



Full wwPDB NMR Structure Validation Report ⓘ

Mar 19, 2025 – 03:53 AM EDT

PDB ID : 2FQ0
Title : Solution structure of major conformation of holo-acyl carrier protein from malaria parasite plasmodium falciparum
Authors : Sharma, A.K.; Sharma, S.K.; Surolia, A.; Surolia, N.; Sarma, S.P.
Deposited on : 2006-01-17

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

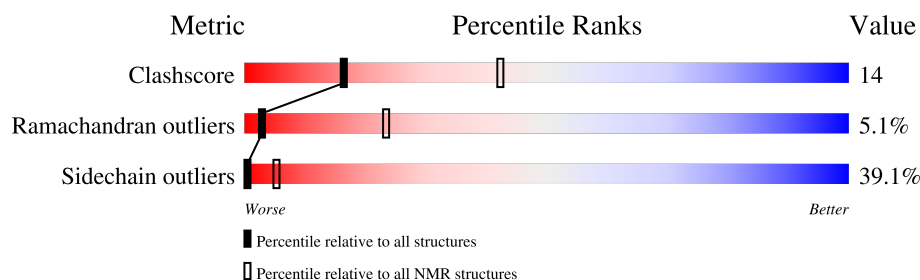
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	79	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
2	A	PNS	137	20	-

2 Ensemble composition and analysis

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:3-A:77 (75)	0.63	2

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 4 single-model clusters were found.

Cluster number	Models
1	2, 4, 6, 9, 13, 16, 17, 18
2	3, 8, 11, 12
3	15, 19
4	1, 14
Single-model clusters	5; 7; 10; 20

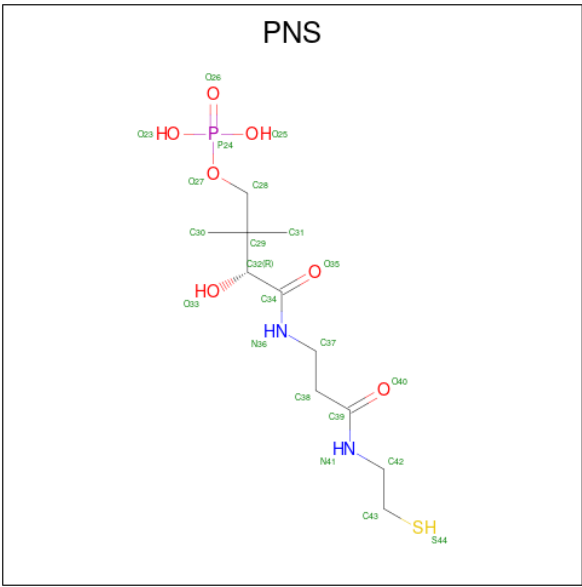
3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1311 atoms, of which 660 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called acyl carrier protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	79	1269	395	639	100	133	2	0

- Molecule 2 is 4'-PHOSPHOPANTETHEINE (three-letter code: PNS) (formula: C₁₁H₂₃N₂O₇PS).



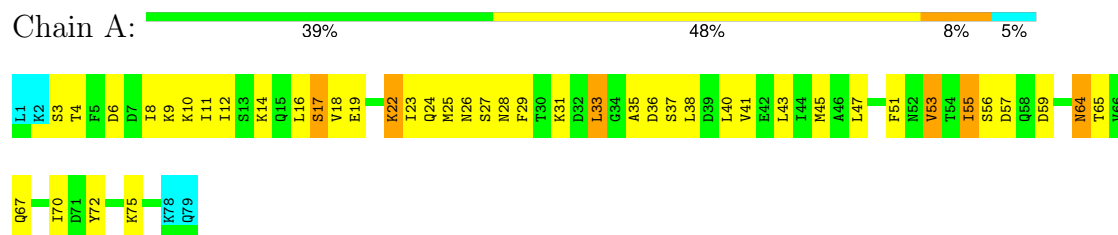
Mol	Chain	Residues	Atoms					
			Total	C	H	N	O	P
2	A	1	42	11	21	2	6	1

