



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 05:00 PM BST

PDB ID : 4WXX
Title : The crystal structure of human DNMT1(351-1600)
Authors : Zhang, Z.M.; Song, J.
Deposited on : 2014-11-14
Resolution : 2.62 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 : 2.13.1
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) : 2.13.1

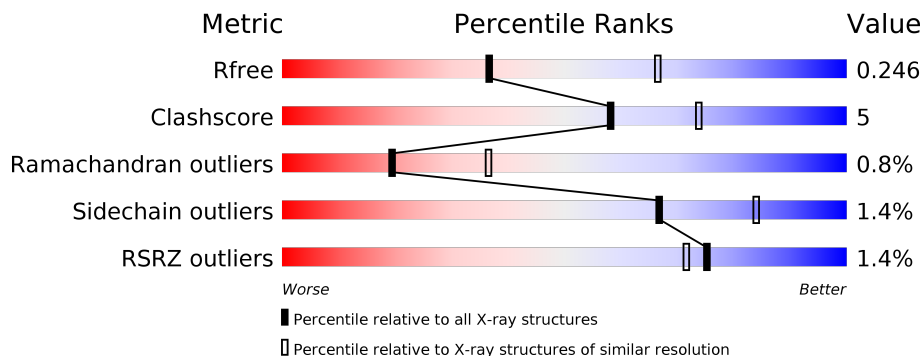
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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	1256	 % 80% 12% • 7%
1	B	1256	 % 82% 11% • 6%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 19035 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 DNA (cytosine-5)-methyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1170	9159	5800	1597	1697	65	0	0	0
1	B	1178	9177	5814	1595	1704	64	0	0	0

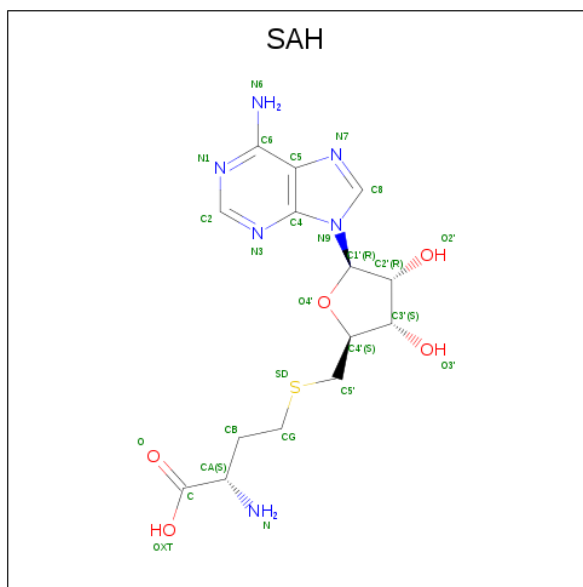
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	350	SER	-	expression tag	UNP P26358
A	1601	LEU	-	expression tag	UNP P26358
A	1602	THR	-	expression tag	UNP P26358
A	1603	ARG	-	expression tag	UNP P26358
A	1604	VAL	-	expression tag	UNP P26358
A	1605	TRP	-	expression tag	UNP P26358
B	350	SER	-	expression tag	UNP P26358
B	1601	LEU	-	expression tag	UNP P26358
B	1602	THR	-	expression tag	UNP P26358
B	1603	ARG	-	expression tag	UNP P26358
B	1604	VAL	-	expression tag	UNP P26358
B	1605	TRP	-	expression tag	UNP P26358

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	5	Total	Zn	0	0
			5	5		
2	A	5	Total	Zn	0	0
			5	5		

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).



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

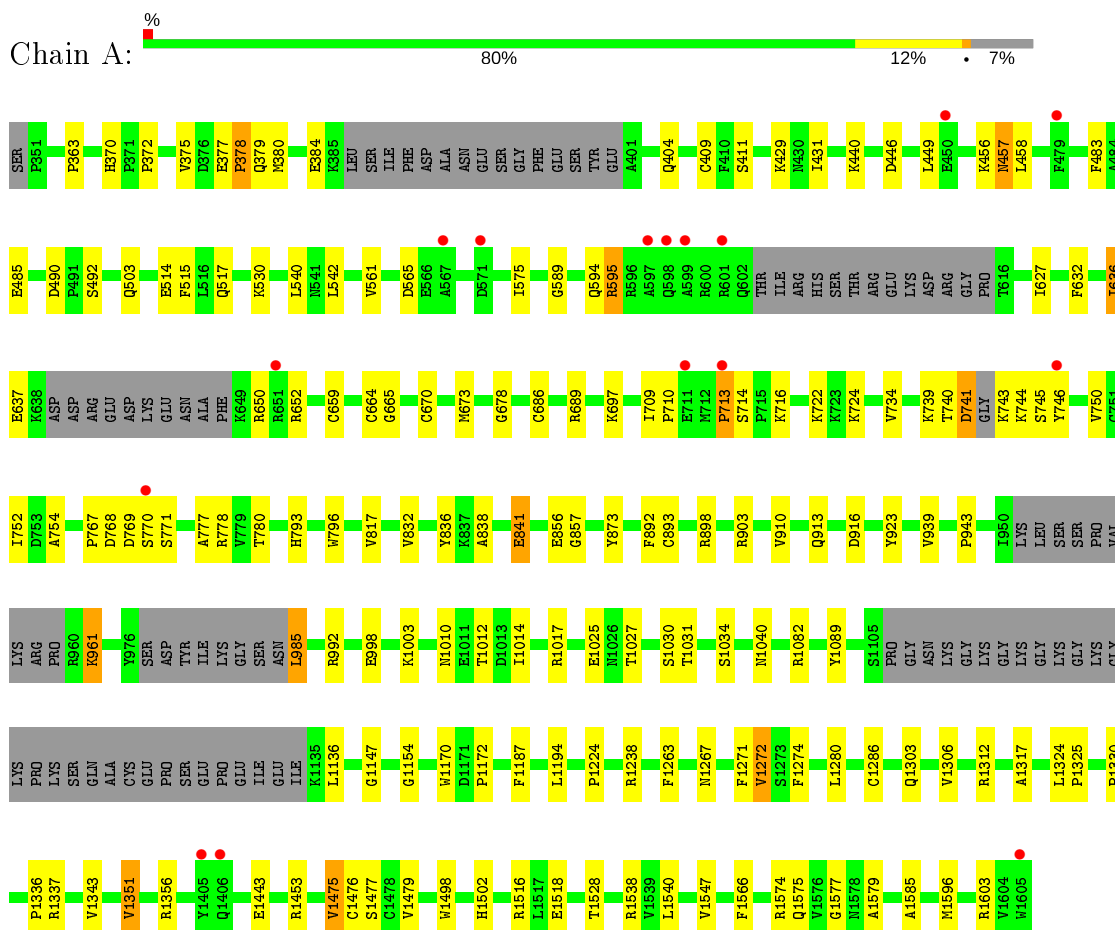
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	311	311	311	0	0
4	B	326	326	326	0	0

