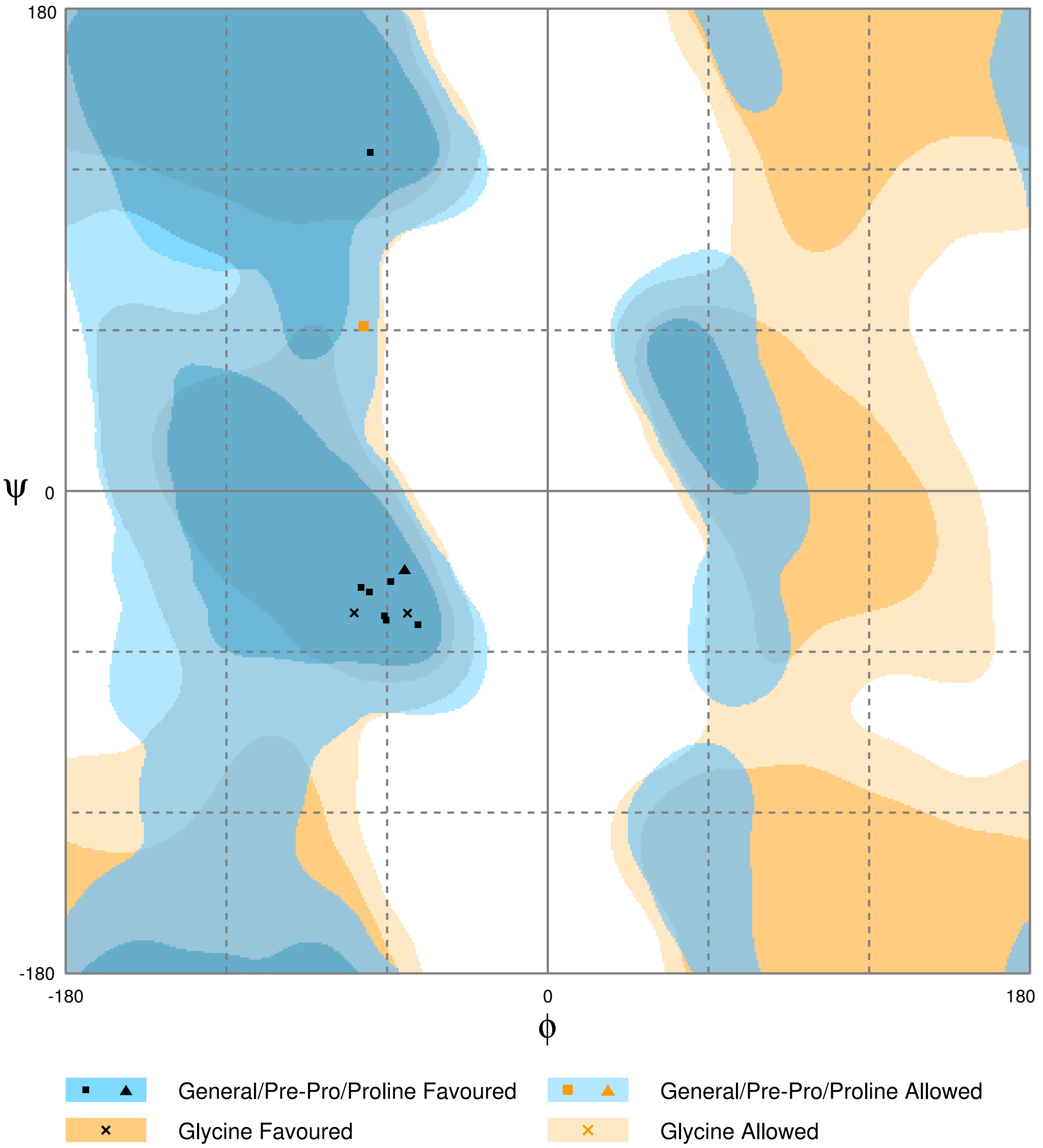
Tem_1ara

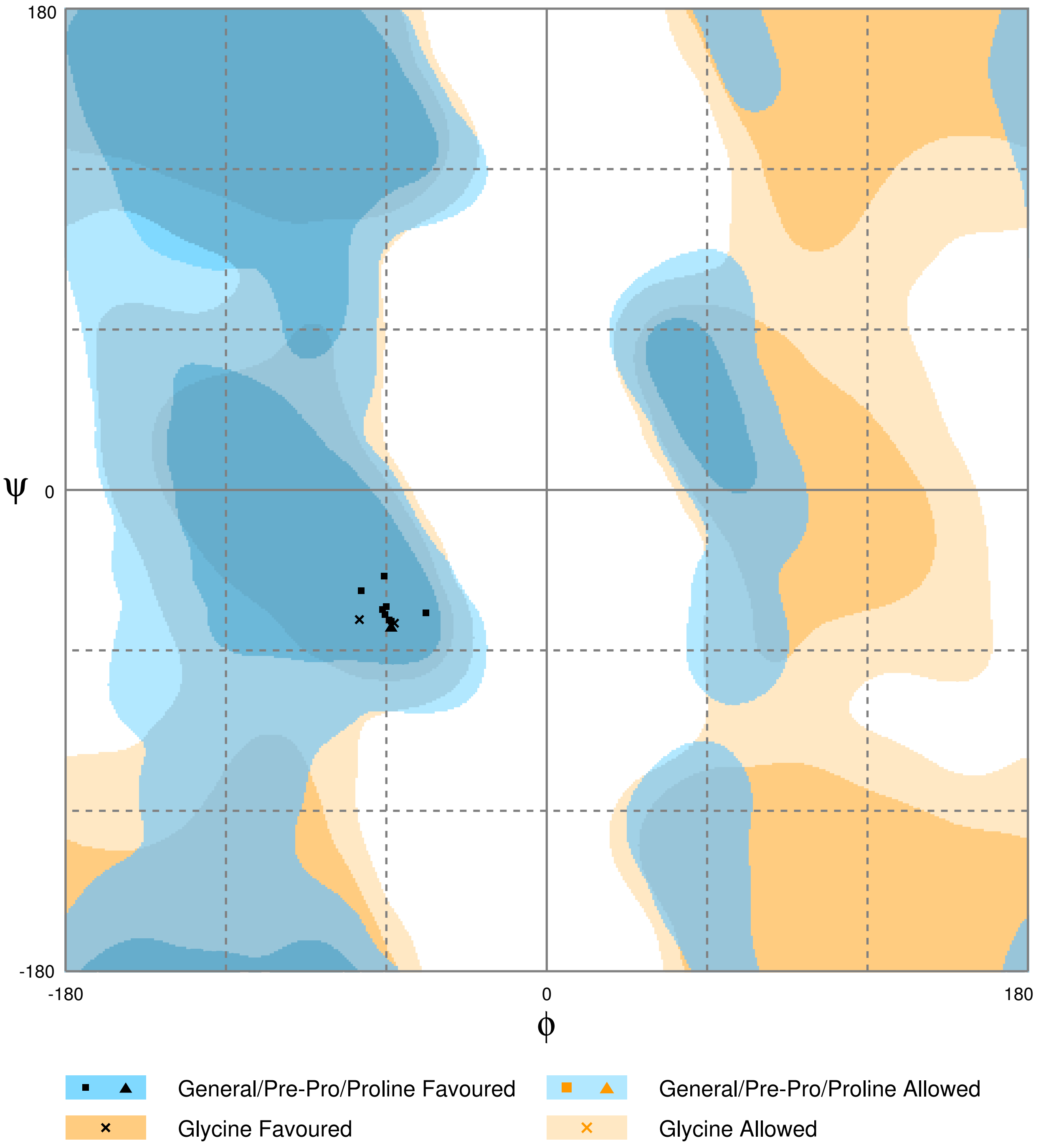


Number of residues in favoured region (~98.0% expected) : 10 (90.9%)
Number of residues in allowed region (~2.0% expected) : 1 (9.1%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1aua

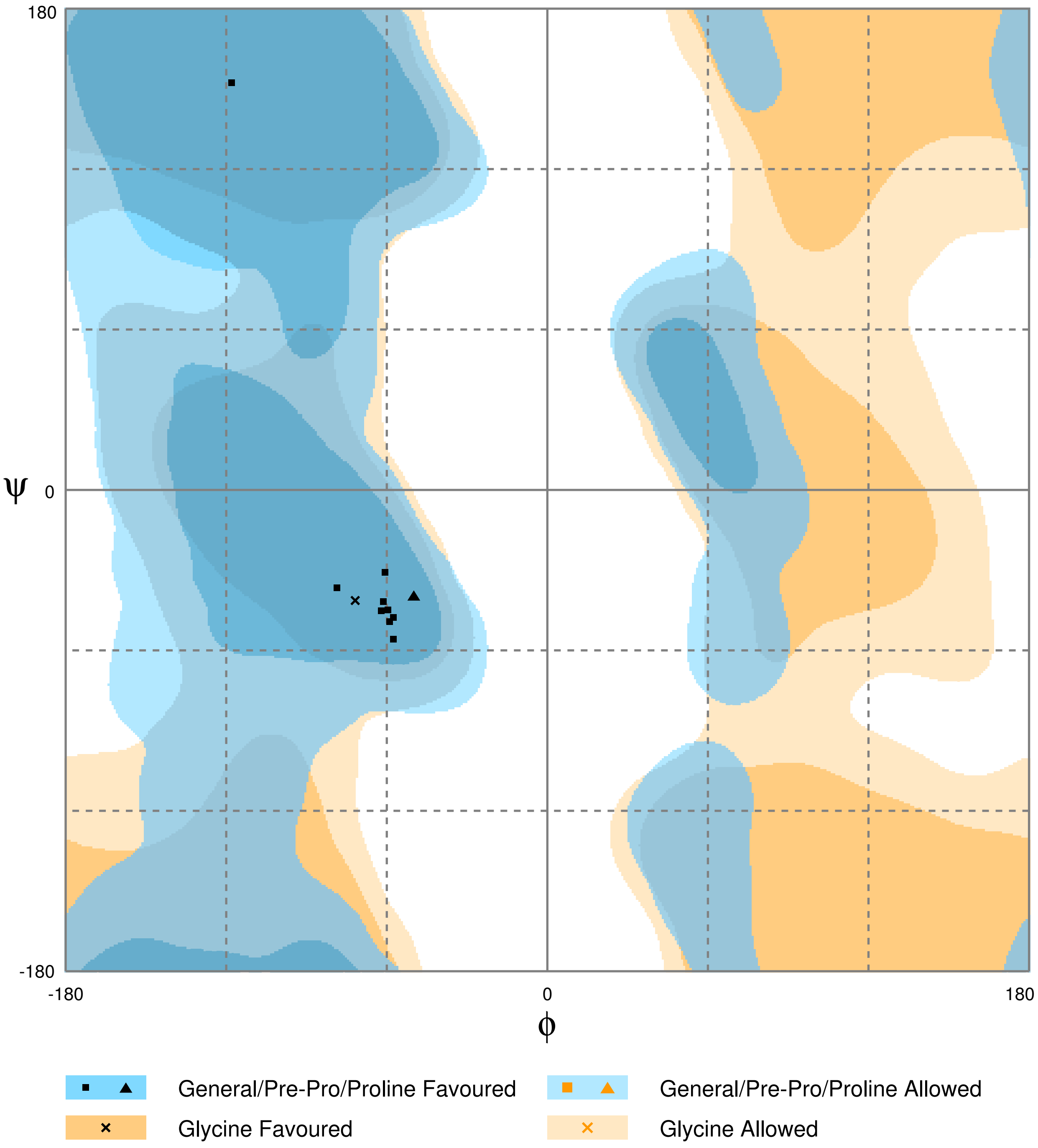


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1bya

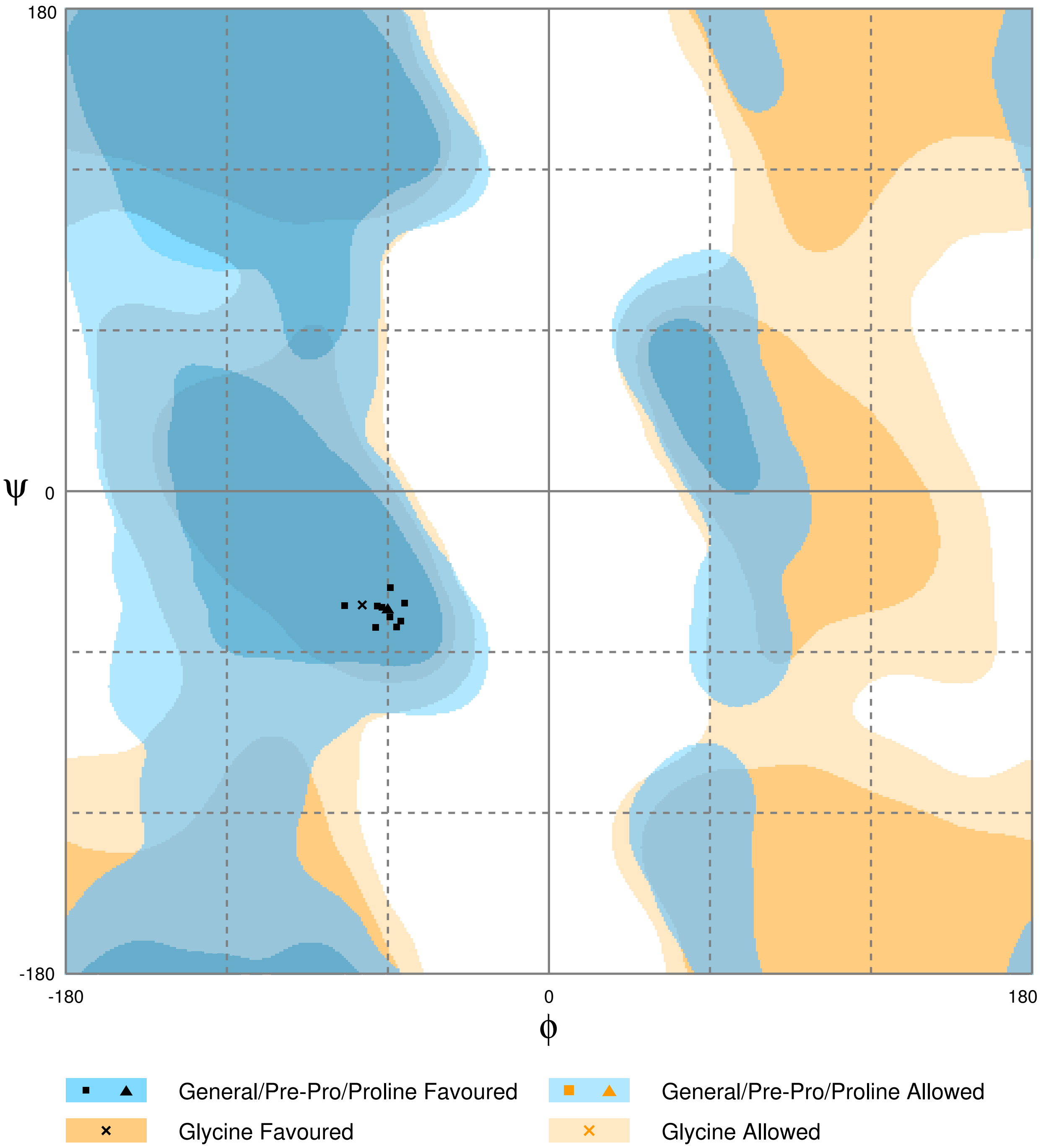


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ca

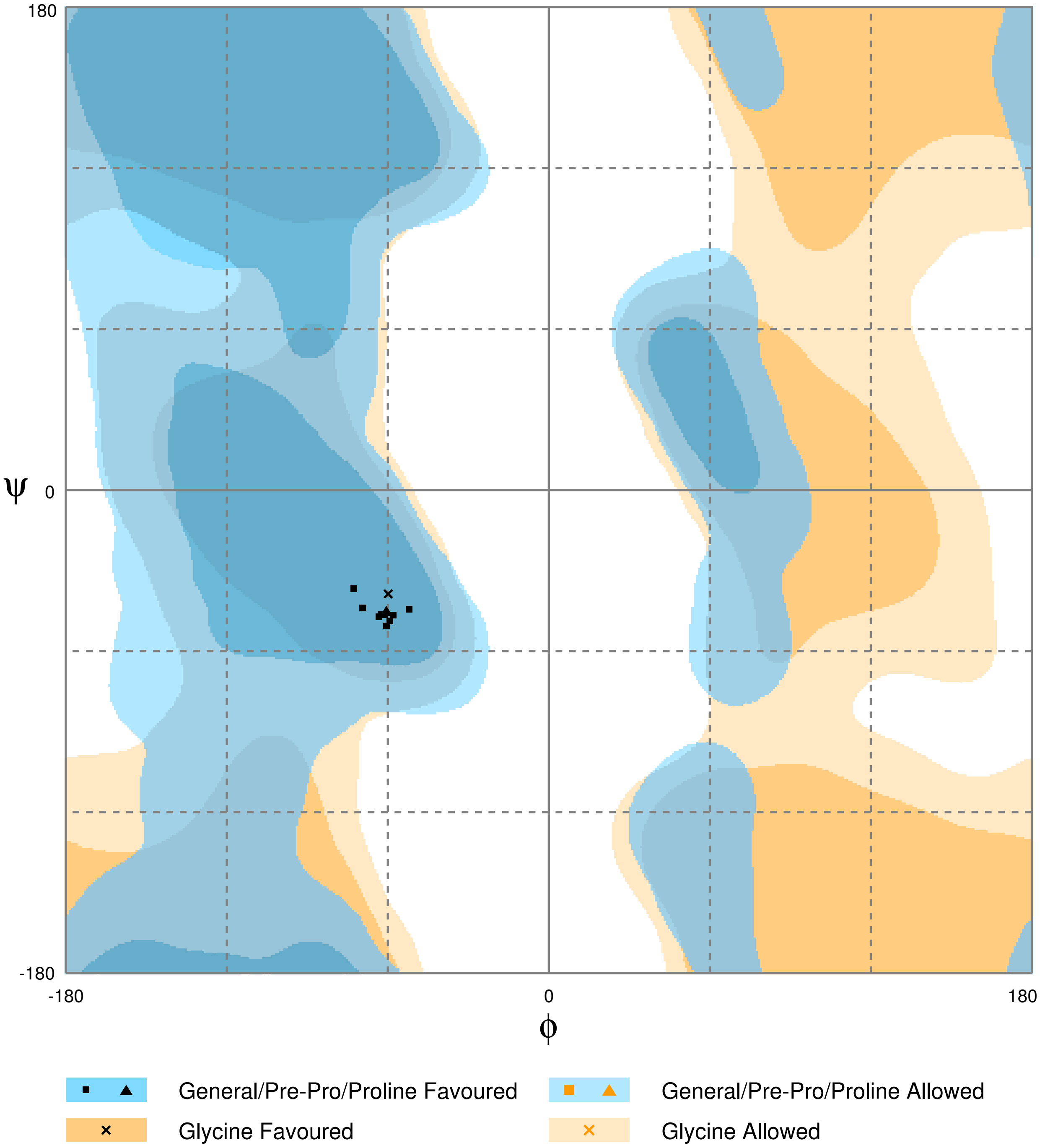


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1cb

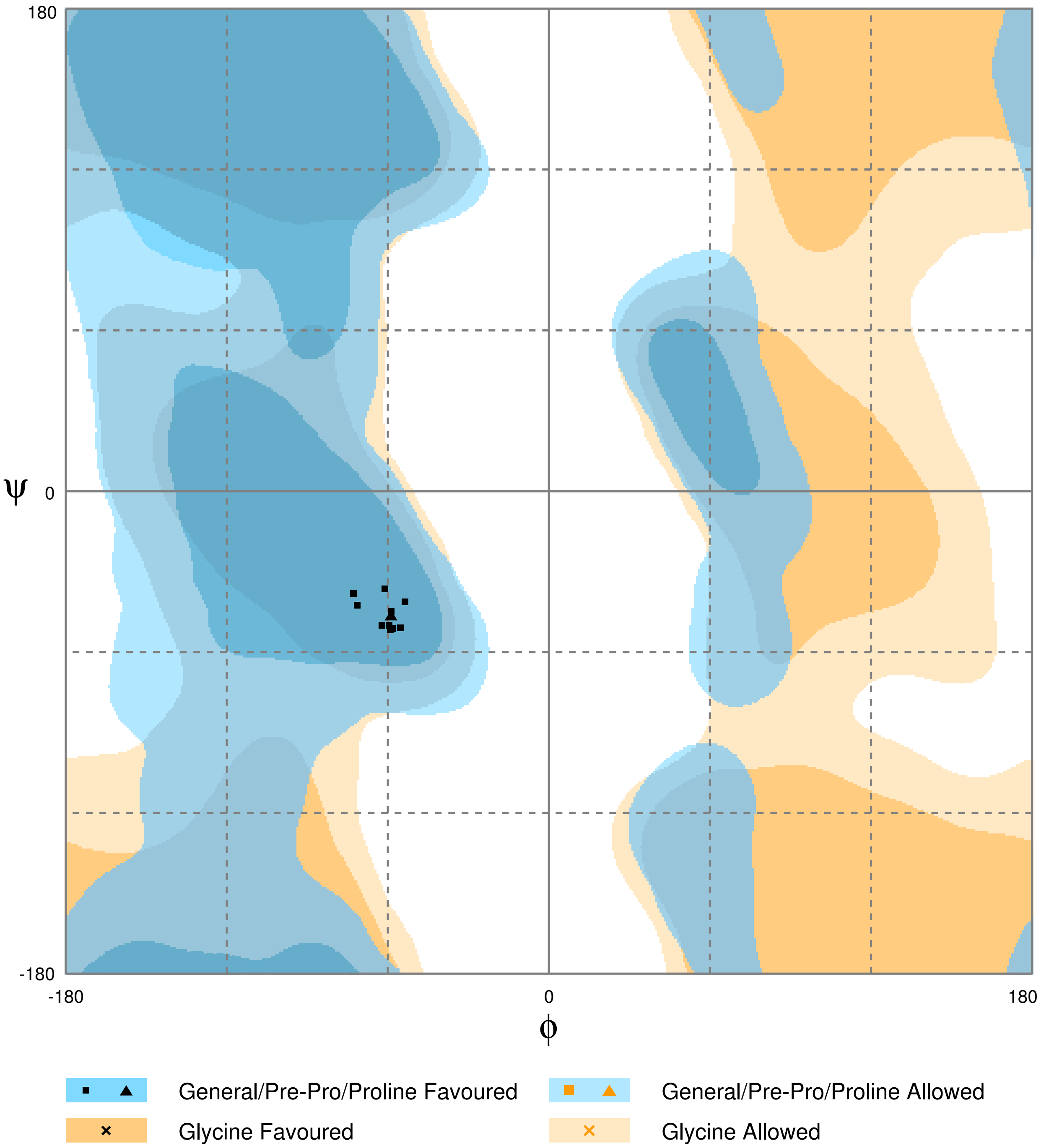


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1cc

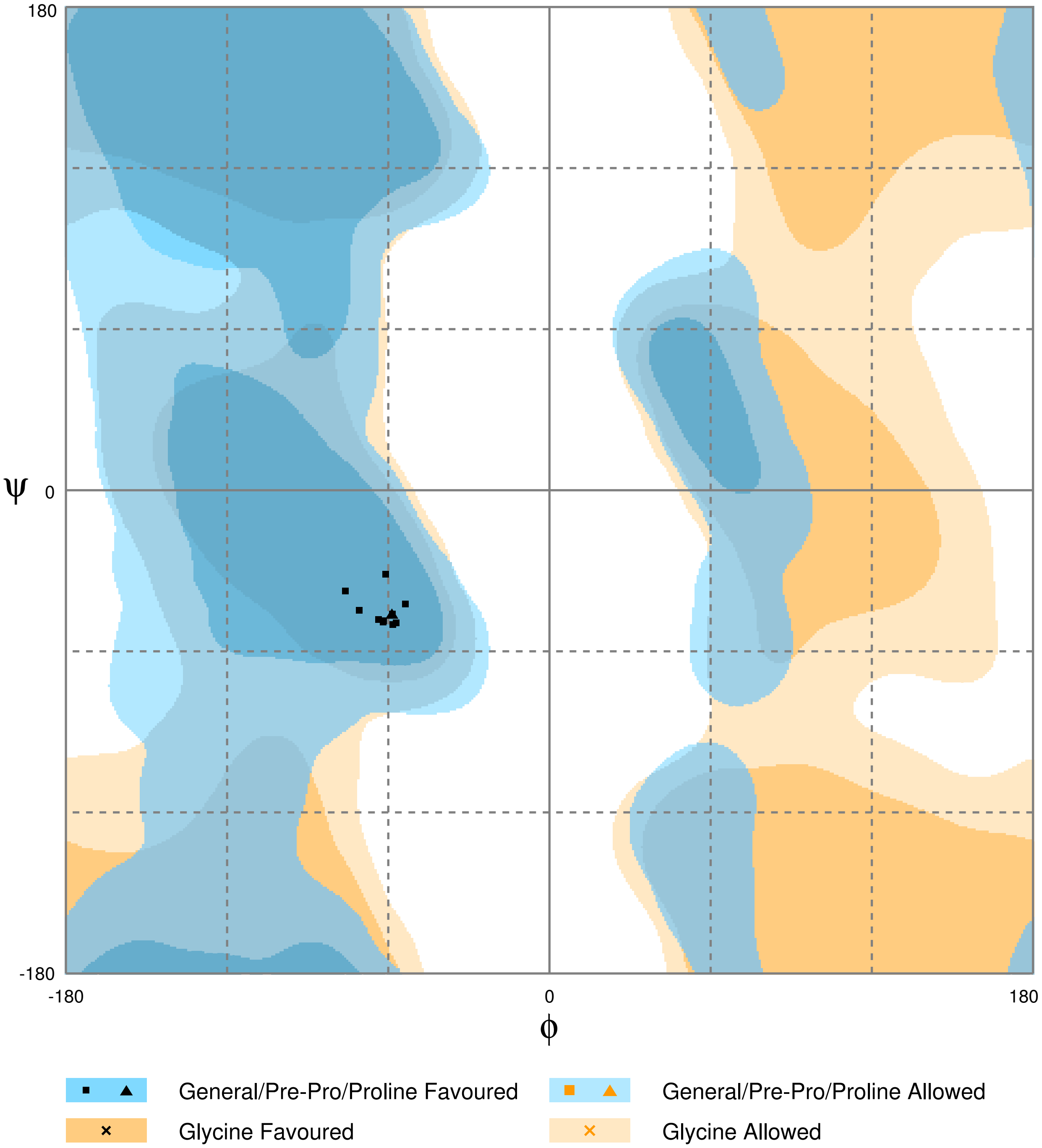


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1cd

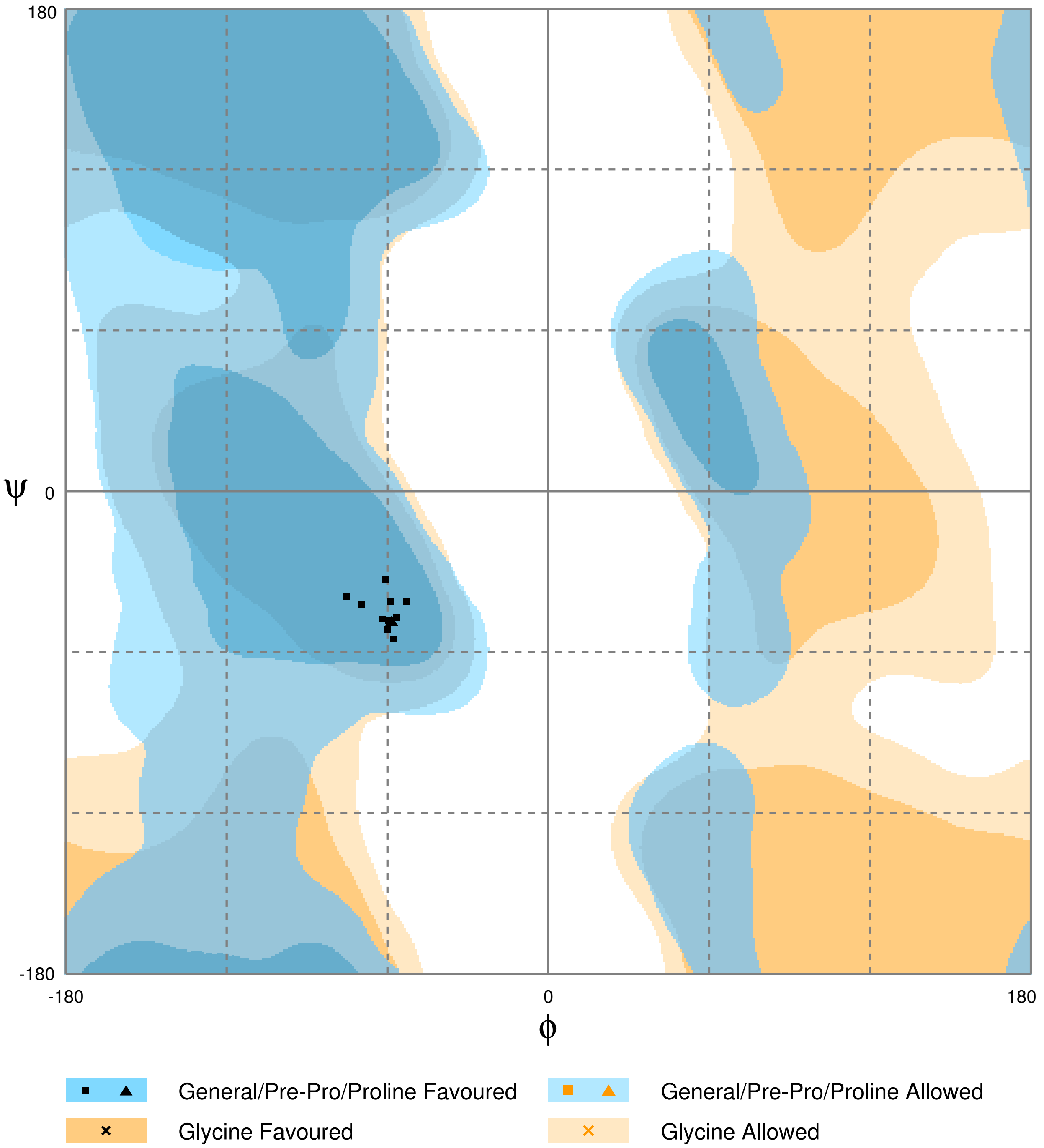


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ce

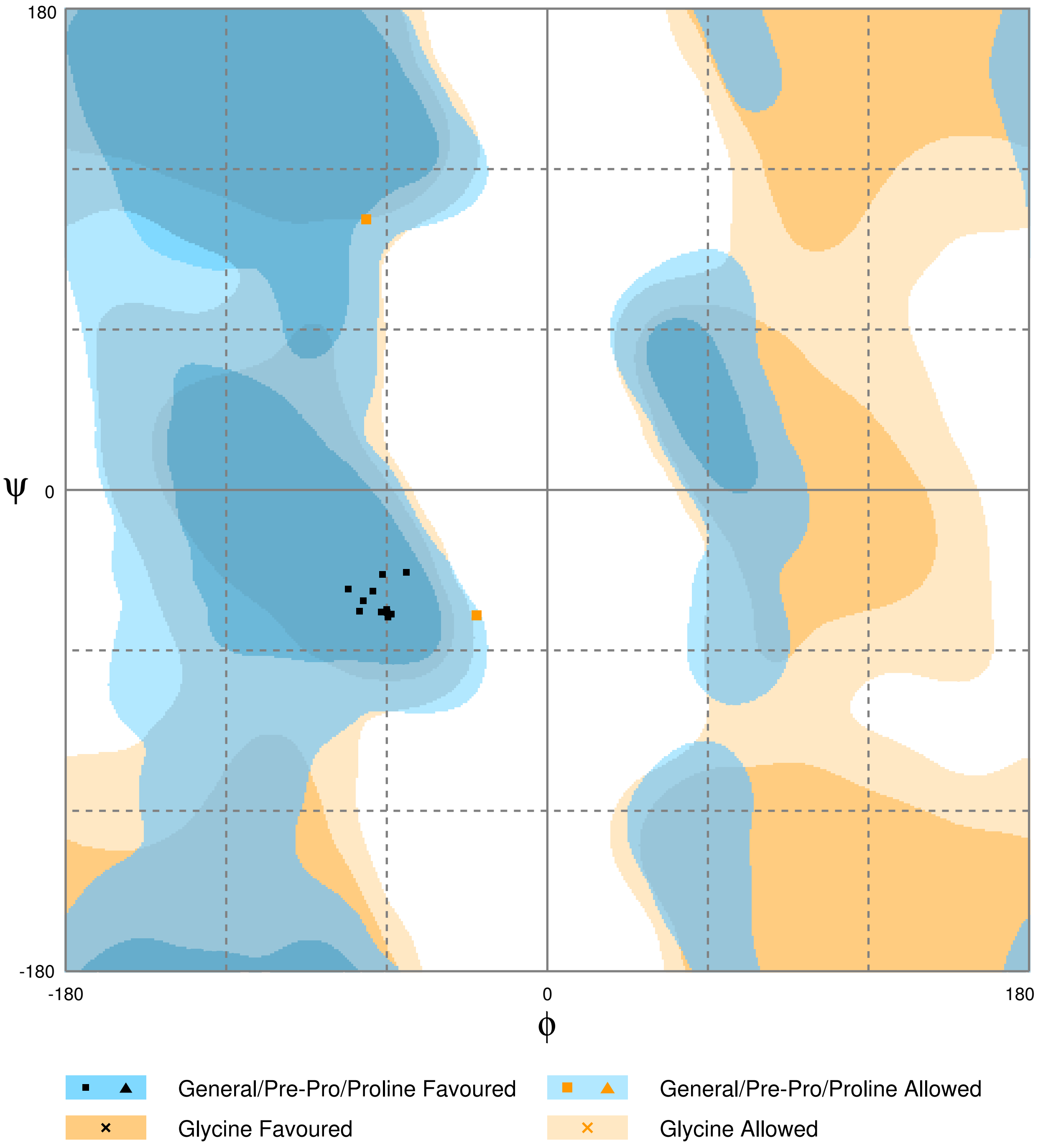


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1cea

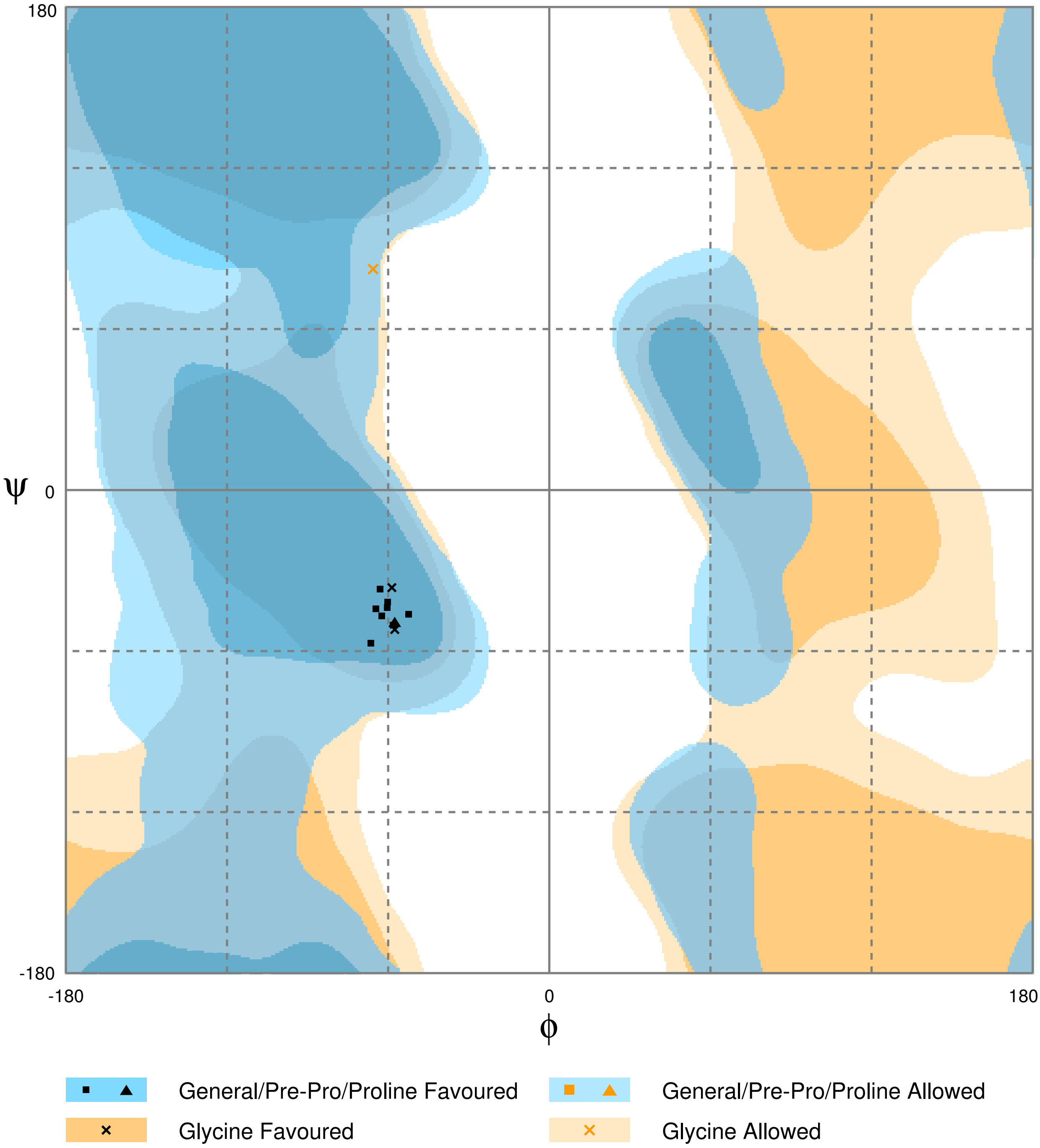


Number of residues in favoured region (~98.0% expected) : 11 (84.6%)
Number of residues in allowed region (~2.0% expected) : 2 (15.4%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ceb

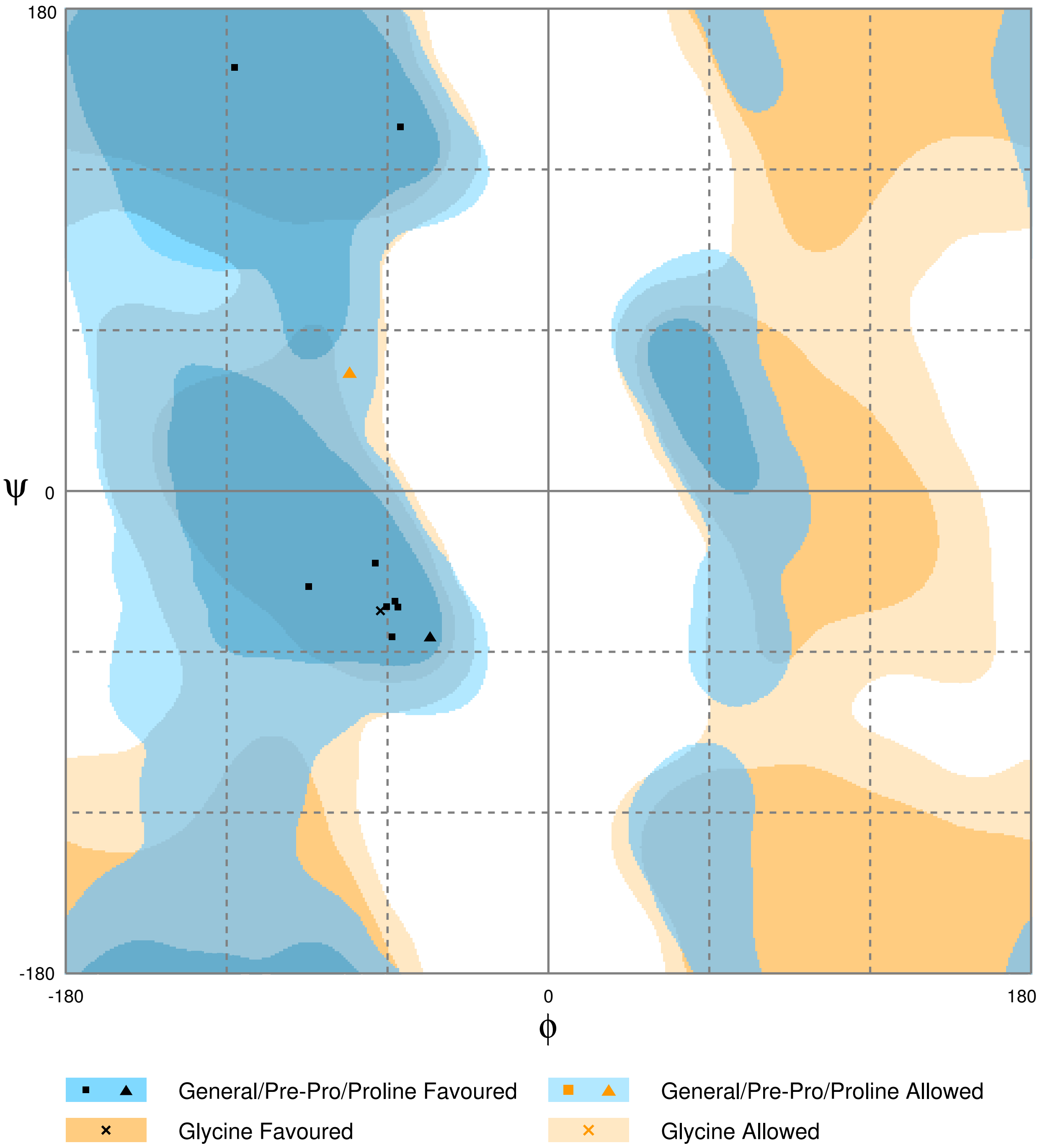


Number of residues in favoured region (~98.0% expected) : 11 (91.7%)
Number of residues in allowed region (~2.0% expected) : 1 (8.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1cec

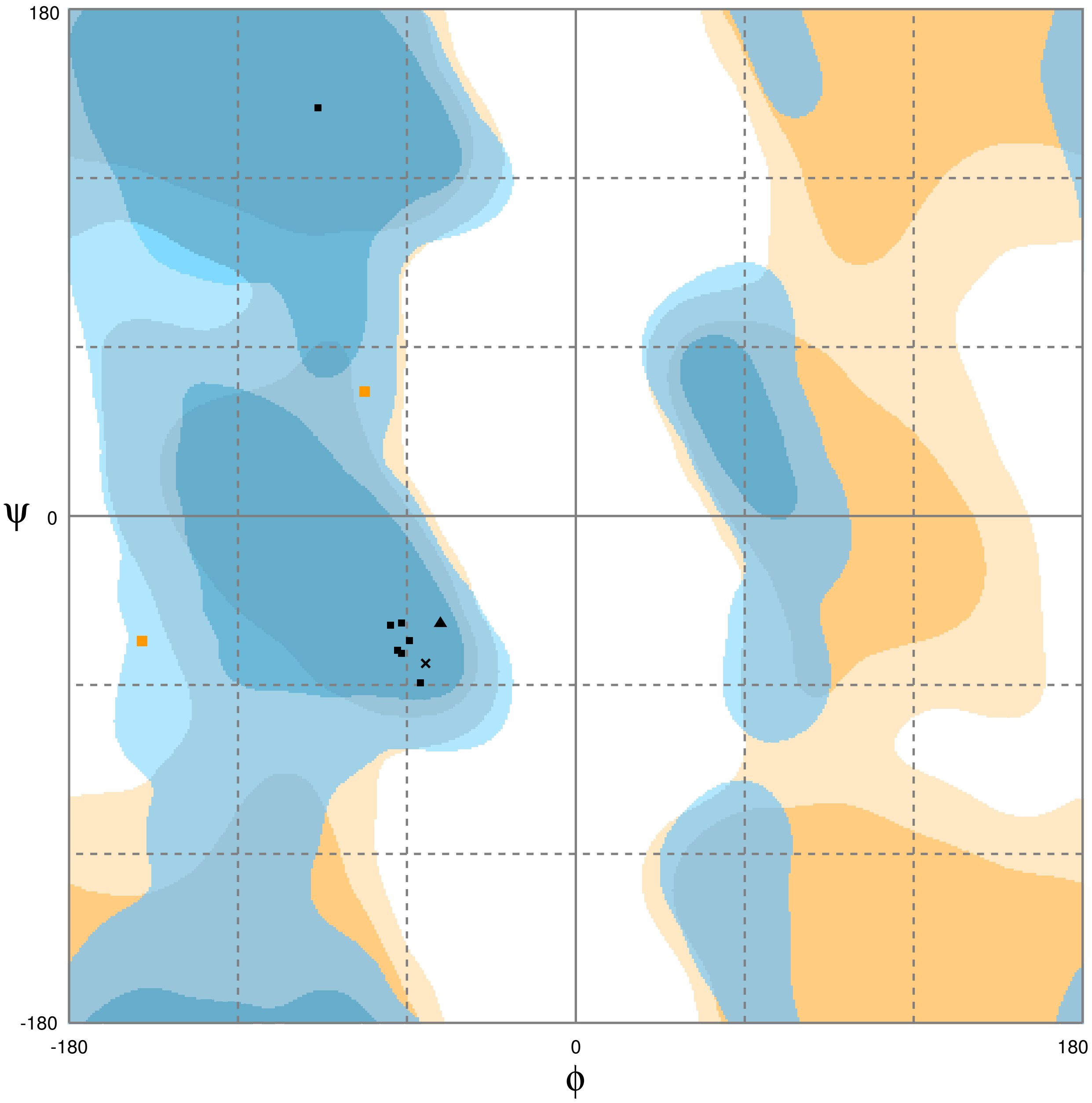


Number of residues in favoured region (~98.0% expected) : 10 (90.9%)
Number of residues in allowed region (~2.0% expected) : 1 (9.1%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1cee



■ ▲ General/Pre-Pro/Proline Favoured

■ ▲ General/Pre-Pro/Proline Allowed

× Glycine Favoured

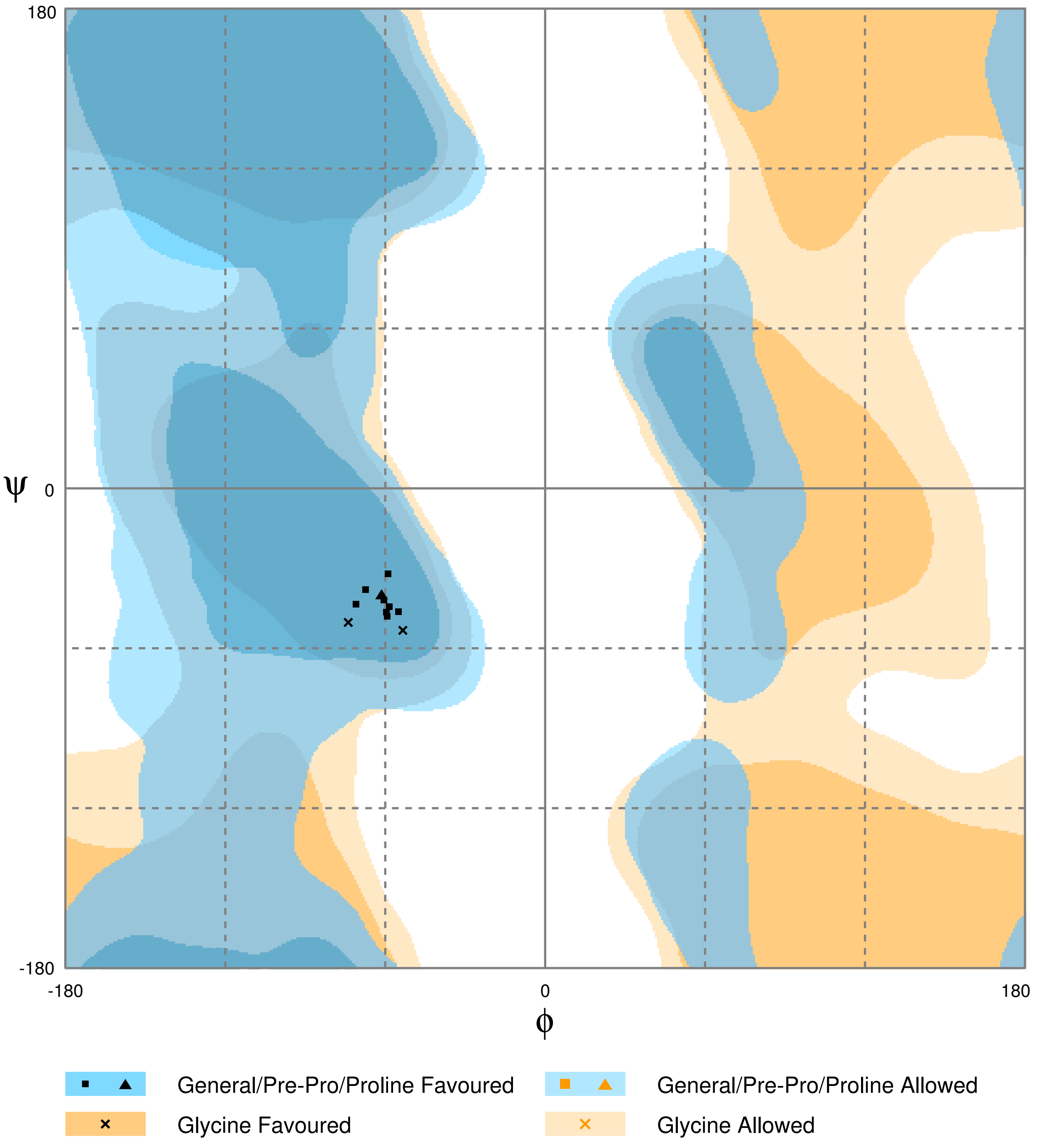
× Glycine Allowed

Number of residues in favoured region (~98.0% expected) : 9 (81.8%)
Number of residues in allowed region (~2.0% expected) : 2 (18.2%)
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

Tem_1csb

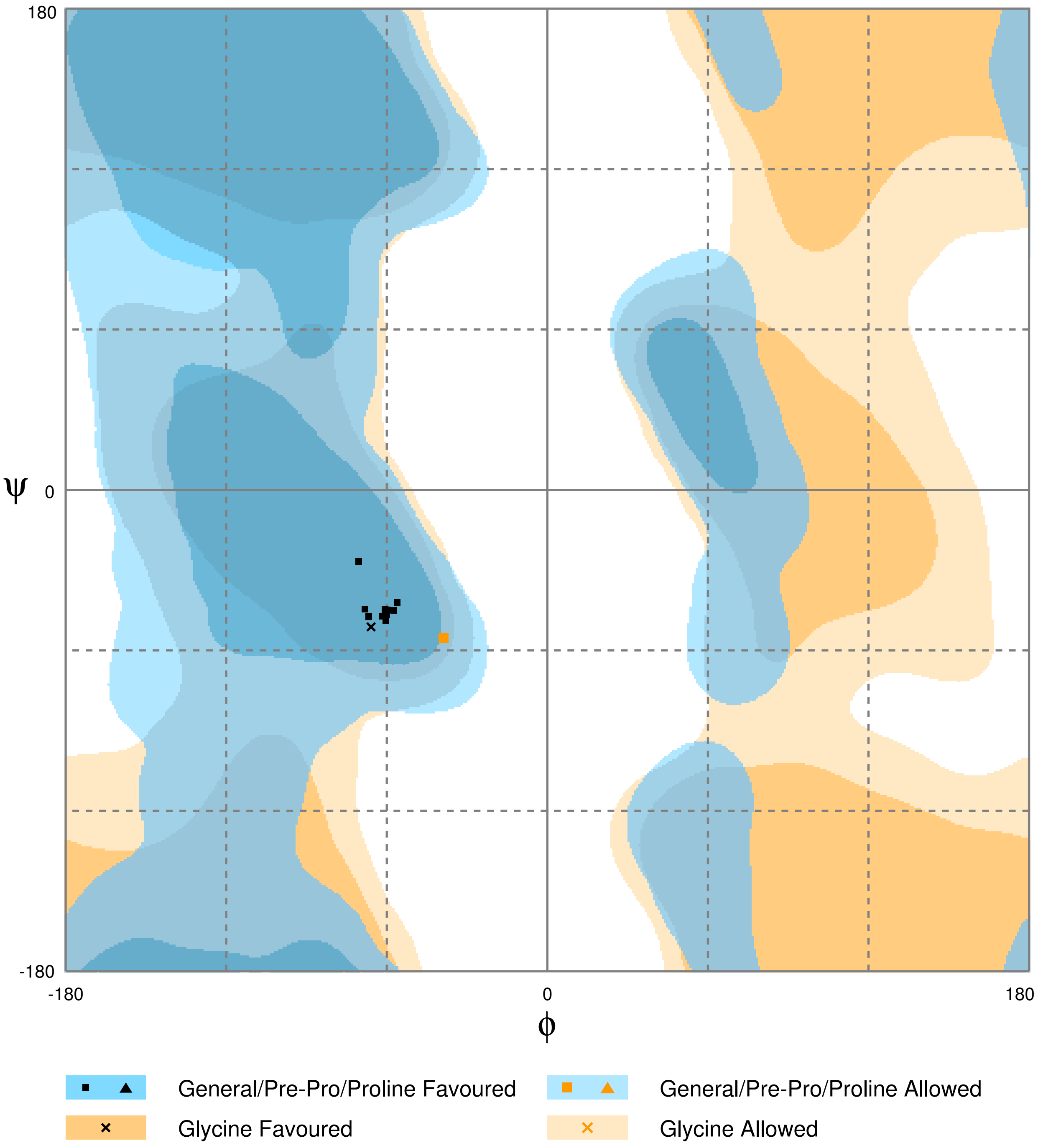


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1csc

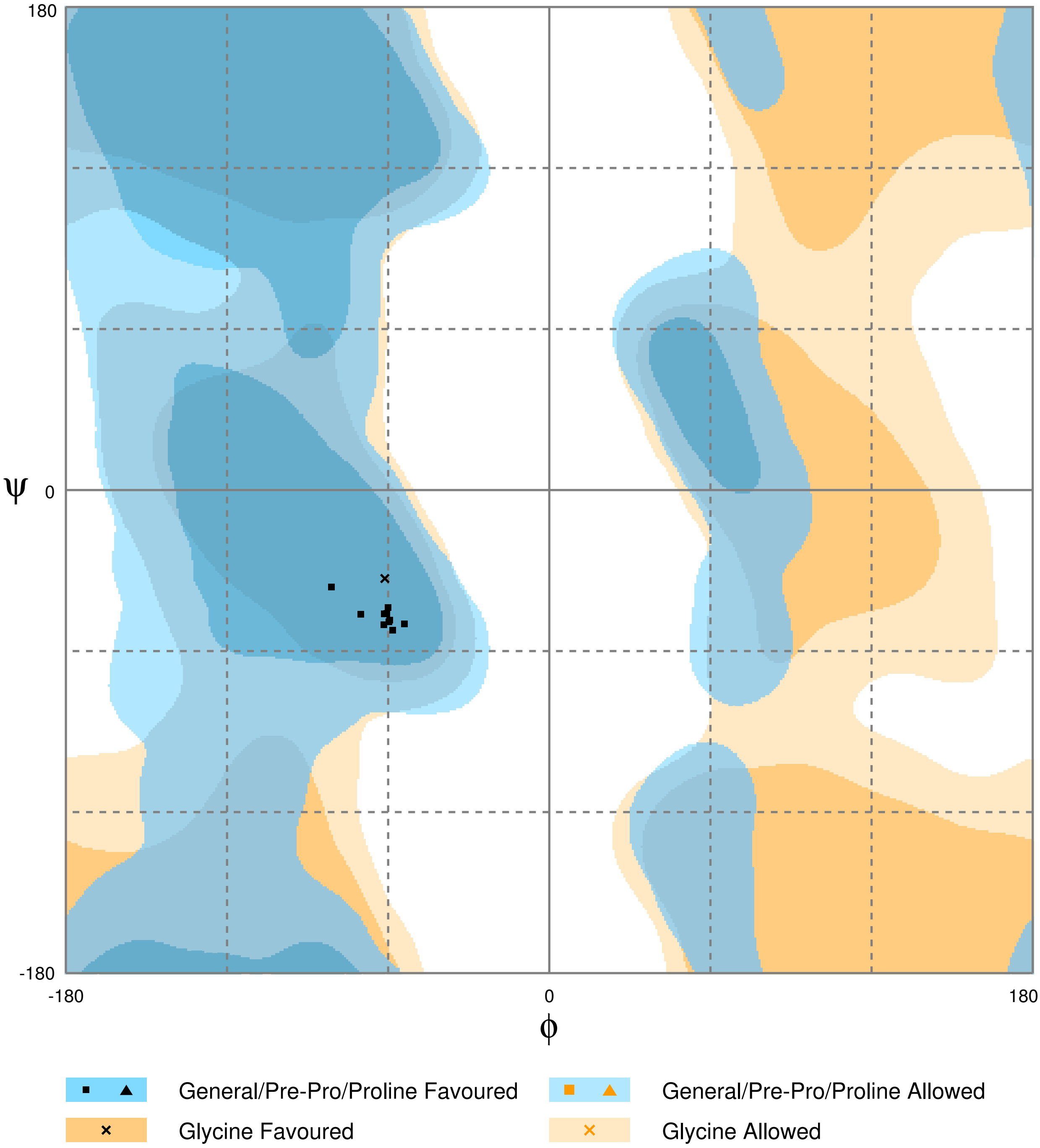


Number of residues in favoured region (~98.0% expected) : 11 (91.7%)
Number of residues in allowed region (~2.0% expected) : 1 (8.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1csd



