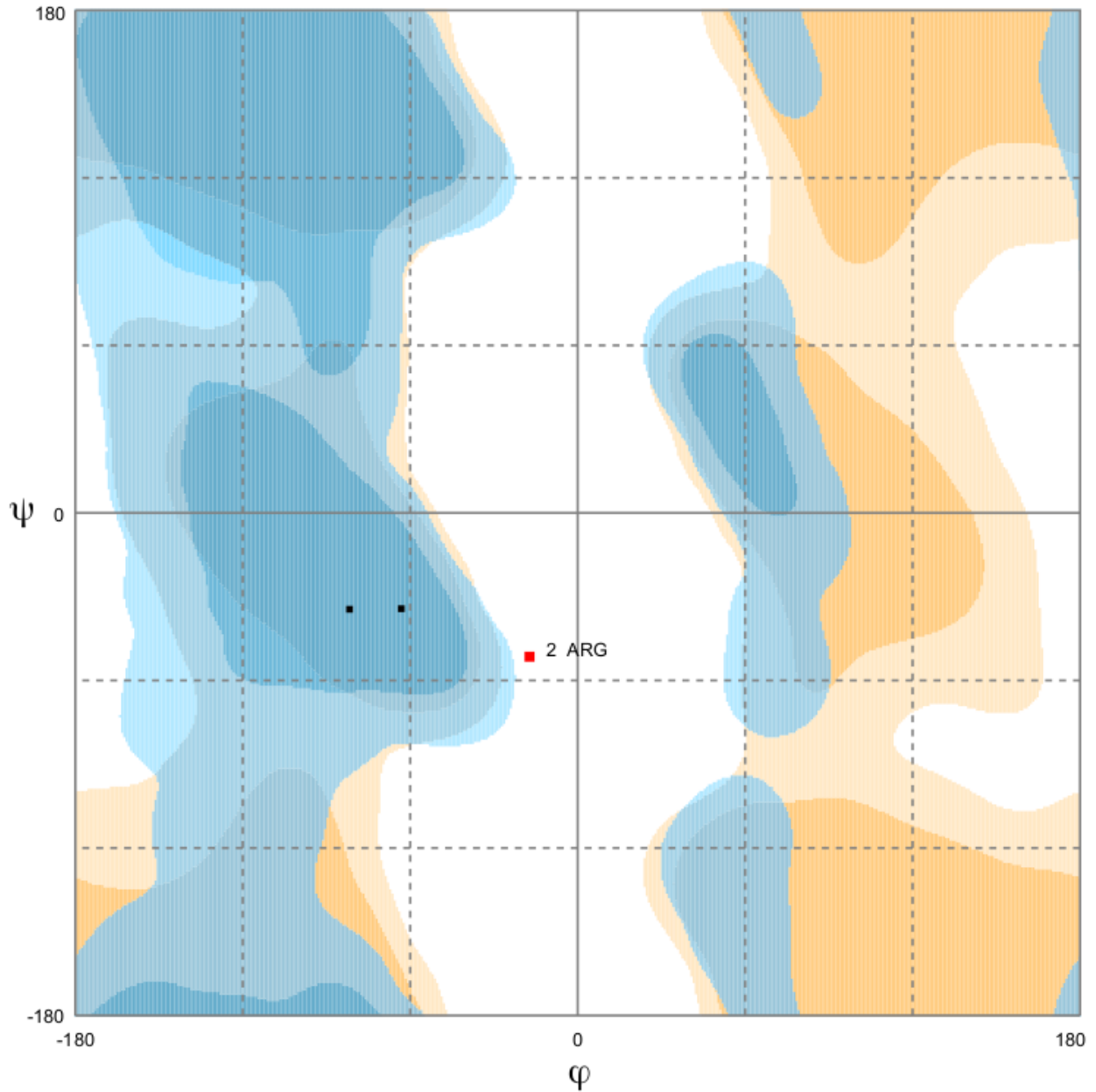
Number of residues in favoured region (~98.0% expected)	: 3 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

TetraF2W-RK



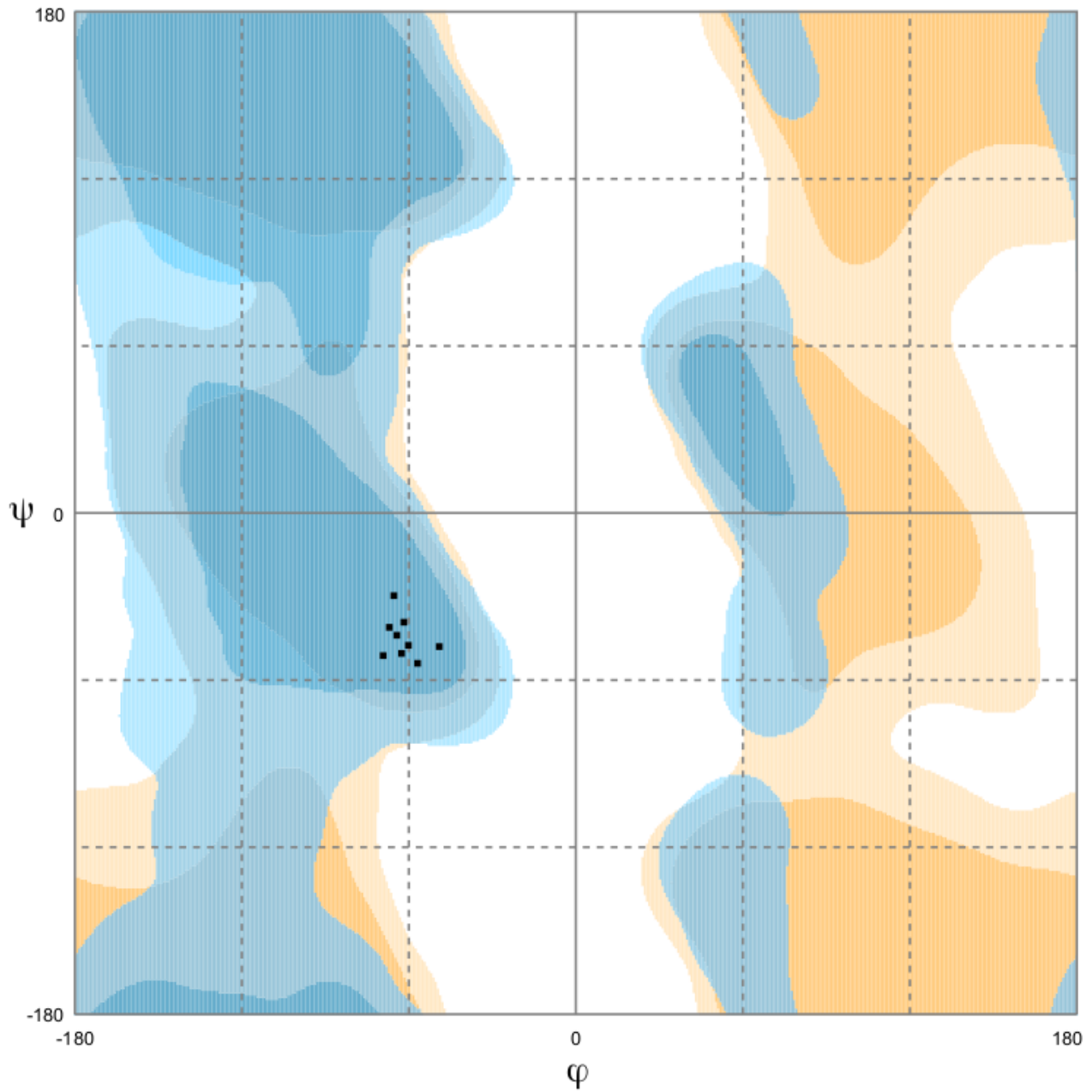
Number of residues in favoured region (~98.0% expected)	: 4 (80.0%)
Number of residues in allowed region (~2.0% expected)	: 1 (20.0%)
Number of residues in outlier region	: 0 (0.0%)

