



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 06:37 pm BST

PDB ID : 2OKC  
Title : Crystal structure of Type I restriction enzyme StySJI M protein (NP\_813429.1) from *Bacteroides thetaiotaomicron* VPI-5482 at 2.20 Å resolution  
Authors : Joint Center for Structural Genomics (JCSG)  
Deposited on : 2007-01-16  
Resolution : 2.20 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

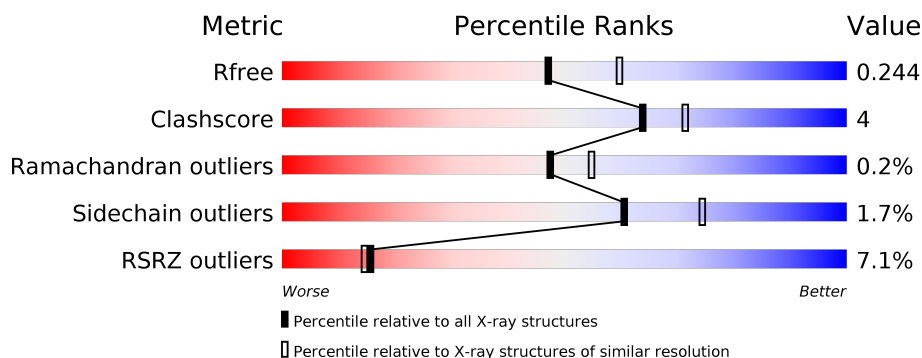
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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  $\leq 5\%$ . 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.

Mol	Chain	Length	Quality of chain
1	A	445	<div> <div>8%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>5%</div> </div> </div>
1	B	445	<div> <div>5%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>• •</div> </div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	IPA	B	501	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7069 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 Type I restriction enzyme StySJI M protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	Se	0	2	0
			3299	2110	542	632	5	10			
1	B	426	Total	C	N	O	S	Se	0	2	0
			3353	2146	548	643	5	11			

There are 26 discrepancies between the modelled and reference sequences:

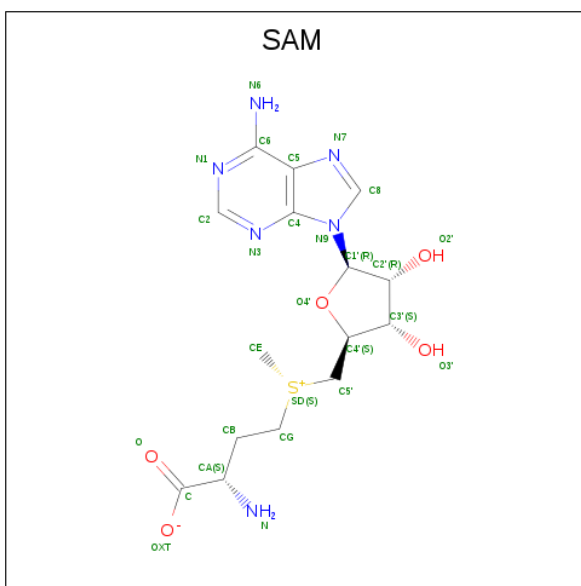
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	LEADER SEQUENCE	UNP Q89Z59
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	44	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	51	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	116	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	125	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	162	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	170	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	192	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	225	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	292	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	293	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	295	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	0	GLY	-	LEADER SEQUENCE	UNP Q89Z59
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	44	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	51	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	116	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	125	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	162	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	170	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	192	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	225	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	292	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	293	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59