Number of residues in favoured region (~98.0% expected) : 11 (100.0%)

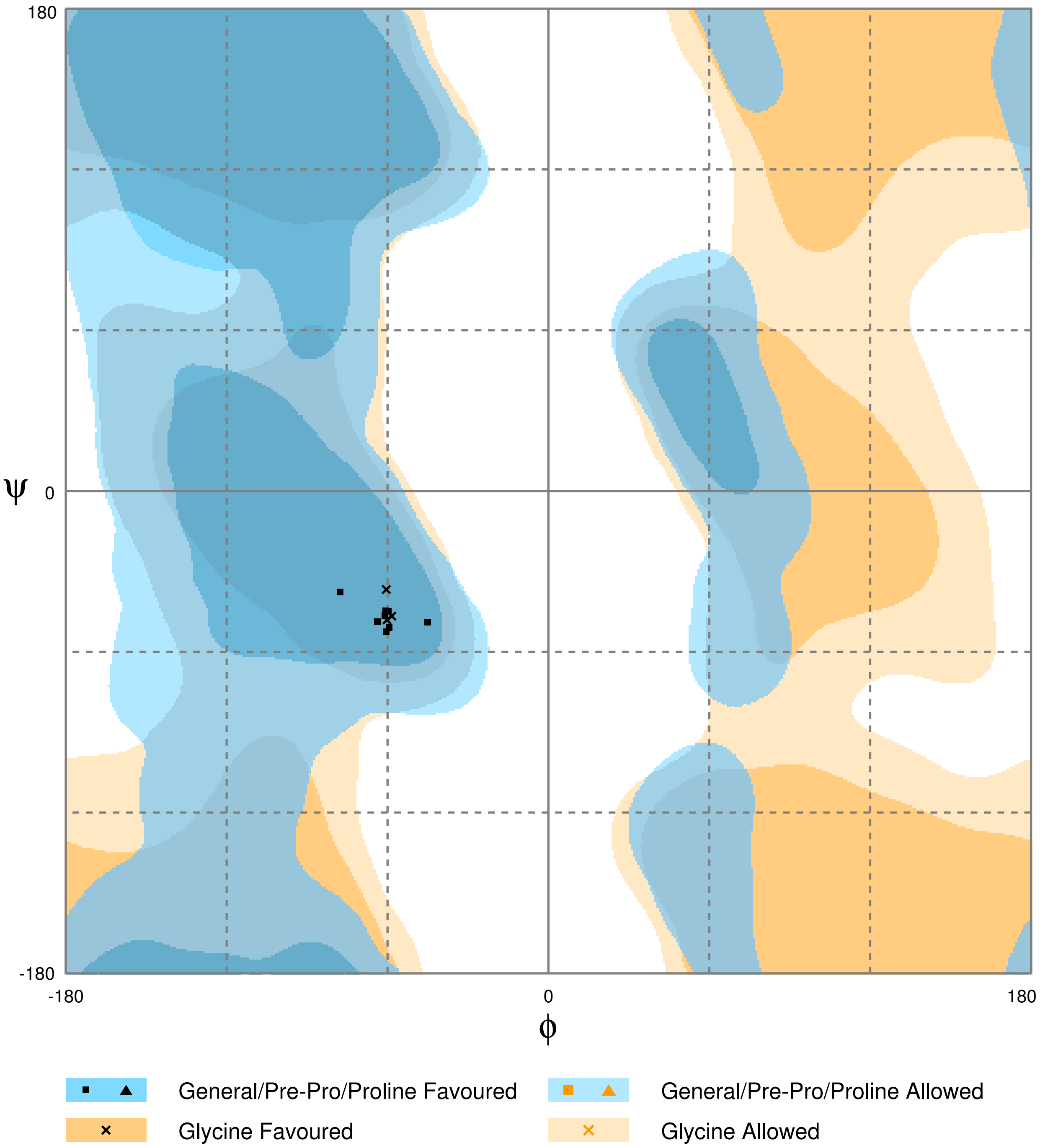
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)

Number of residues in outlier region : 0 (0.0%)

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

Tem_1dra

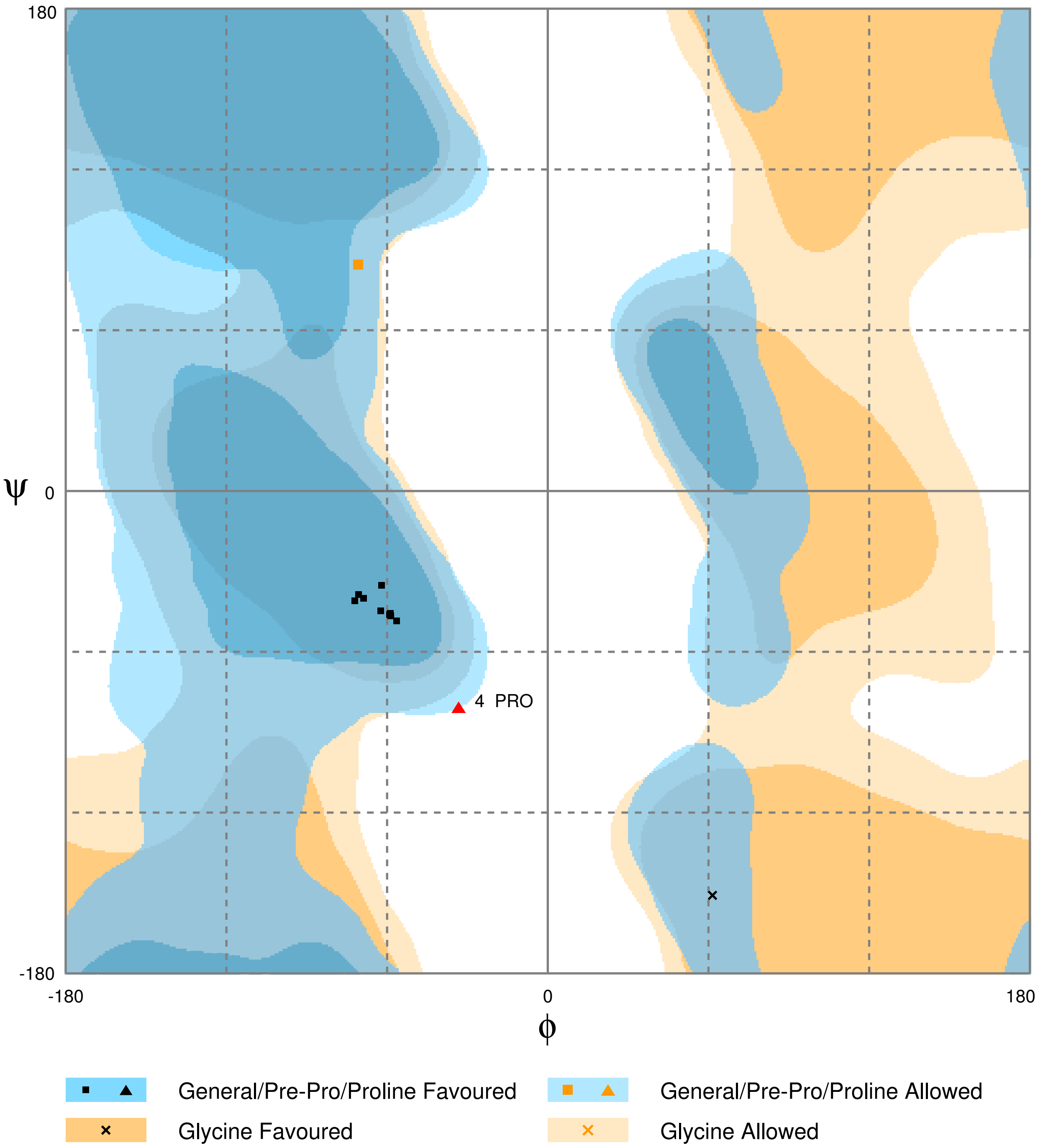


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1dya

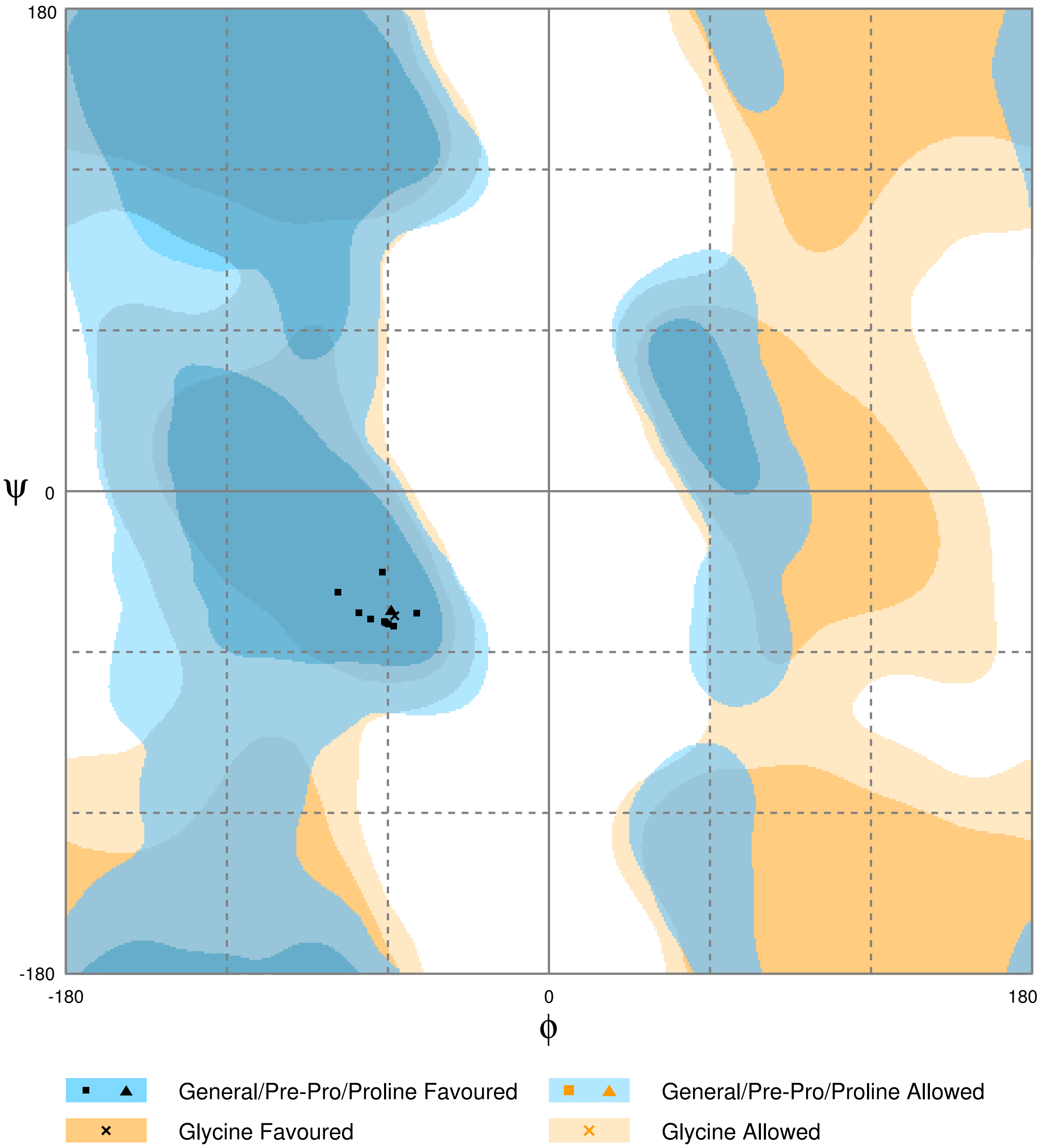


Number of residues in favoured region (~98.0% expected) : 10 (83.3%)
Number of residues in allowed region (~2.0% expected) : 1 (8.3%)
Number of residues in outlier region : 1 (8.3%)

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

Tem_1ec

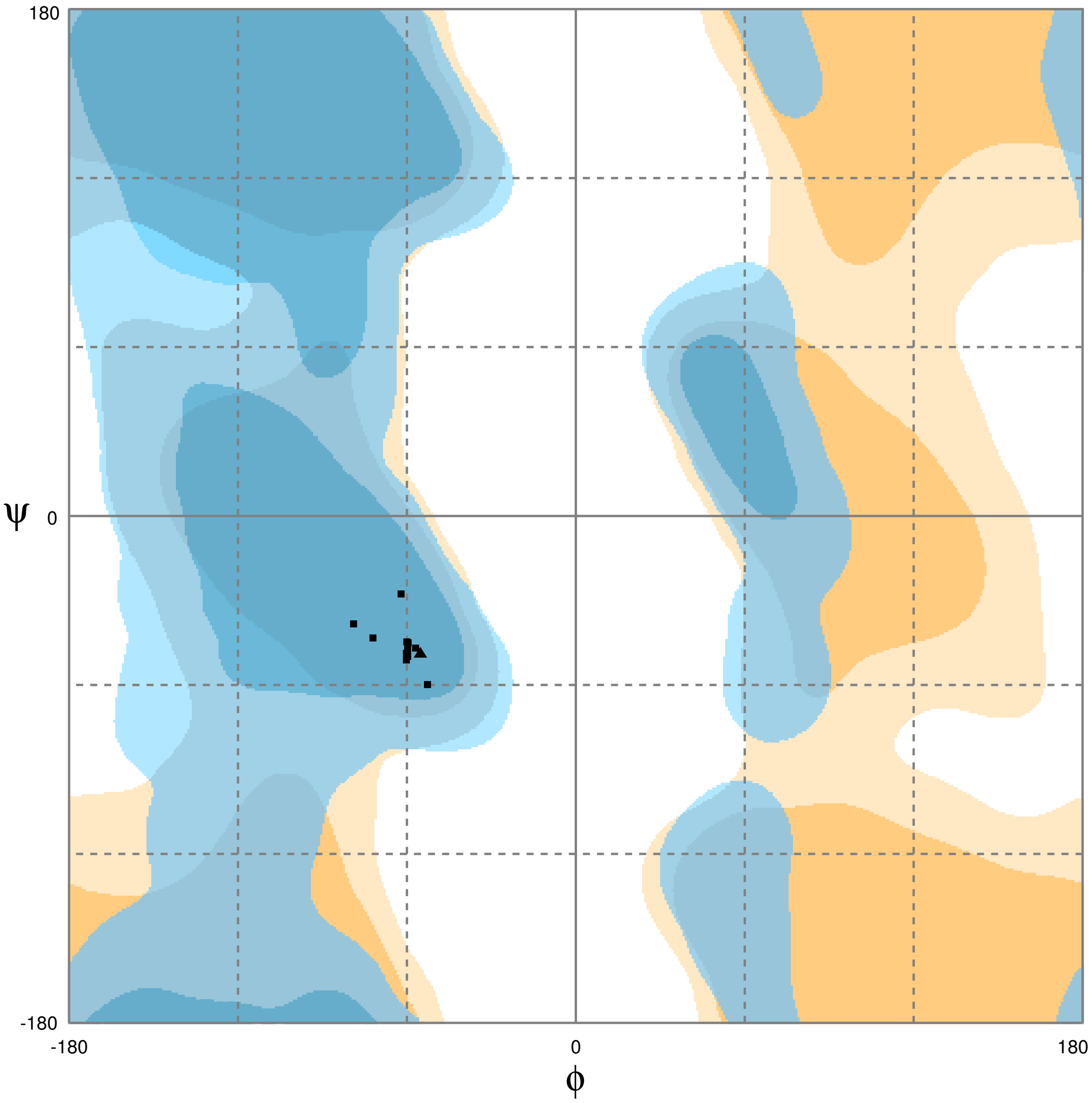


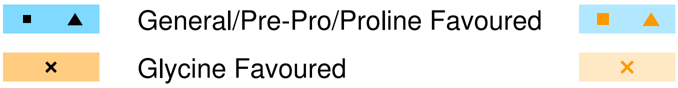
Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ga



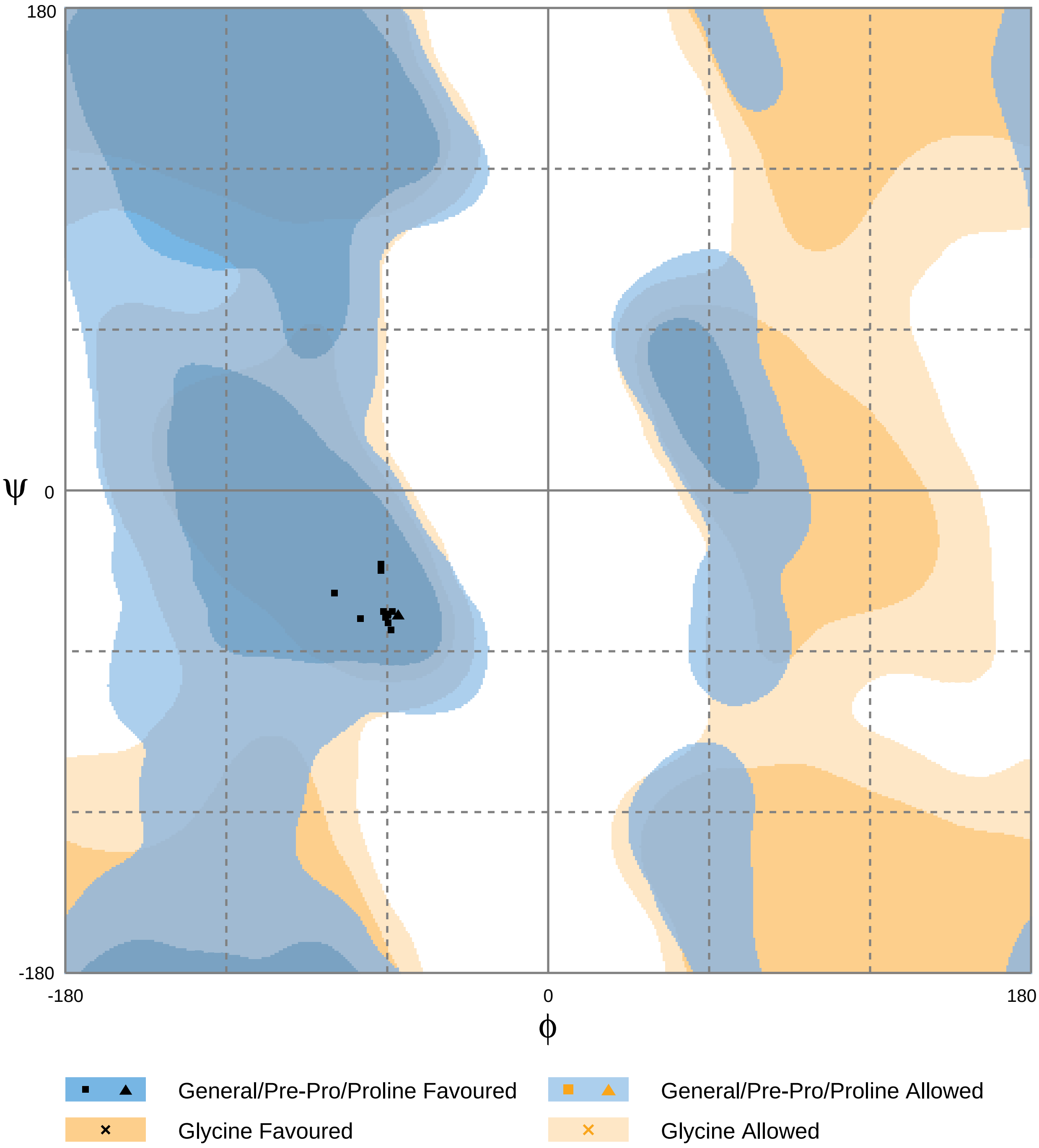


Number of residues in favoured region (~98.0% expected) : 12 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1gb

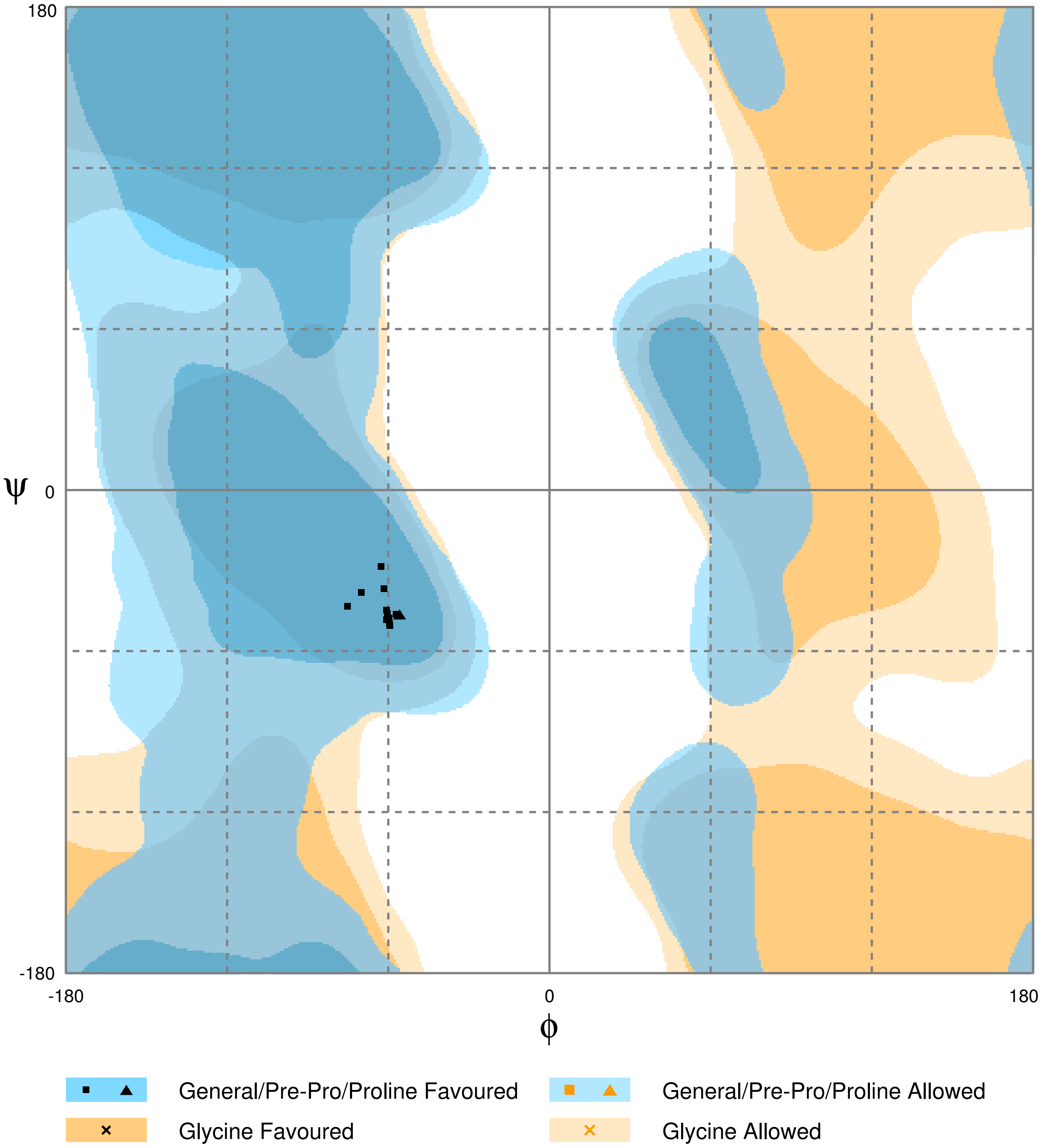


Number of residues in favoured region (~98.0% expected) : 12 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1gc

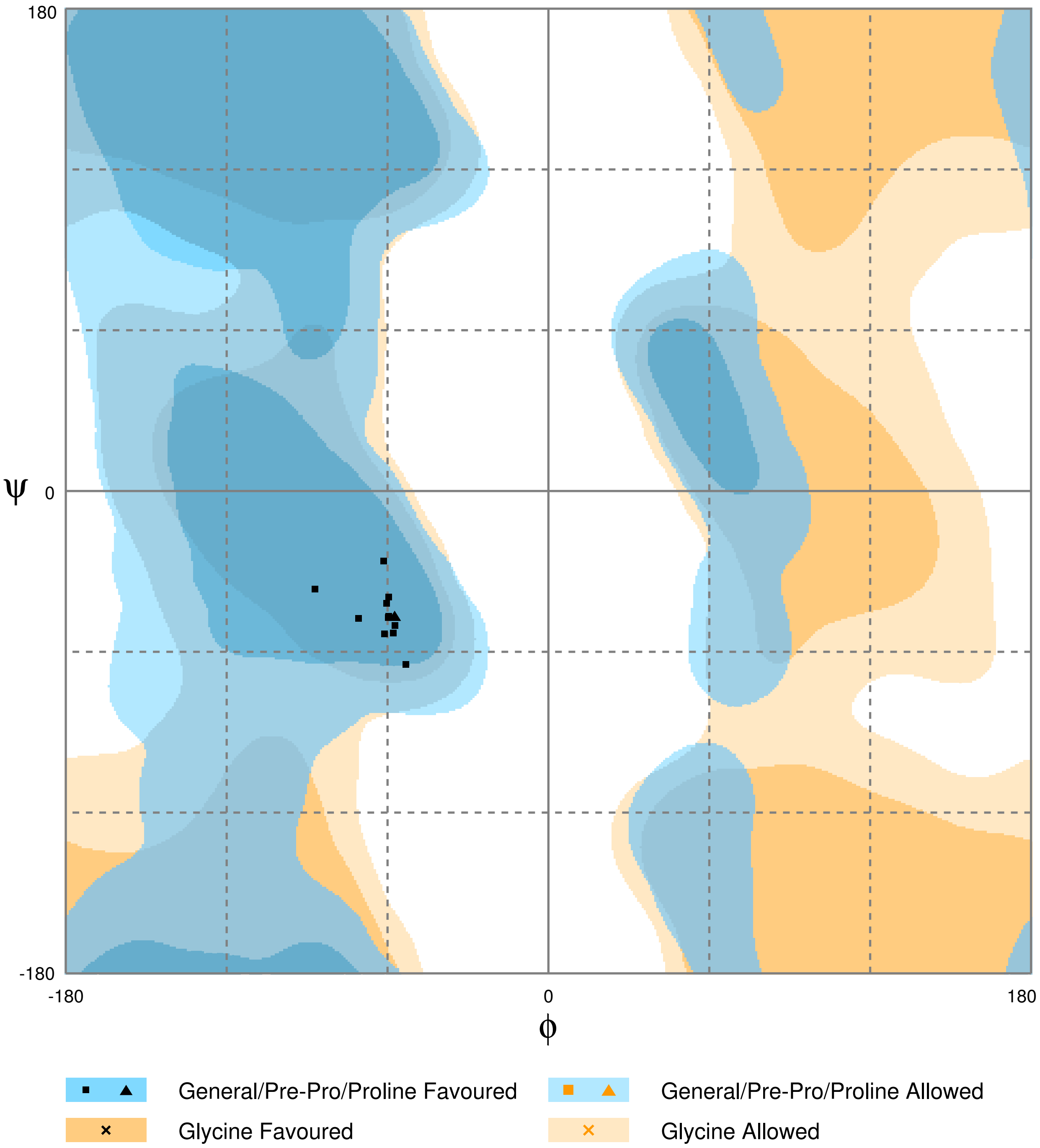


Number of residues in favoured region (~98.0% expected) : 12 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1gd

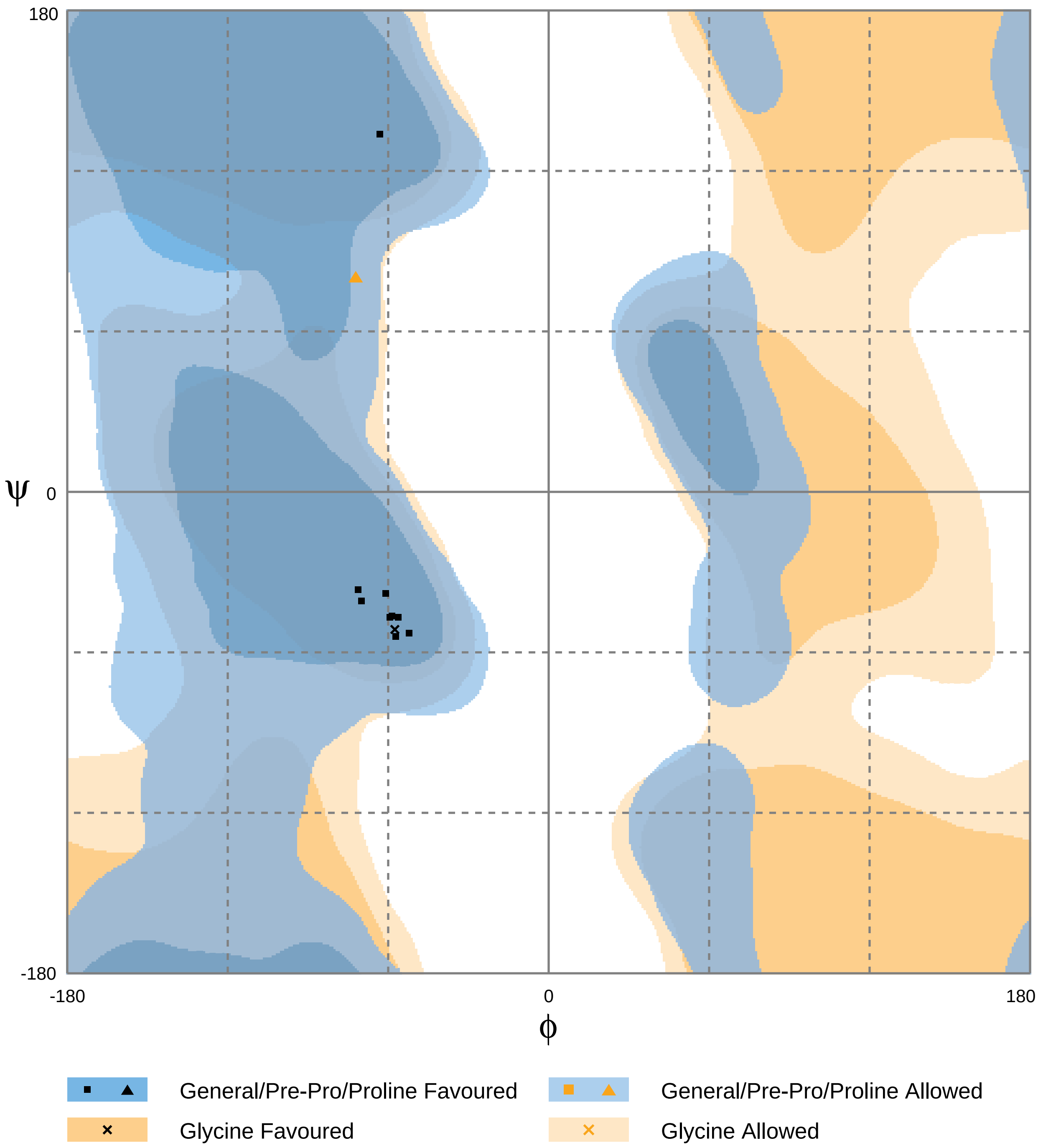


Number of residues in favoured region (~98.0% expected) : 12 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1gy

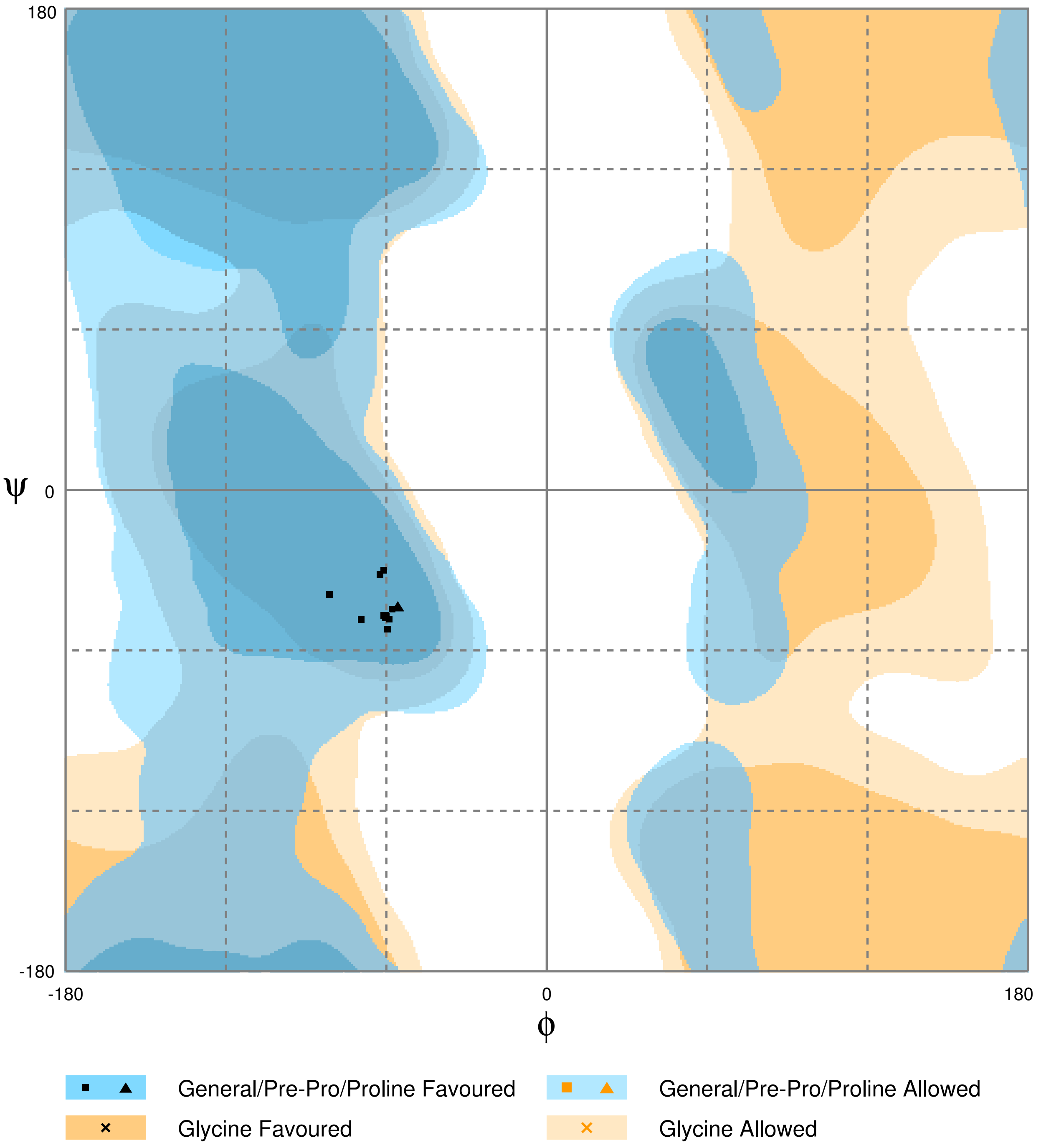


Number of residues in favoured region (~98.0% expected) : 10 (90.9%)
Number of residues in allowed region (~2.0% expected) : 1 (9.1%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1hka

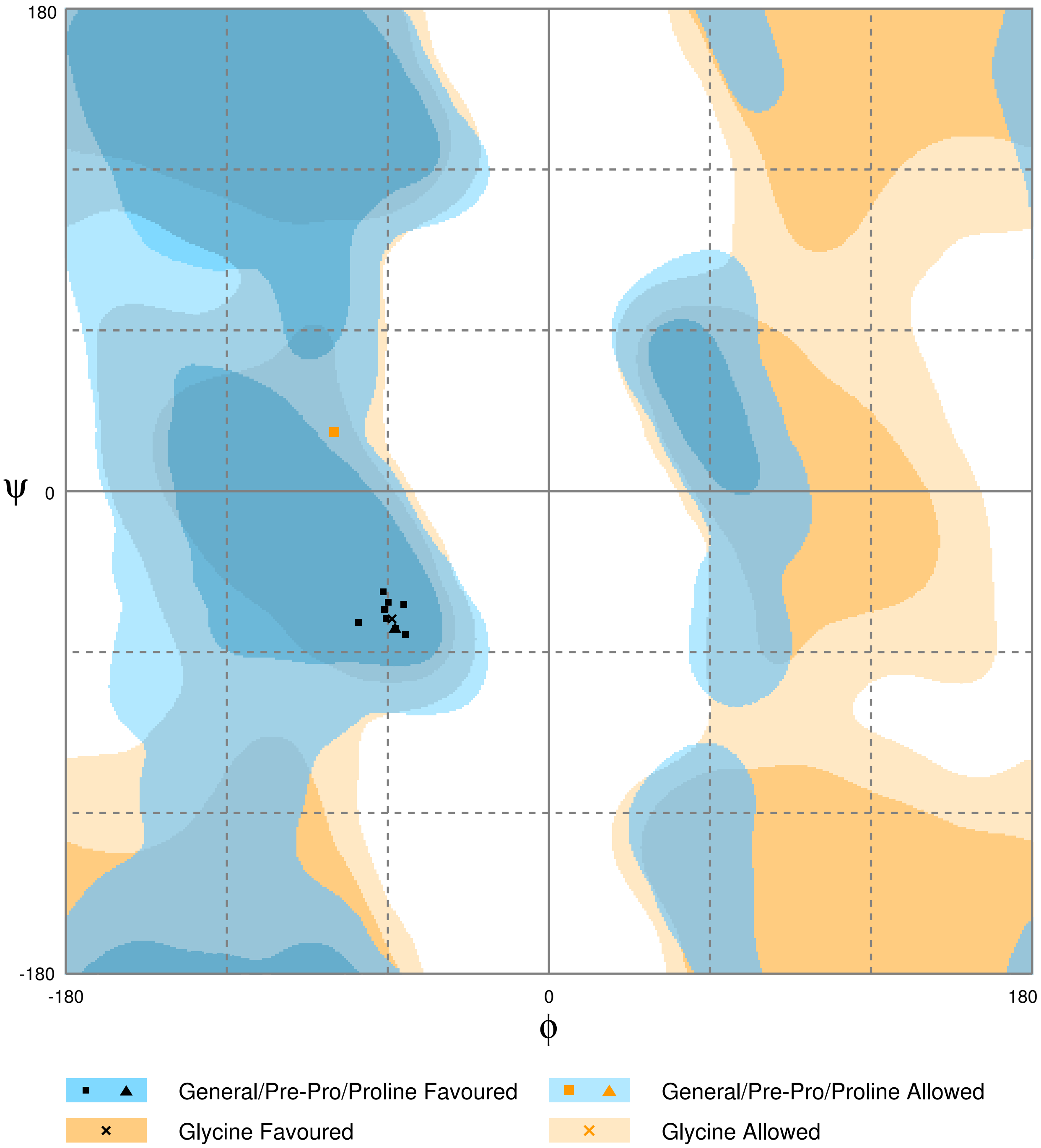


Number of residues in favoured region (~98.0% expected) : 12 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1aua

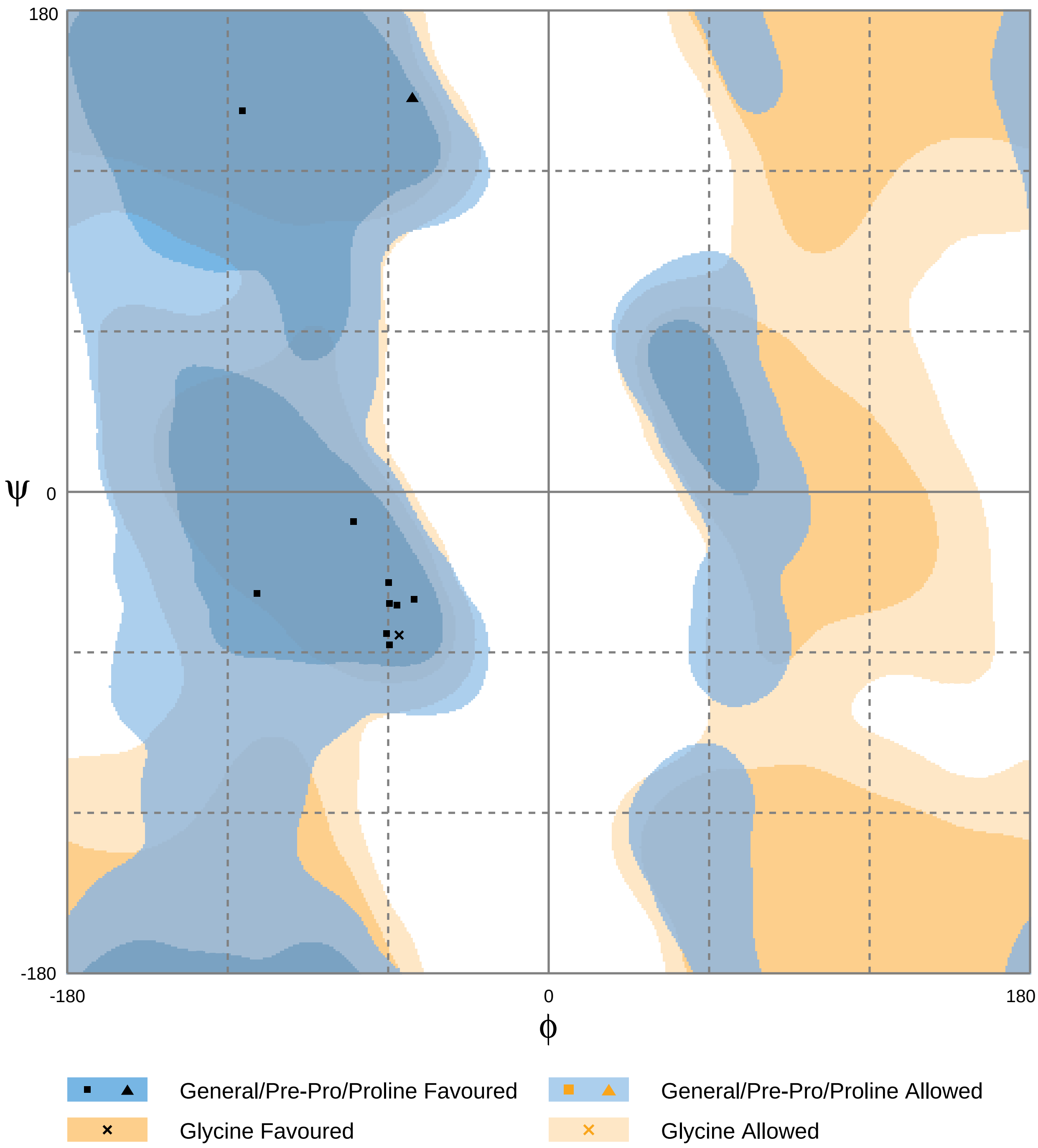


Number of residues in favoured region (~98.0% expected) : 10 (90.9%)
Number of residues in allowed region (~2.0% expected) : 1 (9.1%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1km

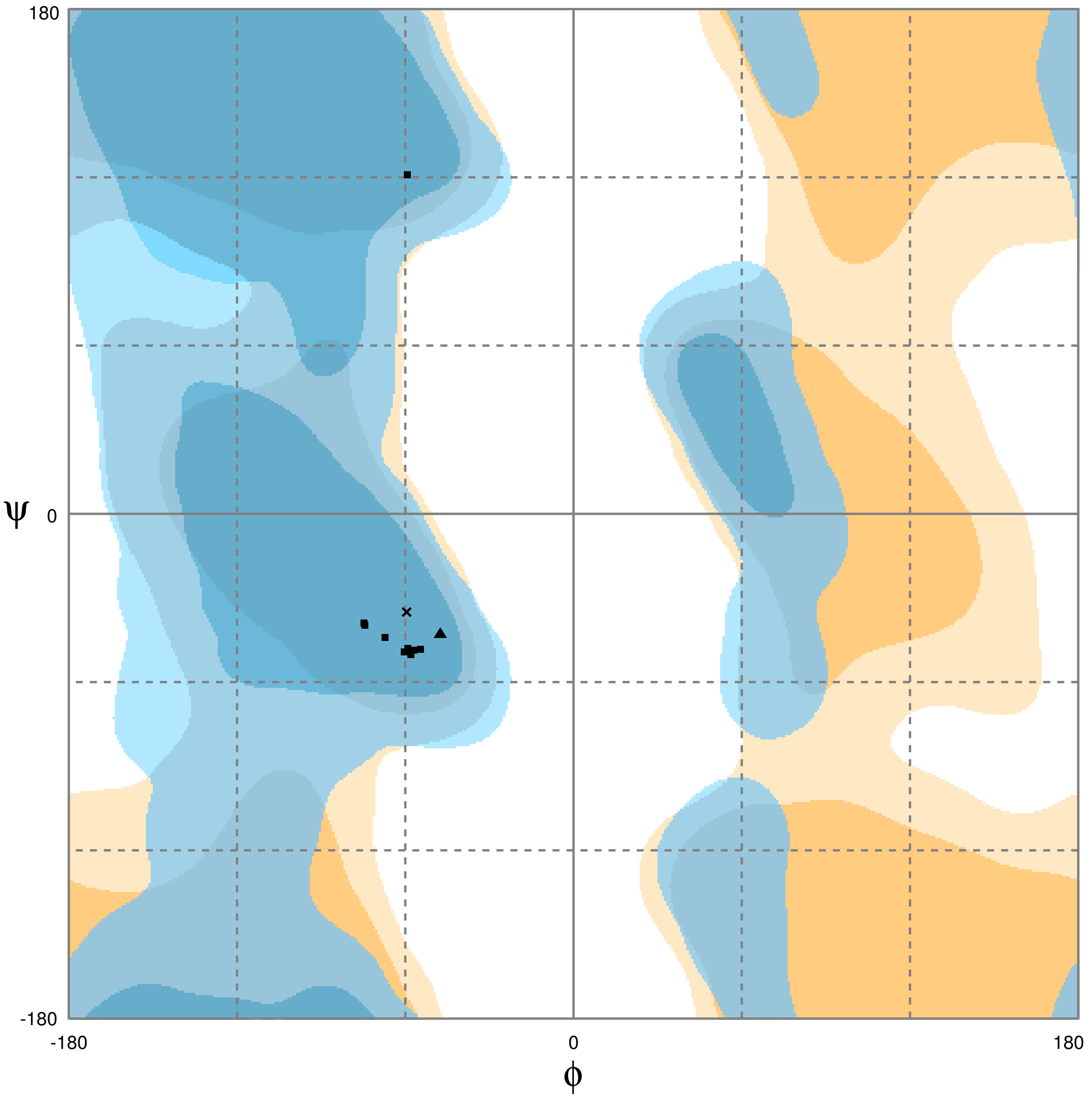


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1la

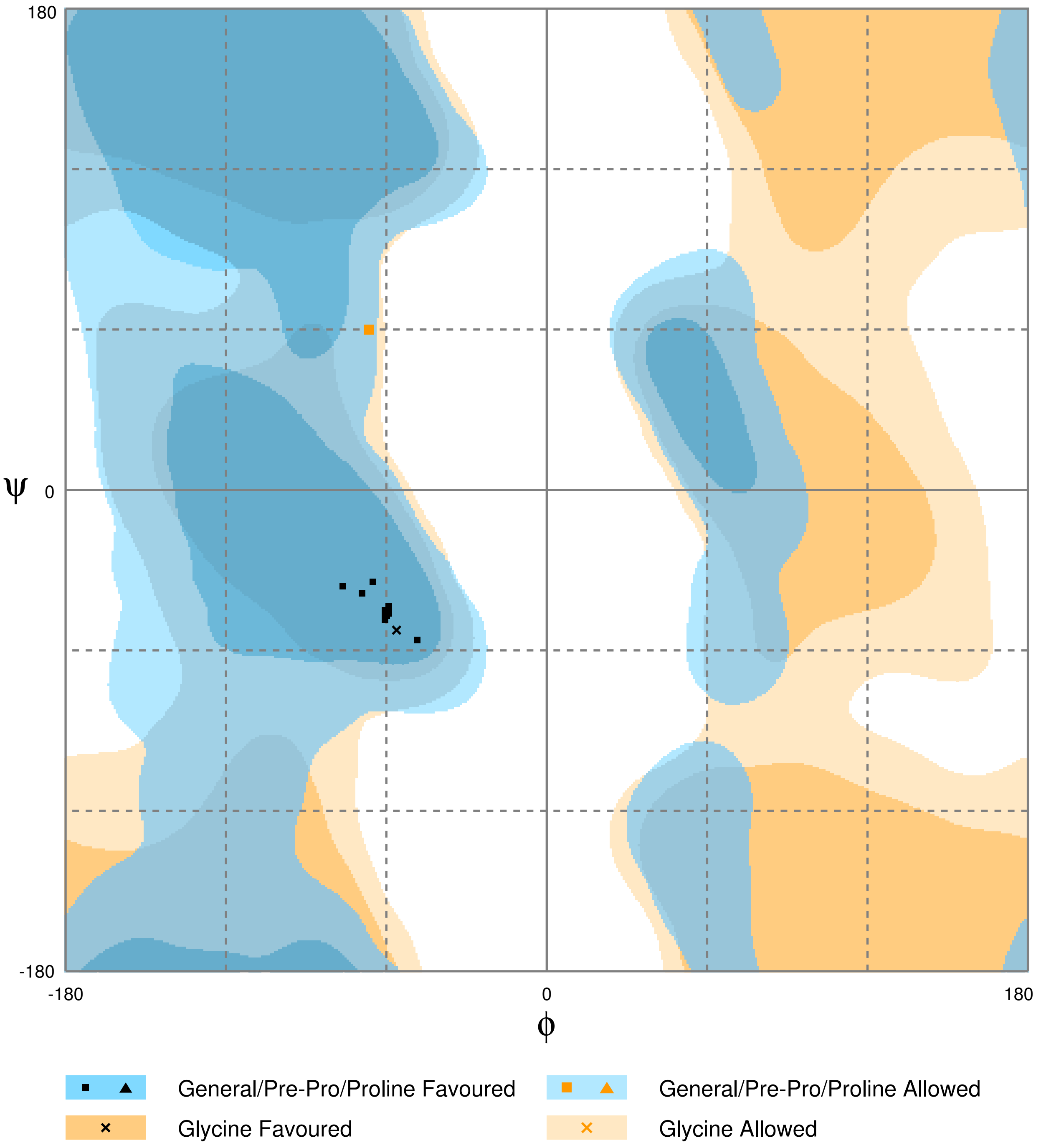


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1lb

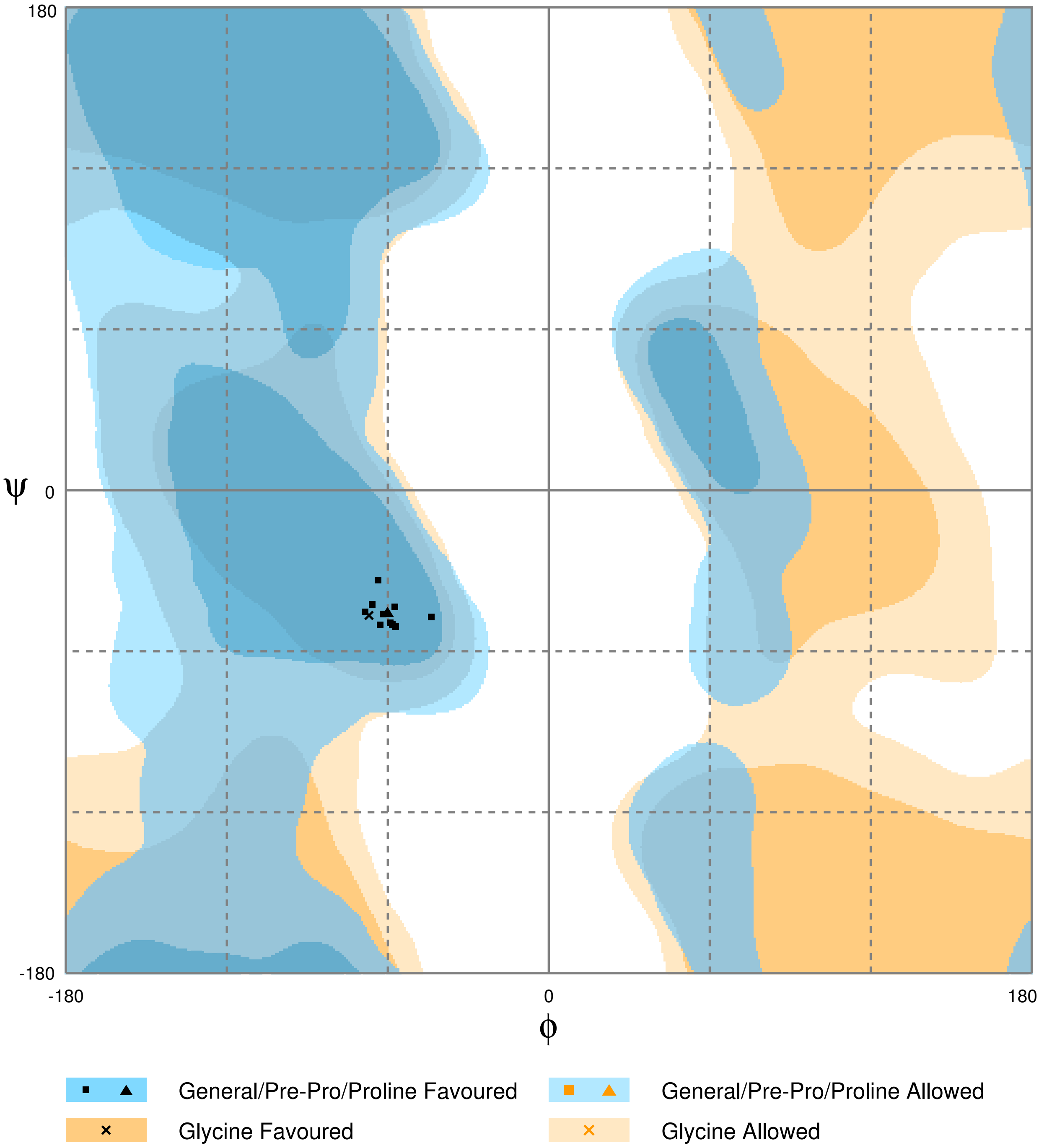


Number of residues in favoured region (~98.0% expected) : 11 (91.7%)
Number of residues in allowed region (~2.0% expected) : 1 (8.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1lc

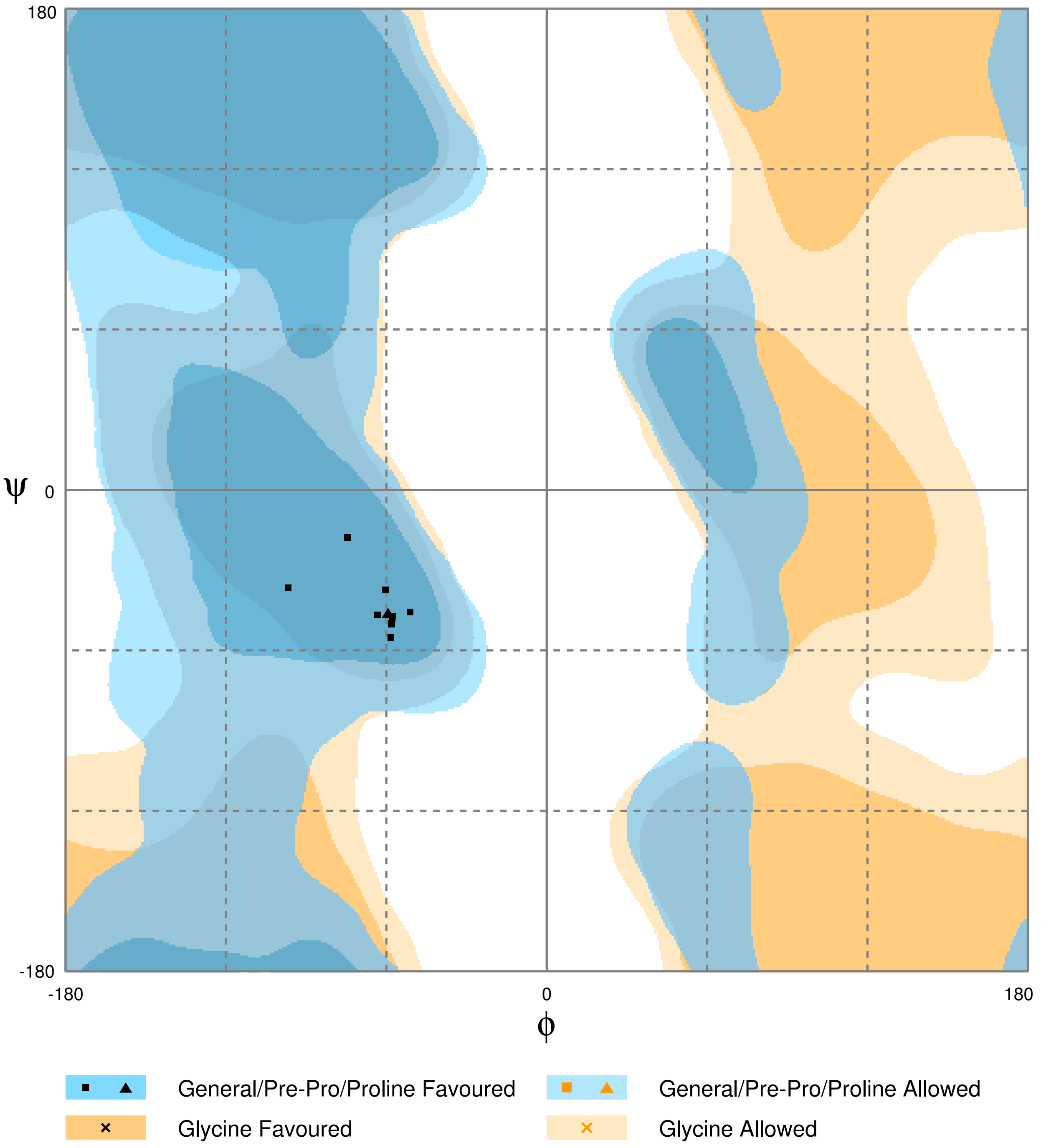


Number of residues in favoured region (~98.0% expected) : 12 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1oa