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: acyl carrier protein

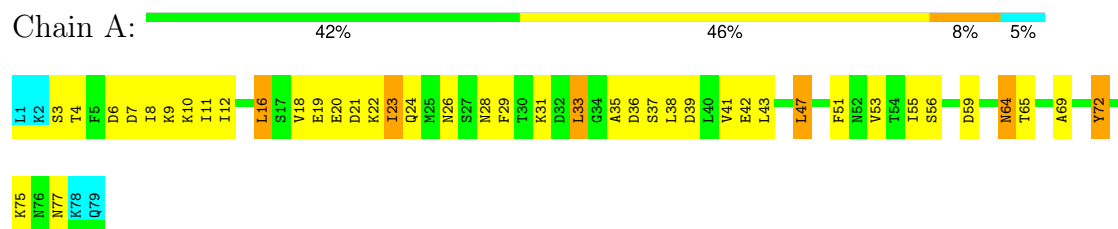


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

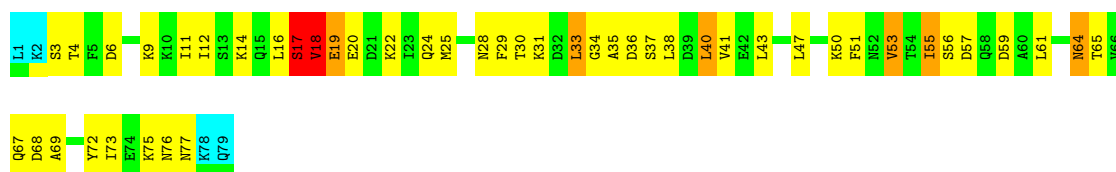
- Molecule 1: acyl carrier protein



4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: acyl carrier protein

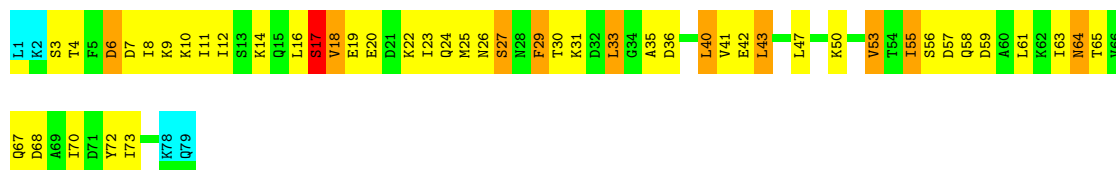




4.2.3 Score per residue for model 3

- Molecule 1: acyl carrier protein

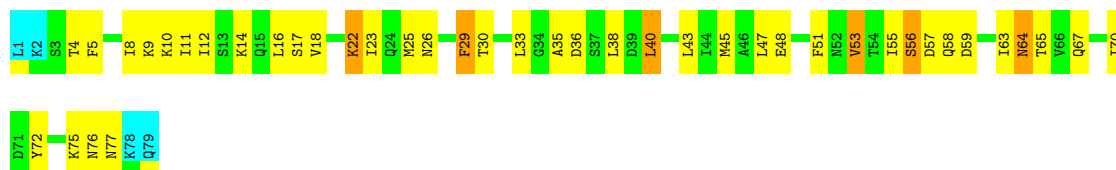
Chain A: 34% 47% 13% 5%



4.2.4 Score per residue for model 4

- Molecule 1: acyl carrier protein

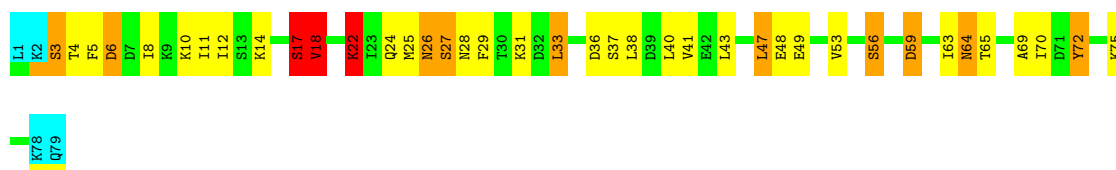
Chain A: 42% 46% 8% 5%



4.2.5 Score per residue for model 5

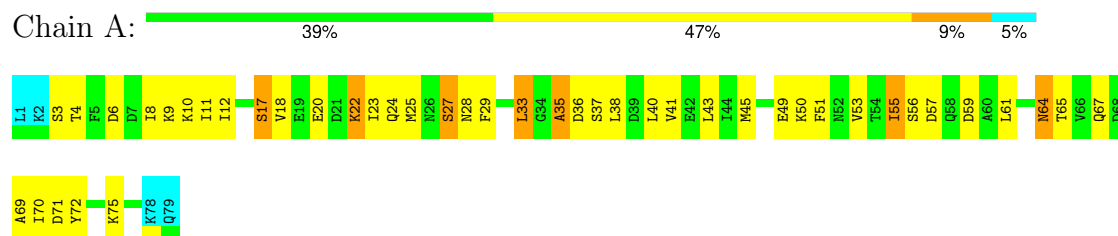
