



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 09:15 PM UTC

PDB ID : 4CXM / pdb_00004cxm
Title : Crystal Structure of Plasmodium Falciparum Spermidine Synthase in Complex with METHYLTHIOADENOSIN AND SPERMIDINE after catalysis in crystal
Authors : Sprenger, J.; Svensson, B.; Al-Karadaghi, S.; Persson, L.
Deposited on : 2014-04-07
Resolution : 1.75 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

A user guide is available at

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

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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

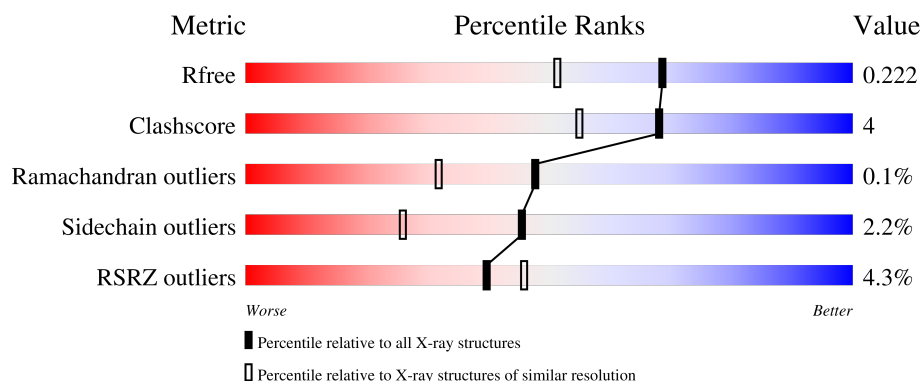
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	283	8% 88% 11% ..
1	B	283	4% 85% 12% ..
1	C	283	% 83% 14% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7336 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.

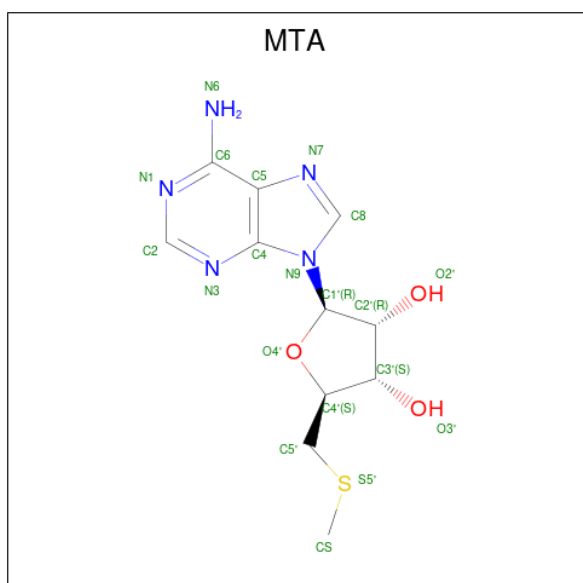
- Molecule 1 is a protein called SPERMIDINE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2254	1463	352	425	14			
1	B	280	Total	C	N	O	S	0	0	0
			2242	1455	350	423	14			
1	C	281	Total	C	N	O	S	0	0	0
			2254	1463	352	425	14			

There are 3 discrepancies between the modelled and reference sequences:

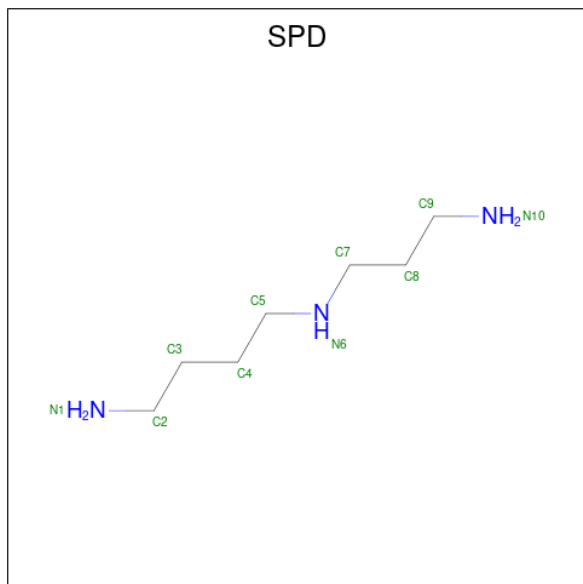
Chain	Residue	Modelled	Actual	Comment	Reference
A	39	GLY	-	expression tag	UNP Q8II73
B	39	GLY	-	expression tag	UNP Q8II73
C	39	GLY	-	expression tag	UNP Q8II73

- Molecule 2 is 5'-DEOXY-5'-METHYLTHIOADENOSINE (CCD ID: MTA) (formula: $C_{11}H_{15}N_5O_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			20	11	5	3	1		
2	B	1	Total	C	N	O	S	0	0
			20	11	5	3	1		
2	C	1	Total	C	N	O	S	0	0
			20	11	5	3	1		

- Molecule 3 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			10	7	3		
3	B	1	Total	C	N	0	0
			10	7	3		
3	C	1	Total	C	N	0	0
			10	7	3		

