



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:26 PM UTC

PDB ID : 4OK6 / pdb_00004ok6
Title : Crystal Structure of Hepatitis C Virus NS3 Helicase Inhibitor Co-complex with Compound 13 [[1-(2-methoxy-5-nitrobenzyl)-1H-indol-3-yl]acetic acid]
Authors : Padyana, A.K.
Deposited on : 2014-01-21
Resolution : 2.40 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

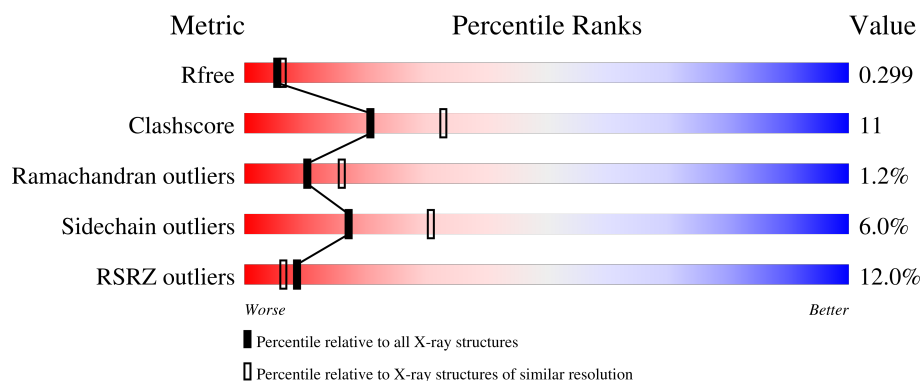
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	464	16% 69% 21% • • 7%
1	B	464	6% 70% 17% • 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6746 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 Serine protease NS3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	1	0
			3250	2058	549	620	23			
1	B	415	Total	C	N	O	S	0	1	0
			3137	1993	527	595	22			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	167	MET	-	expression tag	UNP K4KA16
A	168	GLY	-	expression tag	UNP K4KA16
A	169	SER	-	expression tag	UNP K4KA16
A	170	SER	-	expression tag	UNP K4KA16
A	171	HIS	-	expression tag	UNP K4KA16
A	172	HIS	-	expression tag	UNP K4KA16
A	173	HIS	-	expression tag	UNP K4KA16
A	174	HIS	-	expression tag	UNP K4KA16
A	175	HIS	-	expression tag	UNP K4KA16
A	176	HIS	-	expression tag	UNP K4KA16
A	177	SER	-	expression tag	UNP K4KA16
A	178	SER	-	expression tag	UNP K4KA16
A	179	GLY	-	expression tag	UNP K4KA16
A	403	ASN	SER	conflict	UNP K4KA16
A	505	MET	THR	conflict	UNP K4KA16
B	167	MET	-	expression tag	UNP K4KA16
B	168	GLY	-	expression tag	UNP K4KA16
B	169	SER	-	expression tag	UNP K4KA16
B	170	SER	-	expression tag	UNP K4KA16
B	171	HIS	-	expression tag	UNP K4KA16
B	172	HIS	-	expression tag	UNP K4KA16
B	173	HIS	-	expression tag	UNP K4KA16
B	174	HIS	-	expression tag	UNP K4KA16
B	175	HIS	-	expression tag	UNP K4KA16
B	176	HIS	-	expression tag	UNP K4KA16

Continued on next page...

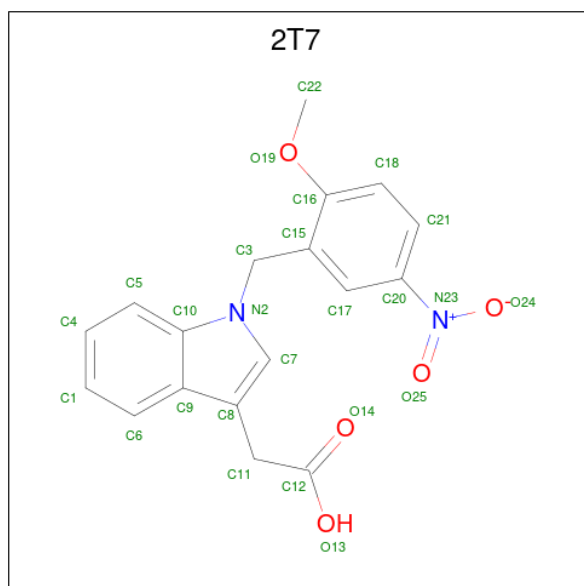
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	SER	-	expression tag	UNP K4KA16
B	178	SER	-	expression tag	UNP K4KA16
B	179	GLY	-	expression tag	UNP K4KA16
B	403	ASN	SER	conflict	UNP K4KA16
B	505	MET	THR	conflict	UNP K4KA16

