



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:08 AM UTC

PDB ID : 6OX4 / pdb_00006ox4
Title : A SETD3 Mutant (N255A) in Complex with an Actin Peptide
Authors : Horton, J.R.; Dai, S.; Cheng, X.
Deposited on : 2019-05-13
Resolution : 2.29 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

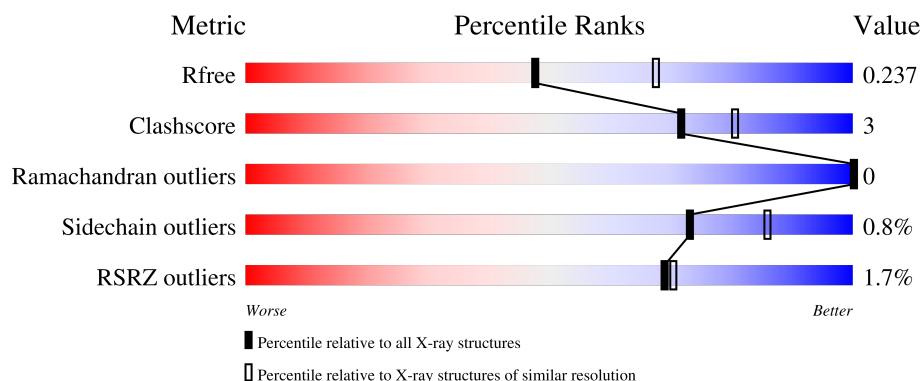
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	Y	15	13% 93% 7%
1	Z	15	13% 100%
2	A	599	% 74% 7% 19%
2	B	599	% 74% 6% 19%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8630 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 Actin Peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	Y	15	Total	C	N	O	0	0	0
			117	78	19	20			
1	Z	15	Total	C	N	O	0	0	0
			120	79	19	22			

- Molecule 2 is a protein called Actin-histidine N-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	483	Total	C	N	O	S	0	7	0
			3880	2487	653	723	17			
2	B	483	Total	C	N	O	S	0	7	0
			3873	2487	650	718	18			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q86TU7
A	-4	PRO	-	expression tag	UNP Q86TU7
A	-3	LEU	-	expression tag	UNP Q86TU7
A	-2	GLY	-	expression tag	UNP Q86TU7
A	-1	SER	-	expression tag	UNP Q86TU7
A	255	ALA	ASN	engineered mutation	UNP Q86TU7
B	-5	GLY	-	expression tag	UNP Q86TU7
B	-4	PRO	-	expression tag	UNP Q86TU7
B	-3	LEU	-	expression tag	UNP Q86TU7
B	-2	GLY	-	expression tag	UNP Q86TU7
B	-1	SER	-	expression tag	UNP Q86TU7
B	255	ALA	ASN	engineered mutation	UNP Q86TU7

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



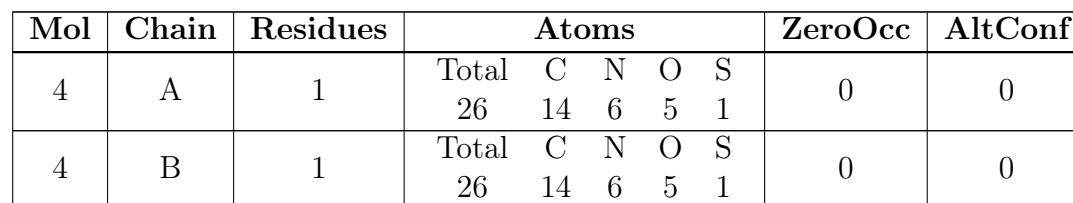
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	Y	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total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

Continued on next page...

Continued from previous page...

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

- Molecule 4 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).



- GOL
-
- The diagram shows the skeletal structure of 1,2,3-propanetriol (glycerol). The carbon chain is represented by a zigzag line with three vertices labeled C1, C2, and C3 in green. C1 is at the left end, C2 is in the middle, and C3 is at the right end. Each carbon is bonded to a hydroxyl group (OH) in red. The OH group on C1 is labeled O1 in green below it. The OH group on C2 is labeled O2 in green below it. The OH group on C3 is labeled O3 in green to its right. The entire structure is set against a light gray background with a white border.

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



Continued from previous page...

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

- Molecule 6 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	Y	3	Total	O	0	0
			3	3		
7	A	234	Total	O	0	0
			234	234		
7	Z	7	Total	O	0	0
			7	7		
7	B	190	Total	O	0	0
			190	190		

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.

