



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 05:06 pm BST

PDB ID : 1TV8
Title : Structure of MoaA in complex with S-adenosylmethionine
Authors : Haenzelmann, P.; Schindelin, H.
Deposited on : 2004-06-28
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (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

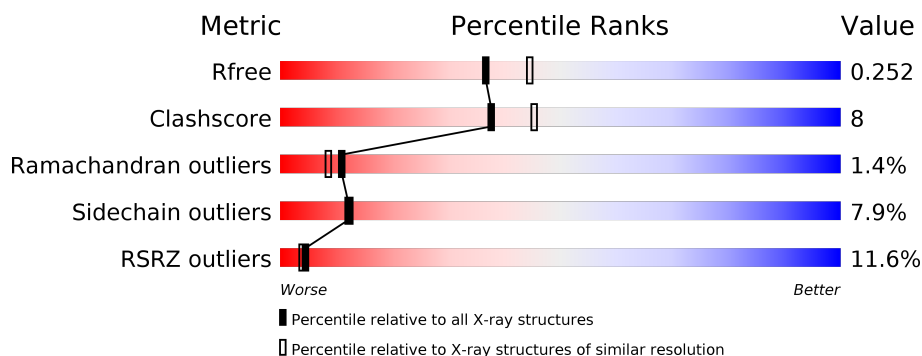
1 Overall quality at a glance

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 ≥ 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	340	
1	B	340	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5505 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 Molybdenum cofactor biosynthesis protein A.

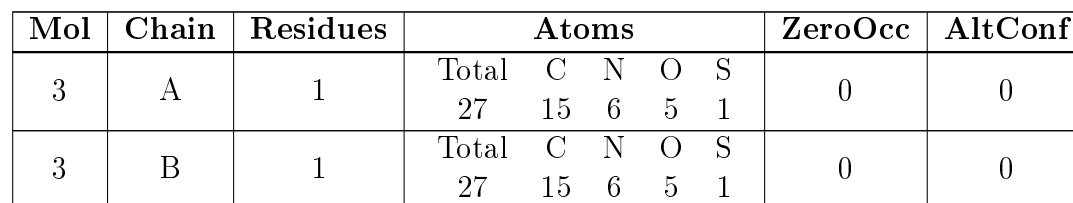
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	0	0
			2641	1673	455	500	13			
1	B	326	Total	C	N	O	S	0	0	0
			2632	1668	454	497	13			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: C₁₅H₂₂N₆O₅S).



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- The diagram shows a cubane-like complex with four iron (Fe) atoms at the corners of a cube and four sulfur (S) atoms at the centers of the edges. The atoms are color-coded: Fe atoms are purple and S atoms are yellow. The bonds between Fe and S atoms are shown as thin purple lines. The labels for the atoms are as follows: SF4 (top), S3 (top-left), FE1 (top-right), FE2 (middle-left), S2 (middle-right), S4 (bottom-right), FE3 (bottom-right), S1 (bottom-left), and FE4 (middle-left). The structure is highly symmetric, with each Fe atom bonded to three S atoms and each S atom bonded to two Fe atoms.

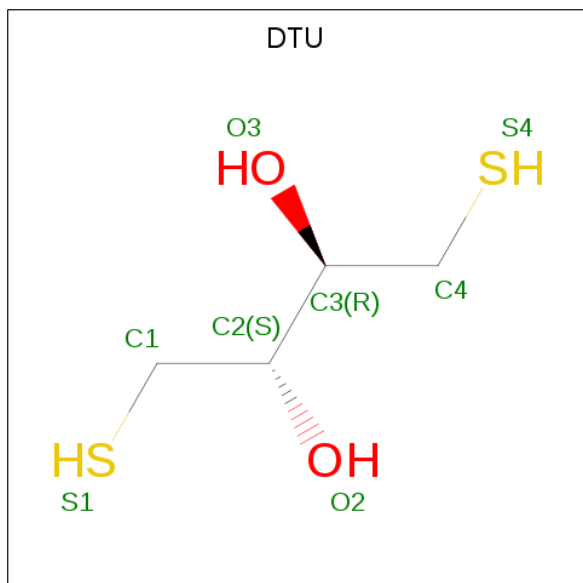
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 8	Fe 4	S 4	0	0
4	A	1	Total 8	Fe 4	S 4	0	0



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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is (2R,3S)-1,4-DIMERCAPTOBUTANE-2,3-DIOL (three-letter code: DTU) (formula: C₄H₁₀O₂S₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	S	0	0
			8	4	2	2		