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Ca 2 2	0	0

- Molecule 3 is [1-(2-methoxy-5-nitrobenzyl)-1H-indol-3-yl]acetic acid (CCD ID: 2T7) (formula: C₁₈H₁₆N₂O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 25 18 2 5	0	0

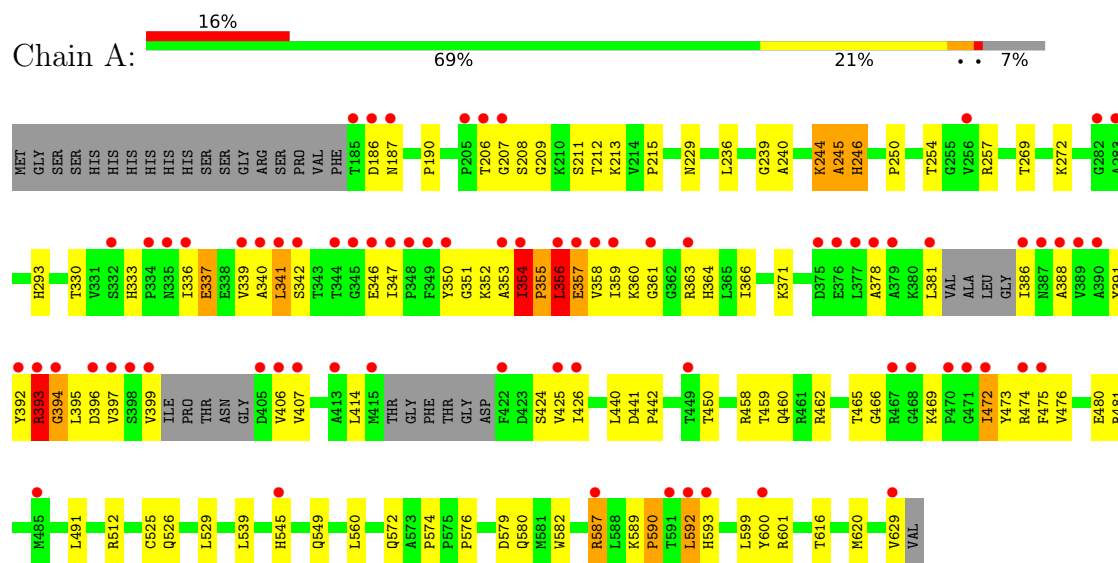
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	153	Total O 153 153	0	0
4	B	179	Total O 179 179	0	0

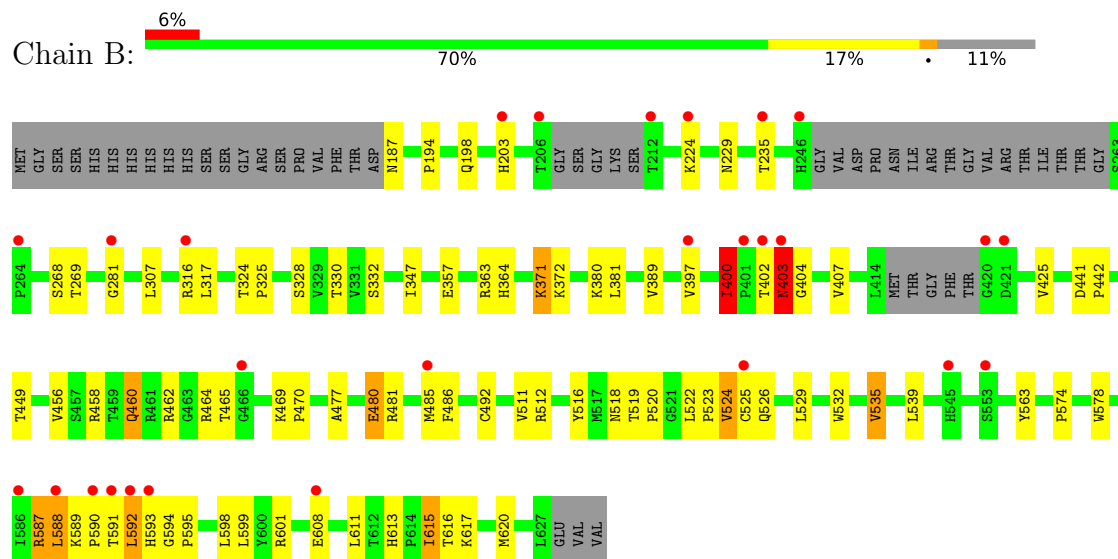
3 Residue-property plots [i](#)

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: Serine protease NS3



• Molecule 1: Serine protease NS3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.15Å 103.32Å 118.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.08 – 2.40 33.08 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (33.08-2.40) 94.4 (33.08-2.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.40Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.239 , 0.300 (Not available) , 0.299	Depositor DCC
R_{free} test set	2005 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	42.7	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6746	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% 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: 2T7, CA