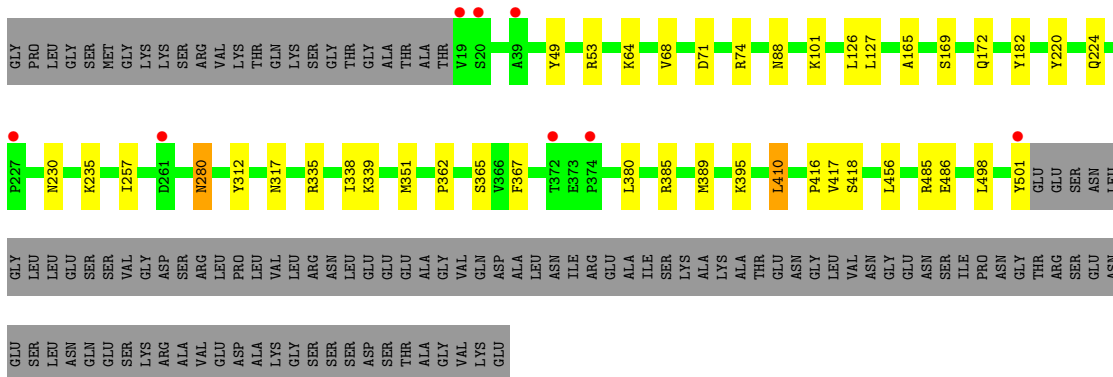
- Molecule 1: Actin Peptide



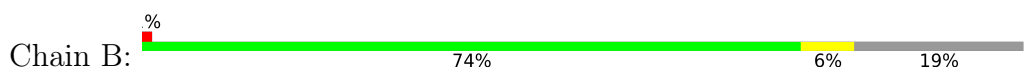
- Molecule 1: Actin Peptide



- Molecule 2: Actin-histidine N-methyltransferase



- Molecule 2: Actin-histidine N-methyltransferase



L160	A166	S169	Q172	Y218	F219	Y220	Q224	H228	A229	N230	L234	F238	E241	R244	C294	E373	P374	P375	R385	M389	V417	E470	K479	Y501	GLU	GLU	SER	ASN	LEU	GLY	LEU	LEU	GLU	SER	GLN	VAL	GLY	ASP	SER	ARG	LEU						
PRO	LEU	VAL	LEU	ARG	ASN	LEU	GLU	GLU	ALA	ALA	ASN	ILE	ARG	GLU	ALA	ILE	ILE	SER	LYS	ALA	LYS	ALA	THR	GLU	ASN	GLY	LEU	VAL	ASN	GLN	ASN	GLU	THR	ARG	SER	GLU	ASN	GLY	SER	LEU	LEU	ASN	GLN	SER	GLU	VAL	GLU
ASP	ALA	LYS	GLY	SER	SER	SER	ASP	THR	ALA	GLY	VAL	GLN	ASP	LEU	LYS	THR	GLY	LEU	VAL	ASN	GLY	ASN	ILE	PRO	ASN	GLY	THR	ARG	SER	GLU	ASN	GLY	SER	LEU	ASN	GLN	SER	LYS	ARG	ALA	VAL	GLU					

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	60.39Å 177.04Å 65.91Å 90.00° 92.50° 90.00°	Depositor
Resolution (Å)	36.73 – 2.29 36.73 – 2.29	Depositor EDS
% Data completeness (in resolution range)	94.7 (36.73-2.29) 94.6 (36.73-2.29)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.15.2_3472)	Depositor
R, R_{free}	0.188 , 0.236 0.189 , 0.237	Depositor DCC
R_{free} test set	2000 reflections (3.24%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.780	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.076 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8630	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SAH, ACT, EDO

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	Y	0.11	0/121	0.25	0/167
1	Z	0.11	0/124	0.28	0/171
2	A	0.15	0/3985	0.32	0/5406
2	B	0.14	0/3975	0.32	0/5393
All	All	0.14	0/8205	0.32	0/11137

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Y	117	0	102	1	0
1	Z	120	0	104	0	0
2	A	3880	0	3778	30	0
2	B	3873	0	3758	24	0
3	A	64	0	96	3	0
3	B	60	0	90	4	0
3	Y	4	0	6	0	0
4	A	26	0	19	2	0
4	B	26	0	19	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	18	0	24	4	0
6	A	8	0	6	1	0
7	A	234	0	0	2	0
7	B	190	0	0	0	0
7	Y	3	0	0	0	0
7	Z	7	0	0	0	0
All	All	8630	0	8002	53	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 3.