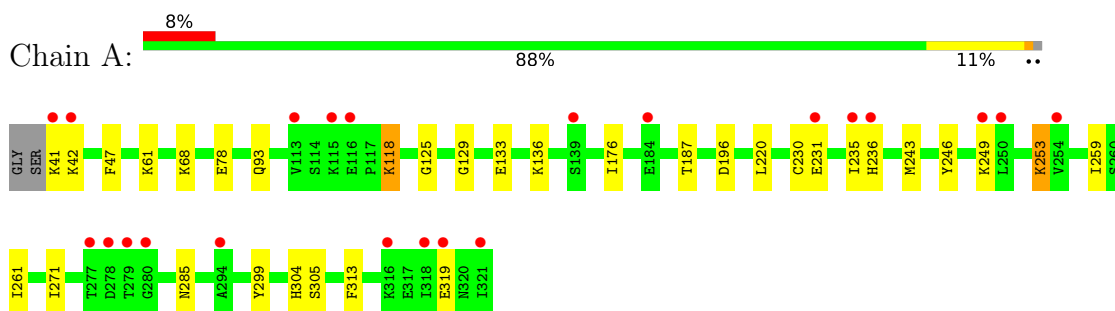
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	112	Total	O	0	0
			112	112		
4	B	175	Total	O	0	0
			175	175		
4	C	209	Total	O	0	0
			209	209		

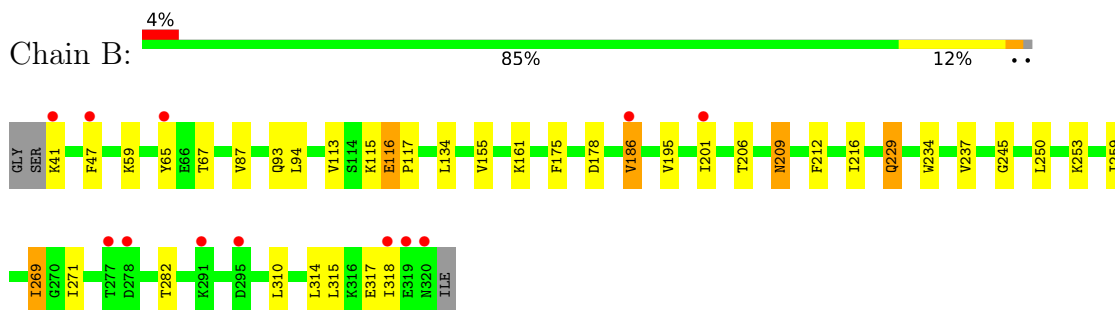
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 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.

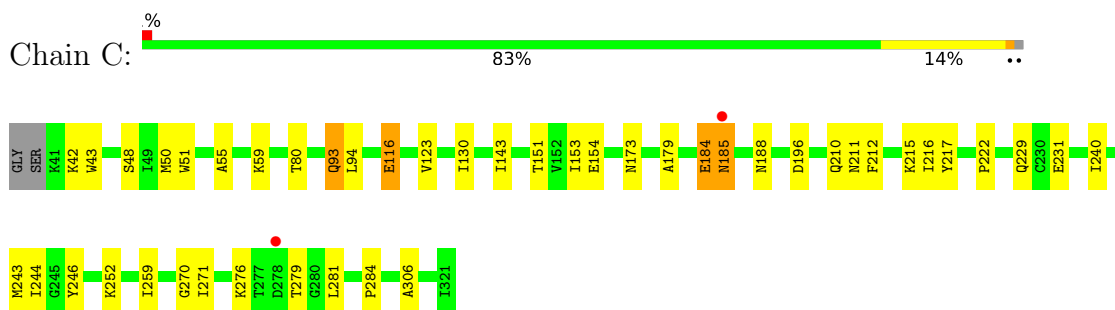
• Molecule 1: SPERMIDINE SYNTHASE



• Molecule 1: SPERMIDINE SYNTHASE



• Molecule 1: SPERMIDINE SYNTHASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	197.90Å 134.40Å 48.30Å 90.00° 95.50° 90.00°	Depositor
Resolution (Å)	44.94 – 1.75 44.94 – 1.75	Depositor EDS
% Data completeness (in resolution range)	98.6 (44.94-1.75) 98.7 (44.94-1.75)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.179 , 0.216 0.187 , 0.222	Depositor DCC
R_{free} test set	6255 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 35.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7336	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: MTA, SPD

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	1.41	9/2304 (0.4%)	1.20	3/3111 (0.1%)
1	B	1.45	12/2292 (0.5%)	1.28	5/3097 (0.2%)
1	C	1.52	15/2304 (0.7%)	1.27	7/3111 (0.2%)
All	All	1.46	36/6900 (0.5%)	1.25	15/9319 (0.2%)

