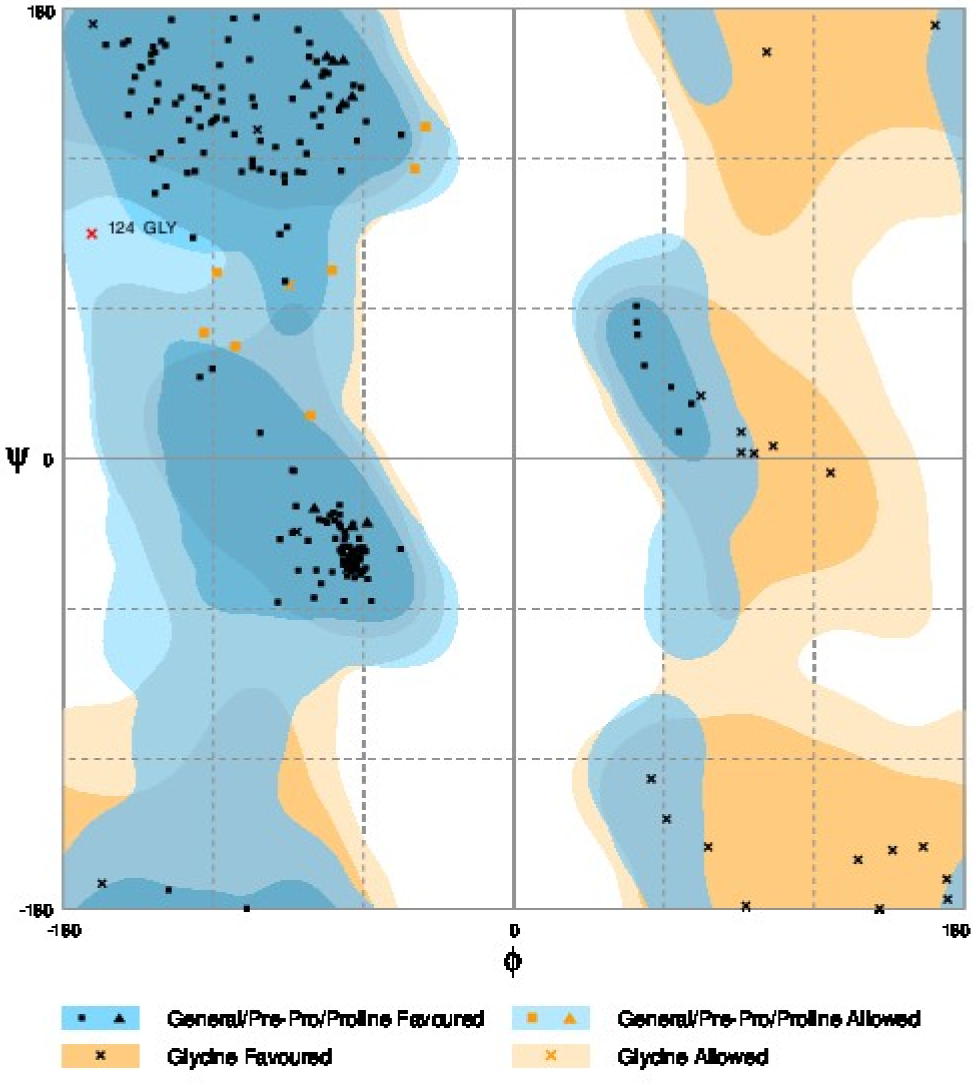
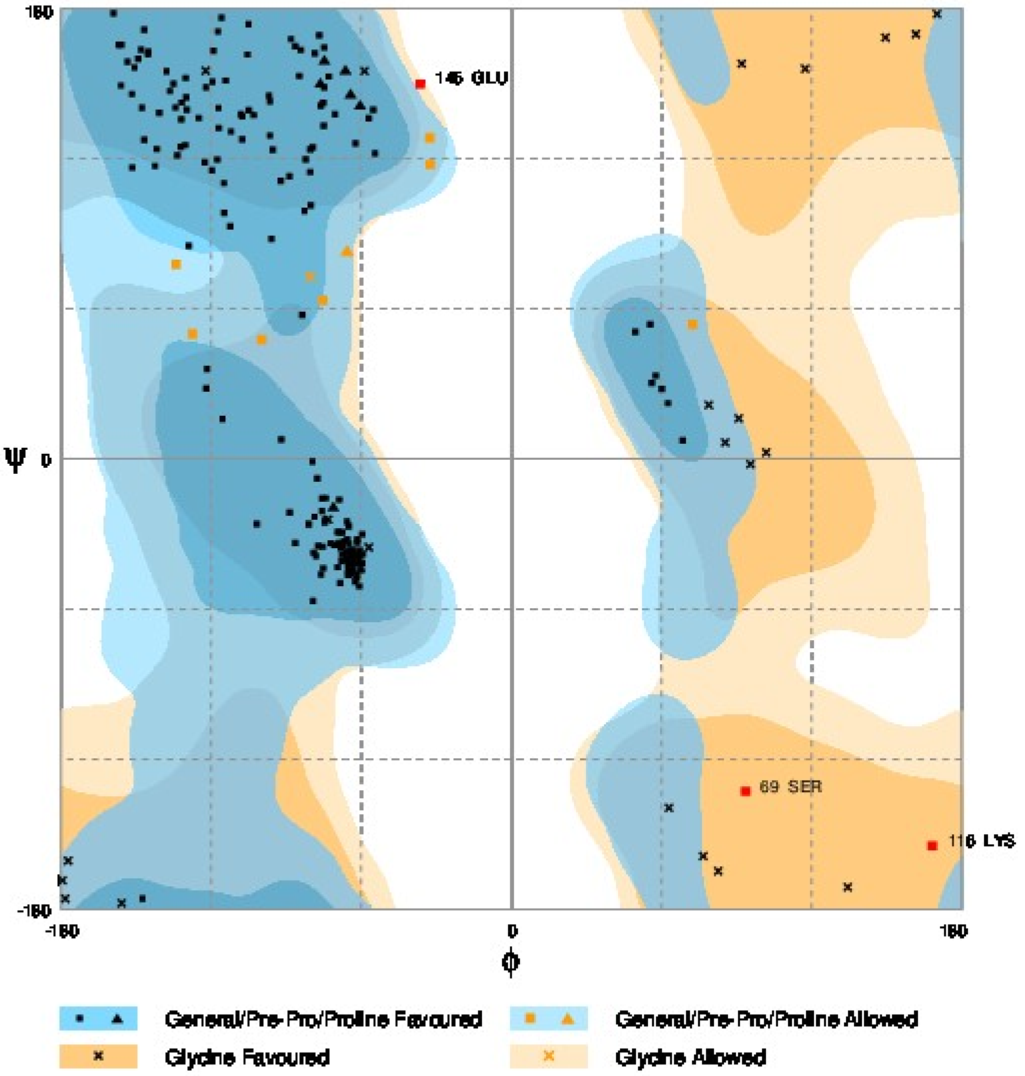
TmL2