Combi-2



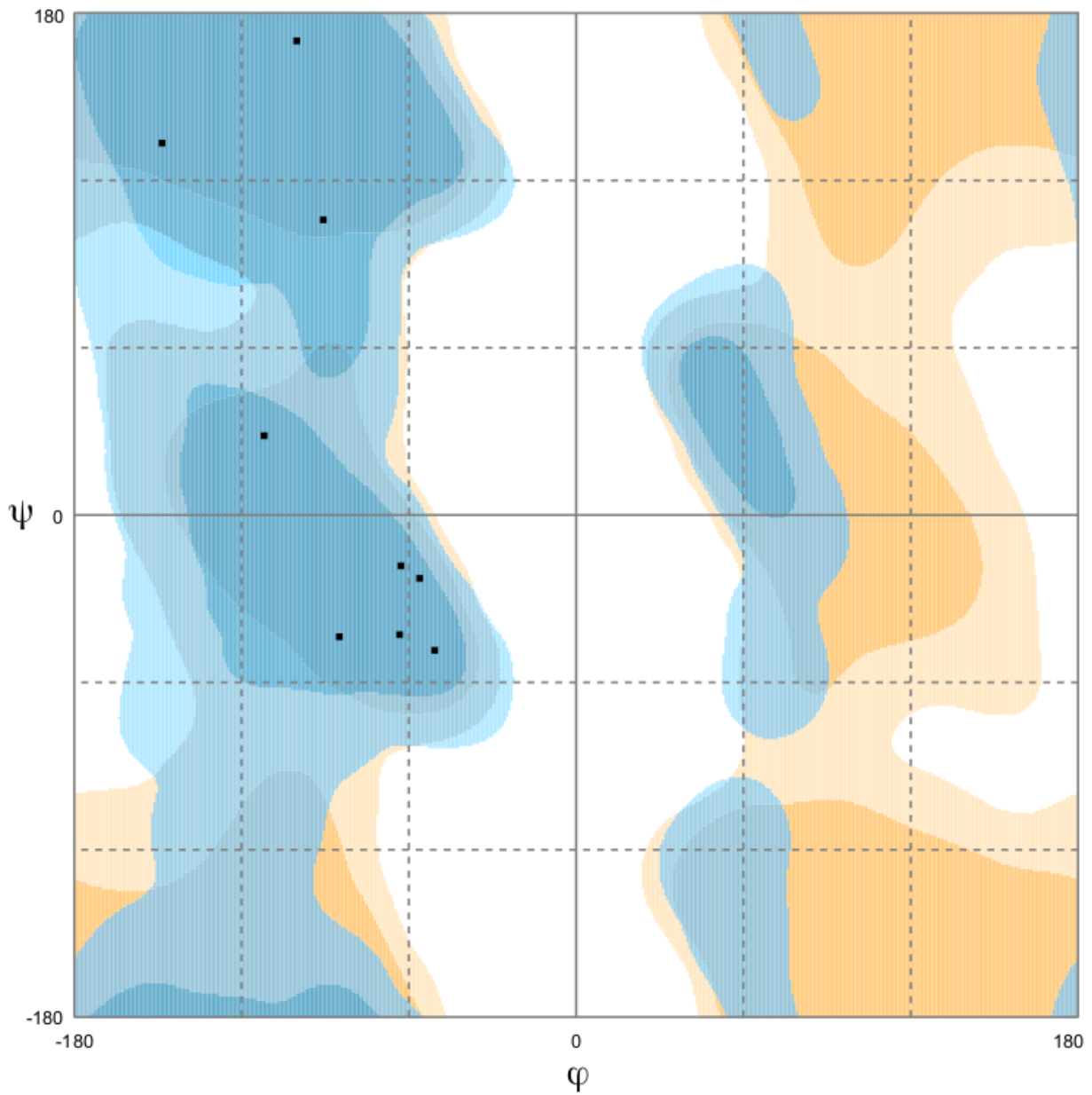
Number of residues in favoured region (~98.0% expected)	: 2 (66.7%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 1 (33.3%)

hLF1-11



Number of residues in favoured region (~98.0% expected)	: 9 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