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	269	ILE	C-O	-9.27	1.14	1.23
1	A	230	CYS	CA-C	7.06	1.61	1.52
1	C	151	THR	C-O	-6.82	1.15	1.24
1	A	187	THR	N-CA	6.68	1.54	1.46
1	C	130	ILE	N-CA	6.61	1.54	1.46
1	B	113	VAL	C-O	6.58	1.30	1.23
1	A	285	ASN	CA-C	-6.48	1.44	1.52
1	C	55	ALA	CA-C	-6.47	1.44	1.52
1	A	220	LEU	C-O	-6.40	1.16	1.23
1	A	313	PHE	N-CA	-6.29	1.38	1.46
1	A	129	GLY	N-CA	5.95	1.53	1.45
1	C	270	GLY	N-CA	5.89	1.51	1.44
1	A	236	HIS	N-CA	5.80	1.54	1.46
1	C	153	ILE	CA-C	5.68	1.59	1.52
1	C	240	ILE	CA-C	5.68	1.59	1.52
1	C	279	THR	CA-C	5.67	1.60	1.52
1	B	206	THR	N-CA	5.59	1.53	1.46
1	B	245	GLY	C-O	-5.58	1.17	1.23
1	B	87	VAL	N-CA	5.53	1.52	1.46
1	A	176	ILE	CA-C	-5.51	1.46	1.52
1	C	116	GLU	CA-CB	5.50	1.60	1.53
1	C	173	ASN	CA-C	-5.41	1.46	1.52
1	B	237	VAL	N-CA	-5.39	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	178	ASP	C-O	-5.33	1.17	1.24
1	C	306	ALA	C-O	-5.29	1.17	1.24
1	B	250	LEU	CA-C	-5.28	1.46	1.52
1	B	195	VAL	C-O	5.26	1.30	1.23
1	C	80	THR	C-O	-5.22	1.17	1.24
1	B	175	PHE	CA-CB	-5.22	1.45	1.53
1	A	231	GLU	N-CA	5.20	1.52	1.46
1	C	93	GLN	CA-C	-5.14	1.45	1.52
1	B	134	LEU	N-CA	5.07	1.52	1.46
1	C	143	ILE	C-O	-5.07	1.18	1.24
1	C	284	PRO	N-CA	-5.07	1.40	1.47
1	C	154	GLU	N-CA	5.03	1.52	1.46
1	B	234	TRP	C-O	-5.01	1.17	1.24

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	185	ASN	N-CA-C	7.95	122.56	112.86
1	C	184	GLU	CA-C-N	-7.29	111.60	123.05
1	C	184	GLU	C-N-CA	-7.29	111.60	123.05
1	B	229	GLN	CA-CB-CG	6.13	126.36	114.10
1	C	184	GLU	O-C-N	-5.99	115.52	122.95
1	B	155	VAL	N-CA-C	5.92	116.66	110.62
1	C	281	LEU	N-CA-C	5.73	120.27	112.88
1	C	50	MET	CG-SD-CE	5.70	113.44	100.90
1	A	304	HIS	N-CA-C	5.68	117.95	111.02
1	B	47	PHE	N-CA-C	-5.67	100.16	109.40
1	B	186	VAL	N-CA-CB	5.59	118.28	110.56
1	C	244	ILE	N-CA-C	-5.32	105.19	110.62
1	A	47	PHE	N-CA-C	-5.14	101.50	109.72
1	B	282	THR	N-CA-C	5.09	119.21	112.89
1	A	125	GLY	N-CA-C	5.02	121.68	114.10

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	2254	0	2265	13	0
1	B	2242	0	2245	17	0
1	C	2254	0	2265	16	0
2	A	20	0	15	1	0
2	B	20	0	15	3	0
2	C	20	0	15	0	0
3	A	10	0	19	3	0
3	B	10	0	19	4	0
3	C	10	0	19	2	0
4	A	112	0	0	1	2
4	B	175	0	0	1	1
4	C	209	0	0	0	1
All	All	7336	0	6877	49	3