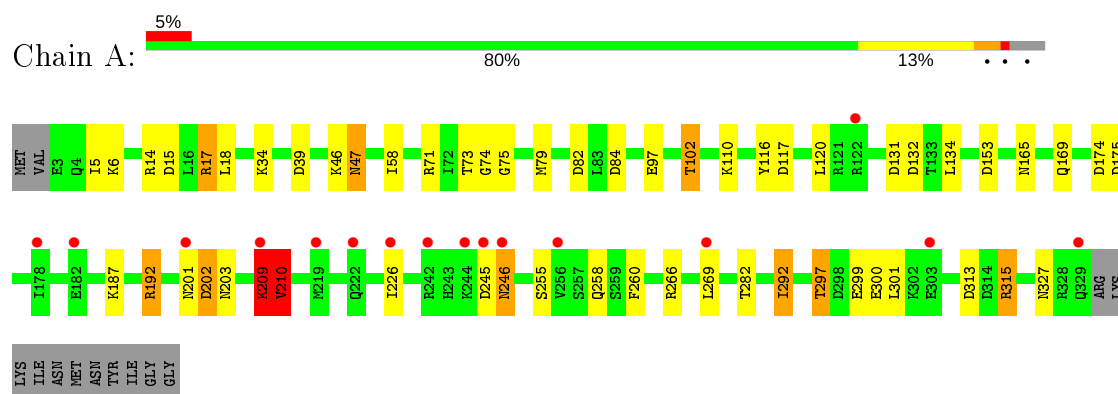
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	96	Total	O	0	0
			96	96		
6	B	32	Total	O	0	0
			32	32		

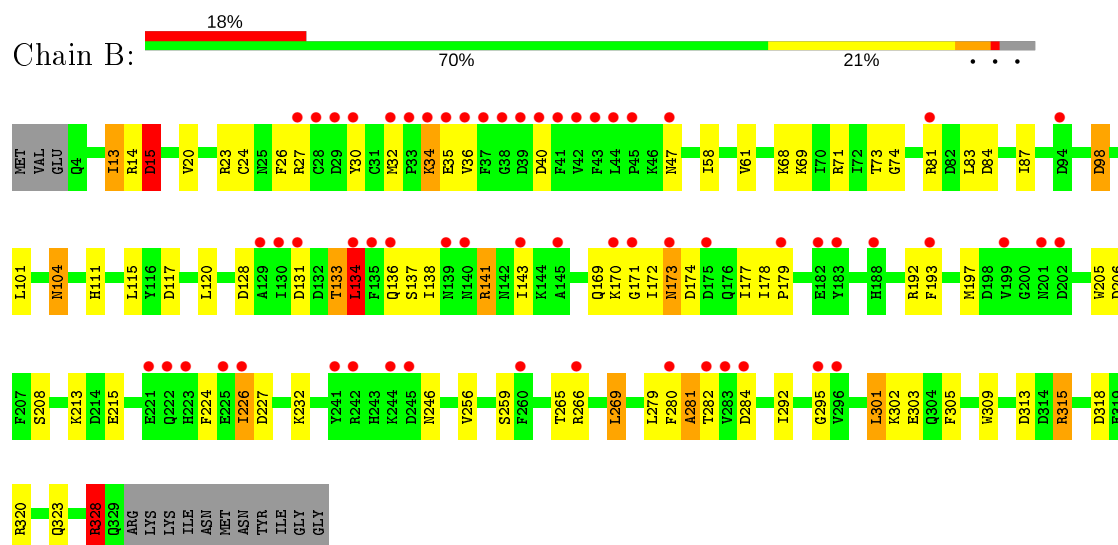
3 Residue-property plots [i](#)

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 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: Molybdenum cofactor biosynthesis protein A



• Molecule 1: Molybdenum cofactor biosynthesis protein A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	47.98Å 103.31Å 189.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	95.35 – 2.20 45.37 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.7 (95.35-2.20) 96.7 (45.37-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.213 , 0.241 0.232 , 0.252	Depositor DCC
R_{free} test set	2399 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	48.9	Xtriage
Anisotropy	0.535	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5505	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: SF4, DTU, SAM, SO4

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	0.84	3/2684 (0.1%)	0.99	16/3613 (0.4%)
1	B	0.89	11/2675 (0.4%)	0.96	11/3601 (0.3%)
All	All	0.86	14/5359 (0.3%)	0.98	27/7214 (0.4%)