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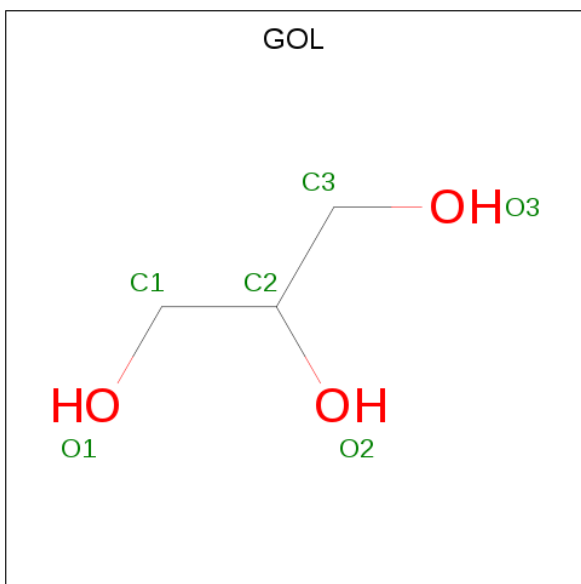
Chain	Residue	Modelled	Actual	Comment	Reference
B	295	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula:  $C_{15}H_{22}N_6O_5S$ ).



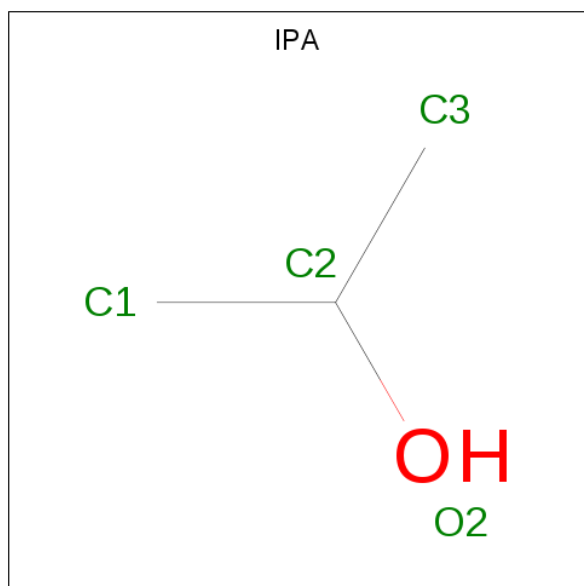
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 27	C 15	N 6	O 5	S 1	0	0
2	B	1	Total 27	C 15	N 6	O 5	S 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $\text{C}_3\text{H}_8\text{O}_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C<sub>3</sub>H<sub>8</sub>O).



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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Cl	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	162	Total	O	0	0
			162	162		
6	B	186	Total	O	0	0
			186	186		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.44Å 85.85Å 152.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.62 – 2.20 28.58 – 2.20	Depositor EDS
% Data completeness (in resolution range)	91.8 (28.62-2.20) 91.6 (28.58-2.20)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.59 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.182 , 0.232 0.194 , 0.244	Depositor DCC
$R_{free}$ test set	2367 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.5	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 48.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7069	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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: GOL, IPA, SAM, CL

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	0.70	1/3363 (0.0%)	0.73	1/4556 (0.0%)
1	B	0.81	4/3420 (0.1%)	0.79	1/4630 (0.0%)
All	All	0.76	5/6783 (0.1%)	0.76	2/9186 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	402	GLU	CD-OE2	15.18	1.42	1.25
1	B	404	ASN	CG-ND2	10.97	1.60	1.32
1	B	402	GLU	CD-OE1	9.76	1.36	1.25
1	B	404	ASN	CG-OD1	8.17	1.42	1.24
1	A	262	PHE	CE1-CZ	5.65	1.48	1.37

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	404	ASN	CB-CG-OD1	-5.62	110.36	121.60
1	A	335	ARG	NE-CZ-NH1	5.39	123.00	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	197	ALA	Peptide
1	B	8	GLU	Peptide

## 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	3299	0	3198	26	0
1	B	3353	0	3280	29	0
2	A	27	0	22	0	0
2	B	27	0	22	1	0
3	A	6	0	8	0	0
4	A	4	0	8	0	0
4	B	4	0	8	1	0
5	B	1	0	0	0	0
6	A	162	0	0	1	0
6	B	186	0	0	1	0
All	All	7069	0	6546	56	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 4.