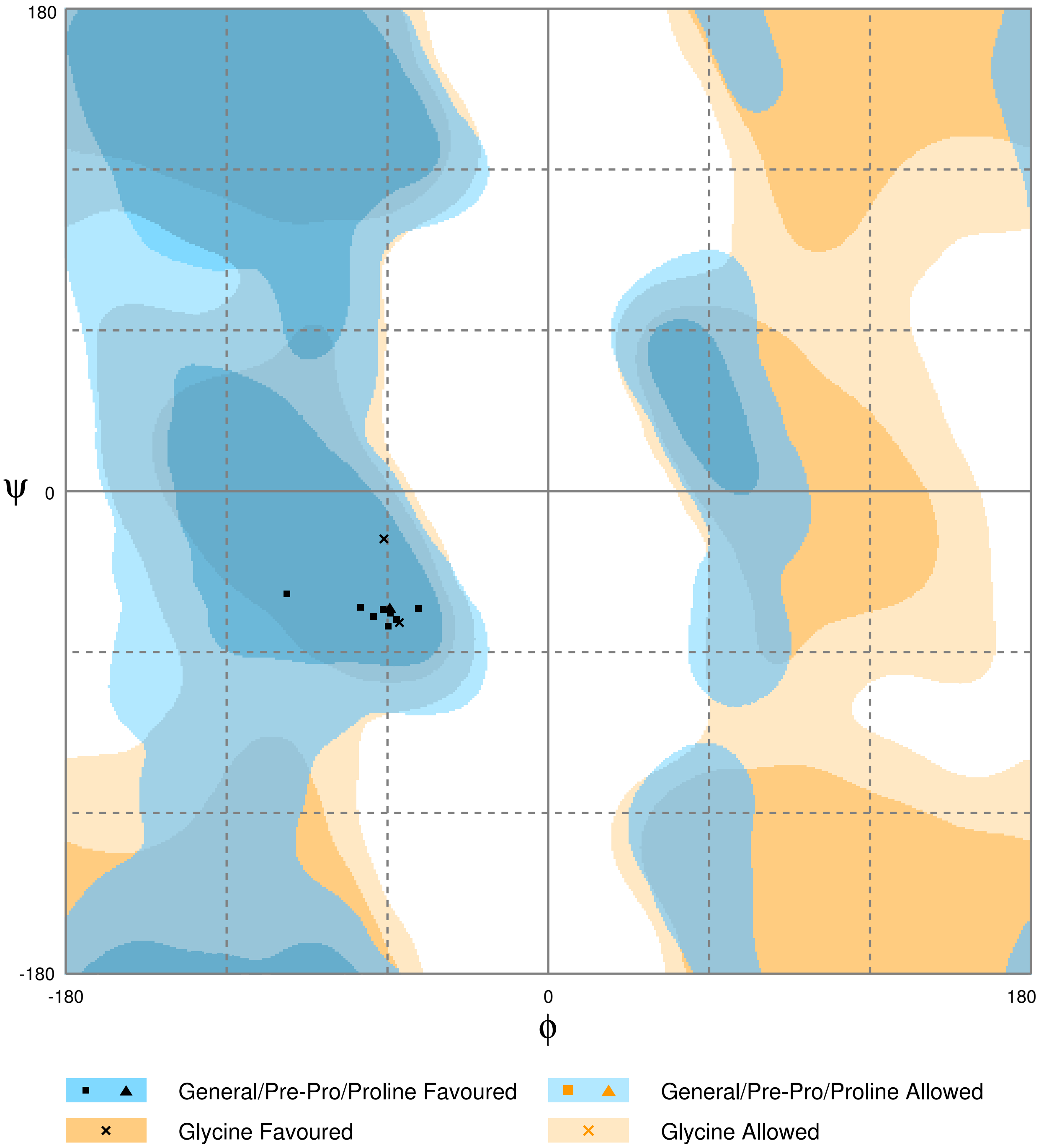


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ob

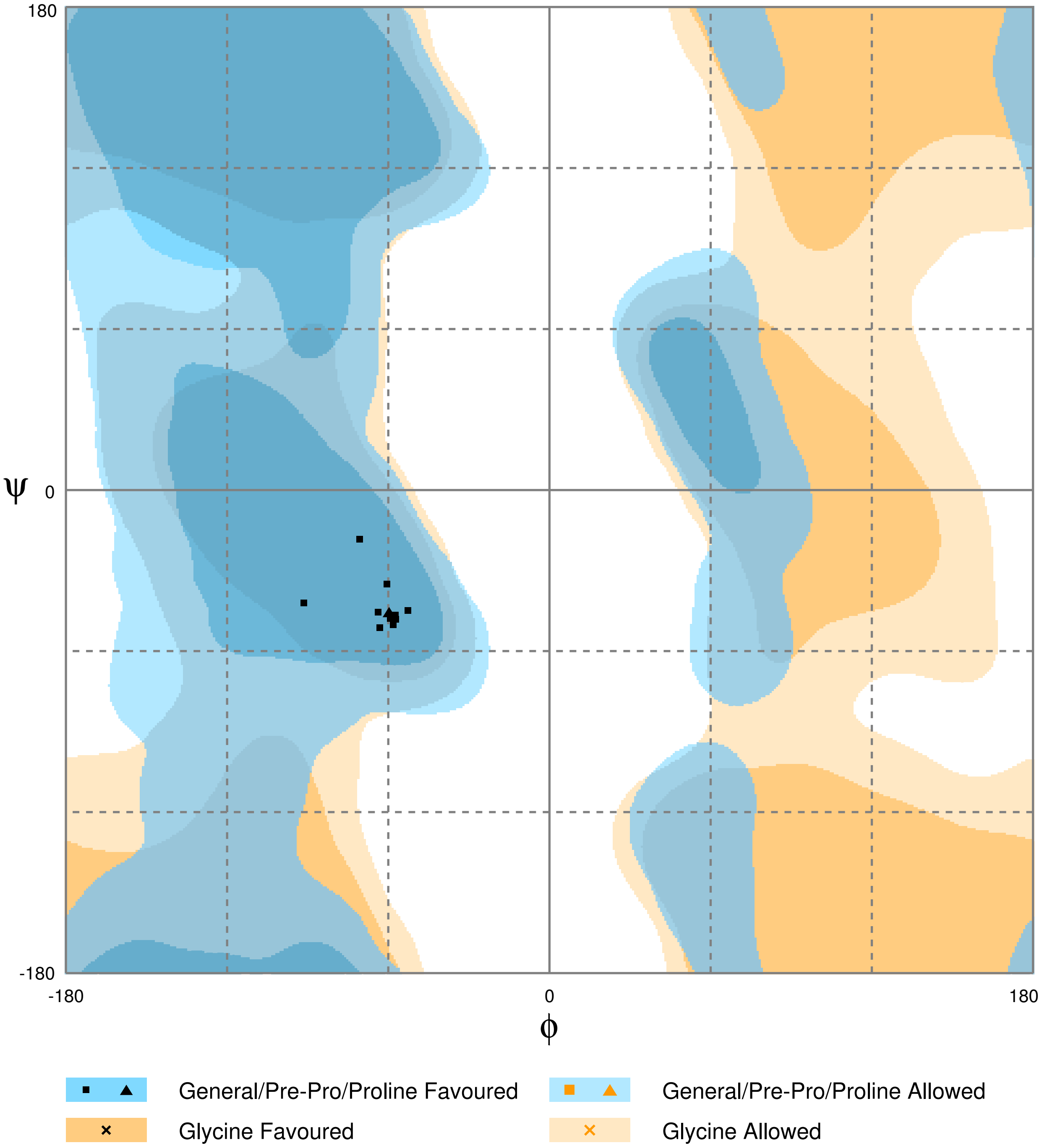


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1oc

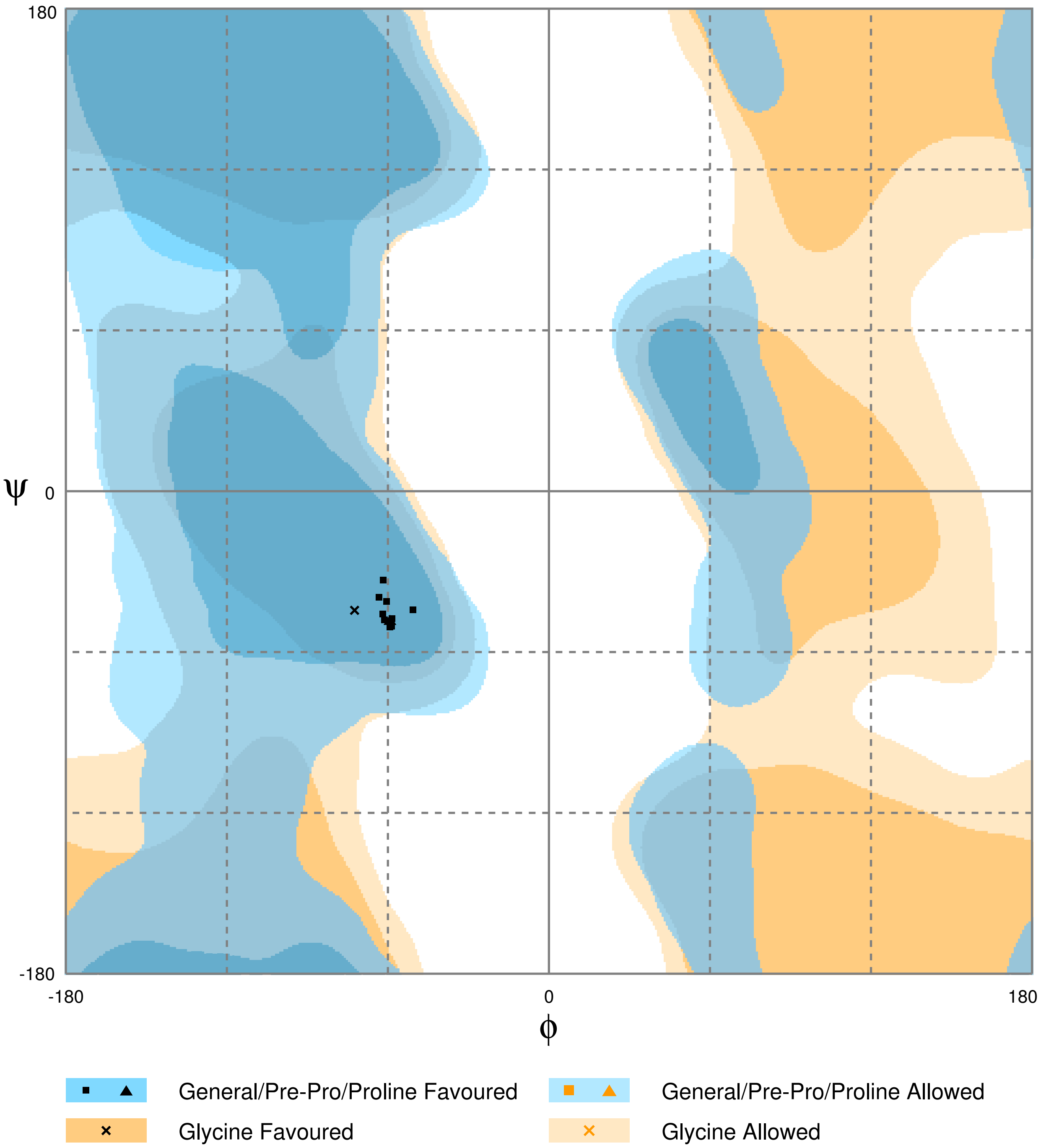


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1od

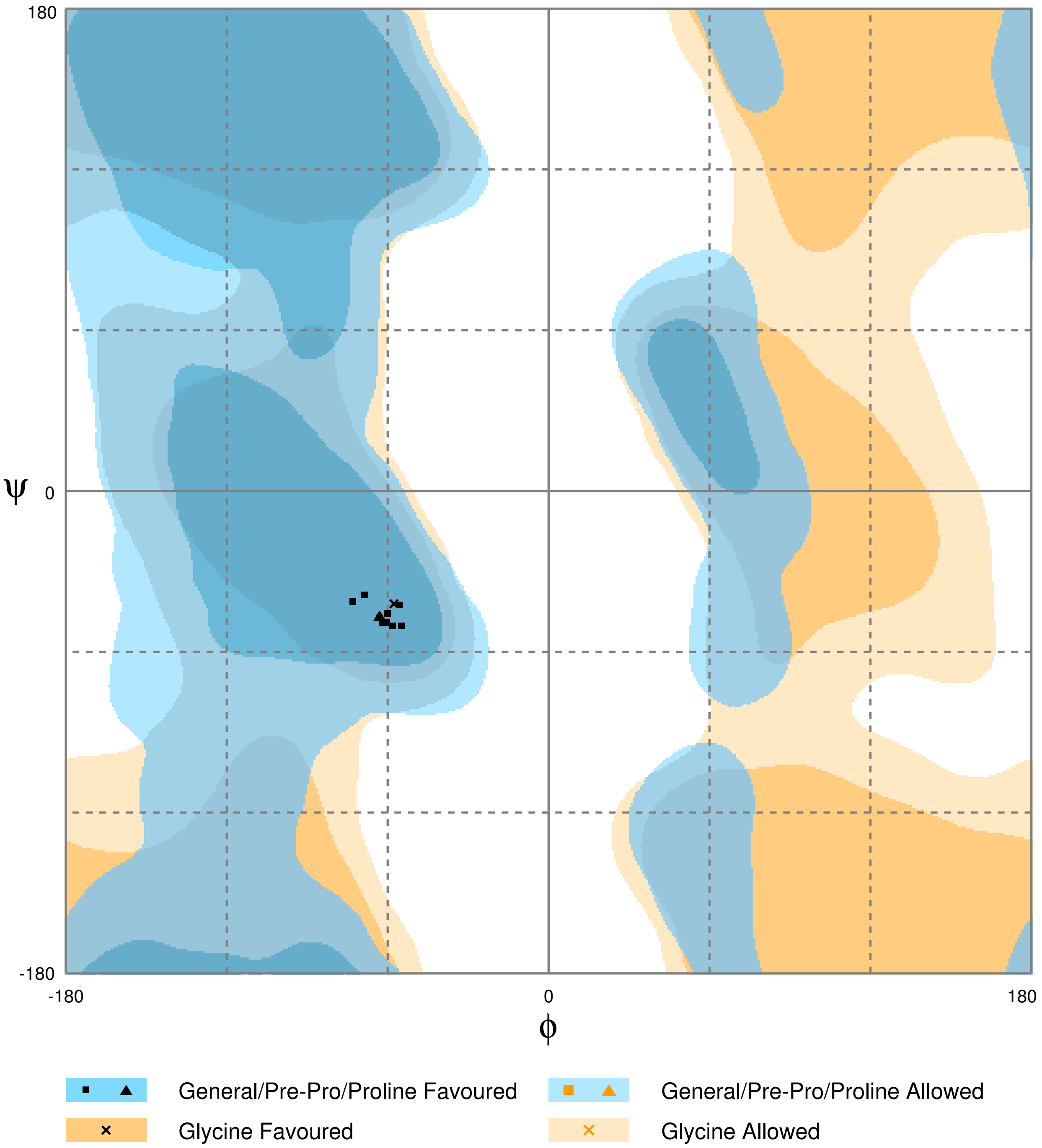


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ola

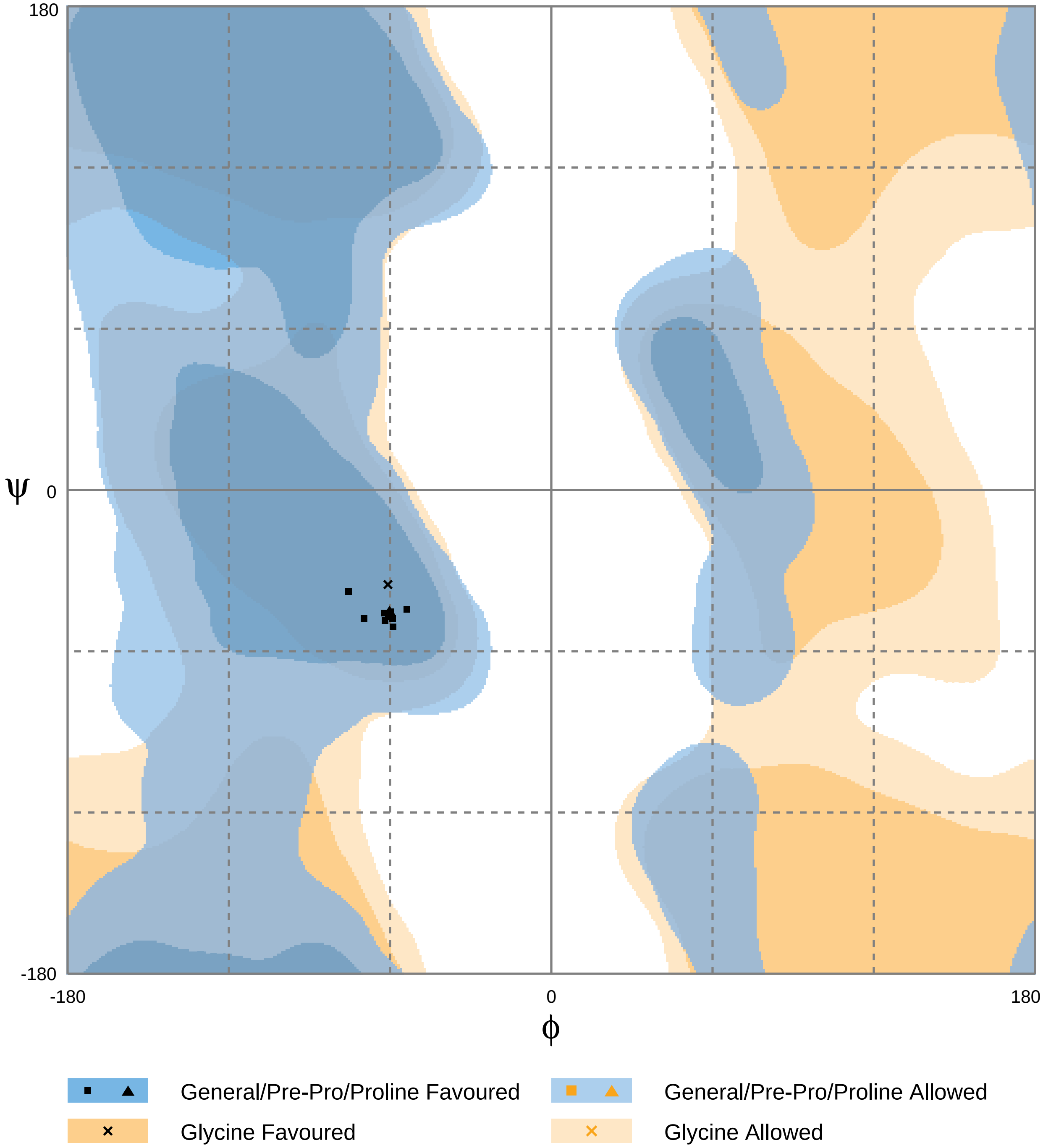


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1olb

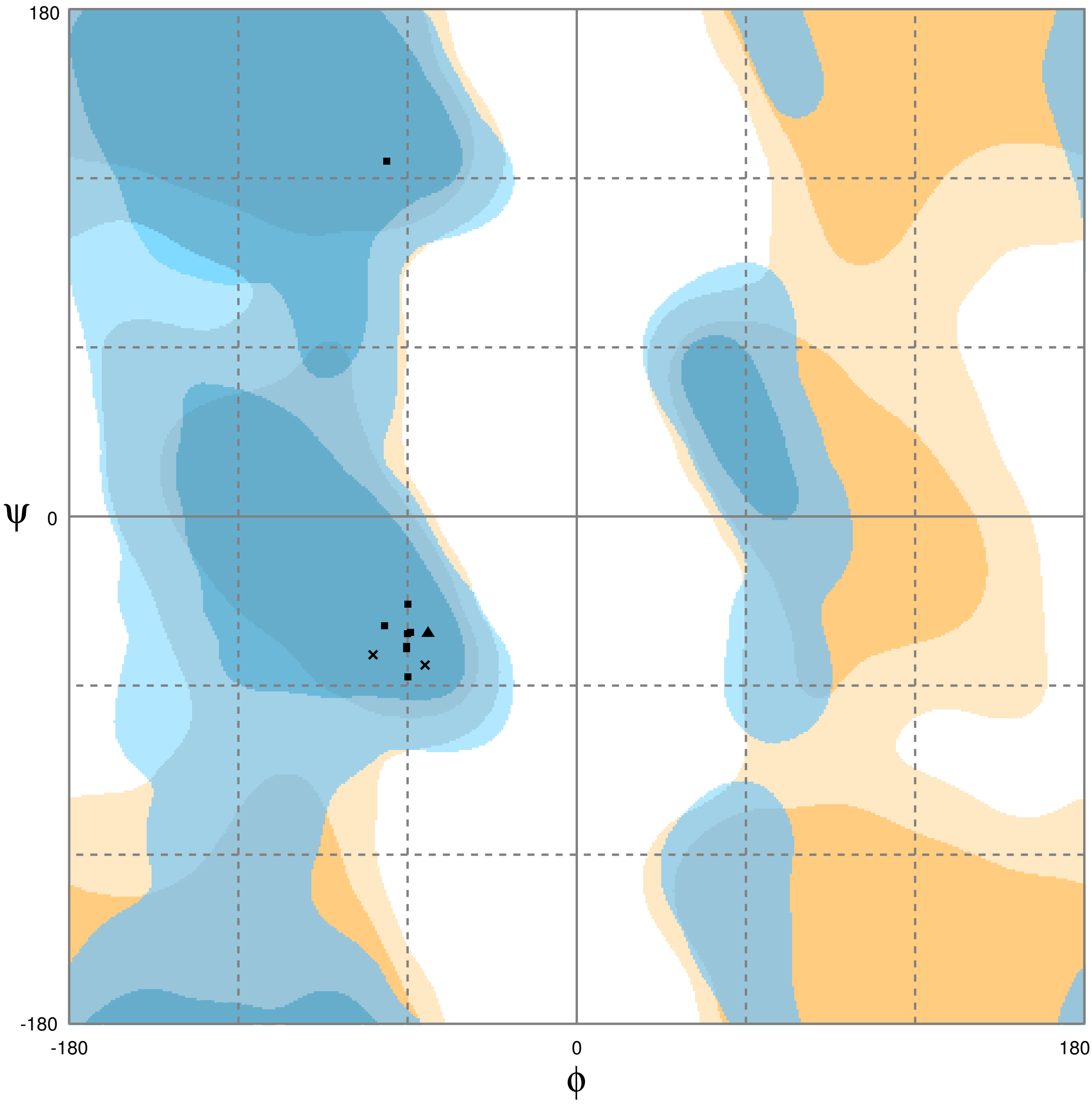


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1p



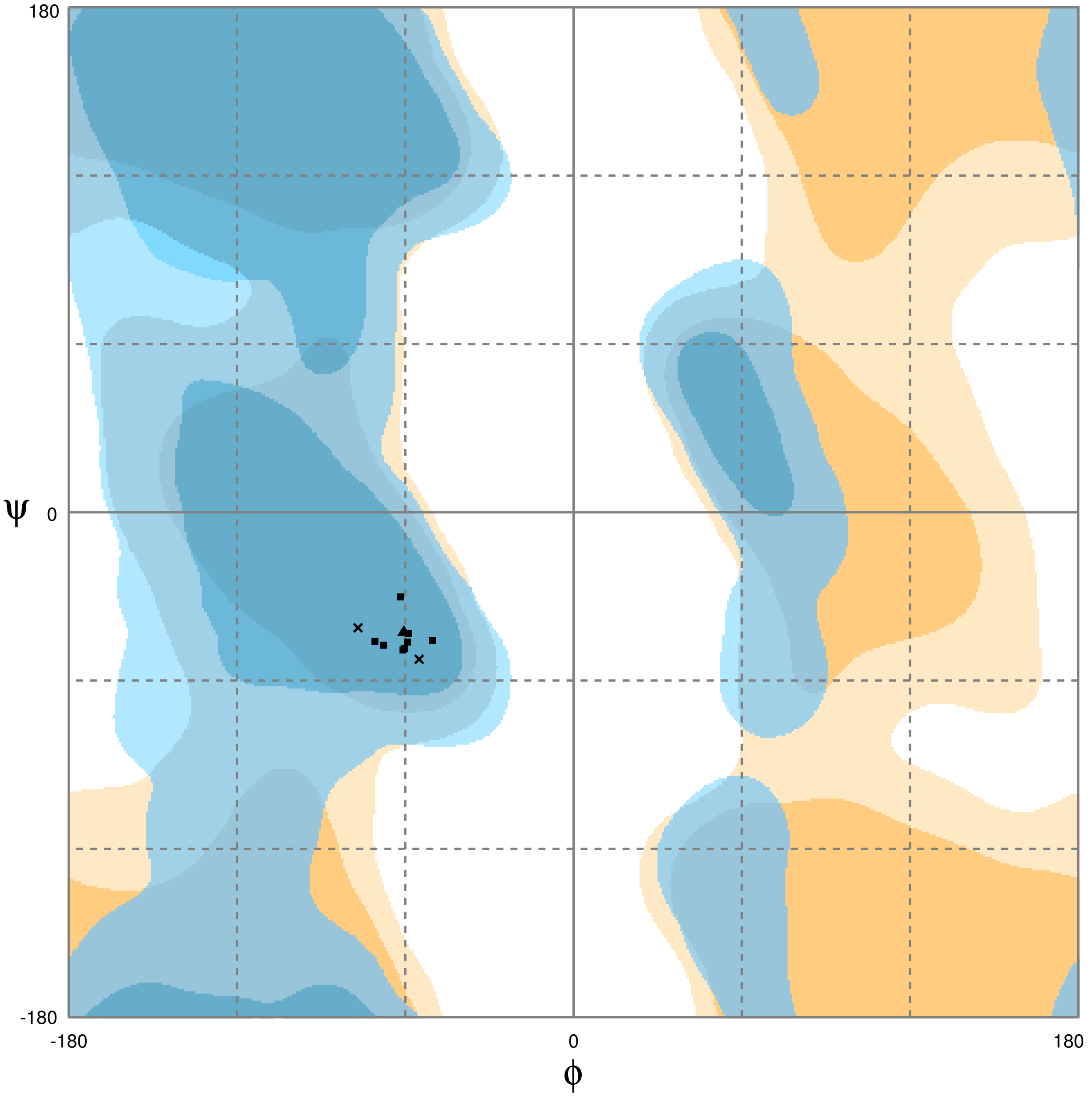
■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

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%)

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

Tem_1pla



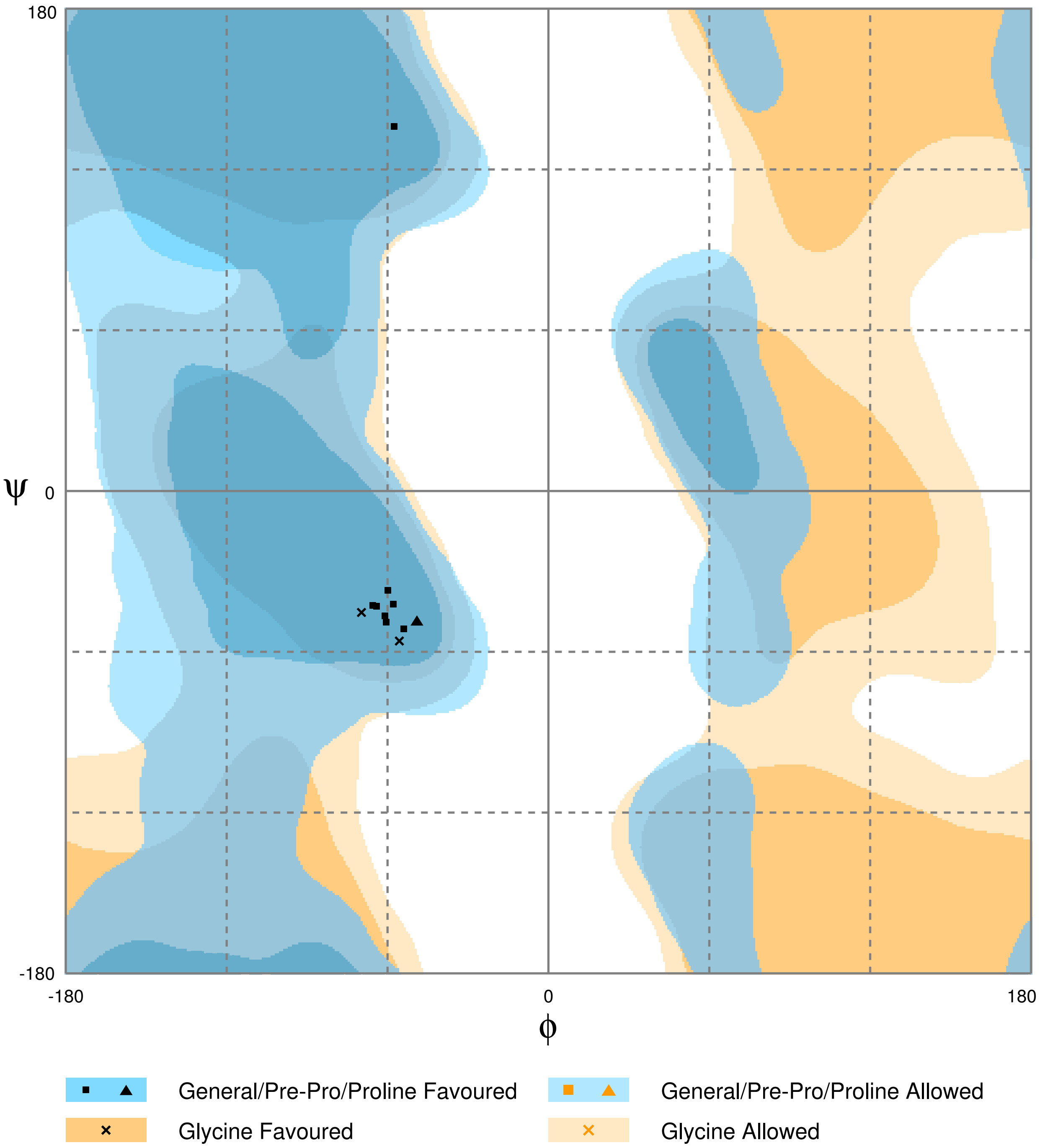
■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

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%)

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

Tem_1pra

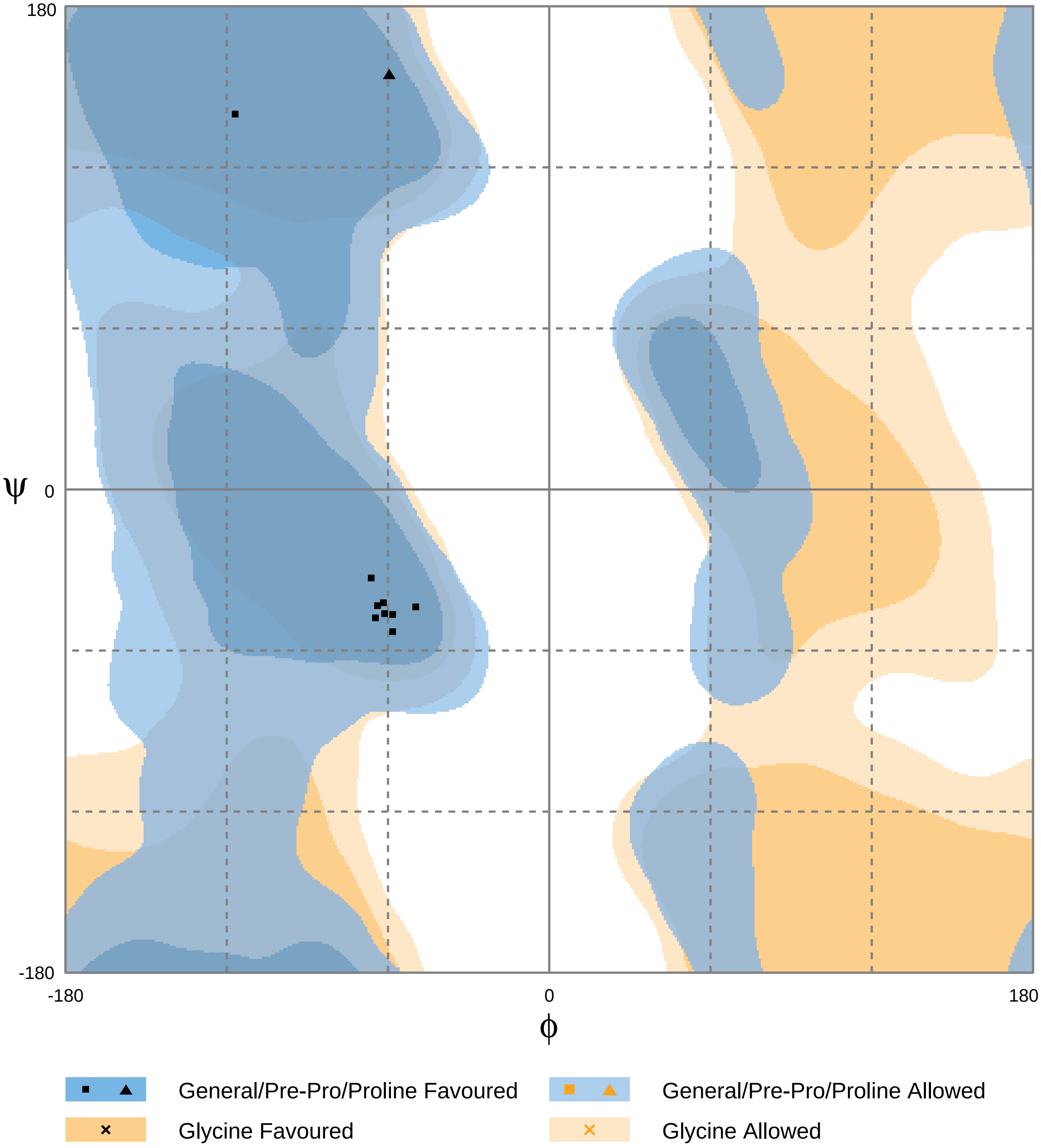


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1rna

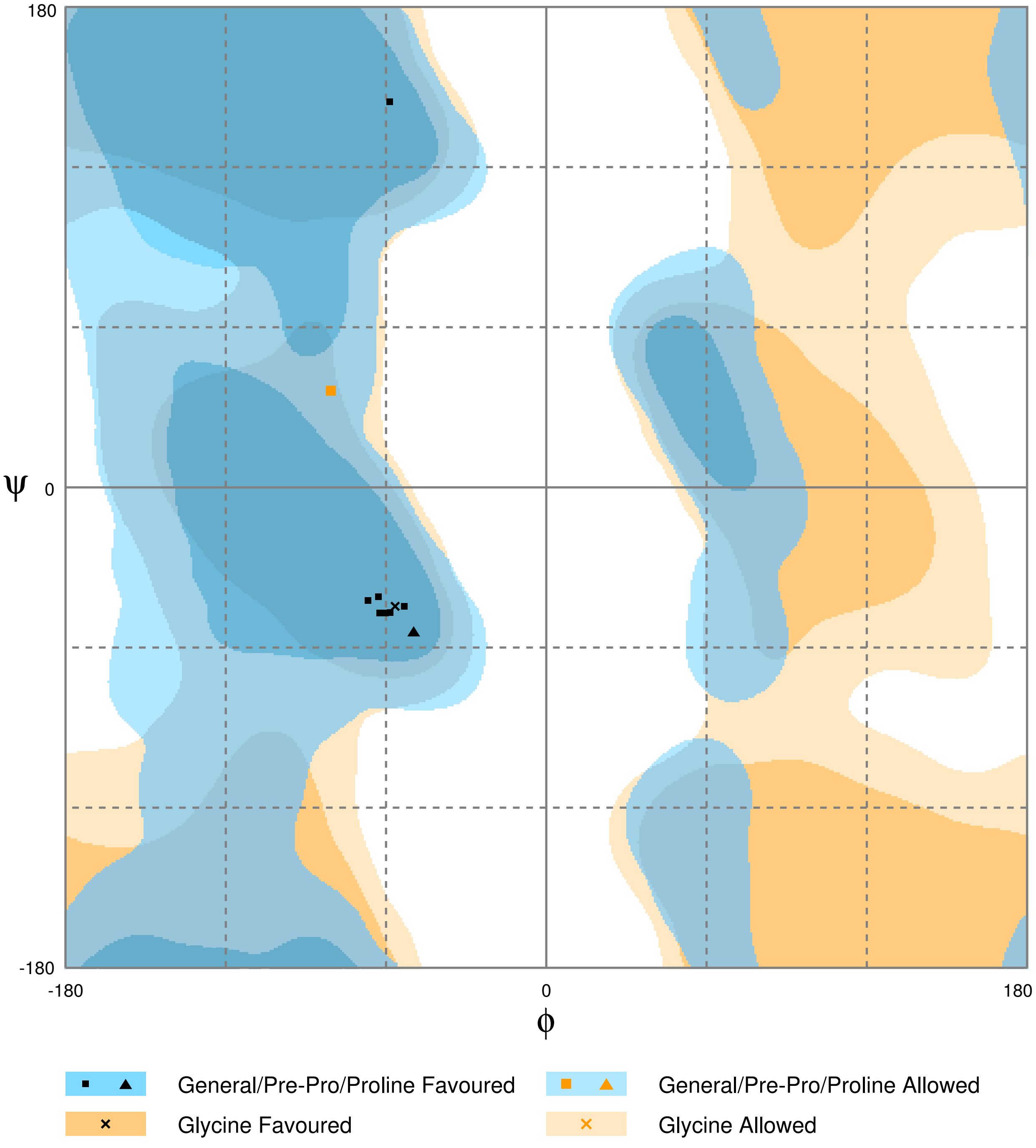


Number of residues in favoured region (~98.0% expected) : 10 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1rnb

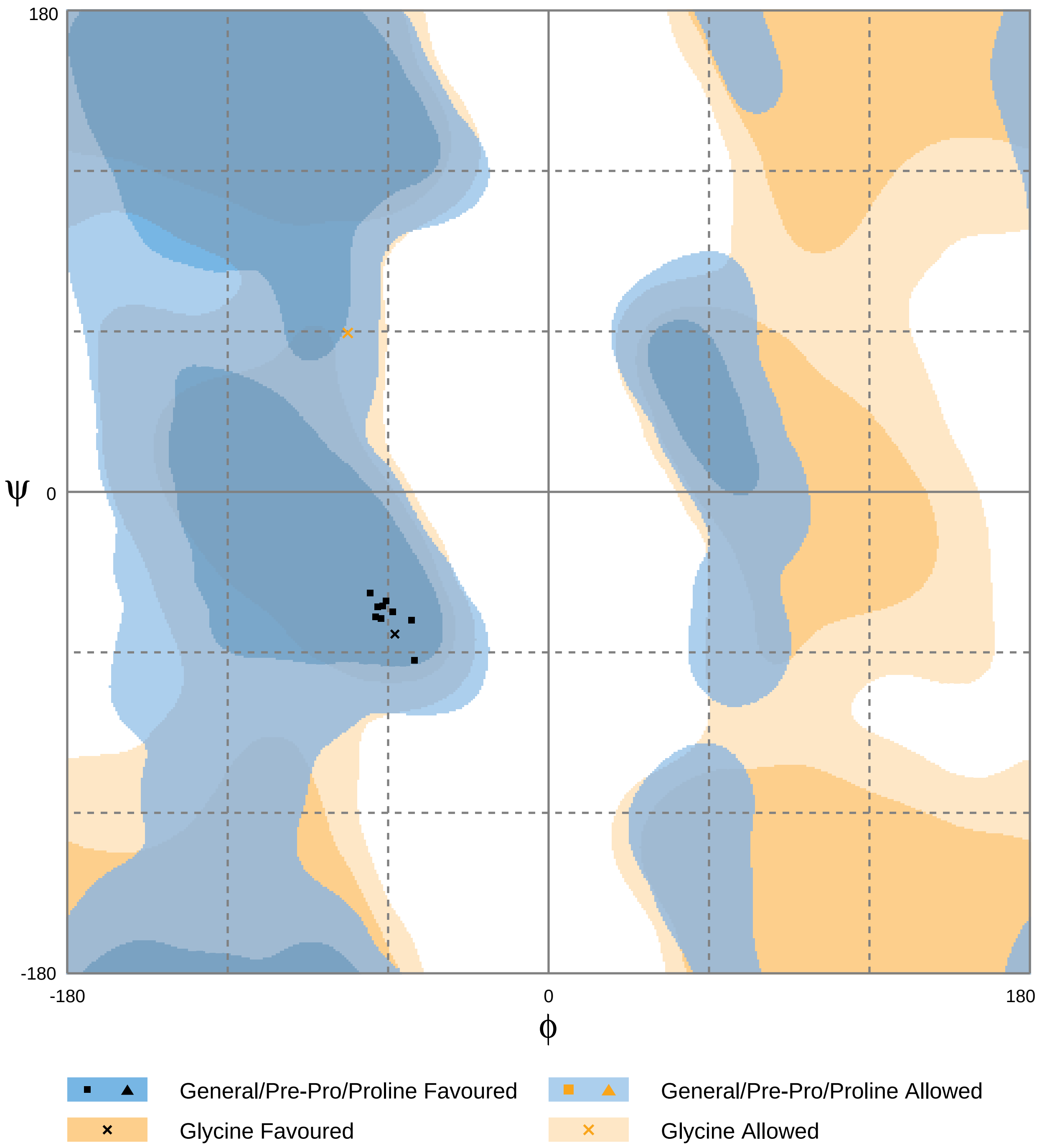


Number of residues in favoured region (~98.0% expected) : 9 (90.0%)
Number of residues in allowed region (~2.0% expected) : 1 (10.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1s

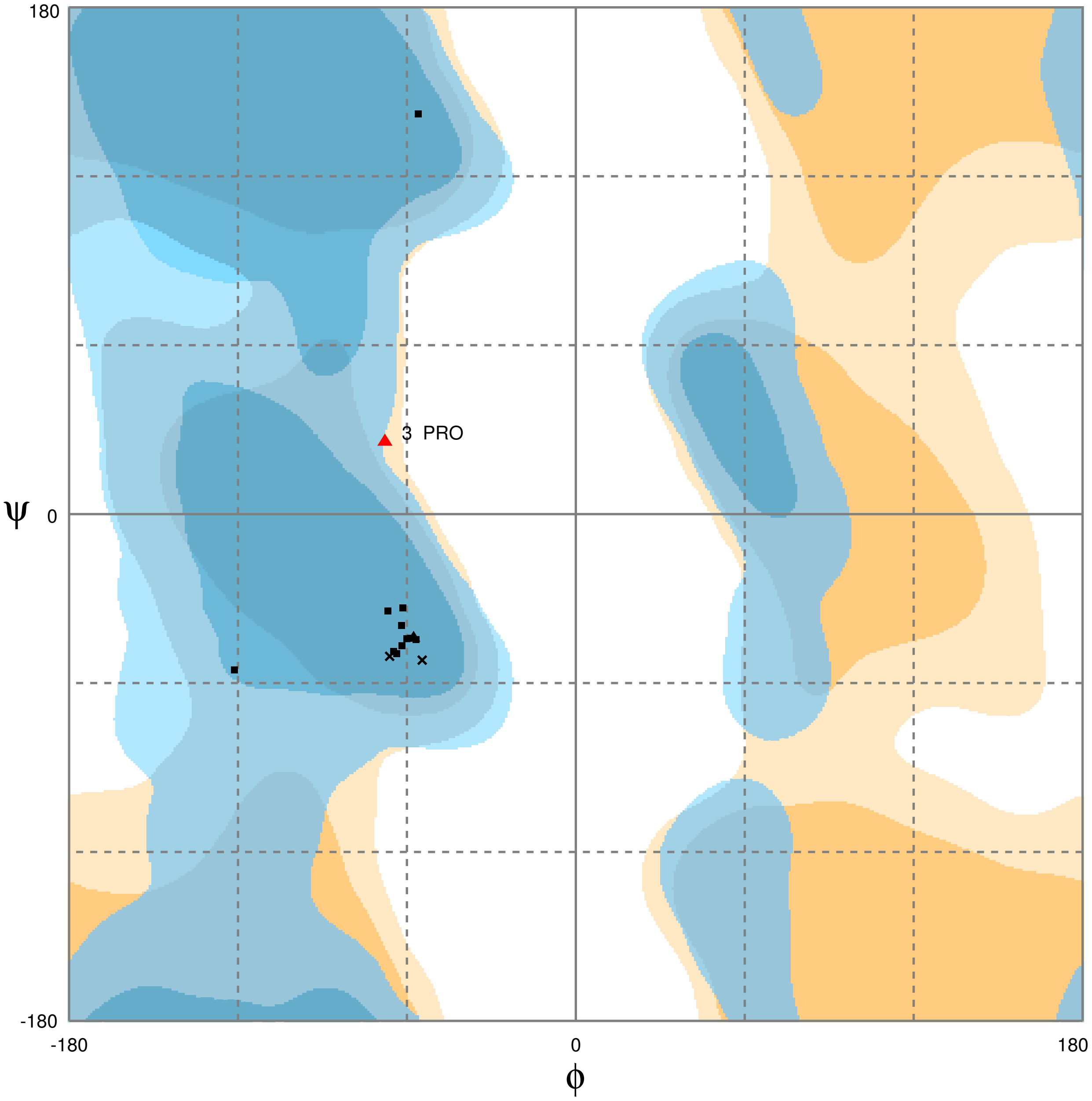


Number of residues in favoured region (~98.0% expected) : 10 (90.9%)
Number of residues in allowed region (~2.0% expected) : 1 (9.1%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ska

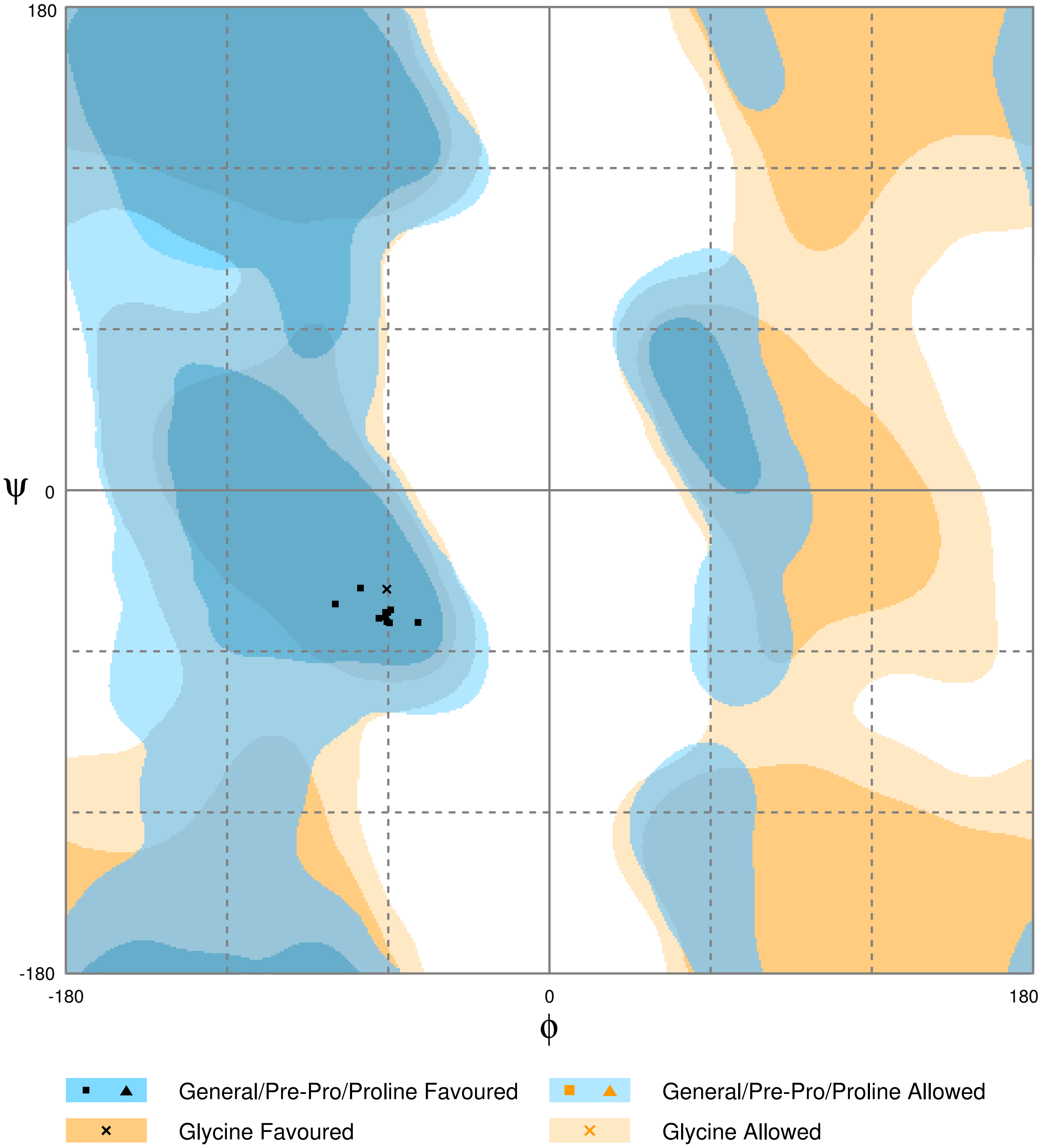


Number of residues in favoured region (~98.0% expected) : 14 (93.3%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 1 (6.7%)

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

Tem_1spa

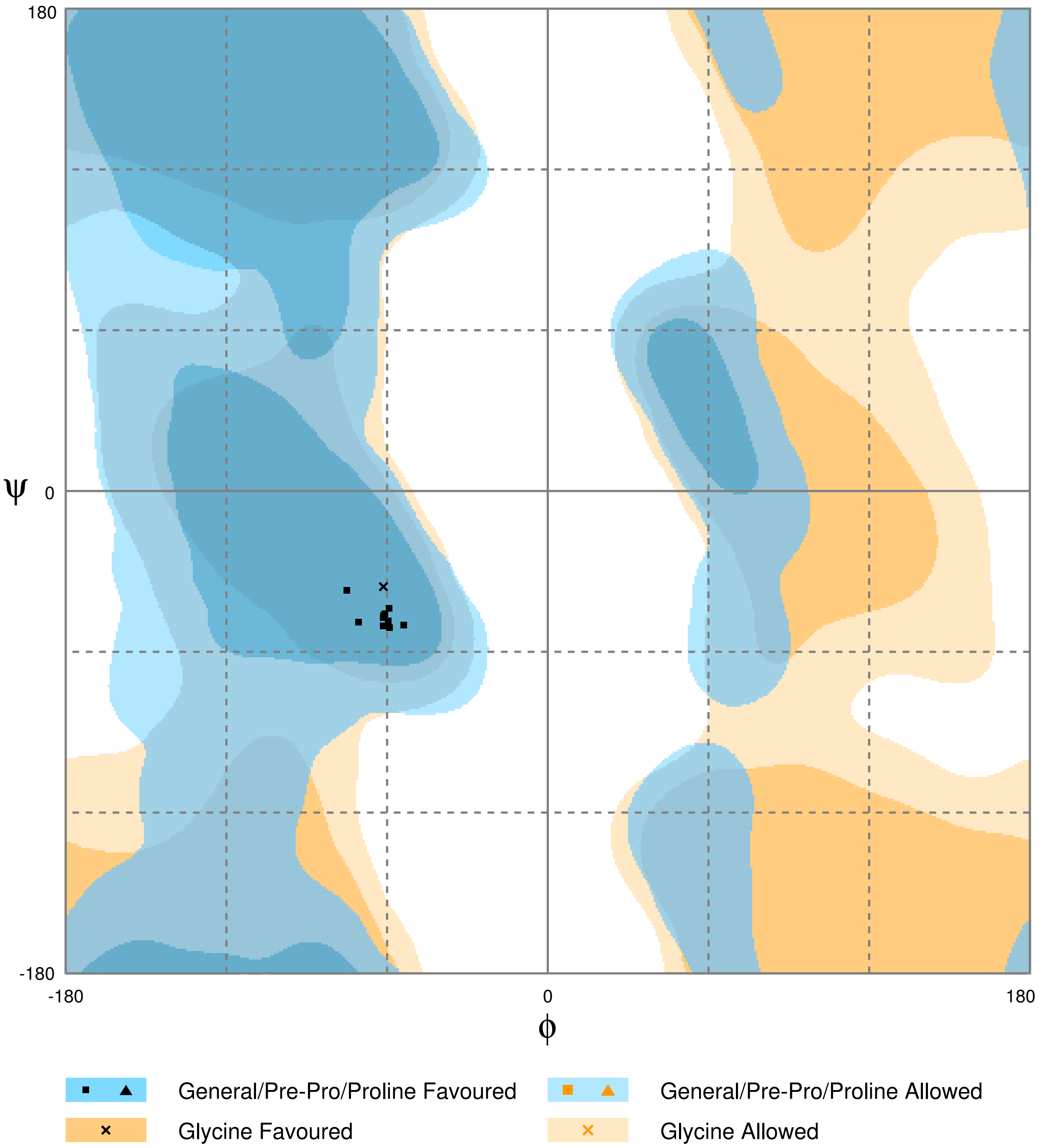


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1spb

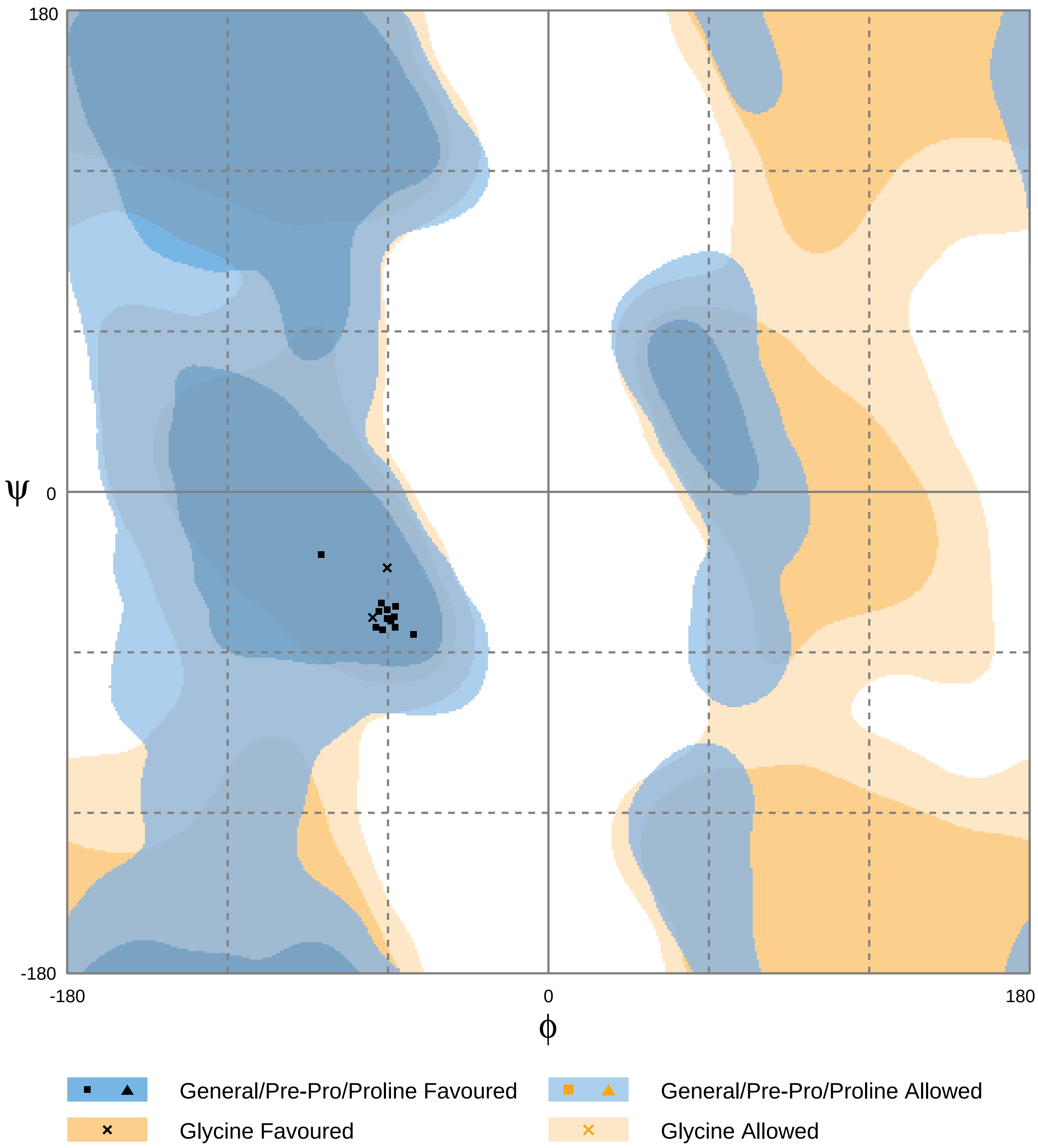


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ta

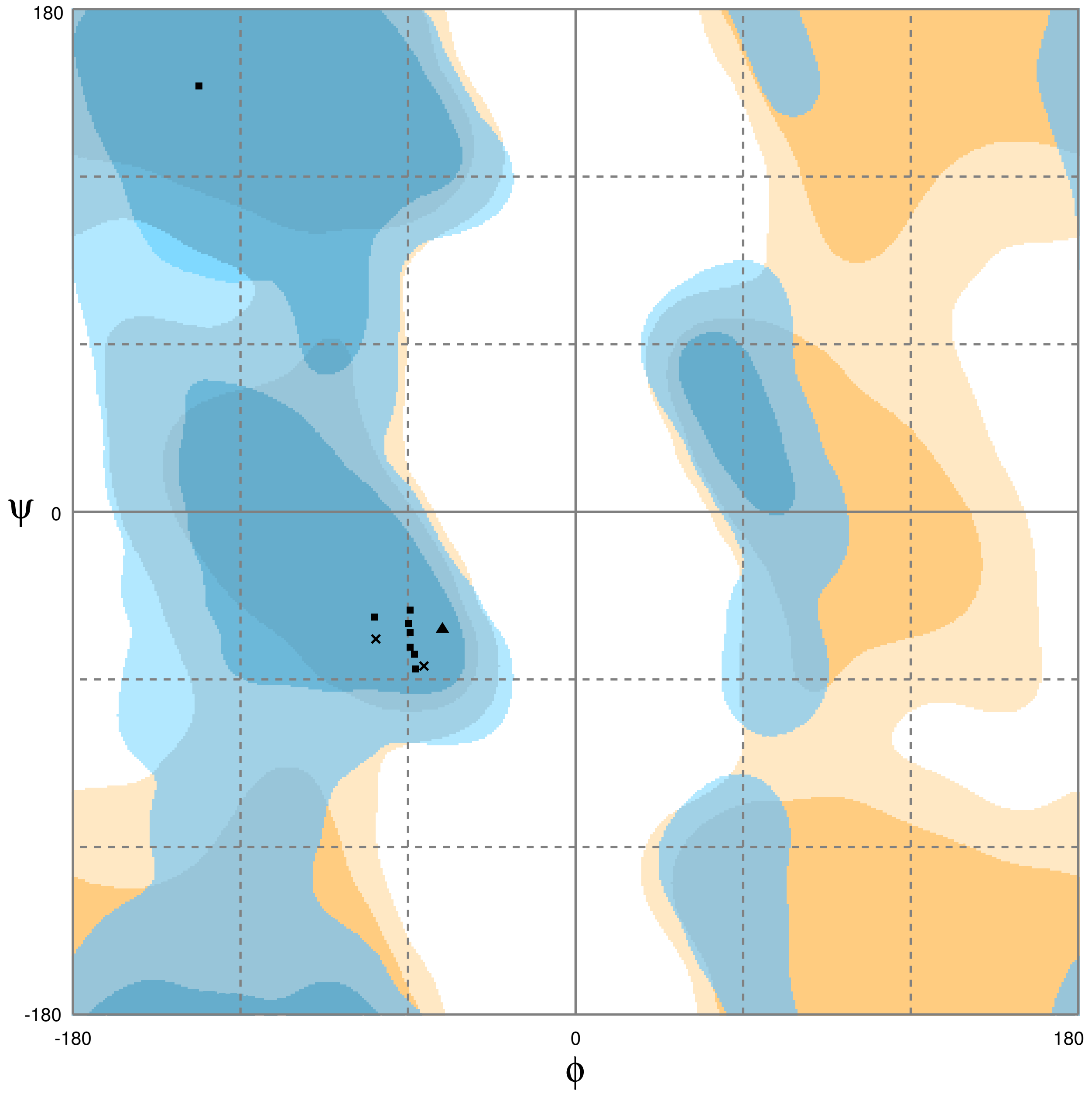


Number of residues in favoured region (~98.0% expected) : 15 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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: ϕ/ψ and $C\beta$ deviation. `Proteins: Structure, Function & Genetics` **50**: 437-450