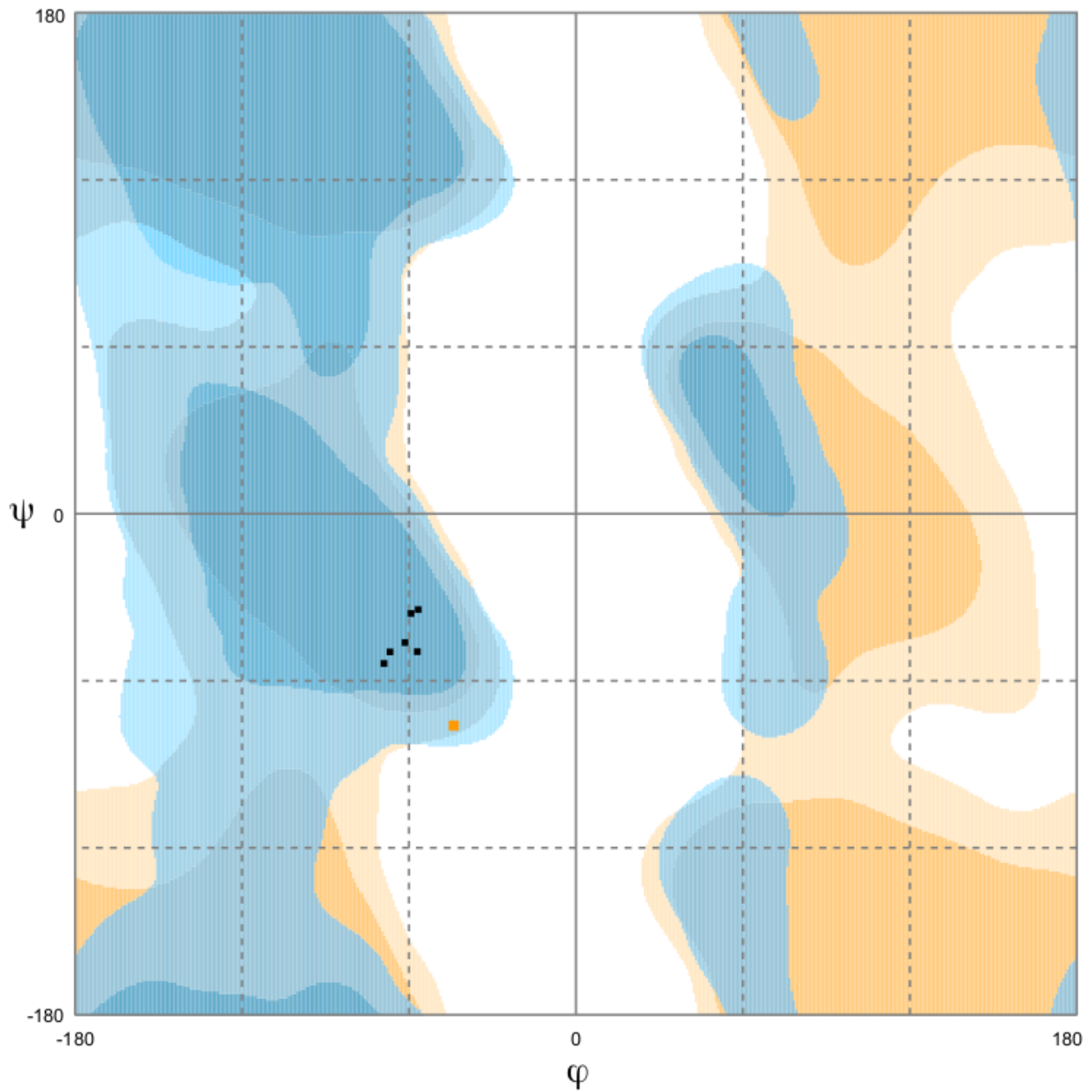
IDR-1010



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

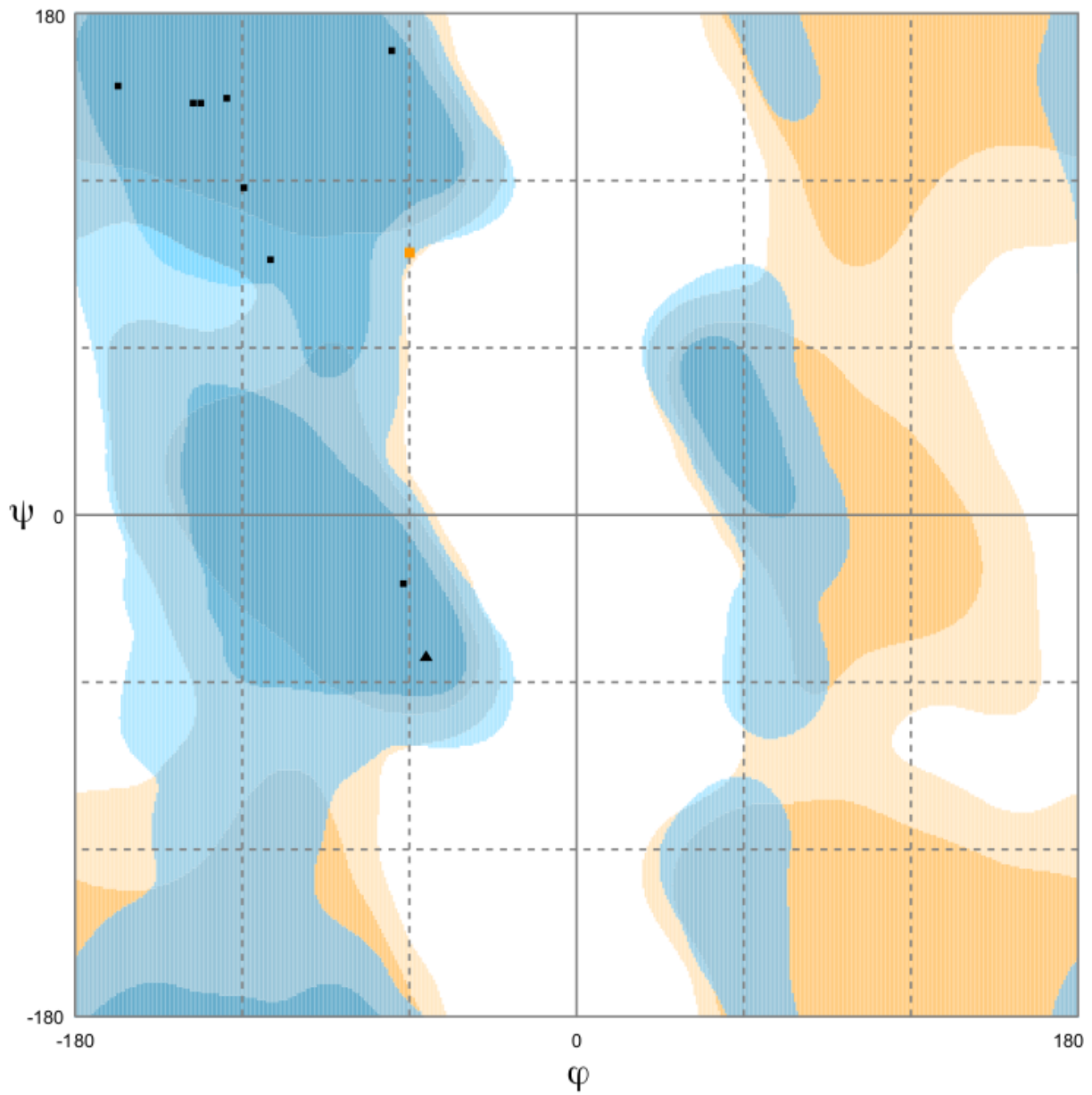
Number of residues in favoured region (~98.0% expected)	: 9 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

PAC- 525



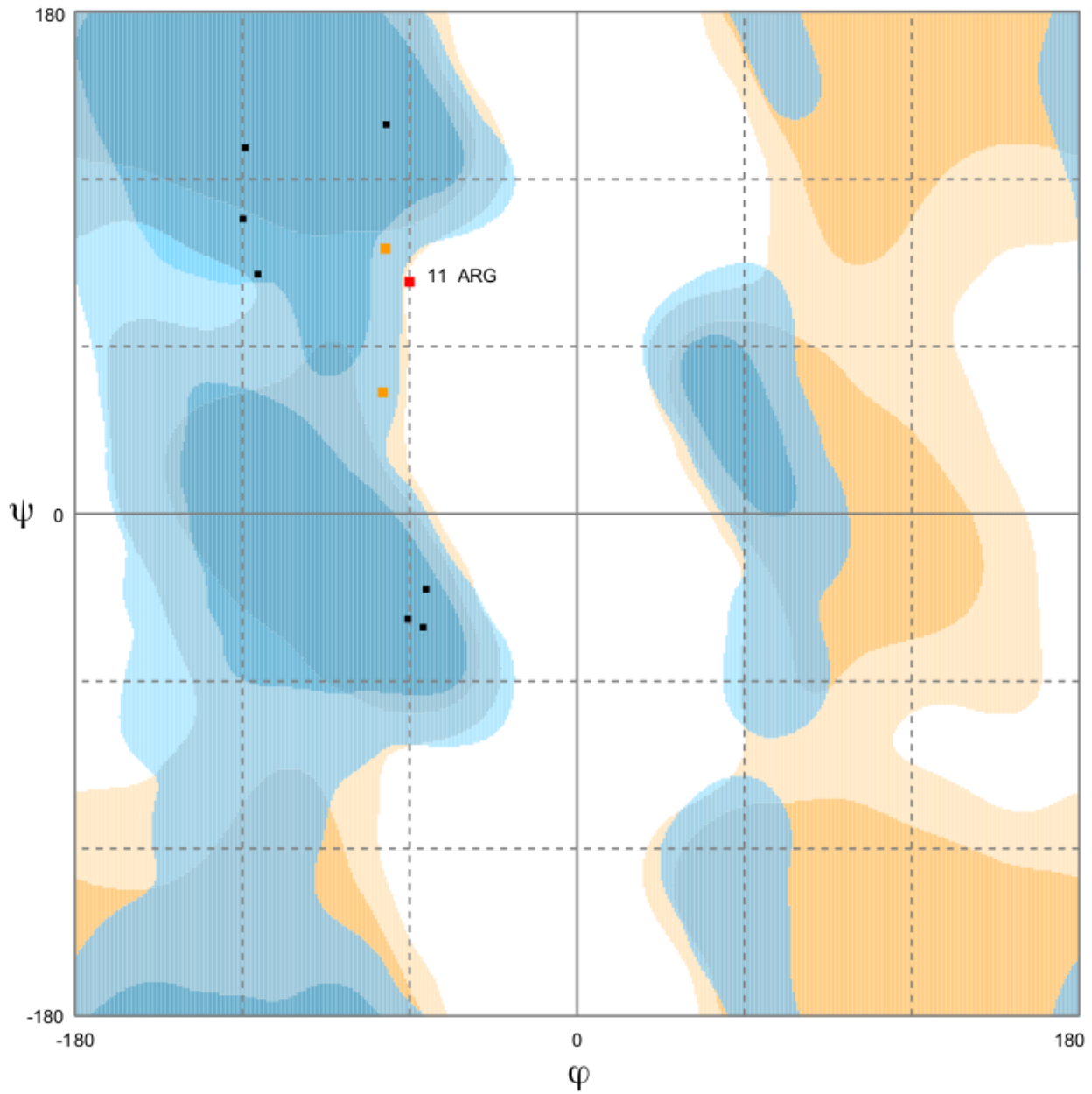
Number of residues in favoured region (~98.0% expected)	: 6 (85.7%)
Number of residues in allowed region (~2.0% expected)	: 1 (14.3%)
Number of residues in outlier region	: 0 (0.0%)