- Molecule 1: acyl carrier protein

Chain A: 46% 33% 13% 5%



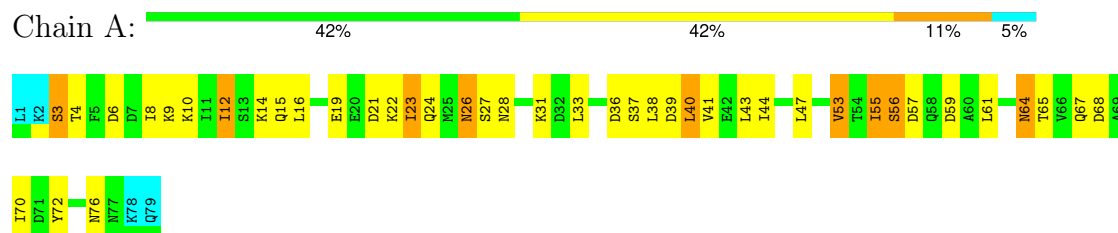
4.2.6 Score per residue for model 6

- Molecule 1: acyl carrier protein



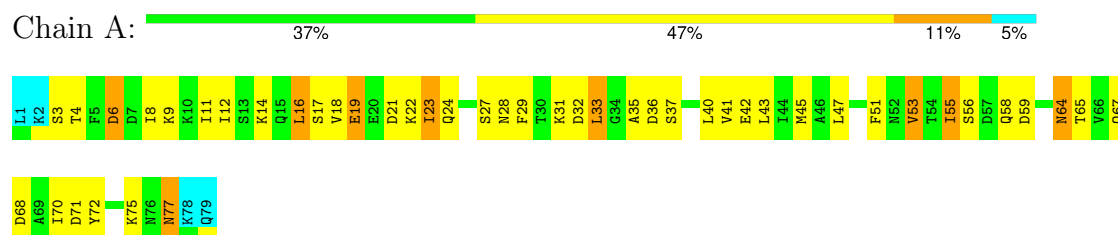
4.2.7 Score per residue for model 7

- Molecule 1: acyl carrier protein



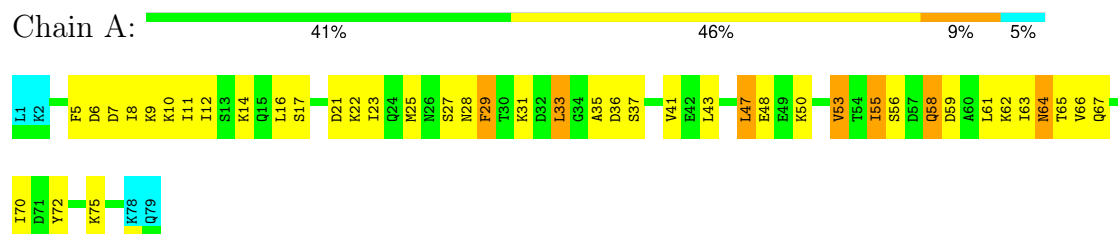
4.2.8 Score per residue for model 8

- Molecule 1: acyl carrier protein



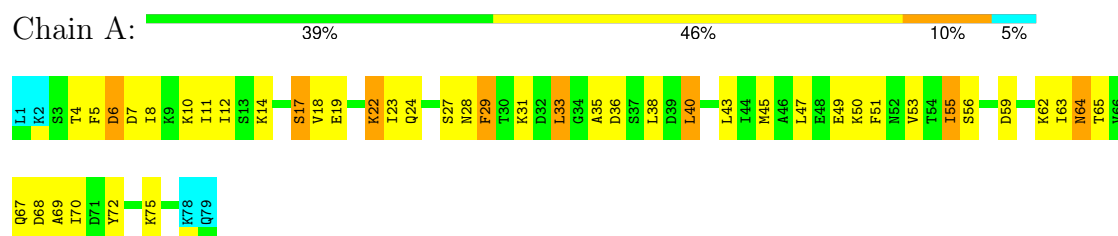
4.2.9 Score per residue for model 9

- Molecule 1: acyl carrier protein



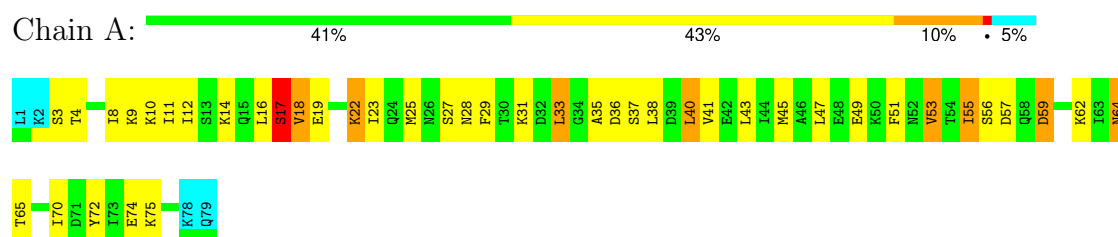
4.2.10 Score per residue for model 10

- Molecule 1: acyl carrier protein



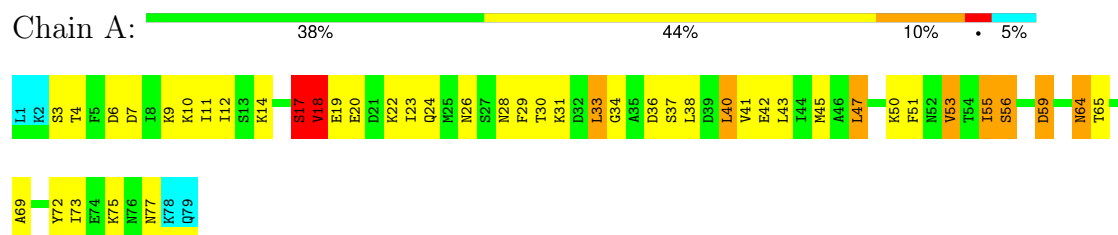