All (56) 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:170:MSE:HE2	1:B:202:ARG:HA	1.53	0.88
1:A:23:ALA:O	1:A:25:GLN:O	2.04	0.74
1:A:362:ILE:HD12	1:A:417:ILE:HD13	1.69	0.74
1:A:150:GLY:HA3	1:A:342:TYR:CG	2.24	0.72
1:B:400:ASP:OD1	1:B:401:ALA:O	2.09	0.70
1:B:362:ILE:HD12	1:B:417:ILE:HD13	1.75	0.69
1:B:198:SER:HB2	1:B:199:LYS:HA	1.75	0.68
1:B:11:LEU:HD11	1:B:125:MSE:HE1	1.82	0.60
1:B:170:MSE:CE	1:B:202:ARG:HA	2.29	0.60
1:B:84:LYS:NZ	1:B:88:GLU:OE2	2.35	0.59
1:A:123:LEU:O	1:A:124:ILE:HB	2.03	0.57
1:A:342:TYR:CG	1:A:343:ALA:N	2.72	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:SER:O	1:A:57:ALA:HB3	2.06	0.56
1:A:198:SER:HB2	1:A:199:LYS:HA	1.87	0.55
1:B:420:ARG:HD3	1:B:424:SER:O	2.05	0.55
1:B:170:MSE:HE2	1:B:202:ARG:CA	2.35	0.53
1:B:401:ALA:O	1:B:402:GLU:HB2	2.07	0.53
1:A:123:LEU:O	1:A:124:ILE:CB	2.57	0.53
1:A:391:CYS:HB3	1:A:409:TRP:CE2	2.44	0.52
1:A:227:LEU:HD22	1:A:239:ILE:HD11	1.92	0.52
1:B:11:LEU:HD21	1:B:122:TRP:CH2	2.45	0.51
1:A:37:THR:HG23	1:A:225:MSE:HG2	1.92	0.51
1:A:198:SER:CB	1:A:199:LYS:HA	2.41	0.50
1:B:335:ARG:HD2	1:B:349:ASN:OD1	2.12	0.50
1:A:36:LEU:HD12	1:A:117:ILE:HD11	1.94	0.49
1:A:22:LEU:HB3	1:A:27:ILE:HB	1.94	0.49
1:B:198:SER:HB2	1:B:199:LYS:CA	2.41	0.49
1:B:36:LEU:HD12	1:B:117:ILE:HD11	1.94	0.49
1:B:29:PHE:HB3	1:B:141:ASN:ND2	2.28	0.48
1:B:29:PHE:CE1	1:B:33:ILE:HD11	2.49	0.47
1:B:36:LEU:CD1	1:B:117:ILE:HD11	2.44	0.47
1:B:11:LEU:HD11	1:B:125:MSE:CE	2.45	0.47
1:A:260:PRO:HD2	1:A:305:VAL:O	2.16	0.46
1:A:11:LEU:HD11	1:A:125:MSE:HE1	1.97	0.46
1:A:29:PHE:CE1	1:A:33:ILE:HD11	2.51	0.45
1:A:9:GLN:O	1:A:9:GLN:CD	2.55	0.45
1:A:362:ILE:HD12	1:A:417:ILE:CD1	2.44	0.45
1:B:29:PHE:CD1	1:B:33:ILE:HD11	2.52	0.45
1:A:323:ARG:NH1	6:A:588:HOH:O	2.49	0.44
1:B:362:ILE:CD1	1:B:417:ILE:HD13	2.45	0.44
1:B:154:THR:OG1	2:B:500:SAM:N	2.51	0.44
1:B:56:SER:O	1:B:57:ALA:HB3	2.18	0.44
1:B:373:HIS:HA	1:B:378:ASN:O	2.18	0.43
1:A:98:THR:O	1:A:99:LYS:C	2.58	0.42
1:B:125:MSE:HB2	1:B:130:LYS:HD2	2.01	0.42
1:B:198:SER:CB	1:B:199:LYS:HA	2.42	0.42
1:A:420:ARG:HD3	1:A:424:SER:O	2.19	0.42
1:B:7:THR:O	1:B:11:LEU:HB2	2.19	0.42
1:A:365:TYR:HA	1:A:408:ARG:O	2.20	0.42
4:B:501:IPA:H33	6:B:576:HOH:O	2.20	0.41
1:B:156:ARG:N	1:B:157:PRO:CD	2.83	0.41
1:B:198:SER:CB	1:B:199:LYS:CA	2.98	0.41
1:A:43:LYS:HD3	1:A:64:TRP:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:LEU:HD23	1:A:225:MSE:CE	2.51	0.41
1:A:420:ARG:HD2	1:A:427:ILE:HD11	2.03	0.41
1:B:37:THR:HG23	1:B:225:MSE:HG2	2.03	0.40