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	A	0	3
1	B	0	1
All	All	0	4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	170	LYS	C-O	10.92	1.44	1.23
1	B	137	SER	CB-OG	8.62	1.53	1.42
1	B	131	ASP	C-O	7.71	1.38	1.23
1	B	171	GLY	N-CA	7.28	1.56	1.46
1	B	170	LYS	CA-C	7.05	1.71	1.52
1	B	137	SER	CA-CB	6.83	1.63	1.52
1	A	79	MET	CG-SD	-6.43	1.64	1.81
1	A	327	ASN	CG-ND2	5.98	1.47	1.32
1	A	327	ASN	CG-OD1	5.61	1.36	1.24
1	B	133	THR	C-O	5.43	1.33	1.23
1	B	208	SER	CB-OG	5.34	1.49	1.42
1	B	134	LEU	N-CA	5.29	1.56	1.46
1	B	104	ASN	CB-CG	5.22	1.63	1.51
1	B	131	ASP	C-N	5.17	1.46	1.34

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	175	ASP	CB-CG-OD2	7.98	125.48	118.30
1	B	128	ASP	CB-CG-OD2	7.37	124.93	118.30
1	A	315	ARG	NE-CZ-NH1	7.05	123.83	120.30
1	A	84	ASP	CB-CG-OD2	6.47	124.12	118.30
1	A	313	ASP	CB-CG-OD2	6.46	124.12	118.30
1	B	313	ASP	CB-CG-OD2	6.23	123.91	118.30
1	B	206	ASP	CB-CG-OD2	6.08	123.77	118.30
1	B	141	ARG	NE-CZ-NH1	6.07	123.34	120.30
1	A	315	ARG	NE-CZ-NH2	-6.07	117.27	120.30
1	A	39	ASP	CB-CG-OD2	6.01	123.71	118.30
1	A	117	ASP	CB-CG-OD2	5.91	123.61	118.30
1	A	17	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	210	VAL	N-CA-C	5.74	126.49	111.00
1	B	98	ASP	CB-CG-OD2	5.67	123.40	118.30
1	A	132	ASP	CB-CG-OD2	5.65	123.39	118.30
1	B	227	ASP	CB-CG-OD2	5.65	123.38	118.30
1	A	82	ASP	CB-CG-OD1	5.61	123.35	118.30
1	A	202	ASP	N-CA-C	5.59	126.11	111.00
1	A	131	ASP	CB-CG-OD2	5.57	123.31	118.30
1	A	15	ASP	CB-CG-OD2	5.54	123.29	118.30
1	A	17	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	B	84	ASP	CB-CG-OD2	5.43	123.19	118.30
1	B	40	ASP	CB-CG-OD2	5.36	123.13	118.30
1	B	15	ASP	CB-CG-OD2	5.35	123.11	118.30
1	B	117	ASP	CB-CG-OD2	5.24	123.01	118.30
1	A	174	ASP	CB-CG-OD2	5.19	122.97	118.30
1	B	284	ASP	CB-CG-OD2	5.08	122.87	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	201	ASN	Peptide
1	A	209	LYS	Peptide
1	A	210	VAL	Peptide
1	B	328	ARG	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	2641	0	2637	31	0
1	B	2632	0	2631	50	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	27	0	21	2	0
3	B	27	0	21	5	0
4	A	16	0	0	0	0
4	B	16	0	0	0	0
5	A	8	0	9	2	0
6	A	96	0	0	8	0
6	B	32	0	0	12	0
All	All	5505	0	5319	82	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 8.