Tet003



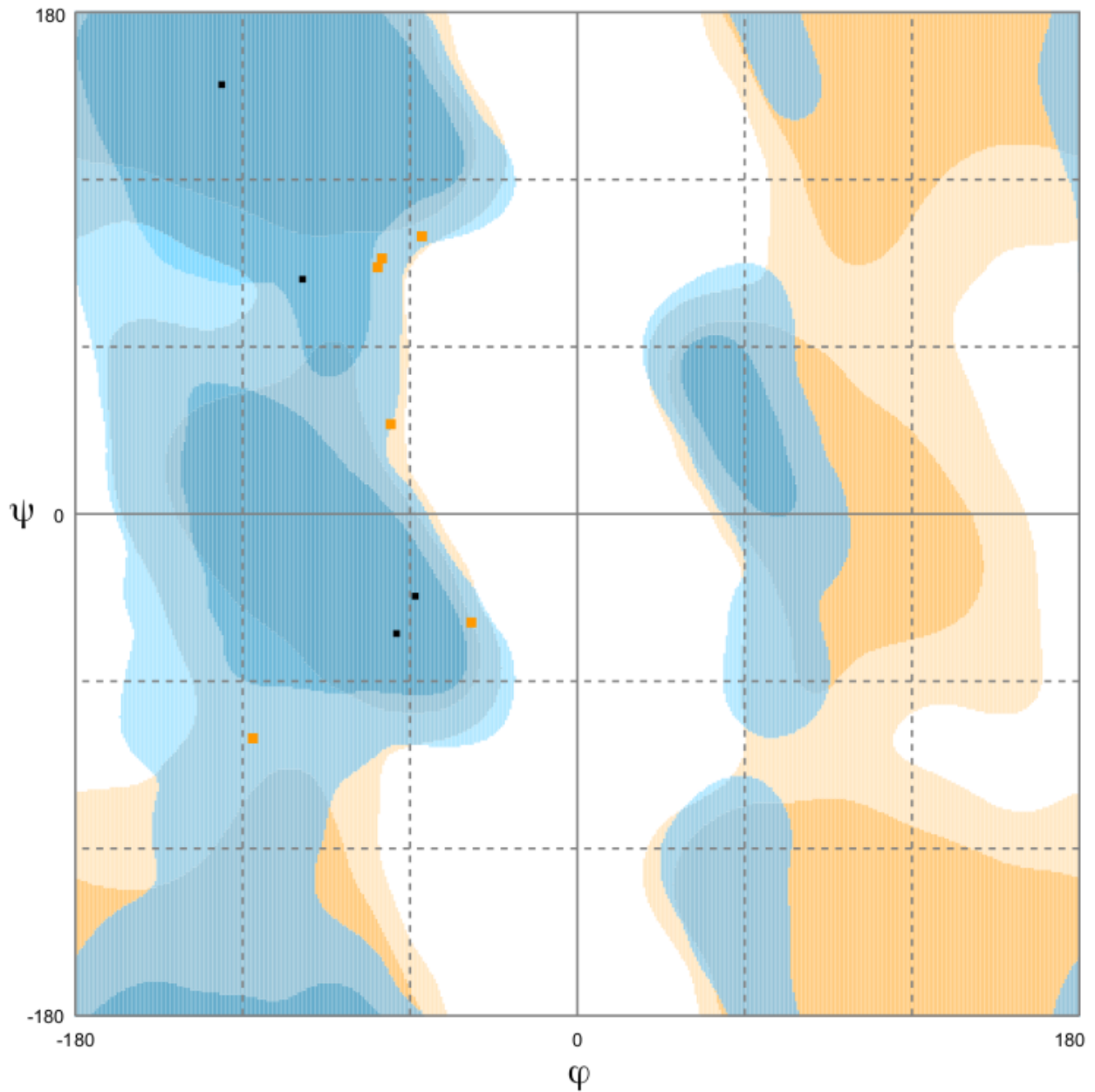
Number of residues in favoured region (~98.0% expected)	: 9 (90.0%)
Number of residues in allowed region (~2.0% expected)	: 1 (10.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet008



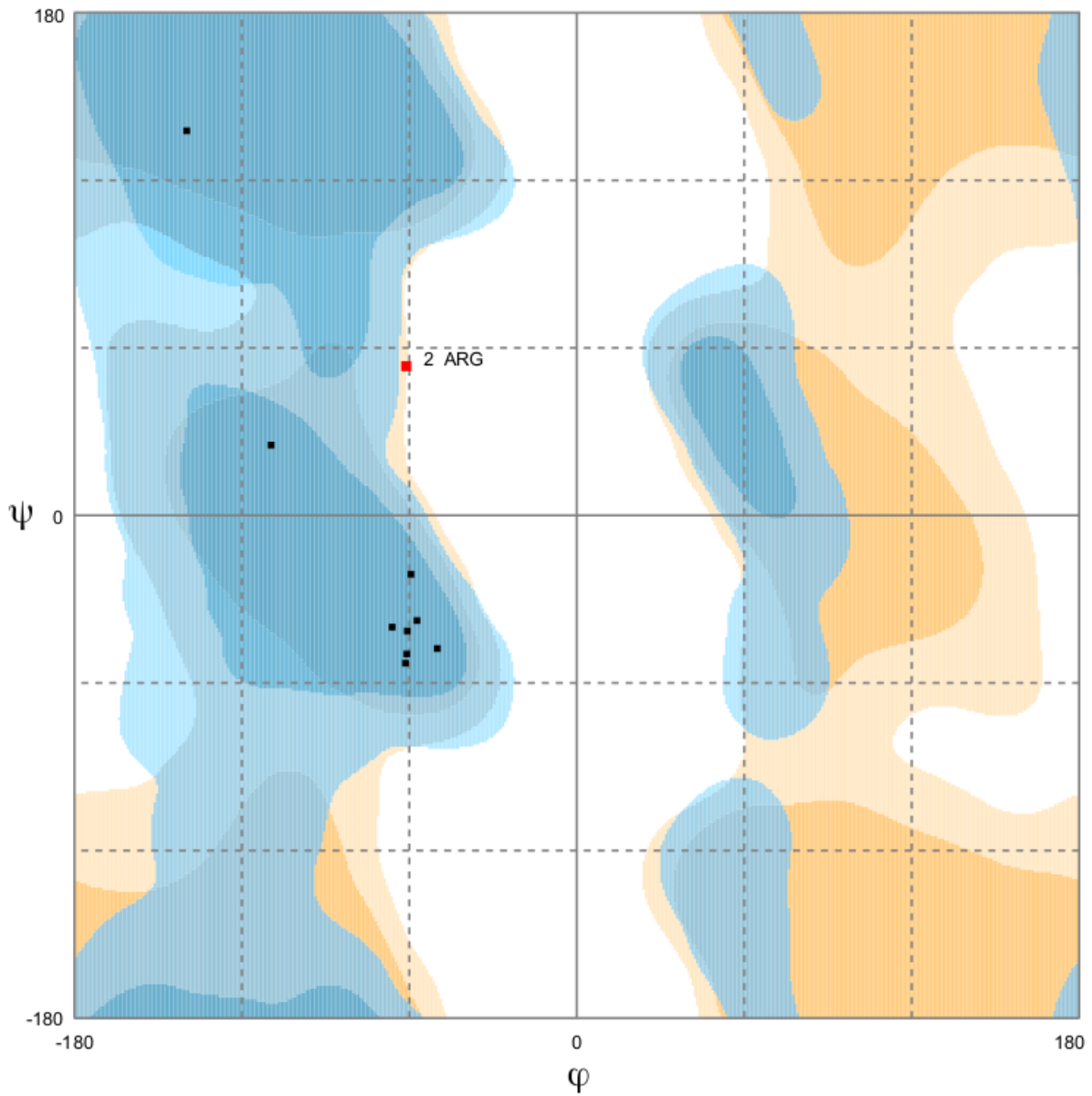
Number of residues in favoured region (~98.0% expected)	: 7 (70.0%)
Number of residues in allowed region (~2.0% expected)	: 2 (20.0%)
Number of residues in outlier region	: 1 (10.0%)

