



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 08:24 pm BST

PDB ID : 1RJE  
Title : Structure of PPM1, a leucine carboxy methyltransferase involved in the regulation of protein phosphatase 2A activity  
Authors : Leulliot, N.; Quevillon-Cheruel, S.; Sorel, I.; de La Sierra-Gallay, I.L.; Collinet, B.; Graille, M.; Blondeau, K.; Bettache, N.; Poupon, A.; Janin, J.; van Tilbeurgh, H.  
Deposited on : 2003-11-19  
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

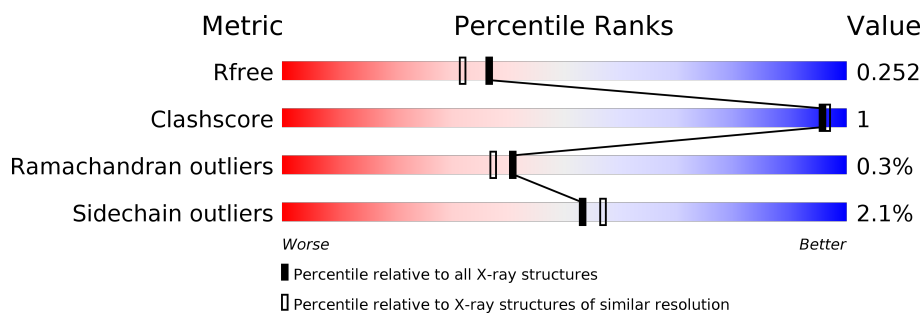
# 1 Overall quality at a glance

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))
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	334	 93% 5% ••
1	B	334	 92% 6% ••
1	C	334	 92% 7% •

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9100 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 carboxy methyl transferase for protein phosphatase 2A catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	0	0
			2644	1681	451	494	18			
1	B	329	Total	C	N	O	S	0	1	0
			2660	1690	454	498	18			
1	C	333	Total	C	N	O	S	0	0	0
			2694	1711	466	499	18			

There are 18 discrepancies between the modelled and reference sequences:

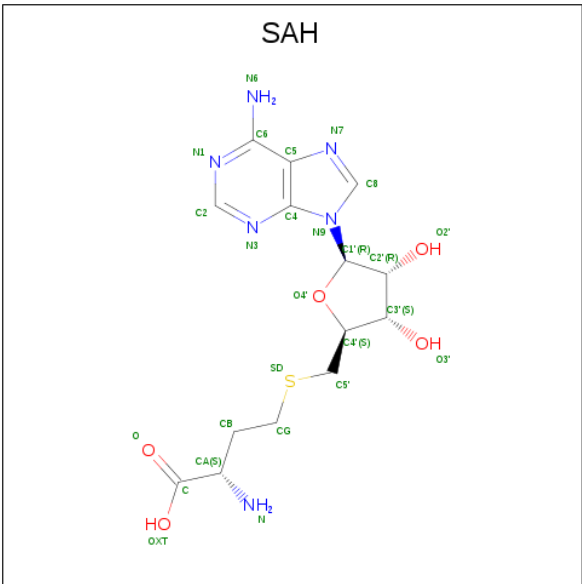
Chain	Residue	Modelled	Actual	Comment	Reference
A	329	HIS	-	EXPRESSION TAG	UNP Q04081
A	330	HIS	-	EXPRESSION TAG	UNP Q04081
A	331	HIS	-	EXPRESSION TAG	UNP Q04081
A	332	HIS	-	EXPRESSION TAG	UNP Q04081
A	333	HIS	-	EXPRESSION TAG	UNP Q04081
A	334	HIS	-	EXPRESSION TAG	UNP Q04081
B	329	HIS	-	EXPRESSION TAG	UNP Q04081
B	330	HIS	-	EXPRESSION TAG	UNP Q04081
B	331	HIS	-	EXPRESSION TAG	UNP Q04081
B	332	HIS	-	EXPRESSION TAG	UNP Q04081
B	333	HIS	-	EXPRESSION TAG	UNP Q04081
B	334	HIS	-	EXPRESSION TAG	UNP Q04081
C	329	HIS	-	EXPRESSION TAG	UNP Q04081
C	330	HIS	-	EXPRESSION TAG	UNP Q04081
C	331	HIS	-	EXPRESSION TAG	UNP Q04081
C	332	HIS	-	EXPRESSION TAG	UNP Q04081
C	333	HIS	-	EXPRESSION TAG	UNP Q04081
C	334	HIS	-	EXPRESSION TAG	UNP Q04081

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C<sub>14</sub>H<sub>20</sub>N<sub>6</sub>O<sub>5</sub>S).