All (82) 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:266:ARG:HB3	6:A:1598:HOH:O	1.49	1.12
1:B:32:MET:HE3	6:B:2529:HOH:O	1.62	0.98
1:B:30:TYR:HE1	3:B:2501:SAM:HN61	1.12	0.98
1:A:245:ASP:HB3	1:A:246:ASN:HB2	1.48	0.96
1:B:136:GLN:CG	1:B:143:ILE:O	2.15	0.95
1:B:136:GLN:HG2	1:B:143:ILE:O	1.71	0.90
1:A:245:ASP:HB2	1:A:246:ASN:HB3	1.54	0.88
1:A:245:ASP:CB	1:A:246:ASN:CB	2.55	0.85
1:A:245:ASP:CB	1:A:246:ASN:HB3	2.07	0.85
1:A:165:ASN:HD21	1:A:192:ARG:HH11	1.25	0.84
1:A:245:ASP:HB3	1:A:246:ASN:CB	2.12	0.78
1:B:136:GLN:HG3	1:B:143:ILE:O	1.80	0.78
1:B:15:ASP:N	6:B:2521:HOH:O	2.15	0.78
1:B:30:TYR:CE1	3:B:2501:SAM:N6	2.56	0.73
1:A:71:ARG:HH11	1:A:102:THR:HG22	1.55	0.71
1:B:34:LYS:NZ	6:B:2510:HOH:O	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:ARG:CA	6:B:2521:HOH:O	2.44	0.66
3:B:2501:SAM:O3'	6:B:2525:HOH:O	2.15	0.64
1:B:73:THR:HG22	1:B:74:GLY:H	1.61	0.64
1:A:169:GLN:HE21	1:A:209:LYS:NZ	1.96	0.63
1:B:14:ARG:HA	6:B:2521:HOH:O	1.98	0.63
1:B:98:ASP:HB3	6:B:2509:HOH:O	1.98	0.62
1:A:165:ASN:HD21	1:A:192:ARG:NH1	1.96	0.61
1:B:301:LEU:HD22	1:B:305:PHE:CE1	2.36	0.60
1:B:280:PHE:O	1:B:281:ALA:HB2	2.04	0.57
1:B:169:GLN:H	1:B:173:ASN:HB2	1.68	0.57
1:A:169:GLN:HE21	1:A:209:LYS:HZ2	1.52	0.56
1:A:245:ASP:HB2	1:A:246:ASN:CB	2.26	0.55
1:A:297:THR:HG22	1:A:300:GLU:H	1.73	0.54
1:A:6:LYS:NZ	1:B:323:GLN:HE22	2.06	0.54
3:A:1501:SAM:O3'	6:A:1570:HOH:O	2.19	0.54
1:B:26:PHE:CE1	1:B:104:ASN:HB2	2.42	0.54
1:B:87:ILE:HD12	1:B:115:LEU:HD22	1.89	0.53
1:B:13:ILE:HG12	1:B:309:TRP:CD2	2.43	0.53
1:B:177:ILE:HA	1:B:193:PHE:CE2	2.44	0.53
1:B:14:ARG:O	1:B:265:THR:O	2.28	0.52
1:B:279:LEU:HD11	6:B:2533:HOH:O	2.09	0.52
1:B:30:TYR:O	1:B:30:TYR:CD1	2.64	0.51
1:B:205:TRP:CE3	1:B:256:VAL:HG22	2.47	0.50
1:B:30:TYR:O	1:B:30:TYR:CG	2.64	0.49
1:B:14:ARG:O	1:B:15:ASP:HB2	2.12	0.49
1:B:23:ARG:NE	6:B:2520:HOH:O	2.46	0.49
1:B:58:ILE:HD13	1:B:269:LEU:HD21	1.95	0.49
1:A:14:ARG:HD3	6:A:1594:HOH:O	2.13	0.48
1:B:134:LEU:O	1:B:138:ILE:HG13	2.14	0.48
1:B:14:ARG:O	1:B:15:ASP:CB	2.61	0.48
1:A:73:THR:OG1	3:A:1501:SAM:HG2	2.12	0.48
1:B:73:THR:CG2	3:B:2501:SAM:HG2	2.44	0.47
1:A:165:ASN:ND2	1:A:192:ARG:HH11	2.02	0.46
1:A:260:PHE:CZ	5:A:1502:DTU:O3	2.64	0.46
1:A:202:ASP:N	1:A:203:ASN:HA	2.30	0.46
6:A:1592:HOH:O	1:B:328:ARG:HG3	2.14	0.46
1:A:58:ILE:HD13	1:A:269:LEU:HD11	1.98	0.46
1:B:172:ILE:HG22	1:B:173:ASN:HD22	1.81	0.46
1:B:259:SER:HB3	1:B:318:ASP:OD1	2.15	0.46
1:A:47:ASN:HD22	1:A:47:ASN:H	1.64	0.45
1:B:24:CYS:O	1:B:27:ARG:NH1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:ARG:NE	6:A:1594:HOH:O	2.49	0.45
1:A:153:ASP:OD2	1:A:187:LYS:NZ	2.50	0.45
1:A:97:GLU:HG2	6:A:1596:HOH:O	2.17	0.45
1:A:266:ARG:CB	6:A:1598:HOH:O	2.31	0.44
1:B:61:VAL:CG1	1:B:302:LYS:HA	2.48	0.44
1:A:292:ILE:HG22	1:A:301:LEU:HD13	1.98	0.44
1:A:260:PHE:HZ	5:A:1502:DTU:O3	1.99	0.44
1:B:178:ILE:HD12	1:B:178:ILE:N	2.33	0.44
1:B:14:ARG:C	6:B:2521:HOH:O	2.50	0.44
1:B:133:THR:O	1:B:136:GLN:N	2.51	0.44
1:B:27:ARG:CZ	1:B:141:ARG:NH2	2.81	0.44
1:B:69:LYS:NZ	1:B:98:ASP:OD2	2.50	0.43
1:B:178:ILE:HD12	1:B:178:ILE:H	1.84	0.43
1:A:14:ARG:CD	6:A:1594:HOH:O	2.67	0.42
1:A:116:TYR:C	1:A:116:TYR:CD2	2.93	0.42
1:B:178:ILE:HB	1:B:179:PRO:HD3	2.01	0.42
1:B:205:TRP:CD2	1:B:256:VAL:HG22	2.54	0.42
1:B:224:PHE:HB3	1:B:226:ILE:HD12	2.02	0.41
1:B:232:LYS:NZ	6:B:2532:HOH:O	2.47	0.41
1:B:73:THR:HG22	3:B:2501:SAM:HG2	2.01	0.41
1:A:74:GLY:HA3	1:A:75:GLY:C	2.41	0.41
1:B:266:ARG:CD	6:B:2533:HOH:O	2.68	0.41
1:B:280:PHE:O	1:B:281:ALA:CB	2.68	0.41
1:A:58:ILE:HG21	1:A:269:LEU:HD11	2.03	0.40
1:B:111:HIS:O	1:B:115:LEU:HG	2.21	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	325/340 (96%)	309 (95%)	13 (4%)	3 (1%)	17 16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	324/340 (95%)	312 (96%)	6 (2%)	6 (2%)	8	5
All	All	649/680 (95%)	621 (96%)	19 (3%)	9 (1%)	11	8

