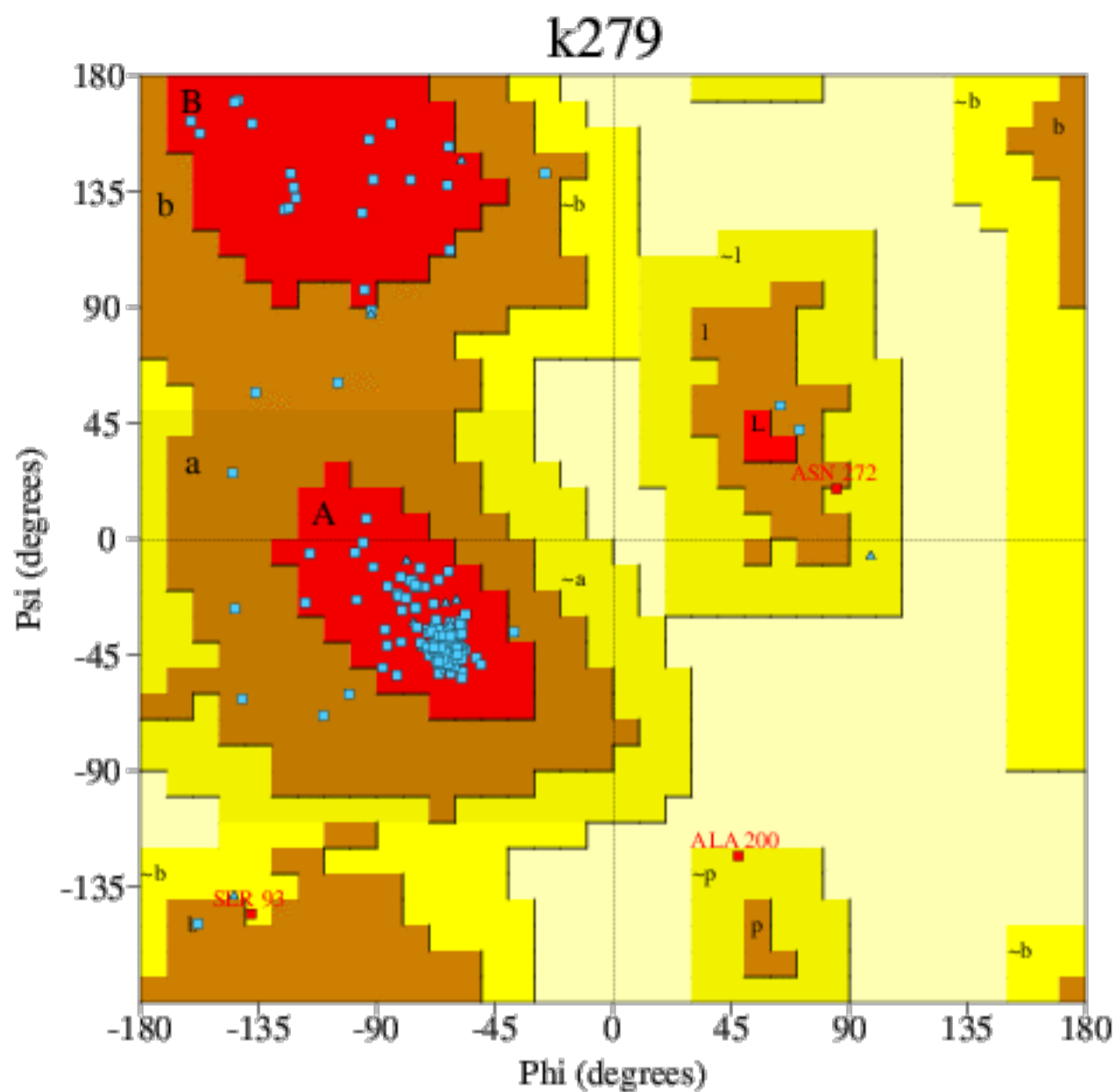**No title**

PDB id

k279

Generate full PROCHECK analyses

PROCHECK summary for k279

Ramachandran plot

Contents

Protein chain

● 274 a.a.

k279

PROCHECK statistics

1. Ramachandran Plot statistics

		No. of residues	%-tage
Most favoured regions	[A,B,L]	230	93.9%
Additional allowed regions	[a,b,l,p]	12	4.9%
Generously allowed regions	[~a,~b,~l,~p]	3	1.2%
Disallowed regions	[XX]	0	0.0%
Non-glycine and non-proline residues		245	100.0%
End-residues (excl. Gly and Pro)		5	
Glycine residues		11	
Proline residues		13	

```
                                              ----
Total number of residues                       274
```

Based on an analysis of **118** structures of resolution of at least **2.0** Angstroms and *R*-factor no greater than **20.0** a good quality model would be expected to have over **90%** in the most favoured regions [A,B,L].

2. G-Factors

```
                                              Average
Parameter                         Score        Score
---------                         -----        -----
Dihedral angles:-
     Phi-psi distribution          0.42
     Chi1-chi2 distribution       -0.42
     Chi1 only                    -0.23
     Chi3 & chi4                   0.59
     Omega                        -0.78*
                                              -0.16
                                              =====

Main-chain covalent forces:-
     Main-chain bond lengths       0.21
     Main-chain bond angles       -0.34
                                              -0.11
                                              =====


     OVERALL AVERAGE                          -0.12
                                              =====
```

G-factors provide a measure of how **unusual**, or out-of-the-ordinary, a property is.

```
Values below -0.5*  - unusual
Values below -1.0** - highly unusual
```

Important note: The main-chain bond-lengths and bond angles are compared with the Engh & Huber (1991) ideal values derived from small-molecule data. Therefore, structures refined using different restraints may show apparently large deviations from normality.

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