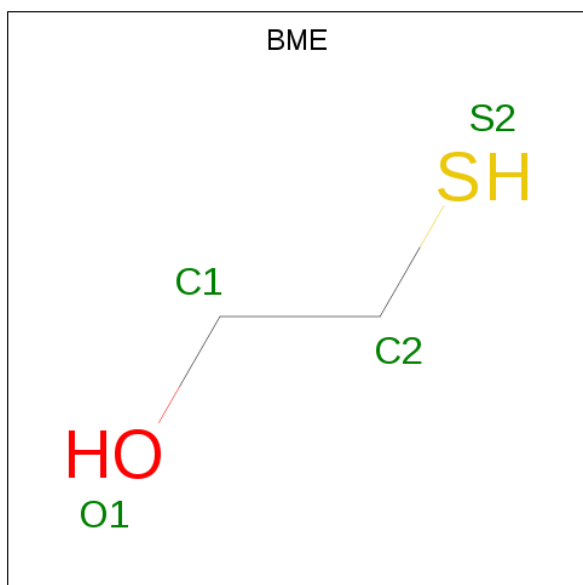
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0
			26	14	6	5	1	

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

- Molecule 4 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C<sub>2</sub>H<sub>6</sub>OS).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	379	Total	O	0	0
			379	379		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	324	Total 324	O 324	0	0
5	C	287	Total 287	O 287	0	0

### 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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

- Molecule 1: carboxy methyl transferase for protein phosphatase 2A catalytic subunit

Chain A:  93% 5% ..



- Molecule 1: carboxy methyl transferase for protein phosphatase 2A catalytic subunit

Chain B:  92% 6% ..



- Molecule 1: carboxy methyl transferase for protein phosphatase 2A catalytic subunit

Chain C:  92% 7% ..



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.75Å 110.75Å 165.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.47 – 2.00 24.45 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.7 (24.47-2.00) 98.7 (24.45-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.159 , 0.210 0.249 , 0.252	Depositor DCC
$R_{free}$ test set	3851 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.0	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 16.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.159 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	9100	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SAH, SO4, BME

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	0.30	1/2694 (0.0%)	0.59	8/3639 (0.2%)
1	B	0.33	1/2714 (0.0%)	0.59	9/3666 (0.2%)
1	C	0.32	1/2749 (0.0%)	0.60	7/3714 (0.2%)
All	All	0.32	3/8157 (0.0%)	0.60	24/11019 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	201	GLU	CD-OE2	6.86	1.33	1.25
1	C	201	GLU	CD-OE2	6.82	1.33	1.25
1	A	201	GLU	CD-OE2	6.74	1.33	1.25