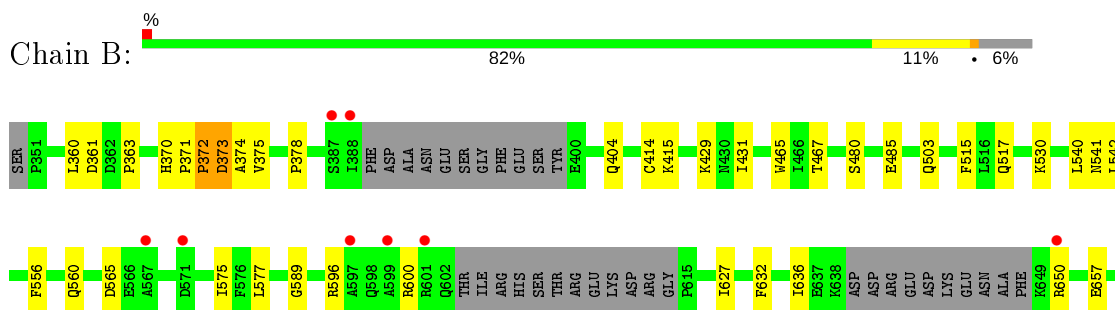
3 Residue-property plots [i](#)

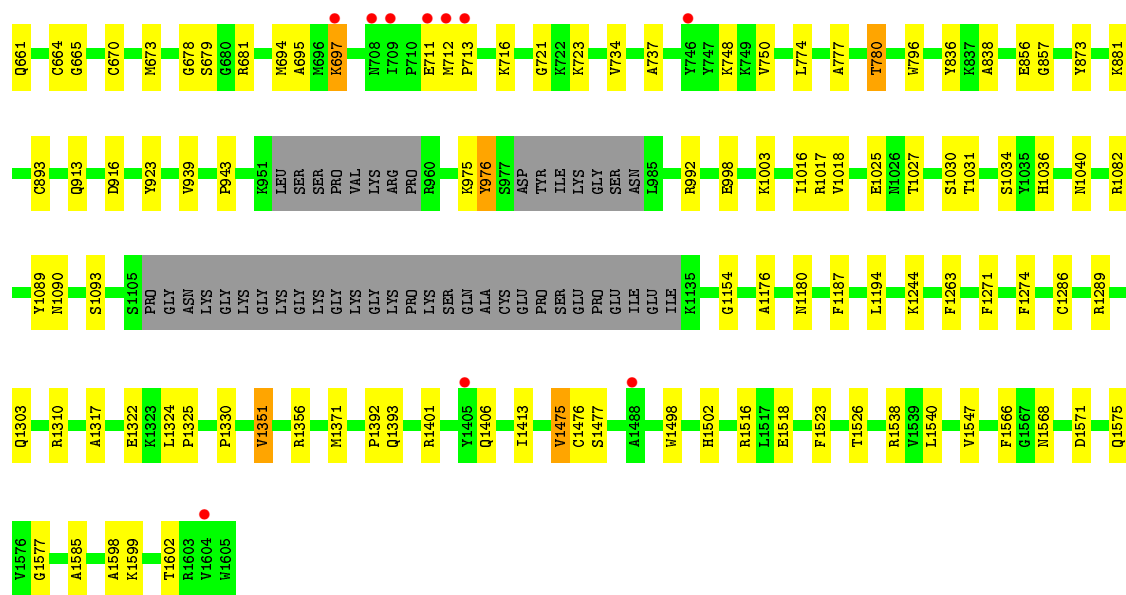
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: DNA (cytosine-5)-methyltransferase 1



- Molecule 1: DNA (cytosine-5)-methyltransferase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	138.57Å 138.57Å 221.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.22 – 2.62 48.21 – 2.62	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.22-2.62) 93.4 (48.21-2.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 2.61Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.205 , 0.245 0.209 , 0.246	Depositor DCC
R_{free} test set	6104 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	41.9	Xtrriage
Anisotropy	0.206	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.477 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	19035	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.23	0/9377	0.42	1/12692 (0.0%)
1	B	0.23	0/9399	0.42	0/12732
All	All	0.23	0/18776	0.42	1/25424 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	449	LEU	CA-CB-CG	8.20	134.16	115.30

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	A	9159	0	8847	96	0
1	B	9177	0	8824	76	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	26	0	19	2	0
3	B	26	0	19	1	0
4	A	311	0	0	6	0
4	B	326	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	19035	0	17709	173	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 5.