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	VAL
1	A	246	ASN
1	B	15	ASP
1	B	174	ASP
1	B	36	VAL
1	B	281	ALA
1	B	295	GLY
1	B	315	ARG
1	A	209	LYS

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	291/302 (96%)	272 (94%)	19 (6%)	17	19
1	B	290/302 (96%)	263 (91%)	27 (9%)	9	8
All	All	581/604 (96%)	535 (92%)	46 (8%)	12	12

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	17	ARG
1	A	18	LEU
1	A	34	LYS
1	A	46	LYS
1	A	47	ASN
1	A	102	THR

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Mol	Chain	Res	Type
1	A	110	LYS
1	A	120	LEU
1	A	134	LEU
1	A	192	ARG
1	A	226	ILE
1	A	255	SER
1	A	258	GLN
1	A	282	THR
1	A	292	ILE
1	A	297	THR
1	A	299	GLU
1	A	315	ARG
1	B	13	ILE
1	B	20	VAL
1	B	34	LYS
1	B	35	GLU
1	B	47	ASN
1	B	68	LYS
1	B	71	ARG
1	B	81	ARG
1	B	83	LEU
1	B	101	LEU
1	B	120	LEU
1	B	134	LEU
1	B	173	ASN
1	B	192	ARG
1	B	197	MET
1	B	213	LYS
1	B	215	GLU
1	B	226	ILE
1	B	246	ASN
1	B	269	LEU
1	B	282	THR
1	B	292	ILE
1	B	301	LEU
1	B	303	GLU
1	B	315	ARG
1	B	320	ARG
1	B	328	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	47	ASN
1	A	91	ASN
1	A	113	GLN
1	A	165	ASN
1	A	169	GLN
1	A	203	ASN
1	B	111	HIS
1	B	136	GLN
1	B	169	GLN
1	B	173	ASN
1	B	222	GLN
1	B	323	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