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	0.63	1/3326 (0.0%)	1.02	7/4539 (0.2%)
1	B	0.60	0/3213	0.95	7/4388 (0.2%)
All	All	0.62	1/6539 (0.0%)	0.99	14/8927 (0.2%)

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	2
1	B	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	354	ILE	CA-CB	5.07	1.60	1.54

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	392	TYR	CA-C-N	-9.37	107.07	122.82
1	A	392	TYR	C-N-CA	-9.37	107.07	122.82
1	A	592	LEU	N-CA-C	-8.38	102.07	112.88
1	A	392	TYR	N-CA-C	-8.15	93.44	110.80
1	B	481	ARG	CA-C-N	-6.82	112.91	120.14
1	B	481	ARG	C-N-CA	-6.82	112.91	120.14
1	B	400	ILE	CA-C-N	-6.01	112.32	119.84
1	B	400	ILE	C-N-CA	-6.01	112.32	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	394	GLY	N-CA-C	-5.31	100.59	113.18
1	A	393	ARG	N-CA-C	5.25	117.40	109.41
1	B	400	ILE	CA-C-O	-5.16	116.23	119.12
1	A	187	ASN	N-CA-C	5.08	115.87	108.14
1	B	594	GLY	CA-C-N	5.06	125.04	120.03
1	B	594	GLY	C-N-CA	5.06	125.04	120.03

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	245	ALA	Peptide
1	A	393	ARG	Peptide
1	B	587	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	3250	0	3208	84	0
1	B	3137	0	3093	61	0
2	A	2	0	0	0	0
3	A	25	0	15	0	0
4	A	153	0	0	4	0
4	B	179	0	0	1	0
All	All	6746	0	6316	141	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 11.