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 (49) 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:A:196:ASP:OD1	3:A:640:SPD:H72	1.80	0.81
2:B:540:MTA:S5'	3:B:640:SPD:H72	2.24	0.77
2:B:540:MTA:S5'	3:B:640:SPD:C7	2.77	0.72
1:C:196:ASP:OD1	3:C:640:SPD:H72	1.91	0.69
1:B:65:TYR:OH	1:B:67:THR:HG21	1.94	0.66
1:A:259:ILE:HD11	1:A:271:ILE:HD11	1.82	0.62
1:A:68:LYS:O	1:B:161:LYS:NZ	2.32	0.62
1:B:229:GLN:HG2	1:B:269:ILE:HD11	1.81	0.62
1:A:243:MET:HE1	1:A:246:TYR:HE2	1.67	0.59
1:A:243:MET:HE1	1:A:246:TYR:CE2	2.40	0.57
1:A:253:LYS:HA	1:A:253:LYS:HE3	1.86	0.57
1:C:43:TRP:CZ2	1:C:59:LYS:HE3	2.41	0.56
2:B:540:MTA:S5'	3:B:640:SPD:H71	2.45	0.55
1:A:42:LYS:HD3	4:A:2003:HOH:O	2.05	0.55
1:A:93:GLN:O	3:A:640:SPD:H81	2.08	0.54
1:C:212:PHE:CE2	1:C:216:ILE:HD11	2.44	0.53
1:B:259:ILE:HD11	1:B:271:ILE:HD11	1.91	0.53
1:C:229:GLN:HE21	1:C:231:GLU:H	1.55	0.53
1:C:94:LEU:C	1:C:94:LEU:HD12	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:LEU:HD12	1:B:94:LEU:C	2.35	0.52
1:B:41:LYS:HG2	1:B:59:LYS:HE2	1.93	0.51
2:A:540:MTA:S5'	3:A:640:SPD:H71	2.51	0.51
1:B:209:ASN:C	1:B:209:ASN:HD22	2.21	0.48
1:C:184:GLU:O	1:C:185:ASN:HB2	2.13	0.48
1:B:65:TYR:CE2	1:B:67:THR:HG22	2.49	0.47
1:A:299:TYR:C	1:A:299:TYR:CD1	2.93	0.47
1:C:229:GLN:NE2	1:C:231:GLU:H	2.13	0.47
1:B:310:LEU:HD13	1:B:314:LEU:HD23	1.97	0.46
1:C:210:GLN:HE22	1:C:246:TYR:HA	1.81	0.46
1:B:116:GLU:N	1:B:117:PRO:CD	2.79	0.46
1:B:317:GLU:HG3	4:B:2175:HOH:O	2.16	0.46
1:C:217:TYR:CE2	1:C:276:LYS:HE2	2.51	0.45
1:C:211:ASN:HD21	1:C:215:LYS:NZ	2.14	0.45
1:A:41:LYS:HE3	1:A:61:LYS:HA	1.99	0.45
1:A:118:LYS:HA	1:A:118:LYS:HD2	1.82	0.44
1:B:209:ASN:ND2	1:B:212:PHE:H	2.16	0.44
1:B:93:GLN:O	3:B:640:SPD:H81	2.17	0.44
1:A:243:MET:CE	1:A:246:TYR:CE2	3.00	0.43
1:C:48:SER:HB3	1:C:51:TRP:CE2	2.53	0.43
1:C:123:VAL:HG13	1:C:179:ALA:CB	2.49	0.43
1:B:209:ASN:C	1:B:209:ASN:ND2	2.77	0.43
1:B:212:PHE:CE2	1:B:216:ILE:HD11	2.53	0.42
1:A:133:GLU:OE1	1:A:136:LYS:NZ	2.44	0.42
1:C:93:GLN:O	3:C:640:SPD:H81	2.20	0.41
1:C:188:ASN:OD1	1:C:222:PRO:HD3	2.20	0.41
1:C:259:ILE:HD11	1:C:271:ILE:HD11	2.03	0.41
1:C:243:MET:HB3	1:C:243:MET:HE3	1.93	0.41
1:B:229:GLN:HG2	1:B:269:ILE:CD1	2.48	0.41
1:B:115:LYS:C	1:B:116:GLU:HG2	2.45	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:2101:HOH:O	4:C:2171:HOH:O[4_444]	1.47	0.73
4:A:2006:HOH:O	4:A:2009:HOH:O[2_555]	1.80	0.40
4:A:2009:HOH:O	4:A:2009:HOH:O[2_555]	1.90	0.30

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	279/283 (99%)	270 (97%)	8 (3%)	1 (0%)	30	15
1	B	278/283 (98%)	272 (98%)	6 (2%)	0	100	100
1	C	279/283 (99%)	271 (97%)	8 (3%)	0	100	100
All	All	836/849 (98%)	813 (97%)	22 (3%)	1 (0%)	48	32

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	235	ILE

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	253/254 (100%)	246 (97%)	7 (3%)	38	18
1	B	251/254 (99%)	244 (97%)	7 (3%)	38	18
1	C	253/254 (100%)	250 (99%)	3 (1%)	63	49
All	All	757/762 (99%)	740 (98%)	17 (2%)	45	26

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	GLU
1	A	118	LYS

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Mol	Chain	Res	Type
1	A	249	LYS
1	A	253	LYS
1	A	261	ILE
1	A	305	SER
1	A	319	GLU
1	B	116	GLU
1	B	186	VAL
1	B	201	ILE
1	B	209	ASN
1	B	253	LYS
1	B	315	LEU
1	B	318	ILE
1	C	42	LYS
1	C	116	GLU
1	C	252	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	73	ASN
1	A	93	GLN
1	A	142	ASN
1	A	173	ASN
1	A	211	ASN
1	A	218	ASN
1	B	72	GLN
1	B	209	ASN
1	B	211	ASN
1	B	285	ASN
1	B	320	ASN
1	C	73	ASN
1	C	93	GLN
1	C	210	GLN
1	C	211	ASN
1	C	218	ASN
1	C	229	GLN
1	C	285	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	MTA	B	540	-	22,22,22	1.49	4 (18%)	32,32,32	2.06	8 (25%)
2	MTA	C	540	-	22,22,22	1.51	4 (18%)	32,32,32	2.06	13 (40%)
3	SPD	C	640	-	9,9,9	1.04	1 (11%)	8,8,8	1.71	2 (25%)
2	MTA	A	540	-	22,22,22	1.19	2 (9%)	32,32,32	1.96	6 (18%)
3	SPD	A	640	-	9,9,9	0.78	0	8,8,8	1.42	1 (12%)
3	SPD	B	640	-	9,9,9	0.45	0	8,8,8	2.10	2 (25%)