Tet009



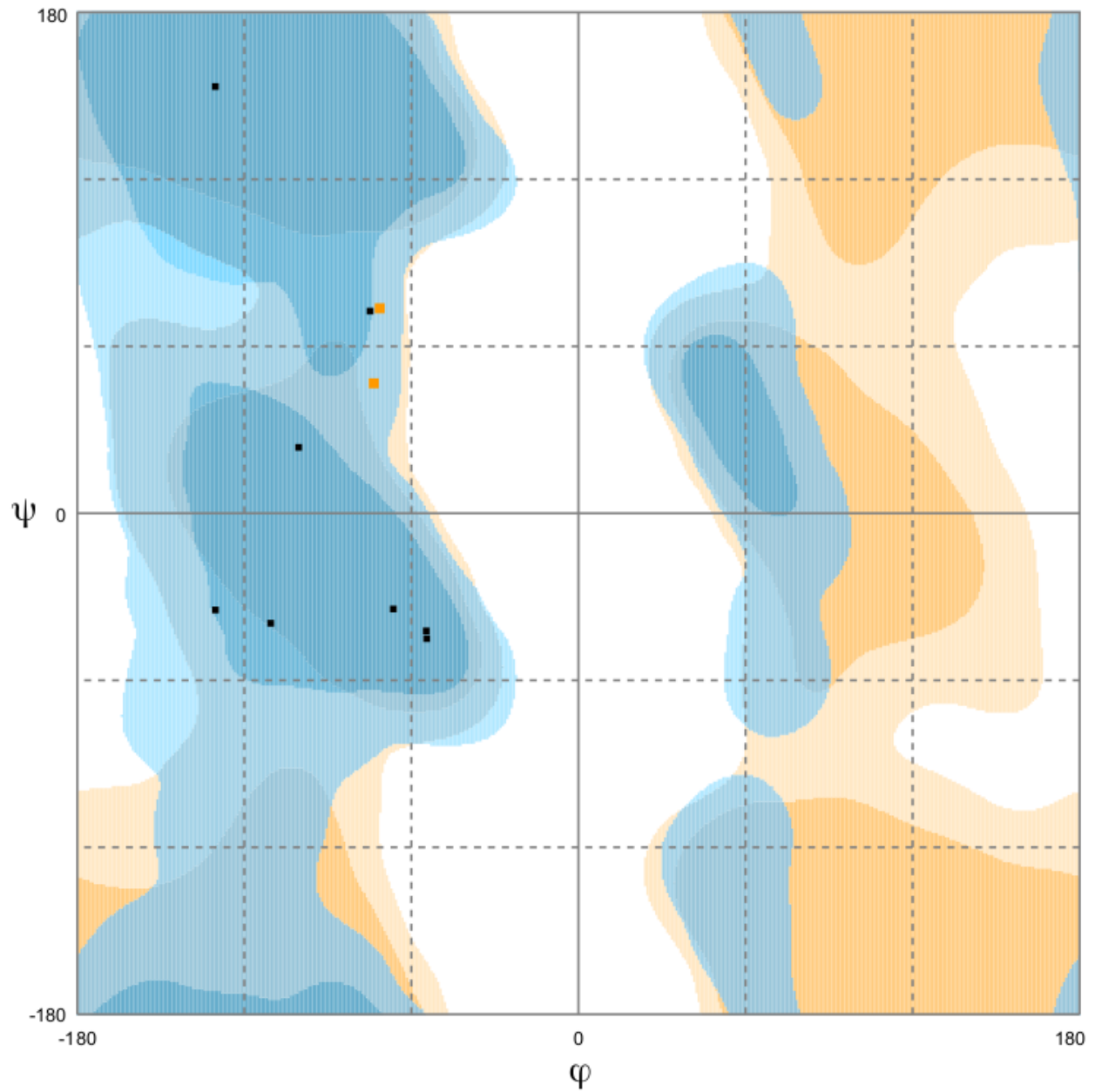
Number of residues in favoured region (~98.0% expected)	: 4 (40.0%)
Number of residues in allowed region (~2.0% expected)	: 6 (60.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet013



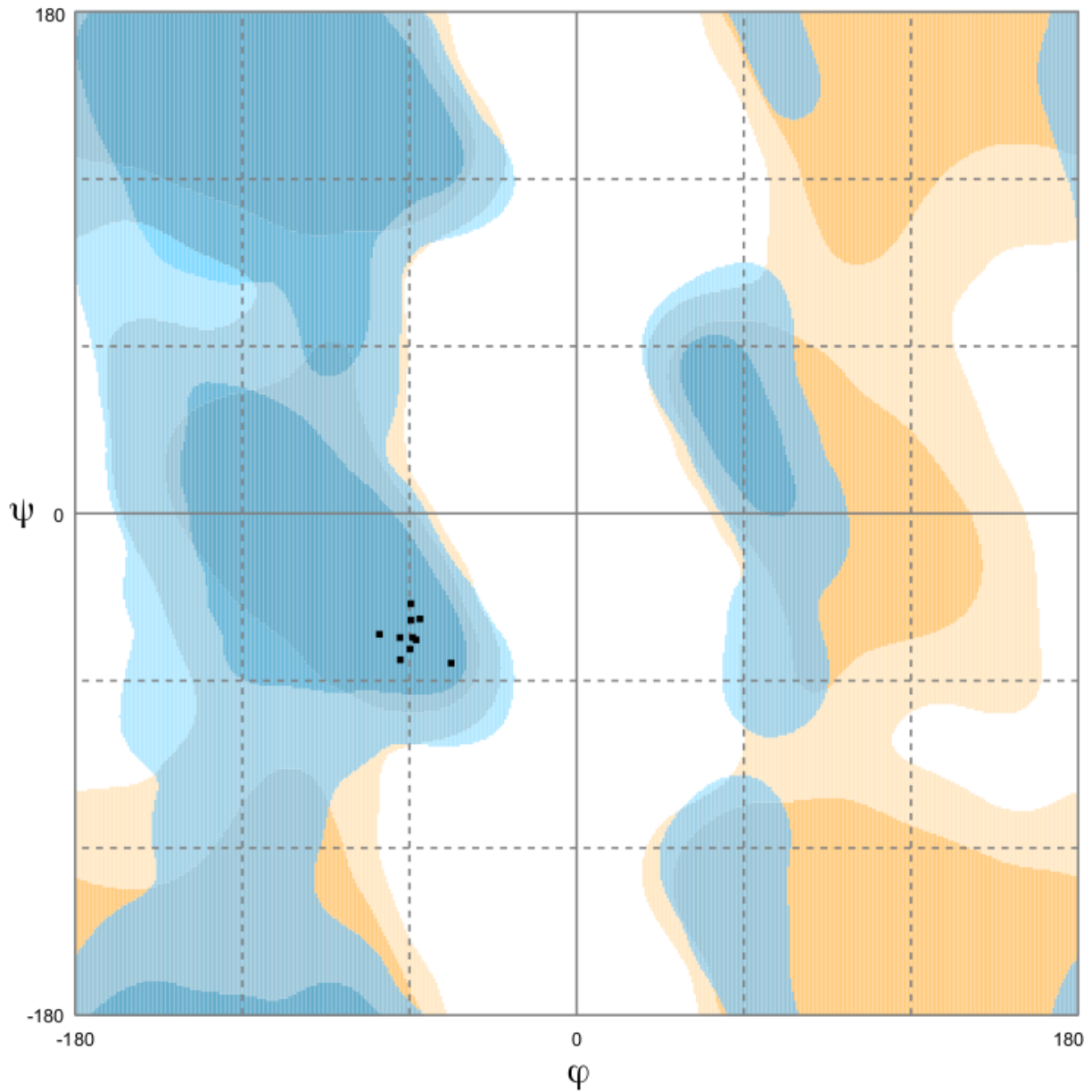
Number of residues in favoured region (~98.0% expected)	: 9 (90.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 1 (10.0%)