All (141) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:ARG:NH2	1:B:400:ILE:O	2.05	0.89
1:B:616:THR:HG22	1:B:620:MET:HE2	1.56	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:587:ARG:NH2	4:A:1138:HOH:O	2.14	0.80
1:B:574:PRO:HG3	1:B:592:LEU:HA	1.63	0.80
1:A:358:VAL:HB	1:A:474:ARG:HH12	1.46	0.79
1:A:358:VAL:HB	1:A:474:ARG:NH1	1.98	0.79
1:A:337:GLU:HB2	1:A:472:ILE:HA	1.67	0.76
1:A:236:LEU:HD22	1:A:257:ARG:HH21	1.51	0.75
1:B:595:PRO:HA	1:B:608:GLU:HG3	1.71	0.72
1:B:330:THR:HG23	1:B:480:GLU:OE1	1.90	0.72
1:B:617:LYS:HA	1:B:620:MET:HE3	1.70	0.71
1:A:481:ARG:HG2	1:B:485:MET:HE3	1.74	0.70
1:A:378:ALA:HA	1:A:381:LEU:HD12	1.73	0.70
1:A:363:ARG:HH22	1:A:399:VAL:HG13	1.59	0.67
1:A:246:HIS:HE1	4:A:1183:HOH:O	1.77	0.67
1:A:245:ALA:O	1:A:246:HIS:CD2	2.47	0.67
1:A:240:ALA:O	1:A:244:LYS:HG2	1.95	0.67
1:A:393:ARG:HG2	1:A:394:GLY:H	1.60	0.66
1:A:245:ALA:O	1:A:246:HIS:HD2	1.77	0.66
1:A:442:PRO:HB2	1:A:620:MET:HE2	1.77	0.66
1:A:350:TYR:HB2	1:A:476:VAL:HG21	1.77	0.65
1:B:381:LEU:HD13	1:B:407:VAL:HG21	1.80	0.64
1:A:341:LEU:HD11	1:A:353:ALA:O	1.98	0.64
1:B:590:PRO:O	1:B:593:HIS:ND1	2.30	0.63
1:A:560:LEU:O	1:A:600:TYR:OH	2.18	0.62
1:A:574:PRO:HG3	1:A:592:LEU:HA	1.82	0.61
1:A:347:ILE:CG2	1:A:354:ILE:HG13	2.32	0.60
1:A:587:ARG:O	1:A:587:ARG:HG2	2.01	0.60
1:B:364:HIS:HB2	1:B:407:VAL:HG12	1.84	0.60
1:A:330:THR:HG22	1:A:459:THR:OG1	2.02	0.60
1:A:337:GLU:HG3	1:A:472:ILE:HG13	1.84	0.59
1:A:358:VAL:HG23	1:A:359:ILE:HG23	1.84	0.59
1:A:366:ILE:HG12	1:A:426:ILE:HB	1.85	0.59
1:A:337:GLU:CG	1:A:472:ILE:HG13	2.34	0.58
1:A:579:ASP:OD1	1:A:580:GLN:N	2.36	0.58
1:B:593:HIS:NE2	4:B:878:HOH:O	2.32	0.57
1:A:396:ASP:CG	1:A:397:VAL:H	2.12	0.57
1:A:351:GLY:C	1:A:352:LYS:HD2	2.29	0.56
1:B:325:PRO:O	1:B:328:SER:OG	2.22	0.56
1:A:347:ILE:HG21	1:A:354:ILE:HG13	1.87	0.56
1:B:371:LYS:HG3	1:B:372:LYS:N	2.20	0.56
1:A:236:LEU:HD22	1:A:257:ARG:NH2	2.20	0.56
1:A:354:ILE:C	1:A:354:ILE:HD12	2.31	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:ASN:O	1:B:203:HIS:N	2.38	0.55
1:B:574:PRO:HB3	1:B:592:LEU:HG	1.88	0.55
1:B:519:THR:HB	1:B:522:LEU:HD12	1.89	0.54
1:B:578:TRP:HZ2	1:B:588:LEU:HD23	1.72	0.54
1:A:616:THR:HG22	1:A:620:MET:HE3	1.88	0.54
1:A:293:HIS:HE1	4:A:1127:HOH:O	1.89	0.54
1:A:450:THR:O	1:B:526:GLN:NE2	2.41	0.53
1:B:458:ARG:NH2	1:B:477:ALA:O	2.36	0.53
1:B:535:VAL:O	1:B:539:LEU:HD13	2.08	0.53
1:B:400:ILE:HG22	1:B:402:THR:CG2	2.39	0.52
1:A:393:ARG:NH1	1:A:393:ARG:HB3	2.24	0.52
1:B:403:ASN:O	1:B:403:ASN:OD1	2.27	0.52
1:A:333:HIS:ND1	1:A:336:ILE:HG13	2.24	0.52
1:A:481:ARG:CG	1:B:485:MET:HE3	2.40	0.51
1:B:486:PHE:CZ	1:B:525:CYS:HB2	2.45	0.51
1:A:254:THR:C	1:A:272:LYS:HG3	2.36	0.51
1:B:485:MET:HE1	1:B:524:VAL:HG12	1.93	0.51
1:B:587:ARG:N	1:B:587:ARG:HD3	2.25	0.51
1:A:351:GLY:O	1:A:352:LYS:HD2	2.10	0.51
1:B:588:LEU:CD2	1:B:592:LEU:HB2	2.41	0.51
1:B:425:VAL:HG23	1:B:465:THR:HB	1.92	0.51
1:A:239:GLY:HA2	1:A:250:PRO:HG2	1.93	0.51
1:A:354:ILE:HD12	1:A:354:ILE:O	2.11	0.51
1:A:616:THR:HG22	1:A:620:MET:CE	2.40	0.50
1:A:393:ARG:HG2	1:A:394:GLY:N	2.26	0.50
1:A:240:ALA:HB1	1:A:244:LYS:HE2	1.92	0.50
1:A:212:THR:C	1:A:215:PRO:HD2	2.36	0.50
1:A:545:HIS:O	1:A:549:GLN:HG3	2.11	0.50
1:B:460:GLN:OE1	1:B:464:ARG:NH2	2.41	0.49