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	11	ASP	CB-CG-OD2	5.37	123.13	118.30
1	C	309	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	11	ASP	CB-CG-OD2	5.25	123.03	118.30
1	B	86	ASP	CB-CG-OD2	5.25	123.03	118.30
1	B	178	ASP	CB-CG-OD2	5.24	123.02	118.30
1	B	9	ASP	CB-CG-OD2	5.24	123.01	118.30
1	B	128	ASP	CB-CG-OD2	5.21	122.99	118.30
1	B	309	ASP	CB-CG-OD2	5.20	122.98	118.30
1	C	128	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	309	ASP	CB-CG-OD2	5.19	122.97	118.30
1	A	178	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	9	ASP	CB-CG-OD2	5.17	122.96	118.30
1	C	9	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	128	ASP	CB-CG-OD2	5.15	122.94	118.30
1	B	11	ASP	CB-CG-OD2	5.14	122.93	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	285	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A	86	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A	64	ASP	CB-CG-OD2	5.13	122.92	118.30
1	B	156	ASP	CB-CG-OD2	5.07	122.87	118.30
1	B	285	ASP	CB-CG-OD2	5.06	122.86	118.30
1	A	285	ASP	CB-CG-OD2	5.04	122.84	118.30
1	C	64	ASP	CB-CG-OD2	5.04	122.84	118.30
1	C	165	ASP	CB-CG-OD2	5.04	122.84	118.30
1	B	64	ASP	CB-CG-OD2	5.03	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 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	2644	0	2672	6	0
1	B	2660	0	2682	6	0
1	C	2694	0	2707	7	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	26	0	19	0	0
3	B	26	0	19	0	0
3	C	26	0	19	0	0
4	A	8	0	12	0	0
4	B	8	0	12	0	0
4	C	8	0	12	0	0
5	A	379	0	0	0	0
5	B	324	0	0	0	0
5	C	287	0	0	0	0
All	All	9100	0	8154	18	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 1.

All (18) 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:160:SER:HB2	1:B:161:PRO:HD3	1.72	0.71
1:C:160:SER:HB2	1:C:161:PRO:CD	2.26	0.66
1:C:160:SER:HB2	1:C:161:PRO:HD3	1.78	0.65
1:C:160:SER:CB	1:C:161:PRO:CD	2.81	0.58
1:B:160:SER:CB	1:B:161:PRO:CD	2.83	0.56
1:A:160:SER:CB	1:A:161:PRO:CD	2.84	0.55
1:B:160:SER:HB2	1:B:161:PRO:CD	2.36	0.54
1:A:160:SER:CB	1:A:161:PRO:HD3	2.39	0.52
1:C:239:PRO:O	1:C:240:ASN:HB2	2.13	0.49
1:A:160:SER:HB3	1:A:161:PRO:HD3	1.95	0.47
1:C:113:LEU:HB2	1:C:114:PRO:HD3	1.96	0.47
1:A:160:SER:HB2	1:A:161:PRO:CD	2.47	0.45
1:B:152:LEU:HD21	1:B:164:ILE:HG23	1.99	0.45
1:A:251:LEU:HD22	1:A:257:LEU:HD23	2.01	0.42
1:C:79:TYR:O	1:C:83:VAL:HG22	2.20	0.41
1:A:36:ASP:H	1:B:117:GLN:HE22	1.67	0.41
1:B:130:ASN:HD22	1:B:173:ALA:CB	2.34	0.41
1:C:45:HIS:CD2	1:C:110:LEU:HD12	2.57	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	326/334 (98%)	311 (95%)	14 (4%)	1 (0%)	41	37
1	B	328/334 (98%)	311 (95%)	16 (5%)	1 (0%)	41	37
1	C	331/334 (99%)	317 (96%)	13 (4%)	1 (0%)	41	37
All	All	985/1002 (98%)	939 (95%)	43 (4%)	3 (0%)	41	37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	160	SER
1	B	160	SER
1	C	160	SER

### 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	297/303 (98%)	292 (98%)	5 (2%)	60	65
1	B	299/303 (99%)	294 (98%)	5 (2%)	60	65
1	C	302/303 (100%)	293 (97%)	9 (3%)	41	41
All	All	898/909 (99%)	879 (98%)	19 (2%)	53	57

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	MET
1	A	128	ASP
1	A	181	GLU
1	A	211	GLU
1	A	253	GLU
1	B	112	MET
1	B	128	ASP
1	B	159	LYS
1	B	255	ARG
1	B	302	LEU
1	C	11	ASP
1	C	68	ARG
1	C	112	MET
1	C	128	ASP
1	C	153	SER
1	C	154	LYS
1	C	155	GLU
1	C	159	LYS
1	C	252	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	ASN
1	A	130	ASN
1	A	166	GLN
1	A	177	ASN
1	A	209	ASN
1	A	210	ASN
1	A	280	ASN
1	A	284	ASN
1	A	306	GLN
1	A	318	GLN
1	B	117	GLN
1	B	130	ASN
1	B	177	ASN
1	B	209	ASN
1	B	210	ASN
1	B	284	ASN
1	C	31	GLN
1	C	75	ASN
1	C	177	ASN
1	C	209	ASN
1	C	256	ASN
1	C	306	GLN
1	C	329	HIS