All (173) 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:740:THR:C	1:A:741:ASP:OD1	1.91	1.09
1:A:739:LYS:HE2	1:A:741:ASP:OD2	1.84	0.77
1:A:741:ASP:N	1:A:741:ASP:OD1	2.21	0.73
1:A:744:LYS:O	1:A:746:TYR:CE2	2.42	0.73
1:A:1147:GLY:HA3	3:A:1706:SAH:HN1	1.56	0.71
1:A:734:VAL:HB	1:A:750:VAL:HB	1.75	0.69
1:A:985:LEU:HD11	1:A:1337:ARG:HB3	1.76	0.68
1:A:1272:VAL:HG22	1:A:1280:LEU:HD22	1.77	0.67
1:A:1263:PHE:HB3	1:A:1317:ALA:HB3	1.77	0.66
1:B:1263:PHE:HB3	1:B:1317:ALA:HB3	1.78	0.65
1:B:780:THR:HG21	1:B:893:CYS:HB2	1.77	0.65
1:A:716:LYS:N	1:A:716:LYS:HD2	2.13	0.64
1:B:1040:ASN:ND2	1:B:1082:ARG:O	2.30	0.64
1:B:503:GLN:HB3	1:B:540:LEU:HD21	1.81	0.63
1:A:713:PRO:HG2	1:A:716:LYS:NZ	2.13	0.62
1:B:694:MET:HA	1:B:697:LYS:HD3	1.80	0.62
1:B:1176:ALA:O	1:B:1180:ASN:ND2	2.32	0.62
1:A:724:LYS:NZ	1:A:768:ASP:OD1	2.24	0.62
1:B:734:VAL:HB	1:B:750:VAL:HB	1.82	0.61
1:B:694:MET:HG3	1:B:697:LYS:NZ	2.16	0.61
1:B:414:CYS:SG	1:B:415:LYS:N	2.74	0.60
1:A:1040:ASN:ND2	1:A:1082:ARG:O	2.35	0.60
1:B:372:PRO:O	1:B:373:ASP:HB2	2.01	0.60
1:B:1392:PRO:HB3	1:B:1401:ARG:HD2	1.85	0.58
1:A:664:CYS:SG	1:A:665:GLY:N	2.77	0.57
1:A:561:VAL:HG13	1:A:575:ILE:HG23	1.86	0.57
1:A:741:ASP:O	1:A:744:LYS:HA	2.04	0.57
1:B:673:MET:O	1:B:678:GLY:N	2.29	0.56
1:A:370:HIS:HB2	1:A:372:PRO:HB3	1.86	0.56
1:A:713:PRO:HG2	1:A:716:LYS:HZ1	1.70	0.56
1:A:770:SER:OG	1:A:771:SER:N	2.39	0.56
1:A:780:THR:OG1	1:A:892:PHE:O	2.23	0.56
1:A:985:LEU:HD13	1:A:1336:PRO:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1579:ALA:HA	3:A:1706:SAH:HA	1.88	0.56
1:B:721:GLY:O	1:B:723:LYS:NZ	2.38	0.56
1:B:404:GLN:HG2	1:B:485:GLU:HB2	1.88	0.56
1:A:650:ARG:HD3	1:A:697:LYS:HB3	1.87	0.55
1:B:465:TRP:HE1	1:B:467:THR:HG22	1.70	0.55
1:B:657:GLU:O	1:B:661:GLN:HG2	2.06	0.55
1:A:411:SER:OG	1:A:492:SER:OG	2.24	0.54
1:B:627:ILE:HD13	1:B:1286:CYS:HA	1.89	0.54
1:B:1244:LYS:NZ	4:B:2106:HOH:O	2.38	0.53
1:A:1574:ARG:NH2	4:A:1863:HOH:O	2.41	0.53
1:A:716:LYS:H	1:A:716:LYS:HD2	1.72	0.53
1:B:1566:PHE:O	1:B:1575:GLN:NE2	2.38	0.53
1:B:465:TRP:NE1	1:B:467:THR:HG22	2.23	0.53
1:A:379:GLN:HE22	1:A:483:PHE:HB3	1.72	0.53
1:A:744:LYS:O	1:A:746:TYR:CD2	2.60	0.53
1:A:1010:ASN:OD1	1:A:1012:THR:OG1	2.23	0.53
1:B:998:GLU:HB2	1:B:1017:ARG:HB3	1.91	0.53
1:A:780:THR:HG21	1:A:893:CYS:HB2	1.92	0.52
1:B:1310:ARG:HE	1:B:1526:THR:HG22	1.74	0.52
1:B:540:LEU:HB3	1:B:542:LEU:HD12	1.90	0.52
1:A:722:LYS:HE3	1:A:768:ASP:HB3	1.92	0.51
1:B:711:GLU:HA	1:B:712:MET:O	2.10	0.51
1:B:943:PRO:HA	1:B:992:ARG:HG2	1.91	0.51
1:B:1324:LEU:HD12	1:B:1325:PRO:HD2	1.92	0.51
1:A:910:VAL:HG23	1:A:1014:ILE:HG12	1.93	0.51
1:B:916:ASP:OD1	1:B:1003:LYS:NZ	2.38	0.51
