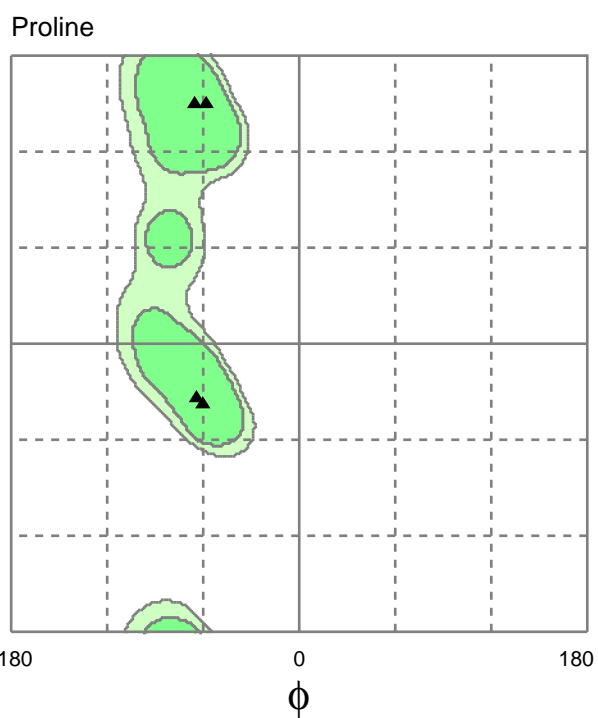
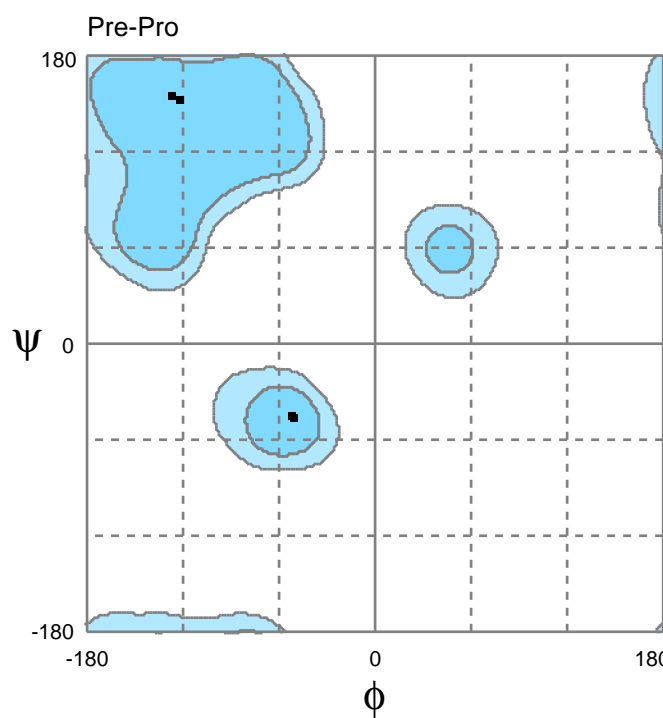
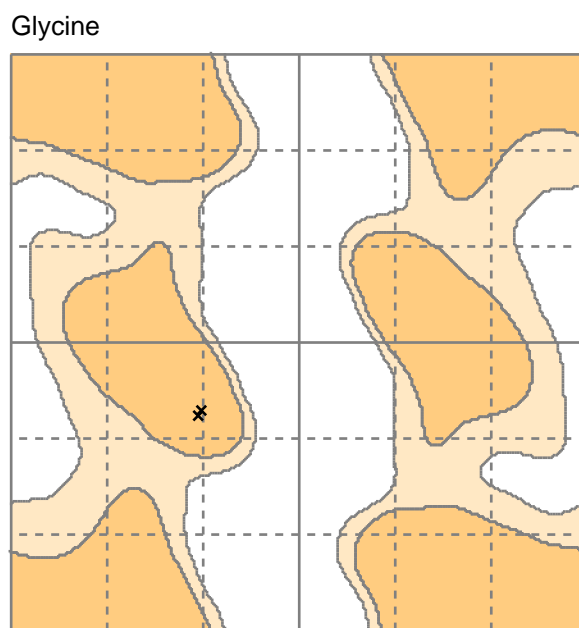
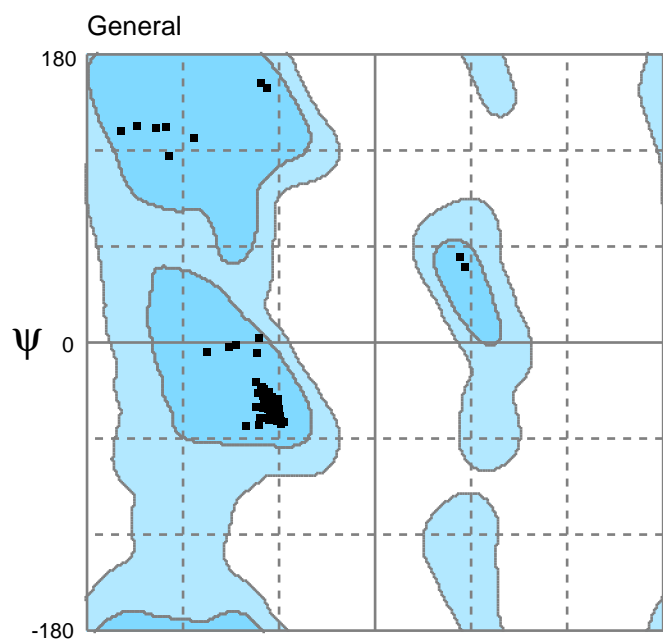


■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

Number of residues in favoured region (~98.0% expected)	: 96 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

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 C $\alpha$  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) : 96 (100.0%)  
 Number of residues in allowed region (~2.0% expected) : 0 (0.0%)  
 Number of residues in outlier region : 0 (0.0%)

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