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	MTA	B	540	-	-	1/7/23/23	0/3/3/3
2	MTA	C	540	-	-	2/7/23/23	0/3/3/3
3	SPD	C	640	-	-	1/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MTA	A	540	-	-	2/7/23/23	0/3/3/3
3	SPD	A	640	-	-	1/7/7/7	-
3	SPD	B	640	-	-	3/7/7/7	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	540	MTA	C5-C4	4.01	1.46	1.39
2	B	540	MTA	C4-N9	-3.64	1.30	1.37
2	A	540	MTA	C5-C4	3.45	1.45	1.39
2	B	540	MTA	C5-N7	-3.42	1.32	1.39
2	B	540	MTA	C5-C4	3.11	1.44	1.39
2	C	540	MTA	C5-N7	-2.93	1.33	1.39
3	C	640	SPD	C8-C7	2.52	1.61	1.51
2	C	540	MTA	C8-N7	2.23	1.36	1.31
2	A	540	MTA	O2'-C2'	-2.09	1.37	1.43
2	B	540	MTA	C2-N3	-2.01	1.30	1.33
2	C	540	MTA	C5'-S5'	-2.00	1.76	1.81

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	540	MTA	C5-C4-N3	-5.93	118.55	126.72
2	B	540	MTA	C5-C4-N3	-5.49	119.16	126.72
2	A	540	MTA	N3-C4-N9	4.79	135.31	127.17
3	B	640	SPD	C8-C7-N6	4.74	124.80	112.07
2	B	540	MTA	O4'-C4'-C5'	4.37	120.10	108.83
2	C	540	MTA	N3-C4-N9	4.33	134.53	127.17
2	B	540	MTA	N3-C4-N9	4.31	134.50	127.17
2	C	540	MTA	C4-N9-C8	3.97	109.91	105.74
2	B	540	MTA	O4'-C1'-C2'	-3.55	99.02	106.62
2	C	540	MTA	N6-C6-N1	3.52	126.22	118.38
2	C	540	MTA	C2-N1-C6	3.37	124.26	118.73
3	C	640	SPD	C8-C7-N6	3.33	121.01	112.07
2	B	540	MTA	C2-N3-C4	3.33	119.96	111.83
2	C	540	MTA	C5-C4-N3	-3.22	122.28	126.72
2	A	540	MTA	C2-N3-C4	3.20	119.64	111.83
2	B	540	MTA	N3-C2-N1	-2.74	124.43	128.58
2	A	540	MTA	O3'-C3'-C4'	-2.70	103.33	111.08
3	A	640	SPD	C8-C7-N6	2.70	119.32	112.07
3	B	640	SPD	C7-N6-C5	2.68	126.07	113.40
2	A	540	MTA	C4'-O4'-C1'	-2.51	103.92	109.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	540	MTA	N3-C2-N1	-2.50	124.79	128.58
2	C	540	MTA	C5-C4-N9	-2.47	103.12	105.81
2	A	540	MTA	C4-C5-N7	-2.38	107.86	110.58
2	C	540	MTA	O4'-C1'-C2'	-2.34	101.62	106.62
2	C	540	MTA	O4'-C4'-C3'	-2.27	100.65	105.15
2	B	540	MTA	N9-C8-N7	-2.24	110.76	113.94
2	C	540	MTA	O3'-C3'-C2'	2.19	118.83	111.82
2	B	540	MTA	C4-N9-C8	2.19	108.03	105.74
3	C	640	SPD	C4-C5-N6	2.15	117.83	112.07
2	C	540	MTA	C5-C6-N6	-2.10	118.09	123.29
2	C	540	MTA	N9-C8-N7	-2.05	111.03	113.94
2	C	540	MTA	O3'-C3'-C4'	-2.01	105.31	111.08

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	540	MTA	O4'-C4'-C5'-S5'
2	A	540	MTA	C3'-C4'-C5'-S5'
2	B	540	MTA	O4'-C4'-C5'-S5'
2	C	540	MTA	O4'-C4'-C5'-S5'
2	C	540	MTA	C3'-C4'-C5'-S5'
3	B	640	SPD	C8-C7-N6-C5
3	A	640	SPD	N6-C7-C8-C9
3	B	640	SPD	N6-C7-C8-C9
3	C	640	SPD	N6-C7-C8-C9
3	B	640	SPD	C7-C8-C9-N10