1:A:1238:ARG:NH1	4:A:2061:HOH:O	2.44	0.50
1:A:780:THR:HG22	1:A:793:HIS:HB3	1.93	0.50
1:B:1526:THR:OG1	1:B:1577:GLY:O	2.29	0.50
1:A:1566:PHE:O	1:A:1575:GLN:NE2	2.42	0.50
1:B:1187:PHE:CG	1:B:1194:LEU:HD21	2.47	0.50
1:A:1312:ARG:NH1	4:A:1986:HOH:O	2.44	0.50
1:A:913:GLN:HA	1:A:923:TYR:HD1	1.77	0.49
1:B:665:GLY:HA2	1:B:670:CYS:HB3	1.94	0.49
1:A:1271:PHE:HA	1:A:1274:PHE:CD2	2.47	0.49
1:A:1324:LEU:HD12	1:A:1325:PRO:HD2	1.94	0.49
1:A:530:LYS:NZ	4:A:2056:HOH:O	2.45	0.49
1:A:636:ILE:HG13	1:A:637:GLU:N	2.28	0.49
1:B:1025:GLU:HG2	1:B:1034:SER:HB3	1.94	0.49
1:A:515:PHE:CD1	1:A:530:LYS:HG3	2.47	0.49
1:B:1516:ARG:HA	1:B:1540:LEU:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1187:PHE:CG	1:A:1194:LEU:HD21	2.48	0.49
1:B:873:TYR:HA	1:B:1351:VAL:O	2.12	0.48
1:A:540:LEU:HB3	1:A:542:LEU:HD12	1.94	0.48
1:B:589:GLY:HA3	1:B:1502:HIS:CE1	2.49	0.48
1:A:1443:GLU:HG2	1:A:1453:ARG:HA	1.96	0.48
1:B:541:ASN:OD1	1:B:541:ASN:N	2.36	0.48
1:B:975:LYS:O	1:B:976:TYR:HB2	2.14	0.48
1:A:503:GLN:HB3	1:A:540:LEU:HD21	1.96	0.48
1:A:1025:GLU:HG3	1:A:1034:SER:HB3	1.95	0.48
1:A:778:ARG:NH1	4:A:1976:HOH:O	2.33	0.48
1:A:943:PRO:HA	1:A:992:ARG:HG2	1.97	0.47
1:A:873:TYR:HA	1:A:1351:VAL:O	2.15	0.47
1:A:589:GLY:HA3	1:A:1502:HIS:CE1	2.49	0.47
1:A:1224:PRO:O	1:A:1267:ASN:ND2	2.47	0.47
1:A:404:GLN:HG2	1:A:485:GLU:HB2	1.96	0.47
1:A:1154:GLY:HA3	1:A:1585:ALA:HB3	1.96	0.47
1:A:1516:ARG:HA	1:A:1540:LEU:HB2	1.96	0.47
1:A:380:MET:HA	1:A:384:GLU:HB2	1.96	0.47
1:B:370:HIS:HA	1:B:371:PRO:HD3	1.77	0.47
1:B:627:ILE:HD11	1:B:1289:ARG:HG2	1.97	0.46
1:A:777:ALA:HB2	1:A:796:TRP:CE3	2.50	0.46
1:B:694:MET:HG3	1:B:697:LYS:HZ1	1.80	0.46
1:A:1475:VAL:HG13	1:A:1498:TRP:NE1	2.31	0.46
1:B:713:PRO:HB2	1:B:716:LYS:HZ1	1.81	0.46
1:B:515:PHE:CD1	1:B:530:LYS:HG3	2.51	0.46
1:A:1476:CYS:SG	1:A:1477:SER:N	2.89	0.46
1:B:1025:GLU:OE1	4:B:1906:HOH:O	2.21	0.46
1:B:429:LYS:O	1:B:431:ILE:N	2.43	0.46
1:B:1154:GLY:HA3	1:B:1585:ALA:HB3	1.99	0.45
1:A:409:CYS:N	1:A:490:ASP:O	2.50	0.45
1:A:856:GLU:HA	1:A:857:GLY:HA2	1.68	0.45
1:B:1476:CYS:SG	1:B:1477:SER:N	2.90	0.45
1:B:360:LEU:HA	1:B:361:ASP:HA	1.57	0.45
1:B:1027:THR:HG23	1:B:1089:TYR:CE1	2.52	0.45
1:A:1528:THR:HG22	1:A:1577:GLY:HA3	1.97	0.45
1:A:594:GLN:O	1:A:595:ARG:HG2	2.17	0.45
1:B:1598:ALA:O	1:B:1602:THR:HB	2.17	0.45
1:A:1518:GLU:OE2	1:A:1538:ARG:NH2	2.48	0.44
1:B:1568:ASN:ND2	1:B:1571:ASP:OD2	2.51	0.44
1:A:514:GLU:HA	1:A:517:GLN:HE21	1.82	0.44
1:A:752:ILE:HG22	1:A:754:ALA:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1272:VAL:HG11	1:A:1343:VAL:HG22	1.99	0.44
1:A:903:ARG:HA	1:A:903:ARG:HD3	1.77	0.44
1:A:1303:GLN:HB3	1:A:1330:PRO:HB3	1.98	0.44