Tet024



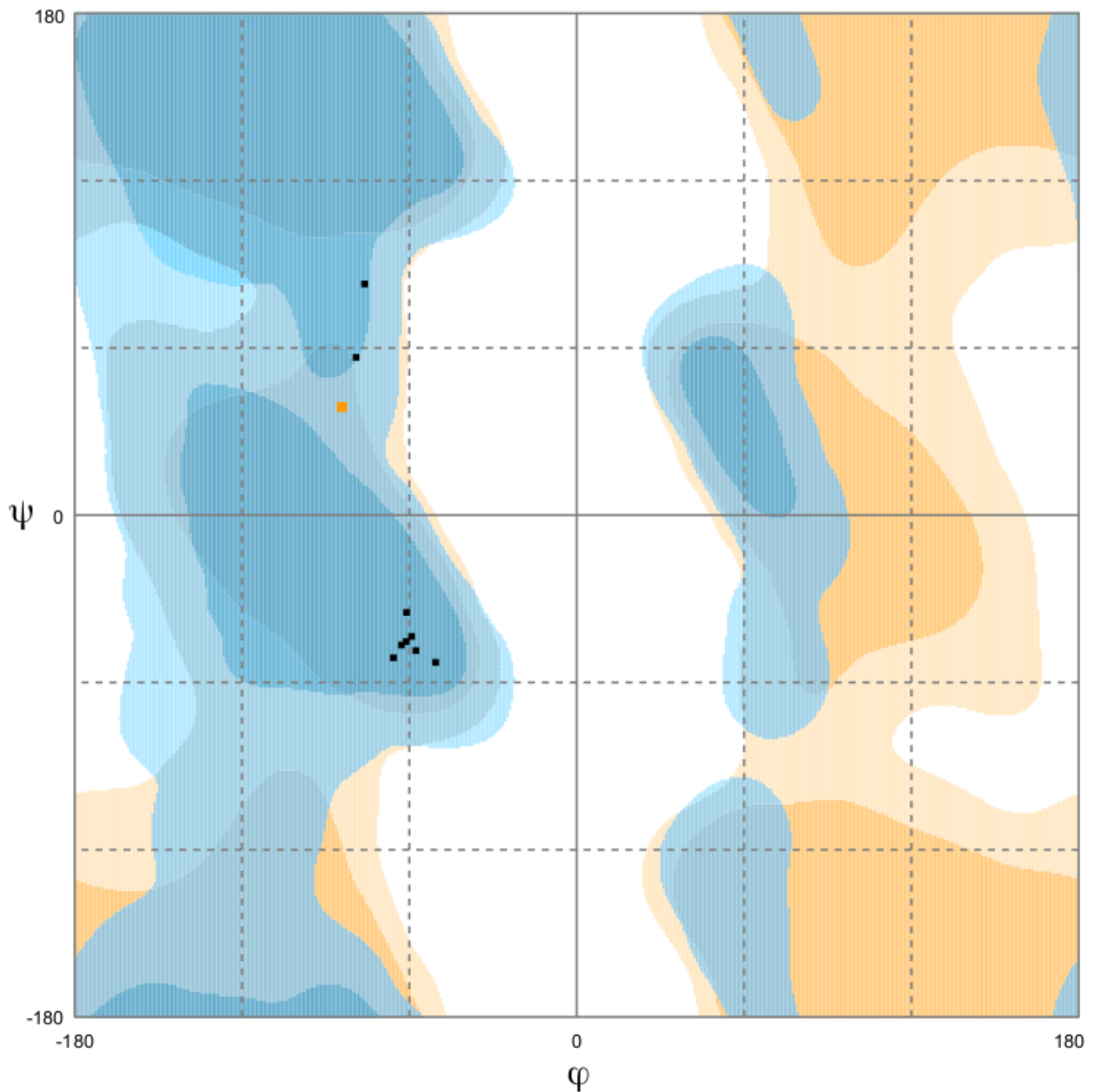
Number of residues in favoured region (~98.0% expected)	: 8 (80.0%)
Number of residues in allowed region (~2.0% expected)	: 2 (20.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet037



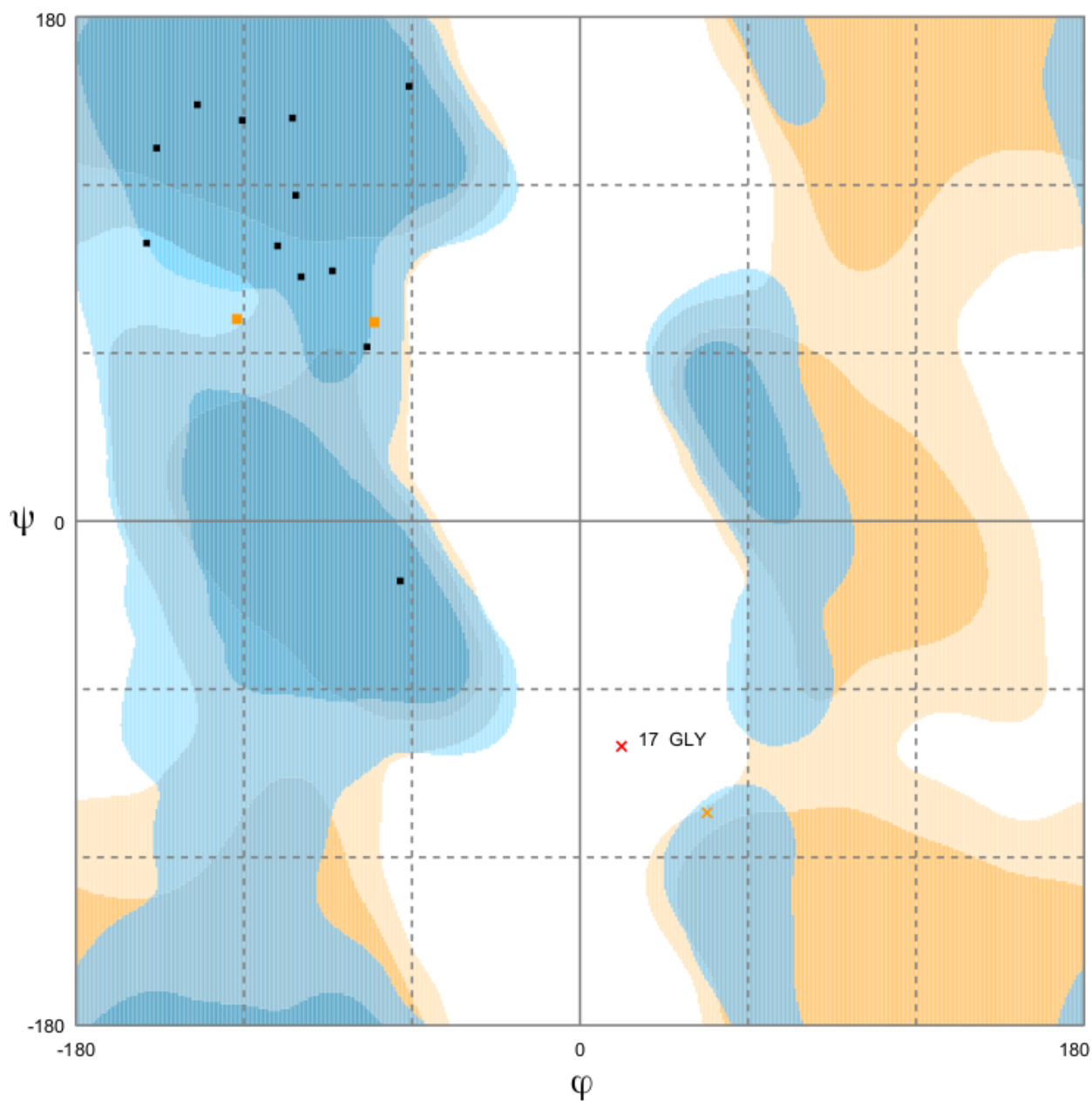
Number of residues in favoured region (~98.0% expected)	: 10 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