9 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	$\# Z > 2$
4	SF4	B	2402	1	0,12,12	0.00	-	-		
3	SAM	B	2501	4	21,29,29	1.37	3 (14%)	18,42,42	2.00	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SAM	A	1501	4	21,29,29	1.24	2 (9%)	18,42,42	1.91	5 (27%)
5	DTU	A	1502	4	7,7,7	0.89	0	4,8,8	2.37	1 (25%)
4	SF4	A	1401	1,3	0,12,12	0.00	-	-		
2	SO4	B	2403	-	4,4,4	0.23	0	6,6,6	0.55	0
2	SO4	A	1403	-	4,4,4	0.31	0	6,6,6	1.12	0
4	SF4	B	2401	1,3	0,12,12	0.00	-	-		
4	SF4	A	1402	1,5	0,12,12	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	SAM	B	2501	4	-	2/8/33/33	0/3/3/3
3	SAM	A	1501	4	-	2/8/33/33	0/3/3/3
5	DTU	A	1502	4	-	4/8/8/8	-
4	SF4	A	1401	1,3	-	-	0/6/5/5
4	SF4	B	2402	1	-	-	0/6/5/5
4	SF4	B	2401	1,3	-	-	0/6/5/5
4	SF4	A	1402	1,5	-	-	0/6/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2501	SAM	C2-N3	4.52	1.39	1.32
3	A	1501	SAM	C2-N3	4.15	1.38	1.32
3	B	2501	SAM	O4'-C1'	2.50	1.44	1.41
3	B	2501	SAM	C2-N1	2.50	1.38	1.33
3	A	1501	SAM	C2-N1	2.40	1.38	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2501	SAM	N3-C2-N1	-6.35	118.75	128.68
3	A	1501	SAM	N3-C2-N1	-5.11	120.69	128.68
5	A	1502	DTU	C3-C4-S4	-4.27	102.04	114.47
3	A	1501	SAM	O4'-C1'-C2'	-4.27	100.69	106.93
3	A	1501	SAM	C5'-SD-CG	-2.88	96.06	103.40
3	B	2501	SAM	O4'-C4'-C5'	2.64	115.55	108.88
3	A	1501	SAM	O4'-C4'-C5'	2.28	114.65	108.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1501	SAM	C4-C5-N7	-2.15	107.16	109.40

There are no chirality outliers.

All (8) torsion outliers are listed below:

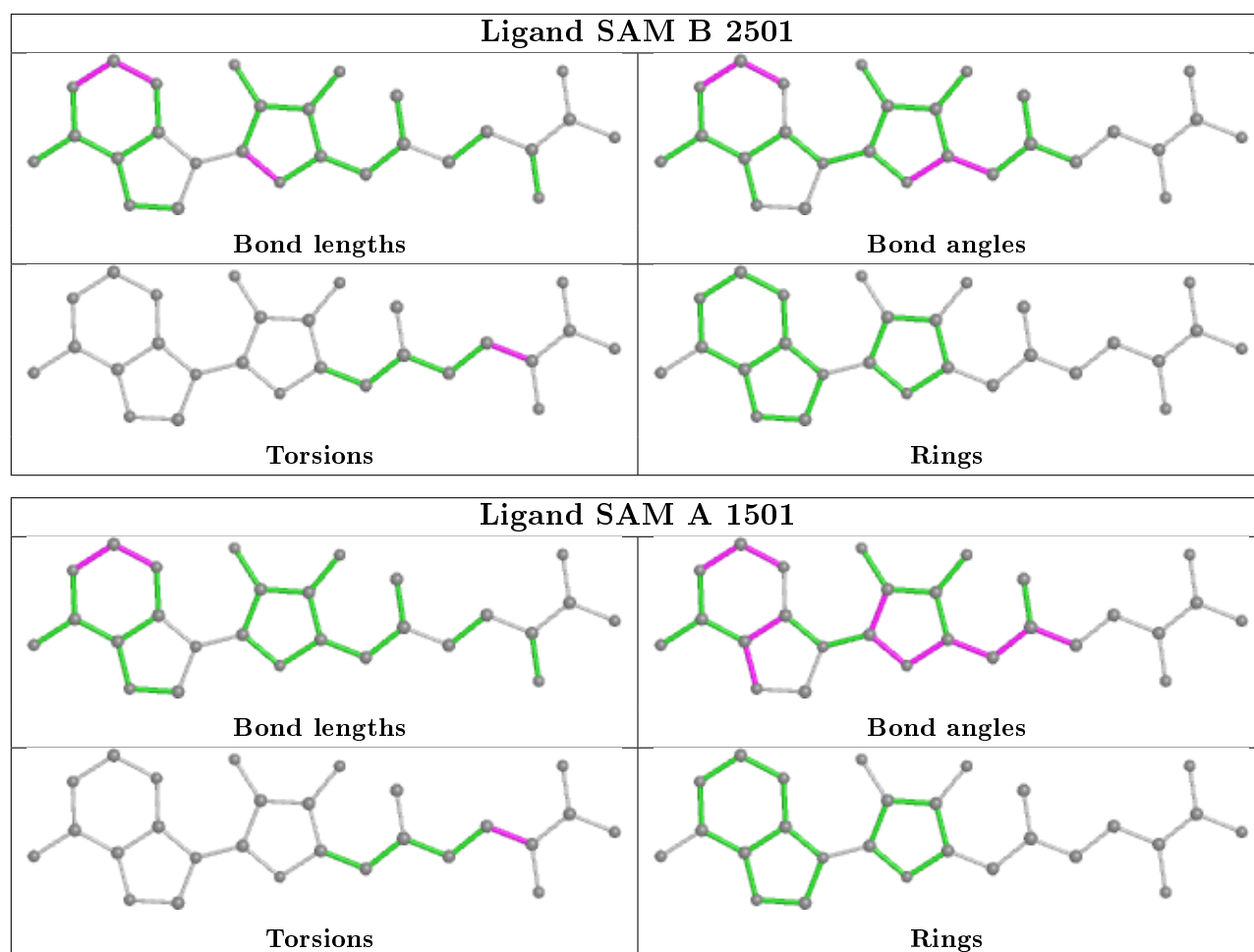
Mol	Chain	Res	Type	Atoms
3	B	2501	SAM	C-CA-CB-CG
3	A	1501	SAM	C-CA-CB-CG
5	A	1502	DTU	O2-C2-C3-C4
5	A	1502	DTU	C2-C3-C4-S4
5	A	1502	DTU	O3-C3-C4-S4
5	A	1502	DTU	O2-C2-C3-O3
3	A	1501	SAM	N-CA-CB-CG
3	B	2501	SAM	N-CA-CB-CG