1:A:652:ARG:HB2	1:A:659:CYS:SG	2.58	0.44
1:B:1016:ILE:HG22	1:B:1018:VAL:HG23	2.00	0.44
1:A:743:LYS:C	1:A:745:SER:N	2.69	0.44
1:B:1030:SER:OG	1:B:1031:THR:N	2.50	0.44
1:B:1036:HIS:ND1	1:B:1393:GLN:O	2.50	0.44
3:B:1706:SAH:HN1	3:B:1706:SAH:HG2	1.58	0.44
1:B:1090:ASN:HB3	1:B:1093:SER:HB3	2.00	0.44
1:A:740:THR:O	1:A:741:ASP:OD1	2.30	0.44
1:B:650:ARG:HB3	1:B:697:LYS:NZ	2.33	0.43
1:B:913:GLN:HG2	1:B:923:TYR:CE1	2.53	0.43
1:A:429:LYS:HG2	1:A:431:ILE:HG13	2.00	0.43
1:A:665:GLY:HA2	1:A:670:CYS:HB3	2.00	0.43
1:A:565:ASP:OD2	1:A:575:ILE:HG22	2.18	0.43
1:B:664:CYS:SG	1:B:665:GLY:N	2.91	0.43
1:A:1027:THR:HG23	1:A:1089:TYR:CE1	2.54	0.43
1:A:627:ILE:HD13	1:A:1286:CYS:HA	2.00	0.43
1:B:1475:VAL:HG13	1:B:1498:TRP:NE1	2.33	0.43
1:B:1303:GLN:HB3	1:B:1330:PRO:HB3	1.99	0.43
1:B:1330:PRO:HD2	1:B:1356:ARG:HB2	2.01	0.43
1:B:465:TRP:HZ3	1:B:480:SER:HB3	1.83	0.43
1:B:632:PHE:O	1:B:636:ILE:HG13	2.18	0.43
1:A:841:GLU:HG2	1:A:841:GLU:H	1.57	0.43
1:B:1518:GLU:OE2	1:B:1538:ARG:NH2	2.52	0.43
1:A:998:GLU:HB2	1:A:1017:ARG:HB3	2.01	0.43
1:A:440:LYS:NZ	1:A:446:ASP:O	2.33	0.43
1:A:375:VAL:O	1:A:378:PRO:HD2	2.19	0.42
1:A:375:VAL:HG23	1:A:457:ASN:HB2	2.00	0.42
1:B:679:SER:OG	1:B:681:ARG:N	2.46	0.42
1:B:711:GLU:HA	1:B:712:MET:C	2.40	0.42
1:B:565:ASP:CG	1:B:575:ILE:H	2.23	0.42
1:A:898:ARG:NH2	4:A:2084:HOH:O	2.53	0.42
1:A:1170:TRP:CD1	1:A:1172:PRO:HD2	2.55	0.42
1:A:1330:PRO:HD2	1:A:1356:ARG:HB2	2.03	0.41
1:A:673:MET:O	1:A:678:GLY:N	2.42	0.41
1:B:556:PHE:O	1:B:560:GLN:HG2	2.20	0.41
1:A:456:LYS:O	1:A:458:LEU:HG	2.19	0.41
1:B:650:ARG:HH11	1:B:697:LYS:HG3	1.84	0.41
1:A:713:PRO:HG2	1:A:716:LYS:HZ2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:916:ASP:OD1	1:A:1003:LYS:NZ	2.49	0.41
1:B:836:TYR:CE2	1:B:838:ALA:HB2	2.56	0.41
1:A:836:TYR:CE2	1:A:838:ALA:HB2	2.56	0.41
1:A:709:ILE:HA	1:A:710:PRO:HD2	1.81	0.41
1:A:686:CYS:HB3	1:A:689:ARG:HB2	2.04	0.40
1:B:1271:PHE:HA	1:B:1274:PHE:CD2	2.56	0.40
1:A:722:LYS:HE3	1:A:768:ASP:CB	2.51	0.40
1:B:881:LYS:HG2	1:B:881:LYS:H	1.67	0.40
1:B:1371:MET:HE1	1:B:1523:PHE:HZ	1.87	0.40
1:B:737:ALA:HA	1:B:748:LYS:HD3	2.02	0.40
1:B:856:GLU:HA	1:B:857:GLY:HA2	1.82	0.40
1:A:1030:SER:OG	1:A:1031:THR:N	2.54	0.40
1:A:379:GLN:NE2	1:A:483:PHE:HB3	2.35	0.40
1:B:577:LEU:HD11	1:B:695:ALA:HB1	2.03	0.40
1:B:777:ALA:HB2	1:B:796:TRP:CE3	2.56	0.40
1:A:1136:LEU:HD23	1:A:1596:MET:HB3	2.04	0.40
1:B:1322:GLU:OE2	1:B:1599:LYS:HD2	2.21	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	1153/1256 (92%)	1076 (93%)	68 (6%)	9 (1%)	19 36
1	B	1164/1256 (93%)	1094 (94%)	61 (5%)	9 (1%)	19 36
All	All	2317/2512 (92%)	2170 (94%)	129 (6%)	18 (1%)	19 36