4.2.11 Score per residue for model 11

- Molecule 1: acyl carrier protein



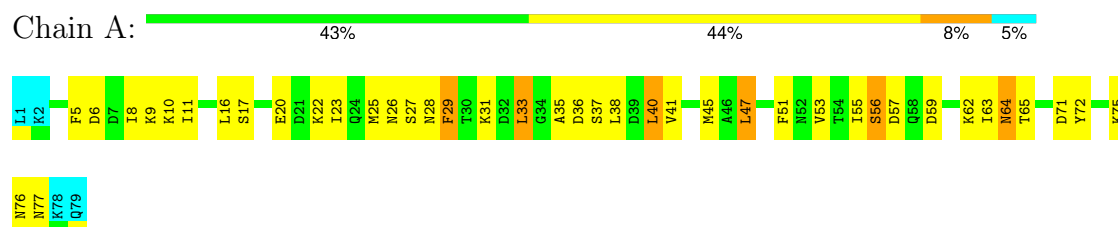
4.2.12 Score per residue for model 12

- Molecule 1: acyl carrier protein



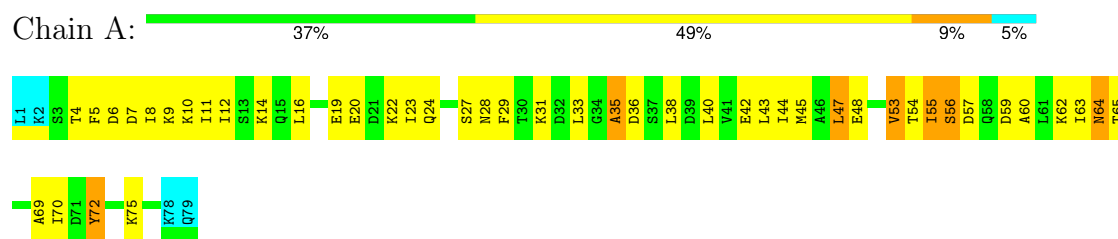
4.2.13 Score per residue for model 13

- Molecule 1: acyl carrier protein



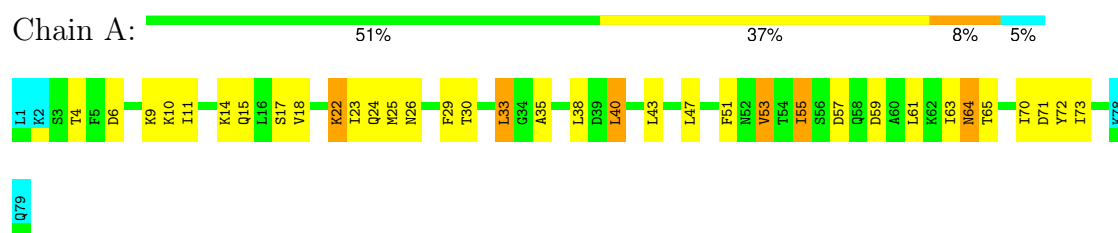
4.2.14 Score per residue for model 14

- Molecule 1: acyl carrier protein



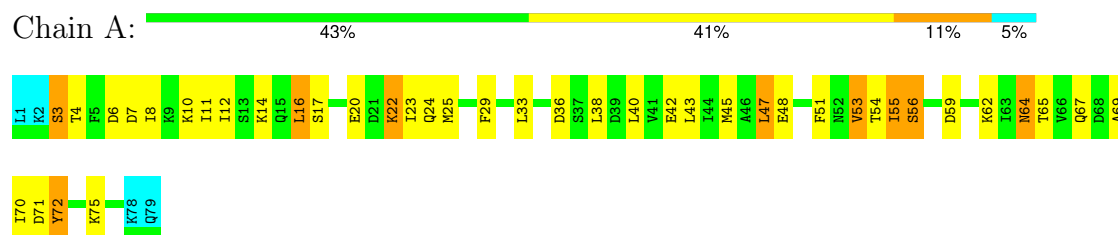
4.2.15 Score per residue for model 15

- Molecule 1: acyl carrier protein



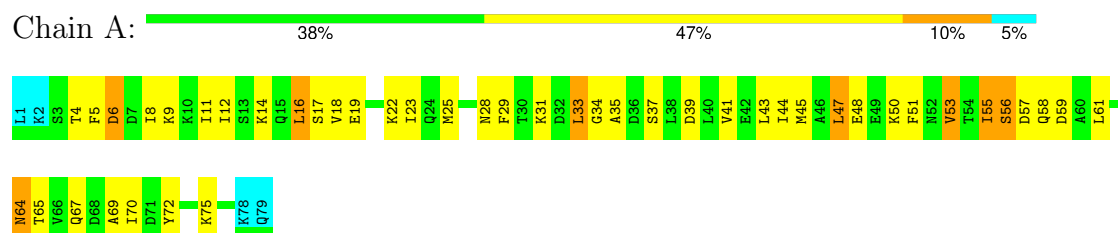
4.2.16 Score per residue for model 16

- Molecule 1: acyl carrier protein



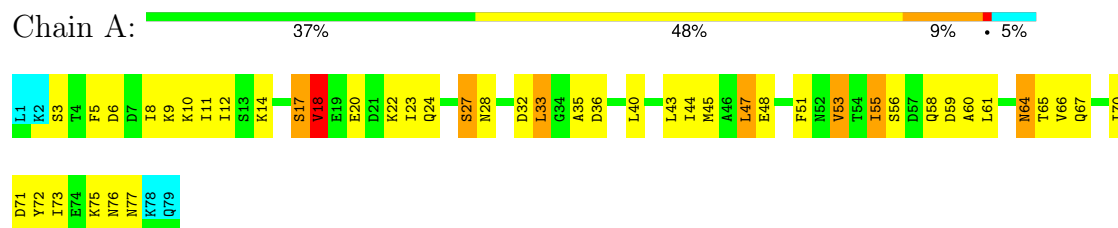
4.2.17 Score per residue for model 17