All (53) 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)
2:A:456:LEU:H	3:A:607:EDO:H22	1.59	0.67
2:B:169:SER:HB3	2:B:172:GLN:HG2	1.76	0.66
2:A:280:ASN:ND2	7:A:706:HOH:O	2.34	0.60
2:A:169:SER:HB3	2:A:172:GLN:HG2	1.83	0.60
2:A:351:MET:HE1	2:A:395:LYS:HG3	1.85	0.58
2:A:485:ARG:NH2	2:A:486:GLU:OE1	2.37	0.58
2:A:182:TYR:HA	5:A:619:GOL:H32	1.87	0.57
2:A:418:SER:HA	2:A:498:LEU:HD11	1.88	0.56
2:A:71:ASP:HA	3:B:611:EDO:H21	1.90	0.54
4:A:601:SAH:O2'	5:A:619:GOL:H2	2.07	0.54
1:Y:72:GLU:HG3	2:A:312:TYR:O	2.07	0.54
2:A:220:TYR:O	2:A:224:GLN:HG2	2.08	0.54
2:A:317:ASN:HB2	3:A:603:EDO:H22	1.91	0.53
2:A:230:ASN:HA	2:A:235:LYS:HD2	1.90	0.53
2:A:74:ARG:HH22	4:A:601:SAH:C	2.21	0.53
2:A:338:ILE:HA	5:A:620:GOL:H11	1.91	0.53
2:A:367:PHE:HA	6:A:621:ACT:H1	1.90	0.52
2:A:101:LYS:NZ	2:B:101:LYS:O	2.40	0.52
2:A:68:VAL:HG21	2:A:165:ALA:HA	1.92	0.51
2:B:244:ARG:HH22	3:B:613:EDO:H21	1.76	0.50
2:A:49:TYR:CZ	2:A:53:ARG:HD2	2.47	0.50
2:B:75:GLU:HA	2:B:78:PHE:CD2	2.48	0.49
2:B:389:MET:HE2	2:B:417:VAL:HG21	1.95	0.49
2:B:144:GLN:HG3	2:B:228:HIS:ND1	2.27	0.48
2:A:362:PRO:HG2	2:A:365:SER:HB2	1.96	0.47
2:A:410:LEU:HD12	2:A:410:LEU:HA	1.76	0.47
2:B:91:SER:HB3	2:B:121:TRP:CE2	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:101:LYS:HE3	2:B:101:LYS:HG3	1.98	0.45
2:B:417:VAL:HA	3:B:612:EDO:H12	1.98	0.45
2:A:385:ARG:O	2:A:389:MET:HG3	2.17	0.45
2:B:91:SER:HB3	2:B:121:TRP:CD2	2.51	0.45
2:A:88:ASN:HB2	2:A:126:LEU:HD21	1.99	0.44
2:B:88:ASN:O	2:B:123:PRO:HG2	2.17	0.44
2:B:373:GLU:HG2	2:B:375:PRO:HD3	2.00	0.44
2:B:470:GLU:N	3:B:608:EDO:H11	2.33	0.44
2:B:147:ILE:HD12	2:B:218:TYR:CE2	2.53	0.43
2:A:339:LYS:O	5:A:620:GOL:O3	2.27	0.43
2:A:416:PRO:HG2	2:A:498:LEU:HD22	2.00	0.43
2:B:68:VAL:HG21	2:B:165:ALA:HA	1.99	0.43
2:B:123:PRO:HD2	2:B:126:LEU:HD12	2.01	0.43
2:B:99:ASN:HB2	2:B:105:PHE:CZ	2.54	0.43
2:B:234:LEU:HB3	2:B:238:PHE:HB2	2.01	0.43
2:A:127:LEU:HD23	2:A:257:ILE:HD13	2.01	0.42
2:A:367:PHE:CG	2:A:380:LEU:HD13	2.54	0.42
2:B:385:ARG:O	2:B:389:MET:HG3	2.20	0.42
2:B:78:PHE:O	2:B:82:MET:HG2	2.20	0.42
2:A:389:MET:HE2	2:A:417:VAL:HG21	2.00	0.42
2:A:53:ARG:HB3	3:A:614:EDO:H21	2.01	0.42
2:A:335:ARG:NH1	7:A:710:HOH:O	2.37	0.41
2:B:241:GLU:CD	2:B:244:ARG:HH21	2.28	0.41
2:B:49:TYR:CZ	2:B:53:ARG:HD2	2.55	0.41
2:B:220:TYR:O	2:B:224:GLN:HG2	2.20	0.41
2:B:373:GLU:CD	2:B:374:PRO:HA	2.46	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	Y	13/15 (87%)	13 (100%)	0	0	100	100
1	Z	13/15 (87%)	12 (92%)	1 (8%)	0	100	100
2	A	488/599 (82%)	482 (99%)	6 (1%)	0	100	100
2	B	488/599 (82%)	487 (100%)	1 (0%)	0	100	100
All	All	1002/1228 (82%)	994 (99%)	8 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	Y	11/14 (79%)	11 (100%)	0	100	100
1	Z	12/14 (86%)	12 (100%)	0	100	100
2	A	413/520 (79%)	409 (99%)	4 (1%)	68	82
2	B	408/520 (78%)	405 (99%)	3 (1%)	76	87
All	All	844/1068 (79%)	837 (99%)	7 (1%)	73	86