Tem_1tga



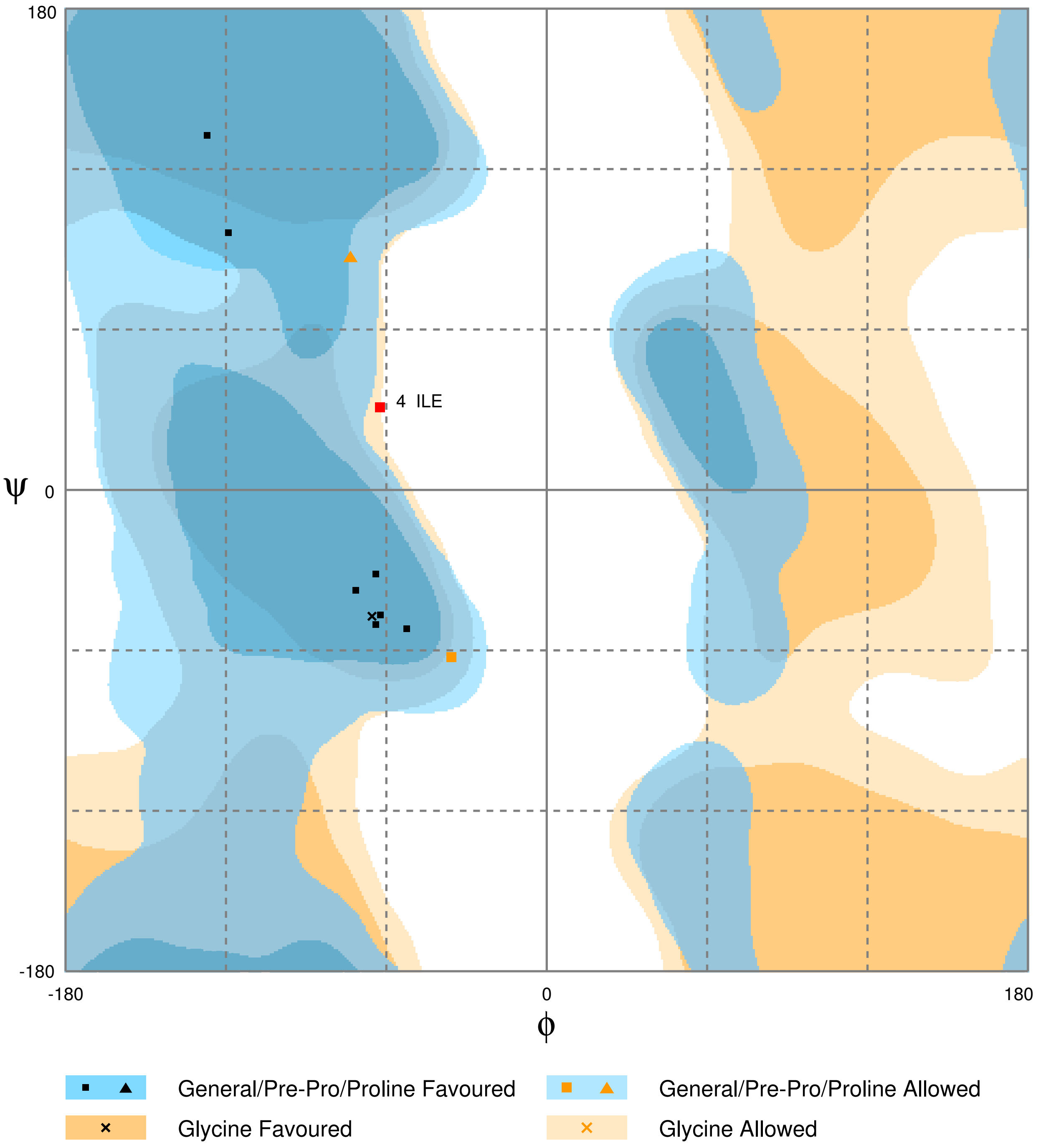
■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

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%)

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

Tem_1tgb

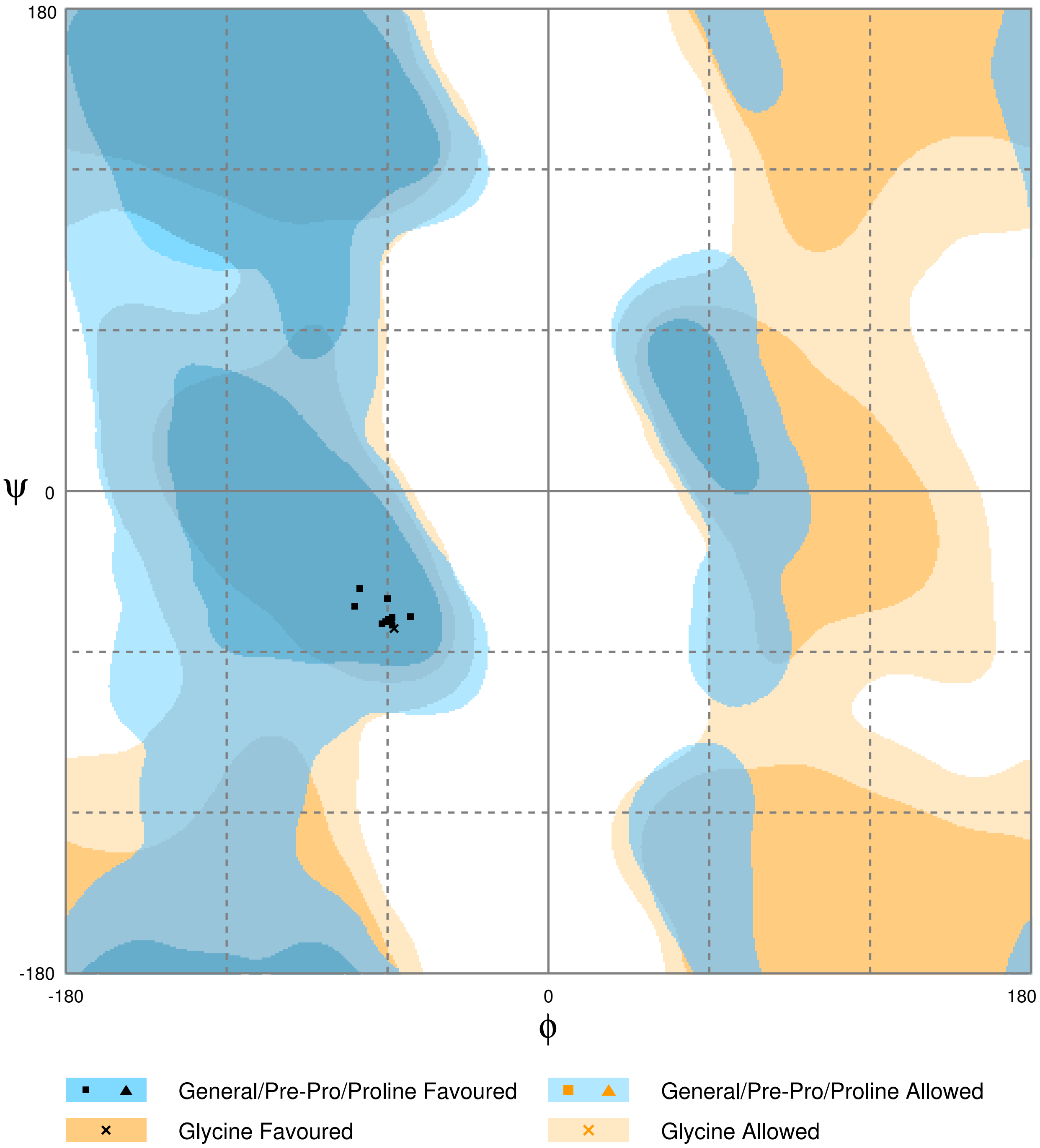


Number of residues in favoured region (~98.0% expected) : 8 (72.7%)
Number of residues in allowed region (~2.0% expected) : 2 (18.2%)
Number of residues in outlier region : 1 (9.1%)

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

Tem_1tgc

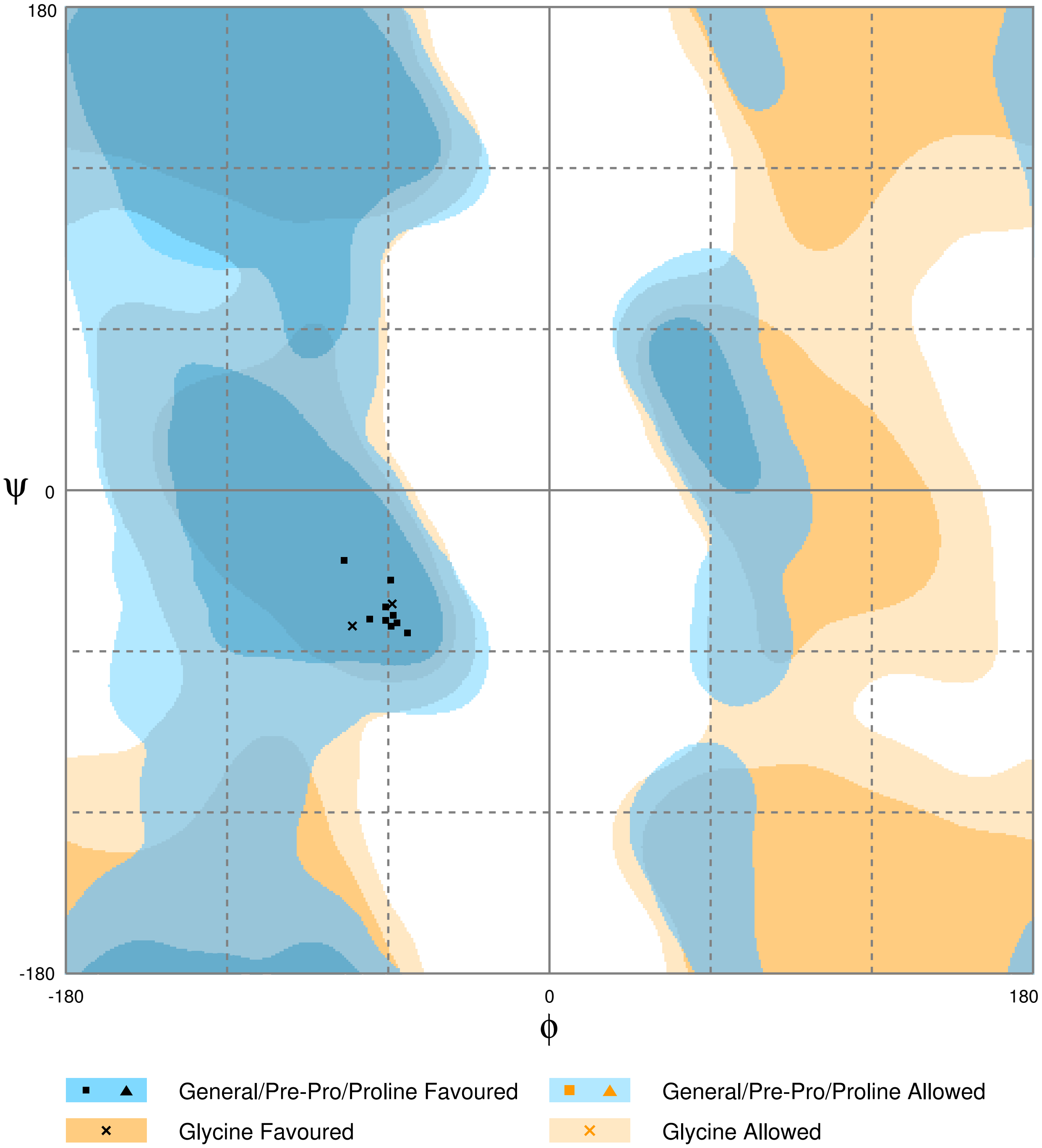


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1tsa

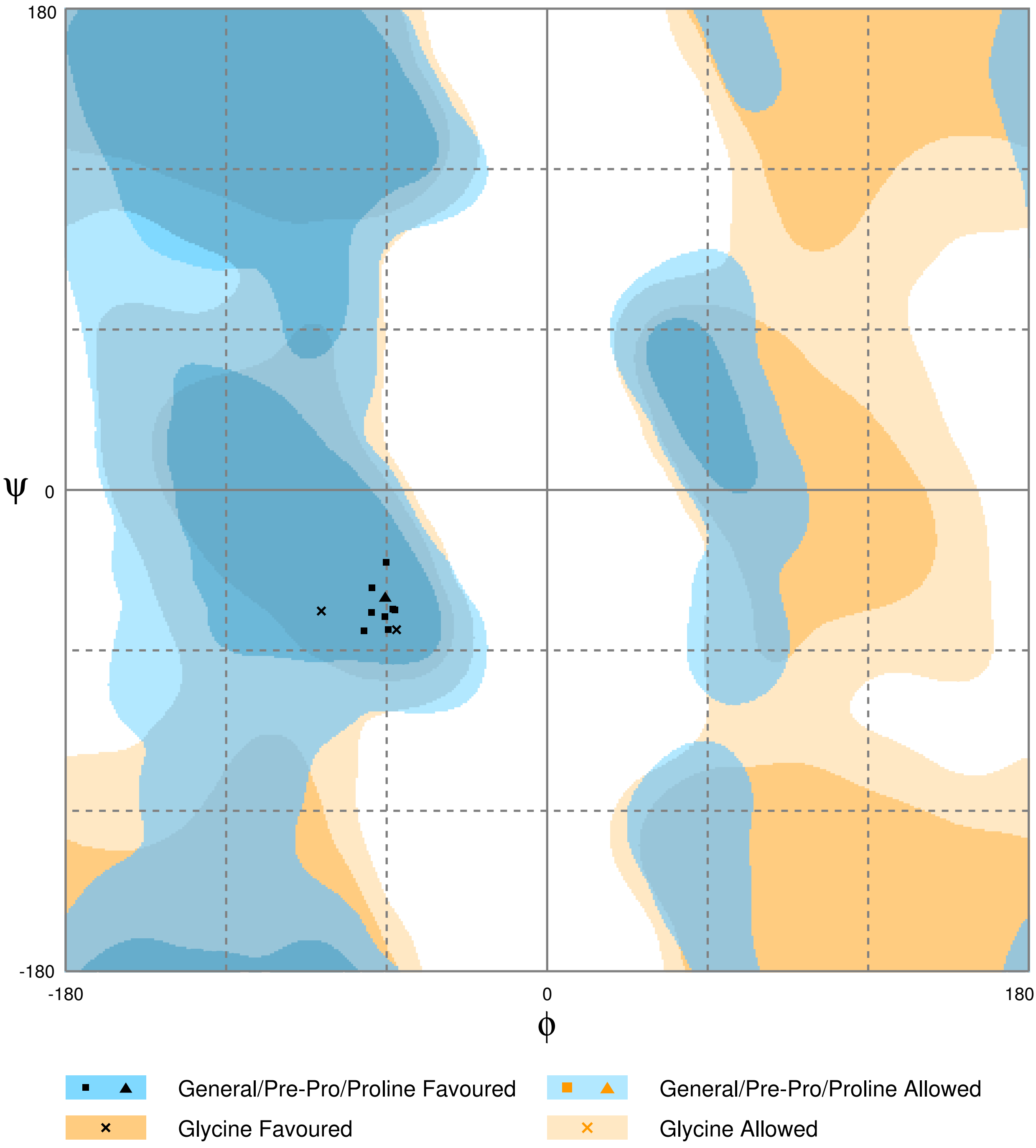


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1tsc

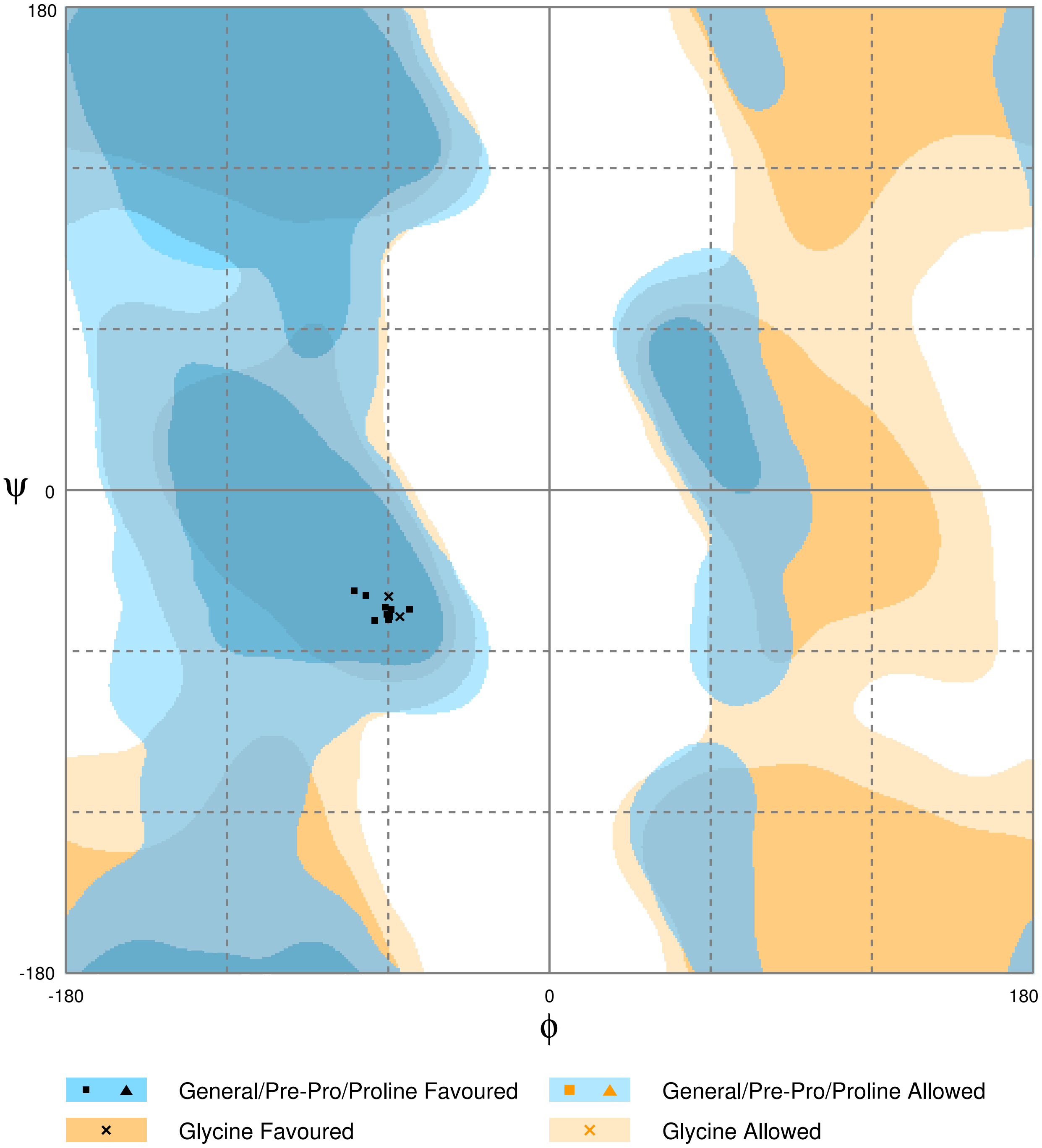


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1va

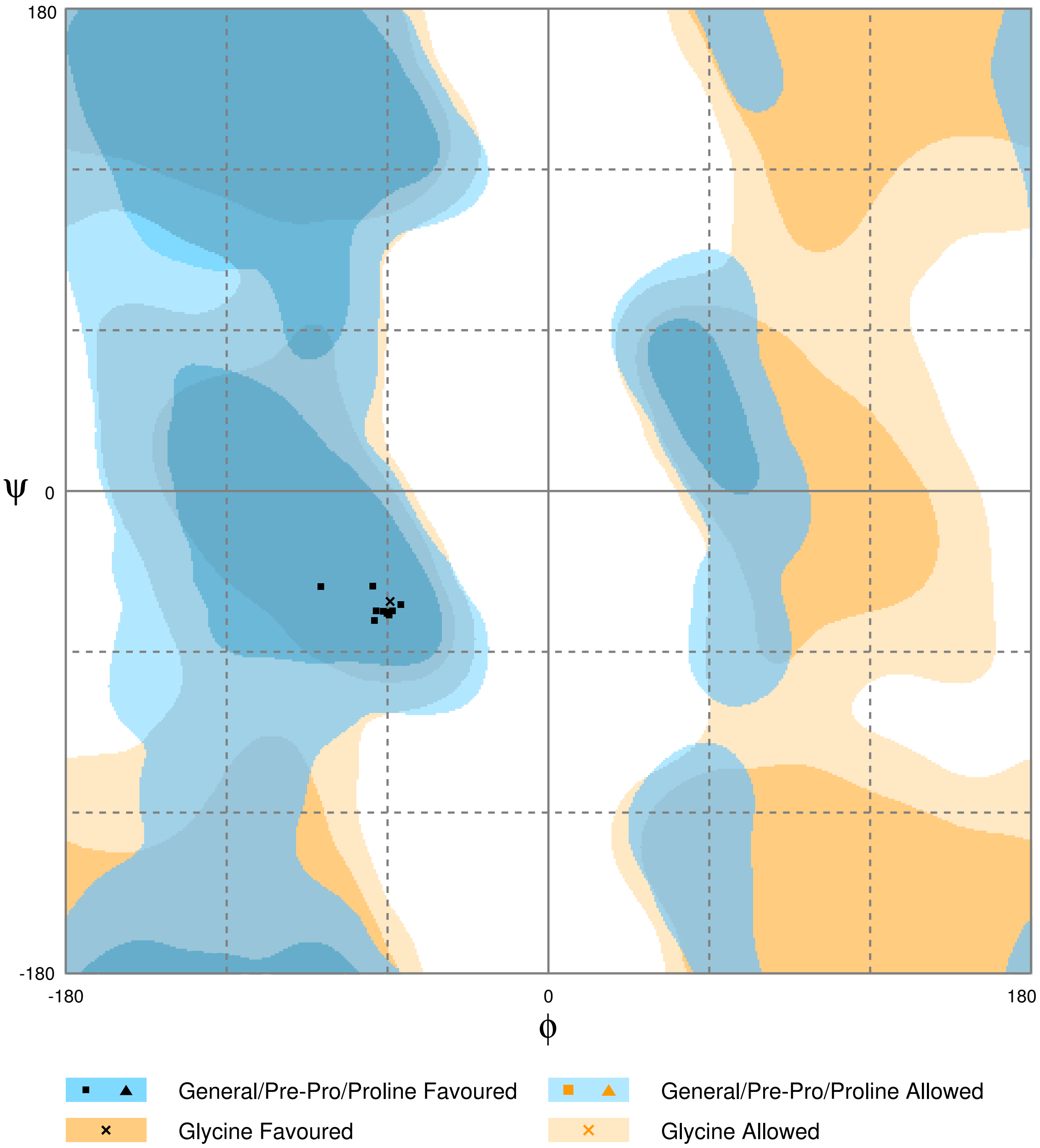


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1vb

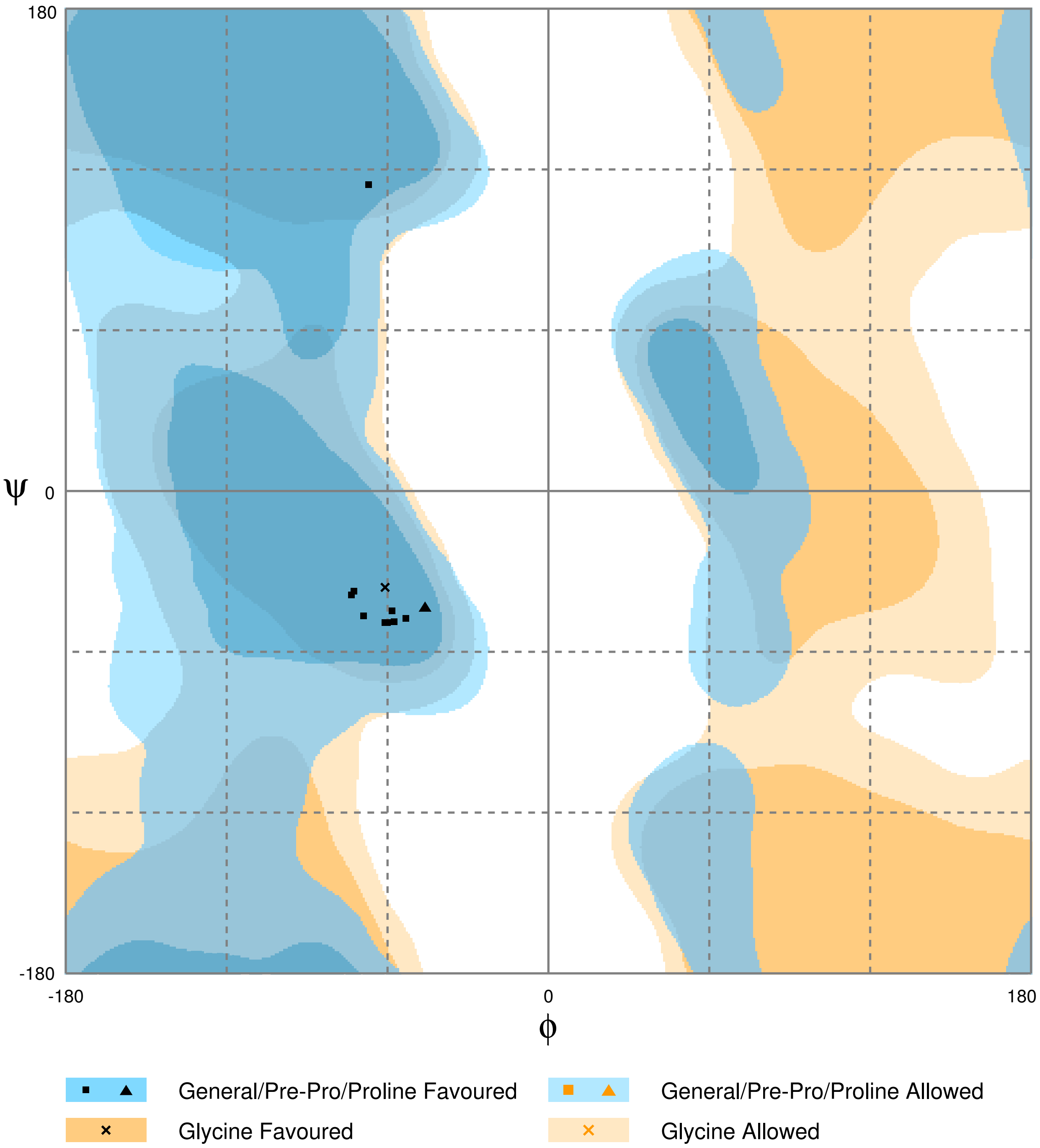


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1vc

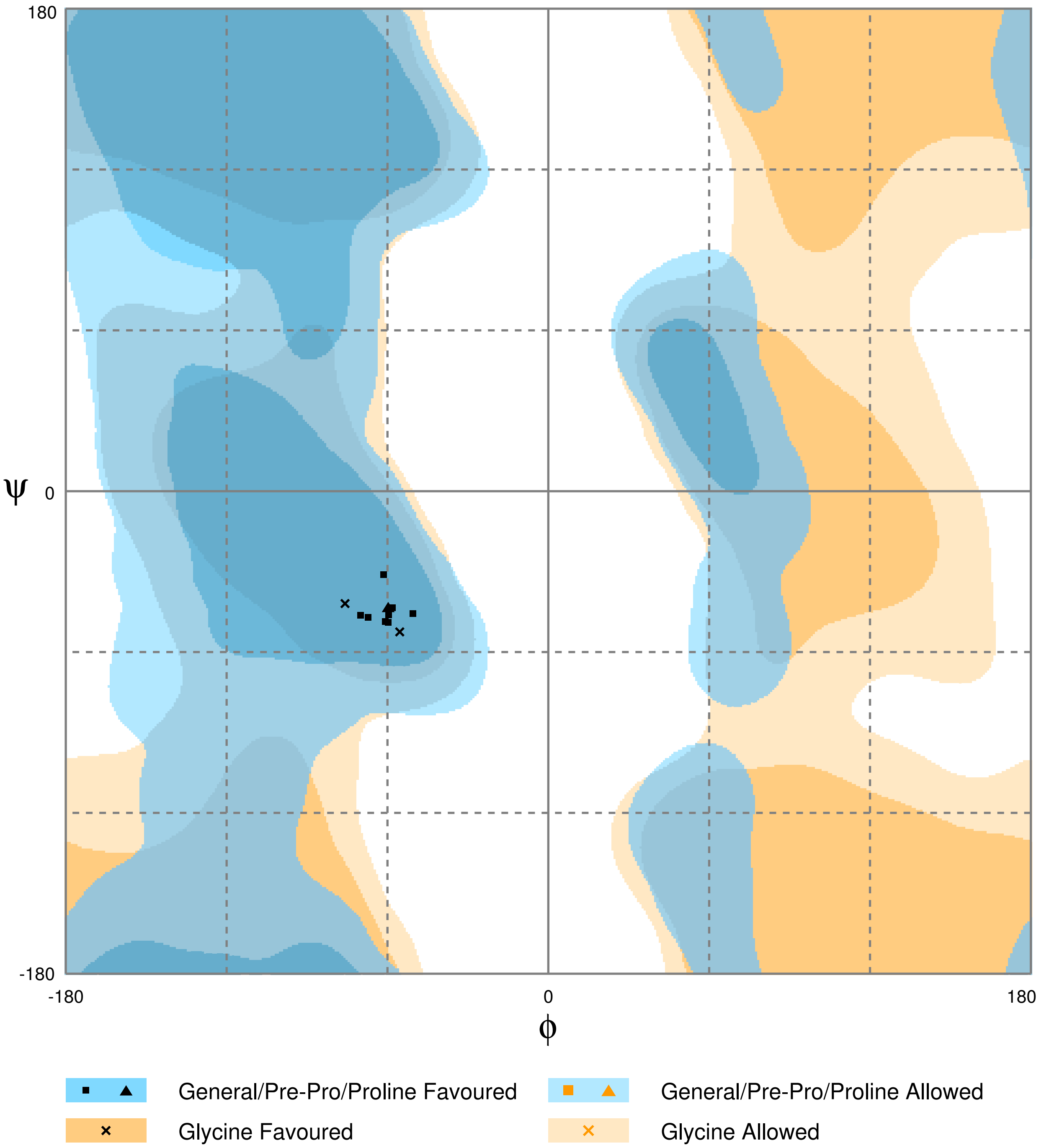


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_1ve

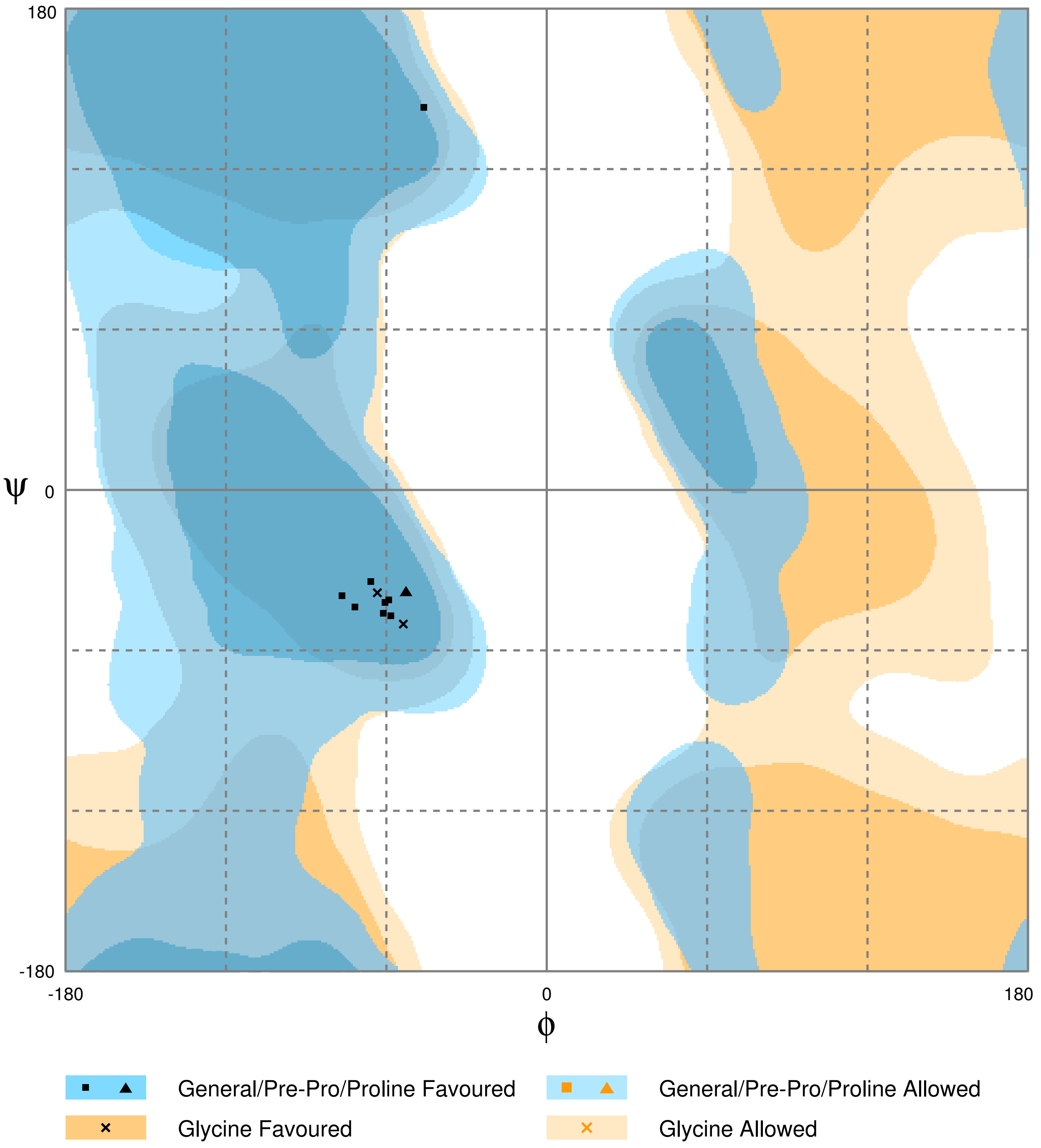


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_aj8

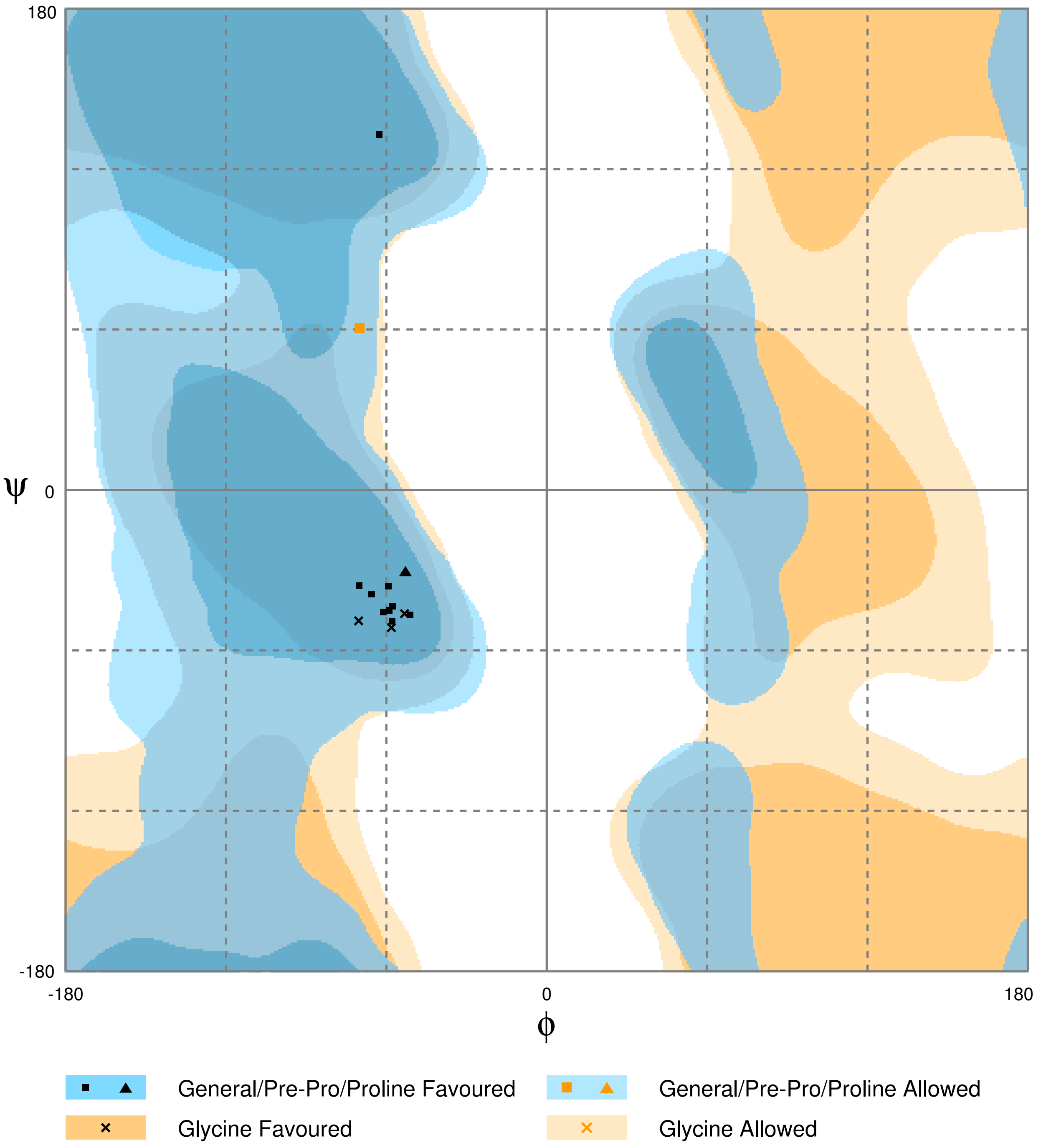


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ala

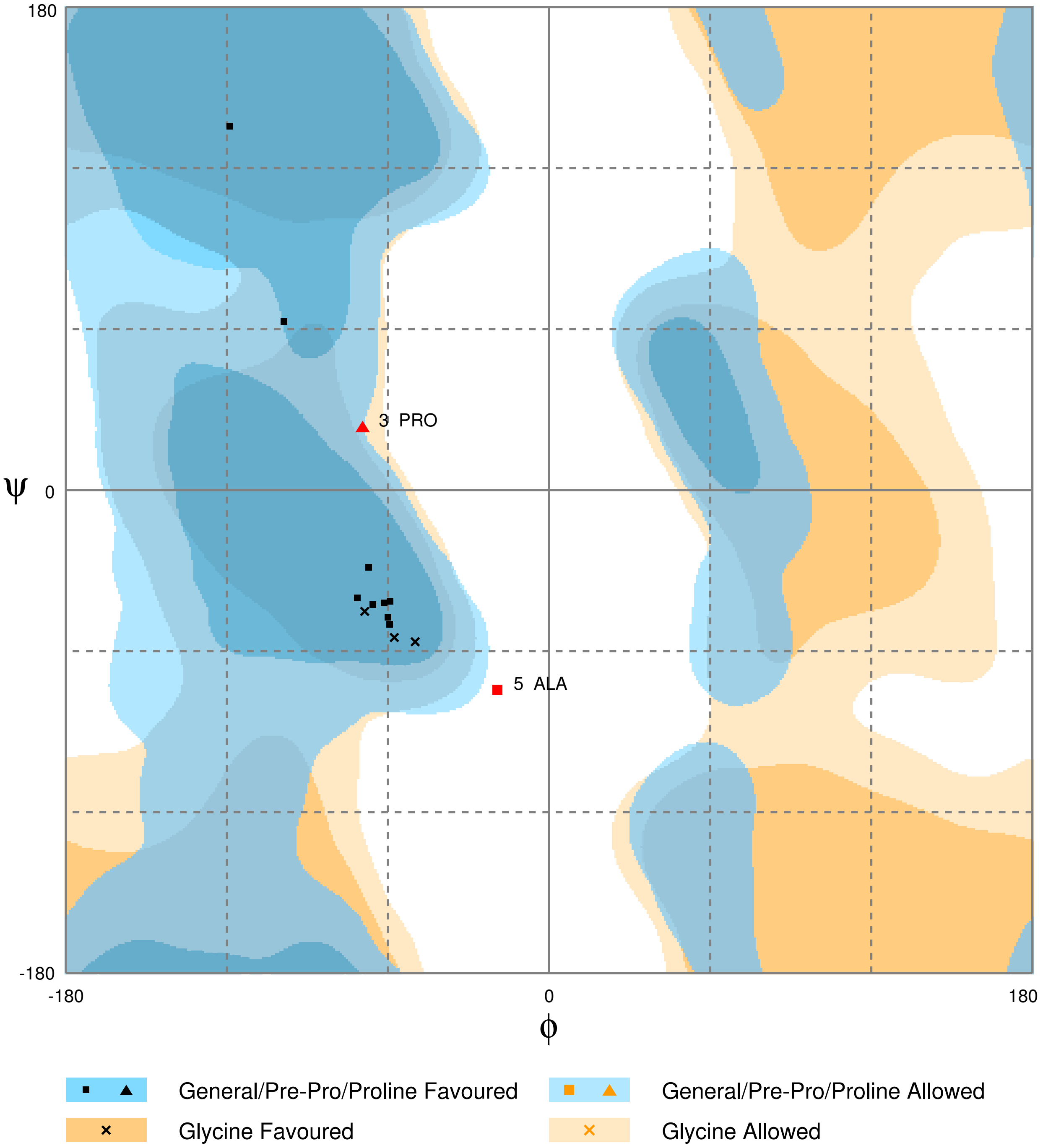


Number of residues in favoured region (~98.0% expected) : 13 (92.9%)
Number of residues in allowed region (~2.0% expected) : 1 (7.1%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ald

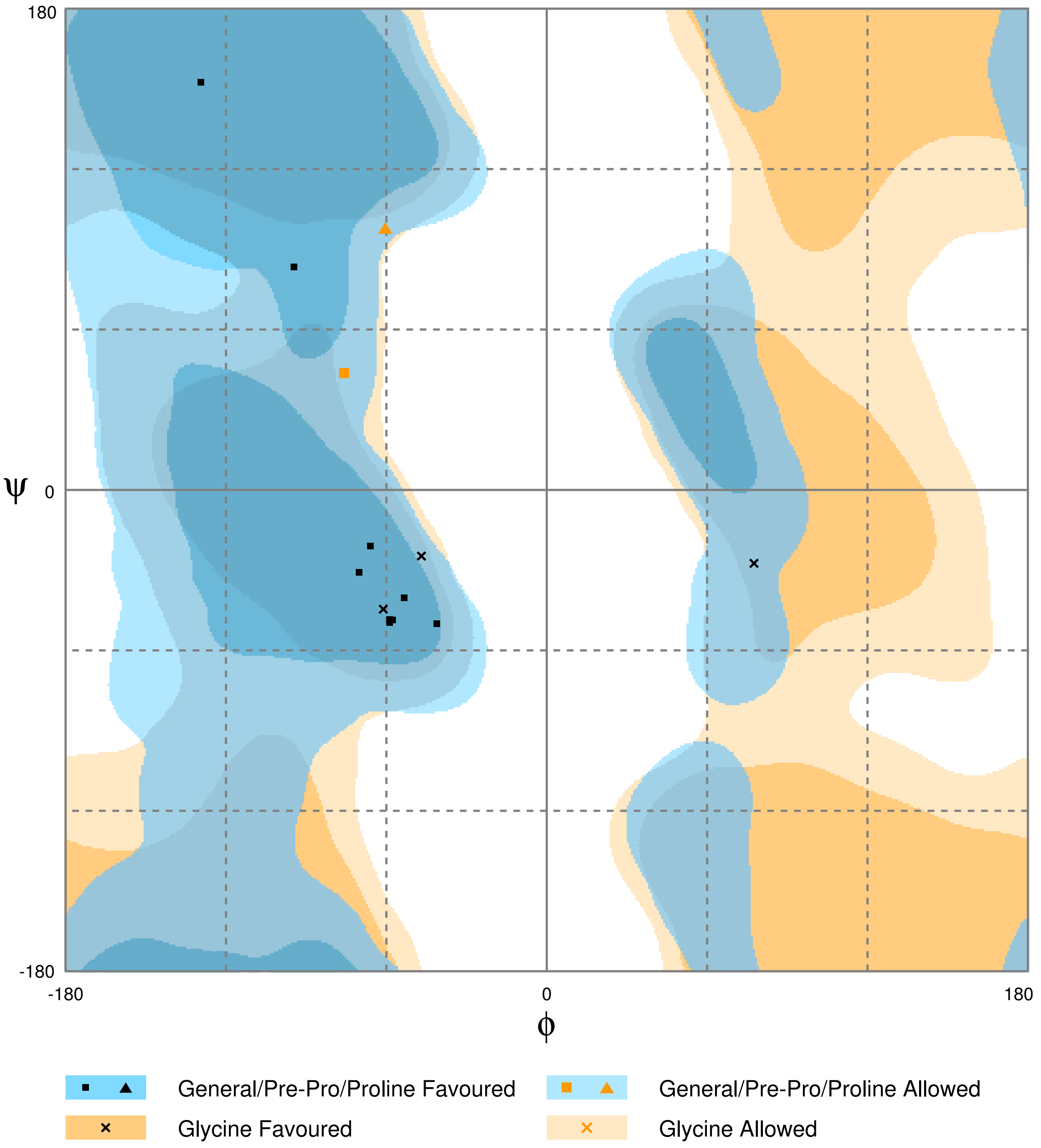


Number of residues in favoured region (~98.0% expected) : 12 (85.7%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 2 (14.3%)

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

Tem_ale

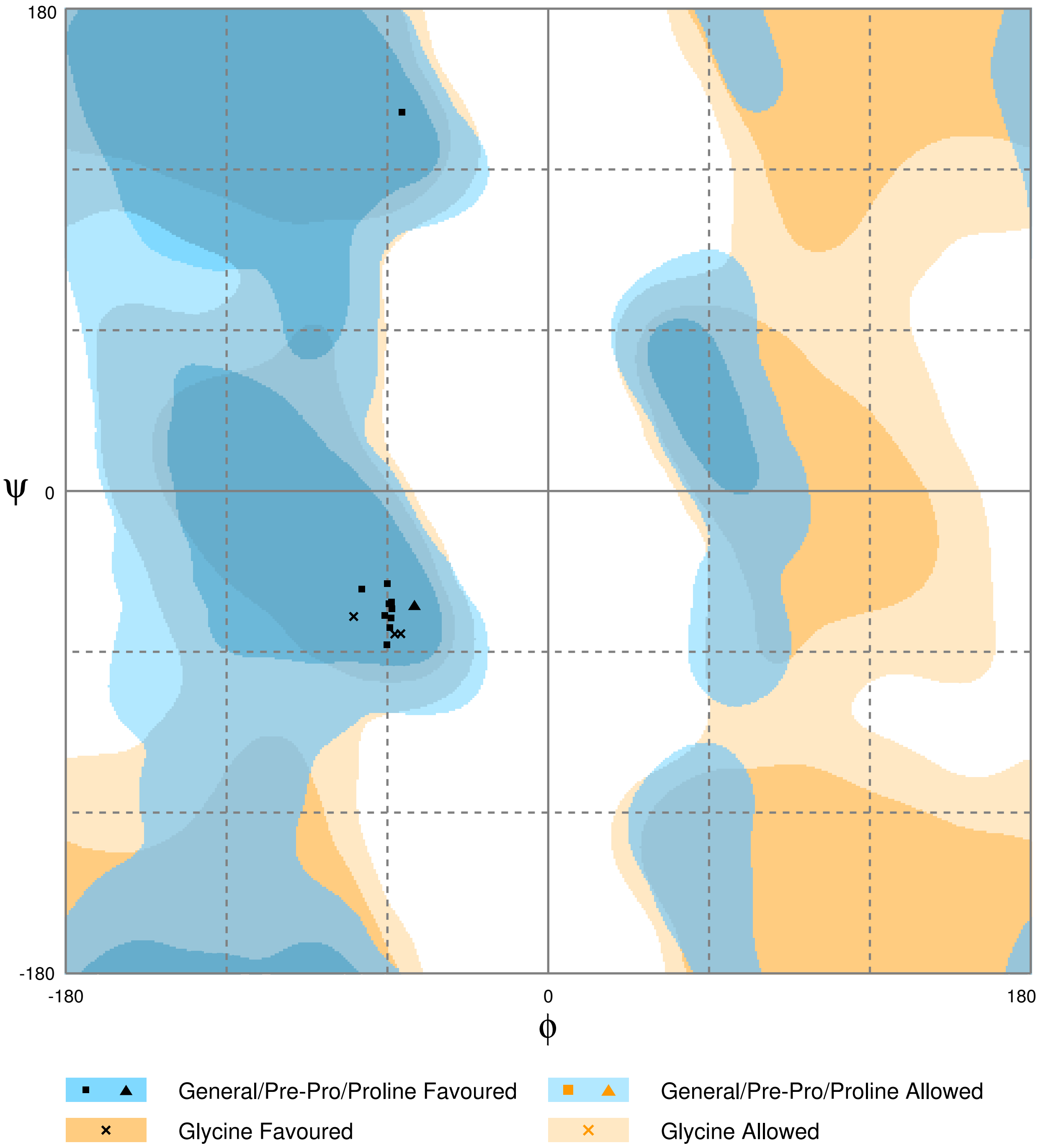


Number of residues in favoured region (~98.0% expected) : 12 (85.7%)
Number of residues in allowed region (~2.0% expected) : 2 (14.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_alf

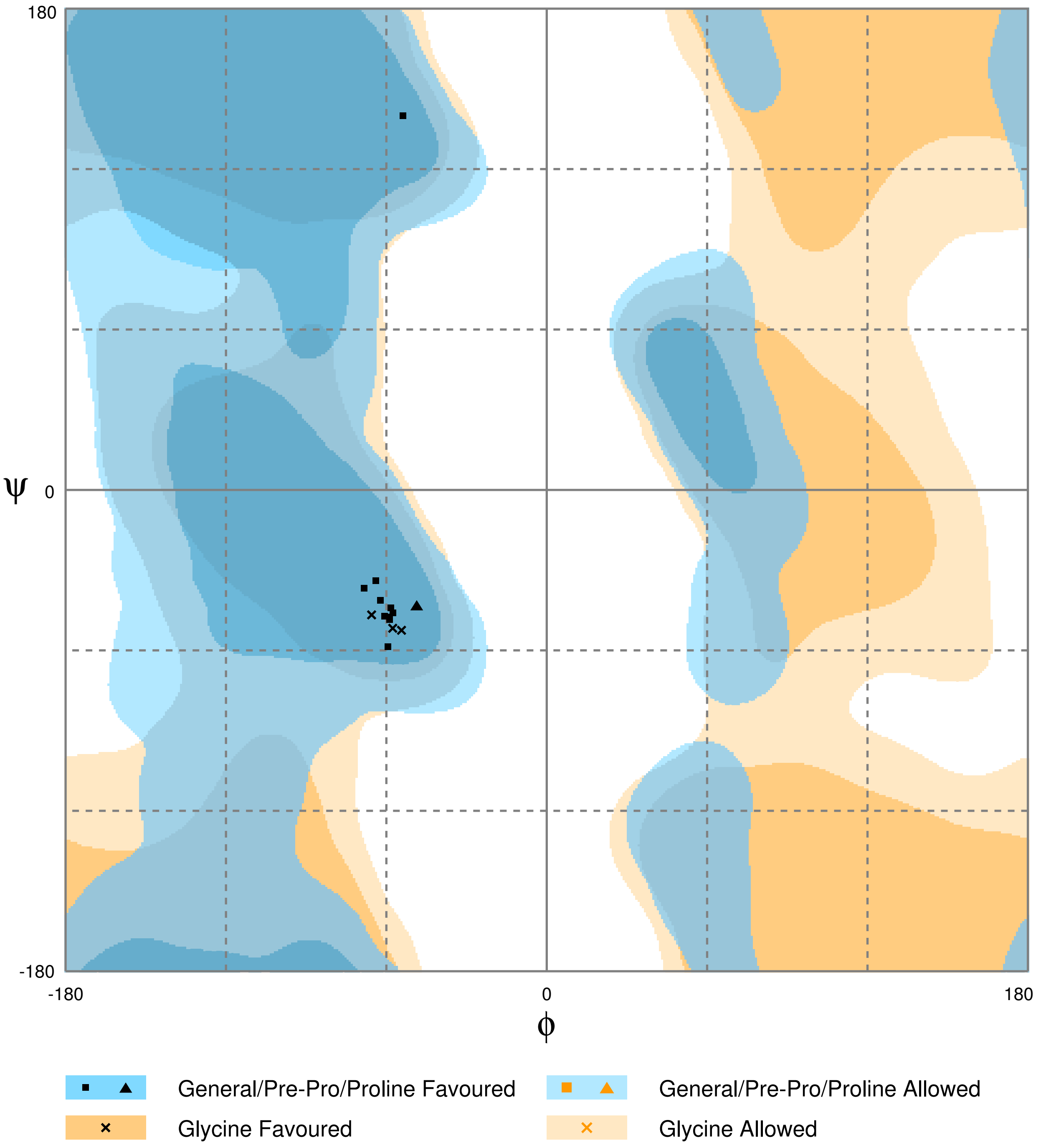


Number of residues in favoured region (~98.0% expected) : 14 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_alg