Tet052



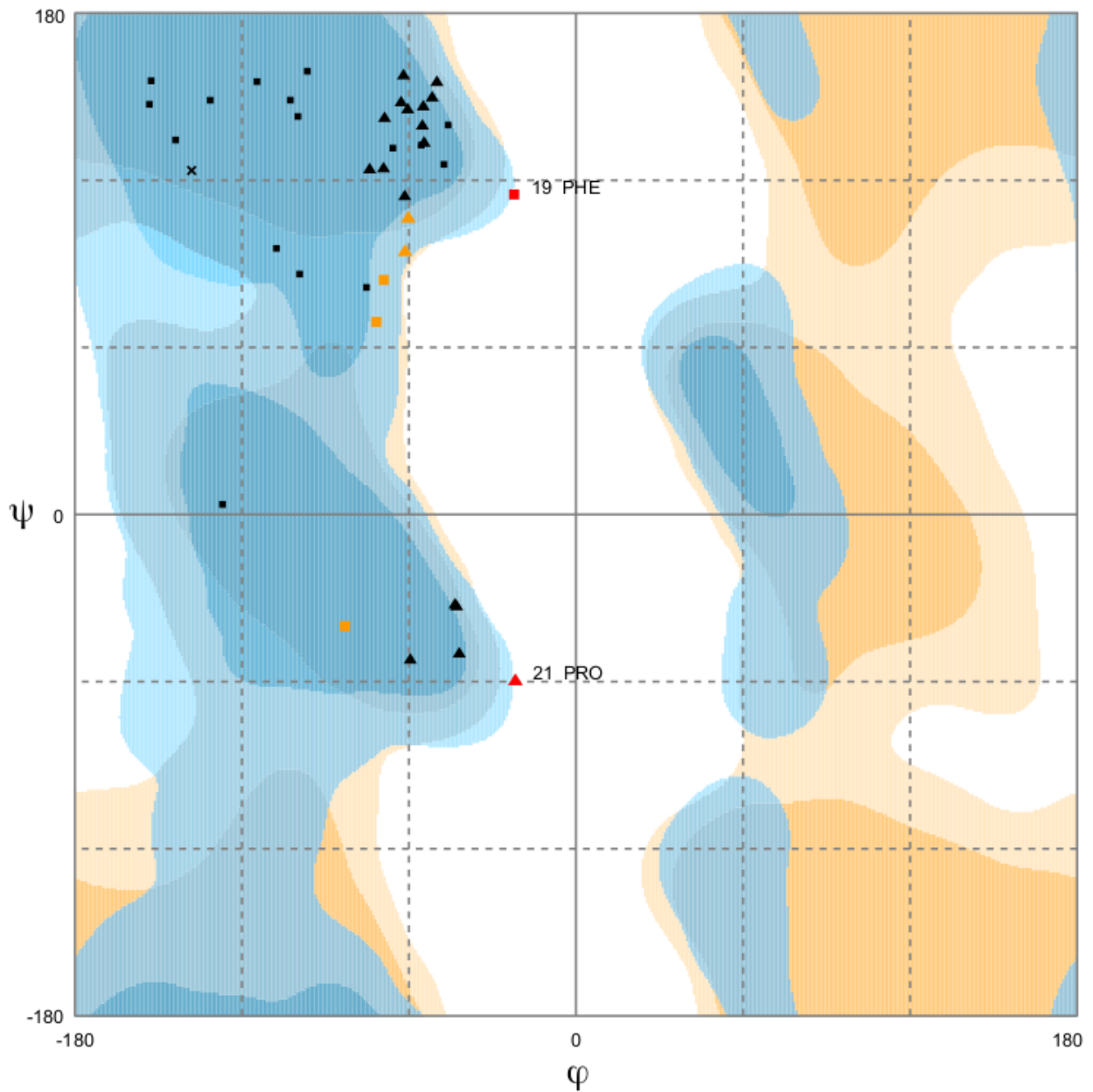
Number of residues in favoured region (~98.0% expected)	: 9 (90.0%)
Number of residues in allowed region (~2.0% expected)	: 1 (10.0%)
Number of residues in outlier region	: 0 (0.0%)

Retrocyclin-3



Number of residues in favoured region (~98.0% expected)	: 12 (75.0%)
Number of residues in allowed region (~2.0% expected)	: 3 (18.8%)
Number of residues in outlier region	: 1 (6.2%)

