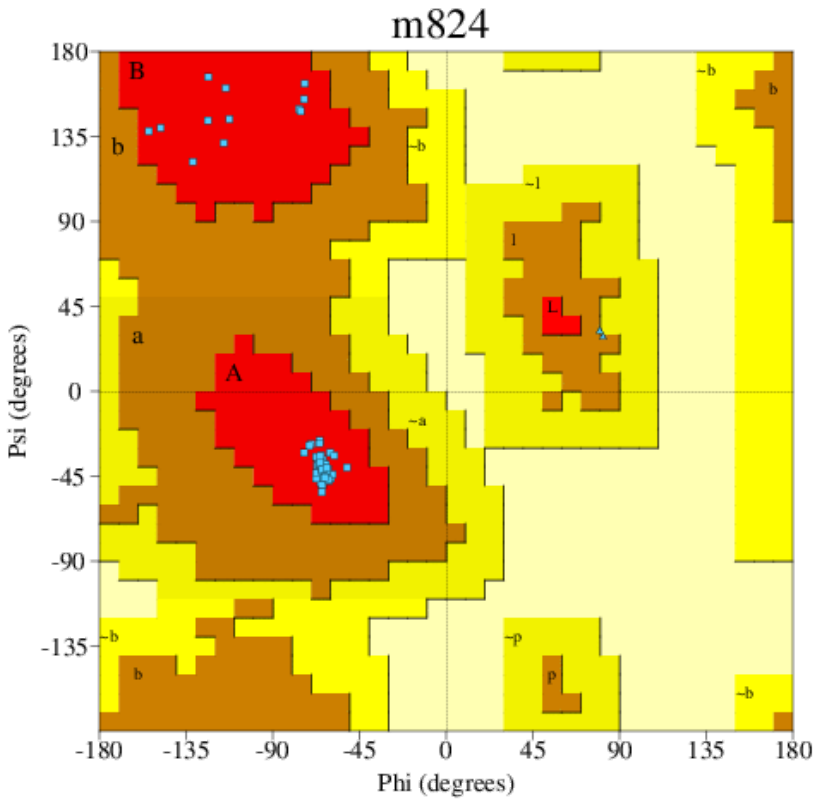
PDBsum entry m824

PROCHECK Generate full PROCHECK analyses

PROCHECK summary for m824

Ramachandran plot



Contents

Protein chains

51 a.a.

Ligands

_DC-_DA-_DA-_DT-_DC-_DA-_DT-_DT-_DG

_DC

_DG-_DC-_DA-_DA-_DT-_DG-_DA-_DT-_DT-_DG

PROCHECK statistics

1. Ramachandran Plot statistics

		No. of residues	%-tage
Most favoured regions	[A,B,L]	92	100.0%
Additional allowed regions	[a,b,l,p]	0	0.0%
Generously allowed regions	[~a,~b,~l,~p]	0	0.0%
Disallowed regions	[XX]	0	0.0%
Non-glycine and non-proline residues		92	100.0%
End-residues (excl. Gly and Pro)		4	
Glycine residues		2	
Proline residues		4	
Total number of residues		102	

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	0.82	
Chi1-chi2 distribution	0.12	
Chi1 only	0.06	
Chi3 & chi4	0.44	
Omega	0.10	
		0.37
Main-chain covalent forces:-		
Main-chain bond lengths	-0.09	
Main-chain bond angles	-0.01	
		-0.05
OVERALL AVERAGE		0.21

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.