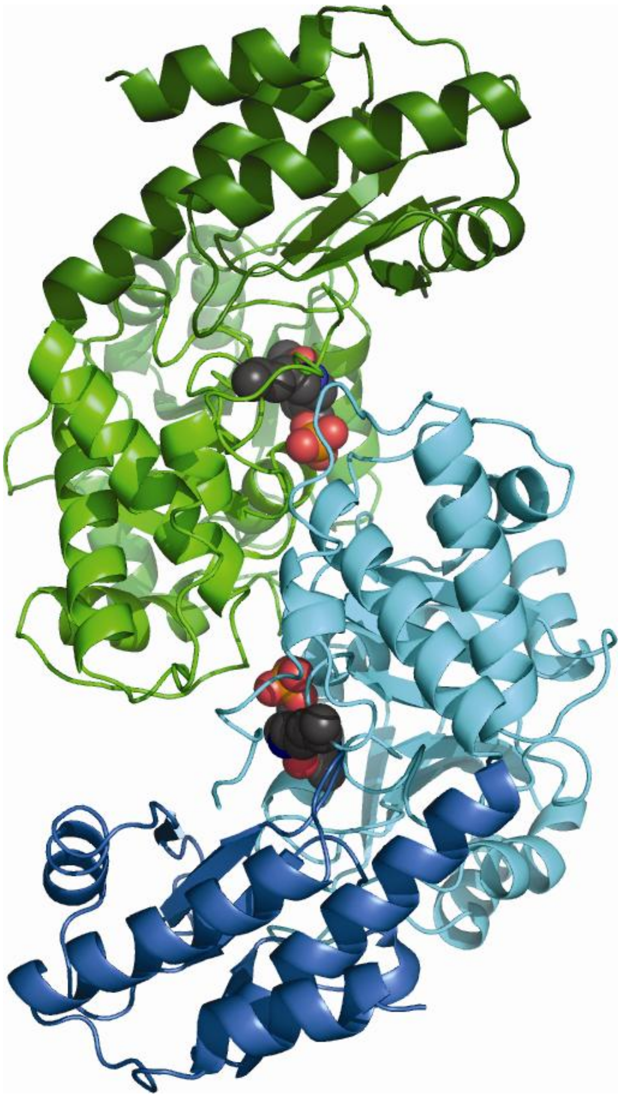
Supplementary Material

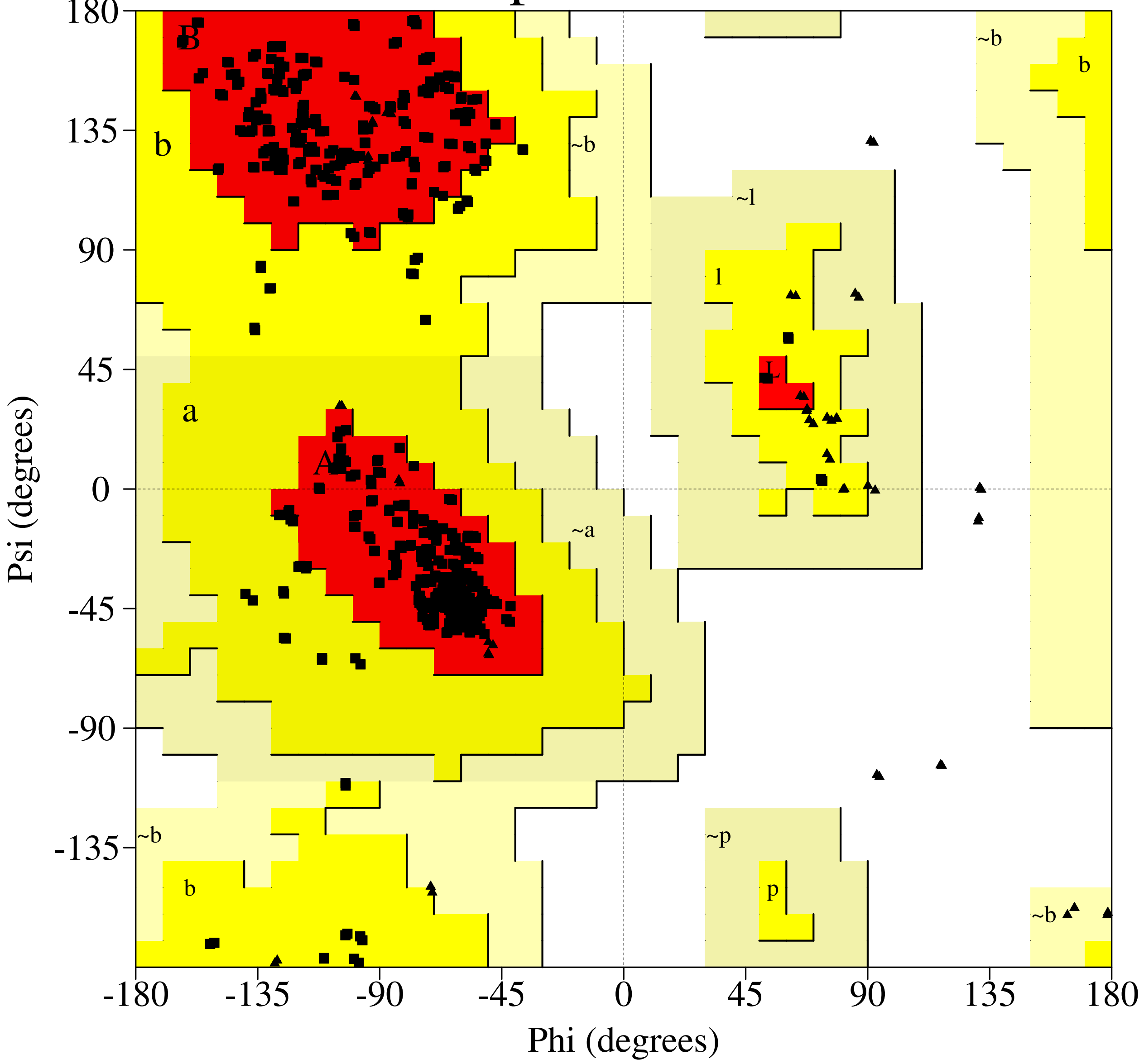


Supplementary Figure 1. A ribbon diagram of the S. sofataricus SPAT dimer viewed along a molecular dyad. The subunits are shown in green and blue with the C-terminal small domains highlighted in a darker shade for each subunit. The cofactor PLP is shown as a space filling model. This figure was prepared using *PyMOL* (DeLano, 2002).

PROCHECK

Ramachandran Plot

deposit_holo



Plot statistics

Residues in most favoured regions [A,B,L]	610	94.4%
Residues in additional allowed regions [a,b,l,p]	36	5.6%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	646	100.0%
Number of end-residues (excl. Gly and Pro)	600	
Number of glycine residues (shown as triangles)	66	
Number of proline residues	38	