1:A:333:HIS:HB3	1:A:336:ILE:HB	1.95	0.49
1:A:525[A]:CYS:SG	1:A:526:GLN:N	2.85	0.48
1:B:588:LEU:HA	1:B:591:THR:CG2	2.43	0.48
1:B:229:ASN:O	1:B:269:THR:HA	2.13	0.48
1:A:587:ARG:O	1:A:590:PRO:HD2	2.14	0.48
1:A:425:VAL:HG23	1:A:465:THR:HB	1.96	0.48
1:A:572:GLN:O	1:A:593:HIS:HB3	2.14	0.48
1:B:268:SER:OG	1:B:269:THR:N	2.46	0.48
1:A:364:HIS:HB2	1:A:407:VAL:HG22	1.96	0.47
1:A:441:ASP:O	1:A:601:ARG:NH1	2.45	0.47
1:B:588:LEU:HD21	1:B:592:LEU:HB2	1.96	0.47
1:B:574:PRO:HD3	1:B:593:HIS:H	1.78	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:GLY:C	1:A:209:GLY:H	2.22	0.46
1:A:474:ARG:NH2	4:A:1204:HOH:O	2.44	0.46
1:A:462:ARG:HG3	1:A:473:TYR:CG	2.49	0.46
1:B:194:PRO:O	1:B:316:ARG:NH2	2.44	0.46
1:B:400:ILE:HG22	1:B:402:THR:HG22	1.97	0.46
1:B:588:LEU:HD22	1:B:588:LEU:O	2.16	0.46
1:B:574:PRO:CG	1:B:592:LEU:HA	2.41	0.46
1:A:600:TYR:C	1:A:600:TYR:CD1	2.94	0.46
1:B:518:ASN:O	1:B:520:PRO:HD3	2.17	0.45
1:B:598:LEU:HD21	1:B:601:ARG:HG2	1.98	0.45
1:B:462:ARG:O	1:B:465:THR:HG22	2.16	0.45
1:A:341:LEU:HD12	1:A:342:SER:N	2.32	0.45
1:B:347:ILE:HD13	1:B:381:LEU:HD21	1.99	0.45
1:B:402:THR:O	1:B:404:GLY:N	2.50	0.45
1:A:360:LYS:HA	1:A:361:GLY:HA2	1.70	0.45
1:A:481:ARG:HG2	1:B:485:MET:CE	2.45	0.45
1:A:207:GLY:O	1:A:209:GLY:N	2.48	0.45
1:B:492:CYS:HB2	1:B:532:TRP:CZ2	2.52	0.45
1:A:340:ALA:HA	1:A:475:PHE:CZ	2.52	0.44
1:A:391:TYR:HE2	1:A:414:LEU:HA	1.82	0.44
1:A:599:LEU:HB2	1:A:600:TYR:CD2	2.53	0.44
1:B:442:PRO:HB3	1:B:611:LEU:HG	2.00	0.44
1:A:587:ARG:O	1:A:587:ARG:CG	2.65	0.44
1:A:616:THR:O	1:A:620:MET:HG3	2.18	0.44
1:B:324:THR:HG23	1:B:328:SER:HB2	2.00	0.43
1:B:563:TYR:HE1	1:B:615:ILE:HD13	1.82	0.43
1:A:391:TYR:CZ	1:A:393:ARG:HG3	2.53	0.43
1:B:307:LEU:HD13	1:B:519:THR:OG1	2.18	0.43
1:A:491:LEU:HD13	1:A:529:LEU:HD23	2.01	0.43
1:A:354:ILE:HA	1:A:355:PRO:HD3	1.86	0.43
1:A:458:ARG:HD2	1:A:480:GLU:OE1	2.19	0.43
1:B:400:ILE:HD13	1:B:400:ILE:N	2.33	0.43
1:B:194:PRO:HD3	1:B:317:LEU:HD13	2.01	0.43
1:B:574:PRO:HG3	1:B:592:LEU:CA	2.40	0.42
1:B:588:LEU:O	1:B:591:THR:N	2.52	0.42
1:A:629:VAL:O	1:A:629:VAL:HG13	2.20	0.42
1:B:599:LEU:HD22	1:B:615:ILE:HG22	2.01	0.42
1:A:440:LEU:HD23	1:A:440:LEU:HA	1.85	0.42
1:B:469:LYS:HG2	1:B:470:PRO:O	2.18	0.42
1:A:388:ALA:HA	1:A:407:VAL:O	2.20	0.42
1:A:229:ASN:O	1:A:269:THR:HA	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:GLU:OE2	1:A:356:LEU:HB2	2.20	0.42
1:B:324:THR:HG21	1:B:456:VAL:HG13	2.02	0.42
1:B:402:THR:C	1:B:404:GLY:H	2.28	0.42
1:A:363:ARG:NH2	1:A:399:VAL:HG13	2.31	0.41
1:A:393:ARG:HB3	1:A:393:ARG:HH11	1.85	0.41
1:A:589:LYS:H	1:A:589:LYS:HG2	1.44	0.41
1:A:391:TYR:CE1	1:A:393:ARG:HG3	2.54	0.41
1:A:473:TYR:C	1:A:474:ARG:HG3	2.45	0.41
1:B:441:ASP:O	1:B:601:ARG:NH1	2.46	0.41
1:A:364:HIS:ND1	1:A:424:SER:OG	2.40	0.41
1:B:516:TYR:OH	1:B:523:PRO:HD2	2.20	0.41
1:B:485:MET:CE	1:B:524:VAL:HG12	2.50	0.41
1:A:466:GLY:HA2	1:A:469:LYS:O	2.21	0.41
1:A:576:PRO:HD2	1:A:582:TRP:CE2	2.57	0.40
1:A:363:ARG:HG2	1:A:406:VAL:HG12	2.02	0.40
1:B:613:HIS:HE1	1:B:615:ILE:HD12	1.87	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	423/464 (91%)	394 (93%)	21 (5%)	8 (2%)	6	8
1	B	408/464 (88%)	384 (94%)	22 (5%)	2 (0%)	24	37
All	All	831/928 (90%)	778 (94%)	43 (5%)	10 (1%)	10	16