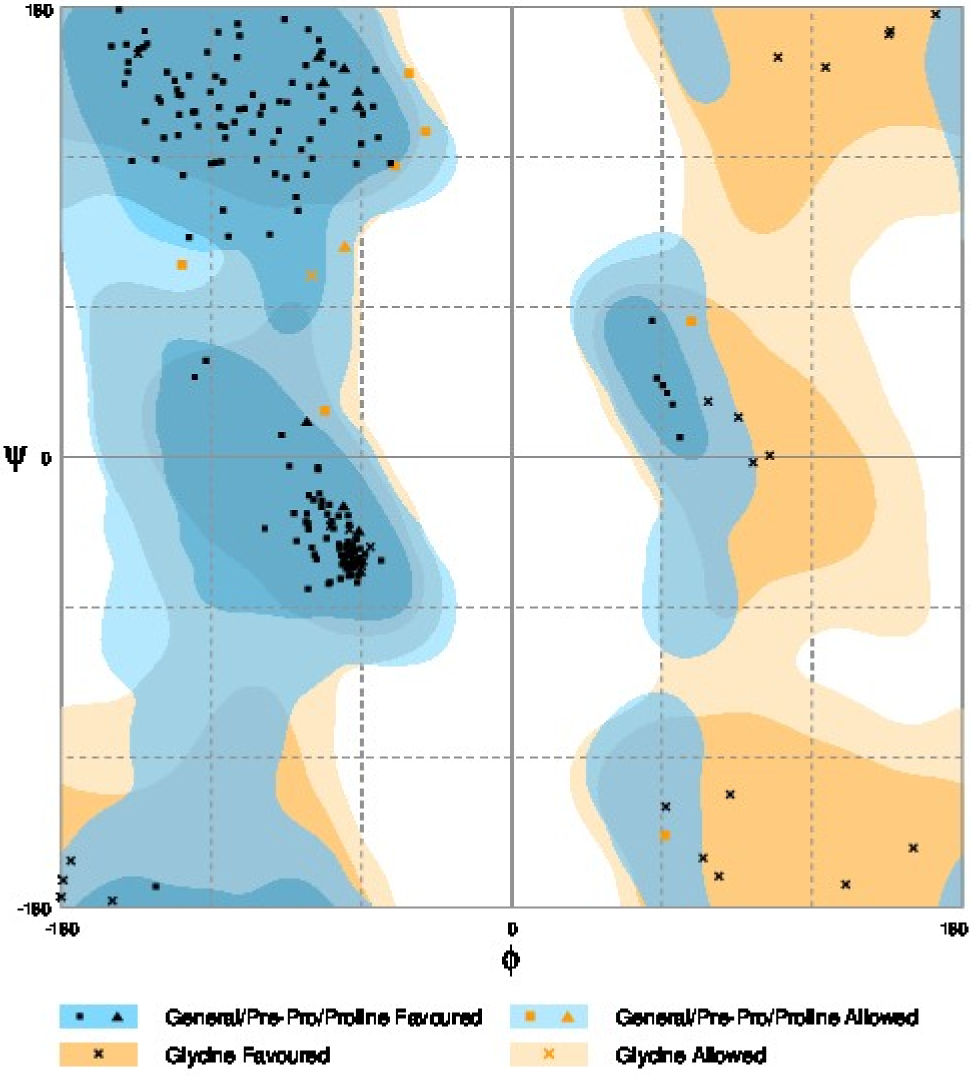
```
Number of residues in favoured region     (~98.0% expected)  :  213 ( 95.9%)
Number of residues in allowed region      ( ~2.0% expected)  :    8 (  3.6%)
Number of residues in outlier region                         :    1 (  0.5%)
```

TmL4



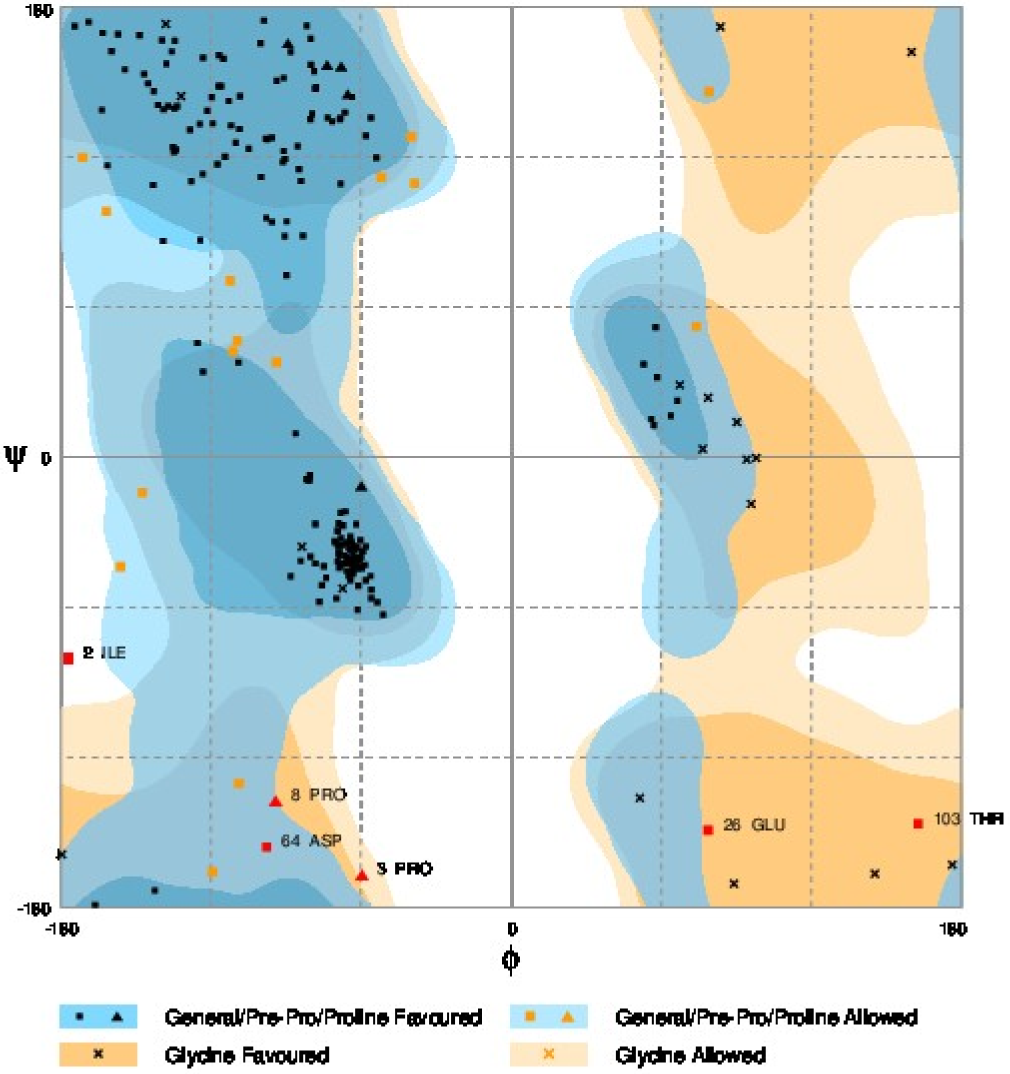
```
Number of residues in favoured region     (~98.0% expected)  :  207 ( 94.5%)
Number of residues in allowed region      ( ~2.0% expected)  :    9 (  4.1%)
Number of residues in outlier region                         :    3 (  1.4%)
```