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	377	GLU

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Mol	Chain	Res	Type
1	A	457	ASN
1	A	961	LYS
1	B	373	ASP
1	B	596	ARG
1	B	976	TYR
1	A	595	ARG
1	B	600	ARG
1	B	363	PRO
1	B	374	ALA
1	B	378	PRO
1	A	363	PRO
1	A	378	PRO
1	A	632	PHE
1	A	769	ASP
1	B	375	VAL
1	A	713	PRO
1	B	372	PRO

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	971/1090 (89%)	954 (98%)	17 (2%)	59	79
1	B	968/1090 (89%)	958 (99%)	10 (1%)	76	89
All	All	1939/2180 (89%)	1912 (99%)	27 (1%)	67	84

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	636	ILE
1	A	714	SER
1	A	741	ASP
1	A	767	PRO
1	A	817	VAL
1	A	832	VAL

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Mol	Chain	Res	Type
1	A	841	GLU
1	A	939	VAL
1	A	961	LYS
1	A	985	LEU
1	A	1272	VAL
1	A	1306	VAL
1	A	1351	VAL
1	A	1475	VAL
1	A	1479	VAL
1	A	1547	VAL
1	A	1603	ARG
1	B	517	GLN
1	B	697	LYS
1	B	774	LEU
1	B	780	THR
1	B	939	VAL
1	B	1351	VAL
1	B	1406	GLN
1	B	1413	ILE
1	B	1475	VAL
1	B	1547	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	379	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 10 are monoatomic - leaving 2 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
3	SAH	B	1706	-	21,28,28	1.19	2 (9%)	20,40,40	1.79	2 (10%)
3	SAH	A	1706	-	21,28,28	1.18	2 (9%)	20,40,40	1.75	3 (15%)

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	SAH	B	1706	-	-	4/7/31/31	0/3/3/3
3	SAH	A	1706	-	-	4/7/31/31	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1706	SAH	C2-N3	3.98	1.38	1.32
3	A	1706	SAH	C2-N3	3.94	1.38	1.32
3	A	1706	SAH	C2-N1	2.41	1.38	1.33
3	B	1706	SAH	C2-N1	2.40	1.38	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1706	SAH	N3-C2-N1	-5.53	120.03	128.68
3	B	1706	SAH	N3-C2-N1	-5.53	120.03	128.68
3	B	1706	SAH	C5'-SD-CG	-4.21	89.64	102.27
3	A	1706	SAH	C5'-SD-CG	-3.82	90.80	102.27
3	A	1706	SAH	C3'-C2'-C1'	2.02	104.02	100.98

There are no chirality outliers.

All (8) torsion outliers are listed below:

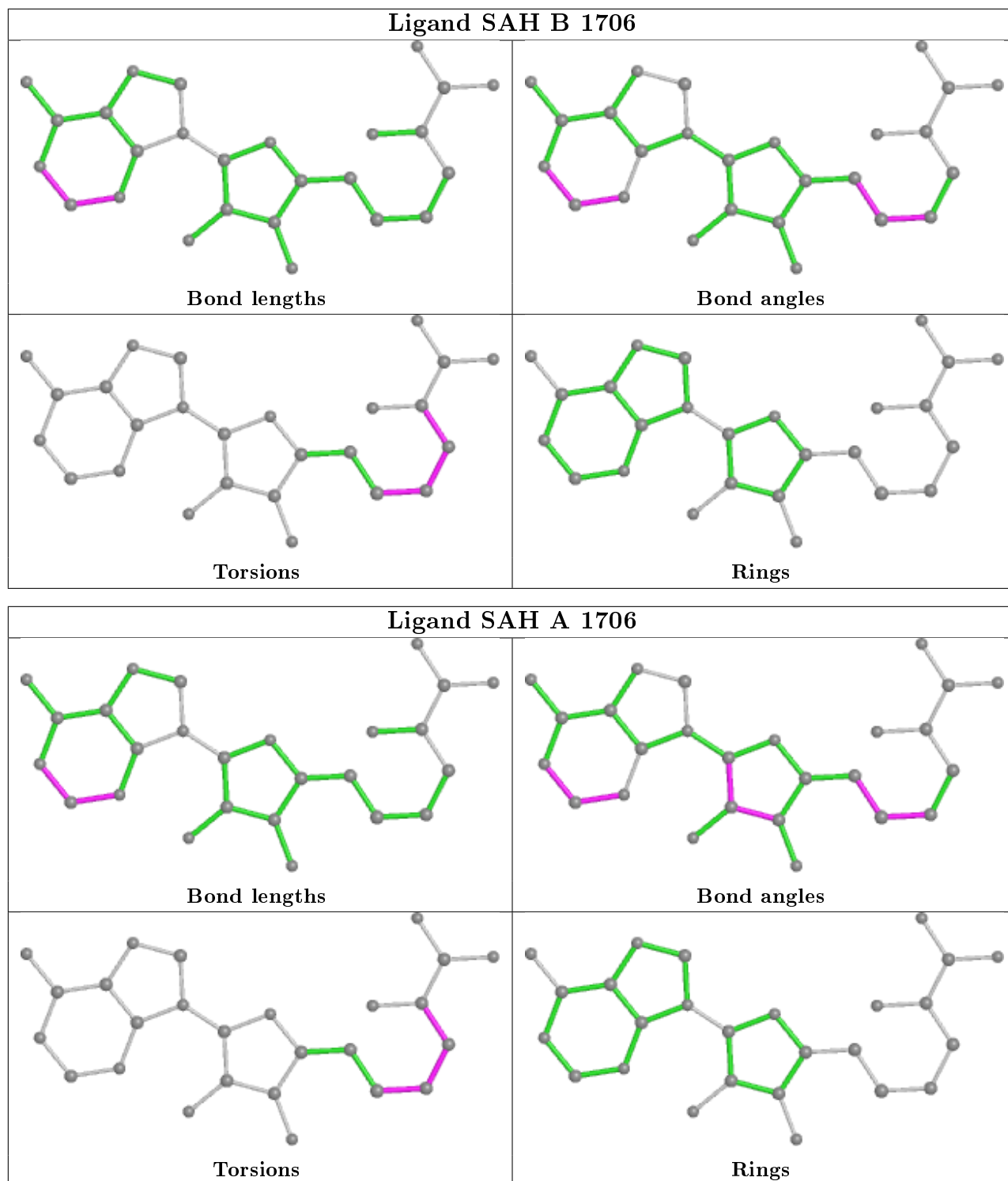
Mol	Chain	Res	Type	Atoms
3	A	1706	SAH	N-CA-CB-CG
3	A	1706	SAH	CA-CB-CG-SD
3	B	1706	SAH	N-CA-CB-CG
3	B	1706	SAH	C-CA-CB-CG
3	B	1706	SAH	CA-CB-CG-SD
3	A	1706	SAH	CB-CG-SD-C5'
3	B	1706	SAH	CB-CG-SD-C5'
3	A	1706	SAH	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1706	SAH	1	0
3	A	1706	SAH	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

