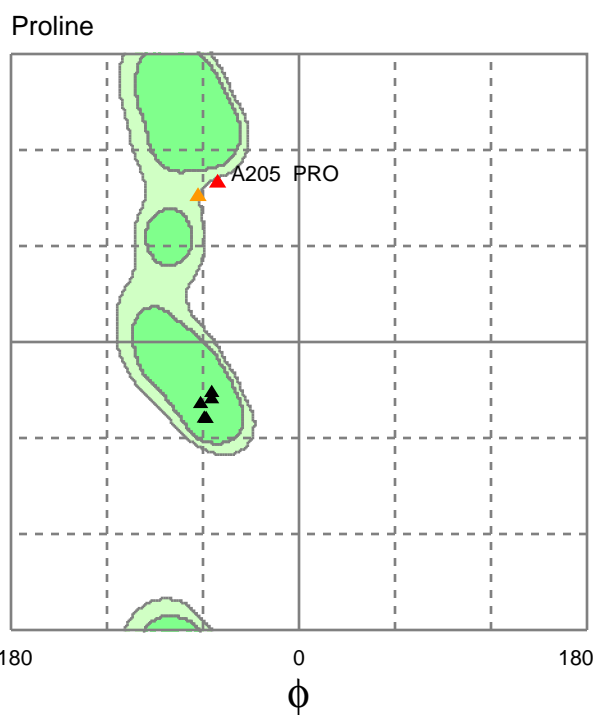
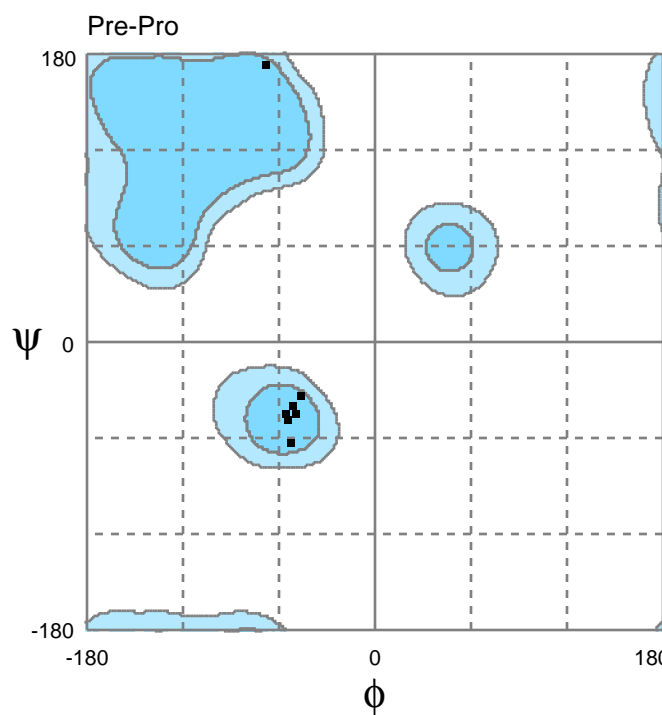
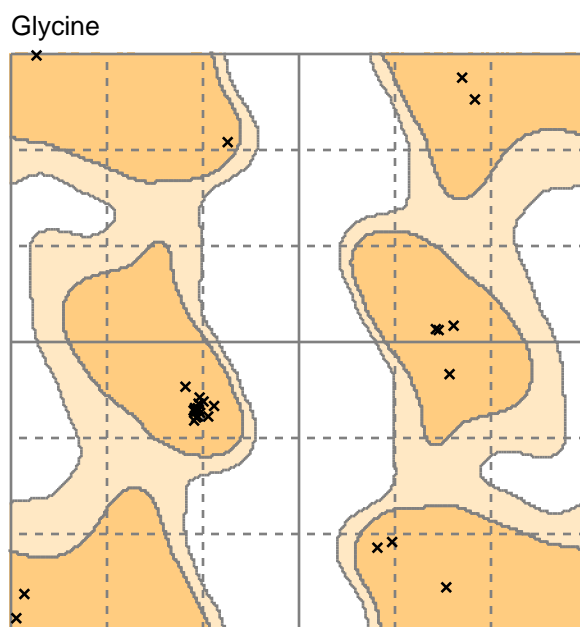
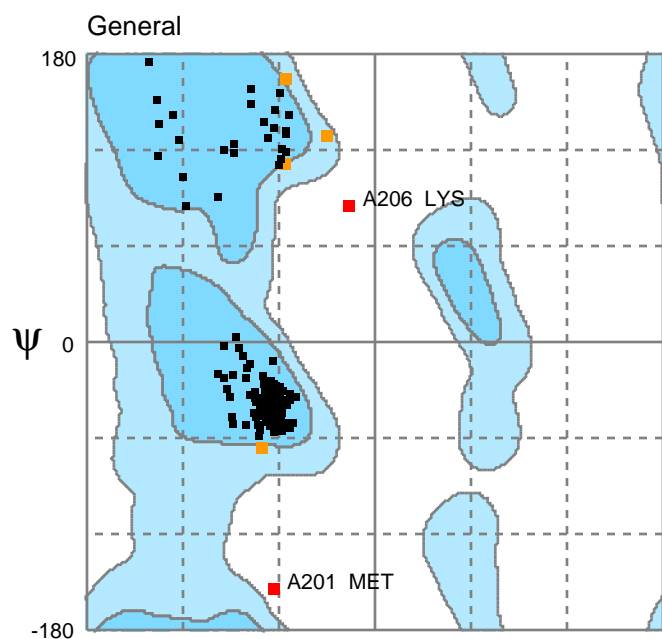


■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
x	Glycine Favoured	x	Glycine Allowed

Number of residues in favoured region (~98.0% expected) : 288 (97.3%)  
 Number of residues in allowed region (~2.0% expected) : 5 (1.7%)  
 Number of residues in outlier region : 3 (1.0%)

RAMPAGE by Paul de Bakker and Simon Lovell available at <http://www-cryst.bioc.cam.ac.uk/rampage/>

Please cite: S.C. Lovell, I.W. Davis, W.B. Arendall III, P.I.W. de Bakker, J.M. Word, M.G. Prisant, J.S. Richardson & D.C. Richardson (2002)  
 Structure validation by  $\alpha$  geometry:  $\phi/\psi$  and  $C\beta$  deviation. *Proteins: Structure, Function & Genetics*. **50**: 437-450



General Favoured

Glycine Favoured

Pre-Pro Favoured

Proline Favoured

General Allowed

Glycine Allowed

Pre-Pro Allowed

Proline Allowed

Number of residues in favoured region (~98.0% expected) : 288 (97.3%)

Number of residues in allowed region (~2.0% expected) : 5 (1.7%)

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