TmL5



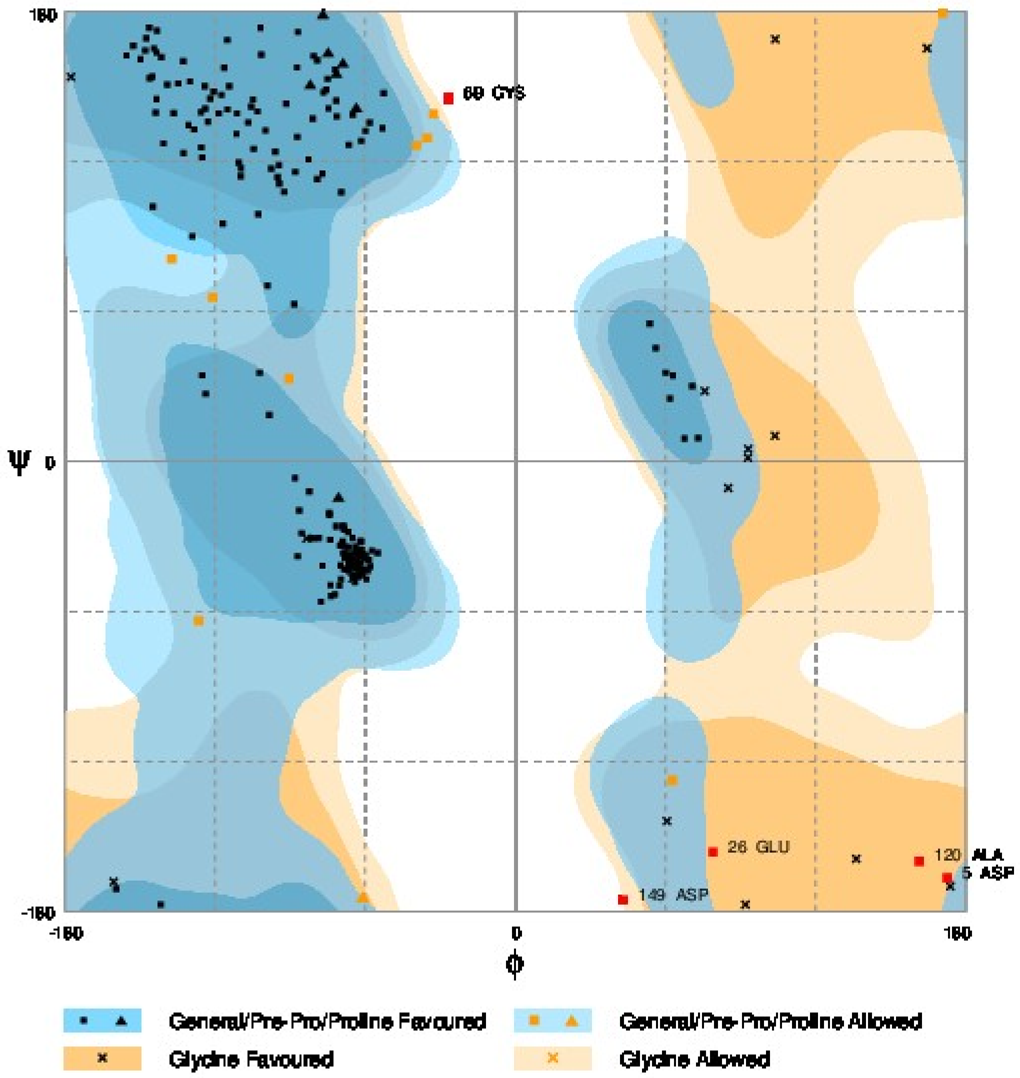
```
Number of residues in favoured region     (~98.0% expected)  :  211  ( 95.9%)
Number of residues in allowed region      ( ~2.0% expected)  :    9  (  4.1%)
Number of residues in outlier region                         :    0  (  0.0%)
```