### 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

11 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$
2	SO4	B	1002	-	4,4,4	0.13	0	6,6,6	0.08	0
4	BME	C	1006	-	3,3,3	0.28	0	1,2,2	0.07	0
3	SAH	C	2003	-	21,28,28	1.22	2 (9%)	20,40,40	1.69	2 (10%)
4	BME	A	1007	-	3,3,3	0.26	0	1,2,2	0.22	0
4	BME	B	1005	-	3,3,3	0.26	0	1,2,2	0.28	0
4	BME	C	1009	-	3,3,3	0.28	0	1,2,2	0.09	0
3	SAH	B	2002	-	21,28,28	1.21	2 (9%)	20,40,40	1.68	2 (10%)
4	BME	A	1004	-	3,3,3	0.28	0	1,2,2	0.23	0
4	BME	B	1008	-	3,3,3	0.26	0	1,2,2	0.21	0
3	SAH	A	2001	-	21,28,28	1.21	2 (9%)	20,40,40	1.67	2 (10%)
2	SO4	A	1001	-	4,4,4	0.14	0	6,6,6	0.06	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
4	BME	C	1006	-	-	1/1/1/1	-
3	SAH	C	2003	-	-	1/7/31/31	0/3/3/3
4	BME	A	1007	-	-	0/1/1/1	-
4	BME	B	1005	-	-	0/1/1/1	-
4	BME	C	1009	-	-	0/1/1/1	-
3	SAH	B	2002	-	-	1/7/31/31	0/3/3/3
4	BME	A	1004	-	-	1/1/1/1	-
4	BME	B	1008	-	-	0/1/1/1	-
3	SAH	A	2001	-	-	1/7/31/31	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2003	SAH	C2-N3	4.09	1.38	1.32
3	B	2002	SAH	C2-N3	4.03	1.38	1.32
3	A	2001	SAH	C2-N3	4.02	1.38	1.32
3	C	2003	SAH	C2-N1	2.62	1.38	1.33
3	A	2001	SAH	C2-N1	2.59	1.38	1.33
3	B	2002	SAH	C2-N1	2.55	1.38	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2003	SAH	N3-C2-N1	-5.95	119.38	128.68
3	B	2002	SAH	N3-C2-N1	-5.94	119.39	128.68
3	A	2001	SAH	N3-C2-N1	-5.92	119.43	128.68
3	C	2003	SAH	C5'-SD-CG	-2.91	93.53	102.27
3	B	2002	SAH	C5'-SD-CG	-2.89	93.61	102.27
3	A	2001	SAH	C5'-SD-CG	-2.83	93.77	102.27

There are no chirality outliers.