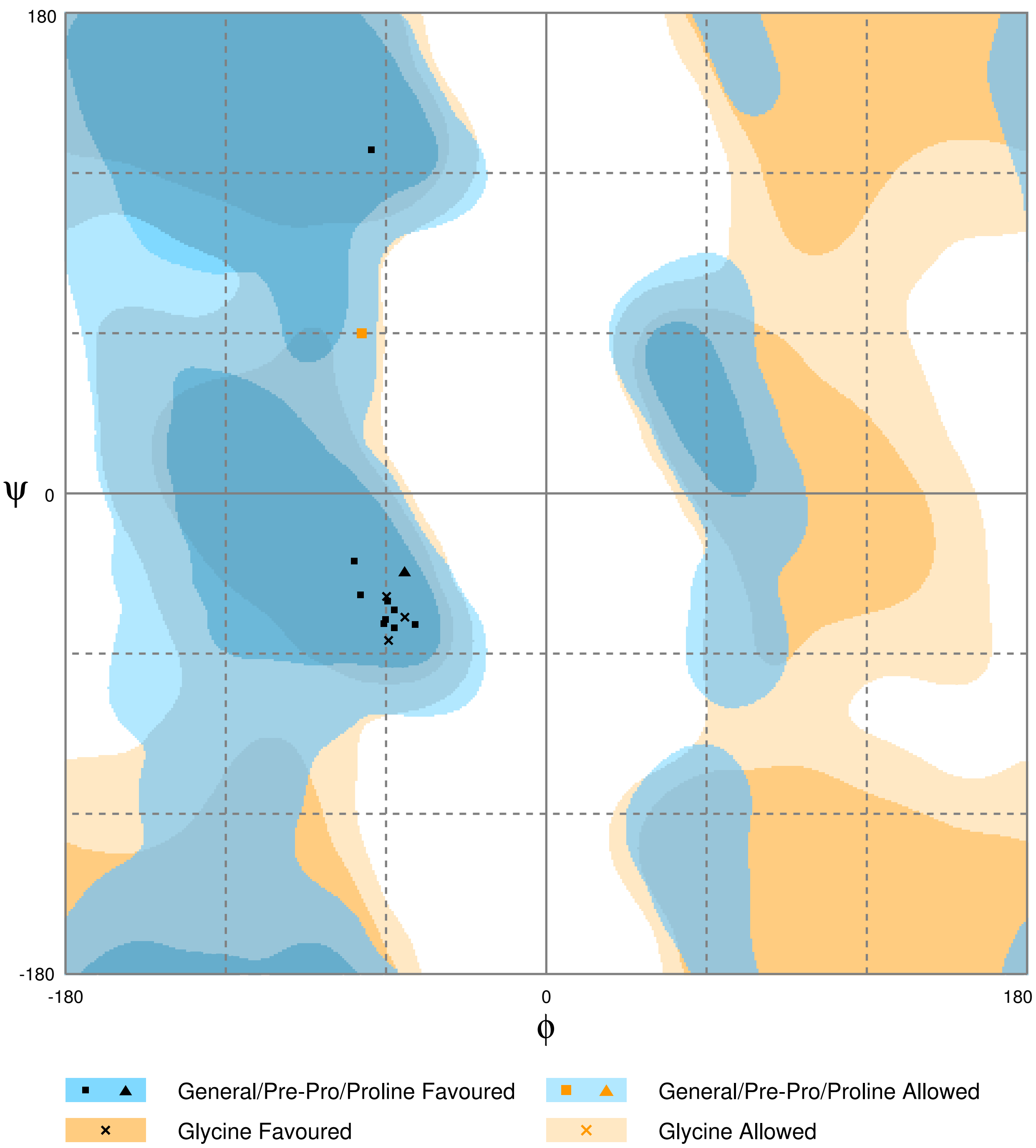


Number of residues in favoured region (~98.0% expected) : 14 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_alh

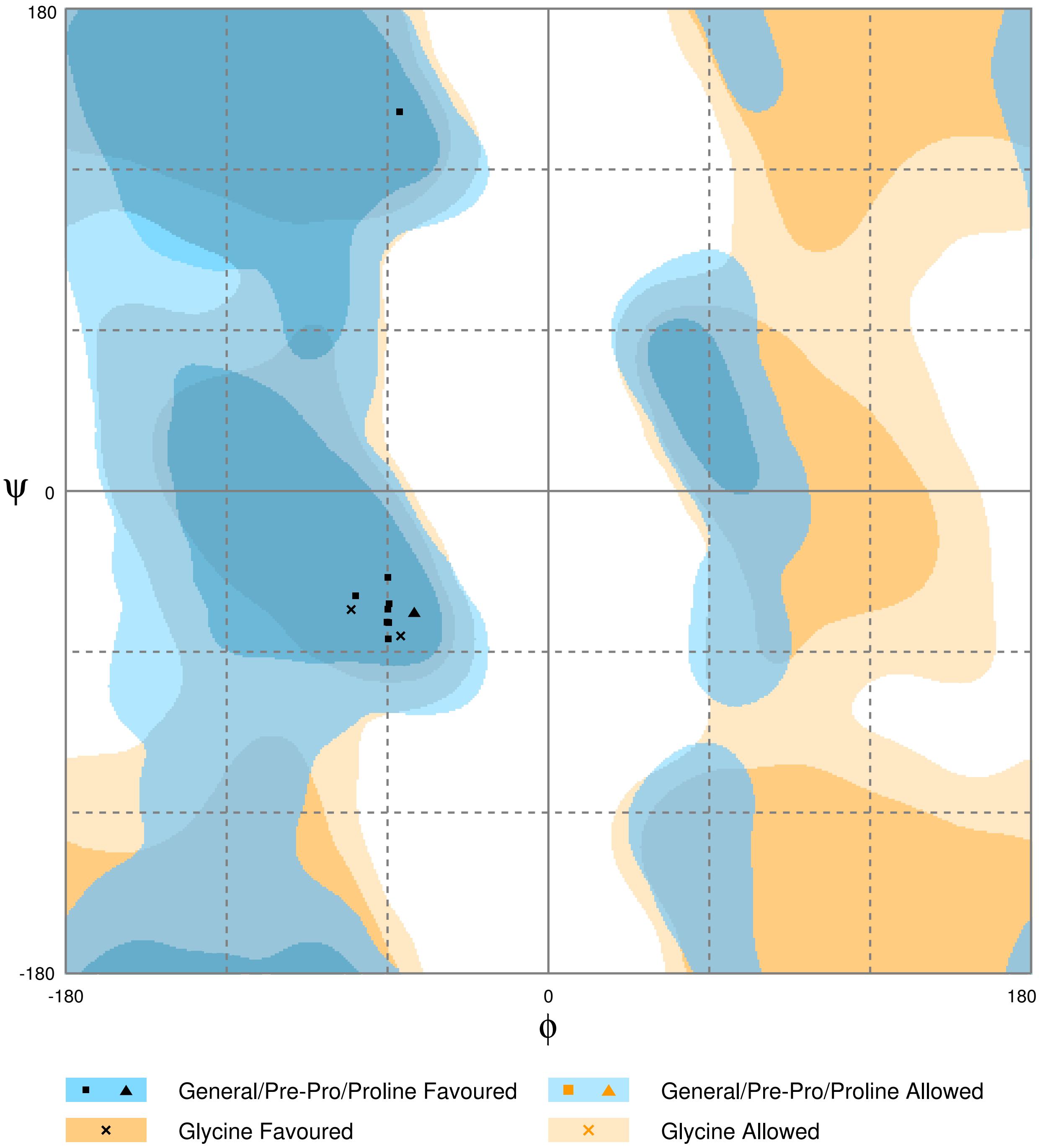


Number of residues in favoured region (~98.0% expected) : 13 (92.9%)
Number of residues in allowed region (~2.0% expected) : 1 (7.1%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ali

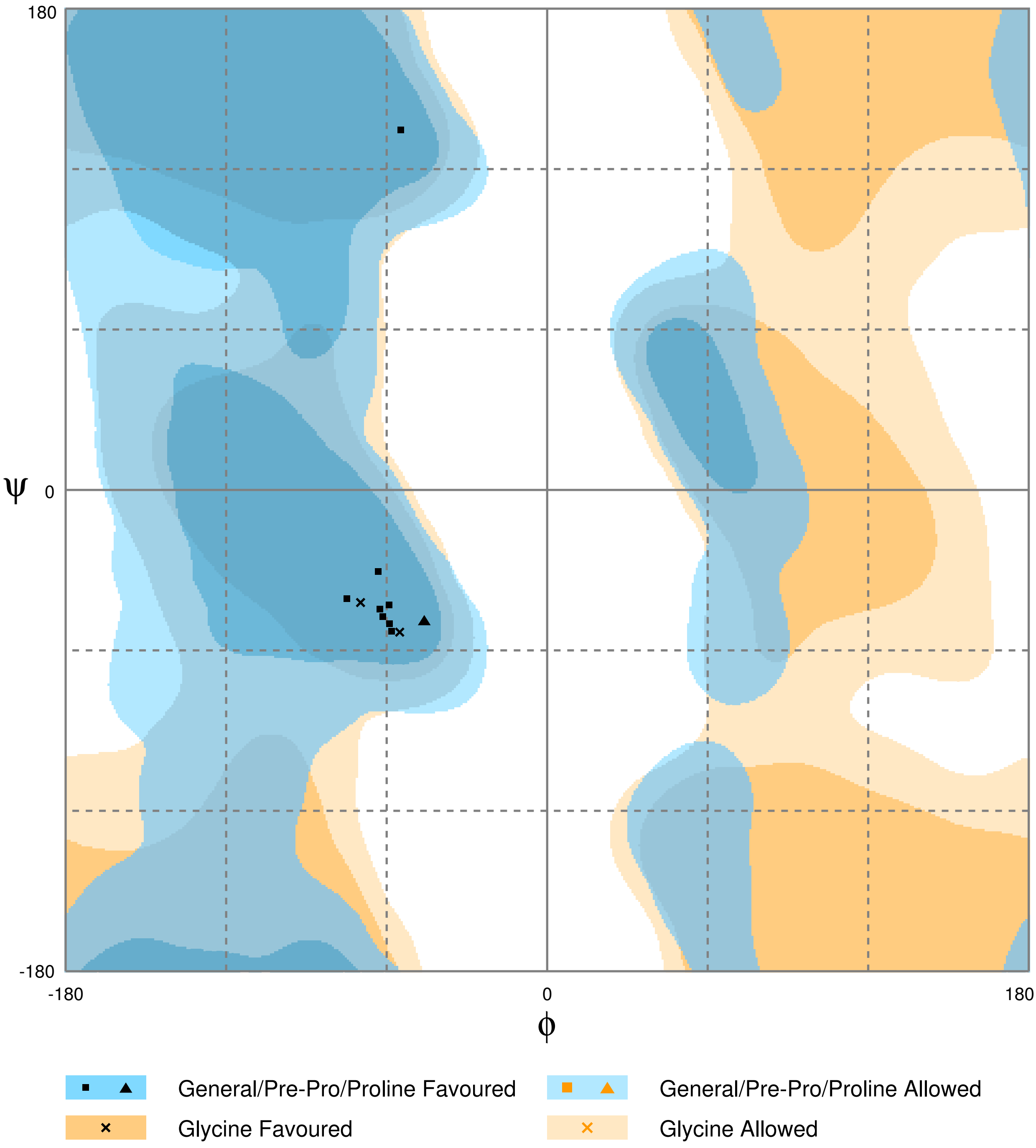


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_alj

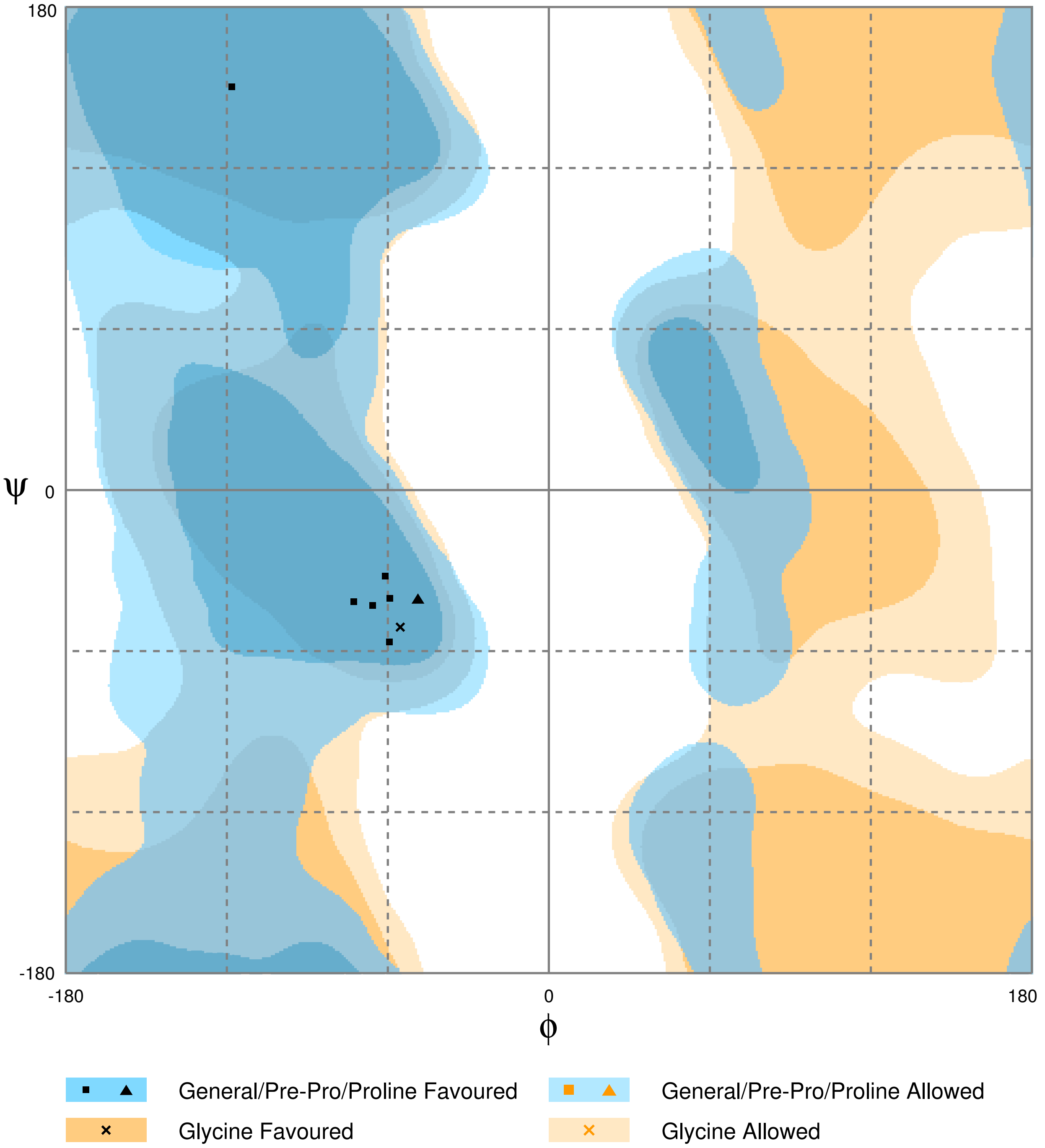


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_alk

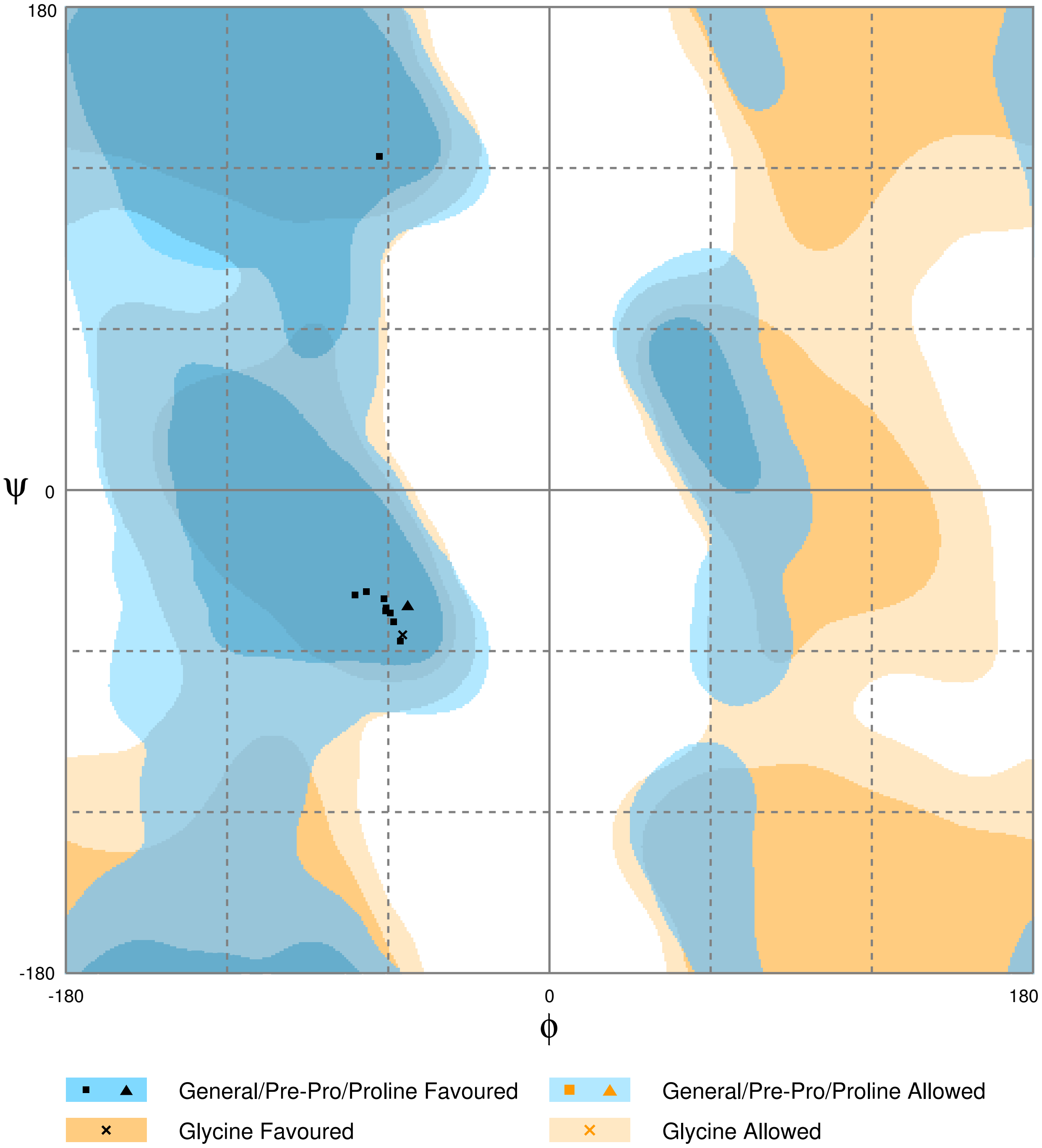


Number of residues in favoured region (~98.0% expected) : 8 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_b

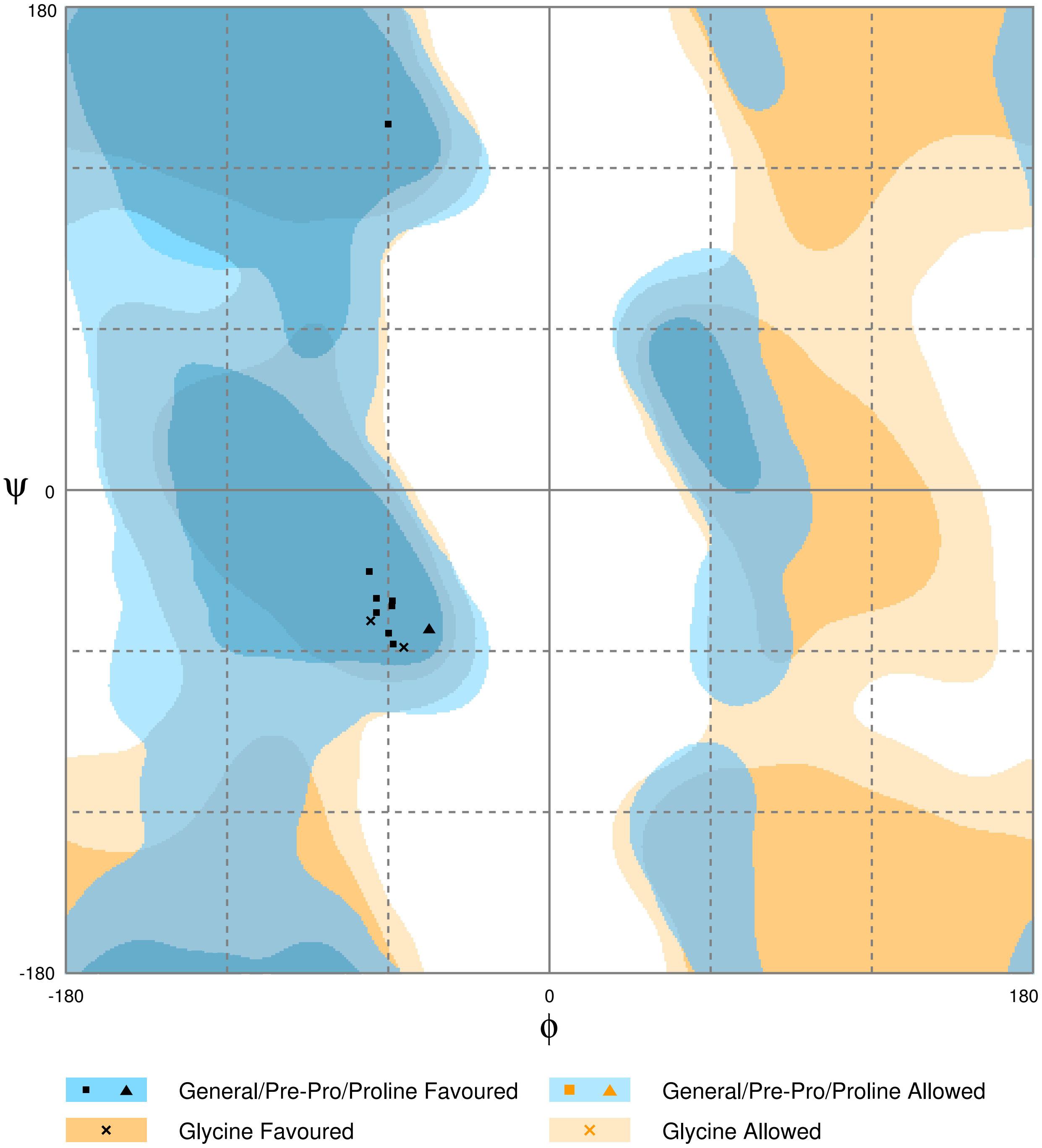


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_c

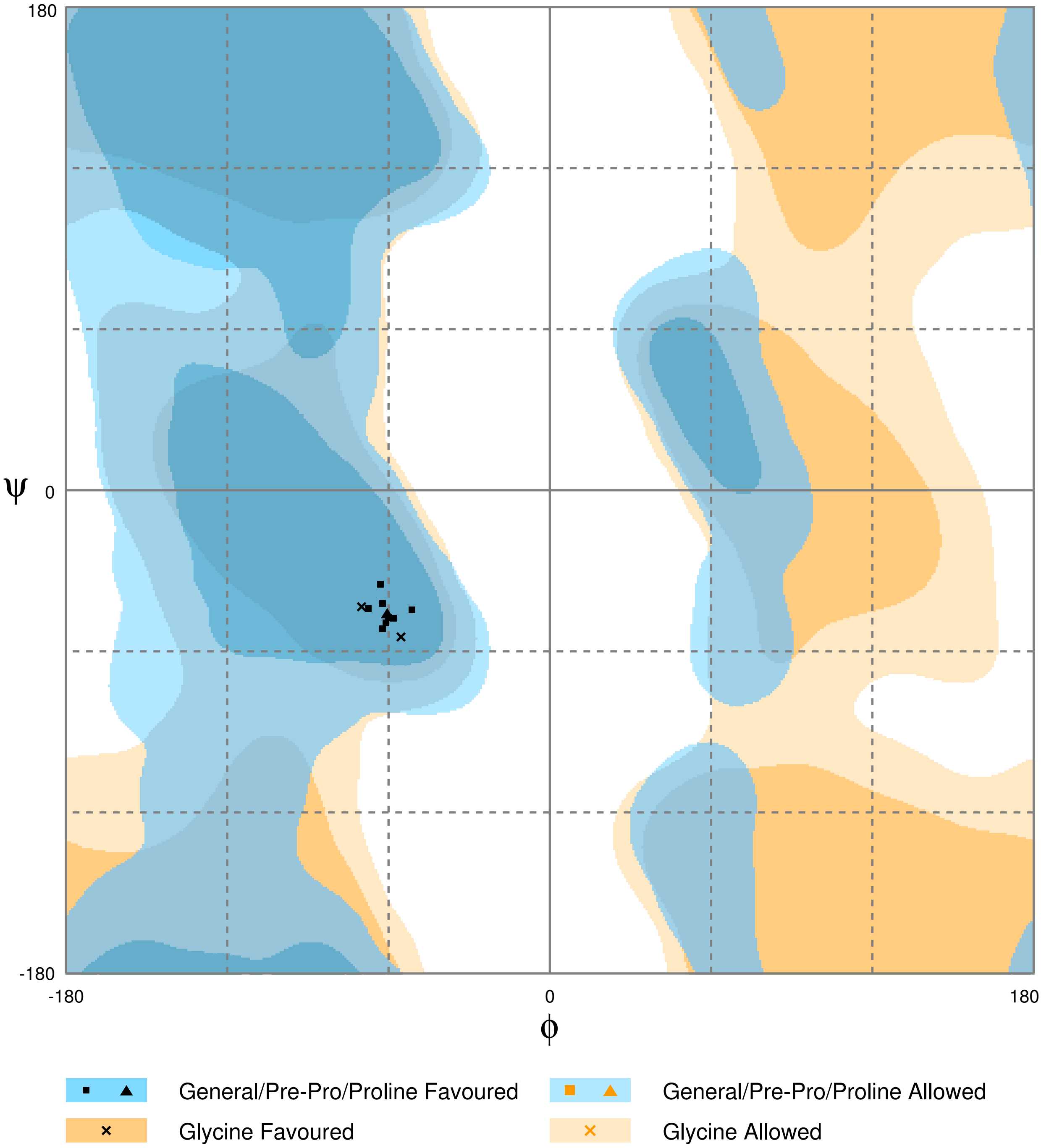


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_cg1

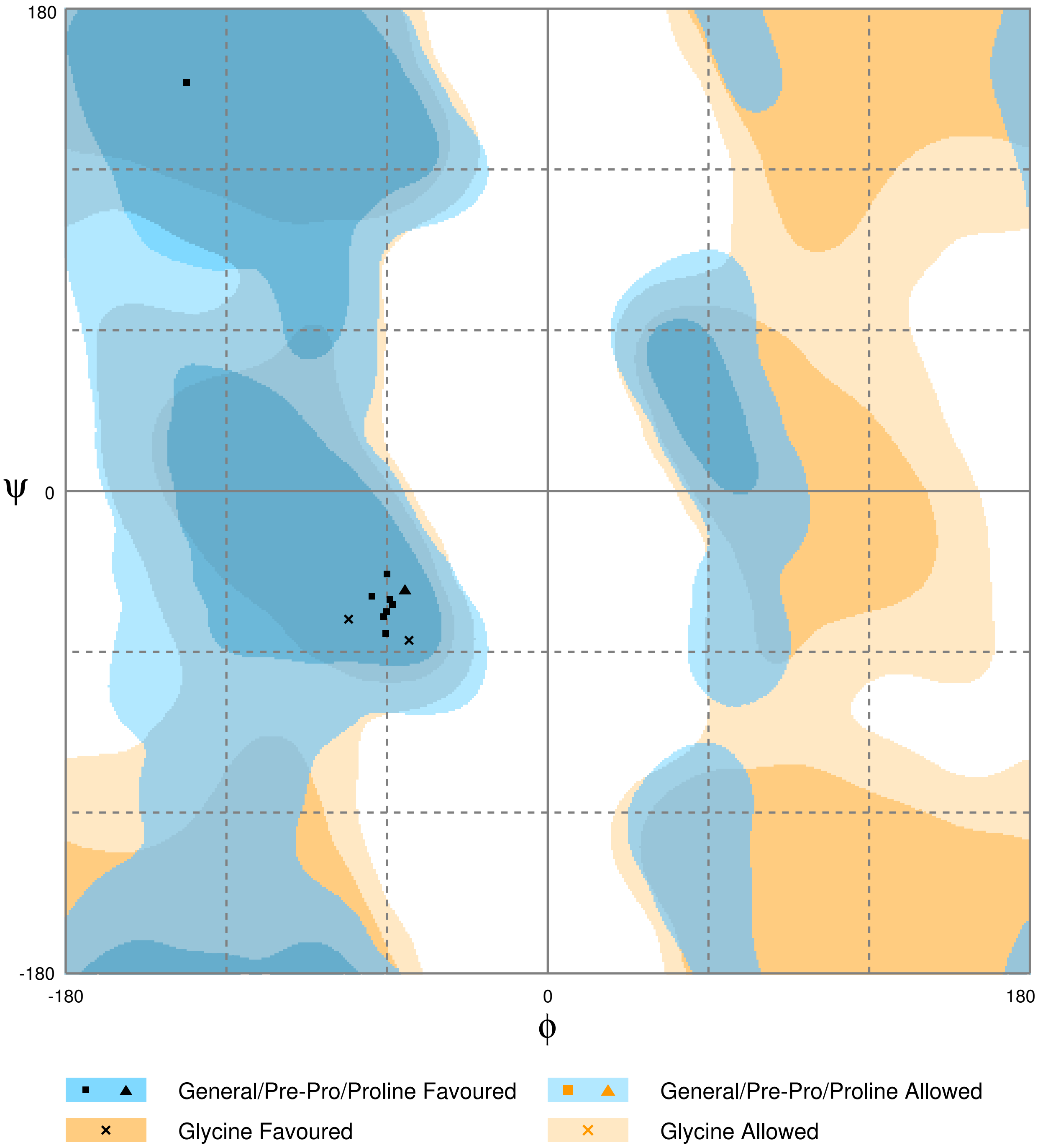


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_cg2

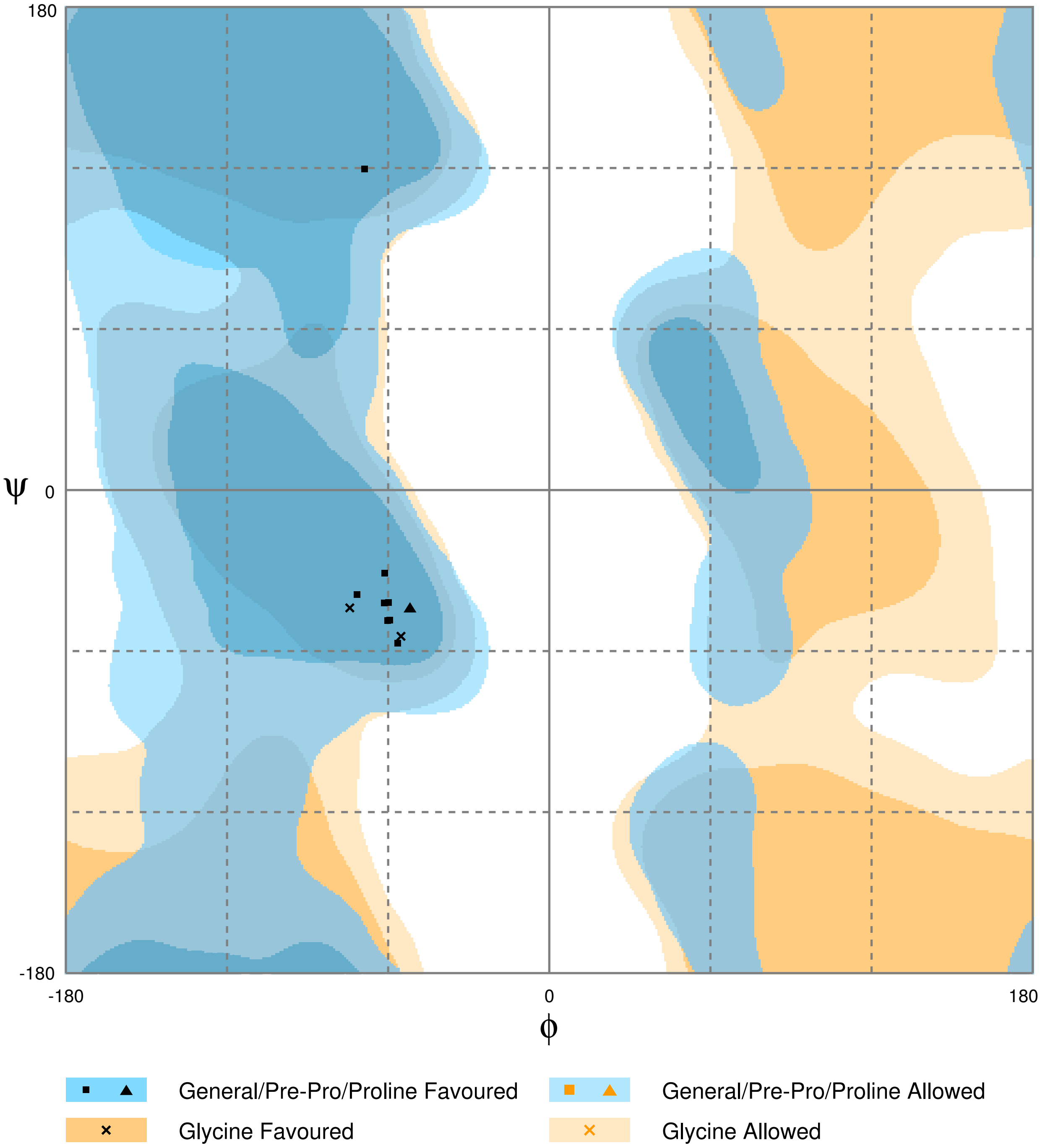


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_cg3

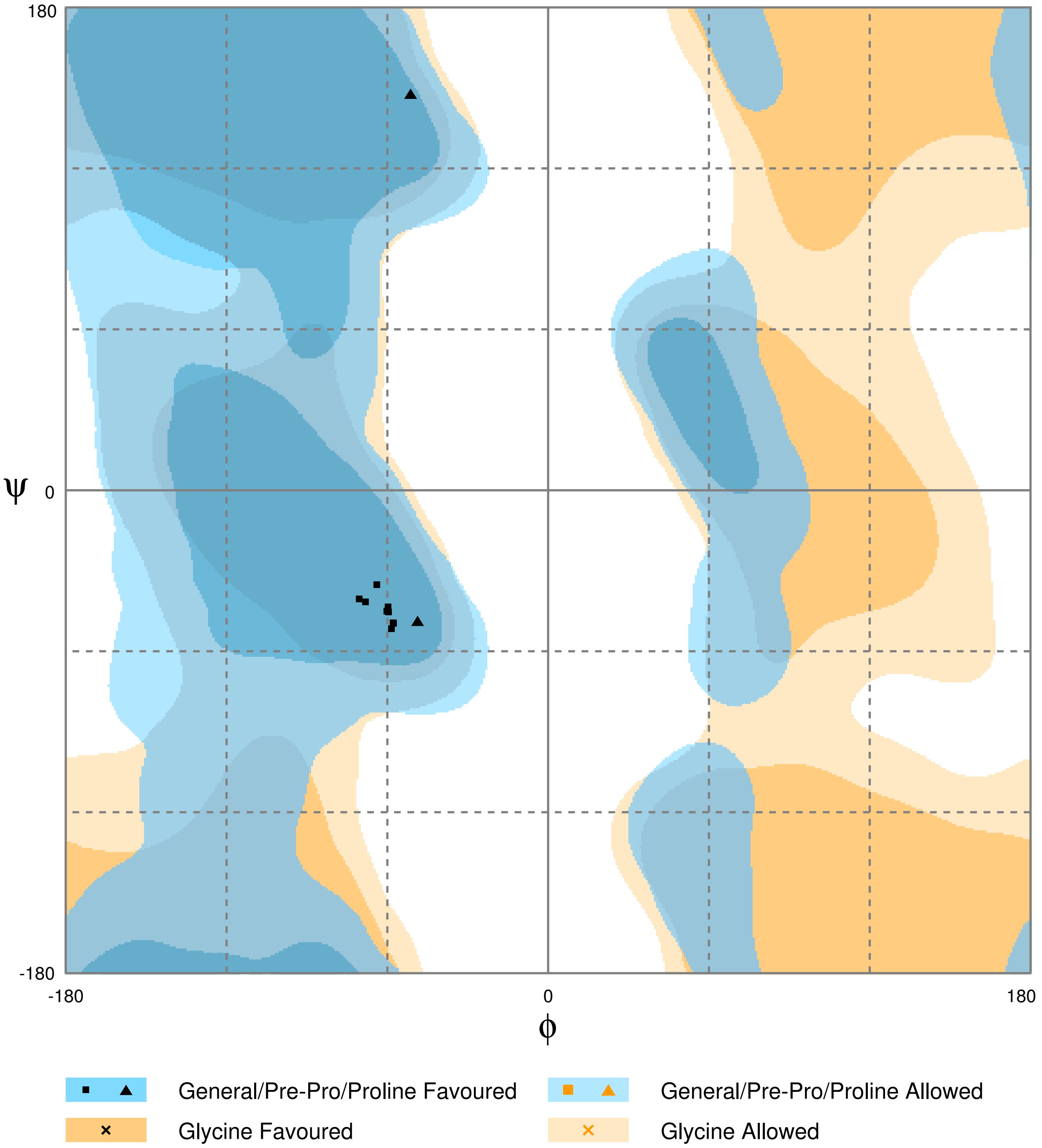


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_cpa

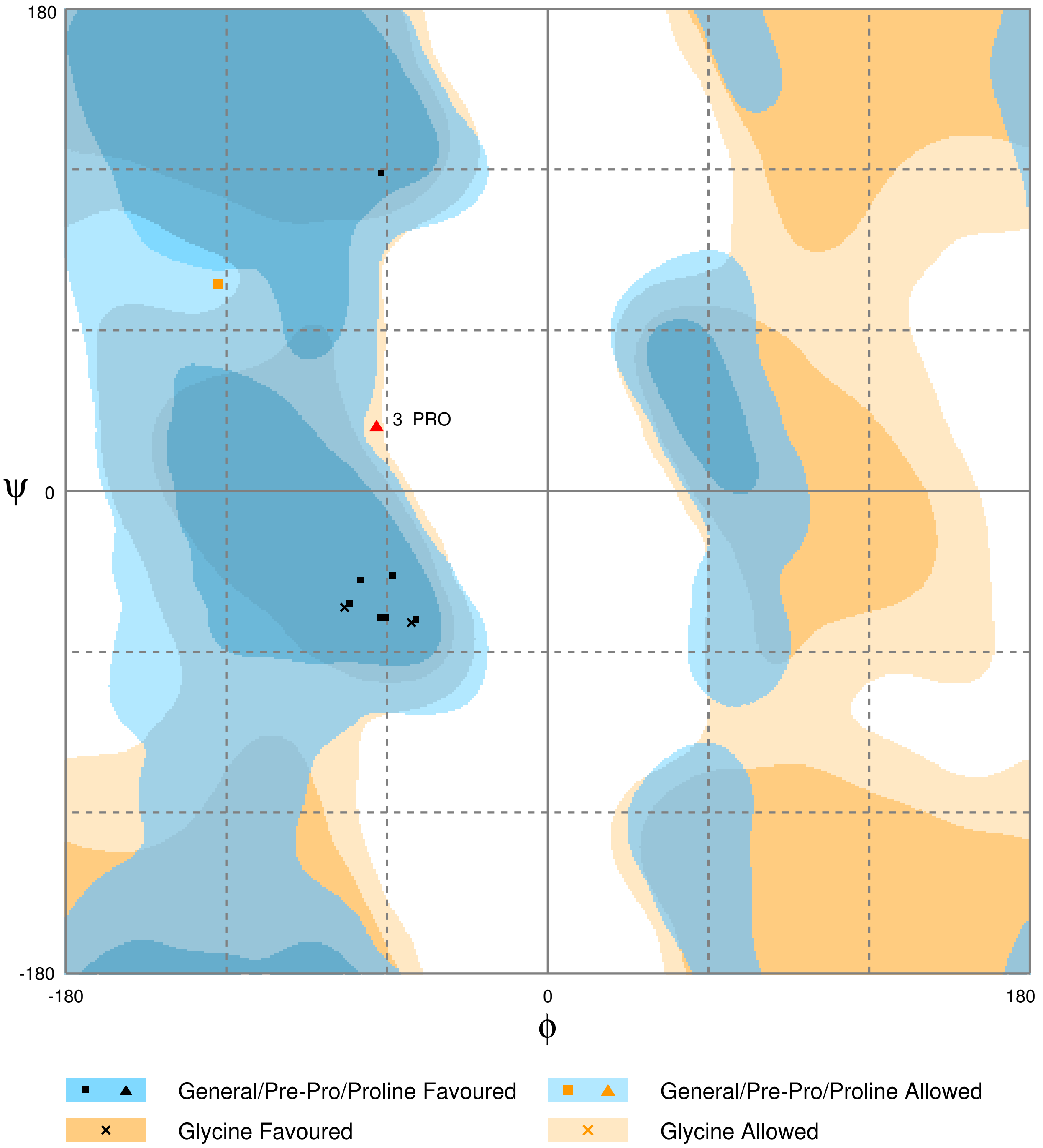


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_cpb

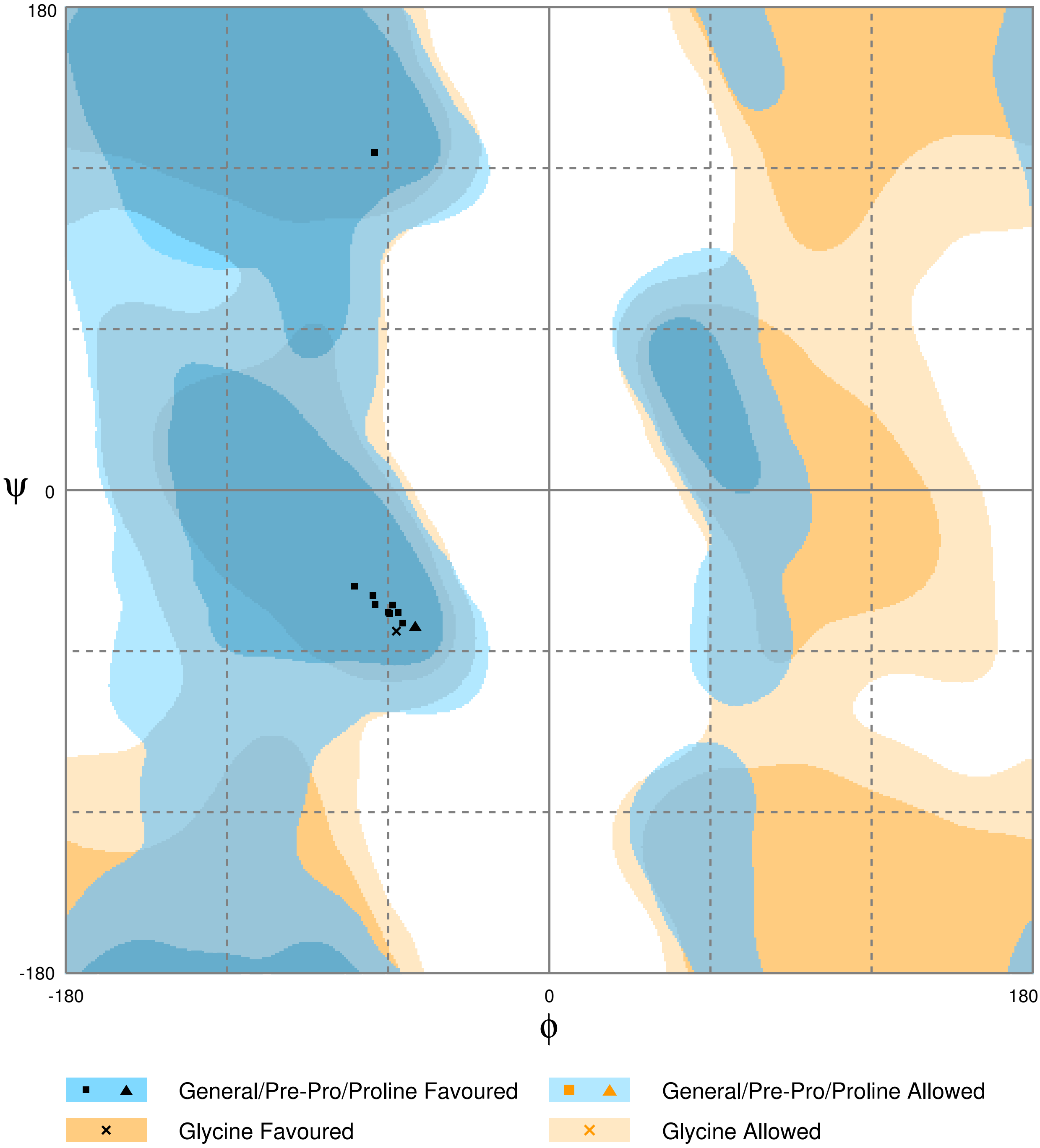


Number of residues in favoured region (~98.0% expected) : 9 (81.8%)
Number of residues in allowed region (~2.0% expected) : 1 (9.1%)
Number of residues in outlier region : 1 (9.1%)

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

Tem_d

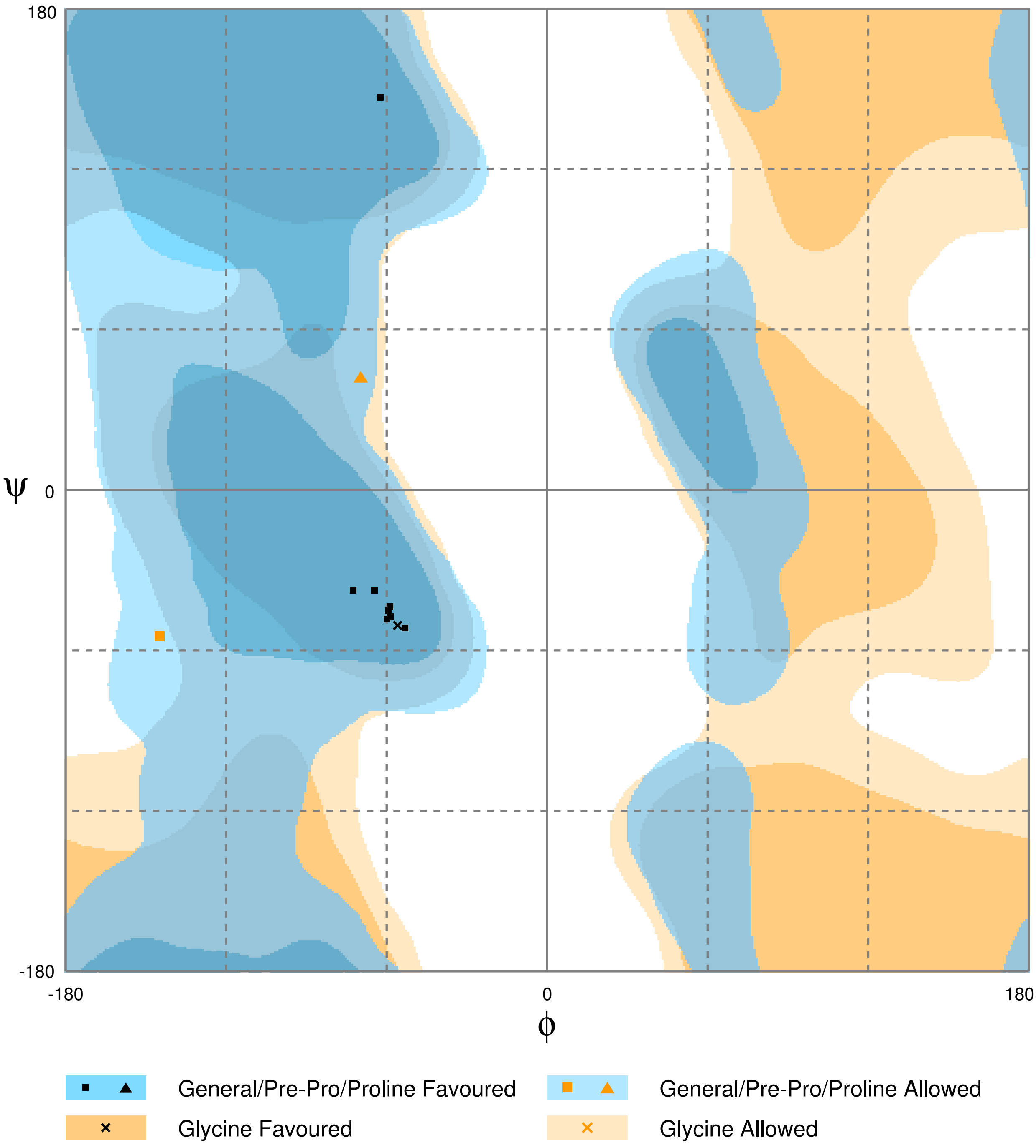


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_e

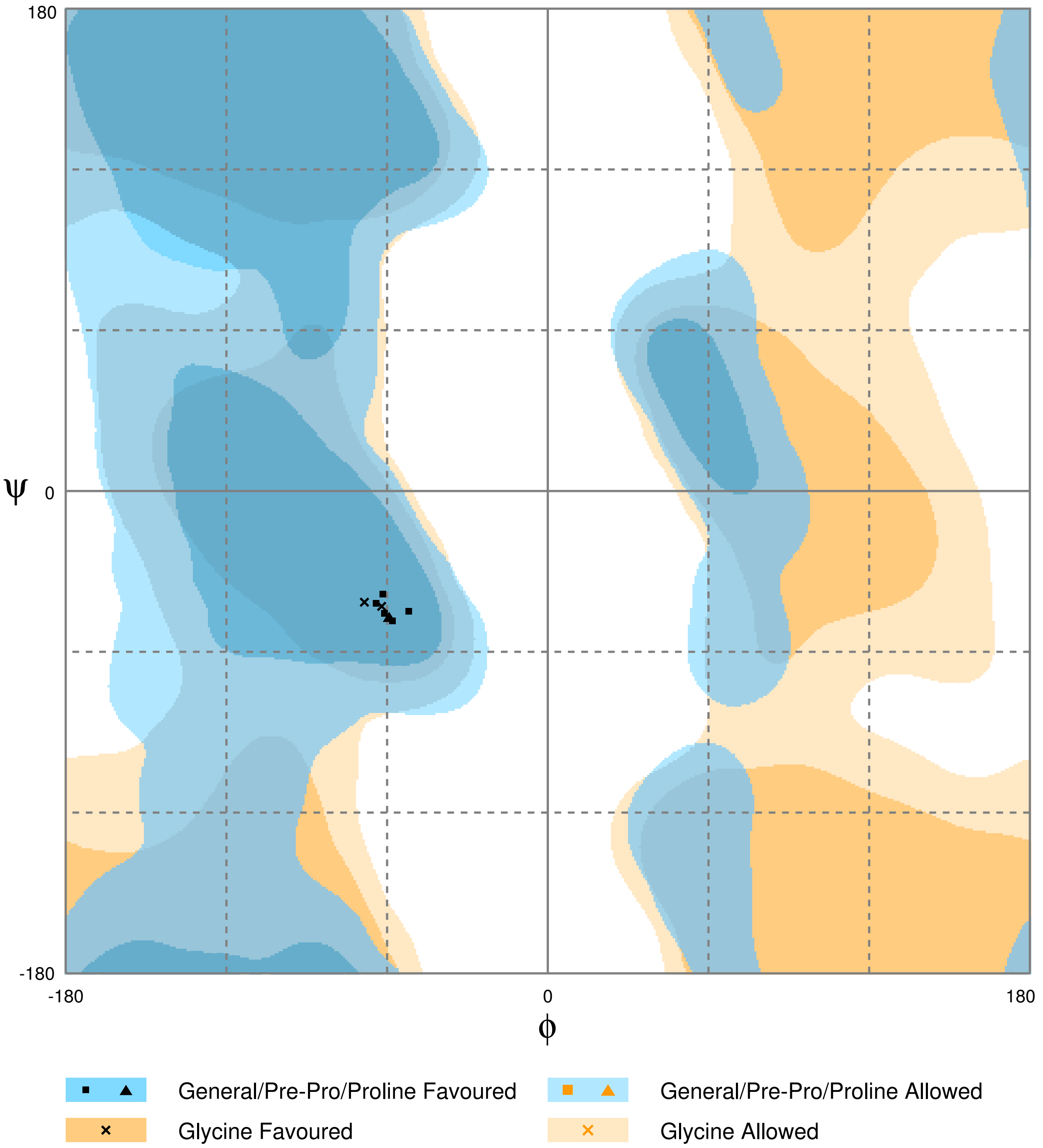


Number of residues in favoured region (~98.0% expected) : 9 (81.8%)
Number of residues in allowed region (~2.0% expected) : 2 (18.2%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_eca

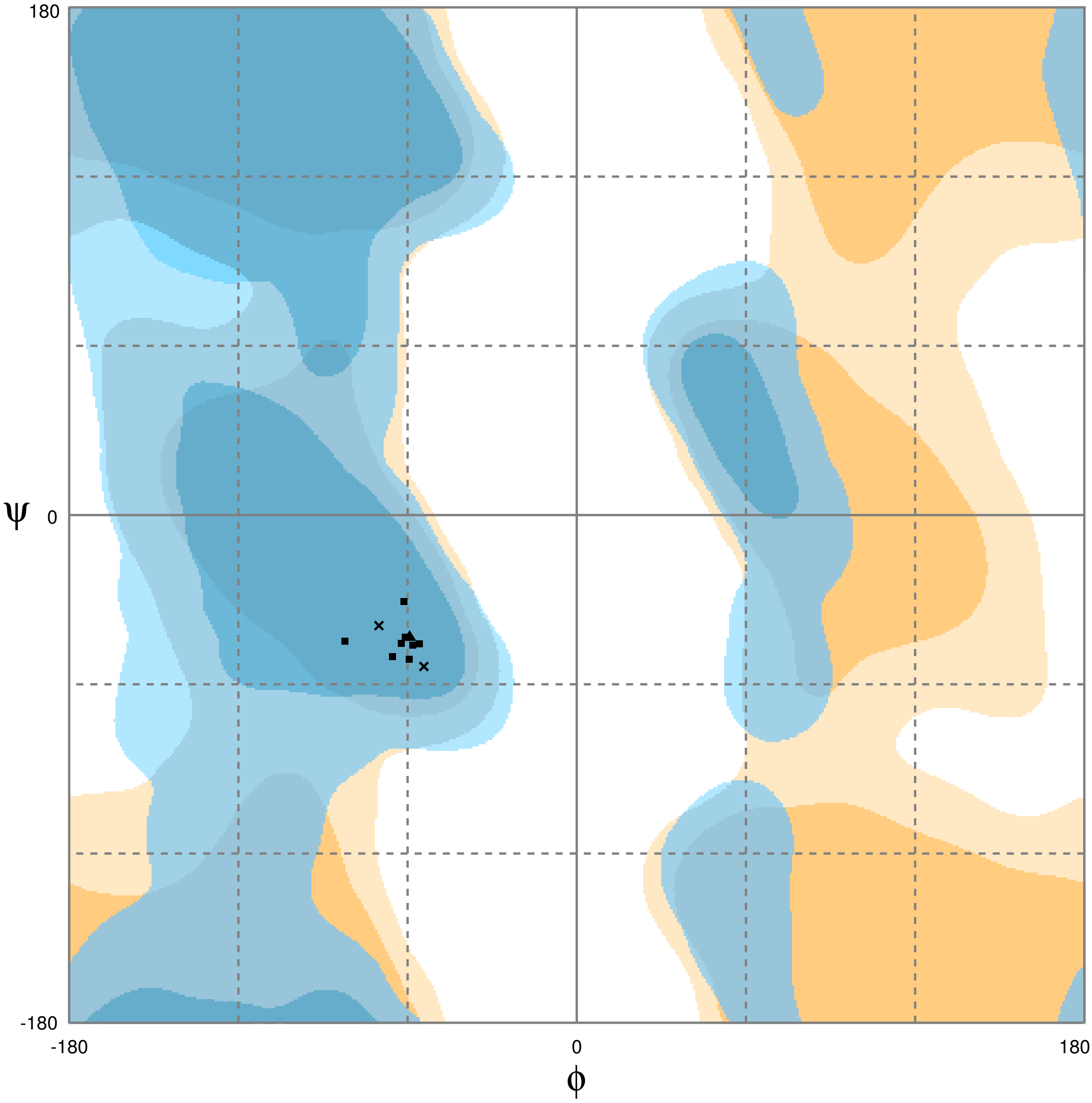


Number of residues in favoured region (~98.0% expected) : 8 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_f



