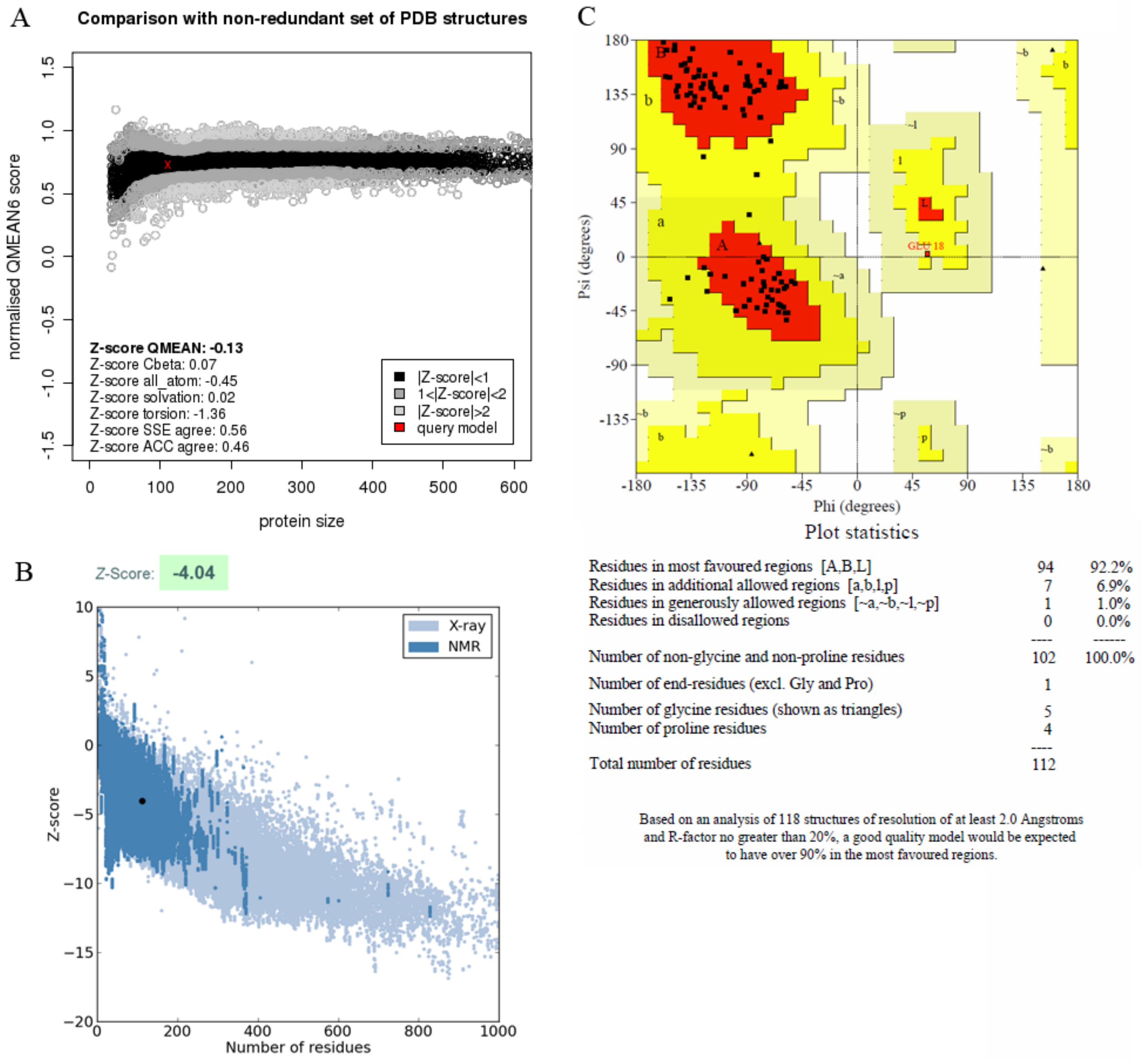
Figure S3. Quality of GAB1 PH domain model. This model was subjected to energy minimization prior to quality assessment. (A) QMEAN; (B) ProSA; (C); Ramachandran plot and summary generated by PROCHECK.



Plot statistics

Residues in most favoured regions [A,B,L]	94	92.2%
Residues in additional allowed regions [a,b,l,p]	7	6.9%
Residues in generously allowed regions [~a,~b,~l,~p]	1	1.0%
Residues in disallowed regions	0	0.0%
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Number of non-glycine and non-proline residues	102	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	5	
Number of proline residues	4	

Total number of residues	112	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.