TmL7



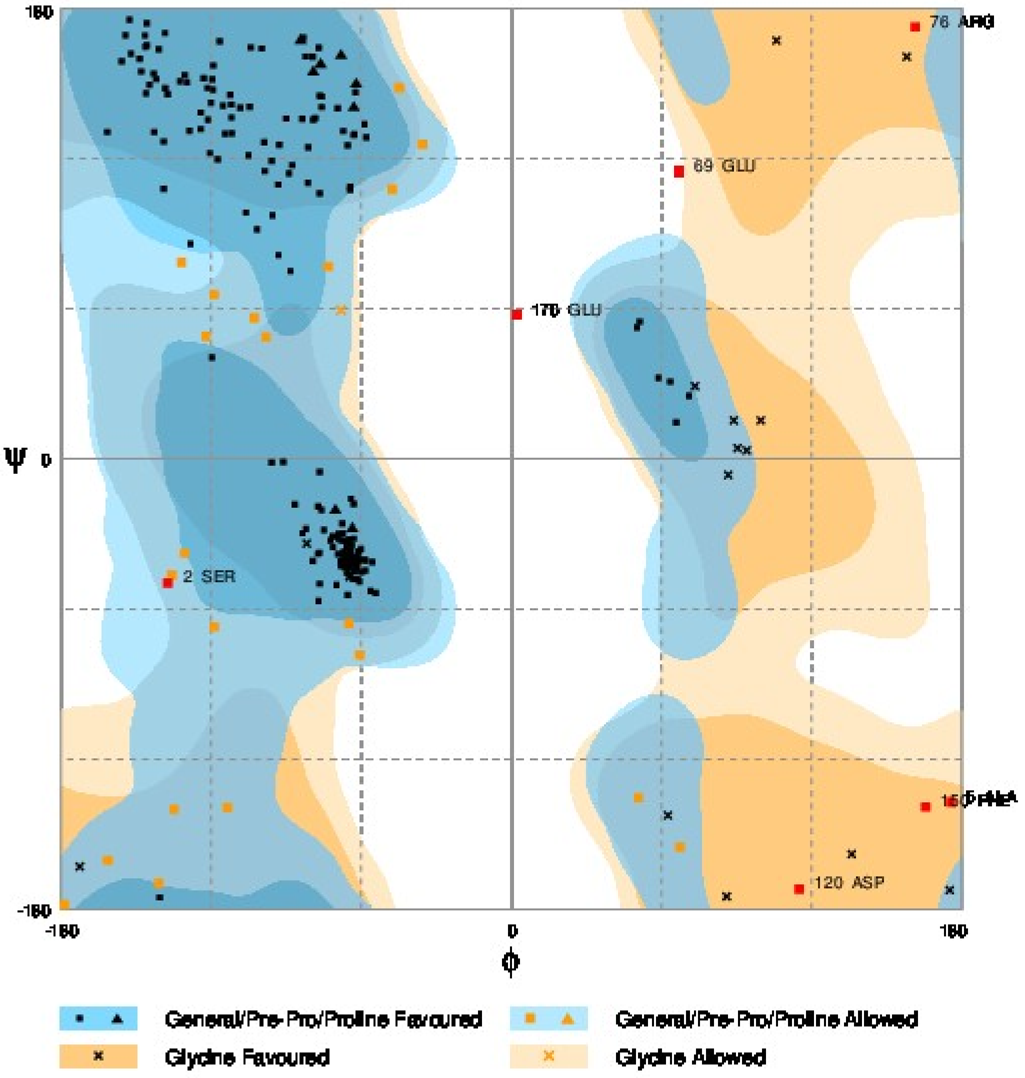
```
Number of residues in favoured region    (~98.0% expected)  :  204 ( 90.7%)
Number of residues in allowed region     ( ~2.0% expected)  :   15 (  6.7%)
Number of residues in outlier region                        :    6 (  2.7%)
```

TmL8



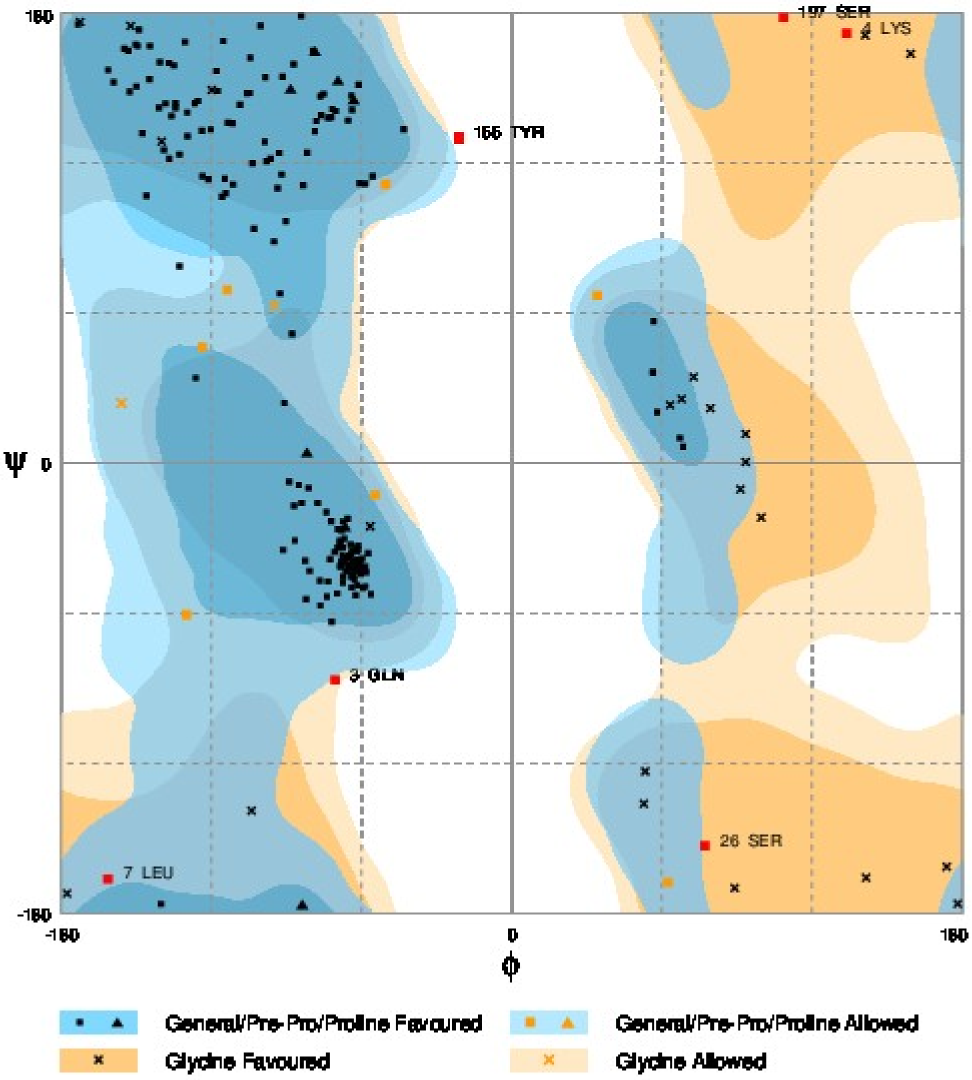
```
Number of residues in favoured region     (~98.0% expected)  :  210 ( 93.3%)
Number of residues in allowed region      ( ~2.0% expected)  :   10 (  4.4%)
Number of residues in outlier region                         :    5 (  2.2%)
```