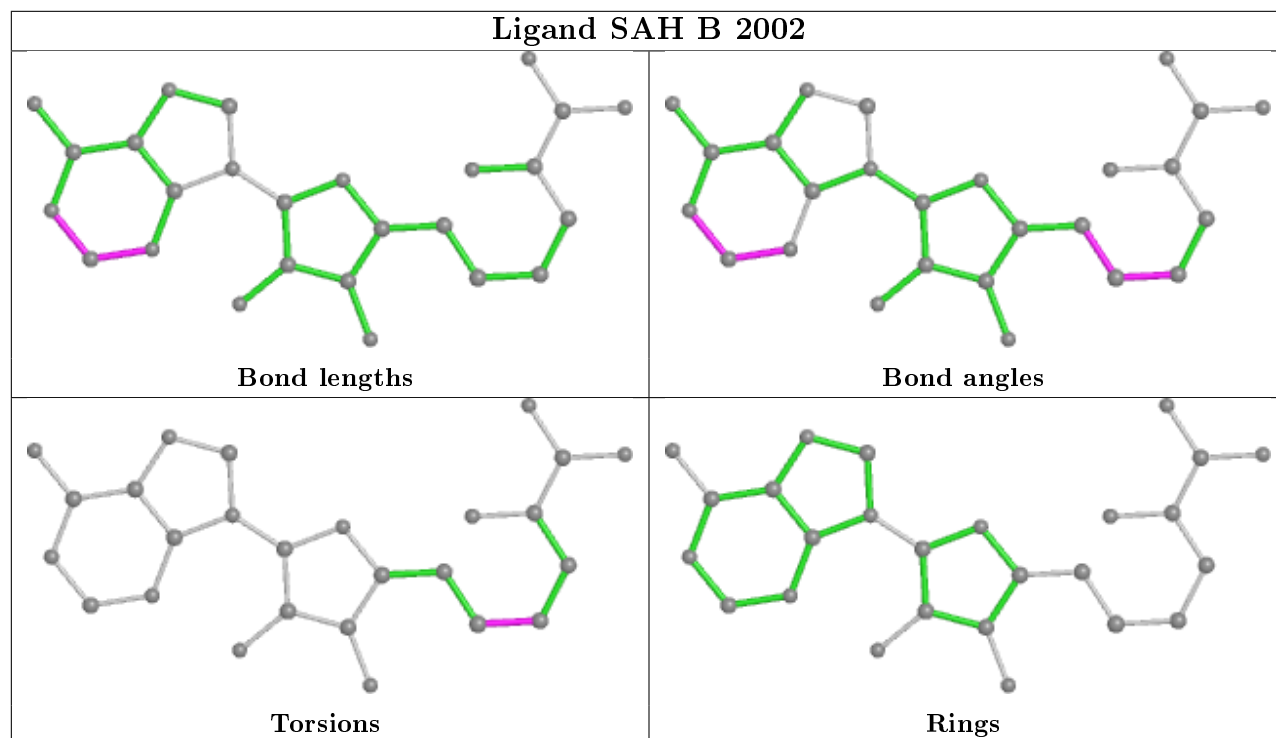
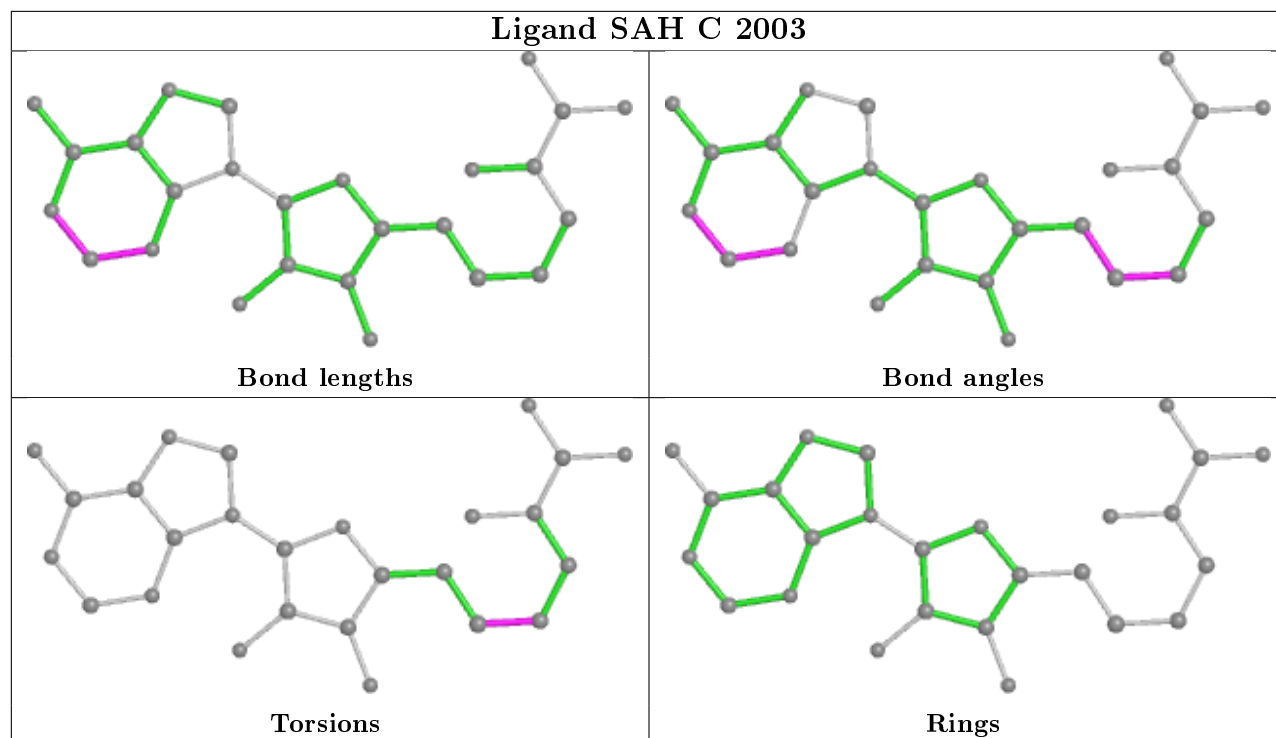
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1004	BME	O1-C1-C2-S2
4	C	1006	BME	O1-C1-C2-S2
3	C	2003	SAH	CB-CG-SD-C5'
3	B	2002	SAH	CB-CG-SD-C5'
3	A	2001	SAH	CB-CG-SD-C5'