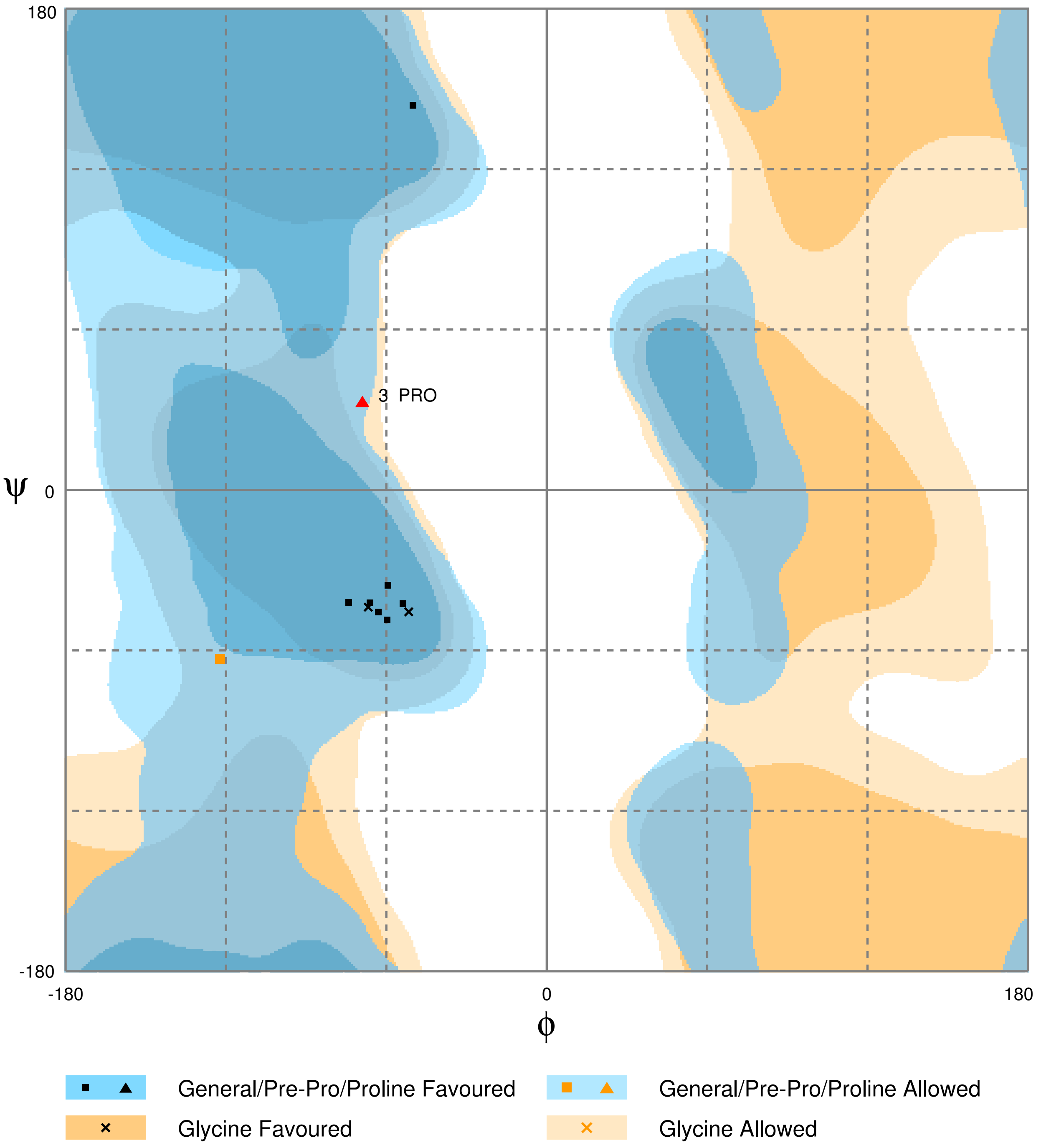
■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

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%)

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

Tem_g

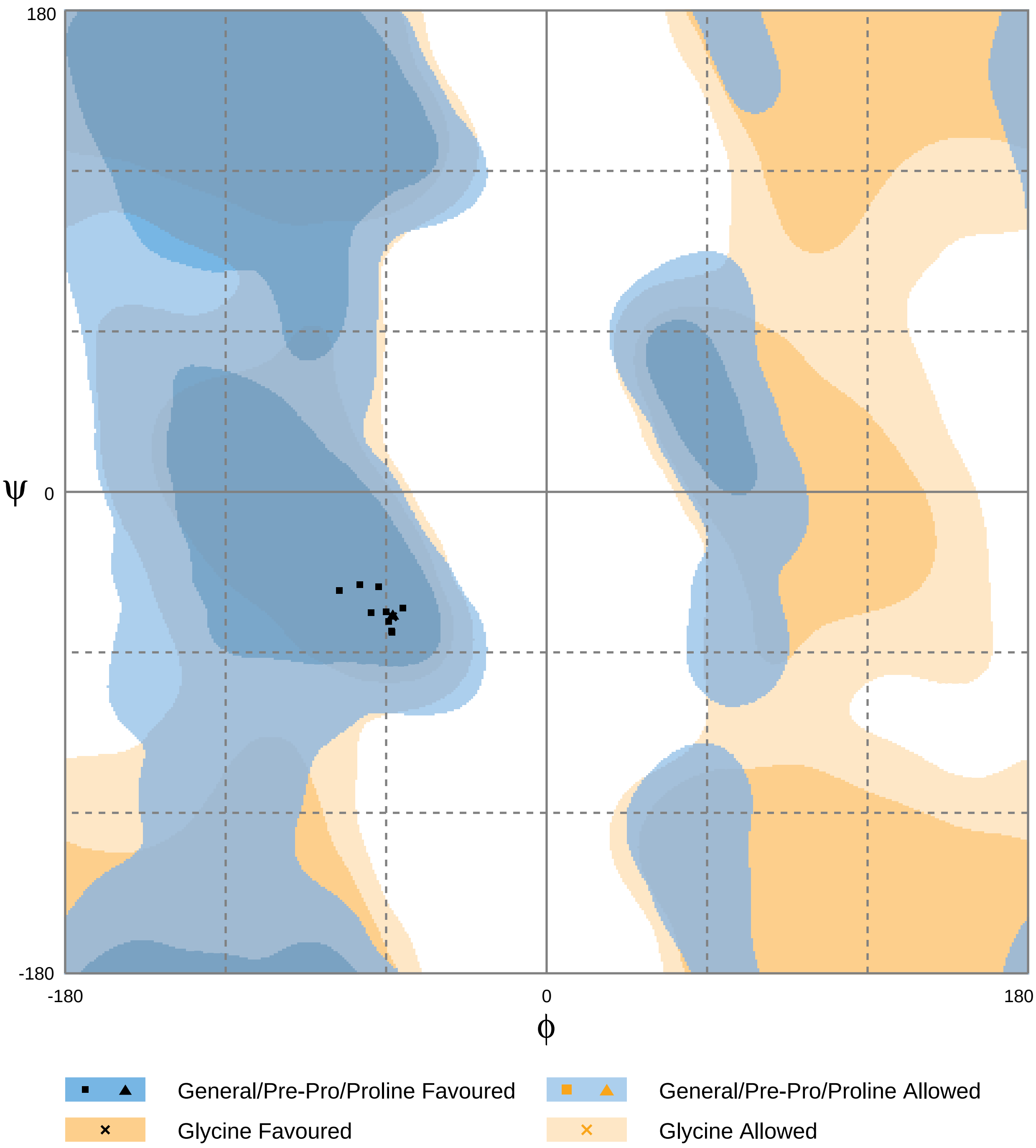


Number of residues in favoured region (~98.0% expected) : 9 (81.8%)
Number of residues in allowed region (~2.0% expected) : 1 (9.1%)
Number of residues in outlier region : 1 (9.1%)

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

Tem_gh

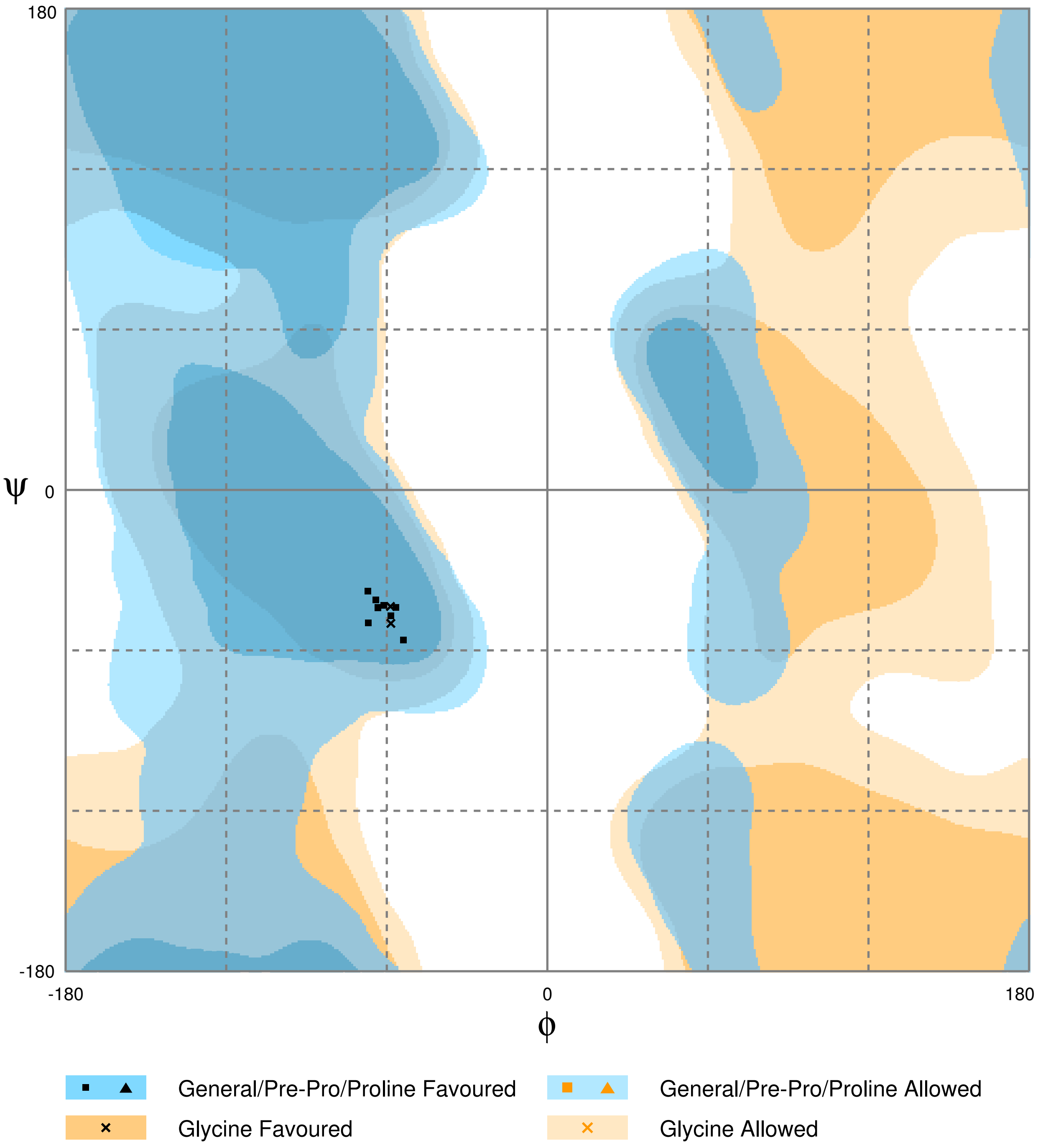


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_gha

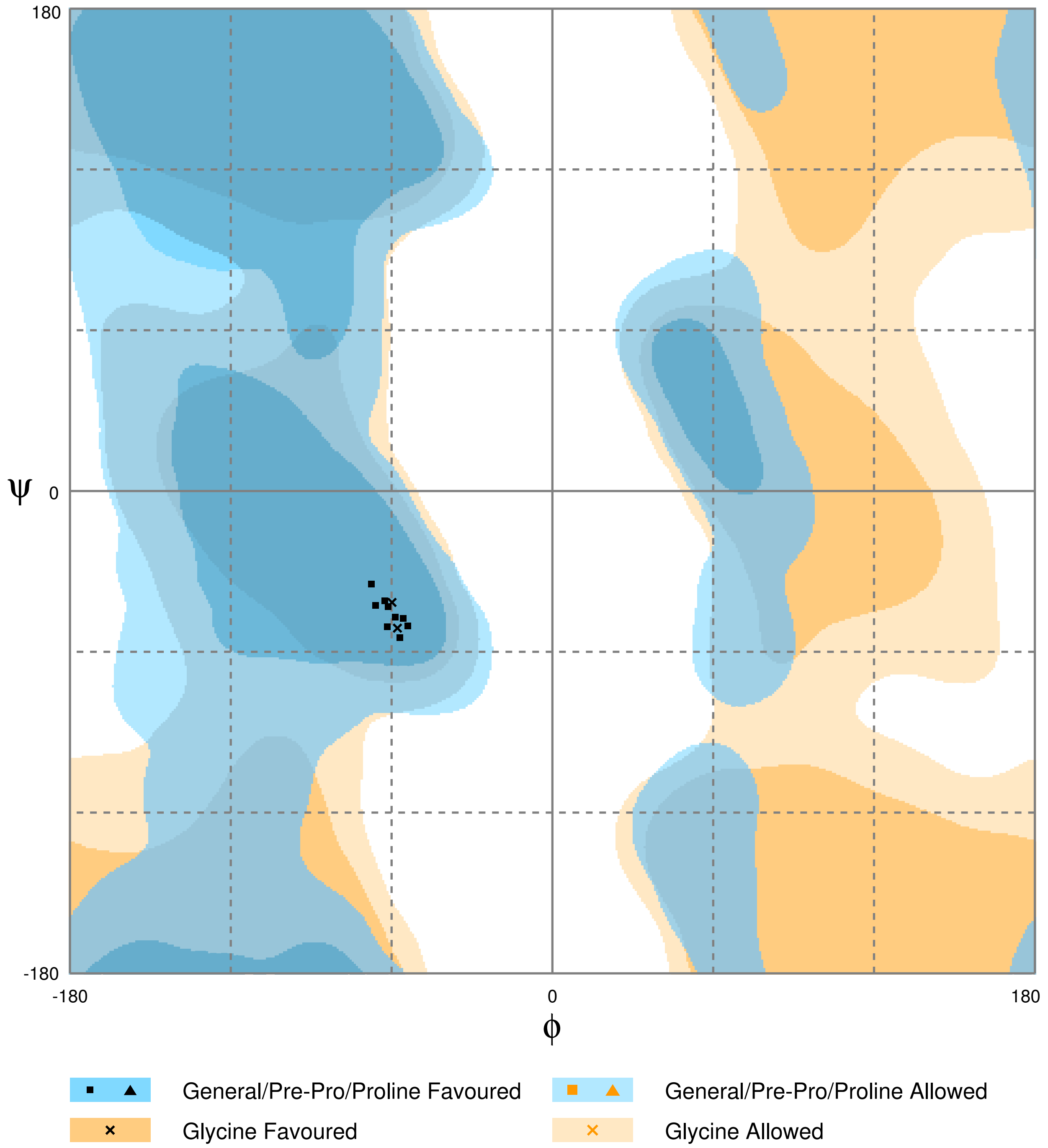


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ghb

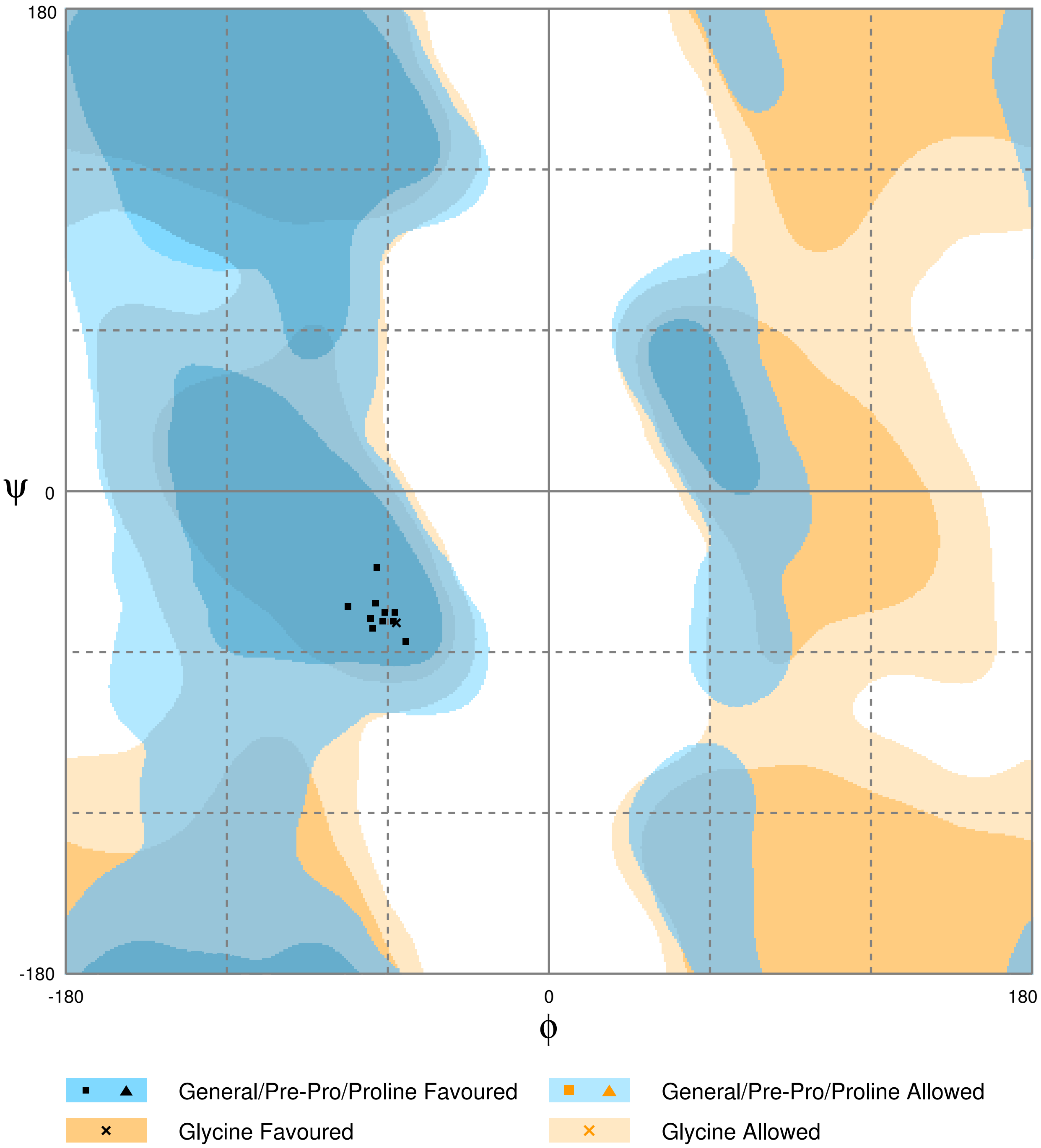


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ghc

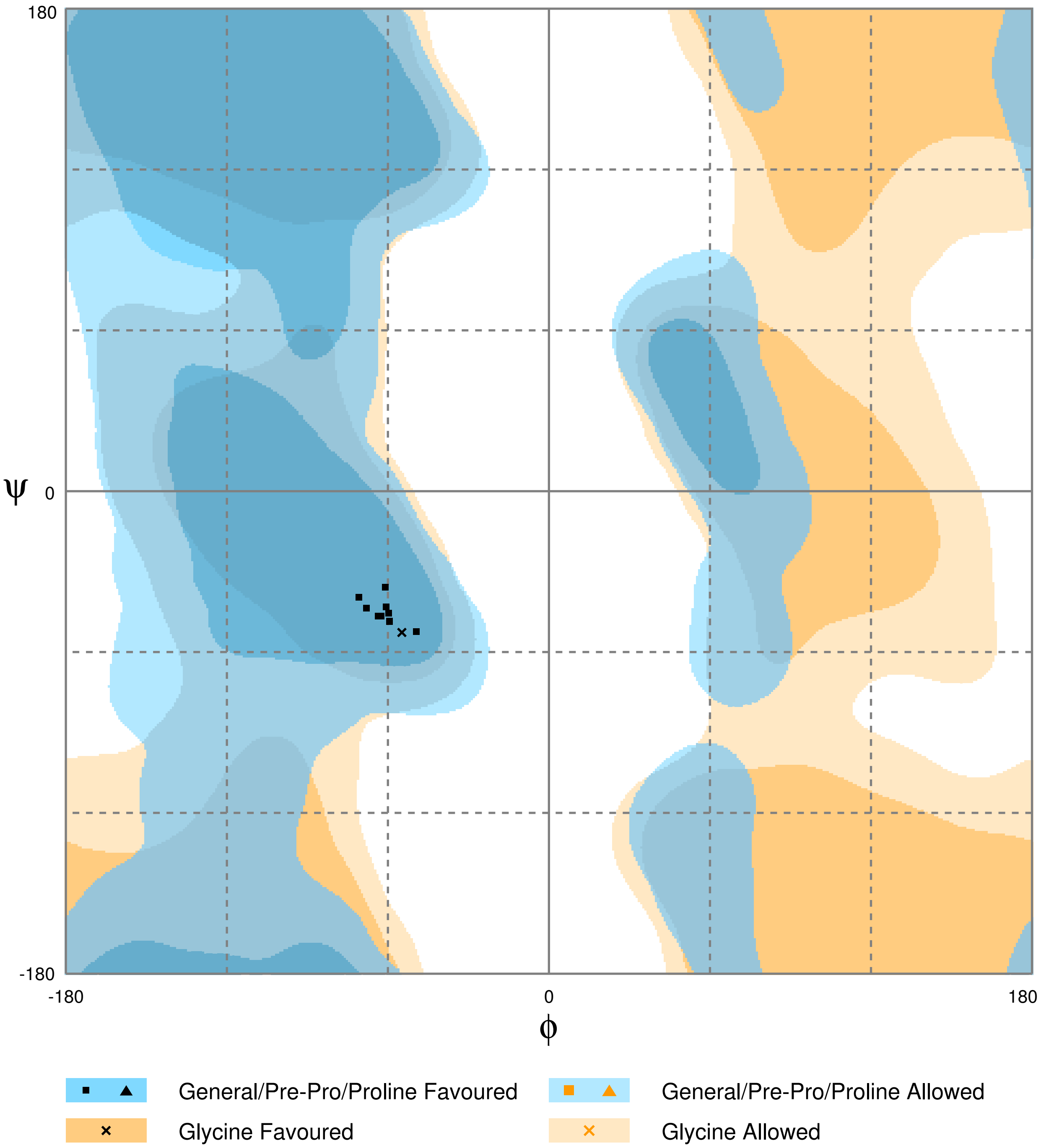


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ghd

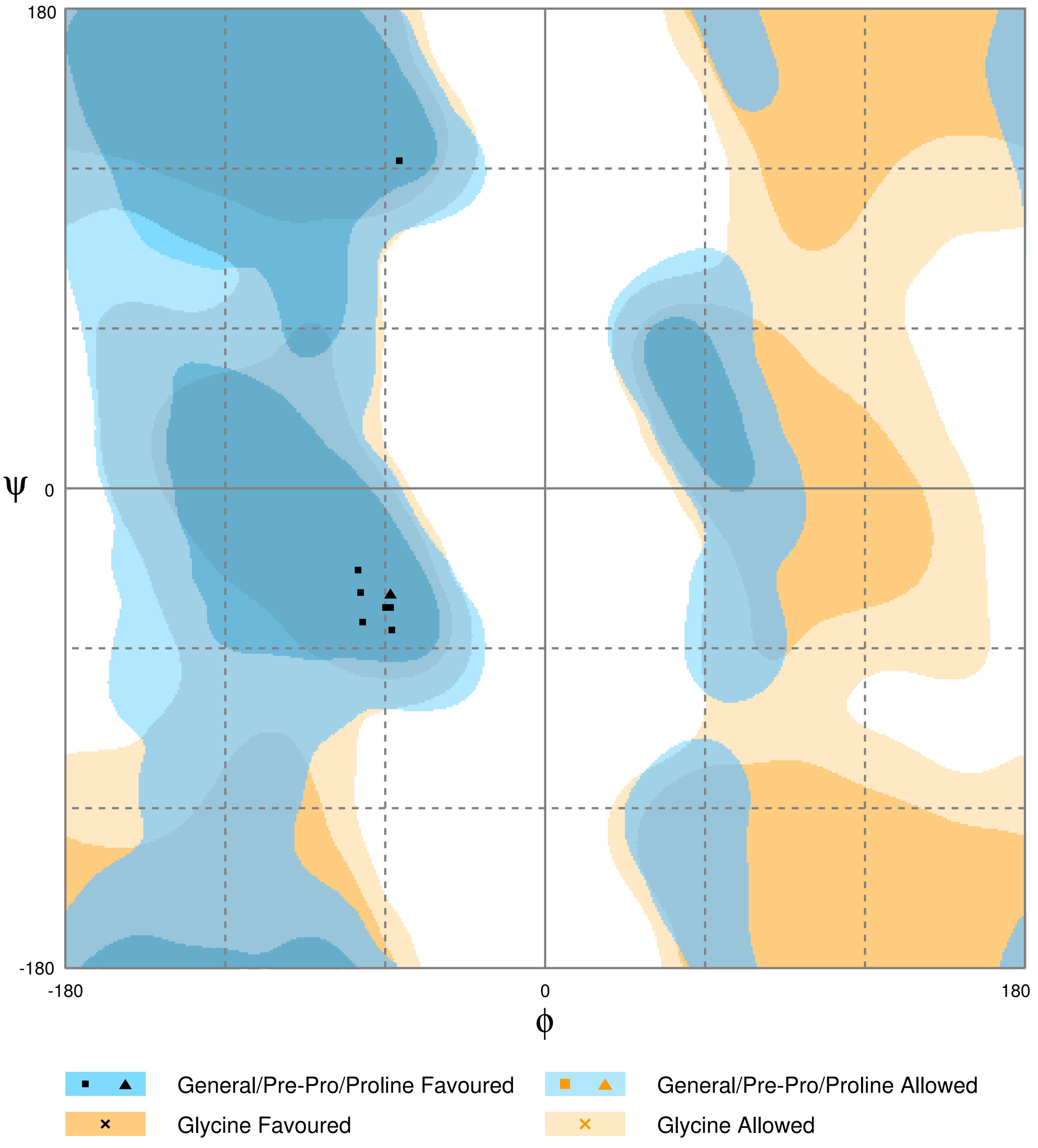


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_h

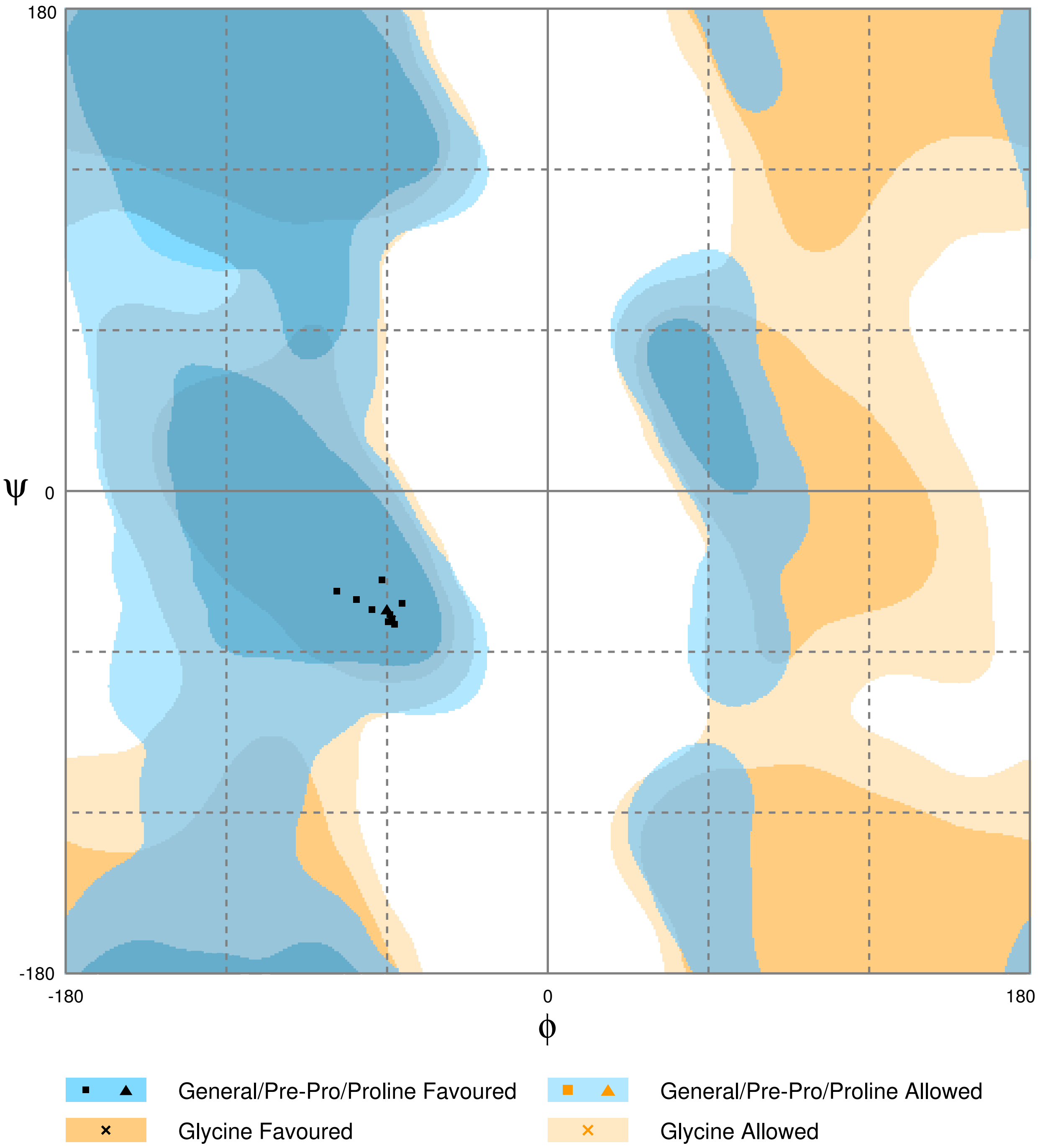


Number of residues in favoured region (~98.0% expected) : 8 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_hb1

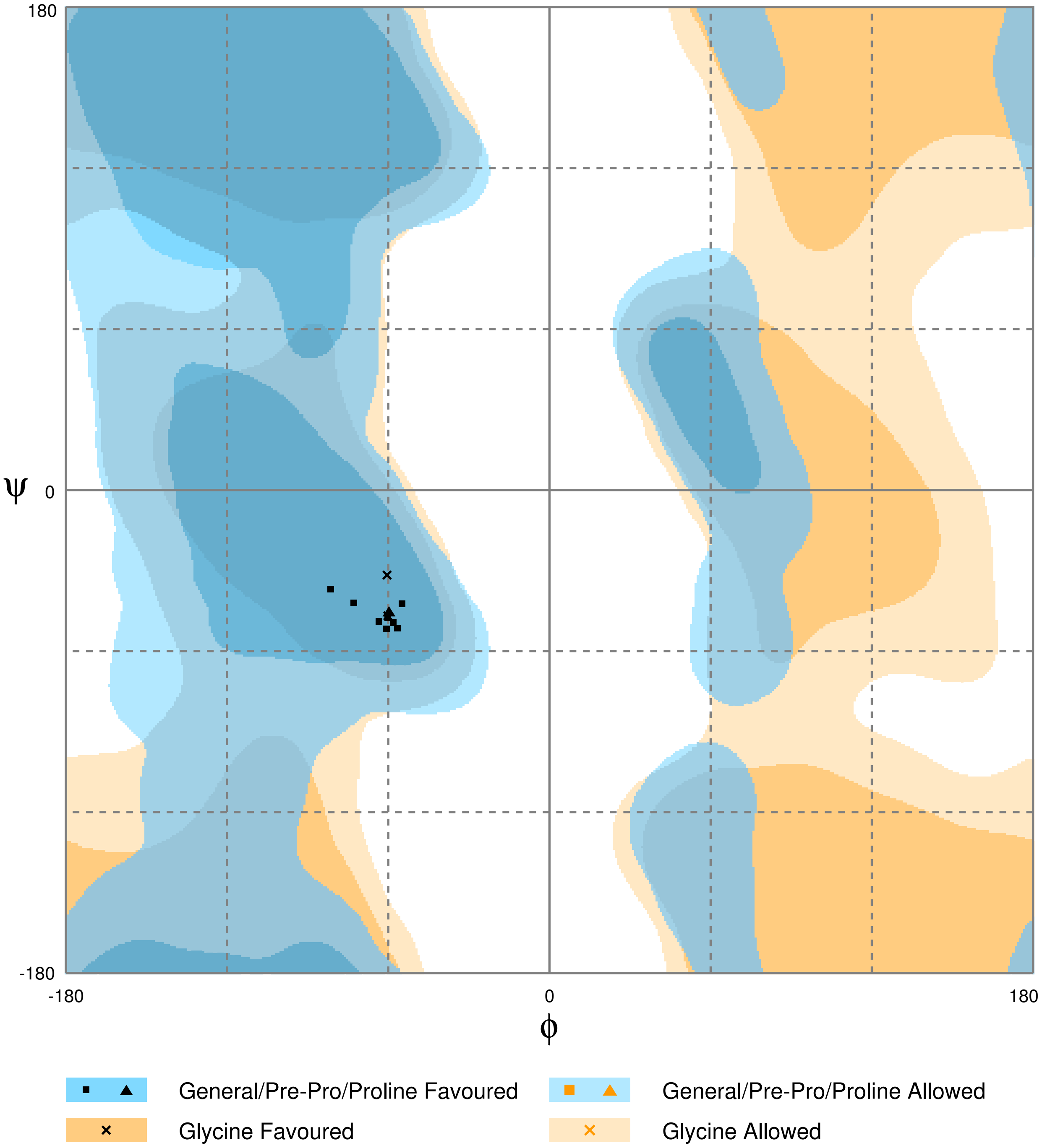


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_hb2

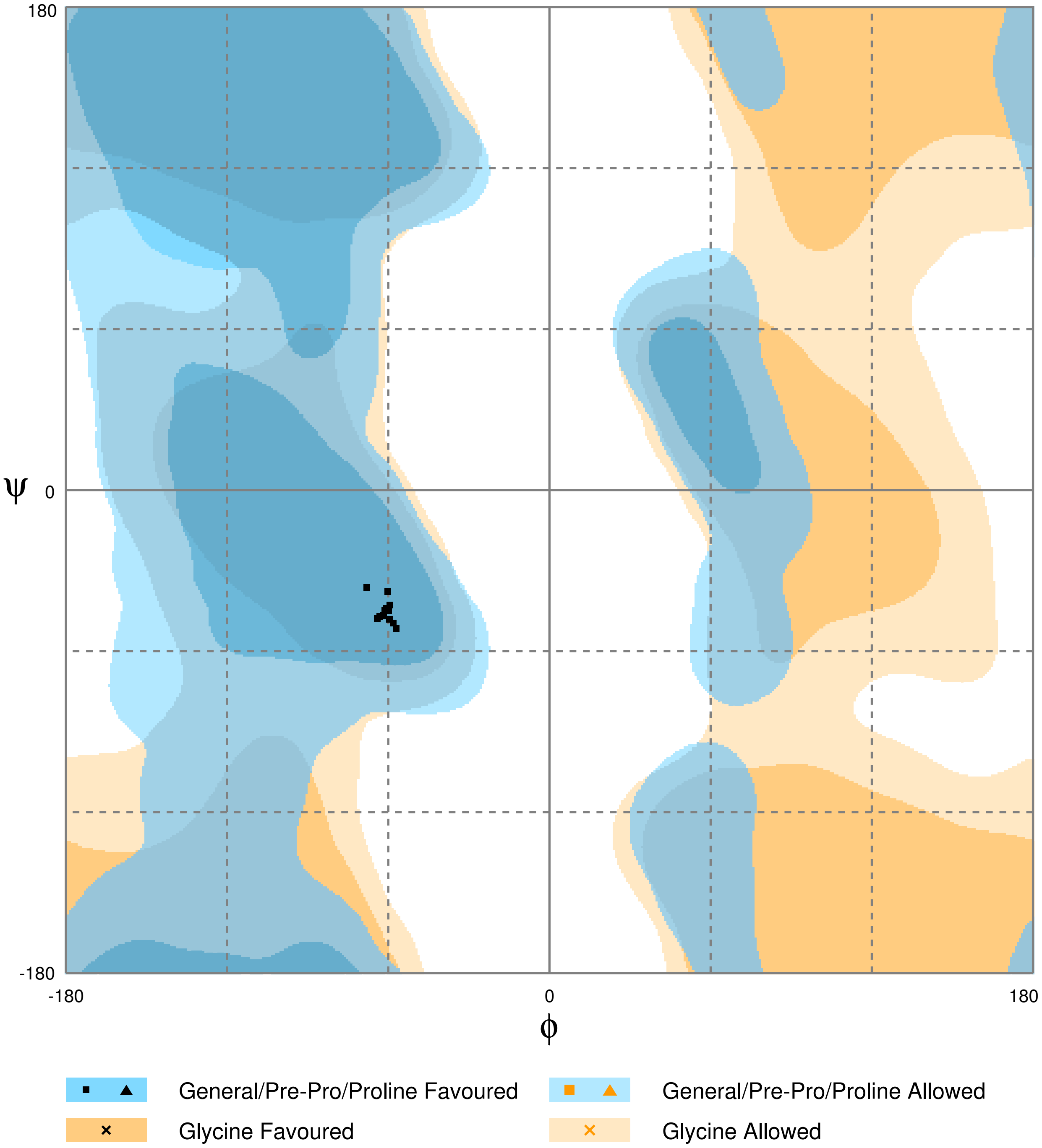


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_hn1

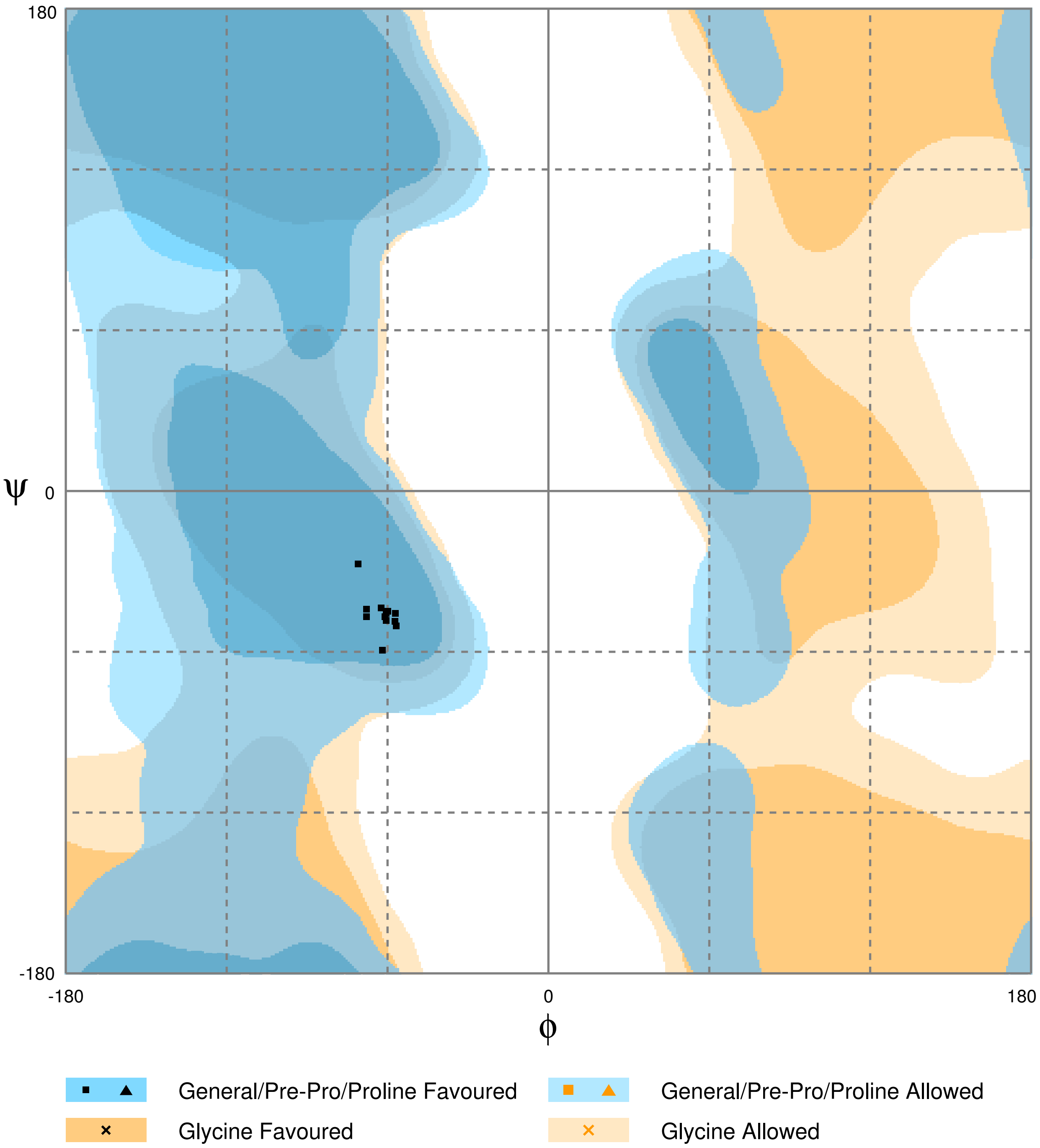


Number of residues in favoured region (~98.0% expected) : 12 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_hn2

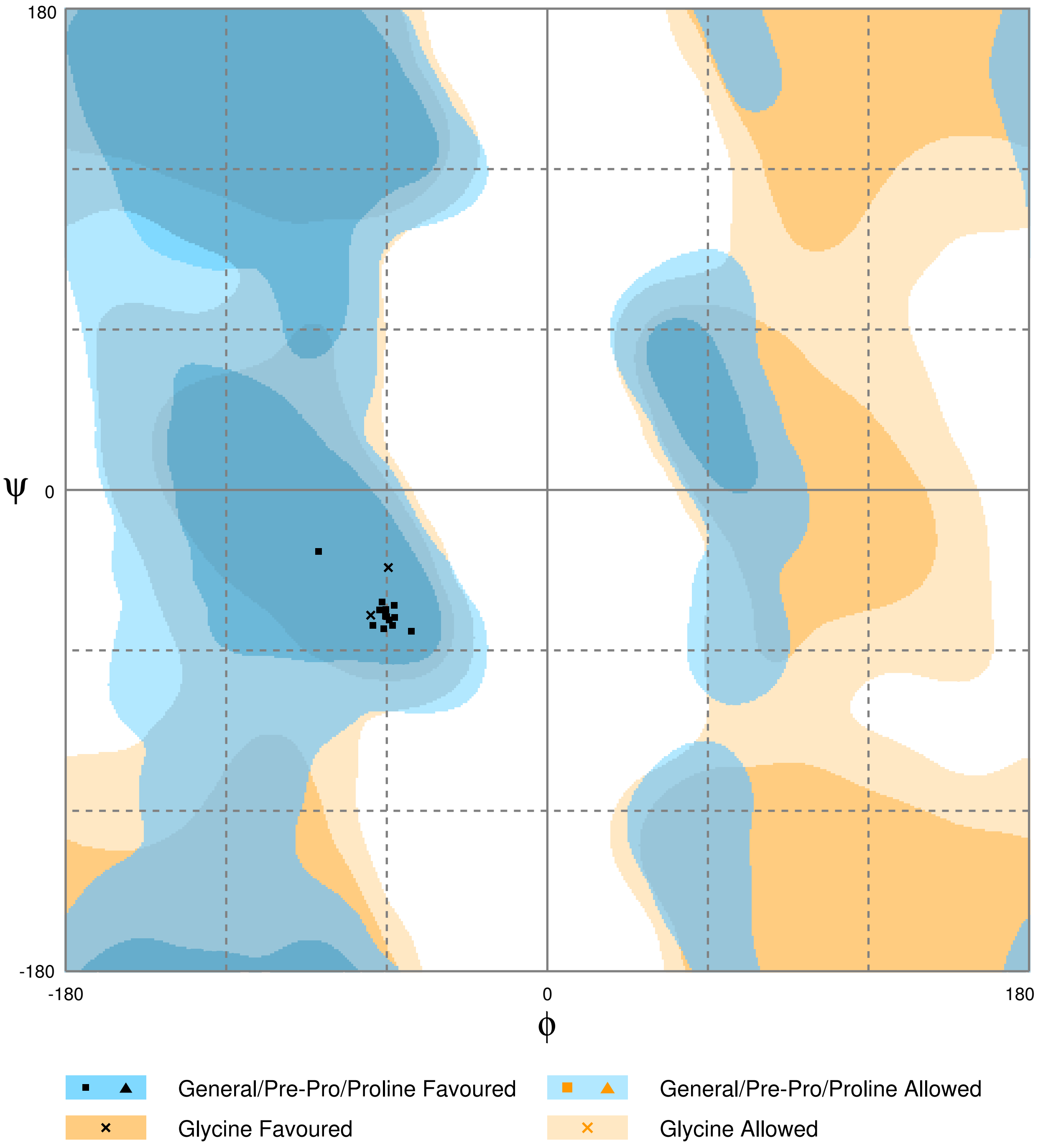


Number of residues in favoured region (~98.0% expected) : 12 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ita

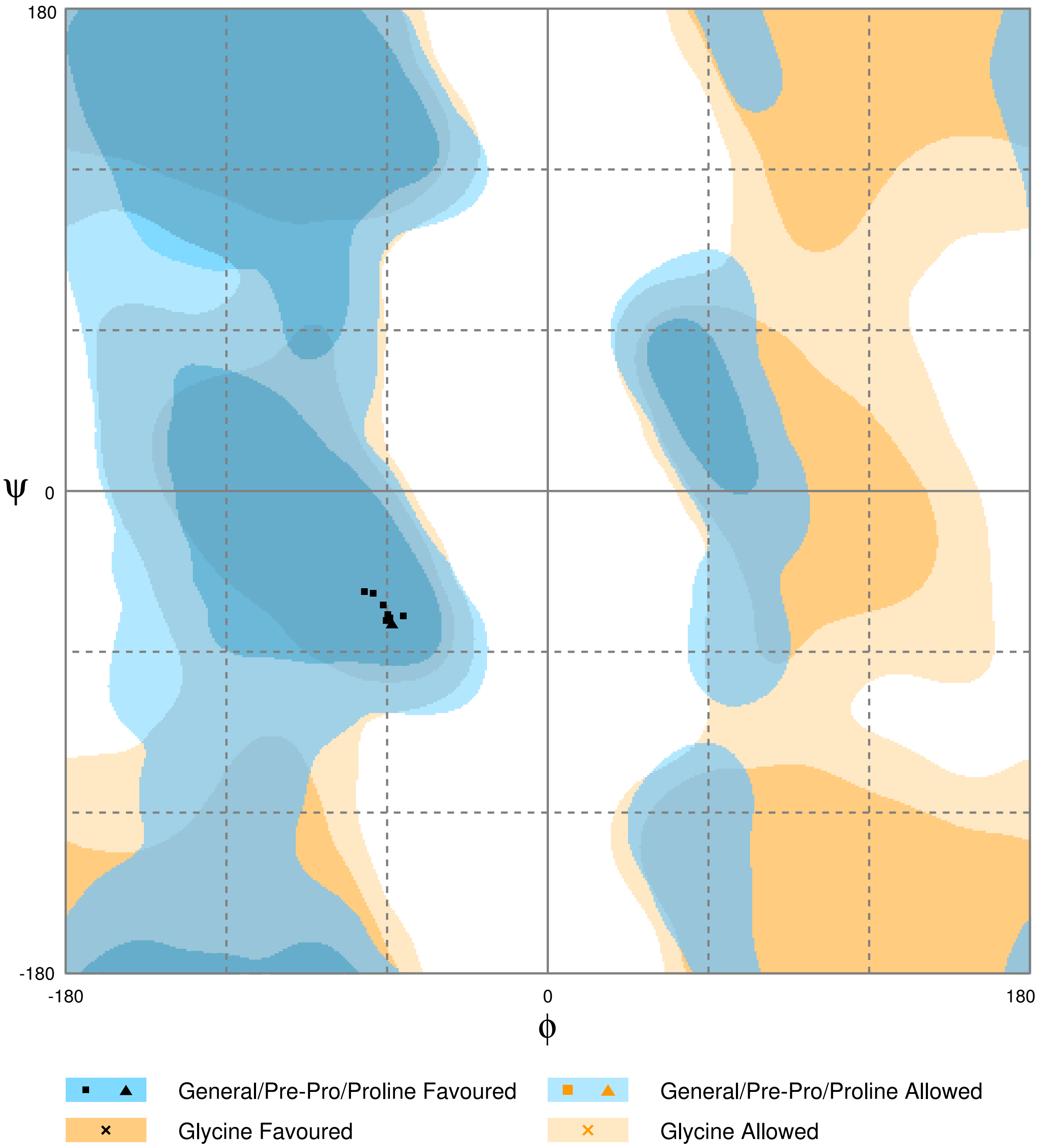


Number of residues in favoured region (~98.0% expected) : 15 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_k

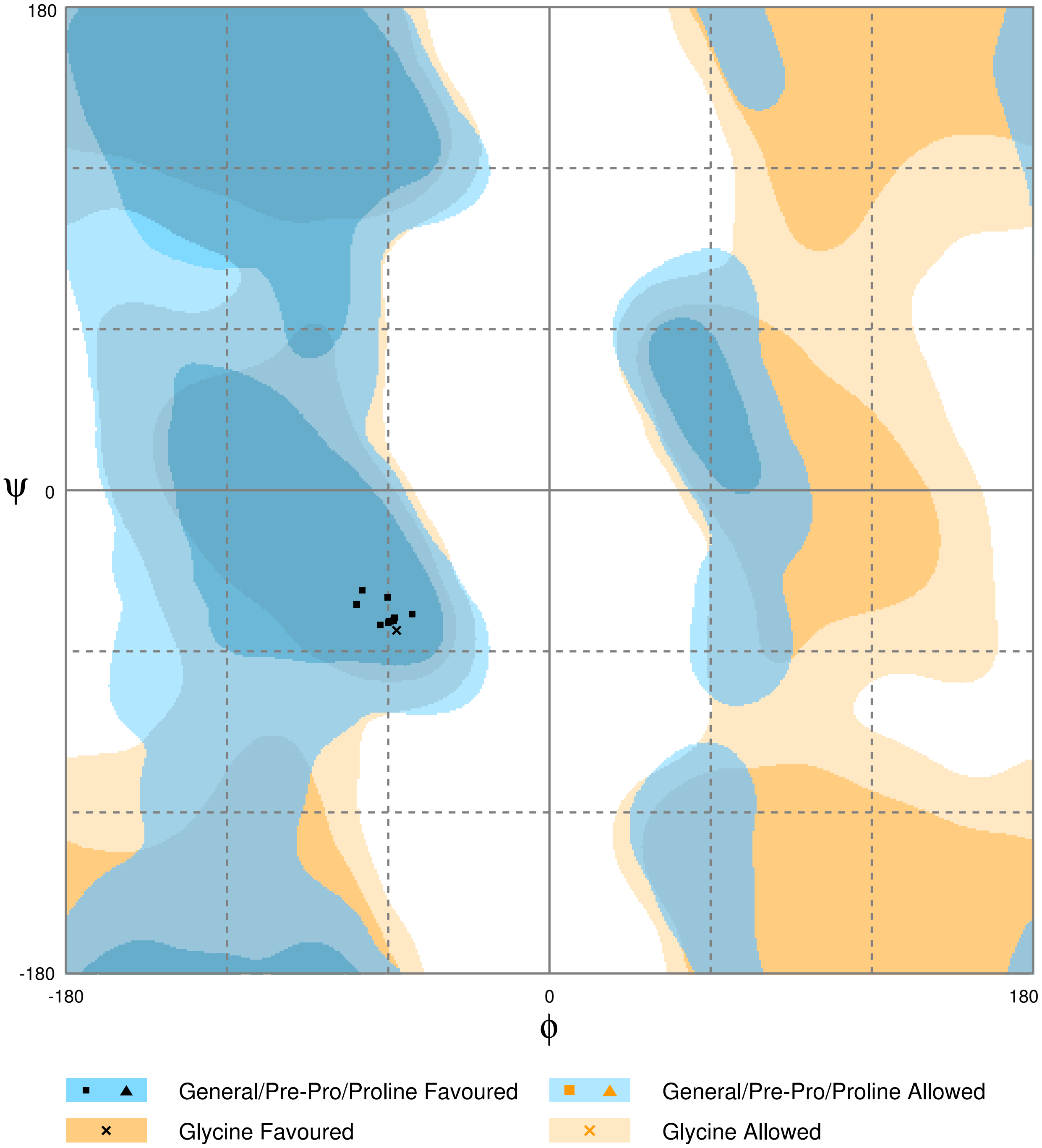


Number of residues in favoured region (~98.0% expected) : 8 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_l

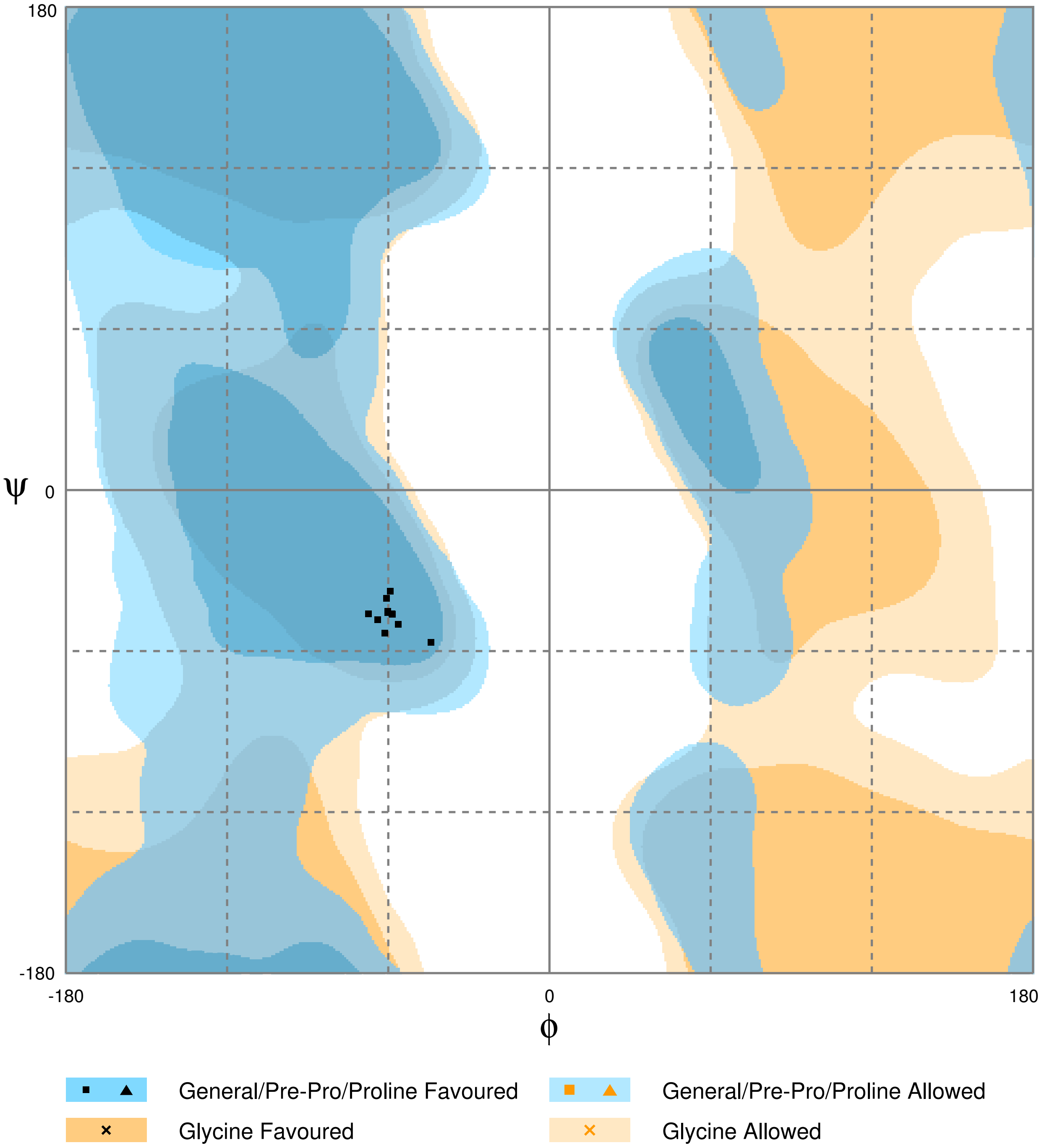


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_la

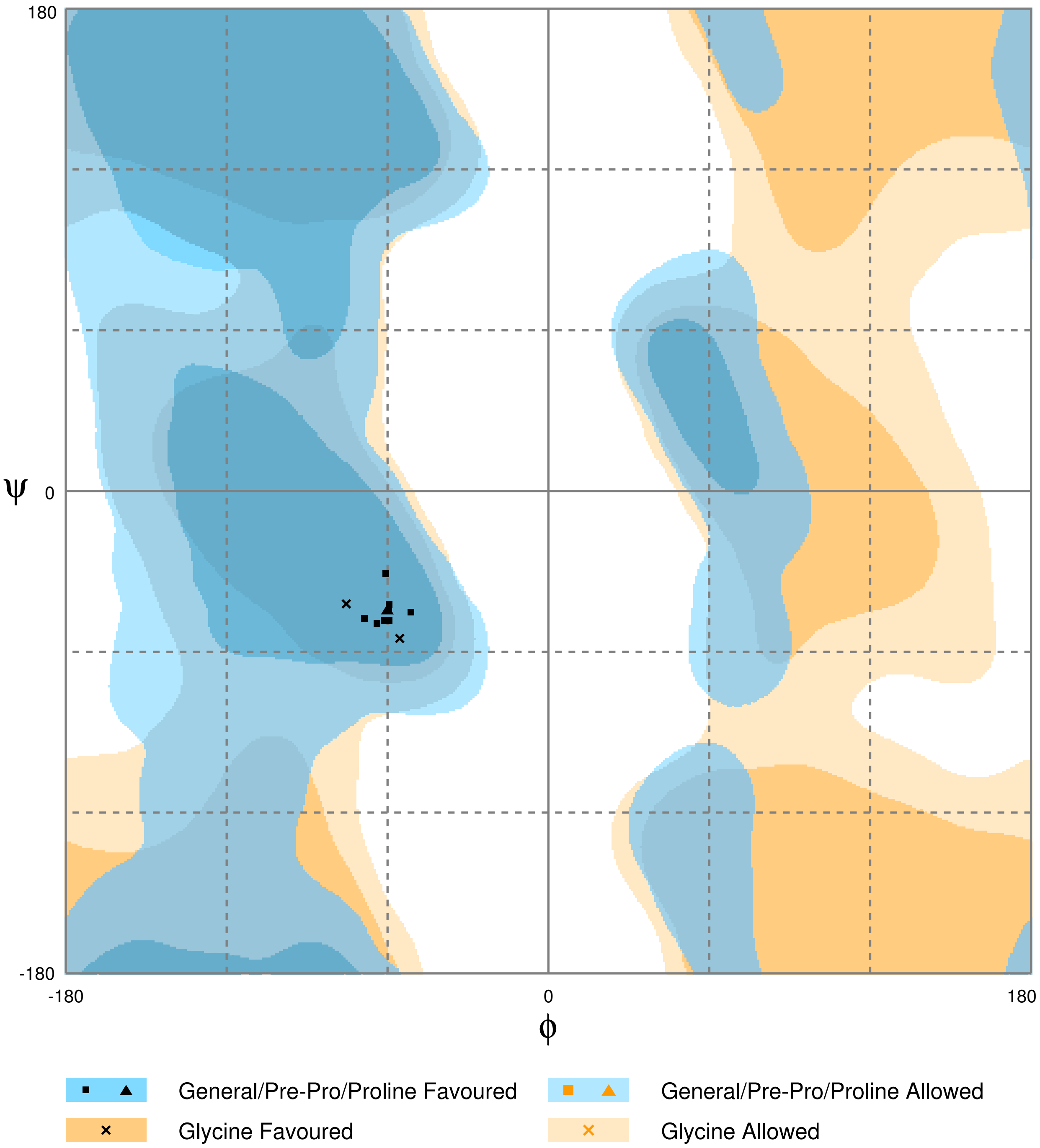


Number of residues in favoured region (~98.0% expected)	: 11 (100.0%)
Number of residues in allowed region (~2.0% expected)	: 0 (0.0%)
Number of residues in outlier region	: 0 (0.0%)