- Molecule 1: acyl carrier protein



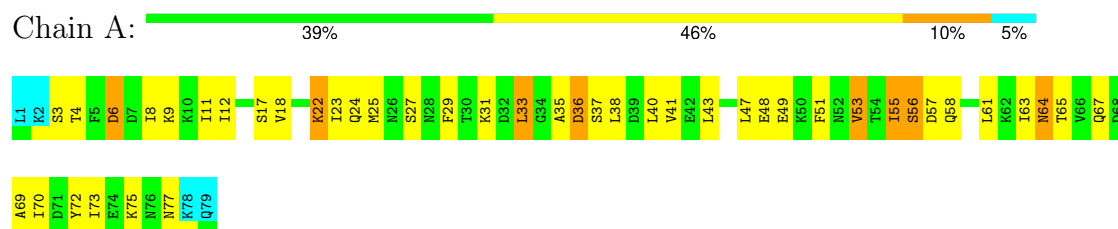
4.2.18 Score per residue for model 18

- Molecule 1: acyl carrier protein



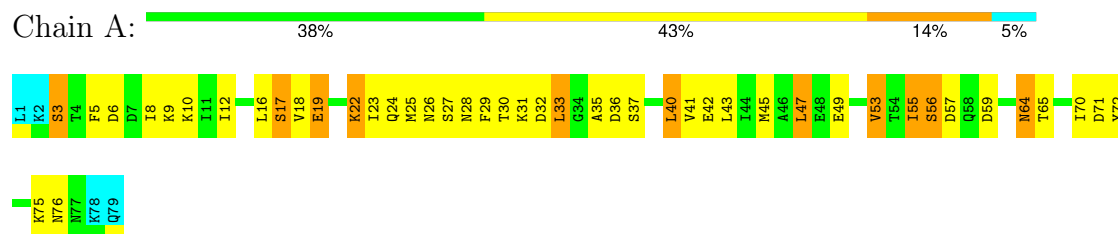
4.2.19 Score per residue for model 19

- Molecule 1: acyl carrier protein



4.2.20 Score per residue for model 20

- Molecule 1: acyl carrier protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS, SIMULATED ANNEALING*.

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *target function*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	2.1

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PNS

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	595	594	594	17±3
All	All	12320	12300	12300	342