TmL9



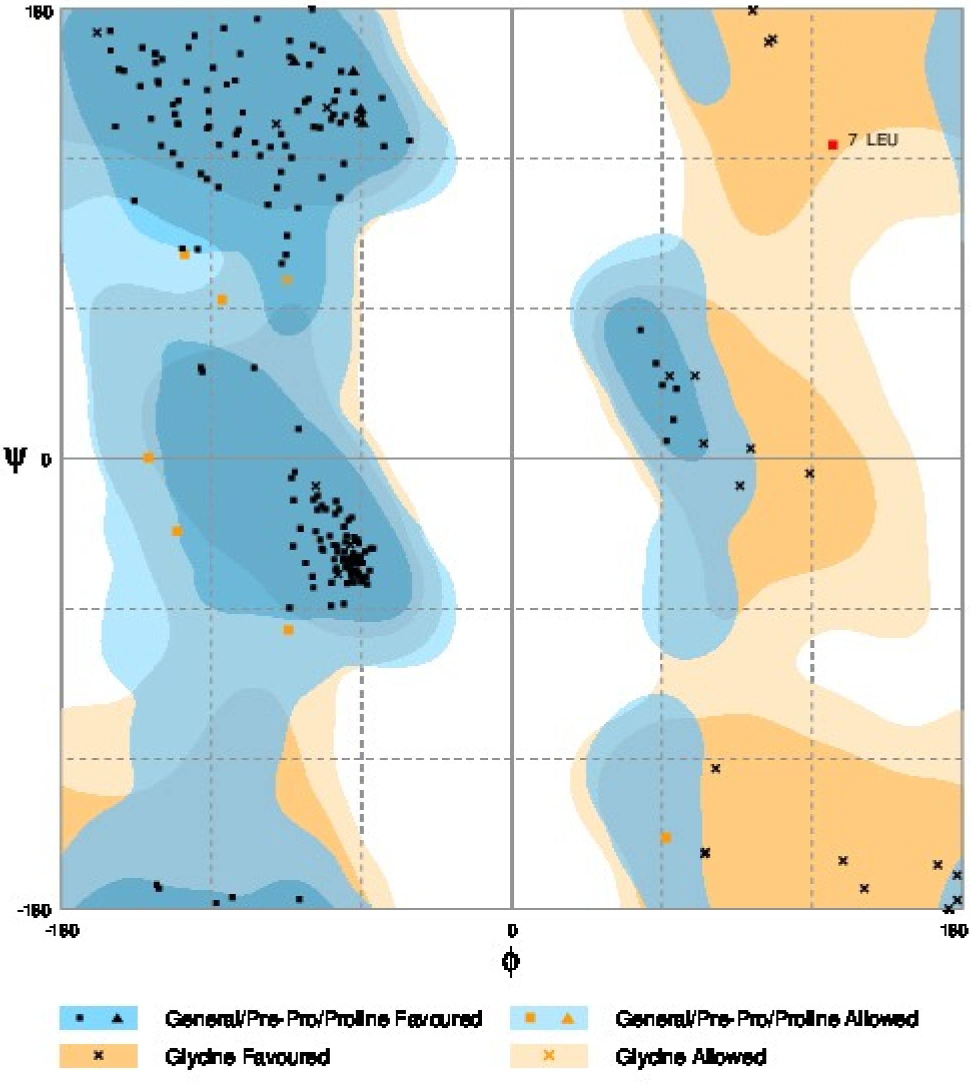
```
Number of residues in favoured region     (~98.0% expected)  :  196 ( 87.1%)
Number of residues in allowed region      ( ~2.0% expected)  :   22 (  9.8%)
Number of residues in outlier region                         :    7 (  3.1%)
```

TmL11



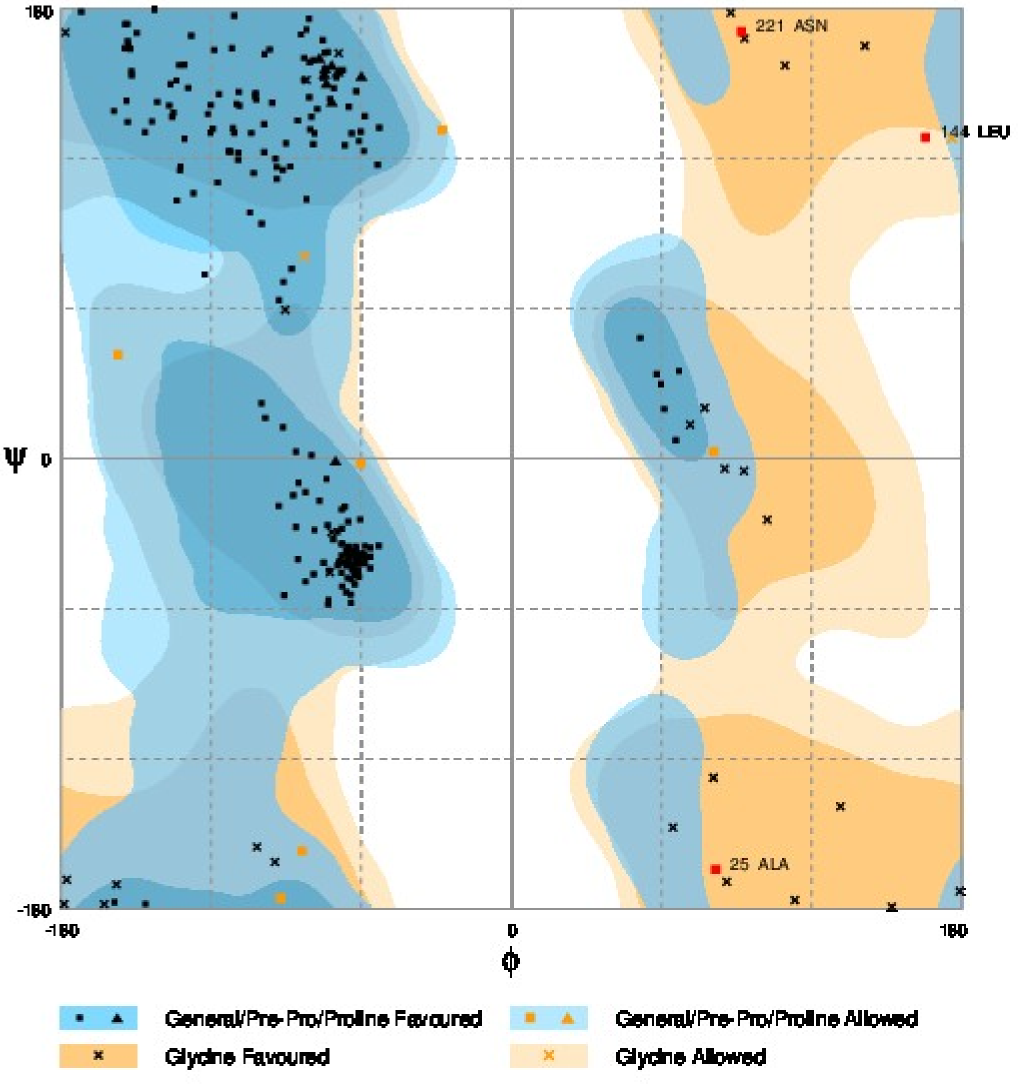
```
Number of residues in favoured region     (~98.0% expected)  :  209 ( 93.3%)
Number of residues in allowed region      ( ~2.0% expected)  :    9 (  4.0%)
Number of residues in outlier region                         :    6 (  2.7%)
```