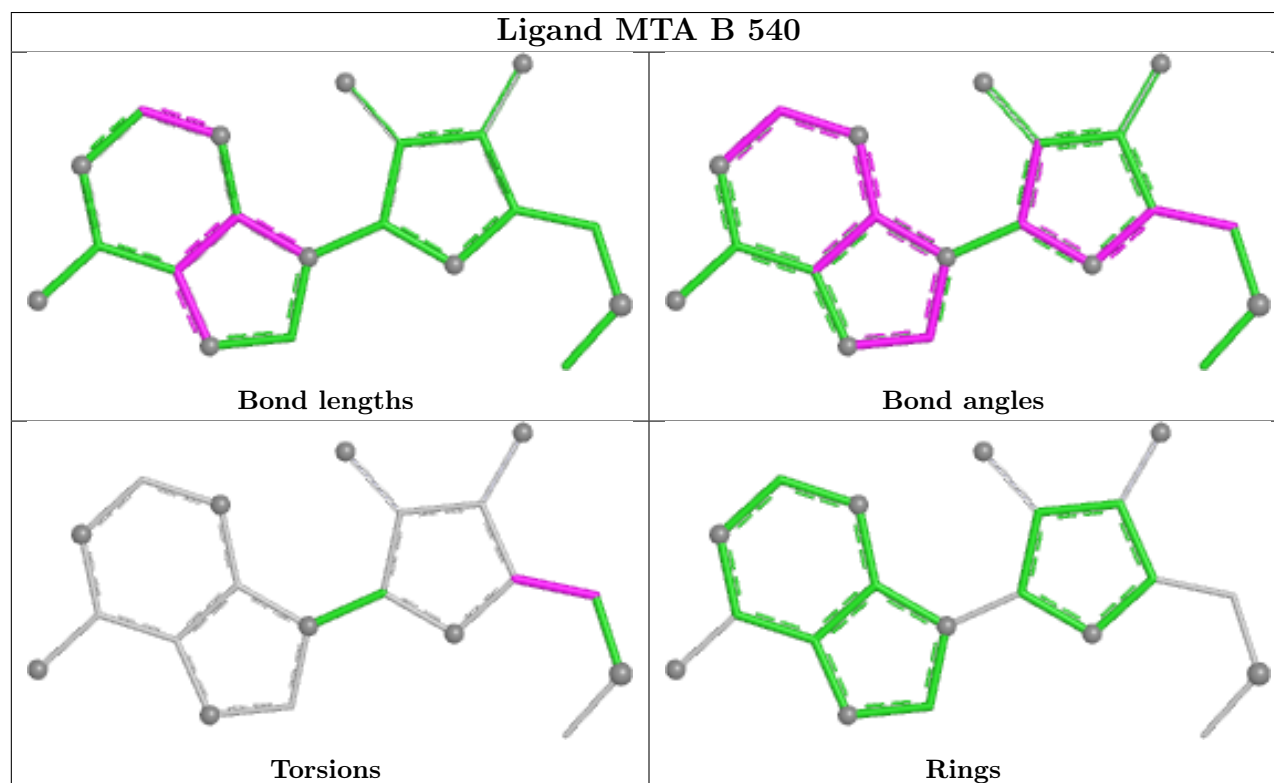
There are no ring outliers.