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:30:THR:HG22	1:A:40:LEU:HD13	0.86	1.47	12	3
1:A:33:LEU:HD22	1:A:33:LEU:O	0.77	1.79	17	2
1:A:33:LEU:HD12	1:A:35:ALA:HB2	0.73	1.60	1	7
1:A:29:PHE:HB3	1:A:40:LEU:HD12	0.65	1.67	20	5
1:A:4:THR:HG21	1:A:69:ALA:HB1	0.65	1.66	2	7
1:A:4:THR:HG21	1:A:69:ALA:CB	0.64	2.23	12	8
1:A:4:THR:HG22	1:A:70:ILE:HG22	0.63	1.69	8	12
1:A:33:LEU:HD13	1:A:34:GLY:N	0.63	2.09	17	2
1:A:23:ILE:HD13	1:A:33:LEU:HD21	0.62	1.70	4	1
1:A:53:VAL:CG2	1:A:55:ILE:HD11	0.62	2.24	2	14
1:A:30:THR:CG2	1:A:40:LEU:HD13	0.62	2.24	3	5
1:A:8:ILE:O	1:A:12:ILE:HG22	0.61	1.95	7	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:ILE:HD13	1:A:23:ILE:HG21	0.60	1.72	7	1
1:A:33:LEU:HD22	1:A:33:LEU:C	0.60	2.17	2	2
1:A:47:LEU:HD23	1:A:48:GLU:N	0.60	2.12	5	3
1:A:57:ASP:O	1:A:61:LEU:HD12	0.60	1.95	15	3
1:A:12:ILE:HG21	1:A:23:ILE:HG12	0.60	1.74	11	1
1:A:16:LEU:O	1:A:18:VAL:HG13	0.59	1.97	1	1
1:A:40:LEU:HD12	1:A:44:ILE:HD11	0.59	1.72	7	1
1:A:12:ILE:HG22	1:A:43:LEU:HD22	0.58	1.72	2	7
1:A:37:SER:O	1:A:41:VAL:HG23	0.58	1.99	7	13
1:A:11:ILE:HD12	1:A:43:LEU:HD12	0.57	1.75	14	17
1:A:64:ASN:ND2	1:A:65:THR:HG23	0.57	2.15	20	11
1:A:27:SER:O	1:A:65:THR:HG22	0.56	2.00	10	11
1:A:66:VAL:O	1:A:70:ILE:HG22	0.55	2.01	18	2
1:A:55:ILE:HG22	1:A:58:GLN:HB2	0.55	1.76	8	2
1:A:16:LEU:HD13	1:A:19:GLU:CD	0.55	2.22	3	1
1:A:23:ILE:HA	1:A:33:LEU:HD22	0.55	1.77	18	2
1:A:16:LEU:HD22	1:A:19:GLU:OE1	0.55	2.02	2	4
1:A:17:SER:O	1:A:18:VAL:HG13	0.55	2.02	5	8
1:A:16:LEU:HD22	1:A:19:GLU:CD	0.55	2.22	11	2
1:A:48:GLU:HG3	1:A:55:ILE:HD12	0.54	1.78	18	1
1:A:29:PHE:CB	1:A:40:LEU:HD12	0.54	2.33	15	3
1:A:35:ALA:HB3	1:A:40:LEU:HD21	0.54	1.80	14	2
1:A:29:PHE:O	1:A:33:LEU:HD22	0.54	2.02	12	1
1:A:47:LEU:HD22	1:A:72:TYR:OH	0.54	2.03	1	1
1:A:59:ASP:HB2	1:A:63:ILE:HD13	0.54	1.79	4	1
1:A:23:ILE:HD11	1:A:29:PHE:CD2	0.54	2.37	17	4
1:A:22:LYS:O	1:A:33:LEU:HD13	0.54	2.03	5	1
1:A:33:LEU:CD1	1:A:35:ALA:HB2	0.53	2.32	10	9
1:A:59:ASP:O	1:A:63:ILE:HD12	0.53	2.03	5	1
1:A:58:GLN:NE2	1:A:61:LEU:HD11	0.53	2.19	18	1
1:A:35:ALA:HB3	1:A:40:LEU:CD2	0.53	2.33	14	2
1:A:44:ILE:HG21	1:A:59:ASP:OD1	0.53	2.03	17	1
1:A:64:ASN:HD22	1:A:65:THR:HG23	0.53	1.64	6	8
1:A:55:ILE:HG21	1:A:59:ASP:OD1	0.52	2.04	6	1
1:A:40:LEU:HD23	1:A:41:VAL:N	0.52	2.19	3	2
1:A:30:THR:CG2	1:A:40:LEU:HD22	0.52	2.35	4	1
1:A:11:ILE:CD1	1:A:47:LEU:HD12	0.51	2.35	12	2
1:A:8:ILE:HG13	1:A:47:LEU:HD11	0.51	1.82	13	5
1:A:33:LEU:HD12	1:A:35:ALA:CB	0.51	2.36	19	1
1:A:29:PHE:CD2	1:A:40:LEU:HD11	0.51	2.41	13	1
1:A:33:LEU:HD12	1:A:35:ALA:N	0.51	2.20	4	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:55:ILE:HG22	1:A:58:GLN:CB	0.50	2.35	9	2
1:A:64:ASN:OD1	1:A:65:THR:HG23	0.50	2.06	5	6
1:A:11:ILE:HD13	1:A:47:LEU:HD12	0.50	1.84	12	2