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

Tem_lf1

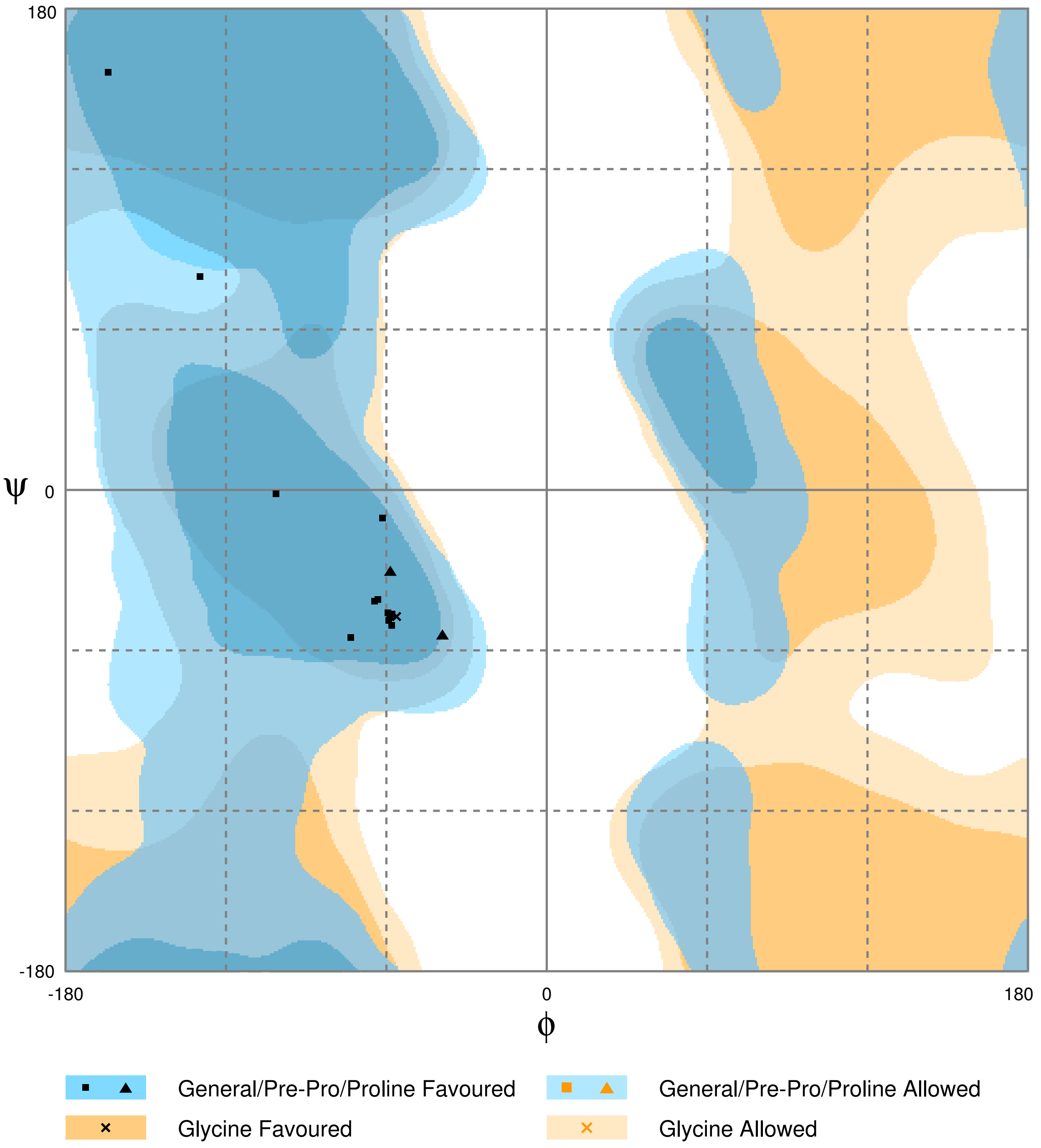


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_lk1

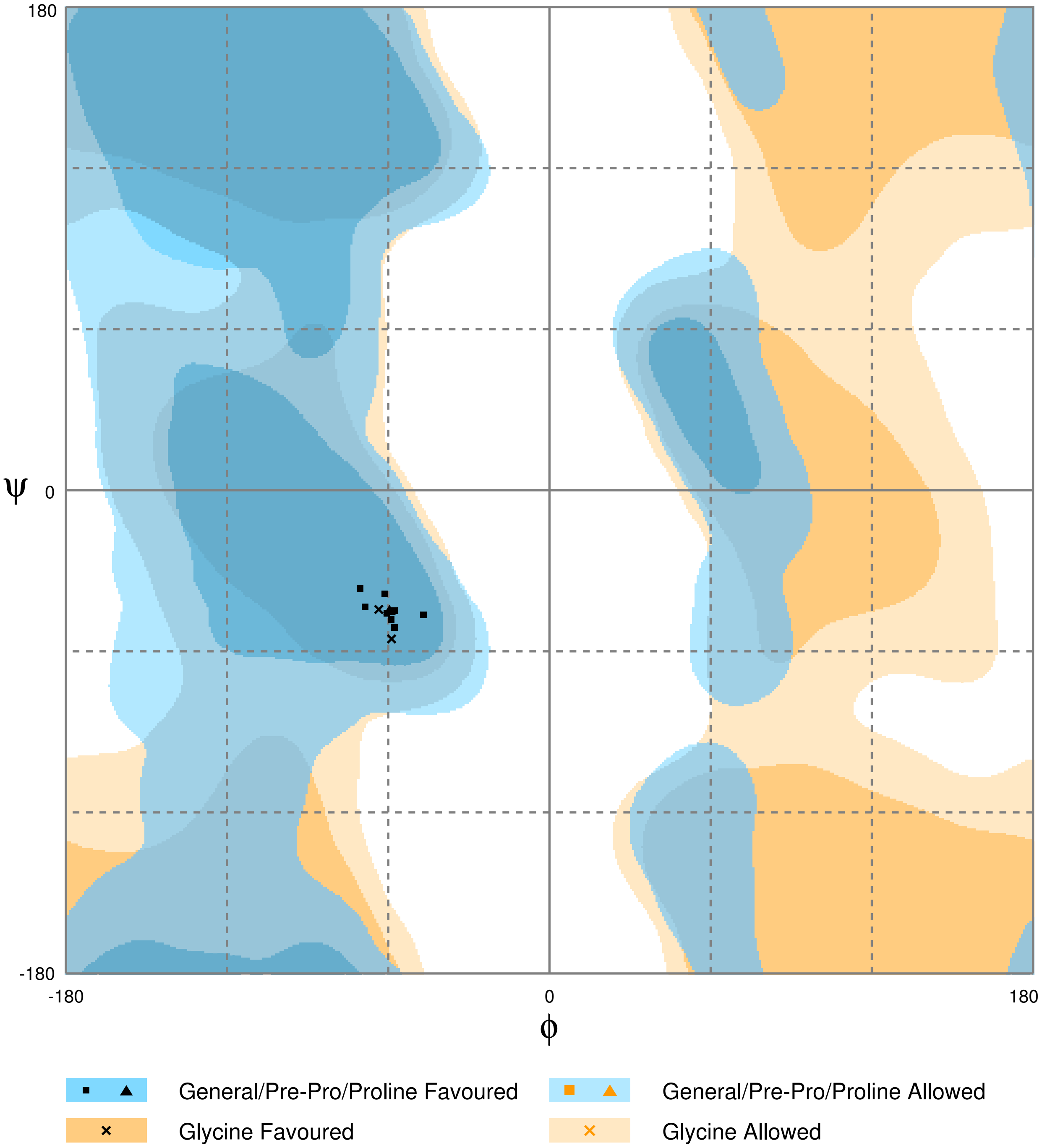


Number of residues in favoured region (~98.0% expected) : 15 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_lt1

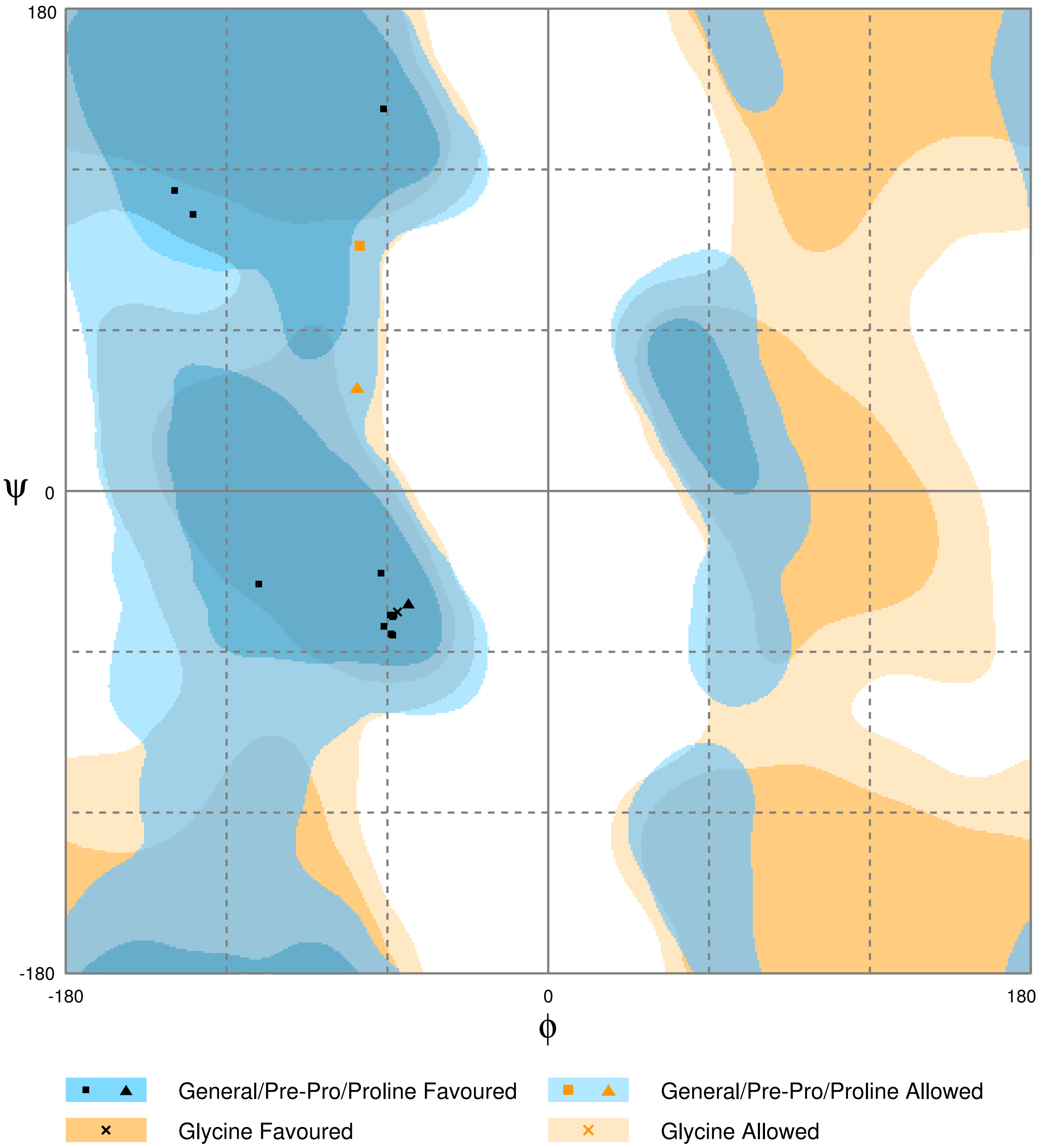


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_lt2

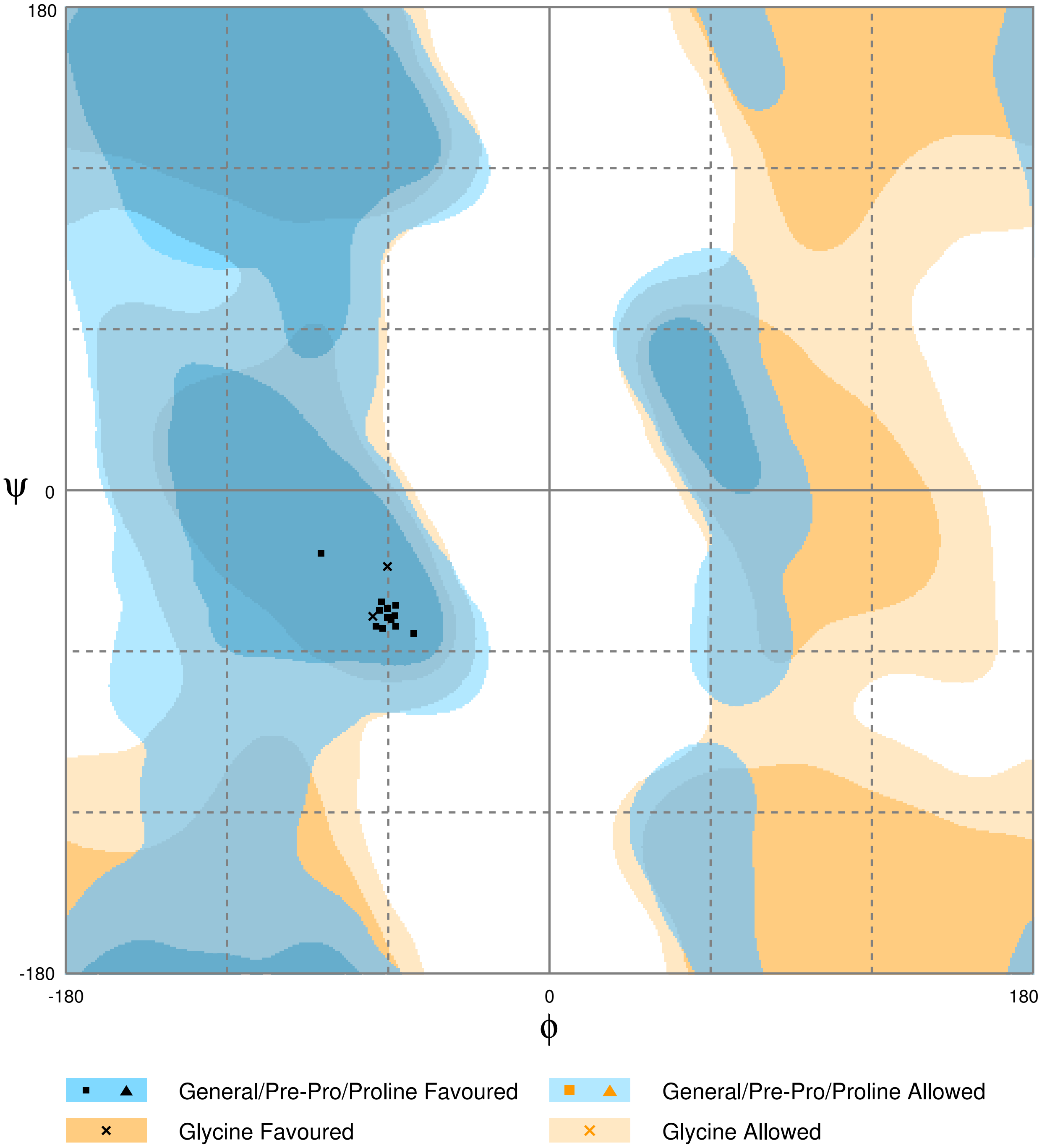


Number of residues in favoured region (~98.0% expected) : 13 (86.7%)
Number of residues in allowed region (~2.0% expected) : 2 (13.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_lta

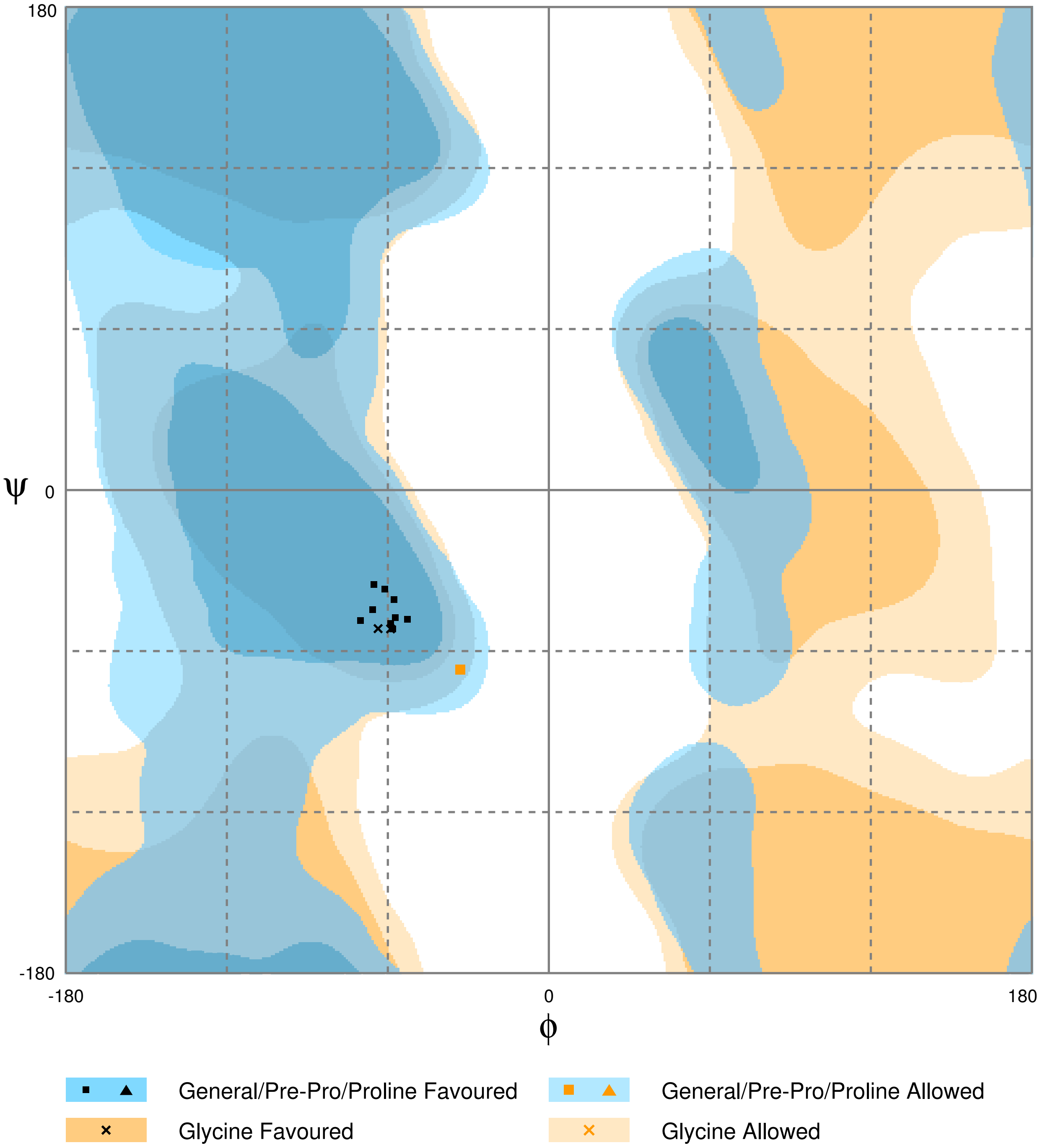


Number of residues in favoured region (~98.0% expected) : 15 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ltb

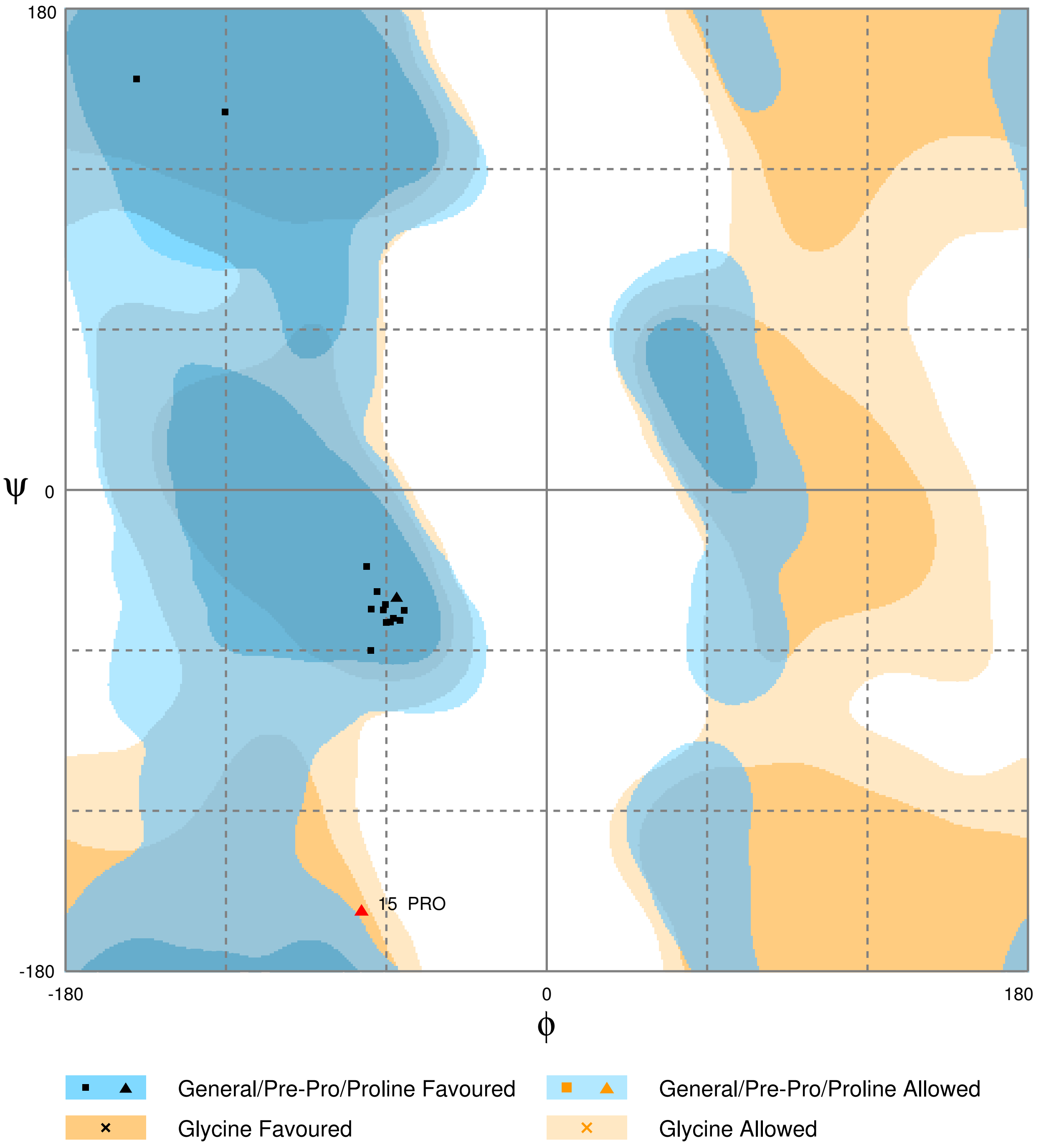


Number of residues in favoured region (~98.0% expected) : 11 (91.7%)
Number of residues in allowed region (~2.0% expected) : 1 (8.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ltc

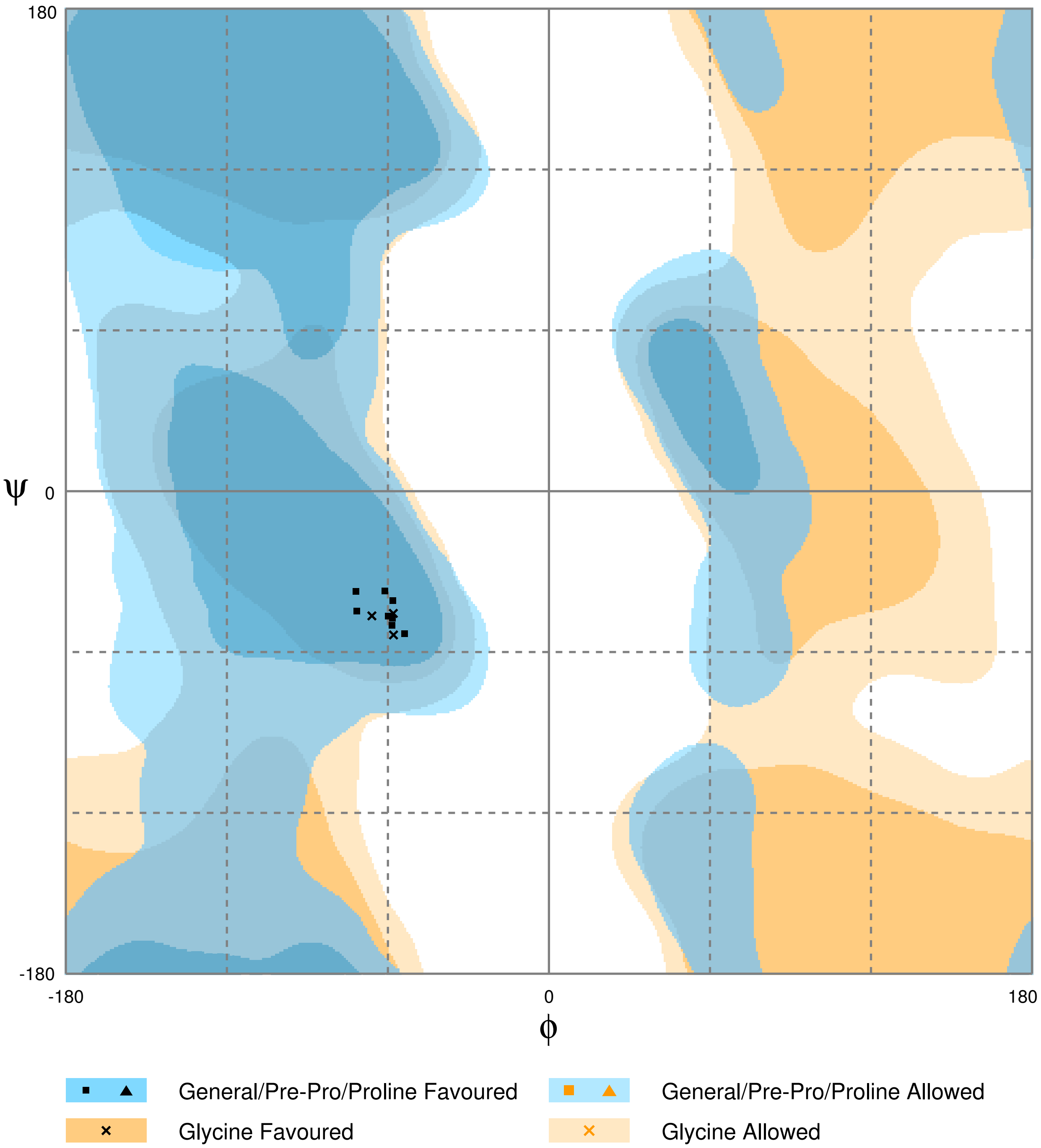


Number of residues in favoured region (~98.0% expected) : 14 (93.3%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 1 (6.7%)

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

Tem_lte

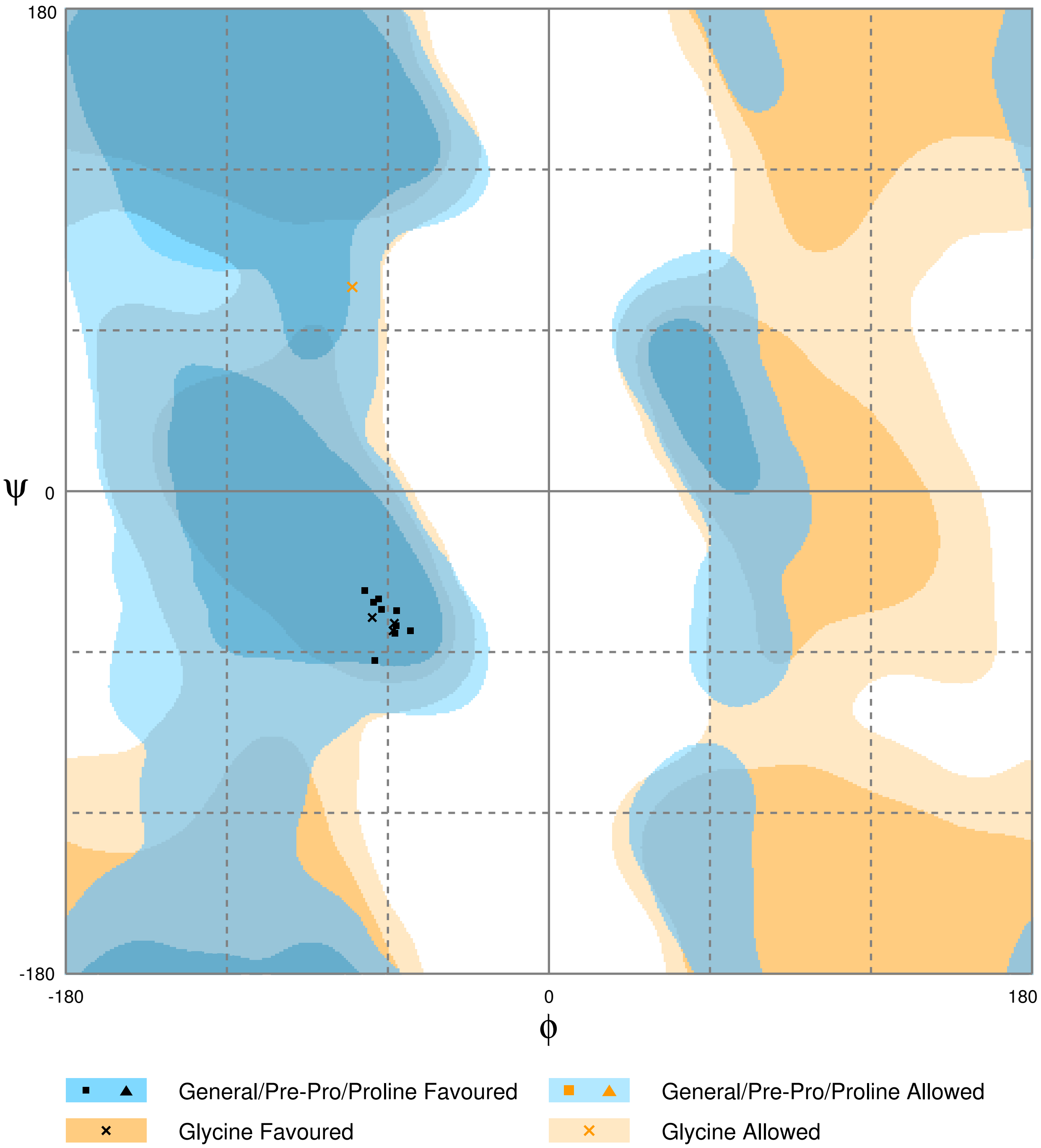


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ms1

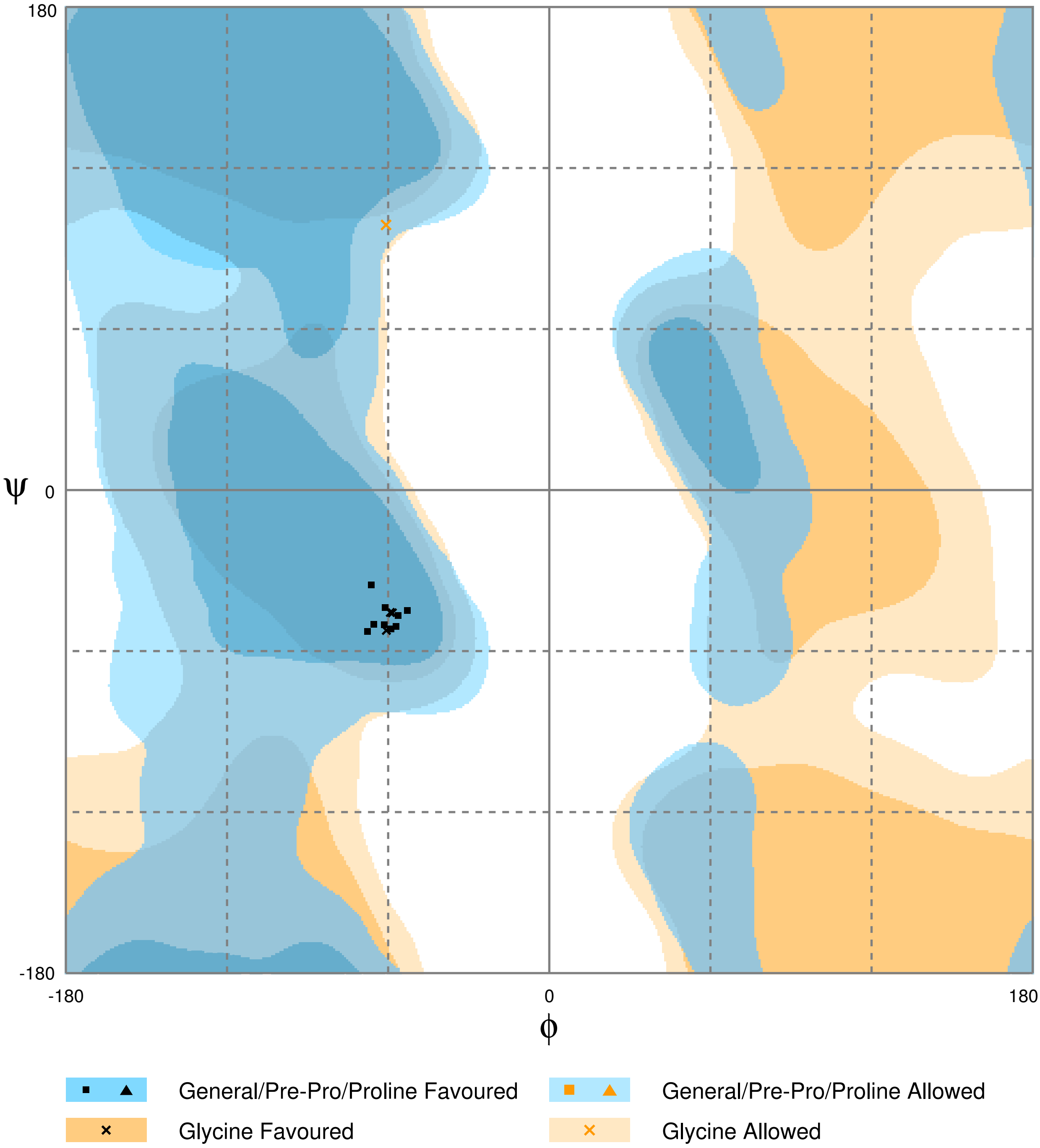


Number of residues in favoured region (~98.0% expected) : 12 (92.3%)
Number of residues in allowed region (~2.0% expected) : 1 (7.7%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ms4

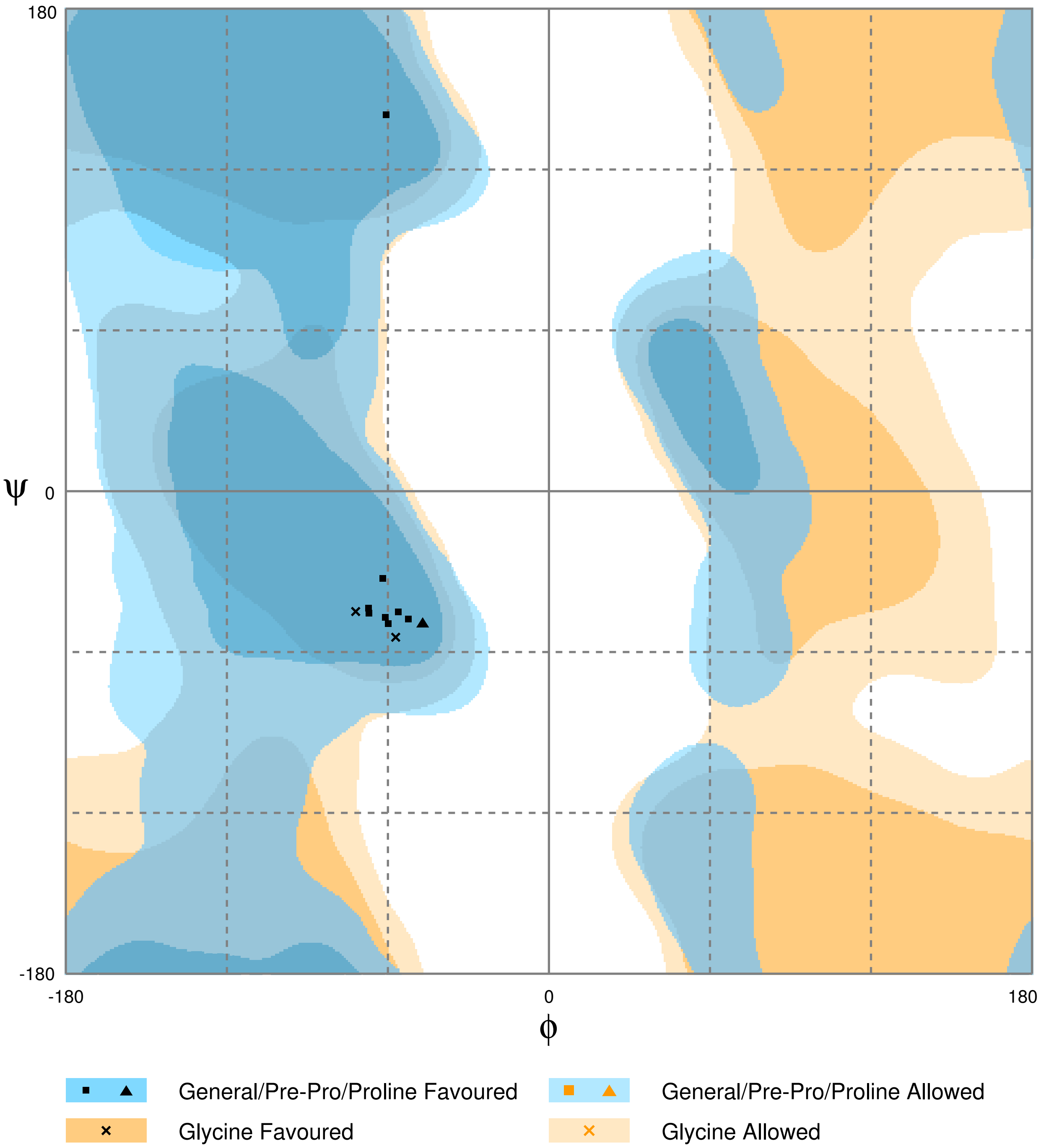


Number of residues in favoured region (~98.0% expected) : 12 (92.3%)
Number of residues in allowed region (~2.0% expected) : 1 (7.7%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_pra

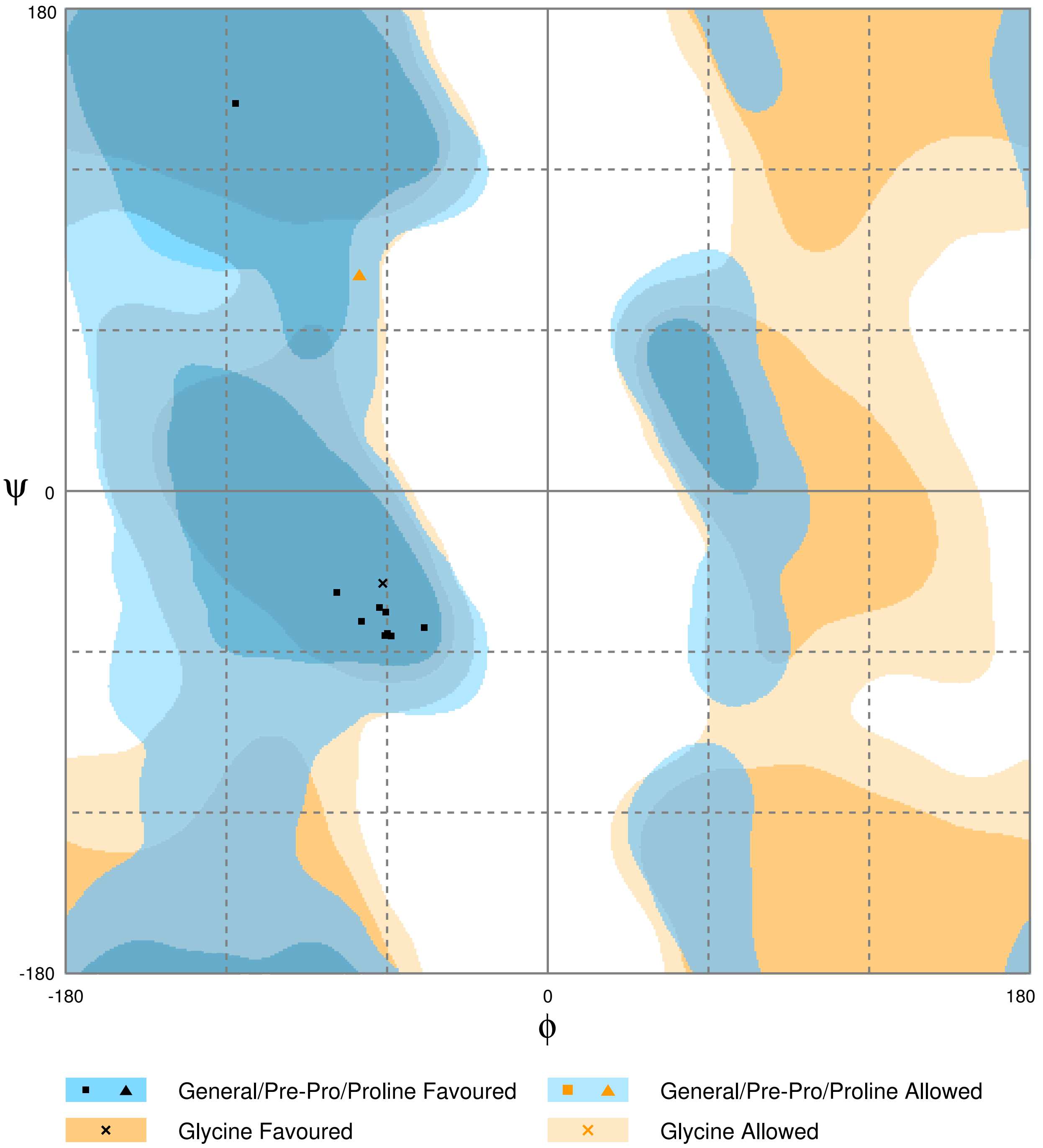


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_prb

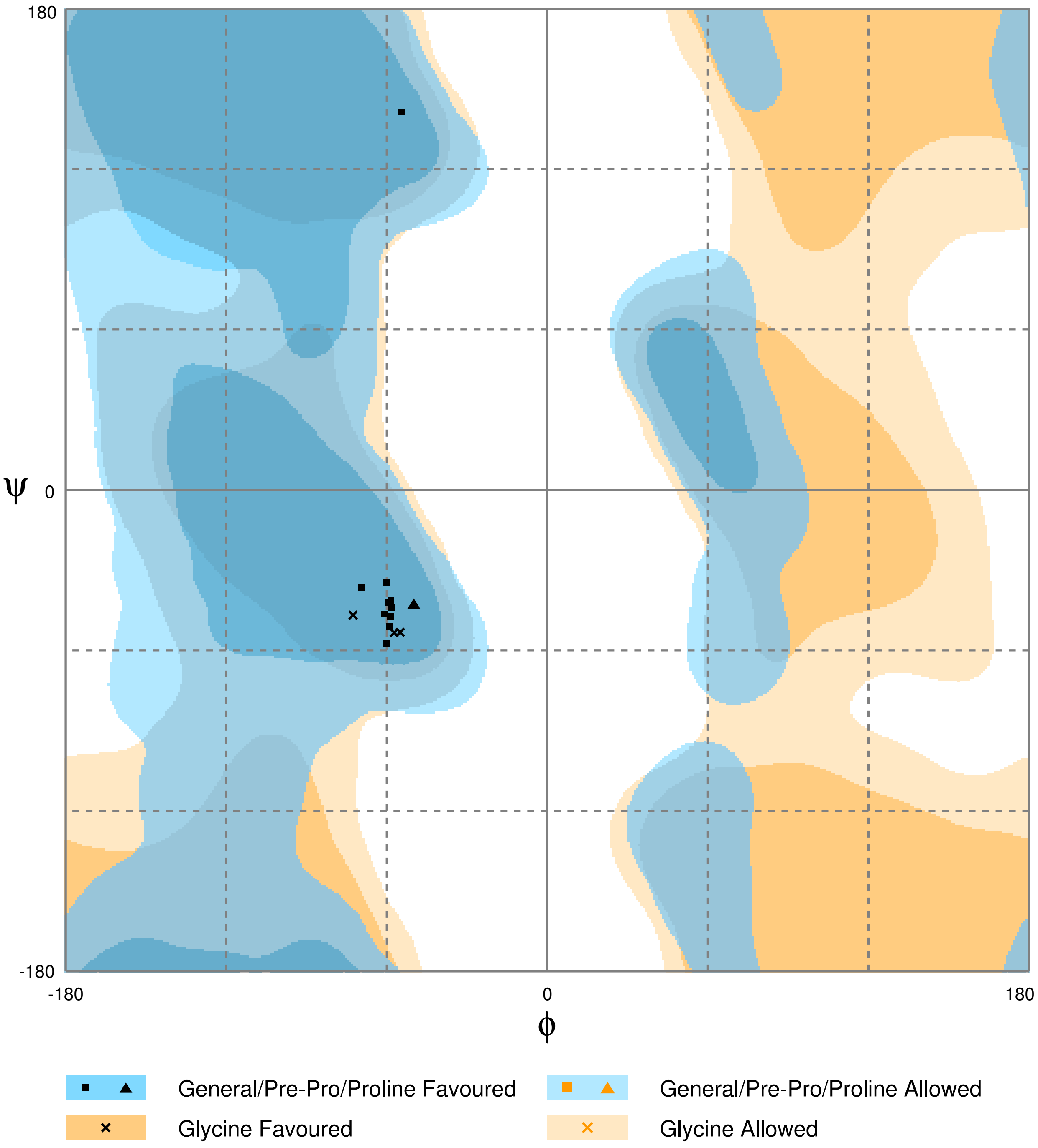


Number of residues in favoured region (~98.0% expected) : 10 (90.9%)
Number of residues in allowed region (~2.0% expected) : 1 (9.1%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_prc

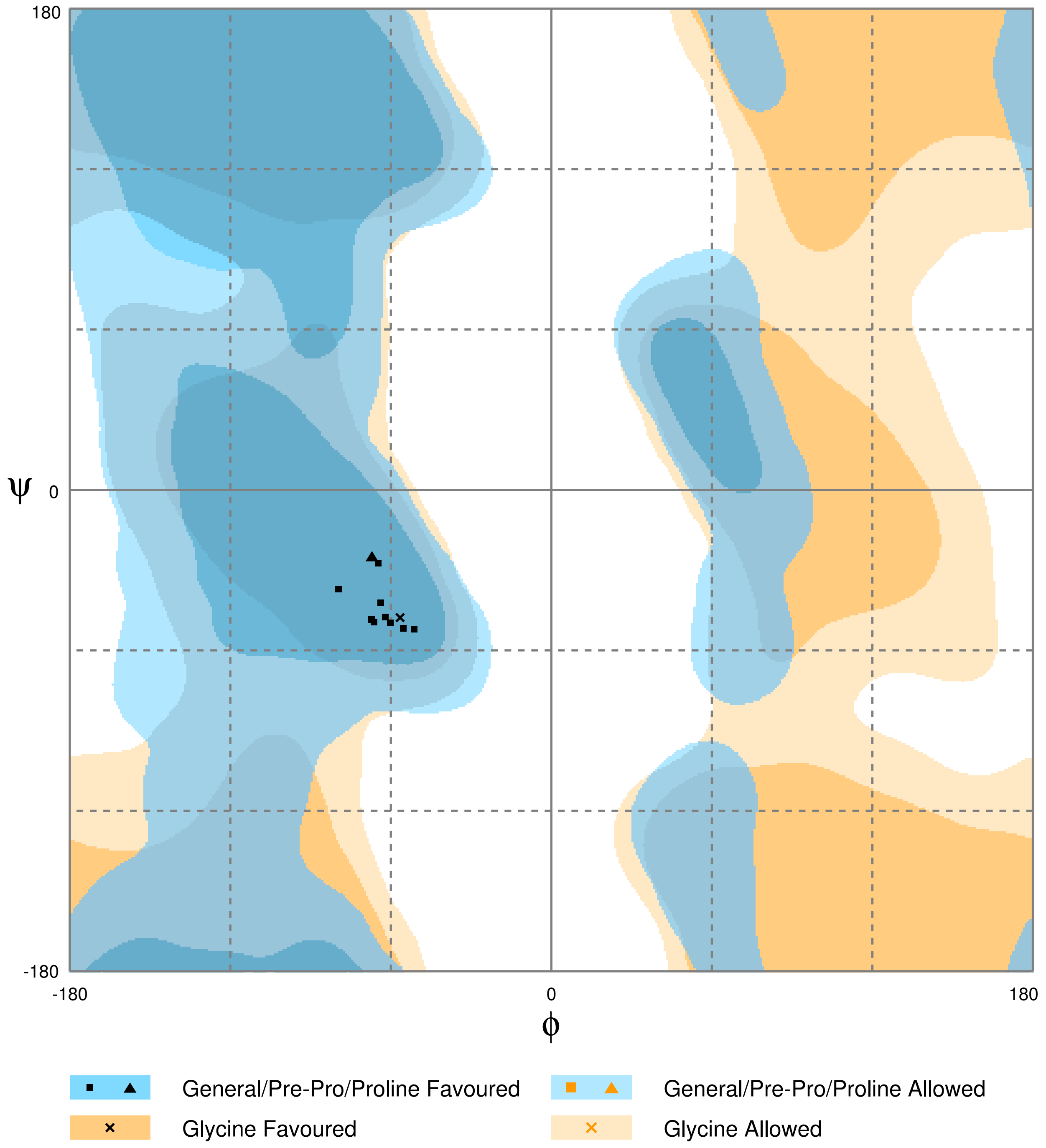


Number of residues in favoured region (~98.0% expected) : 14 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_pta

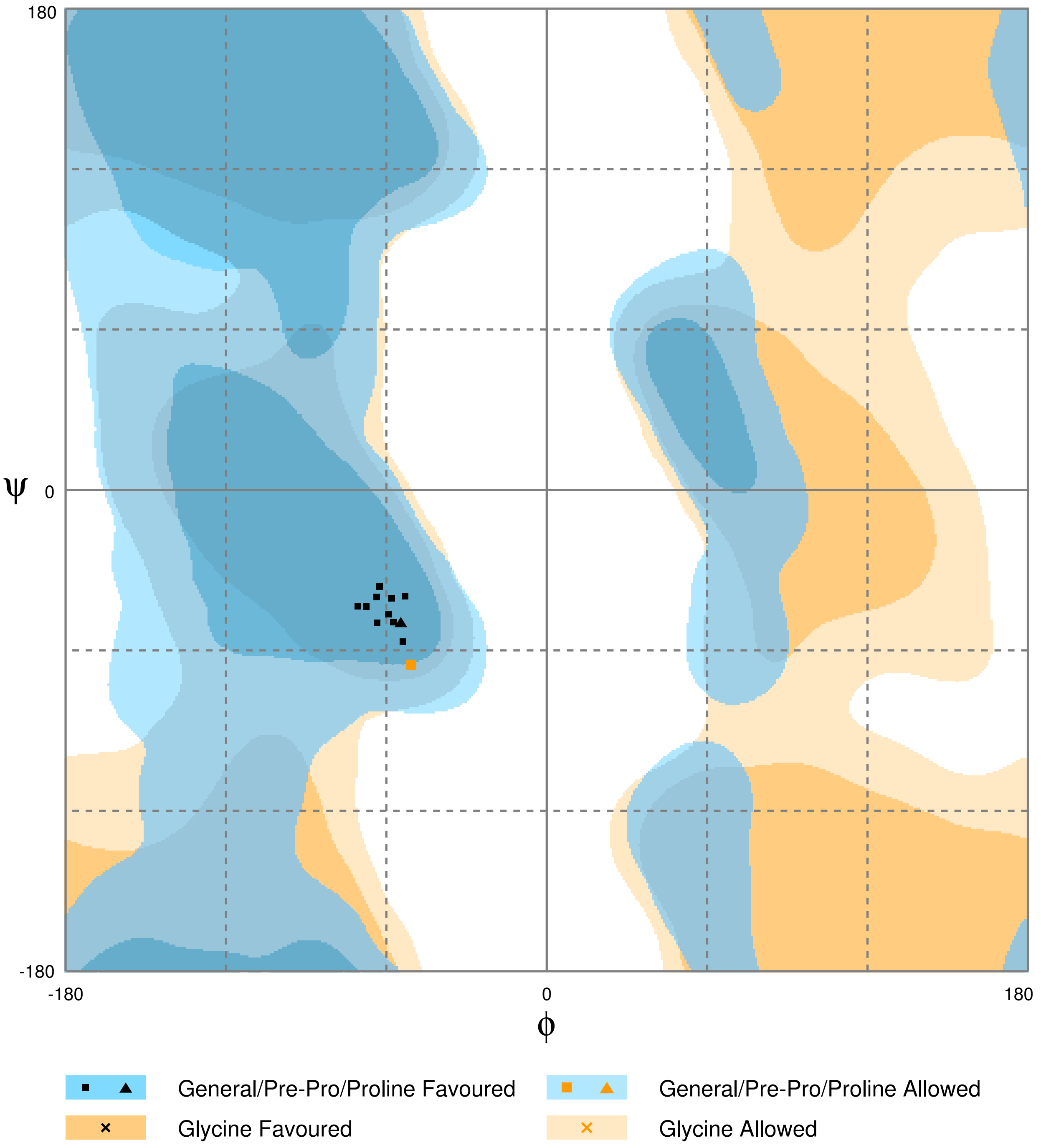


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_ra

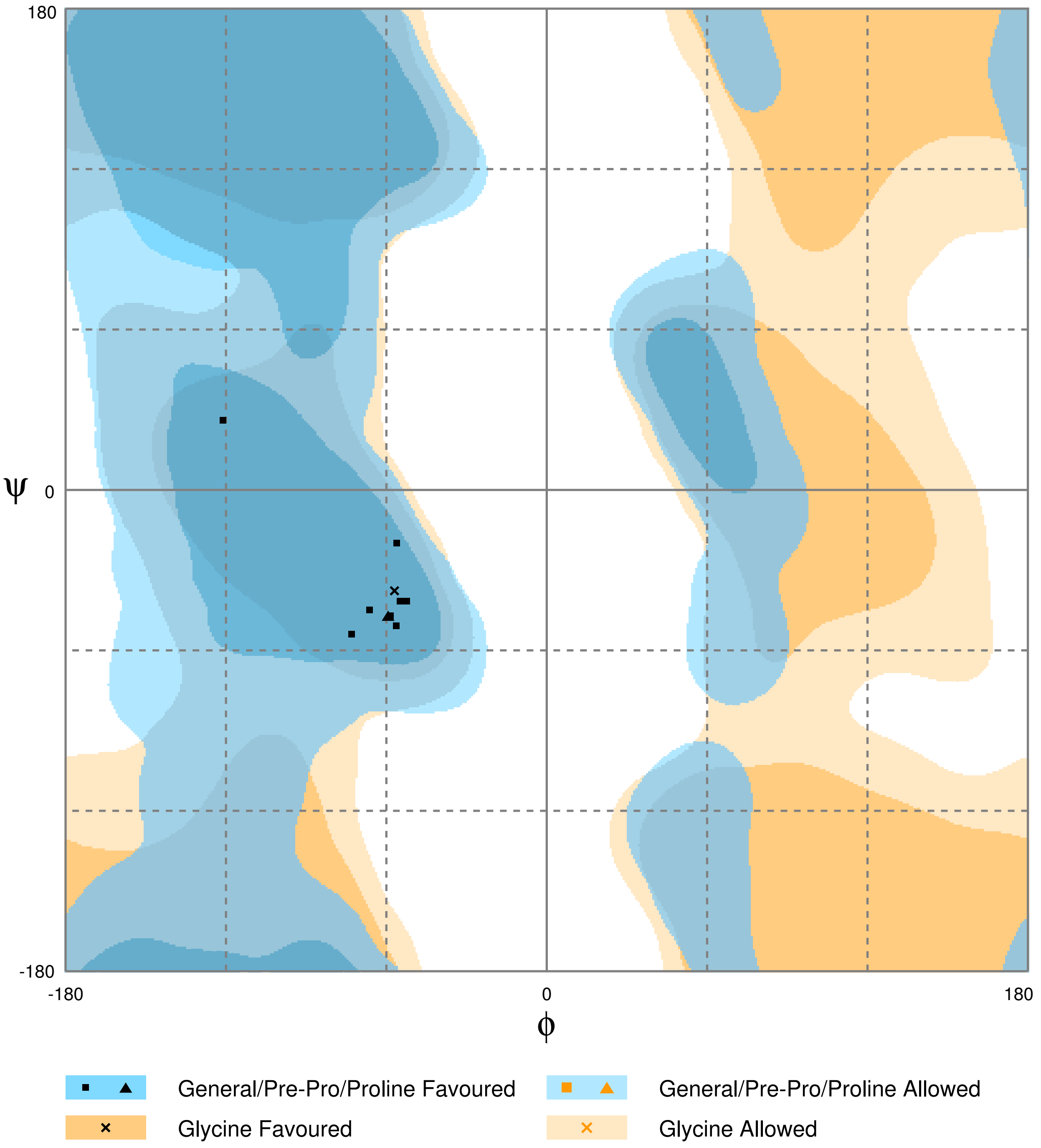


Number of residues in favoured region (~98.0% expected) : 11 (91.7%)
Number of residues in allowed region (~2.0% expected) : 1 (8.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_rb