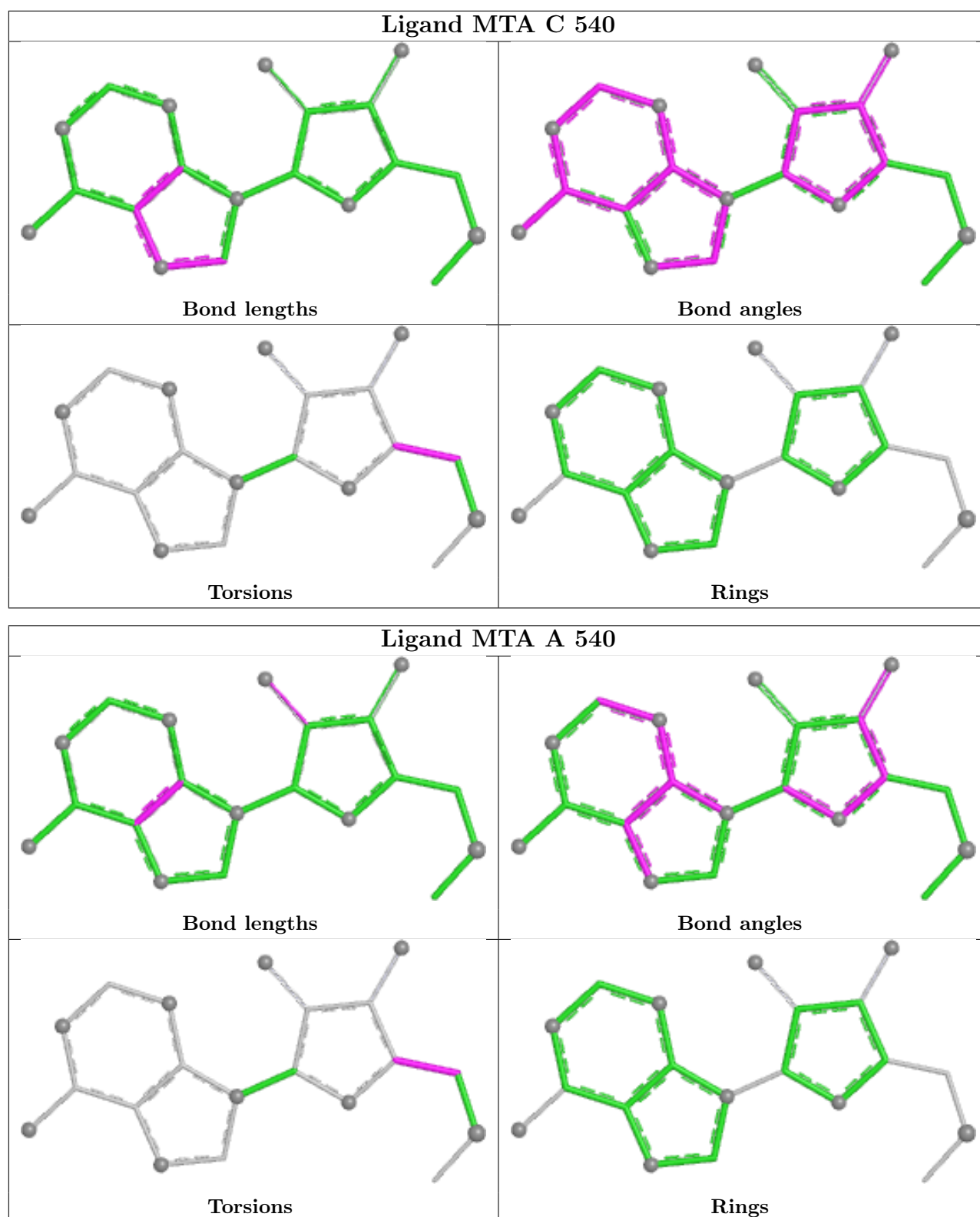
5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	540	MTA	3	0
3	C	640	SPD	2	0
2	A	540	MTA	1	0
3	A	640	SPD	3	0
3	B	640	SPD	4	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 95th 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 ²)	Q<0.9
1	A	281/283 (99%)	0.52	22 (7%) 19 22	19, 27, 48, 63	0
1	B	280/283 (98%)	-0.01	12 (4%) 40 46	13, 21, 39, 81	0
1	C	281/283 (99%)	-0.23	2 (0%) 84 88	12, 18, 36, 46	0
All	All	842/849 (99%)	0.09	36 (4%) 40 46	12, 23, 42, 81	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	236	HIS	3.6
1	B	47	PHE	3.4
1	A	318	ILE	3.2
1	A	321	ILE	3.2
1	B	320	ASN	3.1
1	A	231	GLU	2.9
1	A	278	ASP	2.9
1	A	277	THR	2.8
1	B	186	VAL	2.8
1	A	250	LEU	2.7
1	A	279	THR	2.7
1	B	201	ILE	2.6
1	A	42	LYS	2.6
1	A	319	GLU	2.6
1	B	318	ILE	2.6
1	A	115	LYS	2.6
1	A	235	ILE	2.6
1	A	249	LYS	2.6
1	B	319	GLU	2.6
1	A	280	GLY	2.4
1	C	185	ASN	2.4
1	B	41	LYS	2.3
1	A	294	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	278	ASP	2.3
1	B	278	ASP	2.2
1	B	295	ASP	2.2
1	B	65	TYR	2.2
1	A	113	VAL	2.1
1	A	254	VAL	2.1
1	A	116	GLU	2.1
1	A	184	GLU	2.1
1	A	316	LYS	2.1
1	B	277	THR	2.0
1	B	291	LYS	2.0
1	A	139	SER	2.0
1	A	41	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

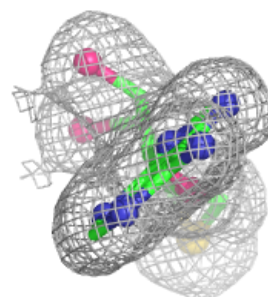
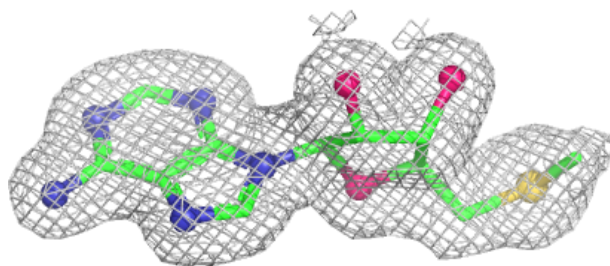
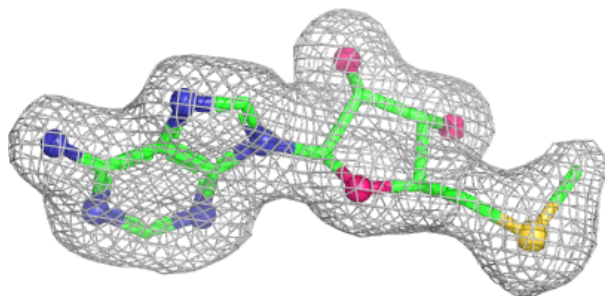
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SPD	A	640	10/10	0.91	0.12	21,34,36,40	0
3	SPD	B	640	10/10	0.92	0.11	18,27,34,37	0
3	SPD	C	640	10/10	0.94	0.10	18,22,29,29	0
2	MTA	A	540	20/20	0.98	0.04	19,21,26,30	0
2	MTA	B	540	20/20	0.98	0.05	17,18,21,24	0
2	MTA	C	540	20/20	0.98	0.04	15,16,19,21	0

