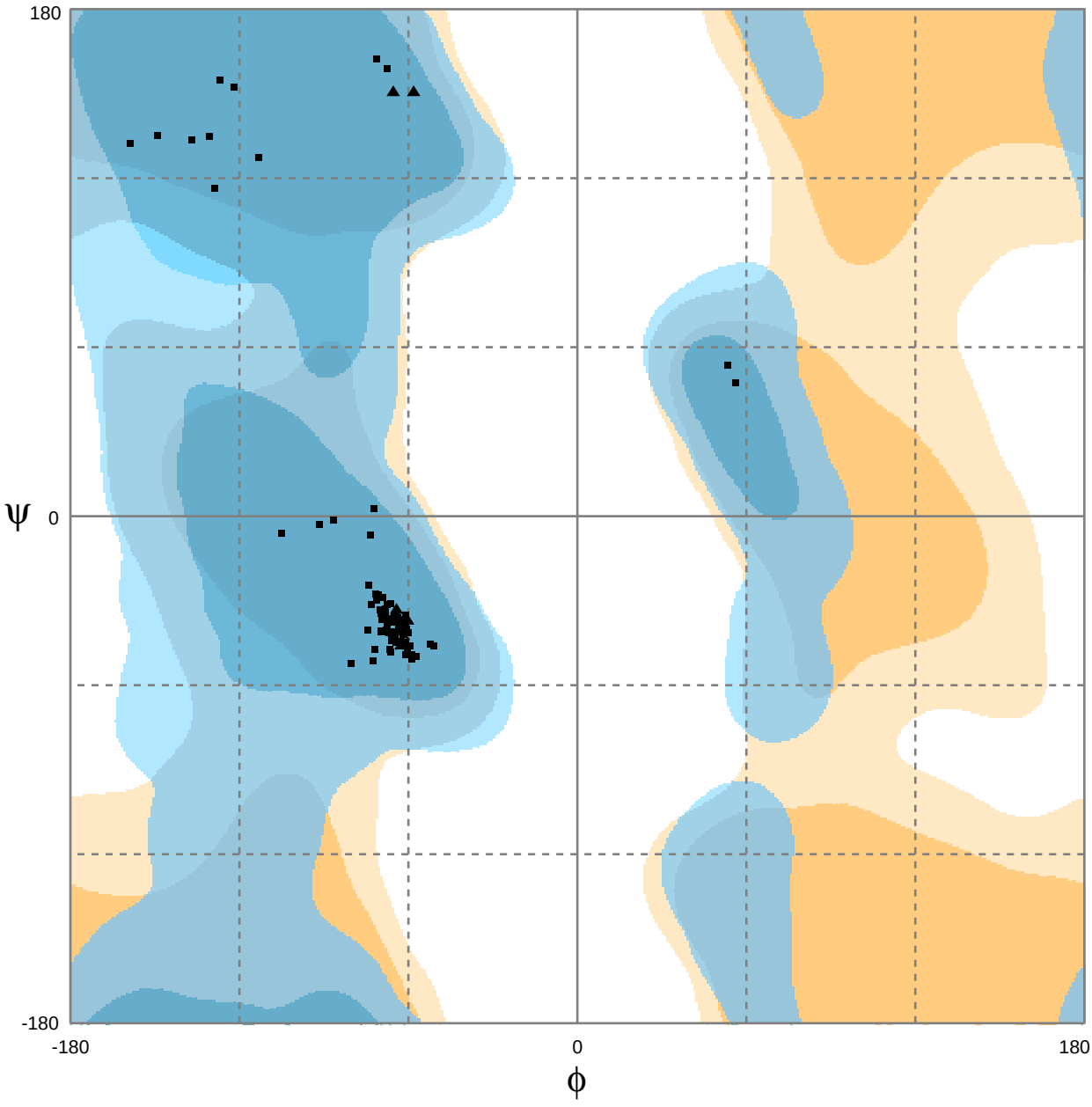
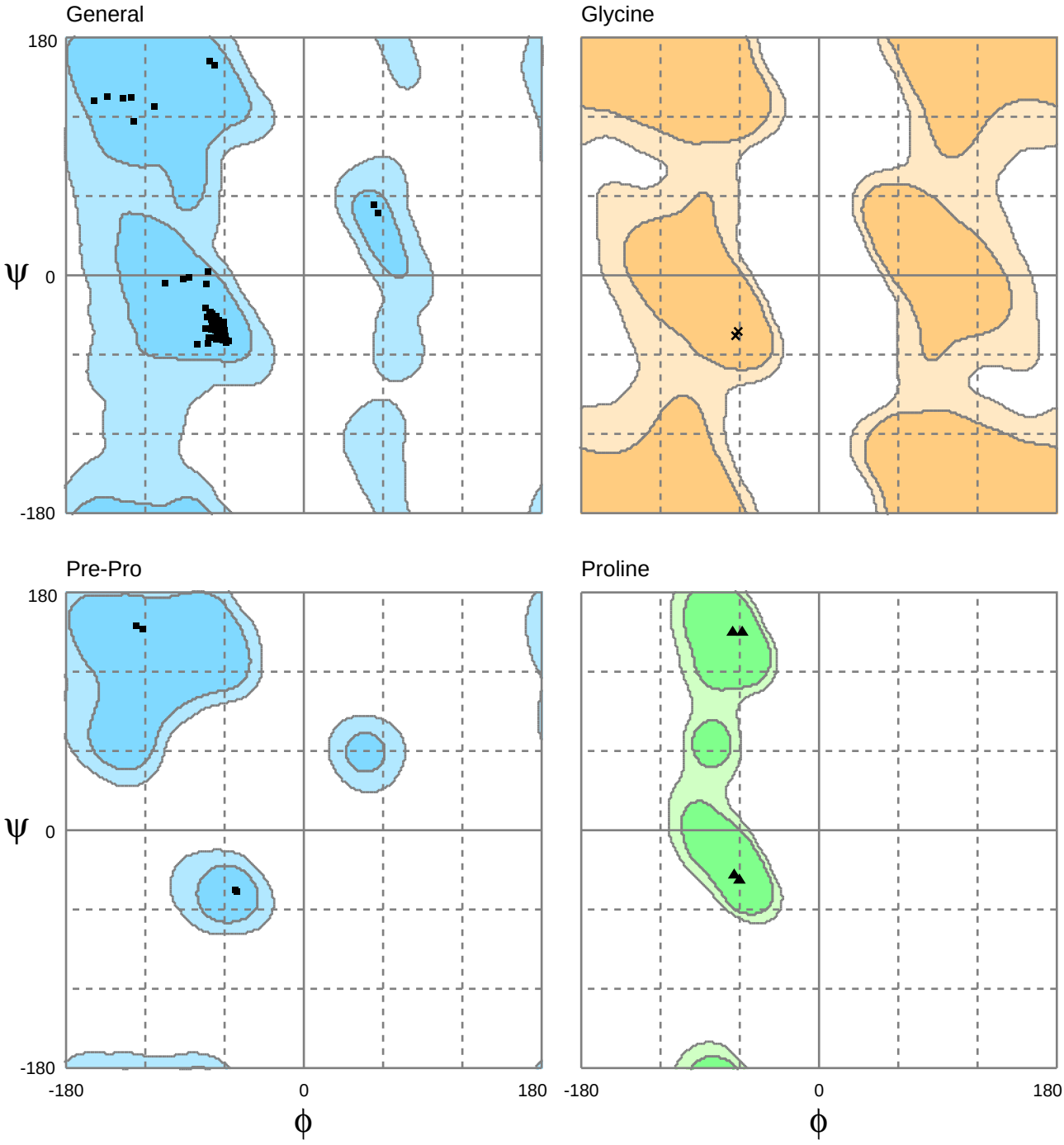


Number of residues in favoured region (~98.0% expected)	:	96 (100.0%)
Number of residues in allowed region (~2.0% expected)	:	0 (0.0%)
Number of residues in outlier region	:	0 (0.0%)

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 Cα geometry: ϕ/ψ and Cβ deviation. *Proteins: Structure, Function & Genetics.* **50**: 437-450



Number of residues in favoured region (~98.0% expected)	: 96 (100.0%)
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