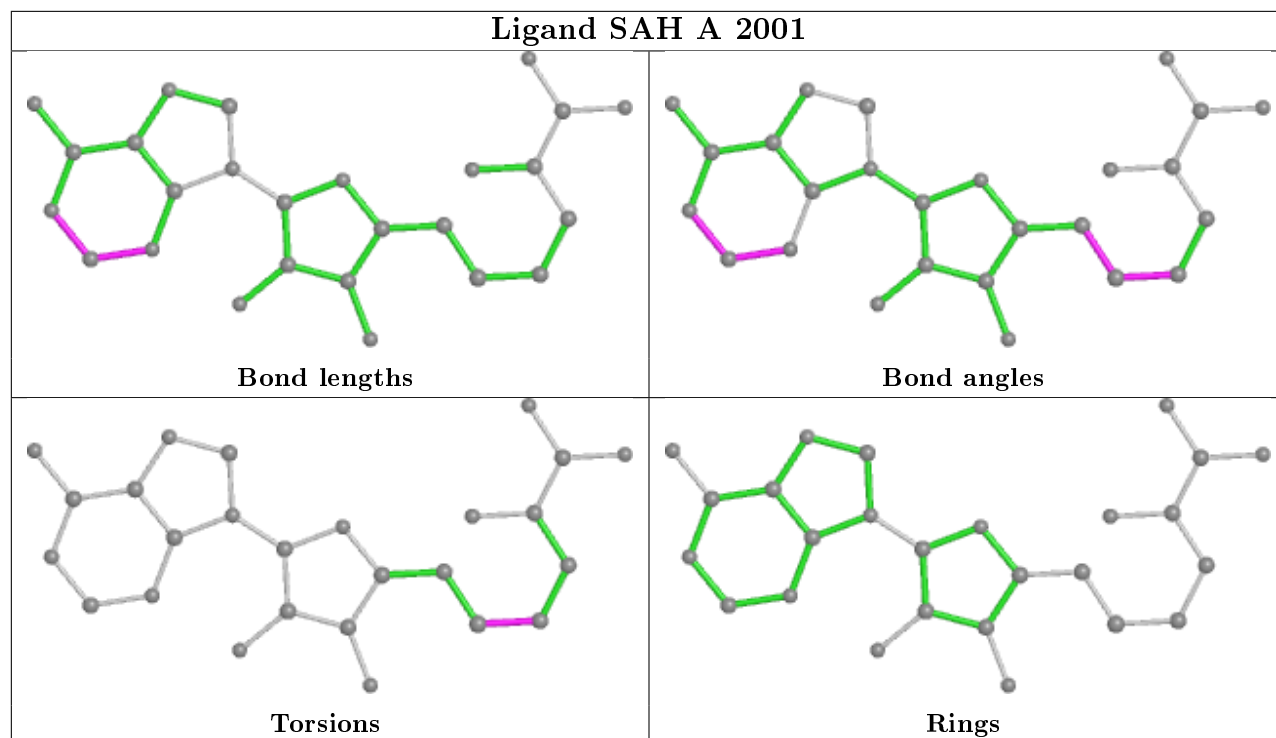
There are no ring outliers.