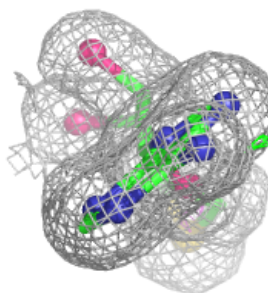
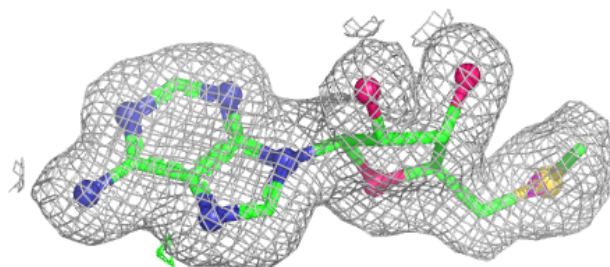
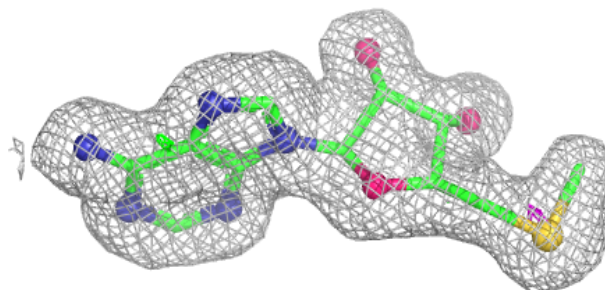
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

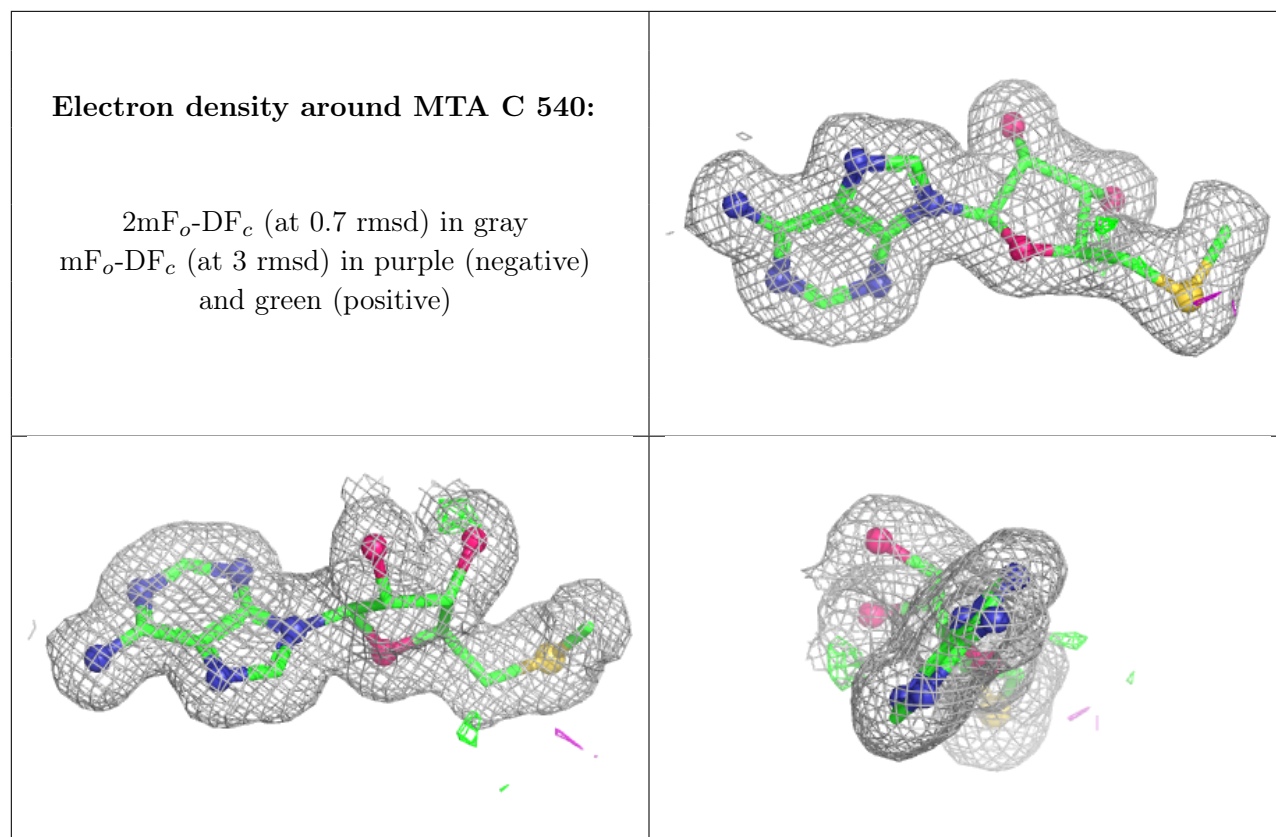
Electron density around MTA A 540:

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

**Electron density around MTA B 540:**

$2mF_o-DF_c$ (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.