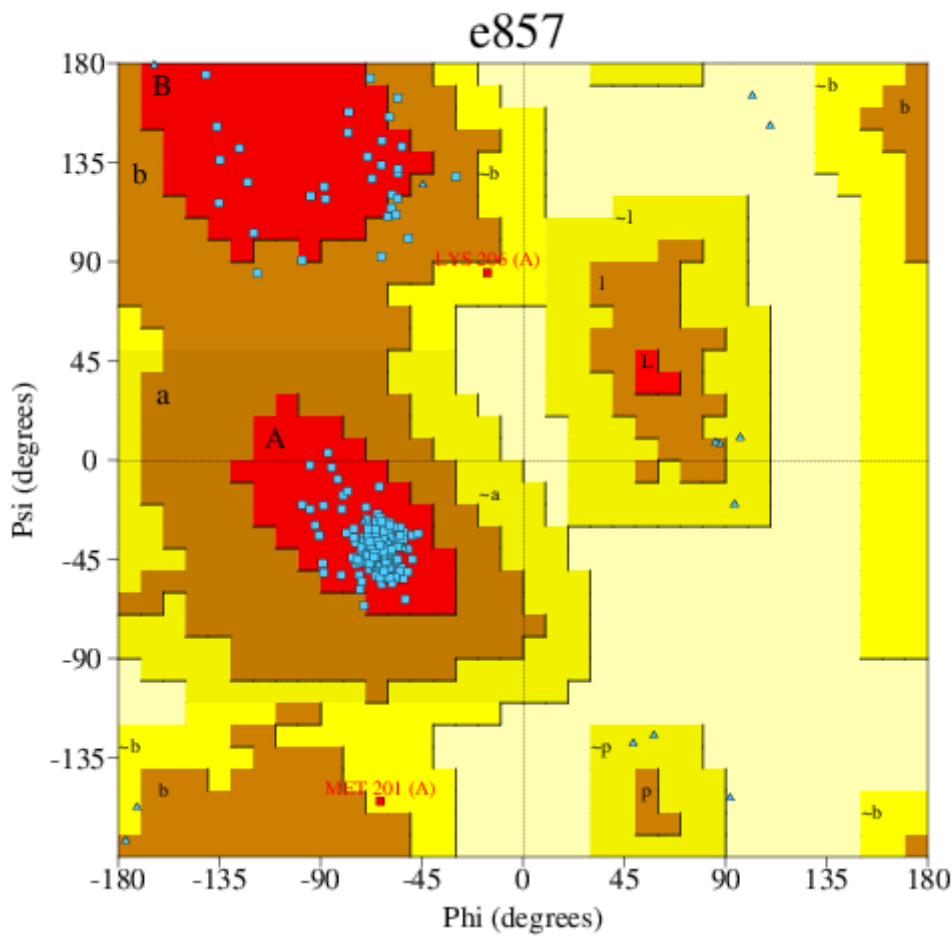


Generate full PROCHECK analyses

PROCHECK summary for e857

Ramachandran plot



PROCHECK statistics

1. Ramachandran Plot statistics

		No. of residues	%-tage
		-----	-----
Most favoured regions	[A,B,L]	246	95.3%
Additional allowed regions	[a,b,l,p]	10	3.9%

Generously allowed regions [~a,~b,~l,~p]	2	0.8%
Disallowed regions [XX]	0	0.0%
	----	-----
Non-glycine and non-proline residues	258	100.0%
End-residues (excl. Gly and Pro)	2	
Glycine residues	31	
Proline residues	7	

Total number of residues	298	

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

Parameter	Score	Average Score
-----	-----	-----
Dihedral angles:-		
Phi-psi distribution	0.49	
Chi1-chi2 distribution	0.09	
Chi1 only	-0.10	
Chi3 & chi4	0.47	
Omega	-0.06	
		0.20
		=====
Main-chain covalent forces:-		
Main-chain bond lengths	0.47	
Main-chain bond angles	0.19	
		0.30
		=====
OVERALL AVERAGE		0.25
		=====

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.