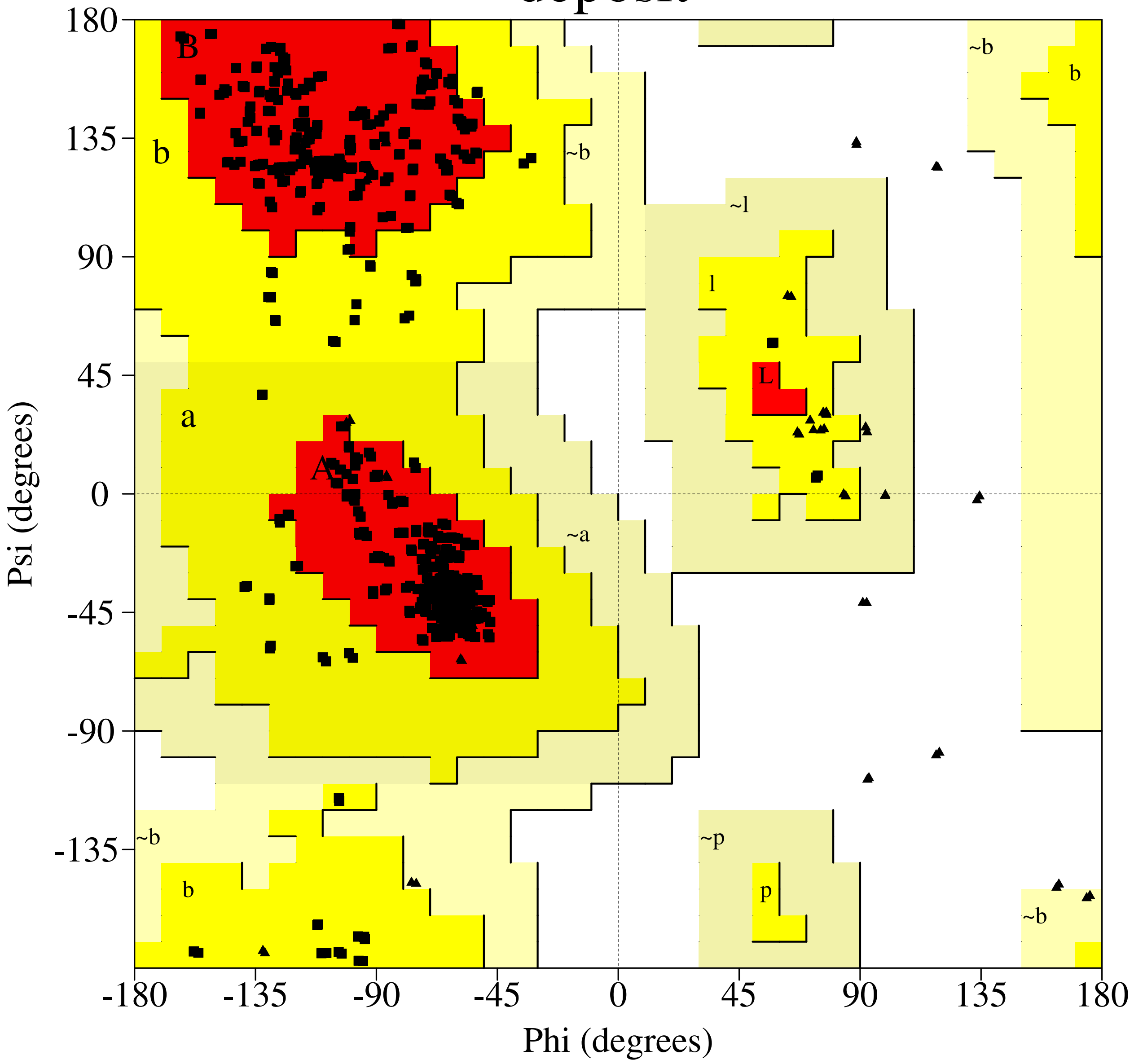
Total number of residues	1350	

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.

PROCHECK

Ramachandran Plot

deposit



Plot statistics

Residues in most favoured regions [A,B,L]	607	92.5%
Residues in additional allowed regions [a,b,l,p]	49	7.5%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
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Number of non-glycine and non-proline residues	656	100.0%
Number of end-residues (excl. Gly and Pro)	513	
Number of glycine residues (shown as triangles)	66	
Number of proline residues	38	