No monomer is involved in short contacts.

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.







## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

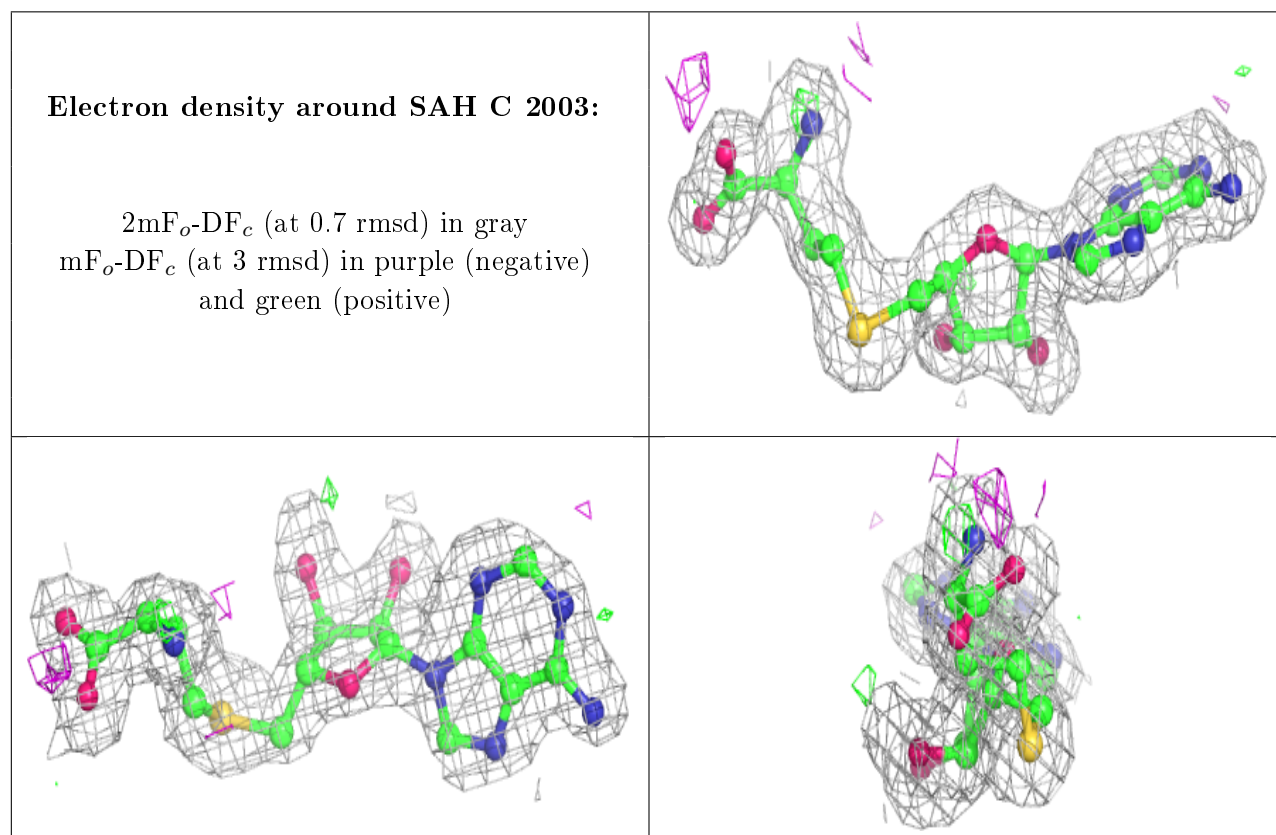
### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