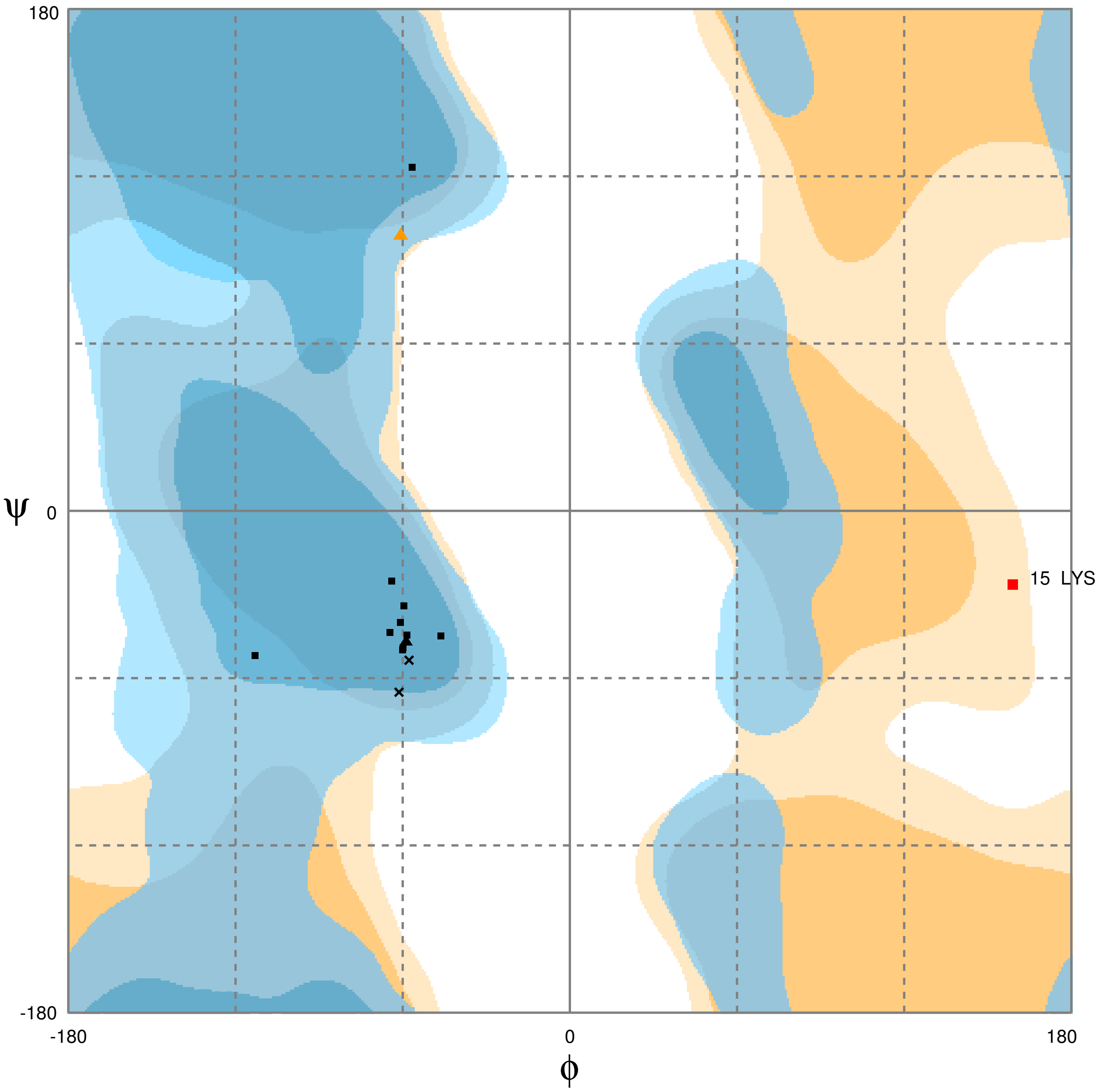


Number of residues in favoured region (~98.0% expected) : 10 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_rn1



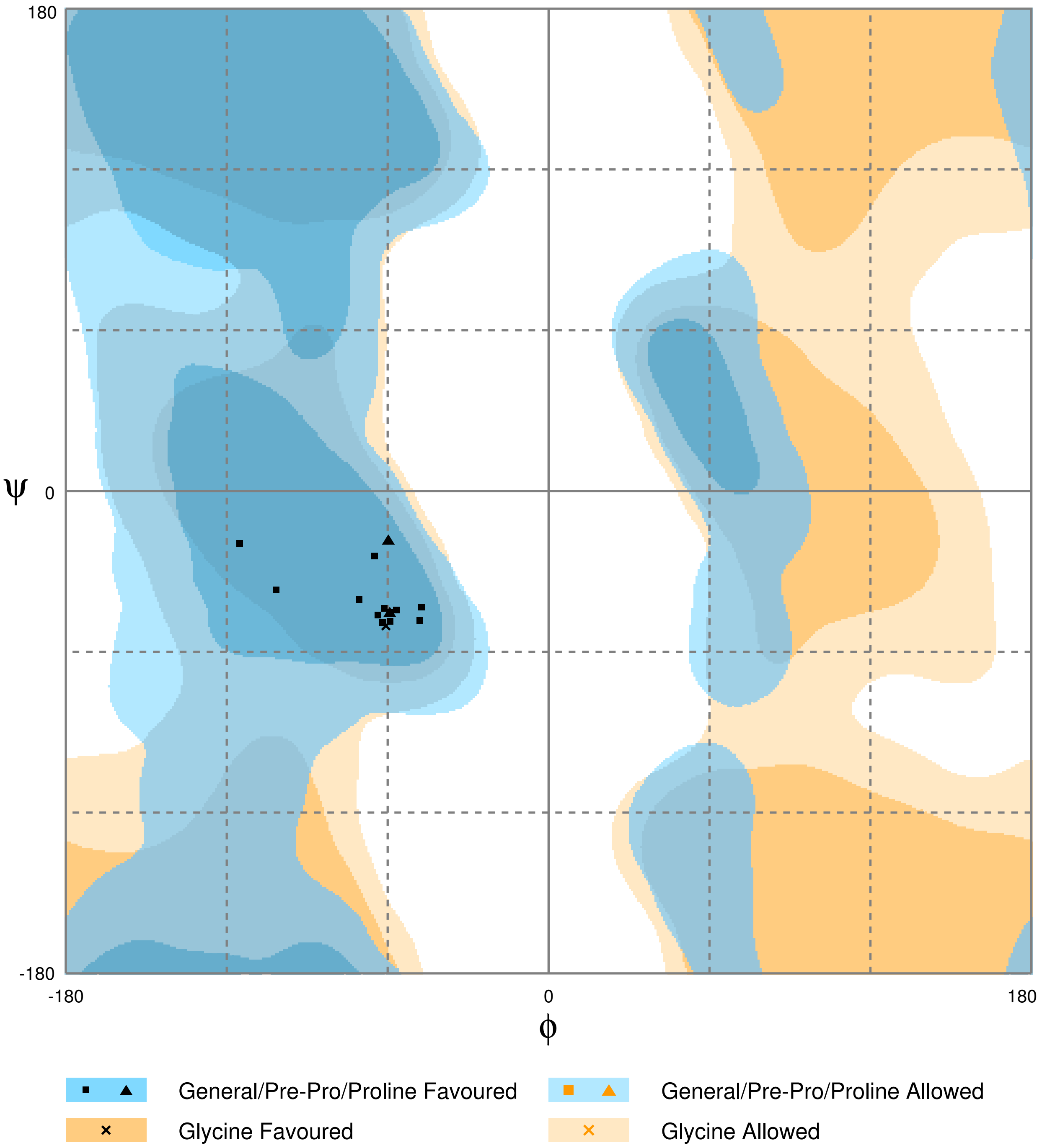
■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

Number of residues in favoured region (~98.0% expected) : 13 (86.7%)
Number of residues in allowed region (~2.0% expected) : 1 (6.7%)
Number of residues in outlier region : 1 (6.7%)

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

Tem_rn3

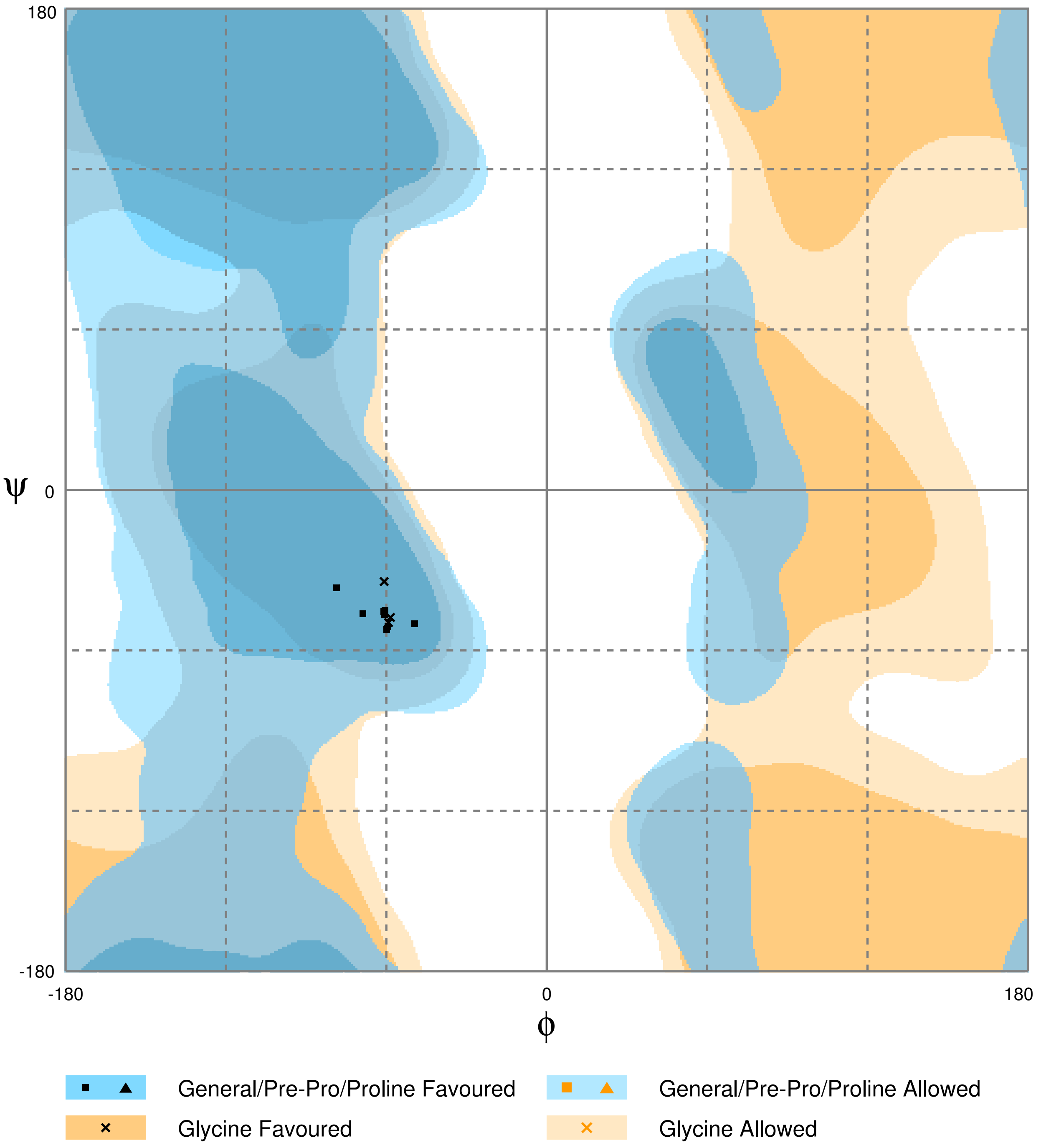


Number of residues in favoured region (~98.0% expected) : 15 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_sha

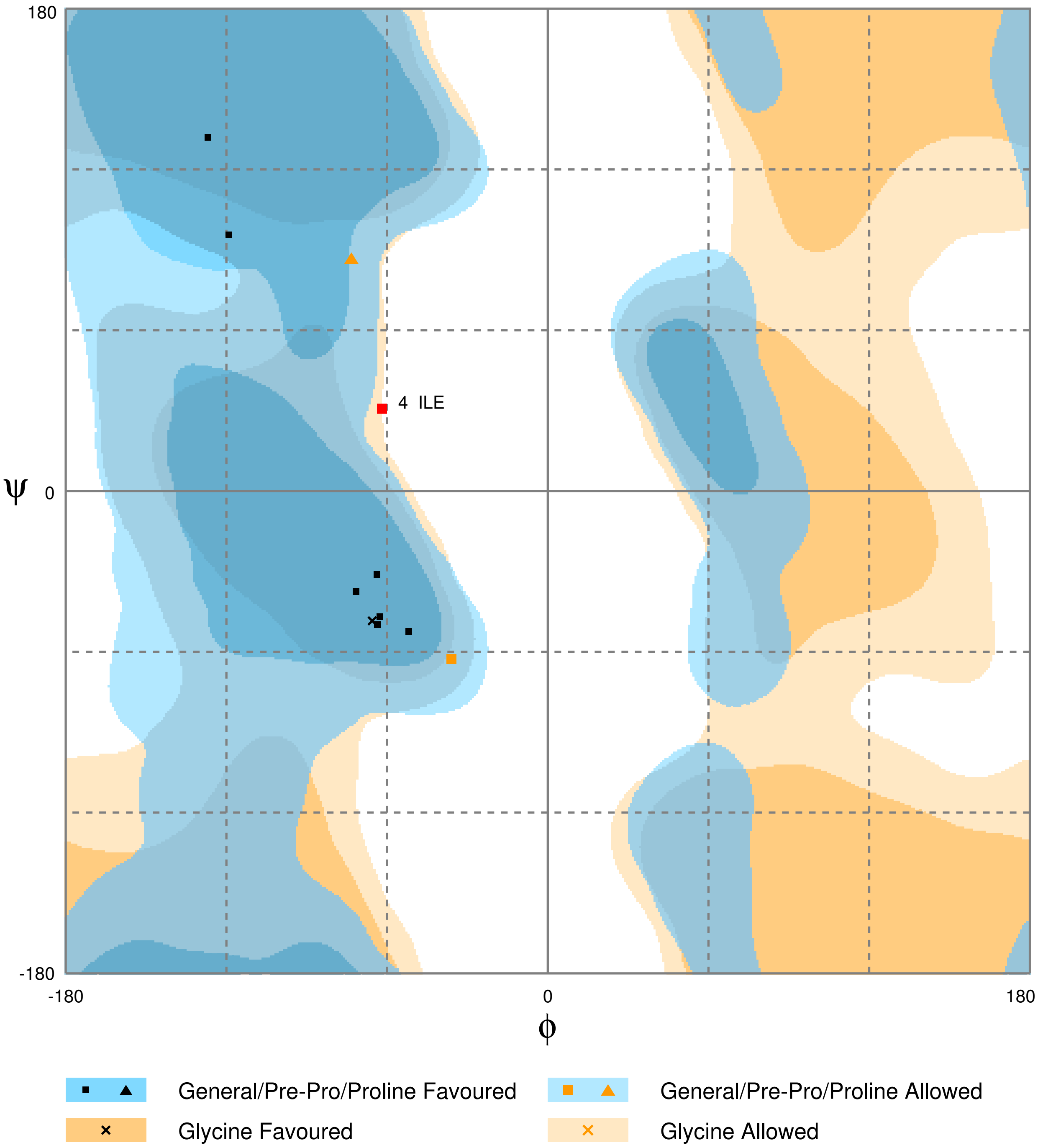


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_shb

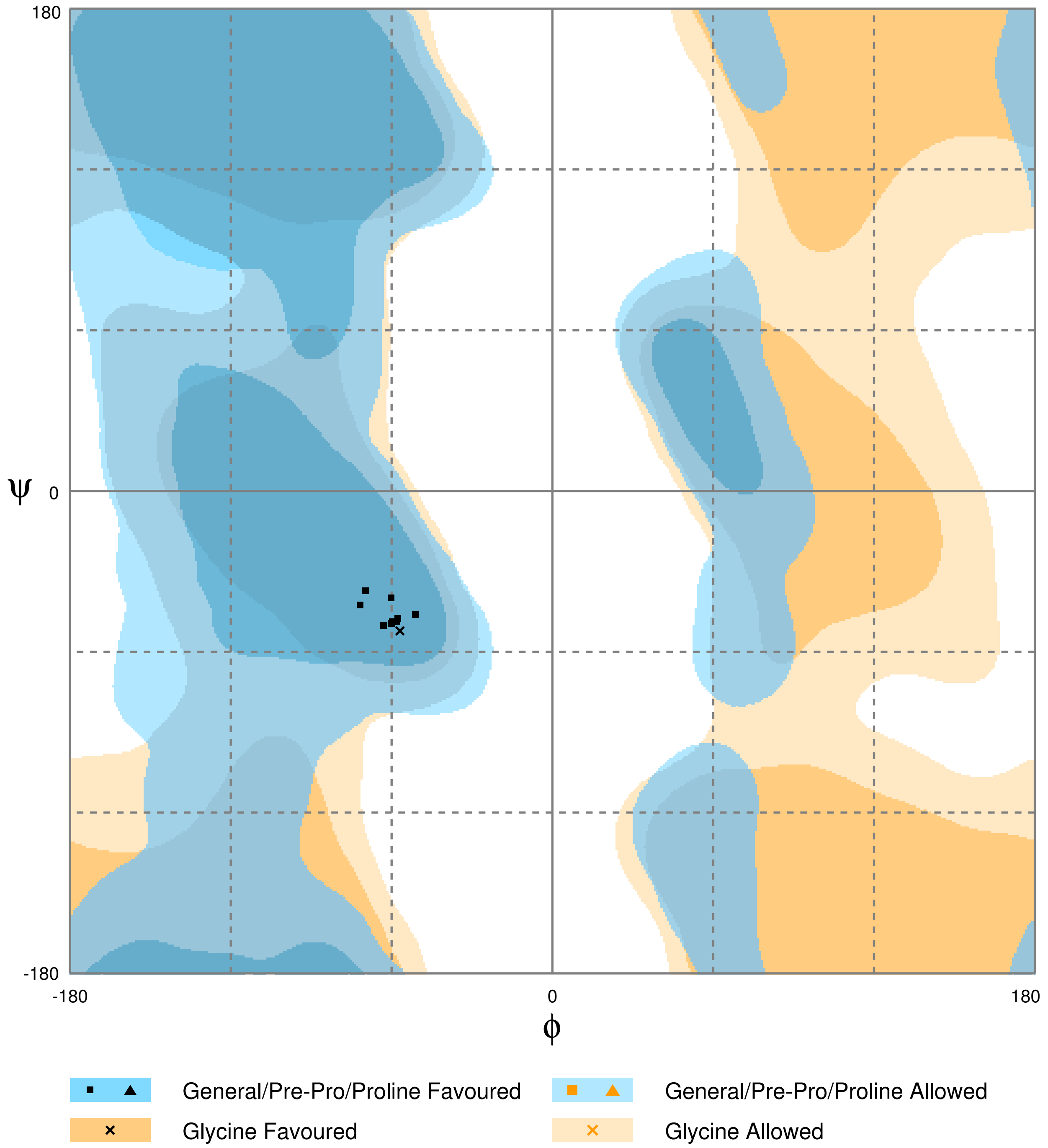


Number of residues in favoured region (~98.0% expected) : 8 (72.7%)
Number of residues in allowed region (~2.0% expected) : 2 (18.2%)
Number of residues in outlier region : 1 (9.1%)

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

Tem_shc

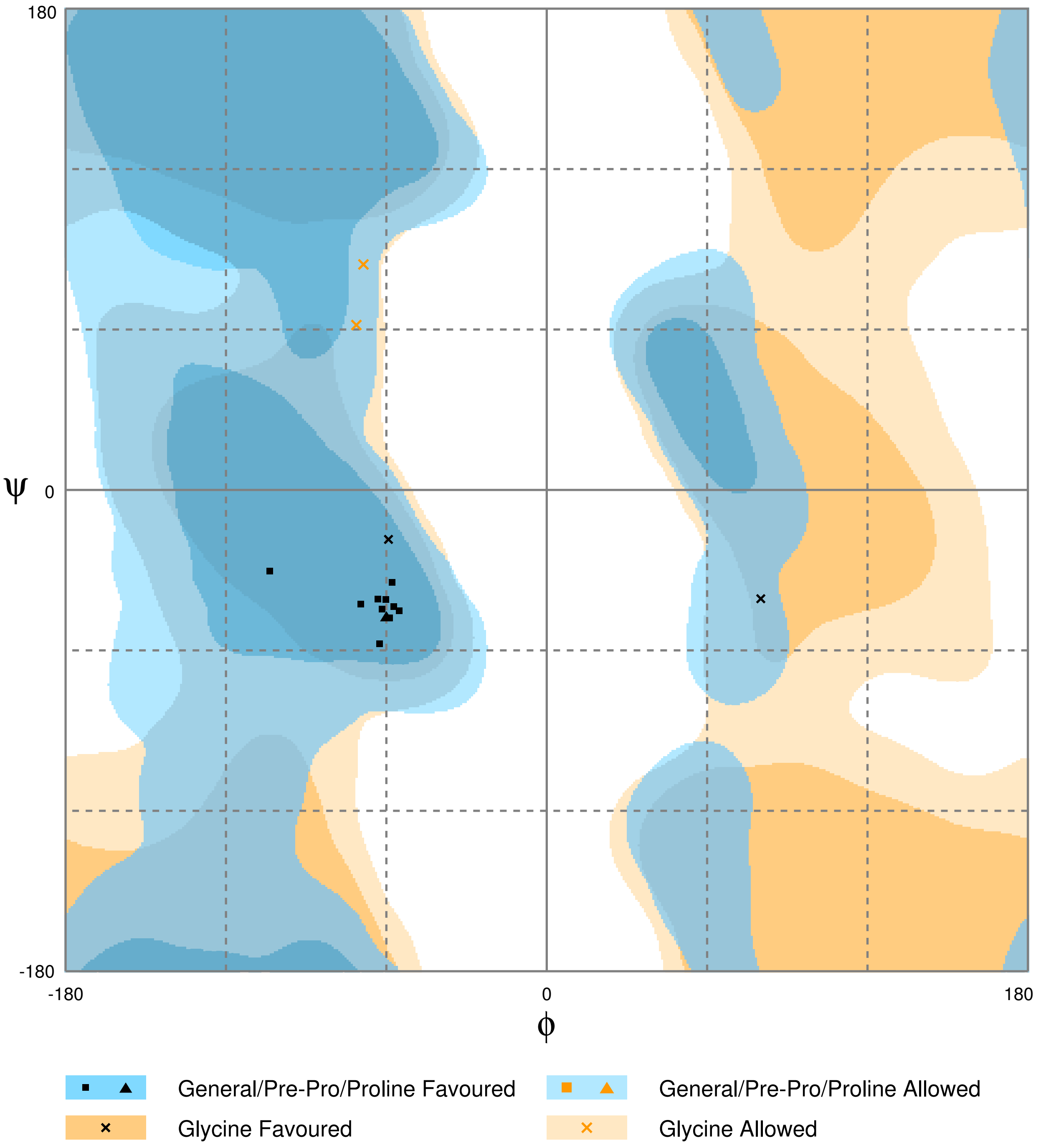


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_shd

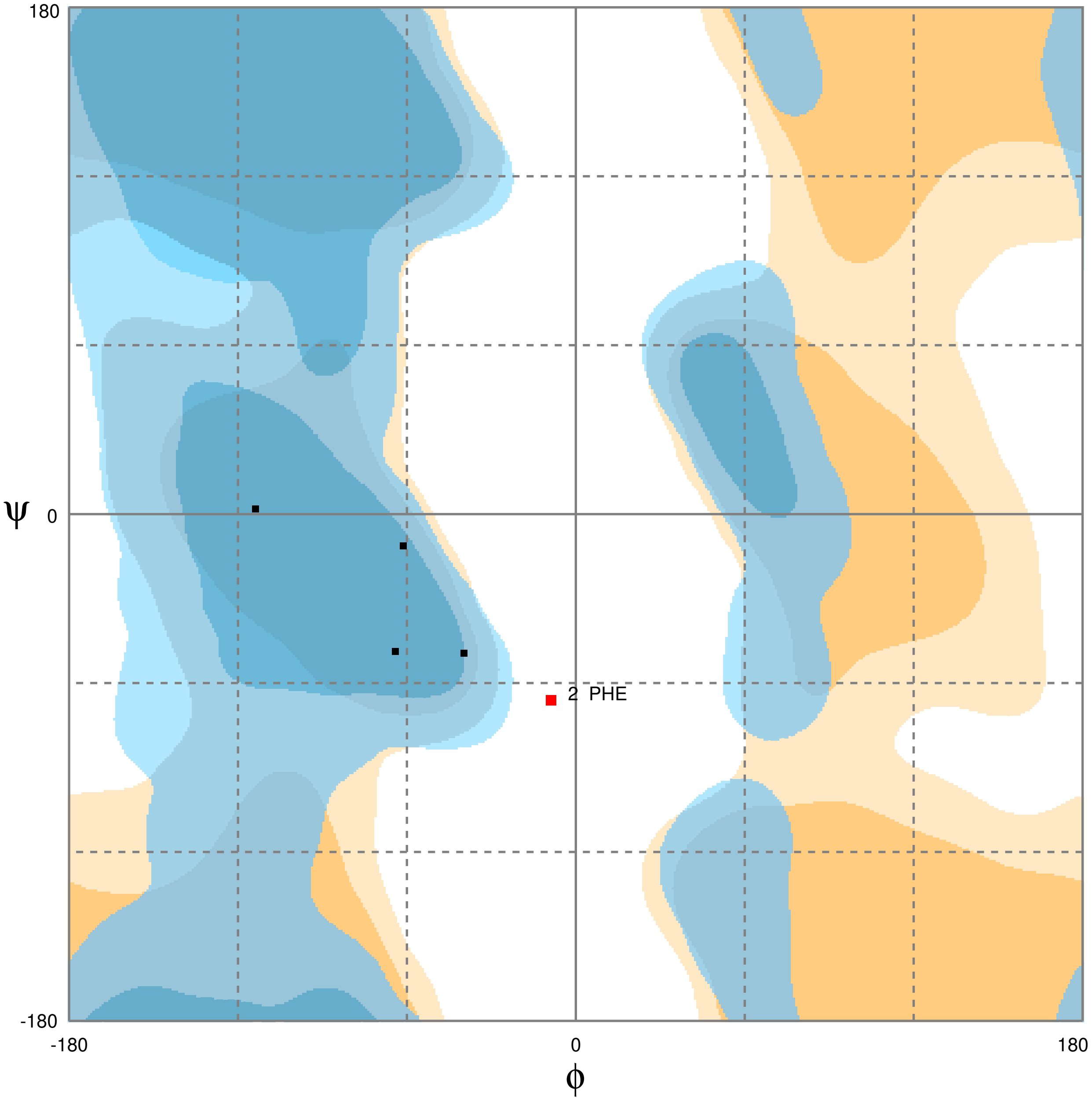


Number of residues in favoured region (~98.0% expected) : 13 (86.7%)
Number of residues in allowed region (~2.0% expected) : 2 (13.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_shf



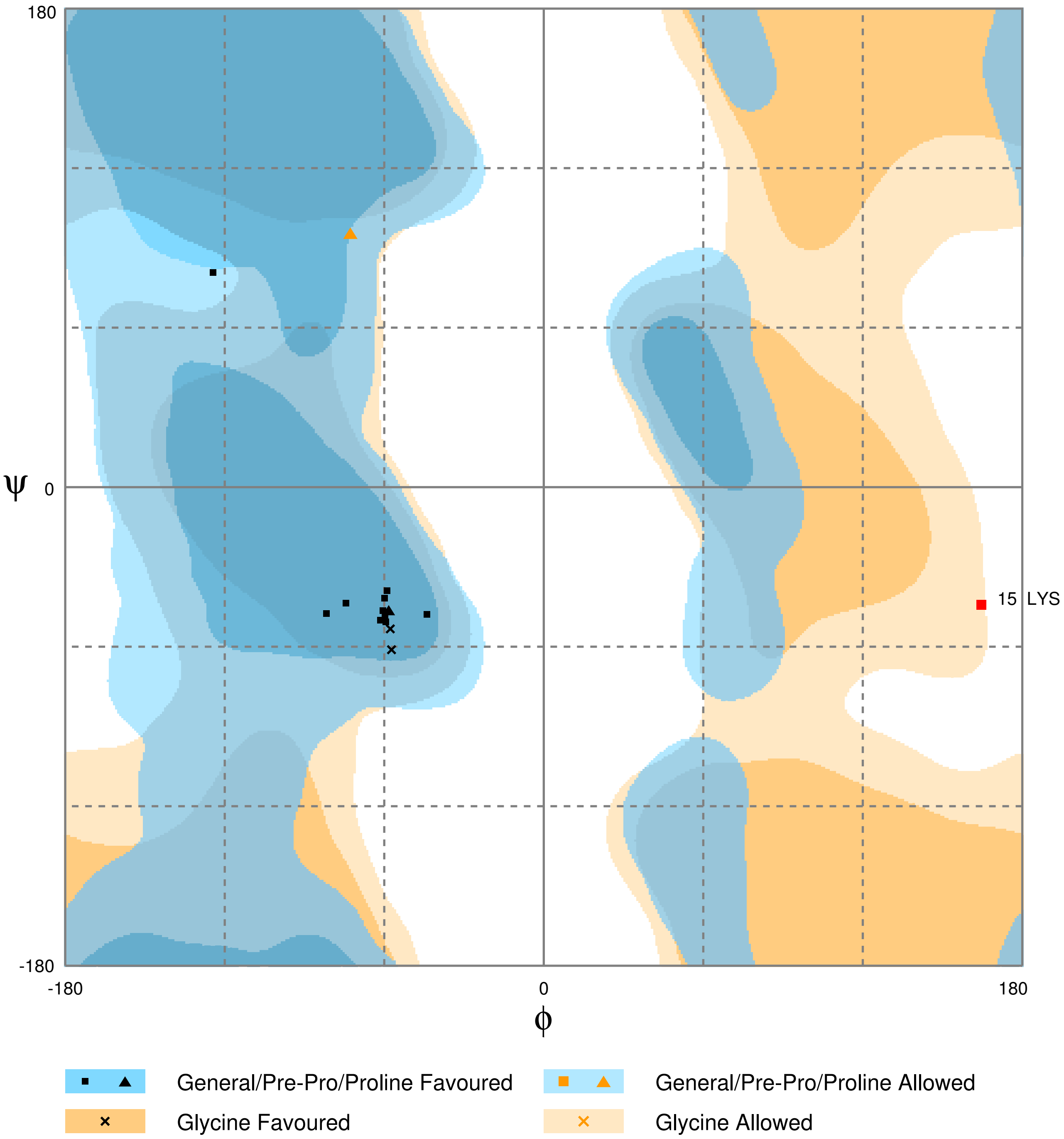
■ ▲	General/Pre-Pro/Proline Favoured	■ ▲	General/Pre-Pro/Proline Allowed
×	Glycine Favoured	×	Glycine Allowed

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

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

Tem_sn1

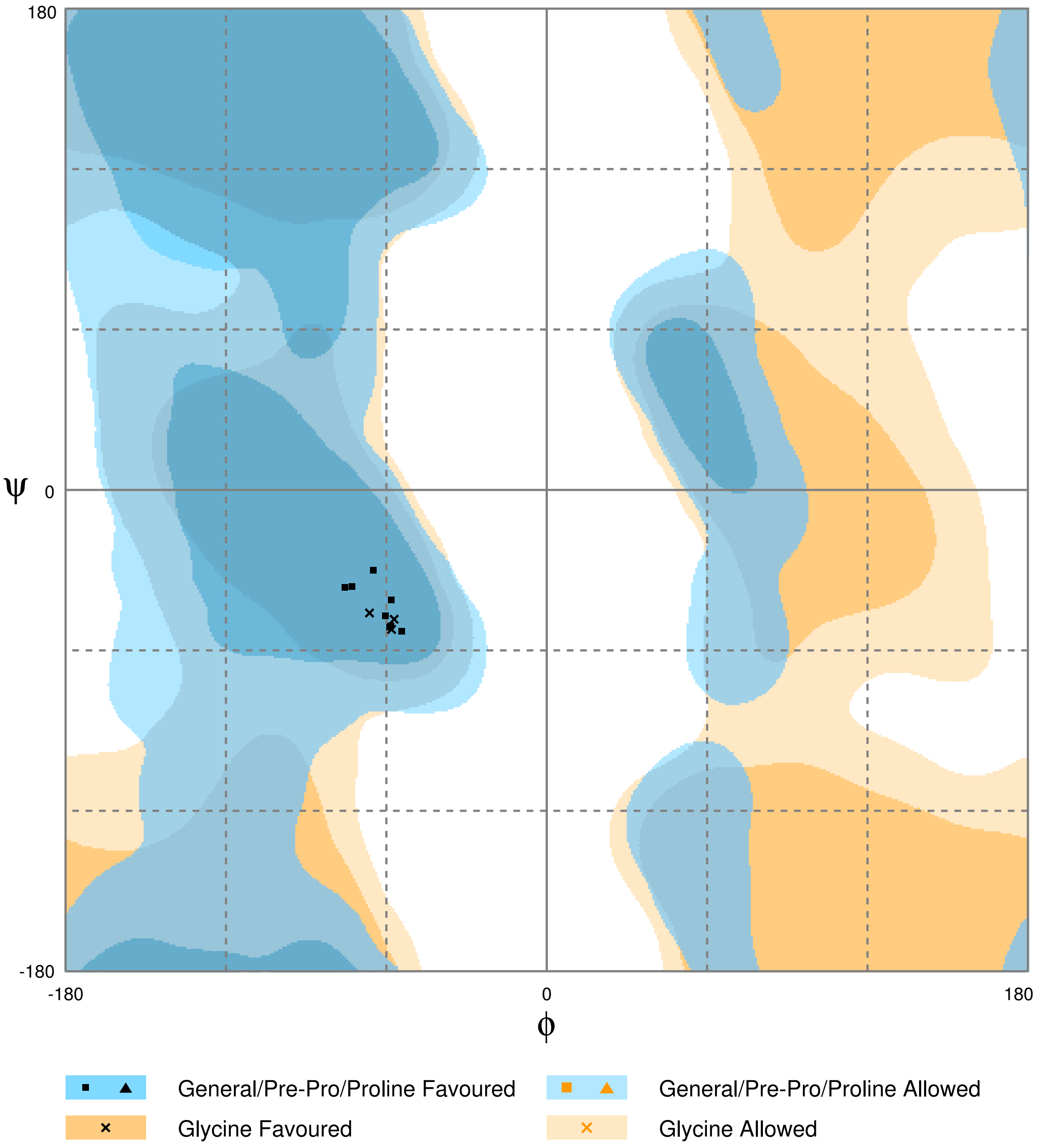


Number of residues in favoured region (~98.0% expected) : 13 (86.7%)
Number of residues in allowed region (~2.0% expected) : 1 (6.7%)
Number of residues in outlier region : 1 (6.7%)

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

Tem_sn2

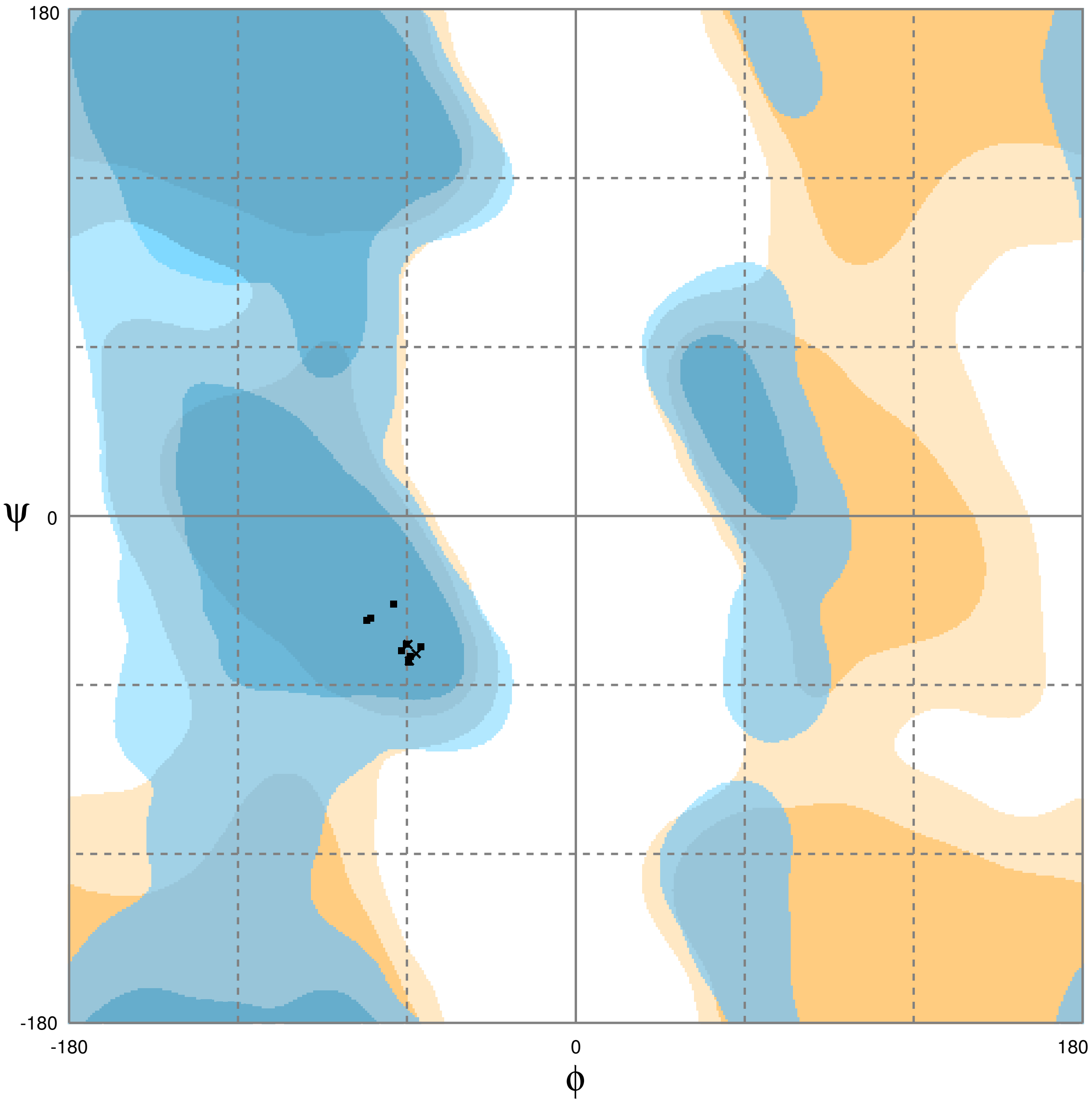


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_sn3



■ ▲ General/Pre-Pro/Proline Favoured

■ ▲ General/Pre-Pro/Proline Allowed

× Glycine Favoured

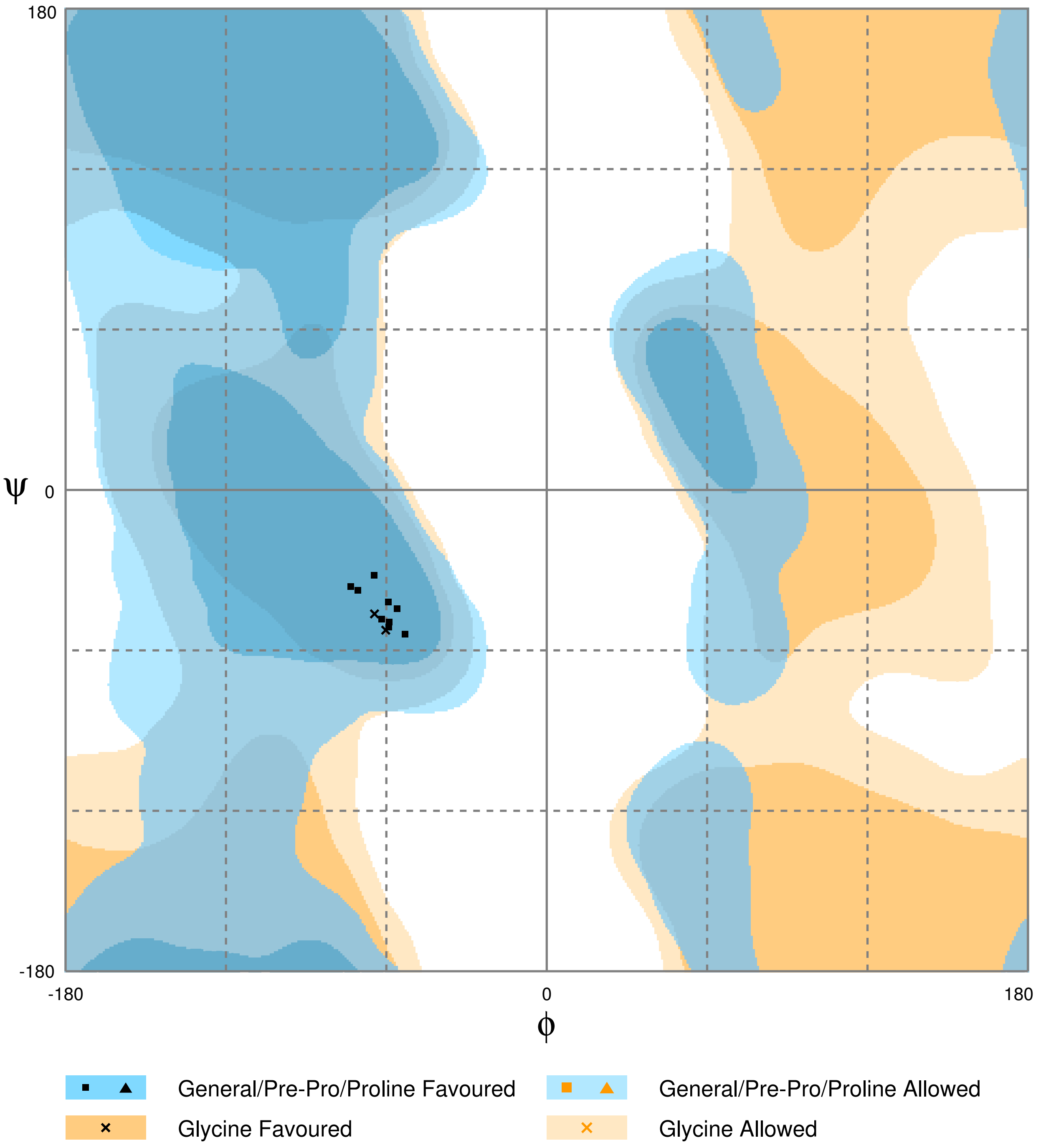
× Glycine Allowed

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%)

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

Tem_sn4

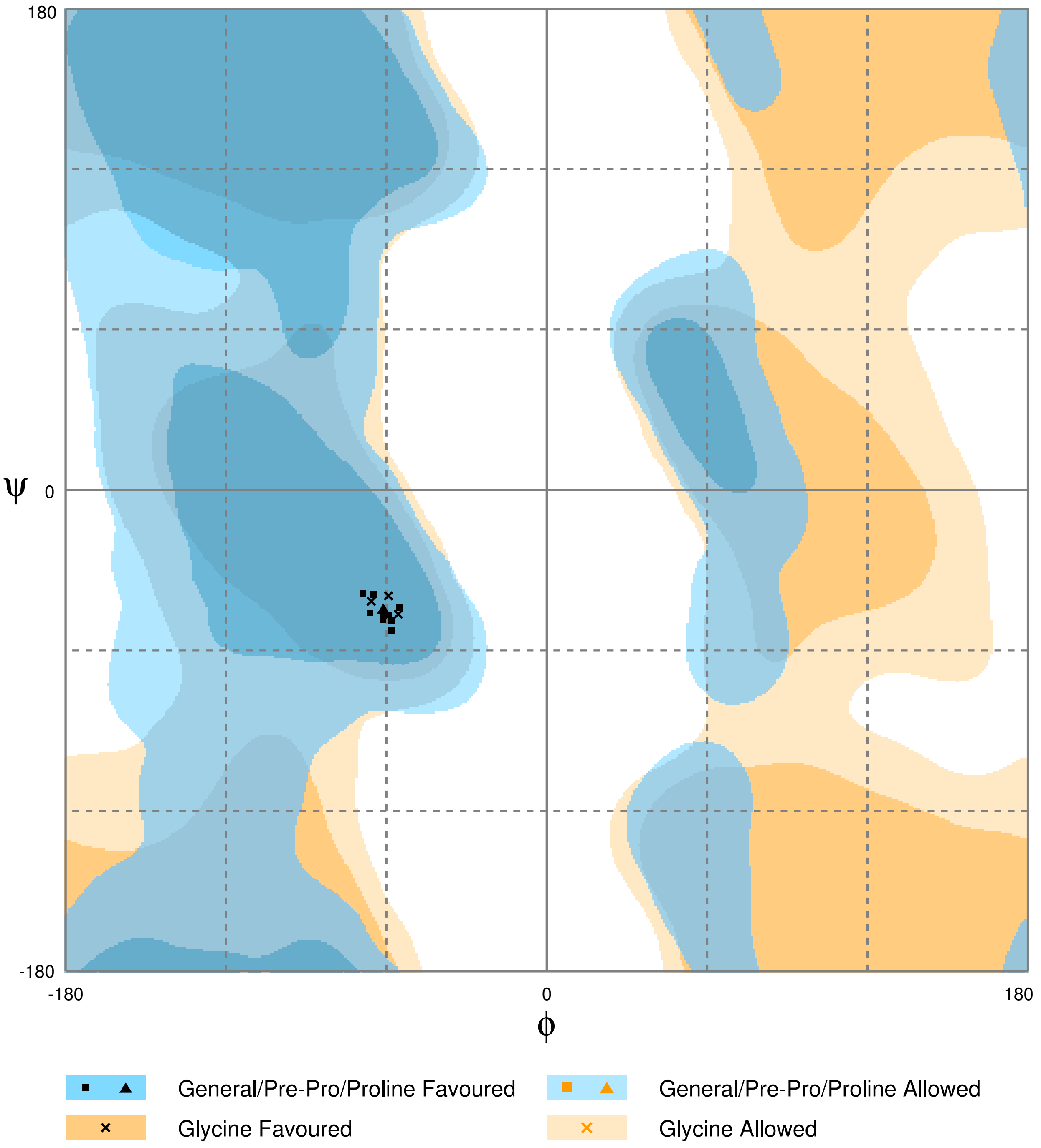


Number of residues in favoured region (~98.0% expected) : 11 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_tp1

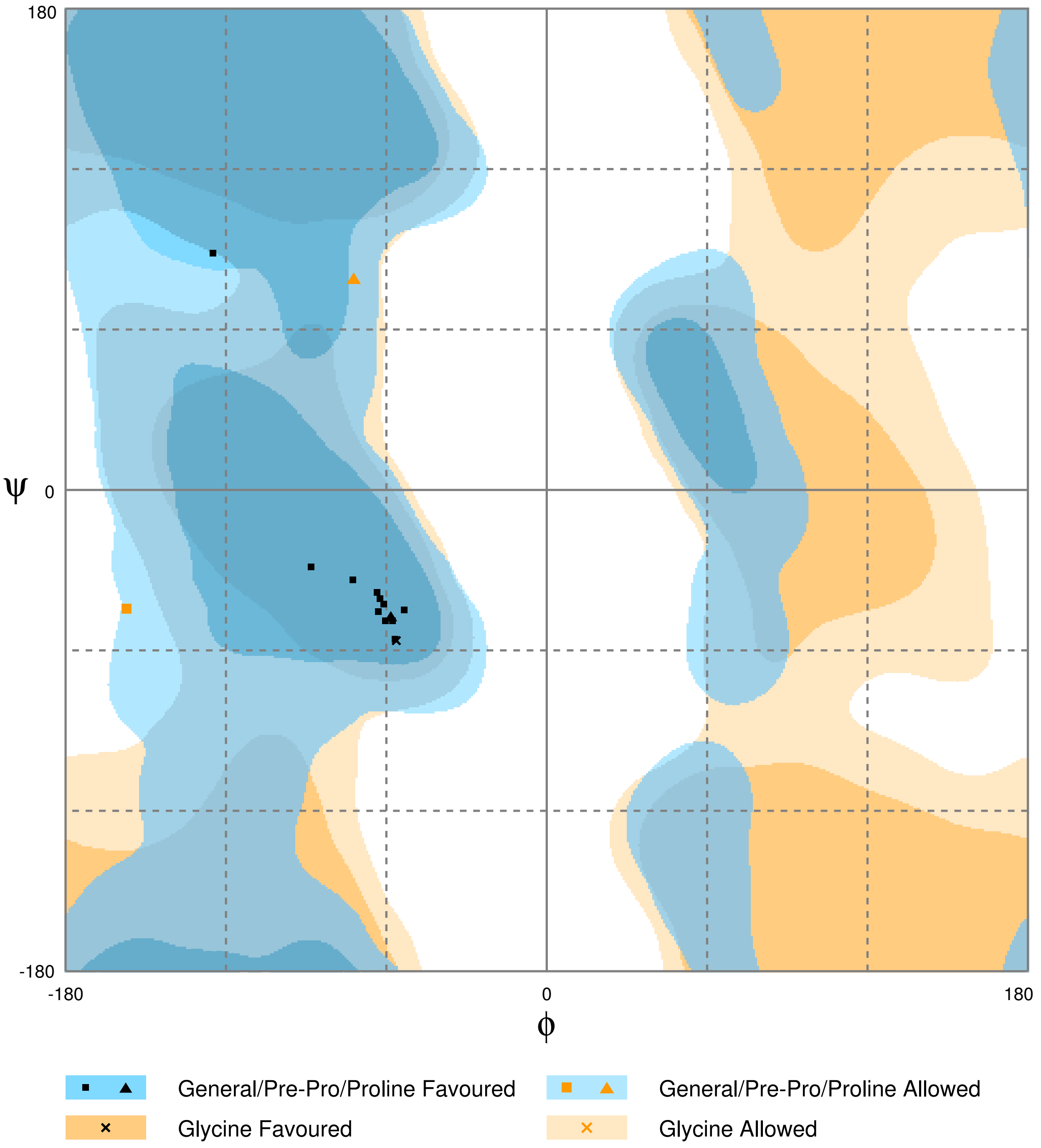


Number of residues in favoured region (~98.0% expected) : 14 (100.0%)
Number of residues in allowed region (~2.0% expected) : 0 (0.0%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_tp2

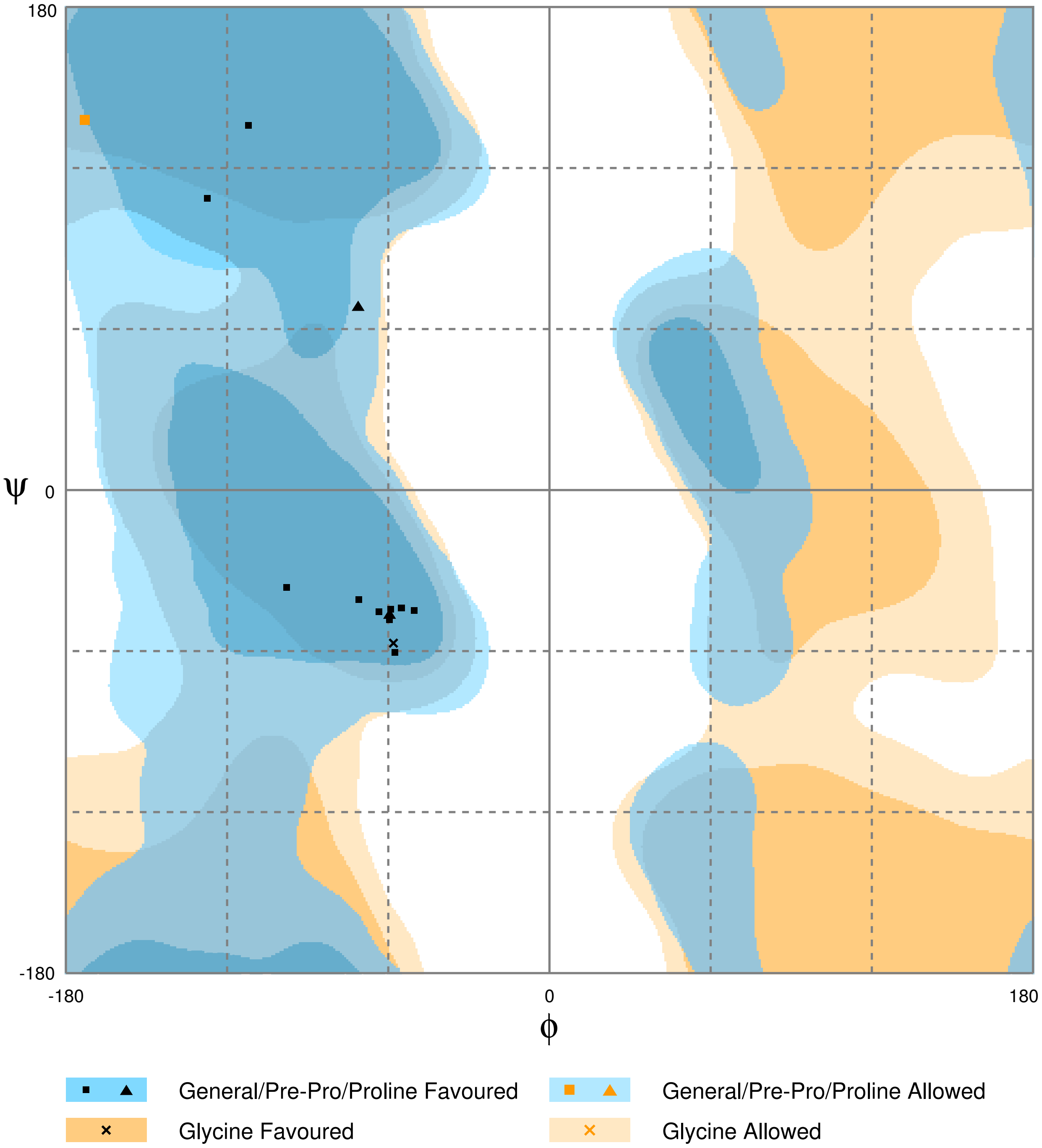


Number of residues in favoured region (~98.0% expected) : 13 (86.7%)
Number of residues in allowed region (~2.0% expected) : 2 (13.3%)
Number of residues in outlier region : 0 (0.0%)

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

Tem_tp3



Number of residues in favoured region (~98.0% expected)	: 14 (93.3%)
Number of residues in allowed region (~2.0% expected)	: 1 (6.7%)
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