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	422/445 (95%)	396 (94%)	25 (6%)	1 (0%)	47	55
1	B	426/445 (96%)	409 (96%)	16 (4%)	1 (0%)	47	55
All	All	848/890 (95%)	805 (95%)	41 (5%)	2 (0%)	47	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	ILE
1	B	9	GLN

### 5.3.2 Protein sidechains [i](#)

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	348/372 (94%)	344 (99%)	4 (1%)	73	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	359/372 (96%)	351 (98%)	8 (2%)	52	65
All	All	707/744 (95%)	695 (98%)	12 (2%)	60	74

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	11	LEU
1	A	234	THR
1	A	374	THR
1	B	9	GLN
1	B	11	LEU
1	B	121	GLN
1	B	156	ARG
1	B	251	THR
1	B	271	ASP
1	B	402	GLU
1	B	415	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	B	25	GLN
1	B	141	ASN
1	B	394	ASN
1	B	403	ASN

### 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

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 for Mogul analysis.

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	SAM	A	500	-	21,29,29	1.19	2 (9%)	18,42,42	1.57	2 (11%)
4	IPA	B	501	-	3,3,3	0.72	0	3,3,3	0.26	0
2	SAM	B	500	-	21,29,29	1.31	2 (9%)	18,42,42	1.71	4 (22%)
4	IPA	A	502	-	3,3,3	0.58	0	3,3,3	0.21	0
3	GOL	A	501	-	5,5,5	0.42	0	5,5,5	0.50	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	SAM	A	500	-	-	0/8/33/33	0/3/3/3
2	SAM	B	500	-	-	0/8/33/33	0/3/3/3
3	GOL	A	501	-	-	1/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	SAM	C2-N3	4.13	1.38	1.32
2	A	500	SAM	C2-N3	3.64	1.38	1.32
2	B	500	SAM	C2-N1	2.76	1.39	1.33
2	A	500	SAM	C2-N1	2.74	1.39	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	SAM	N3-C2-N1	-5.09	120.72	128.68
2	A	500	SAM	N3-C2-N1	-4.99	120.88	128.68
2	A	500	SAM	C1'-N9-C4	-2.68	121.94	126.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	SAM	O4'-C1'-C2'	-2.51	103.26	106.93
2	B	500	SAM	C4-C5-N7	-2.16	107.15	109.40
2	B	500	SAM	O2'-C2'-C3'	2.13	118.71	111.82

There are no chirality outliers.

All (1) torsion outliers are listed below:

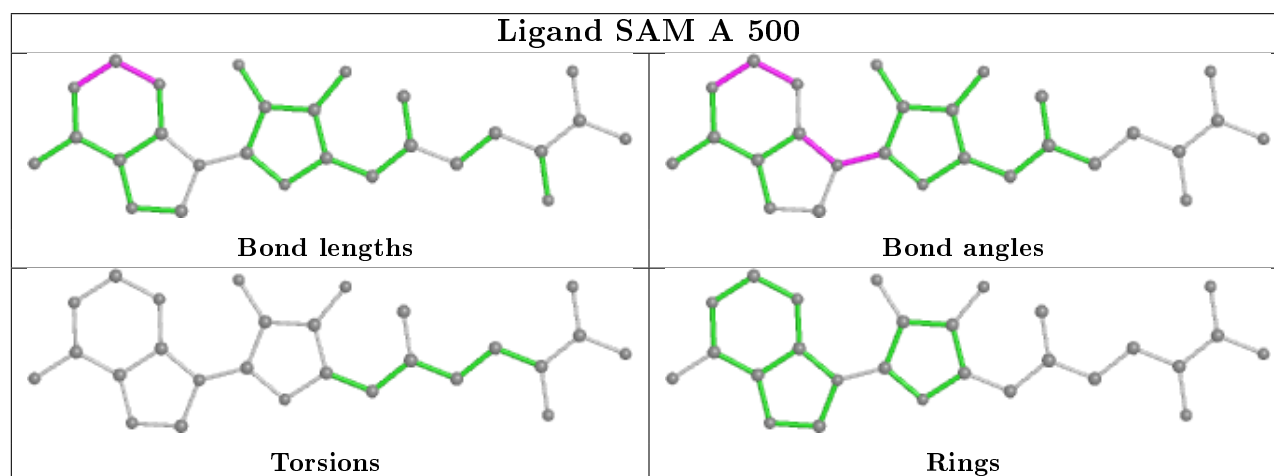
Mol	Chain	Res	Type	Atoms
3	A	501	GOL	O1-C1-C2-C3

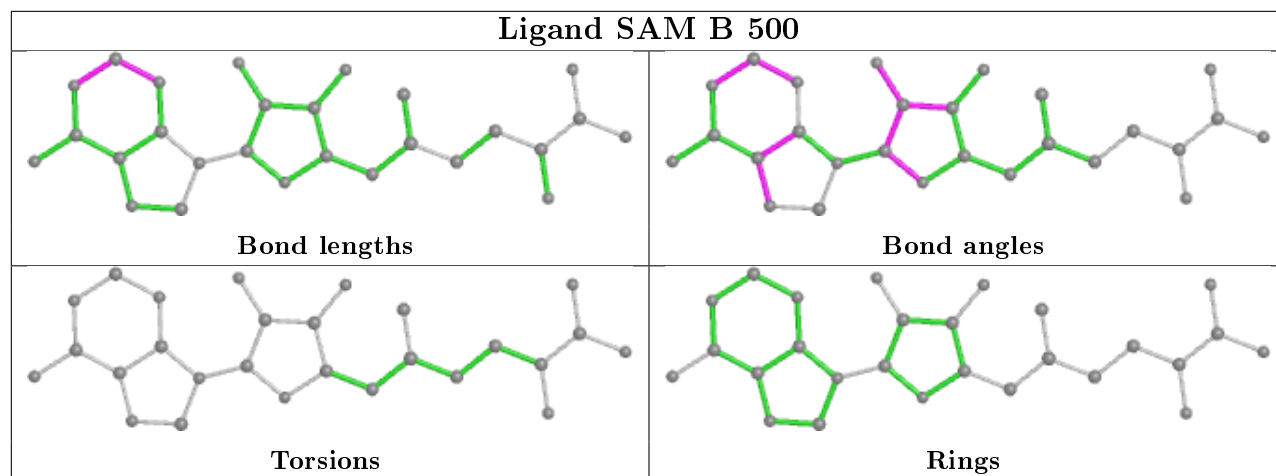
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	501	IPA	1	0
2	B	500	SAM	1	0