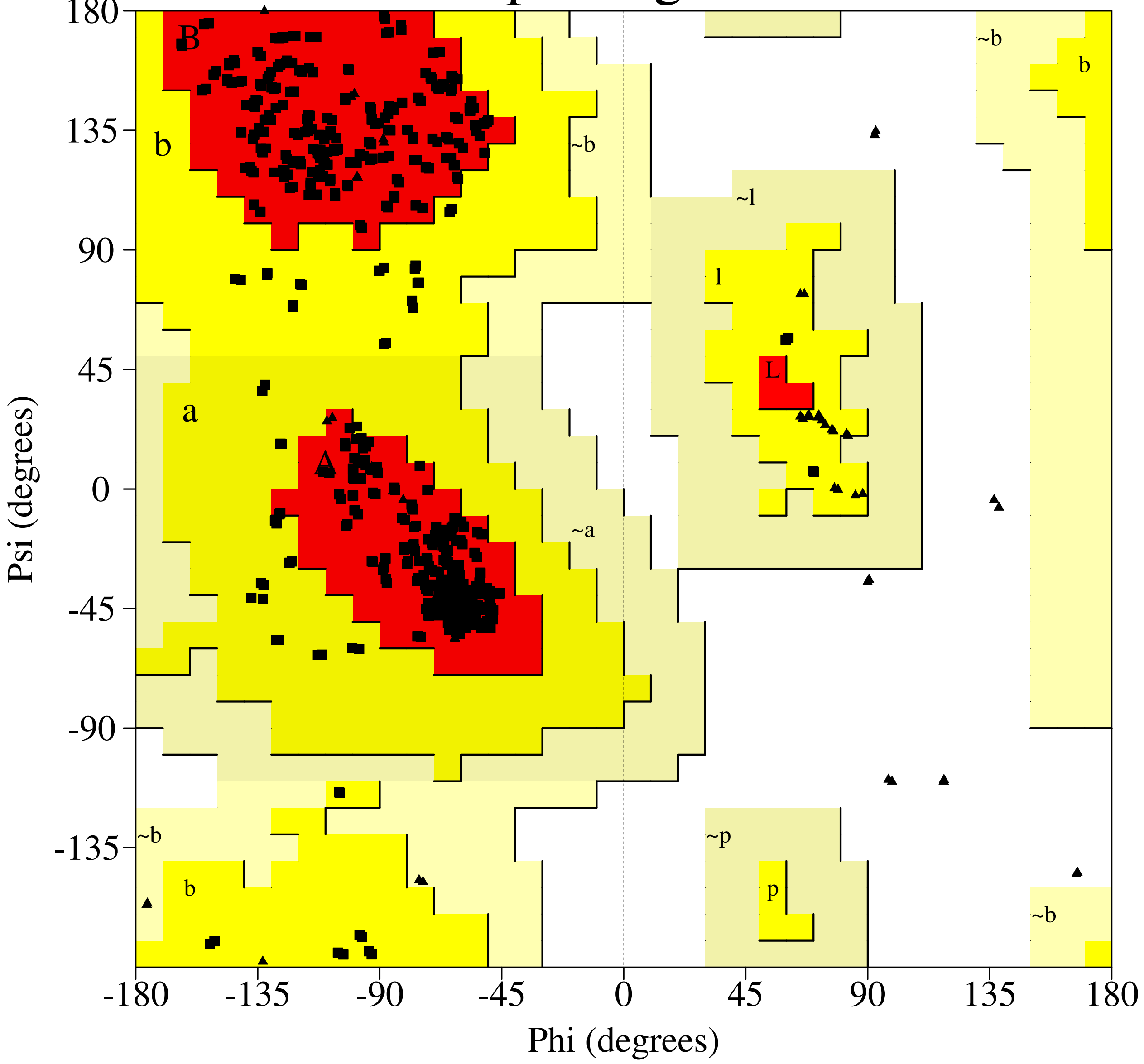
Total number of residues	1273	

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.

PROCHECK

Ramachandran Plot

deposit_gaba



Plot statistics

Residues in most favoured regions [A,B,L]	605	93.1%
Residues in additional allowed regions [a,b,l,p]	45	6.9%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	650	100.0%
Number of end-residues (excl. Gly and Pro)	515	
Number of glycine residues (shown as triangles)	66	
Number of proline residues	38	

Total number of residues	1269	

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.

deposit_gaba_01.ps