



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:31 PM GMT

PDB ID : 1KPH
Title : Crystal Structure of mycolic acid cyclopropane synthase CmaA1 complexed with SAH and DDDMAB
Authors : Huang, C.-C.; Smith, C.V.; Jacobs Jr., W.R.; Glickman, M.S.; Sacchettini, J.C.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2001-12-30
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

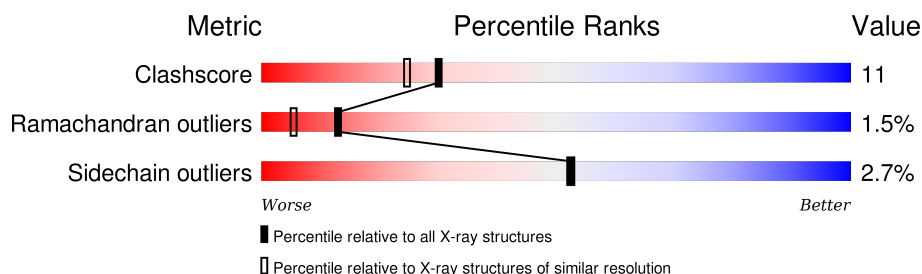
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	287	 71% 25% ..
1	B	287	 80% 18% ..
1	C	287	 78% 21% .
1	D	287	 79% 18% ..

2 Entry composition [i](#)

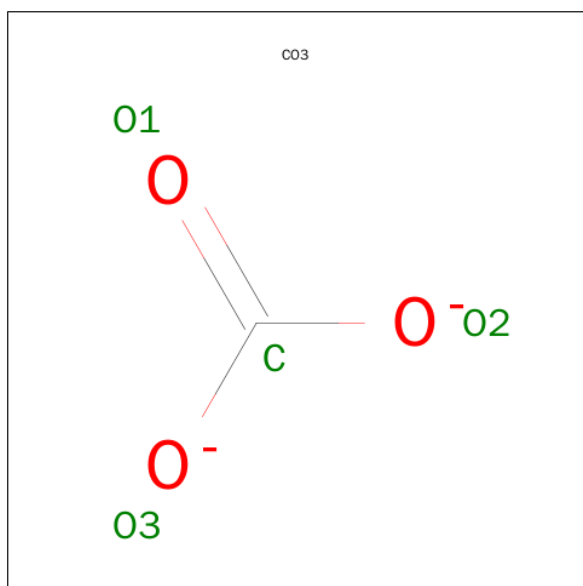
There are 5 unique types of molecules in this entry. The entry contains 10001 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	0	0
			2252	1443	386	409	14			
1	B	285	Total	C	N	O	S	0	0	0
			2269	1452	388	415	14			
1	C	285	Total	C	N	O	S	0	0	0
			2269	1452	388	415	14			
1	D	285	Total	C	N	O	S	0	0	0
			2269	1452	388	415	14			

- Molecule 2 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



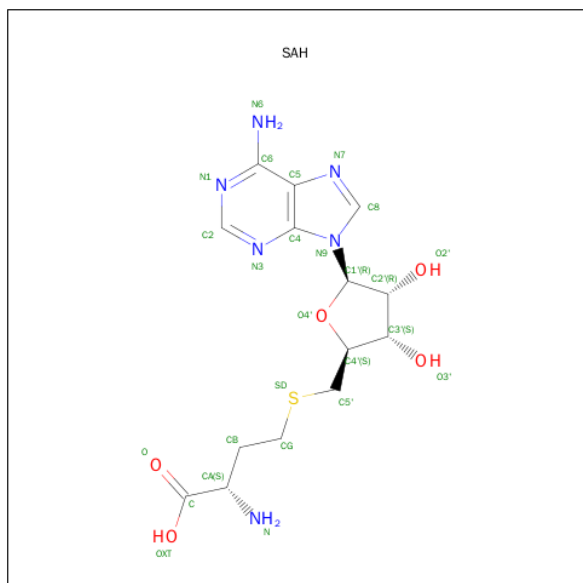
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	1	3		
2	B	1	Total	C	O	0	0
			4	1	3		

