

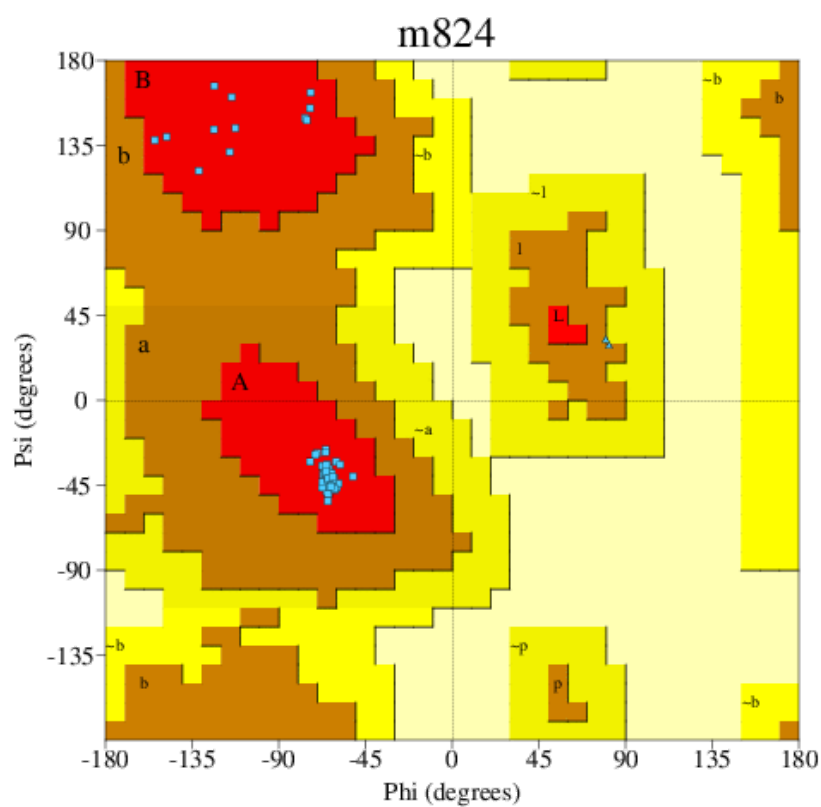
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PDBsum entry m824

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m824**Generate full PROCHECK analyses****PROCHECK summary for m824****Ramachandran plot****Contents****Protein chains****L** **D** 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.



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