TmL13



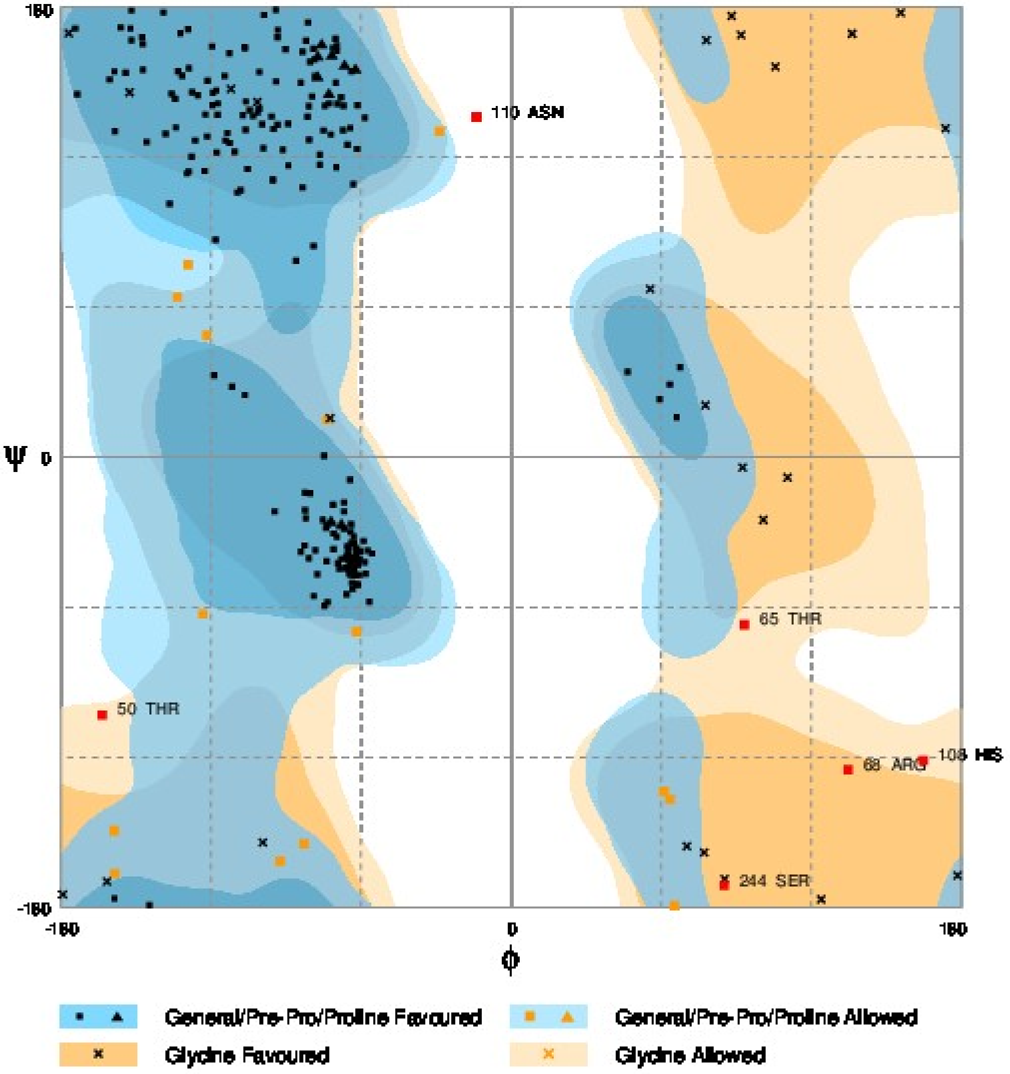
```
Number of residues in favoured region     (~98.0% expected)  :  210 ( 96.3%)
Number of residues in allowed region      ( ~2.0% expected)  :    7 (  3.2%)
Number of residues in outlier region                         :    1 (  0.5%)
```

TmB18



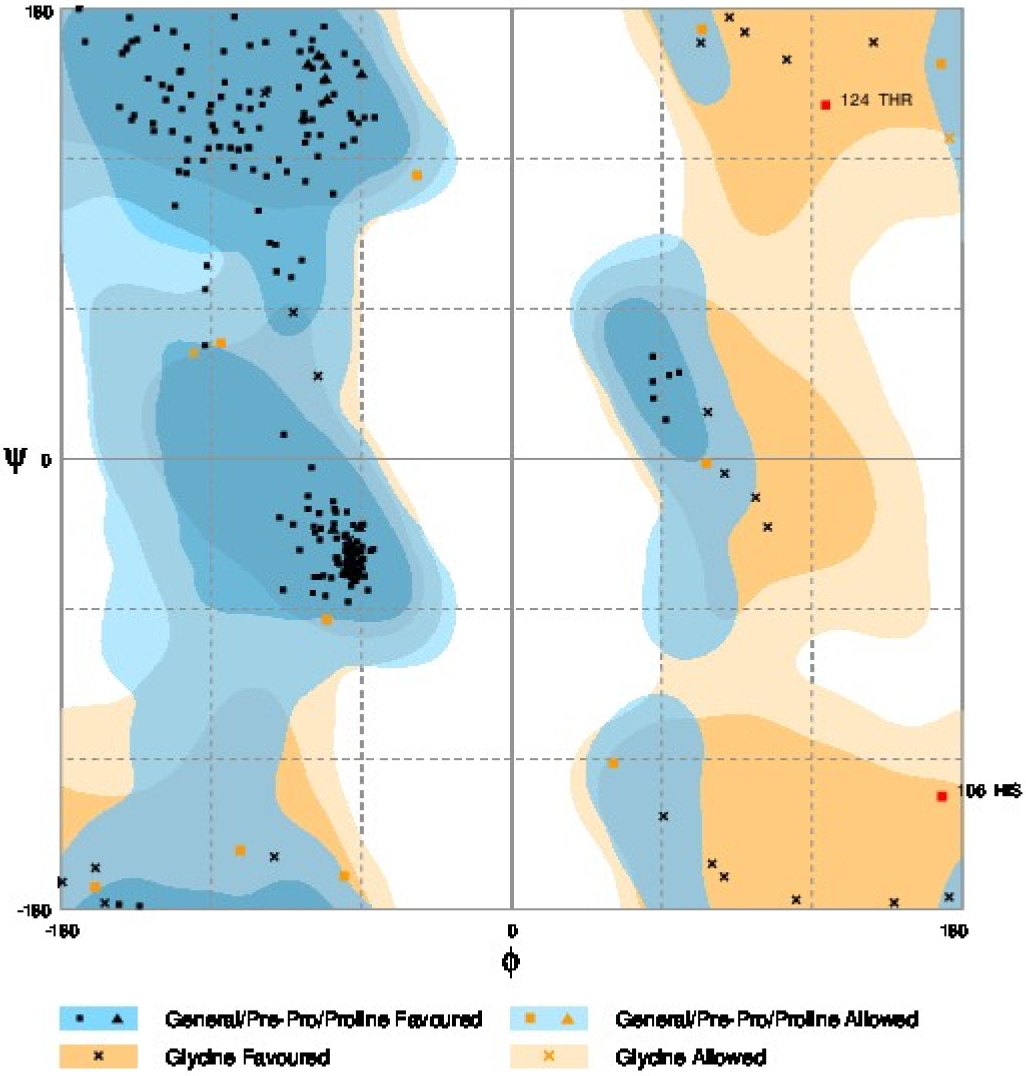
```
Number of residues in favoured region     (~98.0% expected)  :  239 ( 95.6%)
Number of residues in allowed region      ( ~2.0% expected)  :    8 (  3.2%)
Number of residues in outlier region                         :    3 (  1.2%)
```