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2501	SAM	5	0
3	A	1501	SAM	2	0
5	A	1502	DTU	2	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, 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	327/340 (96%)	0.63	16 (4%) 29 28	28, 41, 55, 62	0
1	B	326/340 (95%)	1.07	60 (18%) 1 1	29, 42, 54, 61	0
All	All	653/680 (96%)	0.85	76 (11%) 4 4	28, 41, 55, 62	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	30	TYR	9.4
1	B	283	VAL	7.2
1	B	41	PHE	6.8
1	B	282	THR	6.7
1	B	40	ASP	6.5
1	B	42	VAL	5.8
1	B	37	PHE	5.6
1	B	171	GLY	5.3
1	B	35	GLU	5.1
1	B	38	GLY	4.7
1	B	244	LYS	4.4
1	B	39	ASP	4.2
1	B	131	ASP	4.1
1	B	36	VAL	4.0
1	B	44	LEU	3.9
1	B	43	PHE	3.7
1	A	244	LYS	3.7
1	B	139	ASN	3.7
1	B	260	PHE	3.6
1	B	225	GLU	3.6
1	B	223	HIS	3.6
1	B	175	ASP	3.5
1	B	182	GLU	3.5
1	B	226	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	245	ASP	3.4
1	B	32	MET	3.3
1	A	329	GLN	3.3
1	B	34	LYS	3.3
1	B	47	ASN	3.3
1	B	134	LEU	3.3
1	B	193	PHE	3.2
1	B	284	ASP	3.2
1	B	94	ASP	3.2
1	B	81	ARG	3.2
1	A	245	ASP	3.1
1	B	135	PHE	3.1
1	B	170	LYS	3.0
1	A	226	ILE	3.0
1	A	201	ASN	2.9
1	B	136	GLN	2.9
1	B	183	TYR	2.9
1	A	246	ASN	2.8
1	B	221	GLU	2.8
1	B	266	ARG	2.7
1	B	202	ASP	2.6
1	B	242	ARG	2.6
1	B	280	PHE	2.6
1	B	45	PRO	2.5
1	B	140	ASN	2.5
1	A	178	ILE	2.5
1	B	295	GLY	2.5
1	A	219	MET	2.5
1	A	209	LYS	2.5
1	B	201	ASN	2.5
1	B	29	ASP	2.5
1	A	303	GLU	2.4
1	B	129	ALA	2.4
1	A	122	ARG	2.4
1	B	173	ASN	2.4
1	B	222	GLN	2.3
1	B	28	CYS	2.3
1	B	130	ILE	2.3
1	B	33	PRO	2.3
1	B	241	TYR	2.3
1	B	27	ARG	2.3
1	B	296	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	269	LEU	2.2
1	B	199	VAL	2.2
1	B	179	PRO	2.2
1	A	222	GLN	2.2
1	B	143	ILE	2.1
1	A	242	ARG	2.1
1	A	182	GLU	2.1
1	B	188	HIS	2.1
1	B	145	ALA	2.0
1	A	256	VAL	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 carbohydrates in this entry.

