

## Supplementary Information

### Diffraction Data Statistics

Resolution	$I/\sigma(I)$	$R_{\text{merge}}$	Completeness (%)	% < $3\sigma$
20.00-2.37	18.77	0.059	93.8	0.6
2.37-1.88	22.00	0.061	99.8	1.9
1.88-1.64	20.65	0.070	100.0	4.7
1.64-1.49	18.27	0.077	99.9	8.5
1.49-1.39	14.74	0.091	99.9	14.0
1.39-1.30	12.1	0.109	99.7	18.6
1.30-1.24	6.93	0.131	87.2	26.4
1.24-1.18	5.33	0.146	67.5	29.3
1.18-1.14	3.91	0.173	54.0	29.7
1.14-1.10	2.65	0.199	36.7	25.1
20.00-1.10	17.08	0.067	83.9	15.9

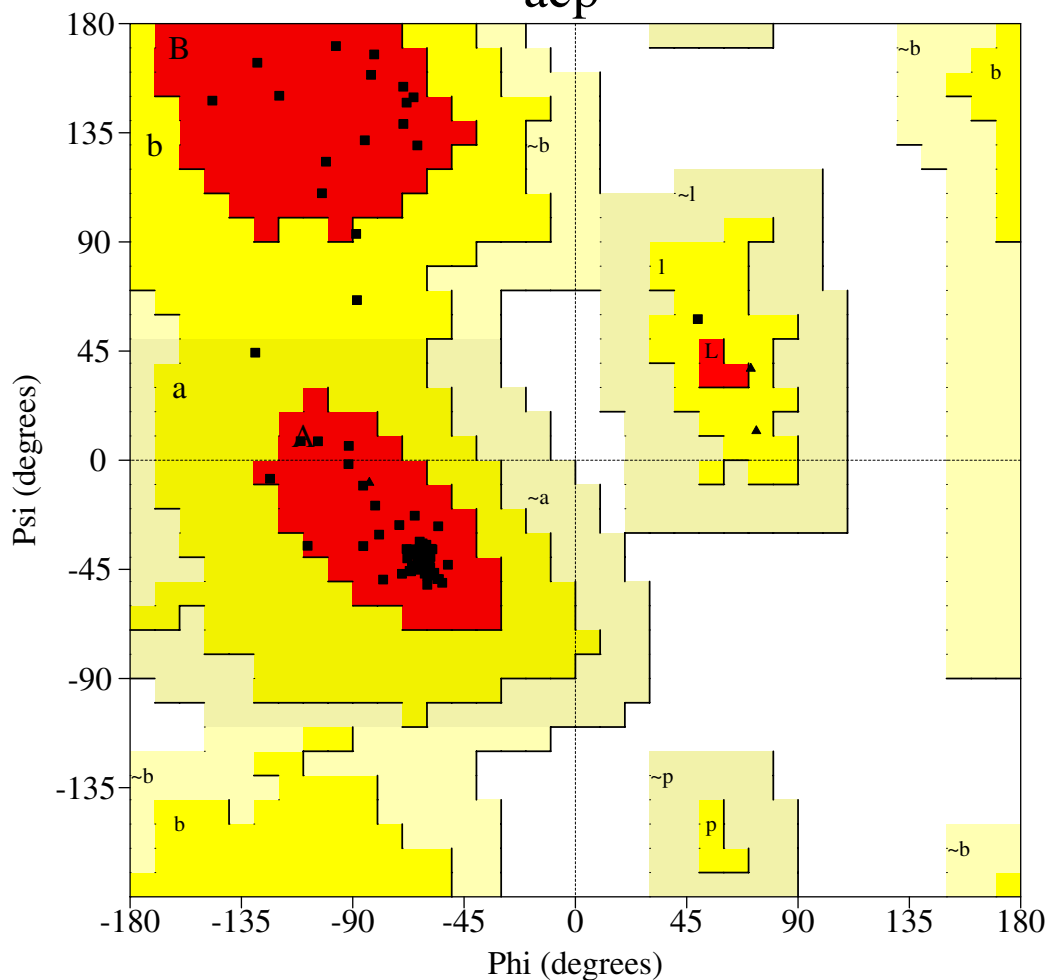
### Structure Refinement Statistics

Resolution (Å)	$R$	$R_{\text{free}}$
20.00-6.69	0.24	0.20
6.69-2.31	0.16	0.15
2.31-1.68	0.13	0.15
1.68-1.39	0.10	0.13
1.39-1.29	0.10	0.11
1.29-1.21	0.11	0.16
1.21-1.14	0.14	0.17
1.14-1.10	0.17	0.15
20.00-1.10	0.13	0.15

PROCHECK

# Ramachandran Plot

acp



## Plot statistics

Residues in most favoured regions [A,B,L]	66	94.3%
Residues in additional allowed regions [a,b,l,p]	4	5.7%
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	70	100.0%
Number of end-residues (excl. Gly and Pro)	126	
Number of glycine residues (shown as triangles)	4	
Number of proline residues	1	
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Total number of residues	201	

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.

**Primary and Secondary Structures of Acyl Carrier Proteins.** Residue numbers are labelled at the top. Helices are shaded in yellow. Six organisms from the Monera kingdom were chosen (3 Gram+, 3 Gram-), plus one from each of the other kingdoms. Red are identical in all the sequences; blue are highly conserved (defined as at least 8 identical residues out of the 10). Ec: *Escherichia coli* (P02901); Hi: *Haemophilus influenzae* (P43709); Hp: *Helicobacter pylori* (P56464); Bs: *Bacillus subtilis* (P80643); Sa: *Staphylococcus aureus* (BAB20936); Mt: *Mycobacterium tuberculosis* acpM (CAA94640); Pf: *Plasmodium falciparum* (AAC63959); Sc: *Saccharomyces cerevisiae* (S33960); So: *Spinacia oleracea* ACP-I (spinach, P07854); Hs: *Homo sapiens* acpM (O14561).

		3	15	28	36	41	47	50	56	61	65	75																																																																	
	$\alpha 1$	$\alpha 2$					$\alpha 3$	$\alpha 4$																																																																					
Ec	1	STIEERVVKKI	IGEQ	L	-	GVKQEEV	TNNAS	F	VE	DL	LG	AD	SL	DT	VE	LV	MA	LE	EE	FD	TE	IP	DE	EA	EK	IT	VQ	AA	ID	YI	NG	HQ	QA																																												
Hi	1	MSIEERVVKKI	I	VE	QL	-	GVKKEED	V	KPEAS	F	VE	DL	LG	AD	SL	DT	VE	LV	MA	LE	EE	FD	TE	IP	DE	EA	EK	IT	VQ	SA	ID	YV	QN	NQ																																											
Hp	1	MALFEDI	Q	AV	IA	EQ	L	-	NVD	AV	Q	V	T	PE	AE	F	V	K	D	L	V	E	L	I	M	A	L	E	E	K	F	G	V	E	I	P	D	E	Q	A	E	K	I	I	N	V	G	D	V	V	K	Y	I	E	D	N	K																				
Bs	2	ADTLERVT	KI	I	V	D	R	L	-	GV	DE	AD	V	K	LE	AS	F	K	E	D	L	G	AD	SL	DL	V	V	E	L	V	M	E	L	E	D	E	F	D	M	E	I	S	D	E	A	E	K	I	A	T	V	G	D	AV	N	Y	I	Q	N	Q																	
Sa	1	MENFD	K	V	K	D	I	I	V	D	R	L	-	GV	D	AD	K	V	T	E	D	A	S	F	K	D	D	L	G	A	D	S	L	D	I	A	E	L	V	M	E	L	E	D	E	F	G	T	E	I	P	D	E	E	A	E	K	I	N	T	V	G	D	AV	K	F	I	N	S	L	E	K					
Mt	6	EEI	I	A	G	I	A	E	I	E	E	V	T	-	G	I	E	P	S	E	I	T	P	E	K	S	F	V	D	D	L	D	I	D	S	L	S	M	V	E	I	A	V	Q	T	E	D	K	Y	G	V	K	I	P	D	E	D	L	A	G	L	R	T	V	G	D	V	V	A	Y	I	Q	K	L	E		
Pf	60	L	S	T	F	D	D	I	K	K	I	S	K	Q	L	-	S	V	E	E	D	K	I	Q	M	N	S	N	T	K	D	L	G	A	D	S	L	D	L	V	E	L	I	M	A	L	E	K	F	N	V	T	S	D	Q	D	L	L	K	I	N	T	V	Q	D	A	I	D	Y	I	E	K	N				
Sc	47	Q	R	V	I	D	V	I	K	A	F	D	K	N	S	P	-	N	I	A	N	K	Q	I	S	S	D	T	Q	F	H	K	D	L	G	L	D	S	L	D	T	V	E	L	L	V	A	I	E	E	E	F	D	I	E	I	P	D	K	V	A	D	E	L	R	S	V	G	E	T	V	D	Y	I	A	S	N
So	59	K	E	T	I	D	K	V	C	D	I	V	K	E	K	L	A	L	G	A	D	V	V	T	A	D	S	E	F	S	K	-	L	G	A	D	S	L	D	T	V	E	I	V	M	N	L	E	E	E	F	G	I	N	V	E	D	E	K	A	Q	D	I	S	T	I	Q	A	A	D	V	I	E	S	L		
Hs	53	E	G	I	Q	D	R	V	L	Y	V	L	K	L	Y	D	-	K	I	D	P	E	K	L	S	V	N	S	H	F	M	K	D	L	G	L	D	S	L	D	Q	V	E	I	I	M	A	M	E	D	E	F	G	F	E	I	P	D	I	D	E	K	L	M	C	P	Q	E	I	V	D	Y	I	A	D	K	