TmB19



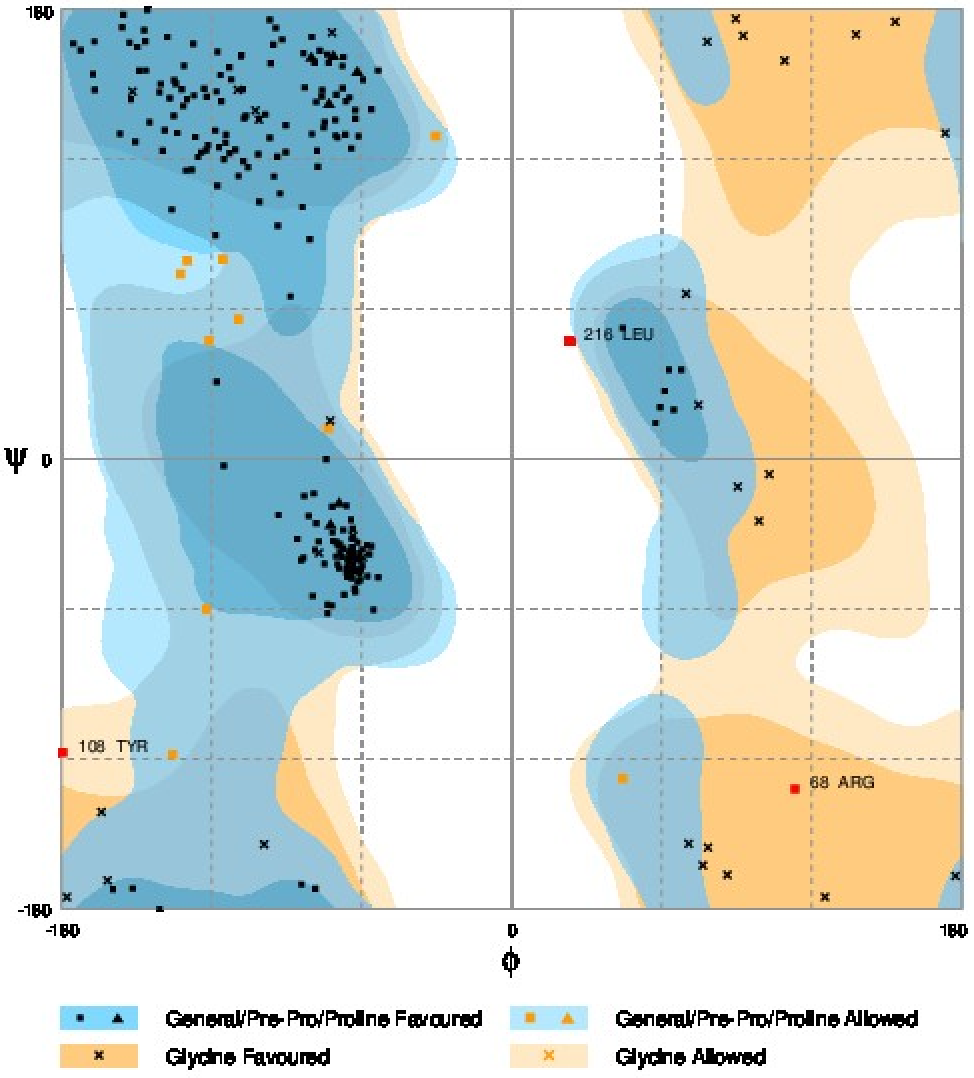
```
Number of residues in favoured region     (~98.0% expected)  :   244 ( 92.4%)
Number of residues in allowed region      ( ~2.0% expected)  :    14 (  5.3%)
Number of residues in outlier region                         :     6 (  2.3%)
```