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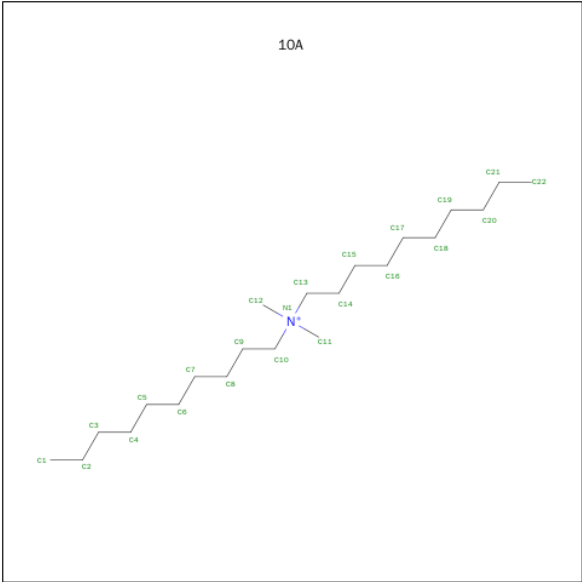
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			4	1	3		
2	D	1	Total	C	O	0	0
			4	1	3		

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			24	14	6	4		
3	B	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	C	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	D	1	Total	C	N	O	S	0
			26	14	6	5	1	

- Molecule 4 is DIDECYL-DIMETHYL-AMMONIUM (three-letter code: 10A) (formula: $C_{22}H_{48}N$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			23	22	1		
4	B	1	Total	C	N	0	0
			23	22	1		
4	C	1	Total	C	N	0	0
			23	22	1		
4	D	1	Total	C	N	0	0
			23	22	1		

- Molecule 5 is water.

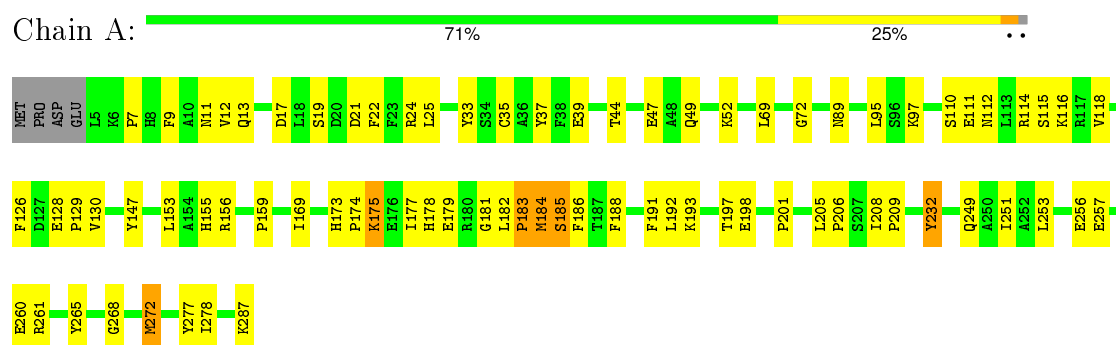
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	156	Total	O	0	0
			156	156		
5	B	185	Total	O	0	0
			185	185		
5	C	210	Total	O	0	0
			210	210		
5	D	181	Total	O	0	0
			181	181		

3 Residue-property plots

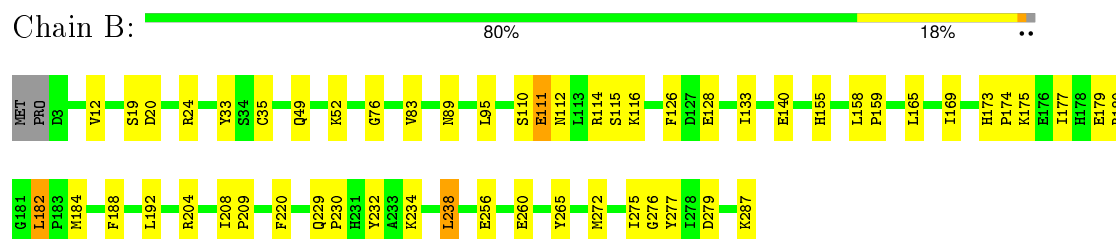
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