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	356	LEU
1	A	587	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	403	ASN
1	B	281	GLY
1	A	208	SER
1	A	246	HIS
1	A	357	GLU
1	A	355	PRO
1	A	590	PRO
1	A	190	PRO

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	356/382 (93%)	337 (95%)	19 (5%)	20	36
1	B	342/382 (90%)	319 (93%)	23 (7%)	15	26
All	All	698/764 (91%)	656 (94%)	42 (6%)	17	31

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	186	ASP
1	A	206	THR
1	A	211	SER
1	A	213	LYS
1	A	244	LYS
1	A	337	GLU
1	A	339	VAL
1	A	341	LEU
1	A	354	ILE
1	A	356	LEU
1	A	357	GLU
1	A	371	LYS
1	A	386	ILE
1	A	393	ARG
1	A	395	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	460	GLN
1	A	472	ILE
1	A	512	ARG
1	A	539	LEU
1	B	198	GLN
1	B	224	LYS
1	B	235	THR
1	B	332	SER
1	B	357	GLU
1	B	371	LYS
1	B	380	LYS
1	B	389	VAL
1	B	397	VAL
1	B	400	ILE
1	B	403	ASN
1	B	449	THR
1	B	460	GLN
1	B	480	GLU
1	B	511	VAL
1	B	512	ARG
1	B	524	VAL
1	B	529	LEU
1	B	535	VAL
1	B	588	LEU
1	B	589	LYS
1	B	592	LEU
1	B	615	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	246	HIS
1	B	541	HIS
1	B	545	HIS

5.3.3 RNA ⓘ

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](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	2T7	A	1003	-	27,27,27	0.78	0	36,38,38	1.27	6 (16%)

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	2T7	A	1003	-	-	7/12/14/14	0/3/3/3

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1003	2T7	C12-C11-C8	-2.94	110.42	114.93
3	A	1003	2T7	C10-N2-C7	2.72	110.11	108.49
3	A	1003	2T7	C21-C20-N23	2.11	121.18	119.34
3	A	1003	2T7	C3-N2-C10	-2.11	123.10	126.13
3	A	1003	2T7	C17-C15-C16	2.08	120.54	118.26
3	A	1003	2T7	O19-C16-C18	-2.03	120.87	124.30

There are no chirality outliers.

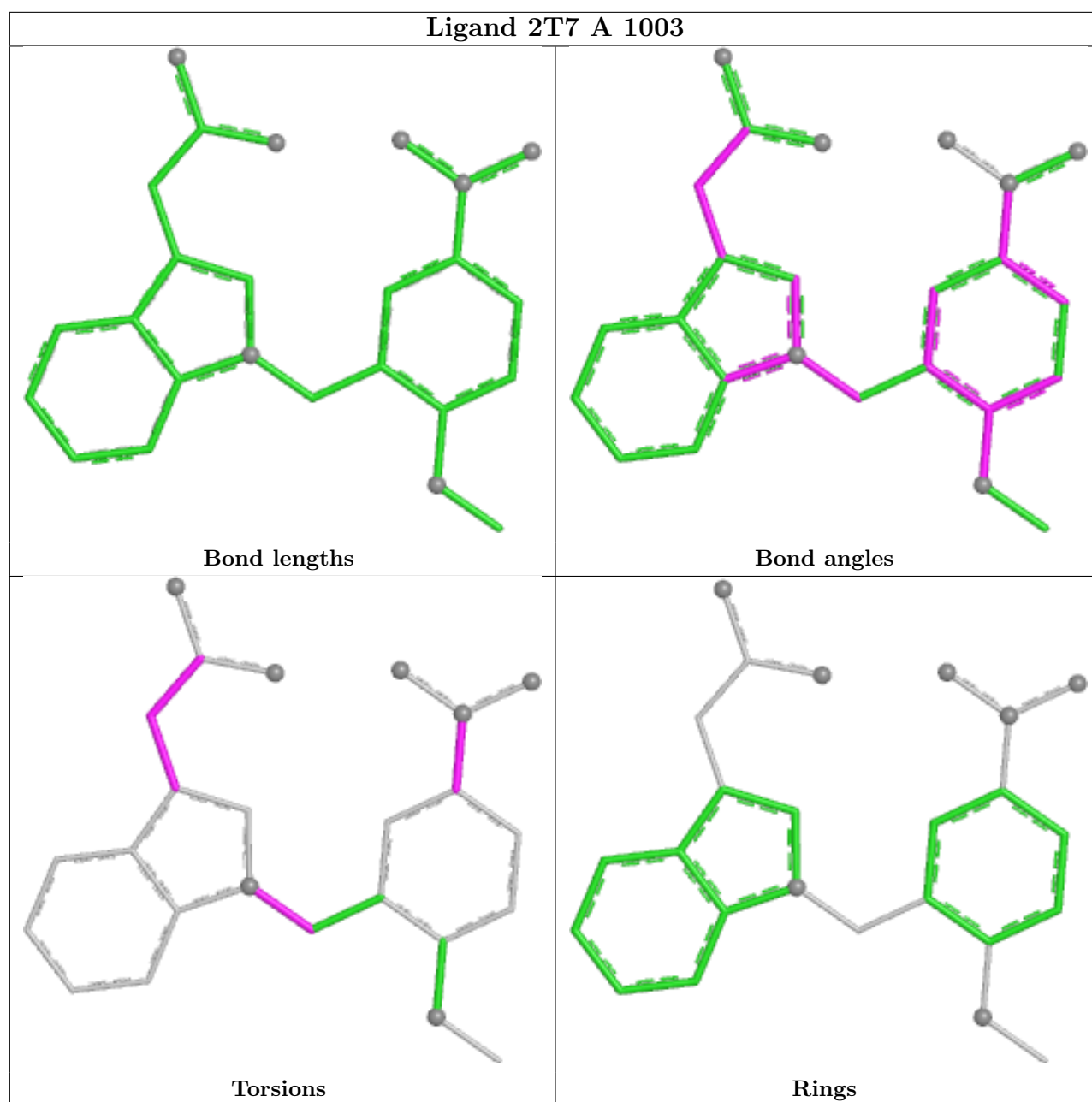
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1003	2T7	C21-C20-N23-O25
3	A	1003	2T7	C17-C20-N23-O25
3	A	1003	2T7	C12-C11-C8-C9
3	A	1003	2T7	C8-C11-C12-O13
3	A	1003	2T7	C12-C11-C8-C7
3	A	1003	2T7	C15-C3-N2-C7
3	A	1003	2T7	C8-C11-C12-O14