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	1170/1256 (93%)	-0.07	16 (1%) 75 71	25, 48, 96, 120	0
1	B	1178/1256 (93%)	-0.08	18 (1%) 73 70	25, 49, 95, 122	0
All	All	2348/2512 (93%)	-0.08	34 (1%) 75 71	25, 48, 95, 122	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	708	ASN	3.7
1	B	1405	TYR	3.7
1	A	567	ALA	3.4
1	A	770	SER	3.3
1	A	571	ASP	3.2
1	B	597	ALA	3.1
1	A	601	ARG	3.0
1	A	599	ALA	3.0
1	A	713	PRO	2.9
1	A	597	ALA	2.8
1	B	746	TYR	2.8
1	A	1605	TRP	2.7
1	B	697	LYS	2.7
1	B	650	ARG	2.5
1	B	571	ASP	2.5
1	B	388	ILE	2.5
1	A	450	GLU	2.4
1	A	1405	TYR	2.4
1	B	1488	ALA	2.4
1	A	598	GLN	2.4
1	B	1604	VAL	2.4
1	A	711	GLU	2.4
1	A	746	TYR	2.3
1	B	712	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	601	ARG	2.3
1	B	711	GLU	2.2
1	B	599	ALA	2.2
1	A	1406	GLN	2.2
1	B	709	ILE	2.2
1	B	567	ALA	2.1
1	B	387	SER	2.1
1	A	479	PHE	2.0
1	B	713	PRO	2.0
1	A	651	ARG	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](#)

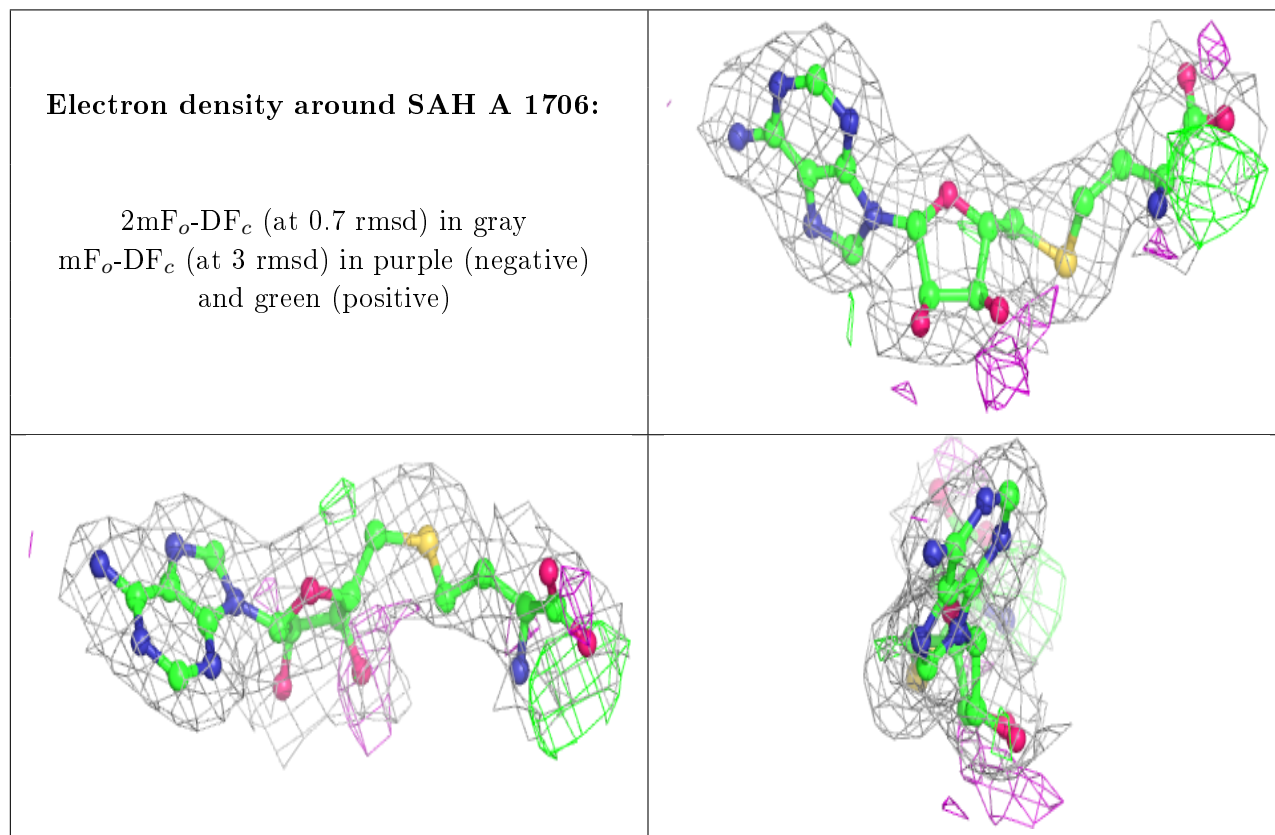
There are no monosaccharides in this entry.