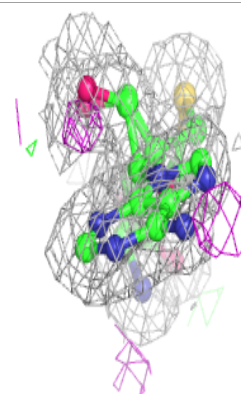
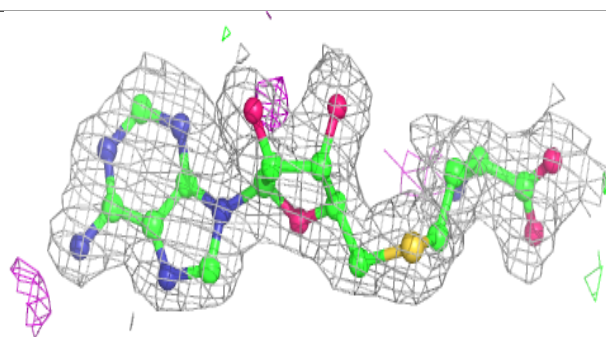
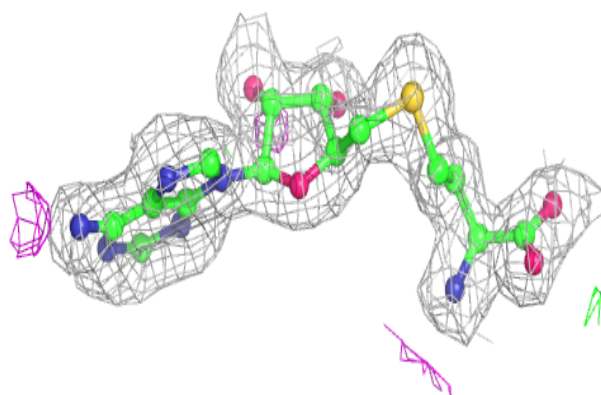
Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

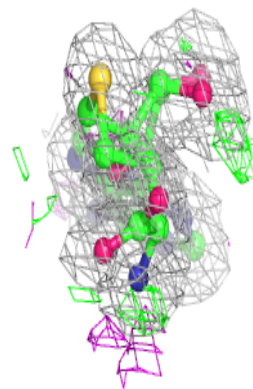
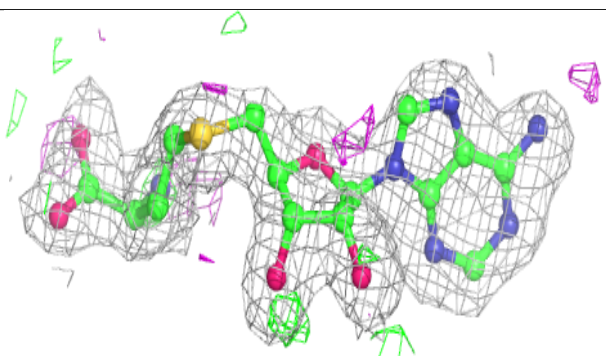
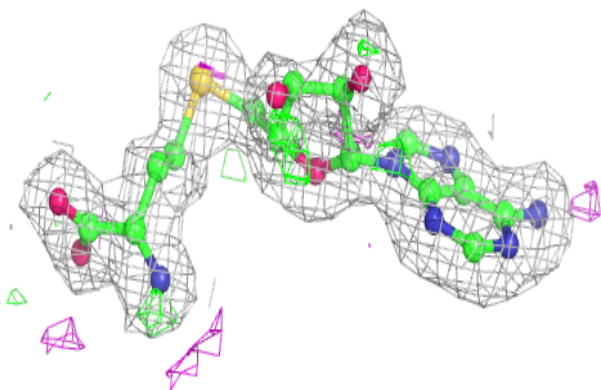


**Electron density around SAH B 2002:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around SAH A 2001:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.