There are no ring outliers.

No monomer is involved in short contacts.

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	430/464 (92%)	0.89	74 (17%) 4 3	19, 46, 87, 109	1 (0%)
1	B	415/464 (89%)	0.56	27 (6%) 25 21	20, 46, 75, 97	1 (0%)
All	All	845/928 (91%)	0.73	101 (11%) 9 6	19, 46, 84, 109	2 (0%)

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	591	THR	8.3
1	A	592	LEU	6.8
1	B	592	LEU	6.0
1	A	354	ILE	5.7
1	A	591	THR	5.6
1	A	356	LEU	5.1
1	A	386	ILE	5.1
1	A	347	ILE	4.9
1	A	353	ALA	4.9
1	B	246	HIS	4.6
1	A	397	VAL	4.5
1	A	405	ASP	4.4
1	B	401	PRO	4.2
1	B	402	THR	4.1
1	A	629	VAL	4.1
1	B	403	ASN	3.9
1	A	399	VAL	3.6
1	A	341	LEU	3.6
1	A	415	MET	3.6
1	A	396	ASP	3.6
1	A	406	VAL	3.5
1	B	281	GLY	3.5
1	B	588	LEU	3.5
1	A	388	ALA	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	390	ALA	3.4
1	A	392	TYR	3.3
1	A	472	ILE	3.1
1	A	471	GLY	3.1
1	A	339	VAL	3.1
1	A	282	GLY	3.0
1	A	345	GLY	3.0
1	B	420	GLY	3.0
1	B	593	HIS	3.0
1	A	393	ARG	3.0
1	A	186	ASP	3.0
1	A	475	PHE	3.0
1	A	425	VAL	2.9
1	A	206	THR	2.9
1	A	358	VAL	2.9
1	A	357	GLU	2.9
1	A	359	ILE	2.9
1	A	344	THR	2.9
1	B	397	VAL	2.8
1	A	205	PRO	2.7
1	A	378	ALA	2.7
1	A	593	HIS	2.7
1	A	394	GLY	2.7
1	A	600	TYR	2.7
1	A	363	ARG	2.7
1	A	422	PHE	2.7
1	B	485	MET	2.7
1	A	375	ASP	2.6
1	B	212	THR	2.6
1	A	474	ARG	2.6
1	A	485	MET	2.6
1	A	389	VAL	2.6
1	A	207	GLY	2.6
1	A	381	LEU	2.6
1	A	283	ALA	2.6
1	A	340	ALA	2.6
1	A	348	PRO	2.5
1	A	349	PHE	2.5
1	A	387	ASN	2.5
1	A	470	PRO	2.5
1	A	377	LEU	2.5
1	B	316	ARG	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	361	GLY	2.4
1	A	467	ARG	2.4
1	A	335	ASN	2.4
1	A	342	SER	2.4
1	A	376	GLU	2.4
1	B	608	GLU	2.4
1	B	421	ASP	2.4
1	A	587	ARG	2.4
1	B	586	ILE	2.4
1	A	545	HIS	2.4
1	B	235	THR	2.3
1	A	413	ALA	2.3
1	B	206	THR	2.3
1	B	466	GLY	2.2
1	B	224	LYS	2.2
1	A	336	ILE	2.2
1	A	398	SER	2.2
1	A	334	PRO	2.2
1	B	590	PRO	2.2
1	B	203	HIS	2.1
1	A	332	SER	2.1
1	A	379	ALA	2.1
1	A	187	ASN	2.1
1	A	468	GLY	2.1
1	B	525	CYS	2.1
1	A	256	VAL	2.1
1	A	407	VAL	2.1
1	A	426	ILE	2.1
1	A	185	THR	2.1
1	A	449	THR	2.1
1	A	346	GLU	2.0
1	A	350	TYR	2.0
1	B	553	SER	2.0
1	B	545	HIS	2.0
1	B	264	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](#)