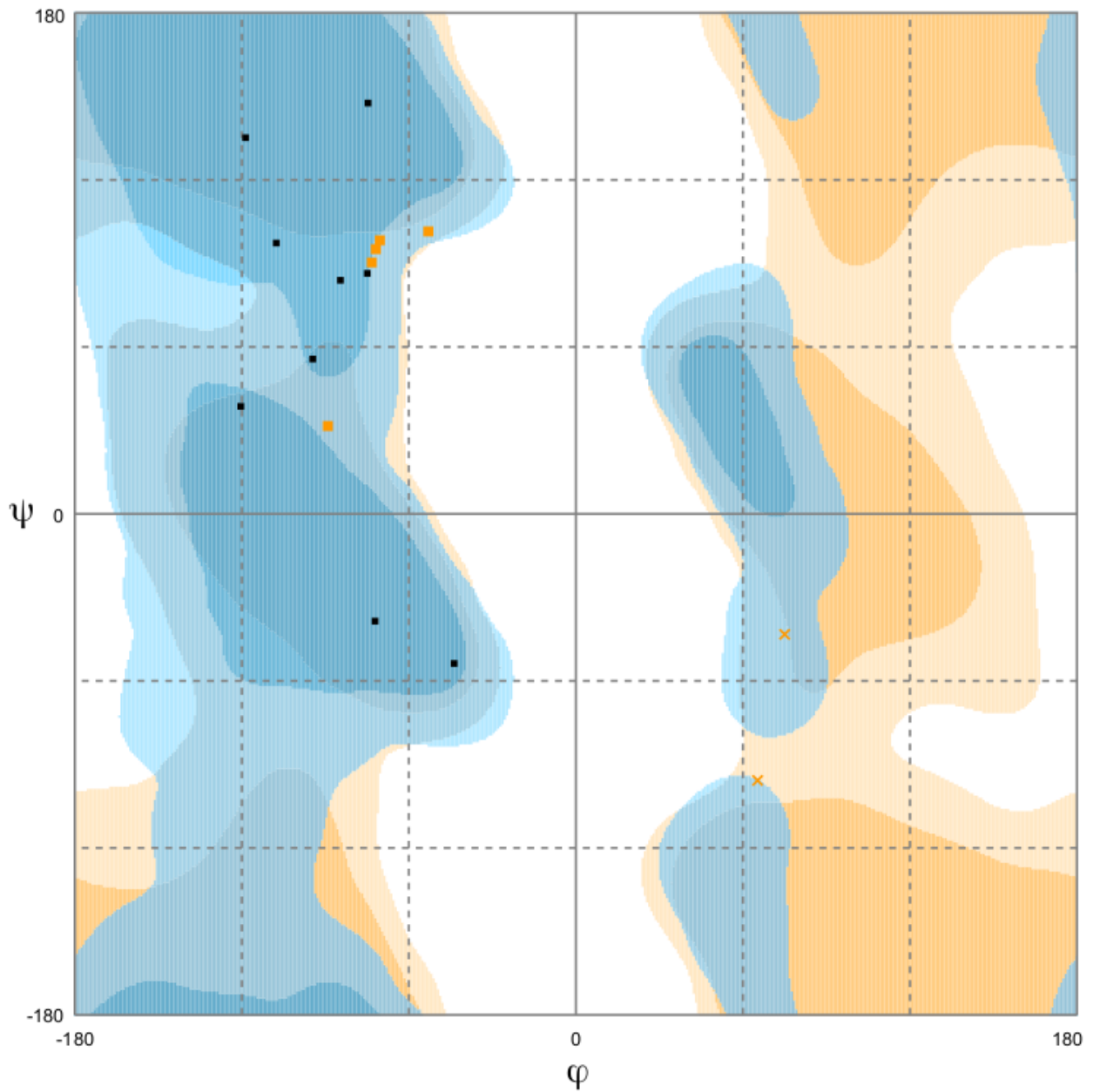
Bactenecin



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

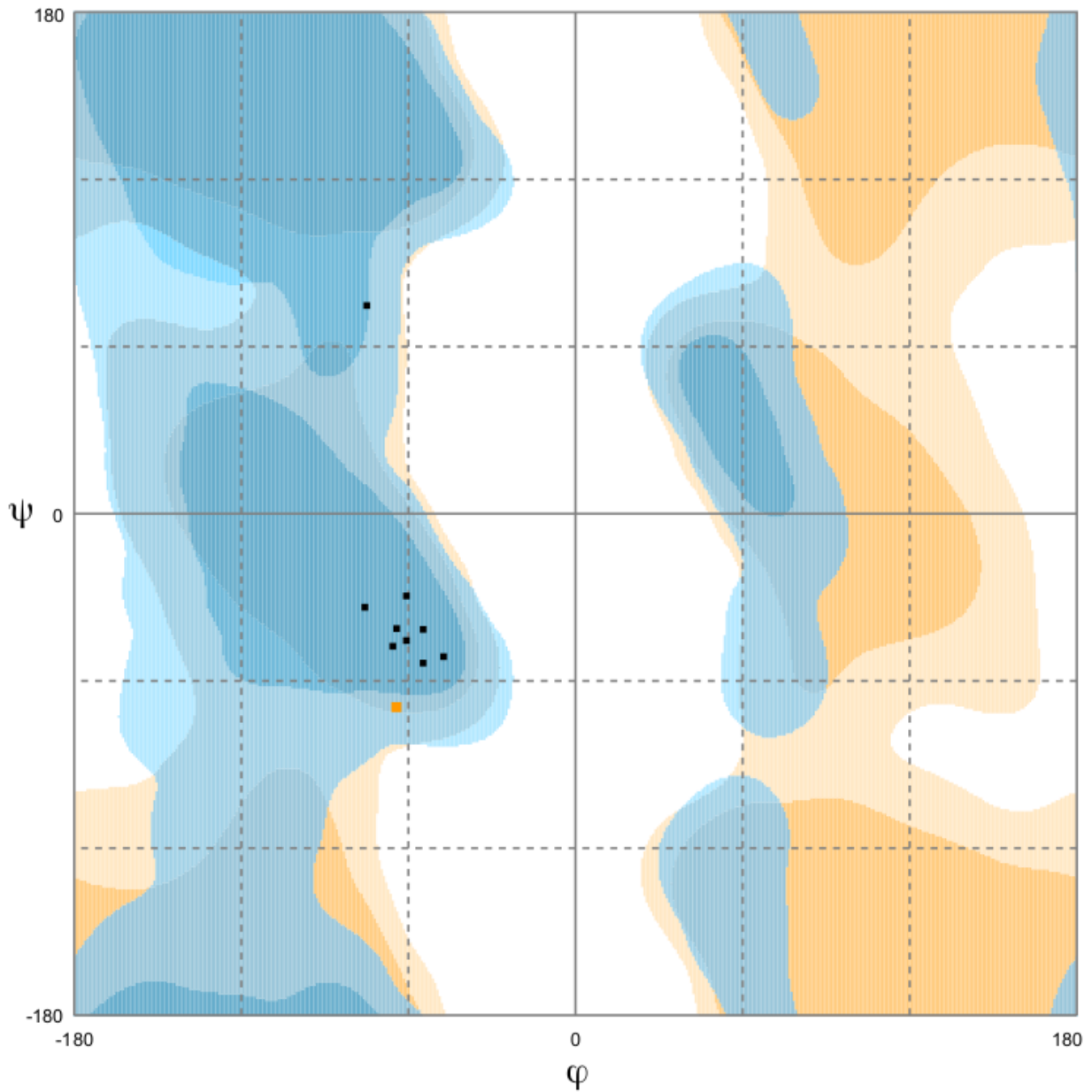
Number of residues in favoured region (~98.0% expected)	: 33 (82.5%)
Number of residues in allowed region (~2.0% expected)	: 5 (12.5%)
Number of residues in outlier region	: 2 (5.0%)

buCATHL4C



Number of residues in favoured region (~98.0% expected)	: 9 (56.2%)
Number of residues in allowed region (~2.0% expected)	: 7 (43.8%)
Number of residues in outlier region	: 0 (0.0%)

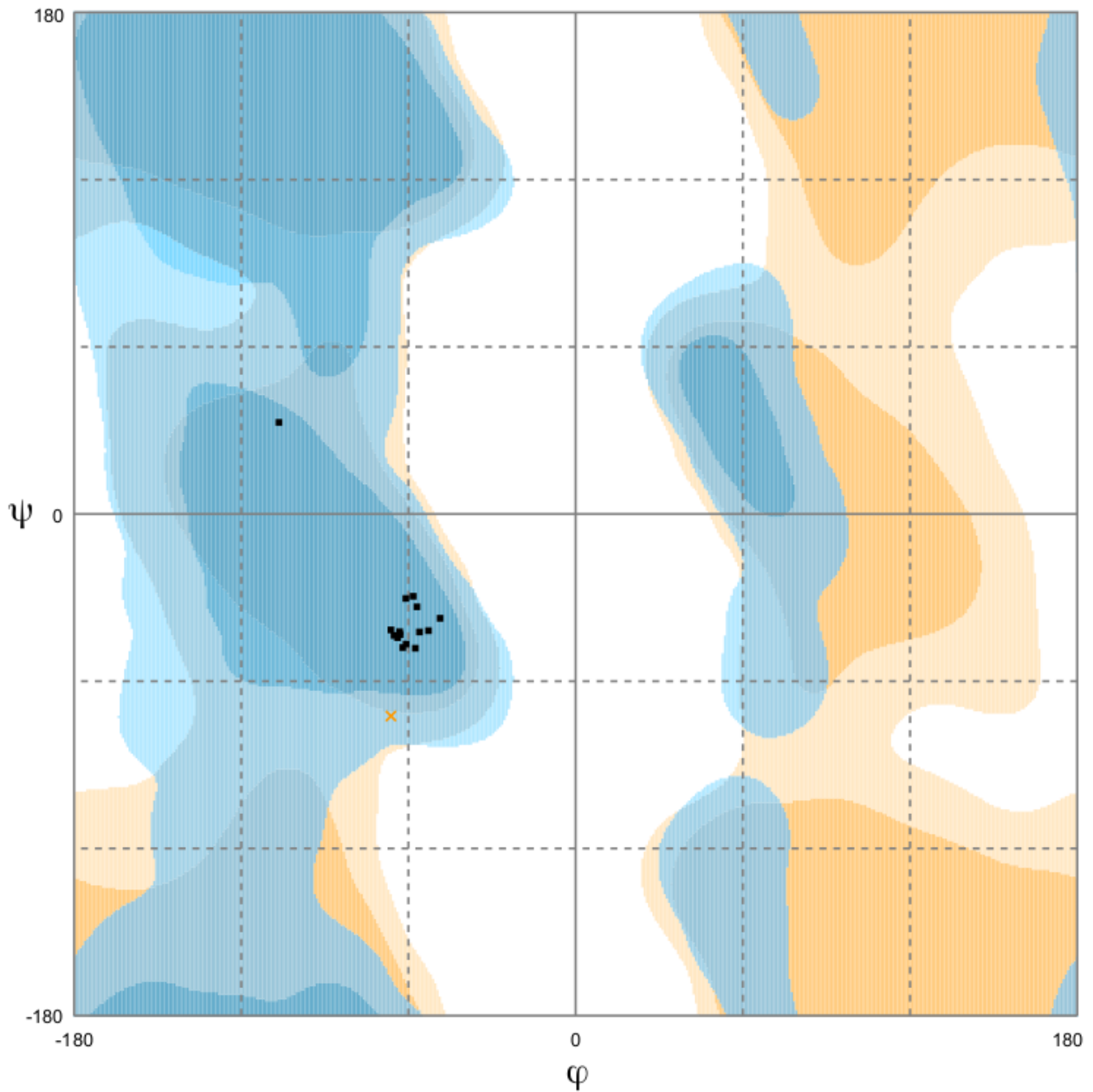
Cyclic dodecapeptide OaDode



■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

Number of residues in favoured region (~98.0% expected)	: 9 (90.0%)
Number of residues in allowed region (~2.0% expected)	: 1 (10.0%)
Number of residues in outlier region	: 0 (0.0%)

RTD-2



Number of residues in favoured region (~98.0% expected)	: 15 (93.8%)
Number of residues in allowed region (~2.0% expected)	: 1 (6.2%)
Number of residues in outlier region	: 0 (0.0%)