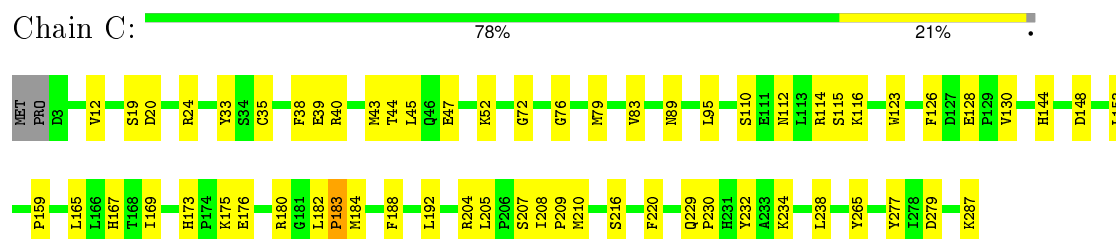
• Molecule 1: CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE 1



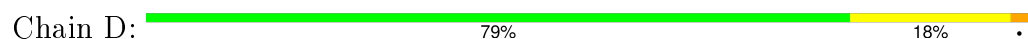
• Molecule 1: CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE 1



• Molecule 1: CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE 1



• Molecule 1: CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE 1



MET	PRO	D3	E4	L5	K6	P7	Y12	S19	D20	R24	Y33	S34	C35	T44	E47	A48	Q49	K52	A77	T78	N79	V83	N89	L95	V103	V107	N112	L113	R114	S115	L119	F126	D127	E128	I136	L165	L166	H167	P174	K175	
E176	I177	H178	E179	R180	G181	L182	P183	M184	S185	F186	T187	F188	L192	V196	L205	I208	P209	M210	Q229	P230	H231	Y232	L243	Q249	M263	K264	Y265	L266	T267	E271	Y277	K287									

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	77.62Å 77.62Å 174.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.83 – 2.00	Depositor
% Data completeness (in resolution range)	97.0 (29.83-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.03	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.194 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10001	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CO3, SAH, 10A

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/2306	0.56	0/3122
1	B	0.32	0/2323	0.59	1/3145 (0.0%)
1	C	0.34	0/2323	0.59	1/3145 (0.0%)
1	D	0.33	0/2323	0.58	0/3145
All	All	0.33	0/9275	0.58	2/12557 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	76	GLY	N-CA-C	5.46	126.76	113.10
1	B	76	GLY	N-CA-C	5.33	126.43	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2252	0	2216	67	0
1	B	2269	0	2226	45	0
1	C	2269	0	2226	43	0
1	D	2269	0	2226	49	0
2	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
3	A	24	0	15	2	0
3	B	26	0	19	0	0
3	C	26	0	19	1	0
3	D	26	0	19	0	0
4	A	23	0	48	4	0
4	B	23	0	48	6	0
4	C	23	0	48	3	0
4	D	23	0	48	1	0
5	A	156	0	0	1	0
5	B	185	0	0	1	0
5	C	210	0	0	2	0
5	D	181	0	0	5	0
All	All	10001	0	9158	205	0

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 11.

The worst 5 of 205 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:ASN:HD22	1:B:115:SER:H	1.26	0.83
1:A:205:LEU:HG	4:A:1901:10A:H31	1.62	0.82
1:A:173:HIS:HB3	1:A:175:LYS:NZ	1.98	0.78
1:A:175:LYS:HZ3	1:A:175:LYS:HB2	1.49	0.78
1:C:234:LYS:O	1:C:238:LEU:HD13	1.86	0.76

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution.