6.4 Ligands [i](#)

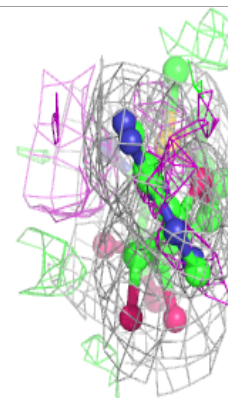
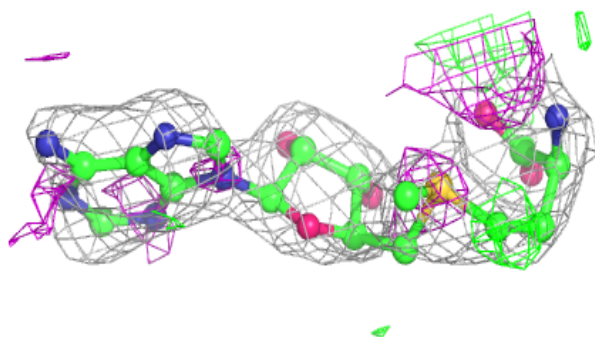
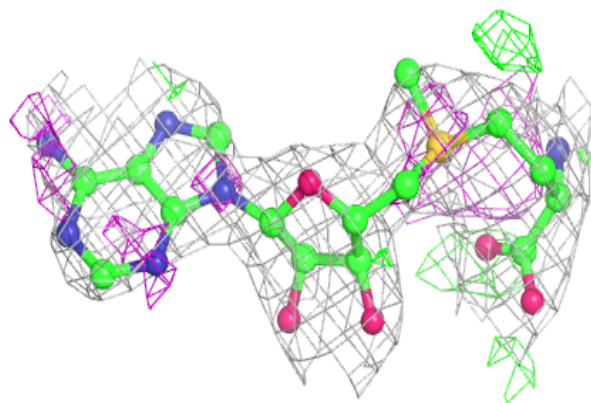
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	DTU	A	1502	8/8	0.84	0.24	77,87,88,95	0
3	SAM	B	2501	27/27	0.87	0.28	67,78,80,80	0
2	SO4	A	1403	5/5	0.87	0.22	70,72,76,79	0
2	SO4	B	2403	5/5	0.91	0.45	81,83,85,86	0
3	SAM	A	1501	27/27	0.92	0.14	54,71,75,75	0
4	SF4	B	2401	8/8	0.95	0.11	37,42,44,44	0
4	SF4	B	2402	8/8	0.97	0.04	35,37,40,45	0
4	SF4	A	1401	8/8	0.98	0.08	36,36,37,37	0
4	SF4	A	1402	8/8	0.98	0.07	35,38,38,44	0

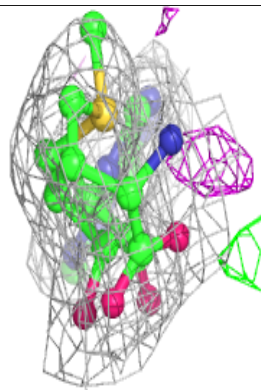
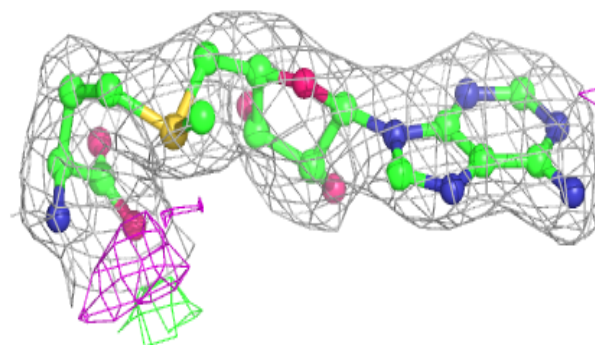
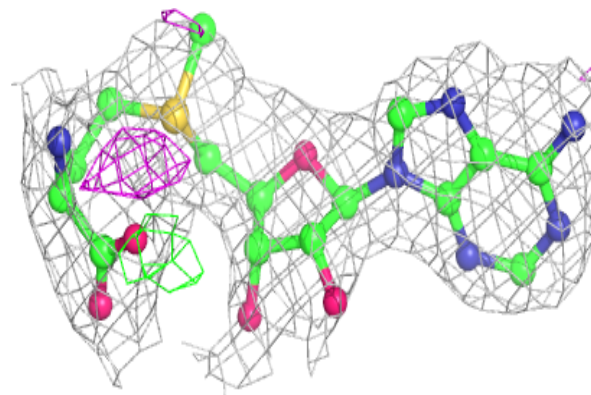
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SAM B 2501:

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

**Electron density around SAM A 1501:**

$2mF_o-DF_c$ (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.