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	64	LYS
2	A	280	ASN
2	A	410	LEU
2	A	501	TYR
2	B	25	LEU
2	B	160	LEU
2	B	479	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	254	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A	256	GLN
2	A	421	ASN
2	A	491	GLN
2	B	149	GLN
2	B	159	HIS

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](#)

39 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	$\# Z > 2$
5	GOL	A	620	-	5,5,5	0.94	0	5,5,5	1.07	0
3	EDO	B	611	-	3,3,3	0.45	0	2,2,2	0.32	0
3	EDO	B	605	-	3,3,3	0.44	0	2,2,2	0.35	0
3	EDO	B	607	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	A	606	-	3,3,3	0.41	0	2,2,2	0.44	0
3	EDO	B	616	-	3,3,3	0.49	0	2,2,2	0.13	0
3	EDO	A	610	-	3,3,3	0.44	0	2,2,2	0.35	0
6	ACT	A	621	-	3,3,3	0.81	0	3,3,3	1.39	0
3	EDO	Y	101	-	3,3,3	0.43	0	2,2,2	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GOL	A	618	-	5,5,5	0.96	0	5,5,5	1.06	0
3	EDO	B	612	-	3,3,3	0.44	0	2,2,2	0.31	0
3	EDO	B	603	-	3,3,3	0.42	0	2,2,2	0.44	0
4	SAH	A	601	-	27,28,28	1.08	2 (7%)	36,40,40	0.69	0
3	EDO	A	615	-	3,3,3	0.44	0	2,2,2	0.34	0
3	EDO	A	604	-	3,3,3	0.43	0	2,2,2	0.35	0
3	EDO	B	614	-	3,3,3	0.43	0	2,2,2	0.38	0
3	EDO	A	613	-	3,3,3	0.43	0	2,2,2	0.35	0
3	EDO	A	609	-	3,3,3	0.41	0	2,2,2	0.45	0
3	EDO	B	610	-	3,3,3	0.44	0	2,2,2	0.33	0
3	EDO	A	608	-	3,3,3	0.42	0	2,2,2	0.34	0
3	EDO	B	606	-	3,3,3	0.44	0	2,2,2	0.32	0
3	EDO	B	608	-	3,3,3	0.44	0	2,2,2	0.27	0
4	SAH	B	601	-	27,28,28	1.03	2 (7%)	36,40,40	0.72	0
3	EDO	A	617	-	3,3,3	0.46	0	2,2,2	0.29	0
3	EDO	B	615	-	3,3,3	0.44	0	2,2,2	0.36	0
5	GOL	A	619	-	5,5,5	0.92	0	5,5,5	1.11	0
3	EDO	A	611	-	3,3,3	0.45	0	2,2,2	0.39	0
3	EDO	A	612	-	3,3,3	0.42	0	2,2,2	0.42	0
3	EDO	A	602	-	3,3,3	0.42	0	2,2,2	0.43	0
3	EDO	B	613	-	3,3,3	0.43	0	2,2,2	0.34	0
3	EDO	A	616	-	3,3,3	0.42	0	2,2,2	0.33	0
3	EDO	B	602	-	3,3,3	0.44	0	2,2,2	0.38	0
6	ACT	A	622	-	3,3,3	0.76	0	3,3,3	1.37	0
3	EDO	A	603	-	3,3,3	0.40	0	2,2,2	0.54	0
3	EDO	A	605	-	3,3,3	0.45	0	2,2,2	0.37	0
3	EDO	B	604	-	3,3,3	0.42	0	2,2,2	0.43	0
3	EDO	A	607	-	3,3,3	0.44	0	2,2,2	0.32	0
3	EDO	B	609	-	3,3,3	0.43	0	2,2,2	0.40	0
3	EDO	A	614	-	3,3,3	0.42	0	2,2,2	0.40	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
5	GOL	A	620	-	-	2/4/4/4	-
3	EDO	B	611	-	-	0/1/1/1	-
3	EDO	B	605	-	-	0/1/1/1	-
3	EDO	B	607	-	-	1/1/1/1	-
3	EDO	A	606	-	-	0/1/1/1	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	616	-	-	0/1/1/1	-
3	EDO	A	610	-	-	0/1/1/1	-
3	EDO	Y	101	-	-	0/1/1/1	-
5	GOL	A	618	-	-	0/4/4/4	-
3	EDO	B	612	-	-	0/1/1/1	-
3	EDO	B	603	-	-	0/1/1/1	-
4	SAH	A	601	-	-	1/15/31/31	0/3/3/3
3	EDO	A	615	-	-	0/1/1/1	-
3	EDO	A	604	-	-	0/1/1/1	-
3	EDO	B	614	-	-	0/1/1/1	-
3	EDO	A	613	-	-	0/1/1/1	-
3	EDO	A	609	-	-	0/1/1/1	-
3	EDO	B	610	-	-	0/1/1/1	-
3	EDO	A	608	-	-	0/1/1/1	-
3	EDO	B	606	-	-	0/1/1/1	-
3	EDO	B	608	-	-	0/1/1/1	-
4	SAH	B	601	-	-	1/15/31/31	0/3/3/3
3	EDO	A	617	-	-	0/1/1/1	-
3	EDO	B	615	-	-	0/1/1/1	-
5	GOL	A	619	-	-	4/4/4/4	-
3	EDO	A	611	-	-	0/1/1/1	-
3	EDO	A	612	-	-	0/1/1/1	-
3	EDO	A	602	-	-	0/1/1/1	-
3	EDO	B	613	-	-	0/1/1/1	-
3	EDO	A	616	-	-	0/1/1/1	-
3	EDO	B	602	-	-	1/1/1/1	-
3	EDO	A	603	-	-	0/1/1/1	-
3	EDO	A	605	-	-	0/1/1/1	-
3	EDO	B	604	-	-	0/1/1/1	-
3	EDO	A	607	-	-	0/1/1/1	-
3	EDO	B	609	-	-	0/1/1/1	-
3	EDO	A	614	-	-	0/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	SAH	C8-N9	2.93	1.42	1.37
4	B	601	SAH	C8-N9	2.54	1.41	1.37
4	A	601	SAH	C5-C4	2.22	1.43	1.39
4	B	601	SAH	C5-C4	2.03	1.42	1.39