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	281/287 (98%)	269 (96%)	8 (3%)	4 (1%)	14	6
1	B	283/287 (99%)	273 (96%)	6 (2%)	4 (1%)	14	6
1	C	283/287 (99%)	267 (94%)	12 (4%)	4 (1%)	14	6
1	D	283/287 (99%)	270 (95%)	8 (3%)	5 (2%)	11	4
All	All	1130/1148 (98%)	1079 (96%)	34 (3%)	17 (2%)	13	5

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	SER
1	A	185	SER
1	C	19	SER
1	C	180	ARG
1	C	182	LEU

5.3.2 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 X-ray entries followed by that with respect to entries of similar resolution.

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	239/243 (98%)	231 (97%)	8 (3%)	45	43
1	B	241/243 (99%)	234 (97%)	7 (3%)	50	49
1	C	241/243 (99%)	236 (98%)	5 (2%)	61	63
1	D	241/243 (99%)	235 (98%)	6 (2%)	55	55
All	All	962/972 (99%)	936 (97%)	26 (3%)	52	52

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	204	ARG
1	B	265	TYR
1	D	232	TYR
1	B	232	TYR
1	B	238	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	112	ASN
1	C	31	GLN
1	D	112	ASN
1	B	246	ASN
1	C	13	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or 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 length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SAH	A	1900	-	20,25,28	1.59	5 (25%)	18,35,40	1.36	2 (11%)
4	10A	A	1901	-	22,22,22	0.55	0	24,24,24	1.30	2 (8%)
2	CO3	A	1902	-	0,3,3	0.00	-	0,3,3	0.00	-
3	SAH	B	2900	-	20,28,28	1.20	3 (15%)	19,40,40	0.93	0
4	10A	B	2901	-	22,22,22	0.56	0	24,24,24	1.19	2 (8%)
2	CO3	B	2902	-	0,3,3	0.00	-	0,3,3	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SAH	C	3900	-	20,28,28	1.13	4 (20%)	19,40,40	0.97	0
4	10A	C	3901	-	22,22,22	0.59	0	24,24,24	1.17	2 (8%)
2	CO3	C	3902	-	0,3,3	0.00	-	0,3,3	0.00	-
3	SAH	D	4900	-	20,28,28	1.20	4 (20%)	19,40,40	0.97	0
4	10A	D	4901	-	22,22,22	0.56	0	24,24,24	1.33	3 (12%)
2	CO3	D	4902	-	0,3,3	0.00	-	0,3,3	0.00	-

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
3	SAH	A	1900	-	-	0/4/24/31	0/3/3/3
4	10A	A	1901	-	-	0/22/22/22	0/0/0/0
2	CO3	A	1902	-	-	0/0/0/0	0/0/0/0
3	SAH	B	2900	-	-	0/7/31/31	0/3/3/3
4	10A	B	2901	-	-	0/22/22/22	0/0/0/0
2	CO3	B	2902	-	-	0/0/0/0	0/0/0/0
3	SAH	C	3900	-	-	0/7/31/31	0/3/3/3
4	10A	C	3901	-	-	0/22/22/22	0/0/0/0
2	CO3	C	3902	-	-	0/0/0/0	0/0/0/0
3	SAH	D	4900	-	-	0/7/31/31	0/3/3/3
4	10A	D	4901	-	-	0/22/22/22	0/0/0/0
2	CO3	D	4902	-	-	0/0/0/0	0/0/0/0

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1900	SAH	OXT-C	-4.06	1.24	1.42
3	B	2900	SAH	C8-N7	-2.39	1.30	1.34
3	D	4900	SAH	C8-N7	-2.38	1.30	1.34
3	A	1900	SAH	C8-N7	-2.37	1.30	1.34
3	C	3900	SAH	C8-N7	-2.14	1.30	1.34

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1900	SAH	C5'-C4'-C3'	-2.62	113.06	115.80
4	D	4901	10A	C11-N1-C10	-2.20	103.83	109.43
4	C	3901	10A	C14-C13-N1	2.55	121.08	115.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1900	SAH	OXT-C-CA	2.55	118.53	111.84
4	B	2901	10A	C14-C13-N1	2.78	121.59	115.57

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1900	SAH	2	0
4	A	1901	10A	4	0
4	B	2901	10A	6	0
3	C	3900	SAH	1	0
4	C	3901	10A	3	0
4	D	4901	10A	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.