TmB20



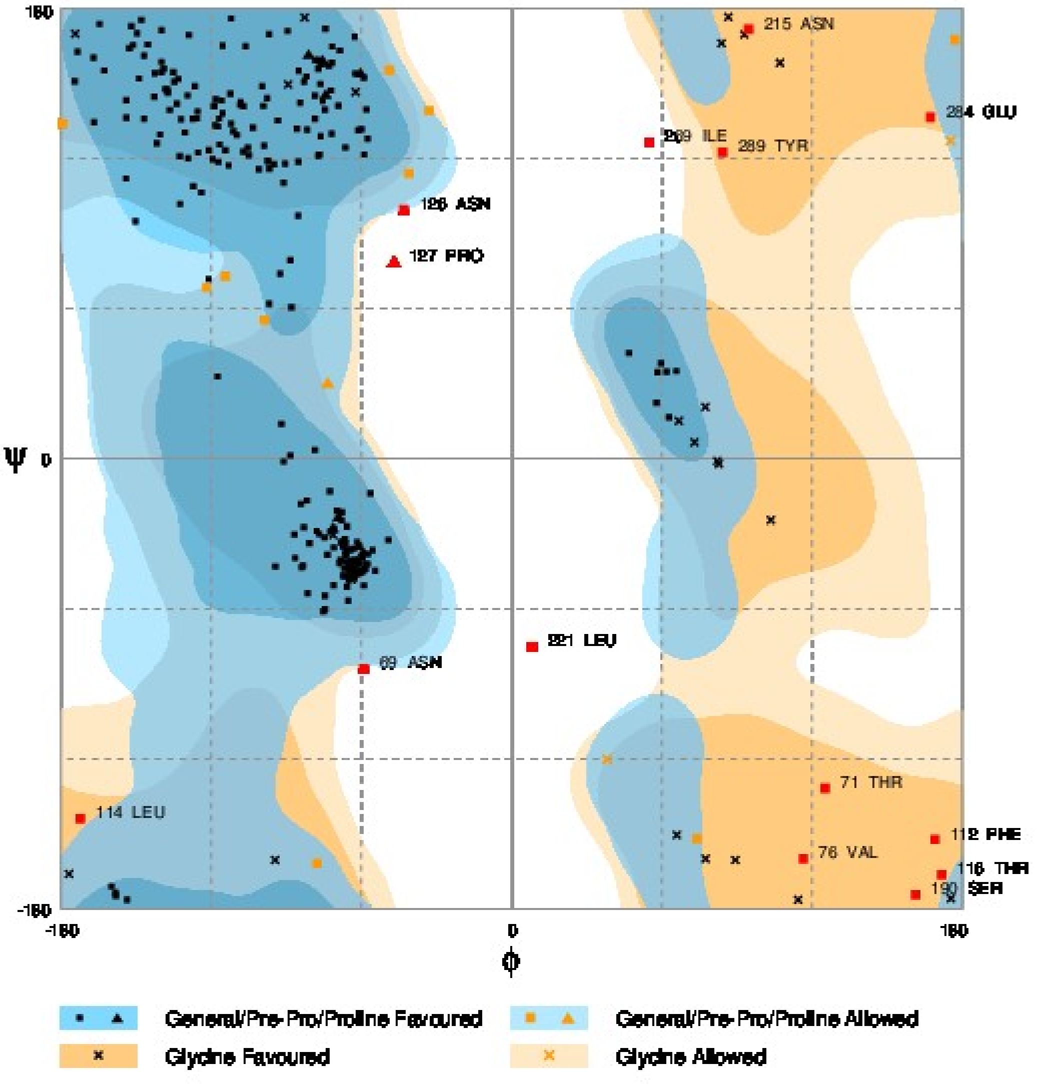
```
Number of residues in favoured region     (~98.0% expected)  :  223  ( 94.1%)
Number of residues in allowed region      ( ~2.0% expected)  :   12  (  5.1%)
Number of residues in outlier region                         :    2  (  0.8%)
```

TmB22



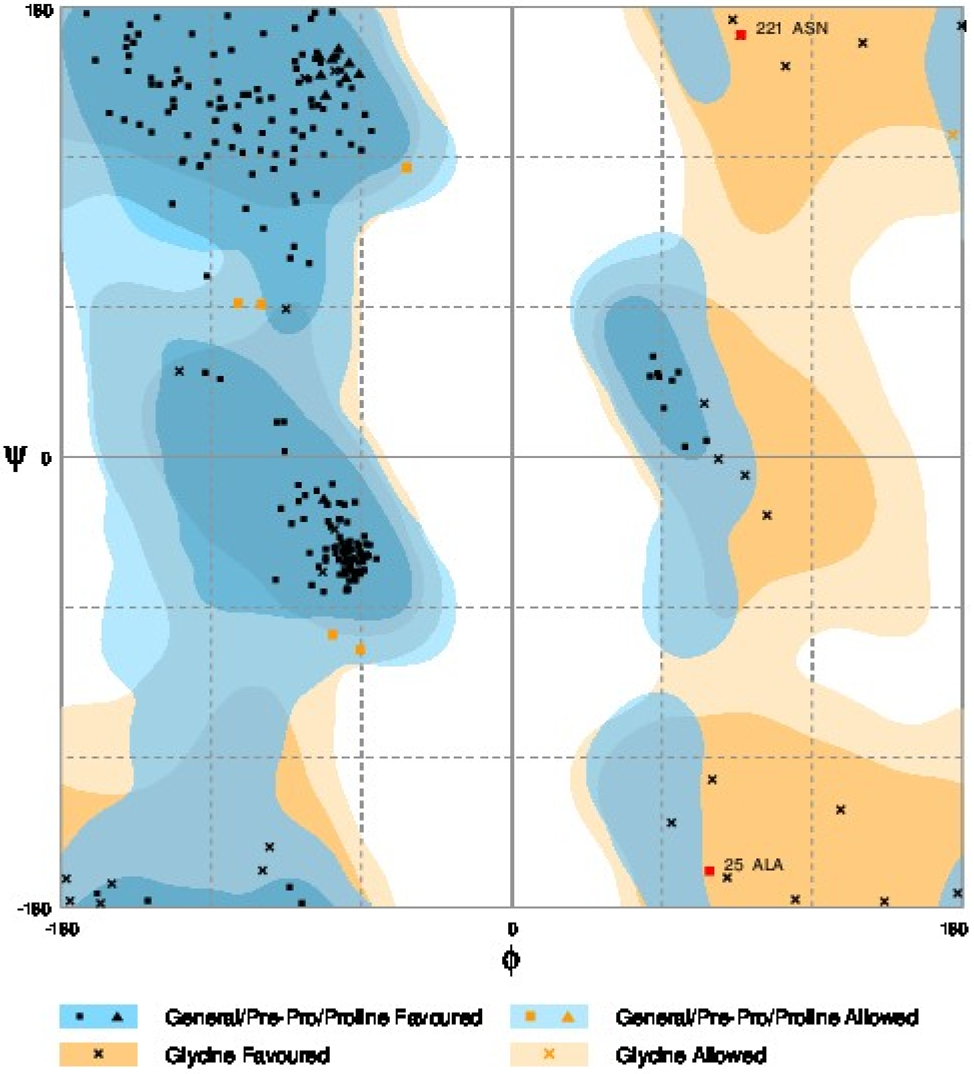
```
Number of residues in favoured region    (~98.0% expected)  :   252 ( 95.1%)
Number of residues in allowed region     ( ~2.0% expected)  :    10 (  3.8%)
Number of residues in outlier region                        :     3 (  1.1%)
```

TmB28



```
Number of residues in favoured region     (~98.0% expected)  :   265 ( 90.8%)
Number of residues in allowed region      ( ~2.0% expected)  :    13 (  4.5%)
Number of residues in outlier region                         :    14 (  4.8%)
```

TmB33



```
Number of residues in favoured region     (~98.0% expected)  :  242 ( 96.8%)
Number of residues in allowed region      ( ~2.0% expected)  :    6 (  2.4%)
Number of residues in outlier region                         :    2 (  0.8%)
```