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

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	413/445 (92%)	0.28	37 (8%) 9 8	31, 43, 65, 84	0
1	B	415/445 (93%)	0.07	22 (5%) 26 25	32, 43, 61, 75	0
All	All	828/890 (93%)	0.17	59 (7%) 16 14	31, 43, 63, 84	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	376	ALA	6.2
1	A	433	GLY	5.8
1	A	145	LYS	5.3
1	A	351	LEU	4.5
1	A	304	VAL	4.5
1	A	126	ASP	4.2
1	A	305	VAL	4.0
1	A	124	ILE	4.0
1	A	350	VAL	4.0
1	A	146	LYS	3.7
1	A	37	THR	3.7
1	A	234	THR	3.7
1	B	304	VAL	3.7
1	B	351	LEU	3.6
1	A	143	GLN	3.6
1	B	350	VAL	3.5
1	B	401	ALA	3.5
1	A	52	PHE	3.4
1	A	402	GLU	3.4
1	B	305	VAL	3.3
1	A	144	ASP	3.2
1	B	124	ILE	3.1
1	A	90	ASP	3.1
1	A	333	ILE	3.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	333	ILE	2.9
1	A	306	LEU	2.9
1	A	303	ALA	2.8
1	A	33	ILE	2.7
1	B	52	PHE	2.7
1	B	306	LEU	2.7
1	A	36	LEU	2.6
1	B	203	ASP	2.6
1	B	404	ASN	2.6
1	A	38	TYR	2.5
1	B	258	ALA	2.5
1	B	235	ASP	2.5
1	A	352	PHE	2.5
1	B	197	ALA	2.5
1	A	39	LEU	2.5
1	B	36	LEU	2.5
1	A	147	SER	2.4
1	A	142	GLY	2.4
1	A	377	THR	2.4
1	B	257	LEU	2.4
1	A	29	PHE	2.3
1	A	257	LEU	2.3
1	A	73	LEU	2.3
1	A	334	LEU	2.3
1	B	334	LEU	2.2
1	B	310	VAL	2.2
1	B	204	PHE	2.2
1	B	303	ALA	2.2
1	B	256	ILE	2.1
1	A	375	LEU	2.1
1	B	9	GLN	2.1
1	A	34	THR	2.1
1	A	258	ALA	2.1
1	A	56	SER	2.1
1	A	349	ASN	2.0

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

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

### 6.3 Carbohydrates [i](#)

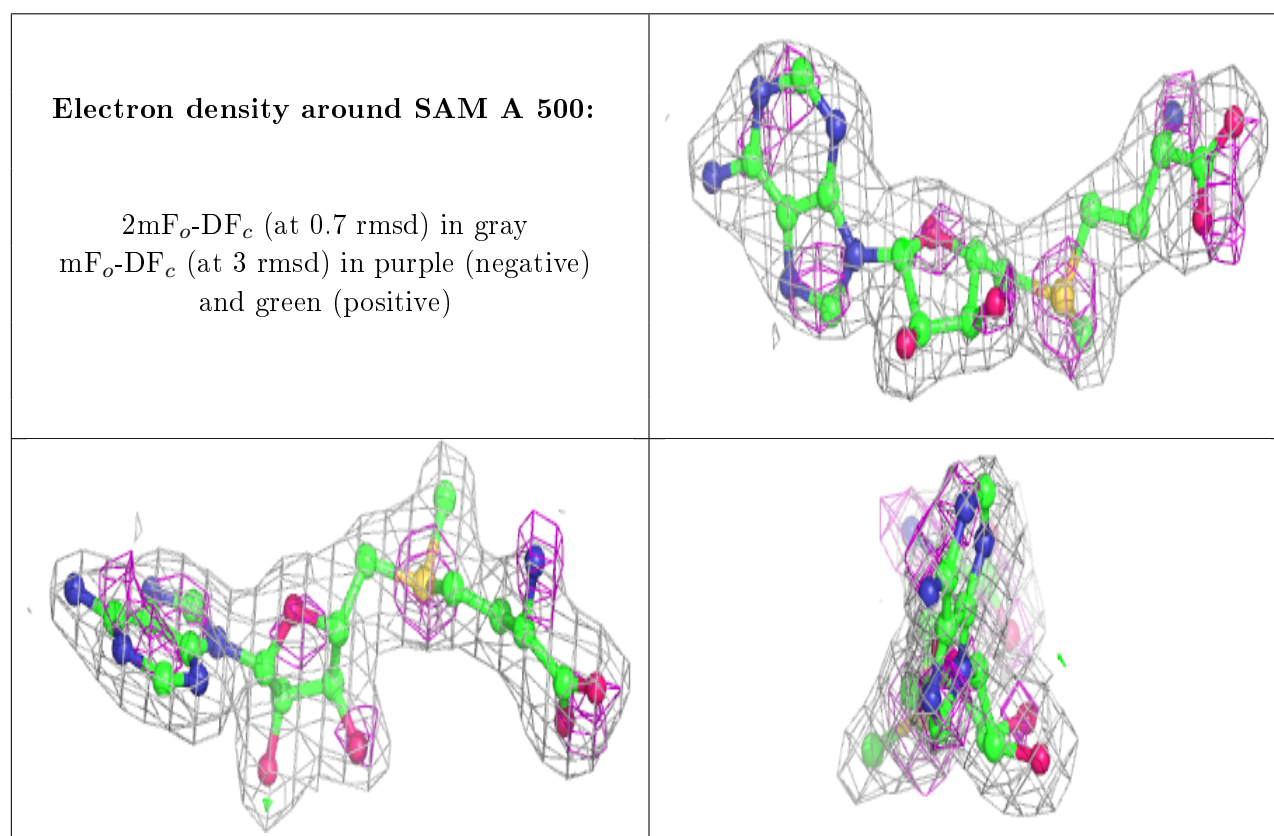
There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