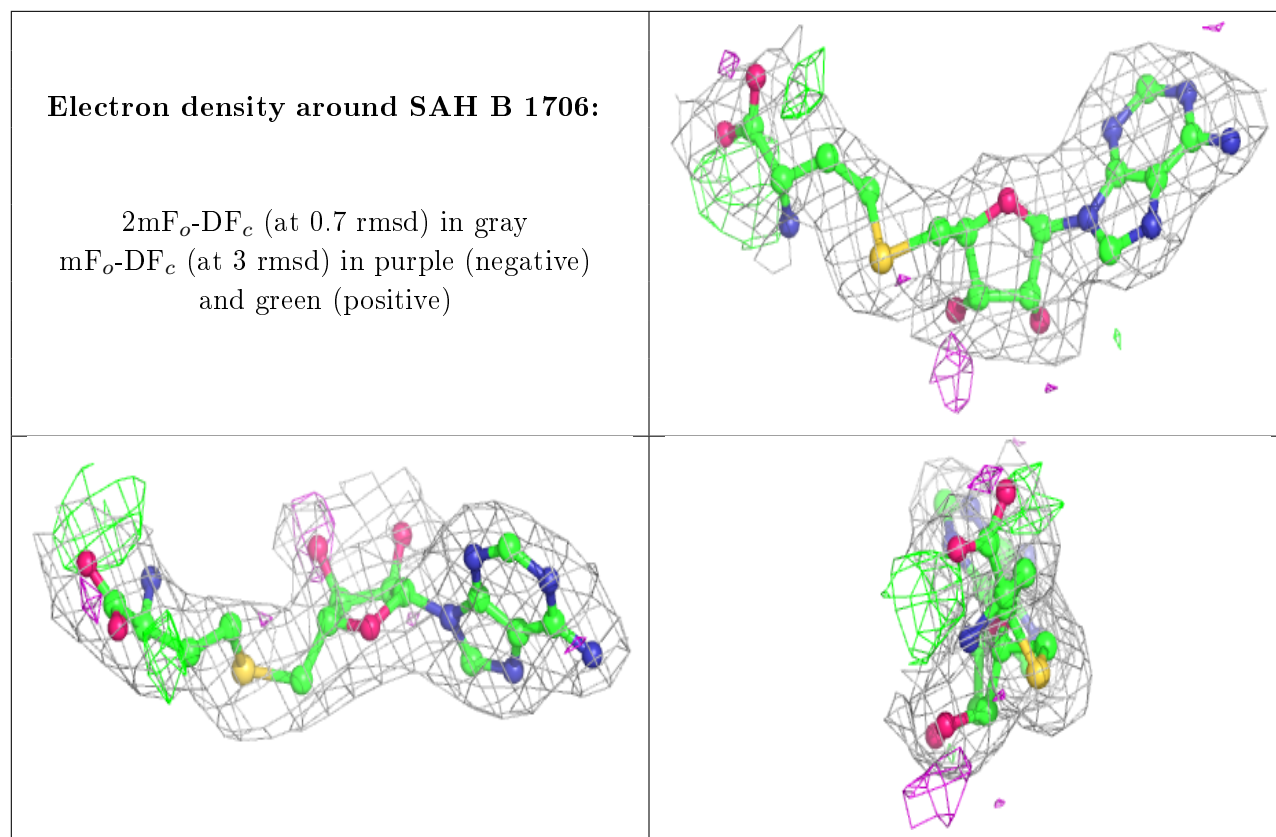
6.4 Ligands [i](#)

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
2	ZN	B	1703	1/1	0.86	0.11	102,102,102,102	0
2	ZN	A	1703	1/1	0.92	0.13	93,93,93,93	0
2	ZN	B	1705	1/1	0.95	0.16	74,74,74,74	0
3	SAH	A	1706	26/26	0.96	0.19	23,34,52,58	0
3	SAH	B	1706	26/26	0.96	0.17	26,37,53,69	0
2	ZN	A	1705	1/1	0.98	0.17	71,71,71,71	0
2	ZN	B	1704	1/1	0.99	0.18	51,51,51,51	0
2	ZN	B	1701	1/1	0.99	0.19	42,42,42,42	0
2	ZN	A	1704	1/1	0.99	0.15	50,50,50,50	0
2	ZN	B	1702	1/1	0.99	0.21	56,56,56,56	0
2	ZN	A	1701	1/1	0.99	0.19	42,42,42,42	0
2	ZN	A	1702	1/1	0.99	0.23	42,42,42,42	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.