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

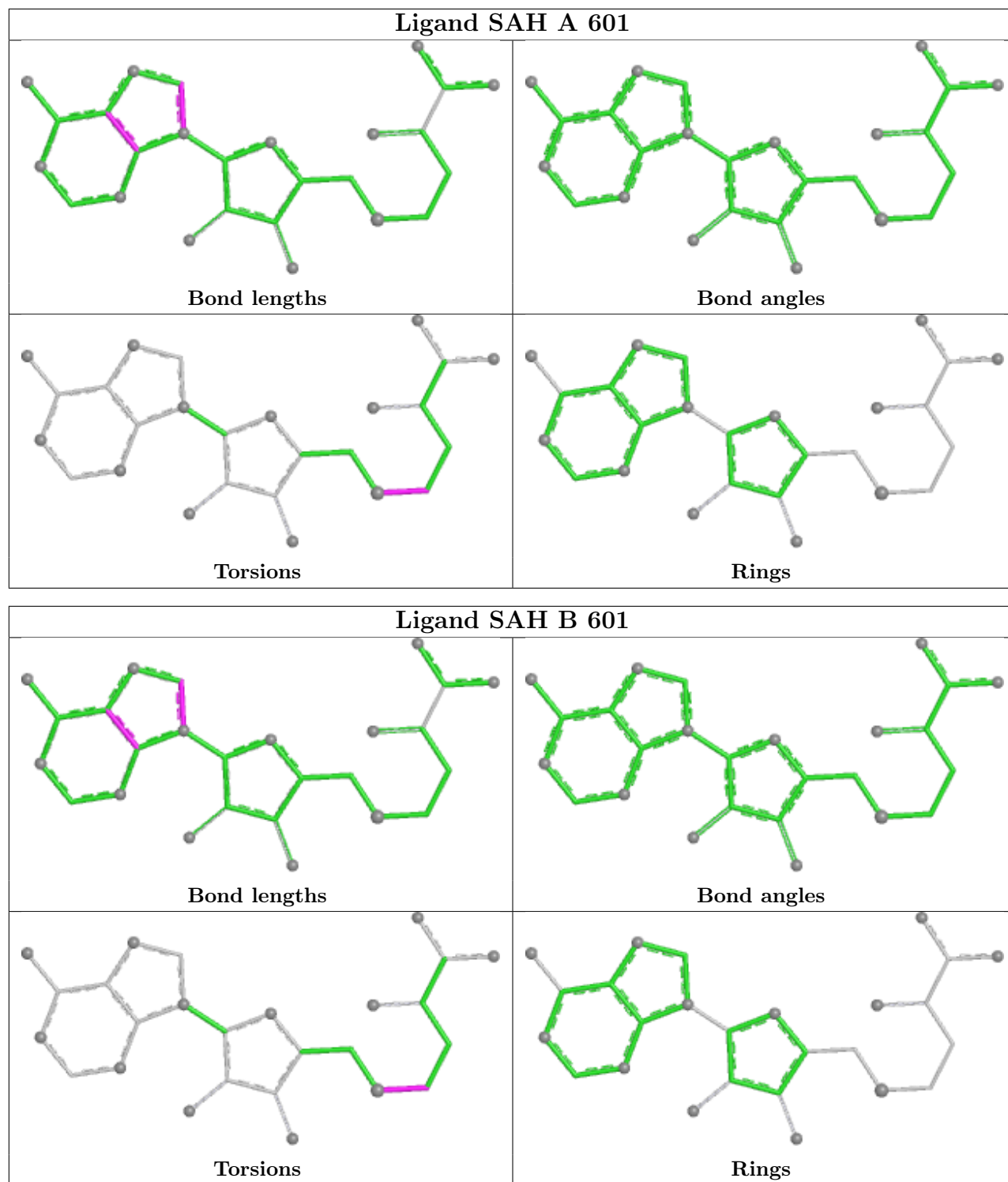
Mol	Chain	Res	Type	Atoms
5	A	619	GOL	O1-C1-C2-C3
5	A	620	GOL	C1-C2-C3-O3
5	A	620	GOL	O2-C2-C3-O3
5	A	619	GOL	C1-C2-C3-O3
5	A	619	GOL	O1-C1-C2-O2
5	A	619	GOL	O2-C2-C3-O3
4	B	601	SAH	CB-CG-SD-C5'
4	A	601	SAH	CB-CG-SD-C5'
3	B	602	EDO	O1-C1-C2-O2
3	B	607	EDO	O1-C1-C2-O2

There are no ring outliers.

11 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	620	GOL	2	0
3	B	611	EDO	1	0
6	A	621	ACT	1	0
3	B	612	EDO	1	0
4	A	601	SAH	2	0
3	B	608	EDO	1	0
5	A	619	GOL	2	0
3	B	613	EDO	1	0
3	A	603	EDO	1	0
3	A	607	EDO	1	0
3	A	614	EDO	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 ⓘ

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	Y	15/15 (100%)	0.74	2 (13%) 7 8	34, 40, 76, 86	0
1	Z	15/15 (100%)	0.68	2 (13%) 7 8	37, 51, 76, 88	0
2	A	483/599 (80%)	0.07	8 (1%) 69 70	15, 37, 69, 97	7 (1%)
2	B	483/599 (80%)	0.10	5 (1%) 79 80	15, 39, 71, 97	7 (1%)
All	All	996/1228 (81%)	0.10	17 (1%) 69 70	15, 39, 71, 97	14 (1%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	501	TYR	4.7
2	B	19	VAL	3.8
2	A	39	ALA	3.5
1	Y	80	ASP	3.4
1	Y	66	THR	3.2
2	A	372	THR	3.2
2	B	501	TYR	3.0
2	B	294[A]	CYS	2.8
2	B	230	ASN	2.6
2	A	19	VAL	2.4
1	Z	66	THR	2.4
2	A	261	ASP	2.2
1	Z	80	ASP	2.1
2	A	20	SER	2.1
2	B	373	GLU	2.1
2	A	227	PRO	2.0
2	A	374	PRO	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 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.

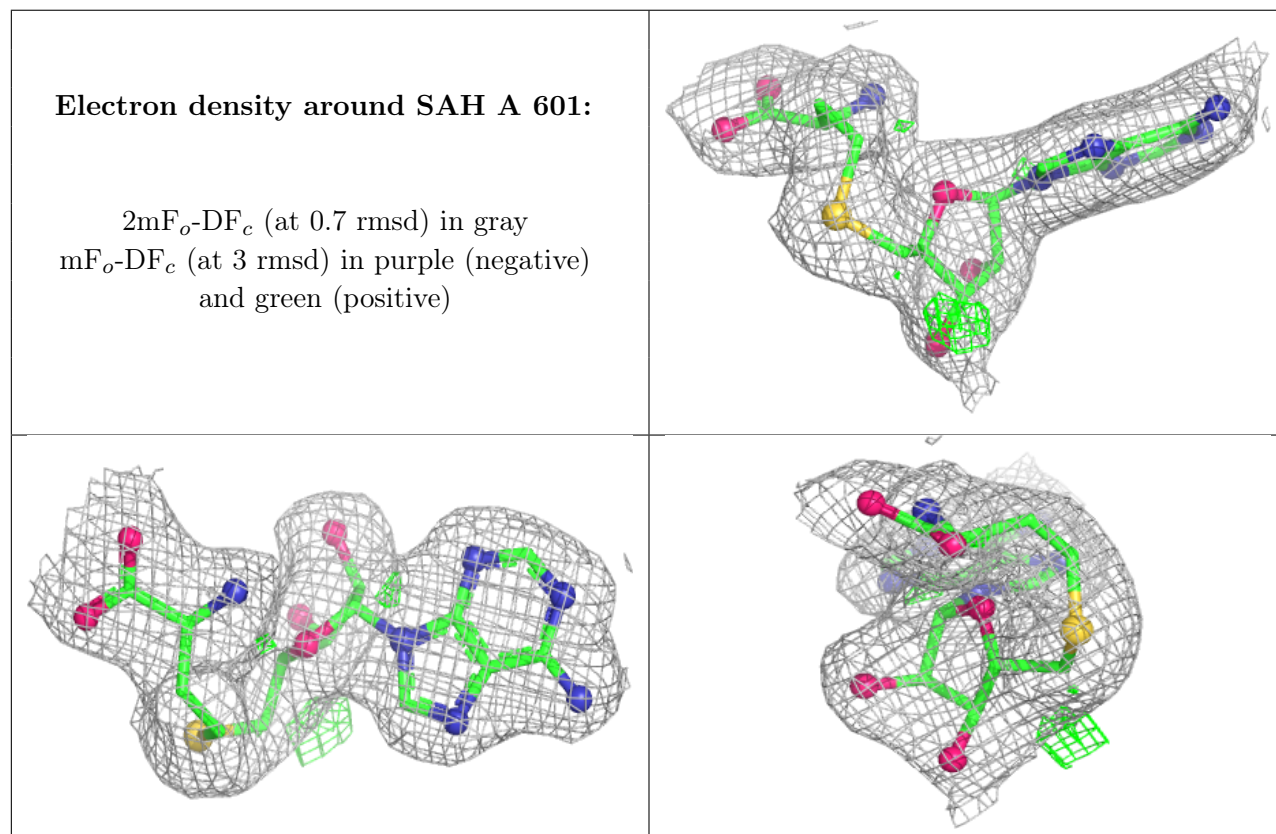
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	EDO	A	617	4/4	0.72	0.21	54,60,62,63	0
3	EDO	B	615	4/4	0.72	0.15	59,61,63,64	0
3	EDO	Y	101	4/4	0.74	0.20	59,63,63,65	0
3	EDO	A	610	4/4	0.75	0.16	71,72,74,75	0
3	EDO	A	613	4/4	0.76	0.16	56,60,64,68	0
3	EDO	B	611	4/4	0.78	0.23	57,60,63,64	0
3	EDO	B	613	4/4	0.79	0.20	65,72,73,75	0
3	EDO	B	607	4/4	0.79	0.17	69,70,71,71	0
3	EDO	B	614	4/4	0.81	0.19	72,73,74,74	0
3	EDO	B	609	4/4	0.81	0.15	70,72,73,74	0
3	EDO	A	602	4/4	0.82	0.17	72,73,73,74	0
3	EDO	A	604	4/4	0.83	0.20	75,76,78,81	0
5	GOL	A	618	6/6	0.83	0.18	65,75,77,77	0
3	EDO	B	605	4/4	0.84	0.21	77,78,79,79	0
3	EDO	A	603	4/4	0.84	0.28	62,63,64,65	0
3	EDO	B	602	4/4	0.85	0.16	58,60,61,61	0
3	EDO	B	603	4/4	0.85	0.17	57,57,61,62	0
3	EDO	A	608	4/4	0.86	0.17	60,62,66,71	0
3	EDO	B	608	4/4	0.86	0.17	50,53,56,61	0
6	ACT	A	621	4/4	0.87	0.14	54,59,61,67	0
3	EDO	B	612	4/4	0.88	0.16	67,67,68,68	0
3	EDO	A	605	4/4	0.88	0.15	66,68,69,70	0
5	GOL	A	620	6/6	0.89	0.22	46,52,61,65	0
3	EDO	A	609	4/4	0.89	0.15	44,52,54,60	0
3	EDO	A	615	4/4	0.90	0.13	43,48,50,55	0
6	ACT	A	622	4/4	0.90	0.12	52,54,58,61	0
3	EDO	A	612	4/4	0.91	0.13	59,61,64,65	0
5	GOL	A	619	6/6	0.91	0.15	46,52,54,54	0
3	EDO	A	607	4/4	0.91	0.15	54,62,67,76	0
3	EDO	A	606	4/4	0.91	0.15	66,66,67,68	0
3	EDO	B	616	4/4	0.91	0.12	30,40,42,44	0
3	EDO	B	604	4/4	0.92	0.10	58,58,58,58	0

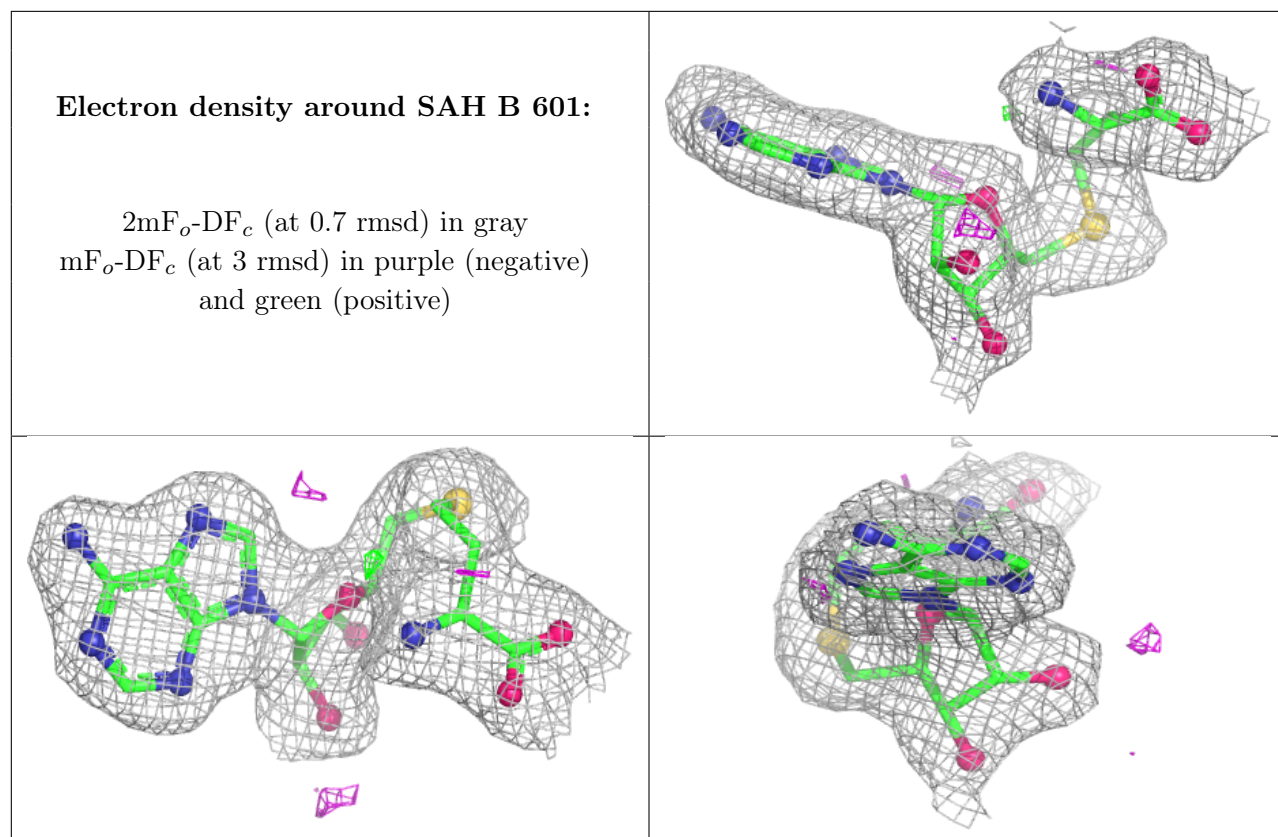
Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	B	610	4/4	0.93	0.11	55,57,58,60	0
3	EDO	B	606	4/4	0.93	0.11	37,39,40,40	0
3	EDO	A	614	4/4	0.93	0.11	59,61,61,65	0
3	EDO	A	616	4/4	0.94	0.09	42,46,47,49	0
3	EDO	A	611	4/4	0.95	0.12	55,56,57,58	0
4	SAH	A	601	26/26	0.96	0.07	16,22,32,42	0
4	SAH	B	601	26/26	0.97	0.06	16,23,33,33	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.