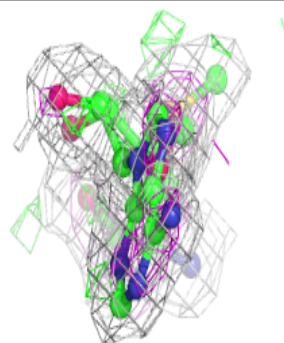
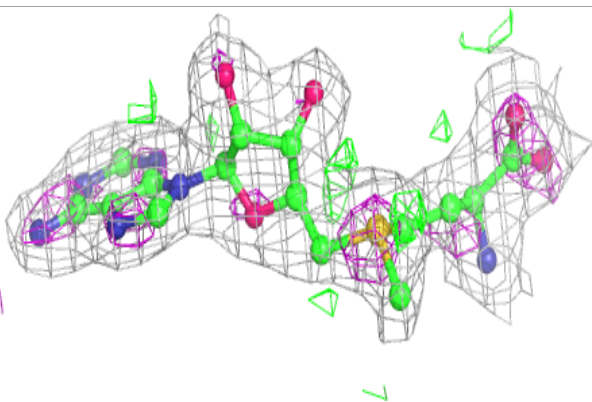
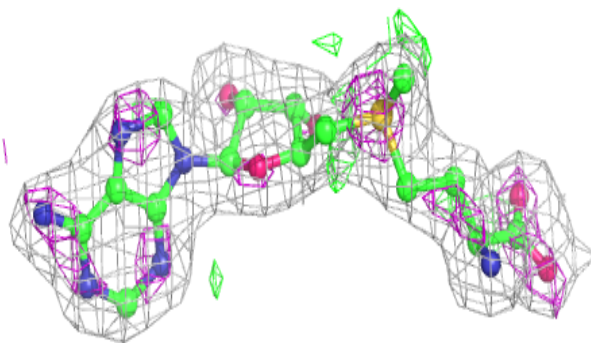
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	IPA	B	501	4/4	0.67	0.68	62,65,65,68	0
3	GOL	A	501	6/6	0.85	0.14	64,67,71,72	0
4	IPA	A	502	4/4	0.85	0.27	51,57,62,67	0
5	CL	B	445	1/1	0.91	0.07	77,77,77,77	0
2	SAM	A	500	27/27	0.95	0.10	35,41,48,52	0
2	SAM	B	500	27/27	0.97	0.09	23,29,34,38	0

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 SAM B 500:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.