1:A:47:LEU:HD21	1:A:72:TYR:OH	0.49	2.07	5	3
1:A:12:ILE:HD12	1:A:19:GLU:HG2	0.49	1.83	10	1
1:A:4:THR:HG22	1:A:70:ILE:CG2	0.49	2.37	6	8
1:A:16:LEU:HD13	1:A:19:GLU:HG2	0.49	1.84	20	1
1:A:30:THR:HB	1:A:40:LEU:HD22	0.49	1.84	4	1
1:A:16:LEU:HD21	1:A:39:ASP:HB3	0.49	1.84	7	2
1:A:29:PHE:HB3	1:A:40:LEU:HD21	0.49	1.85	4	3
1:A:64:ASN:CG	1:A:65:THR:HG23	0.48	2.29	5	11
1:A:33:LEU:HD21	1:A:35:ALA:HB2	0.48	1.85	17	2
1:A:8:ILE:O	1:A:12:ILE:HG23	0.48	2.08	16	15
1:A:23:ILE:HD12	1:A:29:PHE:CE2	0.48	2.43	1	2
1:A:16:LEU:HD21	1:A:39:ASP:CG	0.48	2.29	17	1
1:A:4:THR:HB	1:A:73:ILE:HD13	0.48	1.86	2	3
1:A:23:ILE:HD12	1:A:29:PHE:CD2	0.48	2.44	4	2
1:A:53:VAL:HB	1:A:55:ILE:HD11	0.47	1.86	19	4
1:A:29:PHE:CE1	1:A:63:ILE:HG22	0.47	2.44	4	7
1:A:44:ILE:HD13	1:A:60:ALA:HA	0.47	1.86	14	2
1:A:61:LEU:HD12	1:A:61:LEU:O	0.47	2.10	19	5
1:A:4:THR:CA	1:A:73:ILE:HD13	0.47	2.40	2	5
1:A:11:ILE:HG21	1:A:47:LEU:CB	0.45	2.40	5	1
1:A:29:PHE:HB3	1:A:40:LEU:HD11	0.45	1.88	10	3
1:A:19:GLU:OE2	1:A:23:ILE:HD12	0.45	2.12	12	1
1:A:53:VAL:HG11	1:A:76:ASN:HB3	0.44	1.90	18	4
1:A:15:GLN:HG3	1:A:16:LEU:HD12	0.44	1.88	7	1
1:A:40:LEU:HD12	1:A:44:ILE:CD1	0.44	2.42	7	1
1:A:33:LEU:HD13	1:A:33:LEU:C	0.44	2.31	17	1
1:A:16:LEU:HD21	1:A:39:ASP:CB	0.43	2.43	17	2
1:A:16:LEU:CD1	1:A:43:LEU:HD23	0.43	2.42	7	1
1:A:55:ILE:HG22	1:A:59:ASP:N	0.43	2.28	11	2
1:A:53:VAL:CB	1:A:55:ILE:HD11	0.43	2.44	19	3
1:A:16:LEU:HD13	1:A:19:GLU:OE2	0.43	2.14	8	1
1:A:7:ASP:CB	1:A:47:LEU:HD21	0.43	2.44	12	1
1:A:3:SER:HB3	1:A:73:ILE:HD11	0.42	1.90	18	1
1:A:33:LEU:C	1:A:33:LEU:HD13	0.42	2.34	2	1
1:A:12:ILE:HD11	1:A:20:GLU:HG2	0.42	1.90	18	1
1:A:55:ILE:HG21	1:A:59:ASP:HB3	0.42	1.91	15	1
1:A:33:LEU:HD23	1:A:34:GLY:N	0.42	2.28	12	1
1:A:20:GLU:HA	1:A:23:ILE:HG22	0.42	1.91	16	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:LYS:O	1:A:33:LEU:HD22	0.42	2.15	20	1
1:A:8:ILE:HD13	1:A:29:PHE:HZ	0.42	1.75	6	1
1:A:4:THR:CB	1:A:73:ILE:HD13	0.42	2.45	12	1
1:A:4:THR:HG21	1:A:69:ALA:HB3	0.42	1.90	6	1
1:A:53:VAL:HG21	1:A:55:ILE:HD11	0.42	1.91	15	1
1:A:17:SER:OG	1:A:18:VAL:HG22	0.41	2.15	18	1
1:A:33:LEU:HD11	1:A:35:ALA:HB2	0.41	1.91	10	1
1:A:12:ILE:O	1:A:16:LEU:HD12	0.41	2.16	16	1
1:A:55:ILE:HG21	1:A:59:ASP:CG	0.41	2.35	6	1
1:A:18:VAL:HG23	1:A:18:VAL:O	0.41	2.15	17	1
1:A:40:LEU:HD13	1:A:43:LEU:HD21	0.41	1.92	19	1
1:A:63:ILE:O	1:A:63:ILE:HG22	0.40	2.16	13	1
1:A:54:THR:O	1:A:54:THR:HG23	0.40	2.17	14	2
1:A:48:GLU:HB2	1:A:55:ILE:HD12	0.40	1.93	4	1
1:A:7:ASP:O	1:A:11:ILE:HG23	0.40	2.16	1	1
1:A:30:THR:CB	1:A:40:LEU:HD22	0.40	2.46	4	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	75/79 (95%)	54±2 (72±3%)	17±2 (23±3%)	4±1 (5±2%)	3	23
All	All	1500/1580 (95%)	1086 (72%)	338 (23%)	76 (5%)	3	23