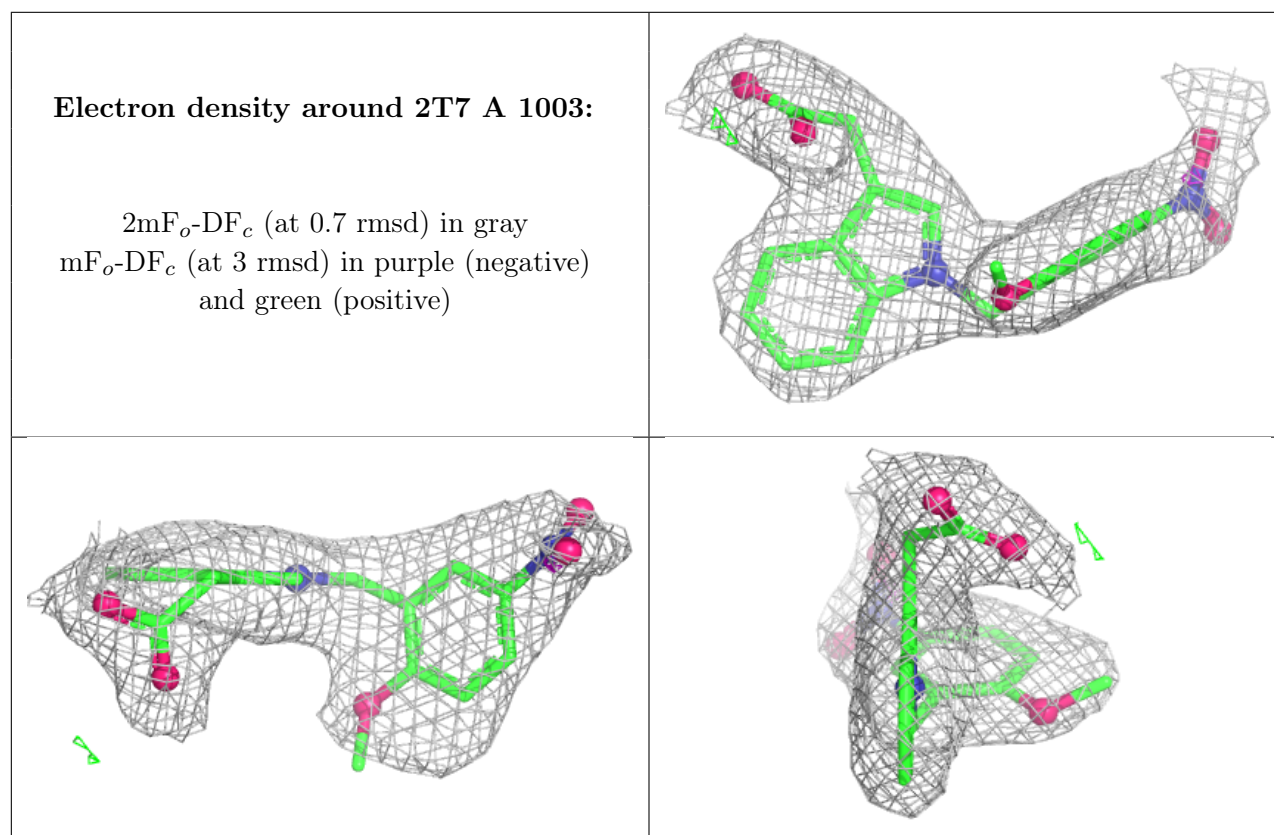
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
3	2T7	A	1003	25/25	0.89	0.10	41,48,65,69	0
2	CA	A	1001	1/1	0.93	0.08	65,65,65,65	0
2	CA	A	1002	1/1	0.94	0.05	60,60,60,60	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 ⓘ

There are no such residues in this entry.