All 12 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	56	SER	18
1	A	17	SER	11
1	A	18	VAL	11
1	A	22	LYS	11
1	A	6	ASP	10
1	A	3	SER	6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	26	ASN	3
1	A	35	ALA	2
1	A	77	ASN	1
1	A	27	SER	1
1	A	55	ILE	1
1	A	36	ASP	1

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	70/74 (95%)	43±3 (61±4%)	27±3 (39±4%)	0	5
All	All	1400/1480 (95%)	852 (61%)	548 (39%)	0	5

All 54 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	53	VAL	20
1	A	64	ASN	20
1	A	72	TYR	20
1	A	33	LEU	19
1	A	47	LEU	19
1	A	36	ASP	18
1	A	55	ILE	18
1	A	9	LYS	17
1	A	22	LYS	17
1	A	75	LYS	17
1	A	10	LYS	16
1	A	24	GLN	15
1	A	28	ASN	15
1	A	31	LYS	15
1	A	59	ASP	15
1	A	14	LYS	15
1	A	6	ASP	14
1	A	38	LEU	14
1	A	51	PHE	14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	40	LEU	14
1	A	25	MET	13
1	A	17	SER	12
1	A	67	GLN	12
1	A	45	MET	12
1	A	23	ILE	11
1	A	56	SER	11
1	A	3	SER	9
1	A	57	ASP	9
1	A	5	PHE	9
1	A	16	LEU	8
1	A	26	ASN	8
1	A	19	GLU	7
1	A	20	GLU	7
1	A	42	GLU	7
1	A	77	ASN	7
1	A	50	LYS	7
1	A	71	ASP	7
1	A	29	PHE	6
1	A	49	GLU	6
1	A	62	LYS	6
1	A	68	ASP	5
1	A	7	ASP	5
1	A	27	SER	5
1	A	58	GLN	5
1	A	21	ASP	4
1	A	18	VAL	4
1	A	32	ASP	3
1	A	48	GLU	3
1	A	76	ASN	2
1	A	43	LEU	2
1	A	12	ILE	1
1	A	74	GLU	1
1	A	15	GLN	1
1	A	70	ILE	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	PNS	A	137	1	14,20,21	0.80±0.00	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	PNS	A	137	1	18,26,29	1.36±0.00	3±0 (16±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PNS	A	137	1	1±0,1,7,7	1±0,24,26,27	-

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	137	PNS	C42-N41-C39	2.52	127.52	122.82	20	20
2	A	137	PNS	C30-C29-C32	2.23	112.57	108.77	20	20
2	A	137	PNS	C37-N36-C34	2.13	126.38	122.55	2	20

All unique chiral outliers are listed below.

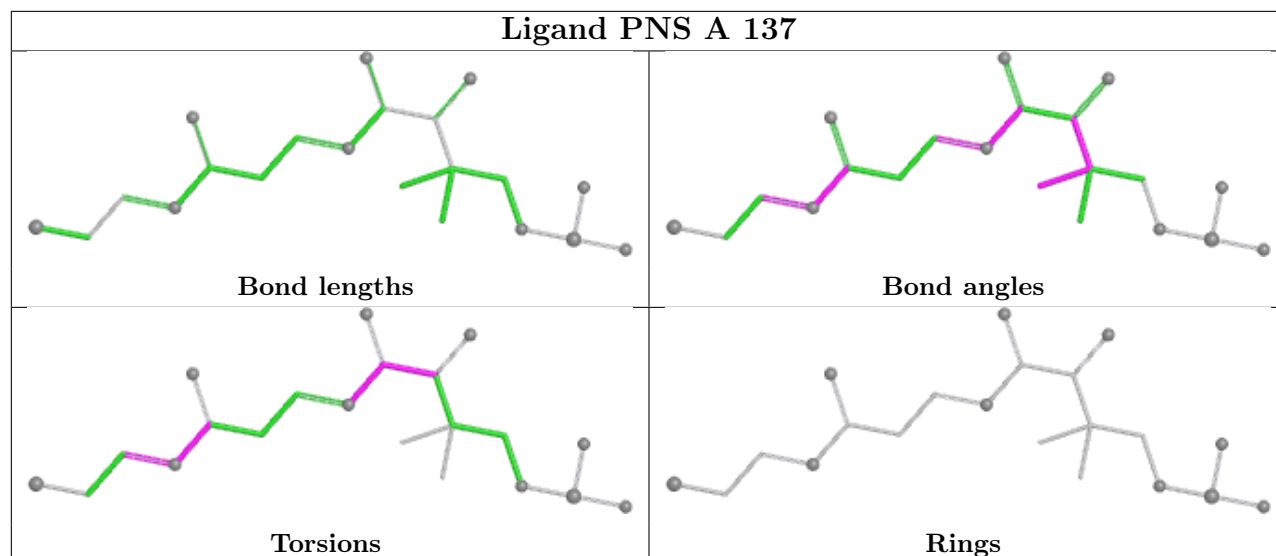
Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	137	PNS	C32	20

All unique torsion outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	137	PNS	C32-C34-N36-C37	20

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided