



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 1, 2026 – 06:08 PM JST

PDB ID : 9VCM / pdb_00009vcm
Title : NAD_dependent dehydrogenase
Authors : Niu, M.; Shen, Y.
Deposited on : 2025-06-06
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 : 1.8.5 (274361), CSD as541be (2020)
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

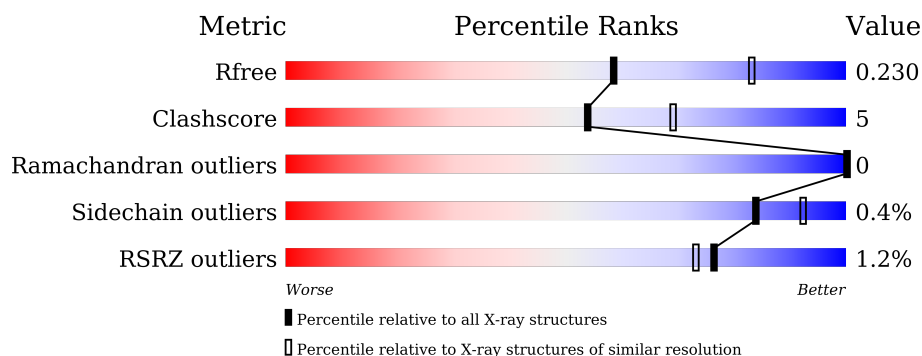
1 Overall quality at a glance

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	342	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>13%</div> <div>6%</div> </div> </div>
1	C	342	<div> <div></div> <div> <div>83%</div> <div>10%</div> <div>6%</div> </div> </div>
2	B	256	<div> <div>0%</div> <div> <div></div> <div>90%</div> <div>9%</div> <div>1%</div> </div> </div>
2	D	256	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>9%</div> <div>1%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8999 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 NADH-dependent dihydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2363	1484	430	445	4			
1	C	321	Total	C	N	O	S	0	0	0
			2347	1472	428	443	4			

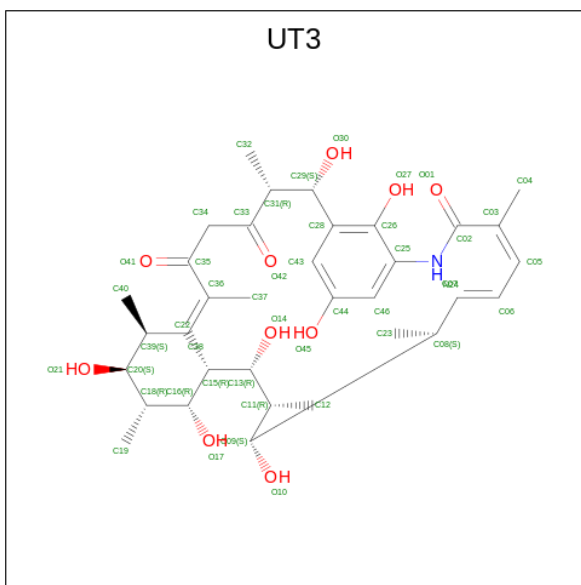
- Molecule 2 is a protein called Rift.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	254	Total	C	N	O	S	0	0	0
			1823	1142	315	361	5			
2	D	253	Total	C	N	O	S	0	0	0
			1825	1143	317	360	5			

There are 4 discrepancies between the modelled and reference sequences:

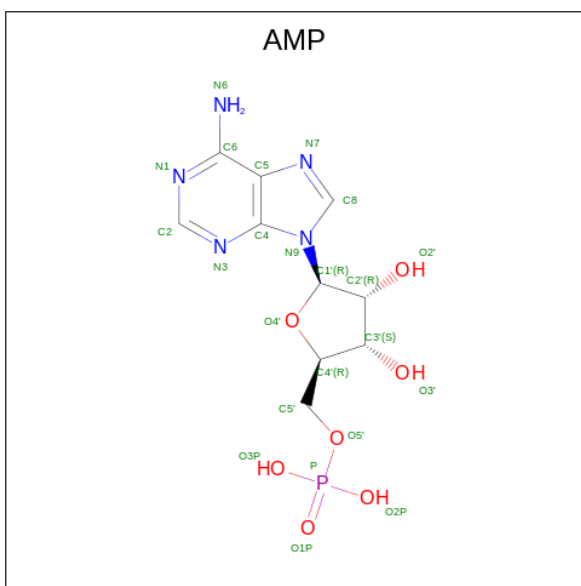
Chain	Residue	Modelled	Actual	Comment	Reference
B	348	MET	-	initiating methionine	UNP O52542
B	349	VAL	-	expression tag	UNP O52542
D	348	MET	-	initiating methionine	UNP O52542
D	349	VAL	-	expression tag	UNP O52542

- Molecule 3 is (4Z,6E,8S,9S,10R,11R,12R,13R,14R,15S,16S,17Z,22R,23S)-4,8,10,12,14,16,18,22-octamethyl-9,11,13,15,23,26,28-heptakis(oxidanyl)-2-azabicyclo[22.3.1]octacos-1(27),4,6,17,24(28),25-hexaene-3,19,21-trione (CCD ID: UT3) (formula: C₃₅H₅₁NO₁₀).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 46	C 35	N 1	O 10	0	0
3	C	1	Total 46	C 35	N 1	O 10	0	0

- Molecule 4 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

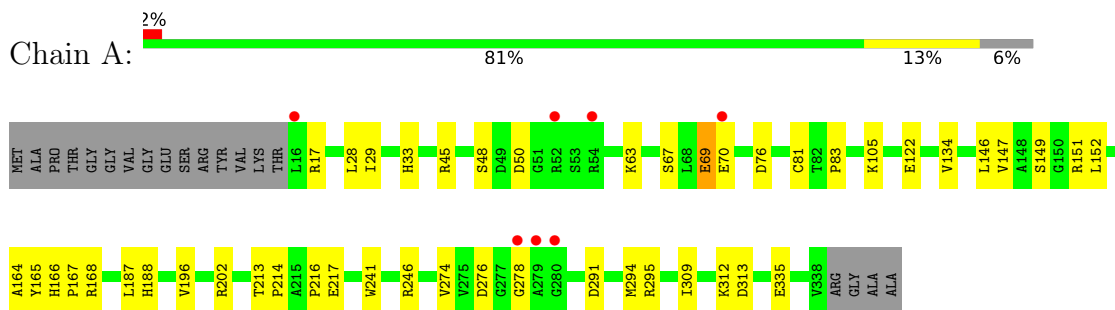
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	125	Total	O	0	0
			125	125		
6	B	114	Total	O	0	0
			114	114		
6	C	183	Total	O	0	0
			183	183		
6	D	94	Total	O	0	0
			94	94		

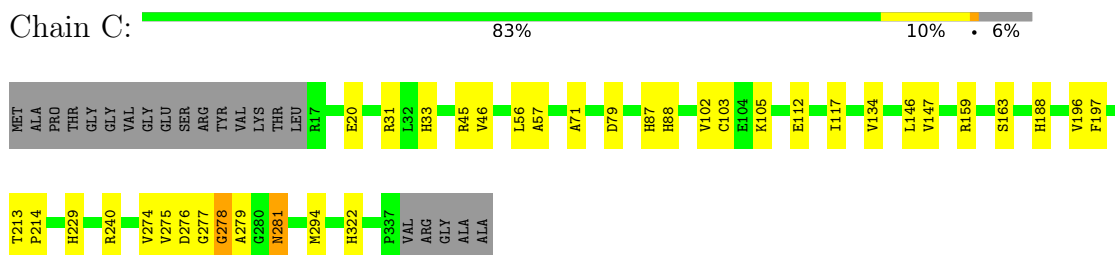
3 Residue-property plots [i](#)

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.

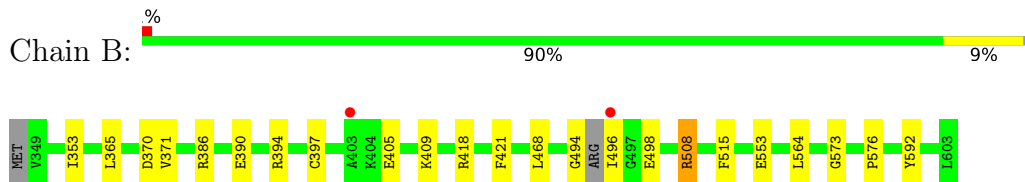
- Molecule 1: NADH-dependent dihydrogenase



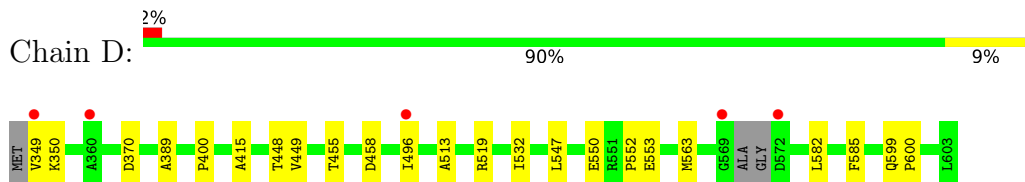
- Molecule 1: NADH-dependent dihydrogenase



- Molecule 2: Rf1T



- Molecule 2: Rf1T



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	192.18Å 81.26Å 90.13Å 90.00° 102.84° 90.00°	Depositor
Resolution (Å)	28.99 – 2.40 28.99 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.5 (28.99-2.40) 96.2 (28.99-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.18.2_3874: ???)	Depositor
R, R_{free}	0.176 , 0.228 0.178 , 0.230	Depositor DCC
R_{free} test set	2000 reflections (3.27%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8999	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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: SO4, UT3, AMP

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	0.49	1/2419 (0.0%)	0.64	4/3301 (0.1%)
1	C	0.57	6/2403 (0.2%)	0.72	4/3278 (0.1%)
2	B	0.48	2/1854 (0.1%)	0.60	0/2524
2	D	0.37	0/1856	0.58	0/2526
All	All	0.49	9/8532 (0.1%)	0.64	8/11629 (0.1%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	371	VAL	C-O	-7.26	1.16	1.24
1	C	276	ASP	C-O	-7.21	1.15	1.23
1	A	276	ASP	C-O	-7.15	1.15	1.23
1	C	275	VAL	C-O	-6.68	1.16	1.24
1	C	274	VAL	C-O	-6.08	1.16	1.23
1	C	276	ASP	CG-OD1	-5.54	1.14	1.25
2	B	508	ARG	C-O	-5.51	1.17	1.24
1	C	281	ASN	C-O	-5.24	1.17	1.24
1	C	277	GLY	C-O	-5.12	1.17	1.24

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	279	ALA	N-CA-C	9.49	124.39	112.24
1	C	278	GLY	N-CA-C	9.13	123.09	112.50
1	C	281	ASN	N-CA-C	9.03	122.77	112.57
1	C	275	VAL	N-CA-C	7.01	117.80	110.72
1	A	69	GLU	CA-C-N	5.87	128.07	120.44
1	A	69	GLU	C-N-CA	5.87	128.07	120.44
1	A	216	PRO	CA-C-N	-5.11	112.36	122.02
1	A	216	PRO	C-N-CA	-5.11	112.36	122.02

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2363	0	2293	35	0
1	C	2347	0	2269	23	0
2	B	1823	0	1793	12	0
2	D	1825	0	1798	13	0
3	A	46	0	0	2	0
3	C	46	0	0	0	0
4	A	23	0	11	2	0
5	A	5	0	0	0	0
5	C	5	0	0	0	0
6	A	125	0	0	1	0
6	B	114	0	0	1	0
6	C	183	0	0	2	0
6	D	94	0	0	0	0
All	All	8999	0	8164	81	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 (81) 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)
4:A:402:AMP:C4'	4:A:402:AMP:O4'	1.65	1.19
1:A:166:HIS:O	1:A:217:GLU:HB2	1.74	0.86
2:B:494:GLY:O	2:B:496:ILE:N	2.20	0.74
1:A:246:ARG:HH12	1:C:278:GLY:HA2	1.53	0.72
1:A:246:ARG:NH1	1:C:278:GLY:HA2	2.05	0.71
1:A:105:LYS:HD2	1:A:187:LEU:HD22	1.73	0.71
1:A:28:LEU:HD23	1:A:168:ARG:HH21	1.57	0.69
1:A:149:SER:OG	1:A:151:ARG:HG3	1.98	0.62
1:C:322:HIS:HE1	6:C:557:HOH:O	1.83	0.62
1:A:45:ARG:HG3	1:A:63:LYS:HE2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:PRO:HD2	4:A:402:AMP:C8	2.38	0.58
1:C:45:ARG:HD2	1:C:71:ALA:O	2.02	0.58
1:A:274:VAL:HG11	1:A:278:GLY:HA2	1.85	0.57
1:A:312:LYS:N	1:A:312:LYS:HD3	2.22	0.55
2:B:394:ARG:HA	2:B:418:ARG:HB3	1.89	0.55
1:C:31:ARG:HG2	1:C:56:LEU:HD13	1.89	0.54
1:A:105:LYS:HE3	1:A:188:HIS:HE1	1.72	0.54
1:A:146:LEU:HB3	1:A:152:LEU:HD23	1.89	0.53
2:D:349:VAL:HG22	2:D:350:LYS:H	1.72	0.53
1:A:291:ASP:O	1:A:295:ARG:HD3	2.09	0.52
1:C:79:ASP:HA	1:C:102:VAL:HG23	1.91	0.52
1:A:48:SER:OG	1:A:50:ASP:OD1	2.27	0.51
2:D:448:THR:HB	2:D:532:ILE:HB	1.93	0.51
2:D:550:GLU:O	2:D:552:PRO:HD3	2.11	0.51
2:B:421:PHE:HB2	2:B:576:PRO:HG2	1.94	0.50
1:A:246:ARG:HH12	1:C:278:GLY:CA	2.22	0.50
1:C:88:HIS:HA	1:C:117:ILE:HD11	1.92	0.50
1:A:312:LYS:NZ	6:A:503:HOH:O	2.34	0.49
1:C:87:HIS:ND1	1:C:103:CYS:SG	2.86	0.49
1:A:28:LEU:HD23	1:A:168:ARG:NH2	2.26	0.49
2:D:400:PRO:HG2	2:D:585:PHE:CE1	2.48	0.48
1:A:69:GLU:H	1:A:69:GLU:CD	2.22	0.48
1:C:105:LYS:HE3	1:C:188:HIS:HE1	1.79	0.48
1:A:146:LEU:HB3	1:A:152:LEU:CD2	2.44	0.48
1:A:33:HIS:HA	1:A:294:MET:HE3	1.97	0.47
1:A:29:ILE:HG23	1:A:81:CYS:HB3	1.95	0.47
1:A:105:LYS:HE3	1:A:188:HIS:CE1	2.49	0.47
1:A:217:GLU:OE1	1:A:217:GLU:N	2.47	0.47
1:C:112:GLU:H	1:C:112:GLU:CD	2.22	0.47
2:D:547:LEU:HB2	2:D:553:GLU:HB2	1.97	0.46
1:A:217:GLU:H	1:A:217:GLU:CD	2.23	0.45
2:B:386:ARG:NH1	2:B:390:GLU:OE2	2.50	0.45
2:D:449:VAL:O	2:D:513:ALA:HA	2.17	0.45
1:A:213:THR:HA	1:A:214:PRO:C	2.42	0.45
1:C:105:LYS:HE3	1:C:188:HIS:CE1	2.51	0.45
1:A:164:ALA:O	1:A:241:TRP:HA	2.17	0.45
1:A:147:VAL:HG21	1:A:196:VAL:HG13	1.99	0.44
1:A:167:PRO:HD2	3:A:401:UT3:O42	2.18	0.44
2:B:405:GLU:O	2:B:409:LYS:HG3	2.18	0.44
2:B:468:LEU:HD13	2:B:515:PHE:HB3	1.99	0.44
2:D:458:ASP:HB3	2:D:496:ILE:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:VAL:HG21	1:C:196:VAL:HG13	1.99	0.43
1:A:67:SER:OG	1:A:70:GLU:OE1	2.26	0.43
1:A:309:ILE:HG13	1:A:313:ASP:HB2	1.99	0.43
1:C:159:ARG:NE	6:C:503:HOH:O	2.34	0.43
2:D:599:GLN:OE1	2:D:600:PRO:HD2	2.19	0.43
1:A:134:VAL:HG21	1:A:188:HIS:HB3	1.99	0.43
2:D:349:VAL:N	2:D:370:ASP:OD2	2.52	0.43
3:A:401:UT3:O14	3:A:401:UT3:O17	2.36	0.43
1:C:33:HIS:HA	1:C:294:MET:HE3	2.01	0.43
2:D:455:THR:O	2:D:519:ARG:HA	2.18	0.42
2:B:353:ILE:HD11	2:B:365:LEU:HD12	2.00	0.42
2:B:498:GLU:OE1	2:B:592:TYR:OH	2.25	0.42
1:C:163:SER:CB	1:C:240:ARG:HB2	2.49	0.42
2:B:365:LEU:HD21	2:B:564:LEU:HD22	2.01	0.42
2:D:582:LEU:HD23	2:D:582:LEU:HA	1.93	0.42
2:B:397:CYS:O	2:B:421:PHE:HA	2.20	0.42
1:A:146:LEU:HD23	1:A:152:LEU:HD21	2.01	0.42
1:A:17:ARG:HH22	1:A:76:ASP:CG	2.27	0.41
2:B:573:GLY:HA3	6:B:806:HOH:O	2.19	0.41
1:C:134:VAL:HG21	1:C:188:HIS:HB3	2.02	0.41
1:A:202:ARG:NH2	1:A:335:GLU:OE2	2.50	0.41
1:C:20:GLU:HG2	1:C:45:ARG:NH2	2.35	0.41
2:B:553:GLU:HG3	1:C:146:LEU:HD11	2.02	0.41
2:D:563:MET:HE2	2:D:563:MET:HB3	1.90	0.41
2:D:389:ALA:HB1	2:D:415:ALA:HB2	2.03	0.41
1:A:165:TYR:O	1:A:167:PRO:HD3	2.20	0.41
1:C:213:THR:HA	1:C:214:PRO:C	2.45	0.41
1:C:281:ASN:OD1	1:C:281:ASN:N	2.42	0.40
1:C:46:VAL:CG2	1:C:57:ALA:HB2	2.51	0.40
1:C:197:PHE:HB2	1:C:229:HIS:CE1	2.56	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	321/342 (94%)	310 (97%)	11 (3%)	0	100	100
1	C	319/342 (93%)	313 (98%)	6 (2%)	0	100	100
2	B	250/256 (98%)	245 (98%)	5 (2%)	0	100	100
2	D	249/256 (97%)	242 (97%)	7 (3%)	0	100	100
All	All	1139/1196 (95%)	1110 (98%)	29 (2%)	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	A	224/236 (95%)	223 (100%)	1 (0%)	84	92
1	C	222/236 (94%)	222 (100%)	0	100	100
2	B	179/181 (99%)	177 (99%)	2 (1%)	65	82
2	D	180/181 (99%)	180 (100%)	0	100	100
All	All	805/834 (96%)	802 (100%)	3 (0%)	84	92

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	GLU
2	B	370	ASP
2	B	508	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	270	GLN
2	B	535	GLN

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Mol	Chain	Res	Type
2	B	589	GLN
1	C	322	HIS
2	D	511	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	$\# Z > 2$
3	UT3	A	401	-	47,47,47	1.19	3 (6%)	64,68,68	2.05	16 (25%)
3	UT3	C	401	-	47,47,47	1.12	2 (4%)	64,68,68	2.65	25 (39%)
4	AMP	A	402	-	25,25,25	4.23	14 (56%)	38,38,38	2.15	12 (31%)
5	SO4	C	402	-	4,4,4	0.15	0	6,6,6	0.20	0
5	SO4	A	403	-	4,4,4	0.17	0	6,6,6	0.49	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
3	UT3	A	401	-	-	27/70/70/70	0/1/2/2
4	AMP	A	402	-	-	1/10/26/26	0/3/3/3
3	UT3	C	401	-	-	26/70/70/70	0/1/2/2

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	402	AMP	C3'-C4'	-11.56	1.23	1.53
4	A	402	AMP	O4'-C4'	9.00	1.65	1.45
4	A	402	AMP	C2'-C1'	-7.15	1.30	1.53
4	A	402	AMP	C2'-C3'	6.32	1.70	1.53
4	A	402	AMP	C6-N6	6.19	1.49	1.34
3	A	401	UT3	C02-N24	4.62	1.45	1.35
4	A	402	AMP	O4'-C1'	4.22	1.52	1.42
3	C	401	UT3	C02-N24	3.99	1.44	1.35
4	A	402	AMP	P-O1P	3.93	1.63	1.50
4	A	402	AMP	O3'-C3'	3.87	1.52	1.43
4	A	402	AMP	C5'-C4'	3.79	1.63	1.51
3	A	401	UT3	C06-C05	2.91	1.52	1.43
4	A	402	AMP	P-O3P	2.57	1.64	1.54
4	A	402	AMP	O5'-C5'	-2.47	1.35	1.44
4	A	402	AMP	P-O5'	2.43	1.68	1.60
3	C	401	UT3	C06-C05	2.40	1.50	1.43
4	A	402	AMP	C1'-N9	2.23	1.52	1.46
4	A	402	AMP	C8-N9	-2.21	1.33	1.37
3	A	401	UT3	C25-N24	2.05	1.45	1.41

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	UT3	C05-C06-C07	-9.24	102.13	124.53
4	A	402	AMP	C5-C4-N3	-6.54	118.21	126.75
3	C	401	UT3	C32-C31-C29	5.25	118.53	112.25
3	C	401	UT3	C40-C39-C20	5.13	122.05	111.31
3	C	401	UT3	C28-C29-C31	5.09	119.94	112.58
4	A	402	AMP	N3-C4-N9	5.01	135.34	127.08
3	C	401	UT3	C18-C16-C15	-4.90	107.22	115.43
3	A	401	UT3	C19-C18-C16	4.75	120.99	111.39
3	C	401	UT3	C05-C03-C02	-4.69	106.75	121.09
3	A	401	UT3	C13-C11-C09	-4.68	103.14	112.54
3	A	401	UT3	C40-C39-C20	4.63	121.02	111.31
3	C	401	UT3	C29-C31-C33	-4.48	102.85	109.34
3	A	401	UT3	C38-C36-C35	-4.45	113.37	121.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	UT3	C13-C11-C09	-4.35	103.79	112.54
3	A	401	UT3	C22-C15-C13	-4.26	102.78	111.39
4	A	402	AMP	N3-C2-N1	-4.25	121.96	128.60
3	C	401	UT3	C38-C36-C35	-4.25	113.75	121.60
3	A	401	UT3	C08-C07-C06	-4.00	117.74	126.16
3	C	401	UT3	C25-N24-C02	-3.90	115.92	126.80
4	A	402	AMP	C2-N3-C4	3.89	120.95	111.75
3	C	401	UT3	C09-C08-C07	-3.76	102.54	111.42
3	C	401	UT3	C06-C05-C03	3.72	137.55	126.61
3	C	401	UT3	C39-C20-C18	3.62	122.35	114.96
3	A	401	UT3	C39-C38-C36	3.53	135.74	126.32
3	A	401	UT3	C16-C15-C13	-3.43	105.64	112.54
3	A	401	UT3	O30-C29-C28	-3.41	104.21	110.32
3	A	401	UT3	C37-C36-C38	3.32	129.68	124.30
3	A	401	UT3	C40-C39-C38	-3.17	104.77	110.05
3	A	401	UT3	C09-C08-C07	-3.12	104.05	111.42
3	A	401	UT3	C39-C20-C18	3.06	121.20	114.96
3	C	401	UT3	C37-C36-C38	3.05	129.24	124.30
3	C	401	UT3	C19-C18-C16	3.04	117.53	111.39
3	C	401	UT3	C46-C25-N24	-2.99	114.00	121.90
3	C	401	UT3	C40-C39-C38	-2.98	105.10	110.05
3	C	401	UT3	C04-C03-C02	2.97	122.77	115.28
3	A	401	UT3	C20-C18-C16	-2.93	106.64	112.54
4	A	402	AMP	C5-N7-C8	2.93	107.68	103.51
3	C	401	UT3	C04-C03-C05	2.82	130.25	123.42
4	A	402	AMP	P-O5'-C5'	2.77	125.91	118.30
3	C	401	UT3	C22-C15-C16	-2.74	105.84	111.39
4	A	402	AMP	N9-C8-N7	-2.71	110.21	113.91
3	C	401	UT3	O01-C02-C03	-2.70	116.75	121.53
3	C	401	UT3	C20-C39-C38	-2.49	104.80	110.56
4	A	402	AMP	C4-C5-N7	-2.48	107.60	110.62
3	A	401	UT3	C43-C28-C26	2.48	120.09	117.49
4	A	402	AMP	O4'-C1'-C2'	-2.46	101.28	106.64
3	C	401	UT3	C22-C15-C13	-2.43	106.48	111.39
3	C	401	UT3	C20-C18-C16	-2.35	107.82	112.54
3	A	401	UT3	C05-C06-C07	-2.28	119.00	124.53
4	A	402	AMP	C4'-O4'-C1'	-2.26	104.49	109.47
4	A	402	AMP	C2'-C3'-C4'	2.16	106.85	102.64
4	A	402	AMP	C4-N9-C8	2.16	108.07	105.73
3	C	401	UT3	C43-C28-C26	2.09	119.69	117.49

There are no chirality outliers.

All (54) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	UT3	C07-C08-C09-O10
3	A	401	UT3	C08-C09-C11-C12
3	A	401	UT3	O10-C09-C11-C12
3	A	401	UT3	O10-C09-C11-C13
3	A	401	UT3	C15-C16-C18-C19
3	A	401	UT3	O17-C16-C18-C19
3	A	401	UT3	C18-C20-C39-C38
3	A	401	UT3	C18-C20-C39-C40
3	A	401	UT3	O21-C20-C39-C38
3	A	401	UT3	O21-C20-C39-C40
3	A	401	UT3	O42-C33-C34-C35
3	A	401	UT3	C36-C38-C39-C20
3	C	401	UT3	C23-C08-C09-O10
3	C	401	UT3	C08-C09-C11-C12
3	C	401	UT3	O10-C09-C11-C12
3	C	401	UT3	O10-C09-C11-C13
3	C	401	UT3	C18-C20-C39-C38
3	C	401	UT3	C18-C20-C39-C40
3	C	401	UT3	O21-C20-C39-C38
3	C	401	UT3	O21-C20-C39-C40
3	C	401	UT3	C26-C28-C29-O30
3	C	401	UT3	C43-C28-C29-O30
3	C	401	UT3	C36-C38-C39-C20
3	C	401	UT3	C36-C38-C39-C40
3	A	401	UT3	C08-C09-C11-C13
3	A	401	UT3	C15-C16-C18-C20
3	C	401	UT3	C08-C09-C11-C13
3	A	401	UT3	O17-C16-C18-C20
3	A	401	UT3	C07-C08-C09-C11
3	A	401	UT3	C23-C08-C09-C11
3	C	401	UT3	C23-C08-C09-C11
3	C	401	UT3	O14-C13-C15-C22
3	A	401	UT3	C26-C25-N24-C02
3	A	401	UT3	C06-C07-C08-C23
3	C	401	UT3	O42-C33-C34-C35
3	C	401	UT3	C07-C08-C09-C11
3	C	401	UT3	C26-C25-N24-C02
3	A	401	UT3	C23-C08-C09-O10
3	A	401	UT3	C34-C35-C36-C37
3	A	401	UT3	O01-C02-C03-C05
3	C	401	UT3	C11-C13-C15-C22
3	A	401	UT3	C36-C38-C39-C40

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Mol	Chain	Res	Type	Atoms
3	A	401	UT3	C34-C35-C36-C38
3	A	401	UT3	N24-C02-C03-C05
3	C	401	UT3	C11-C13-C15-C16
3	C	401	UT3	C46-C25-N24-C02
3	C	401	UT3	C06-C07-C08-C23
3	A	401	UT3	O41-C35-C36-C38
3	C	401	UT3	C07-C08-C09-O10
3	C	401	UT3	C43-C28-C29-C31
3	C	401	UT3	N24-C02-C03-C05
3	C	401	UT3	O01-C02-C03-C05
3	A	401	UT3	C16-C18-C20-C39
4	A	402	AMP	O4'-C4'-C5'-O5'

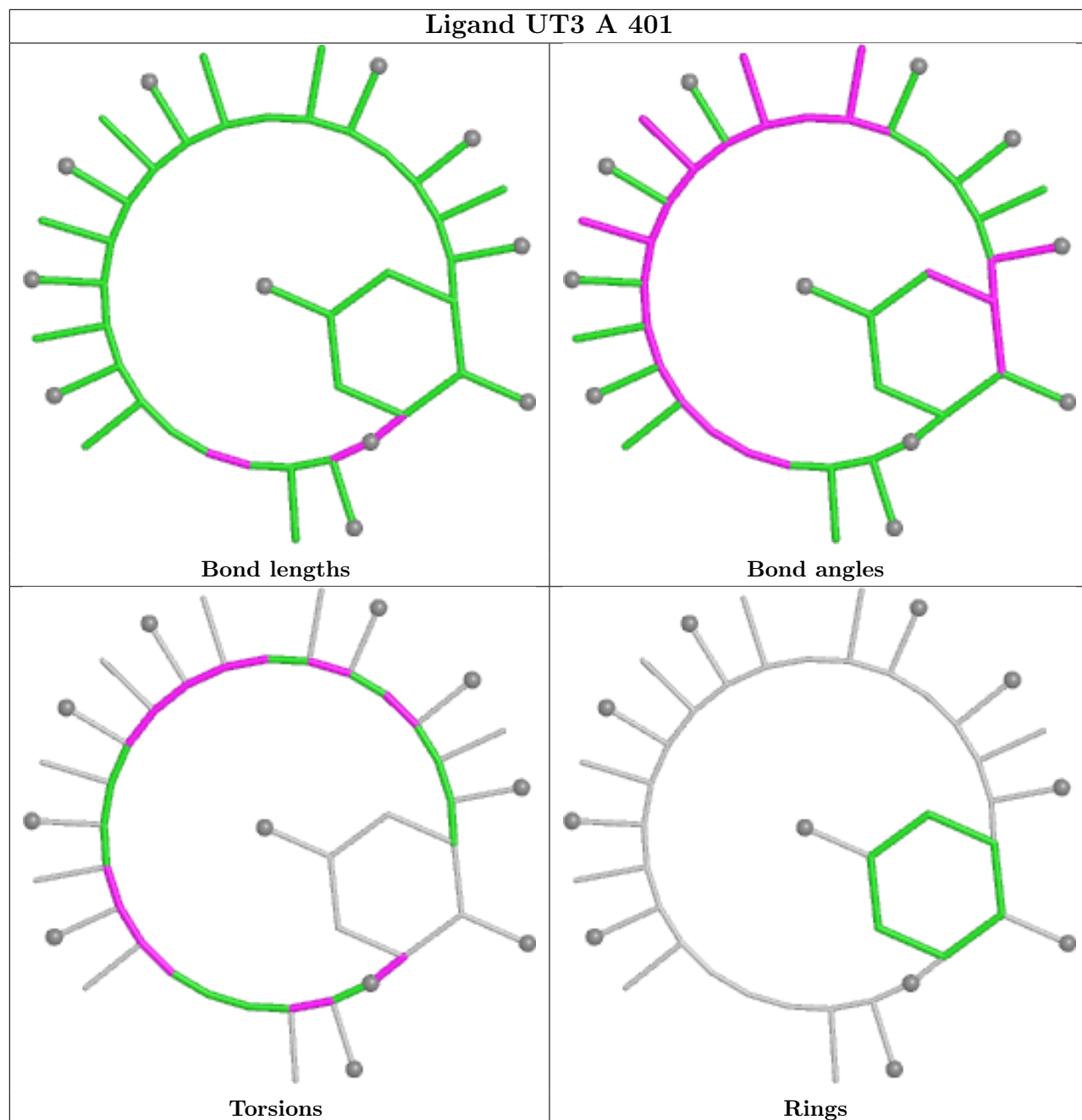
There are no ring outliers.

2 monomers are involved in 4 short contacts:

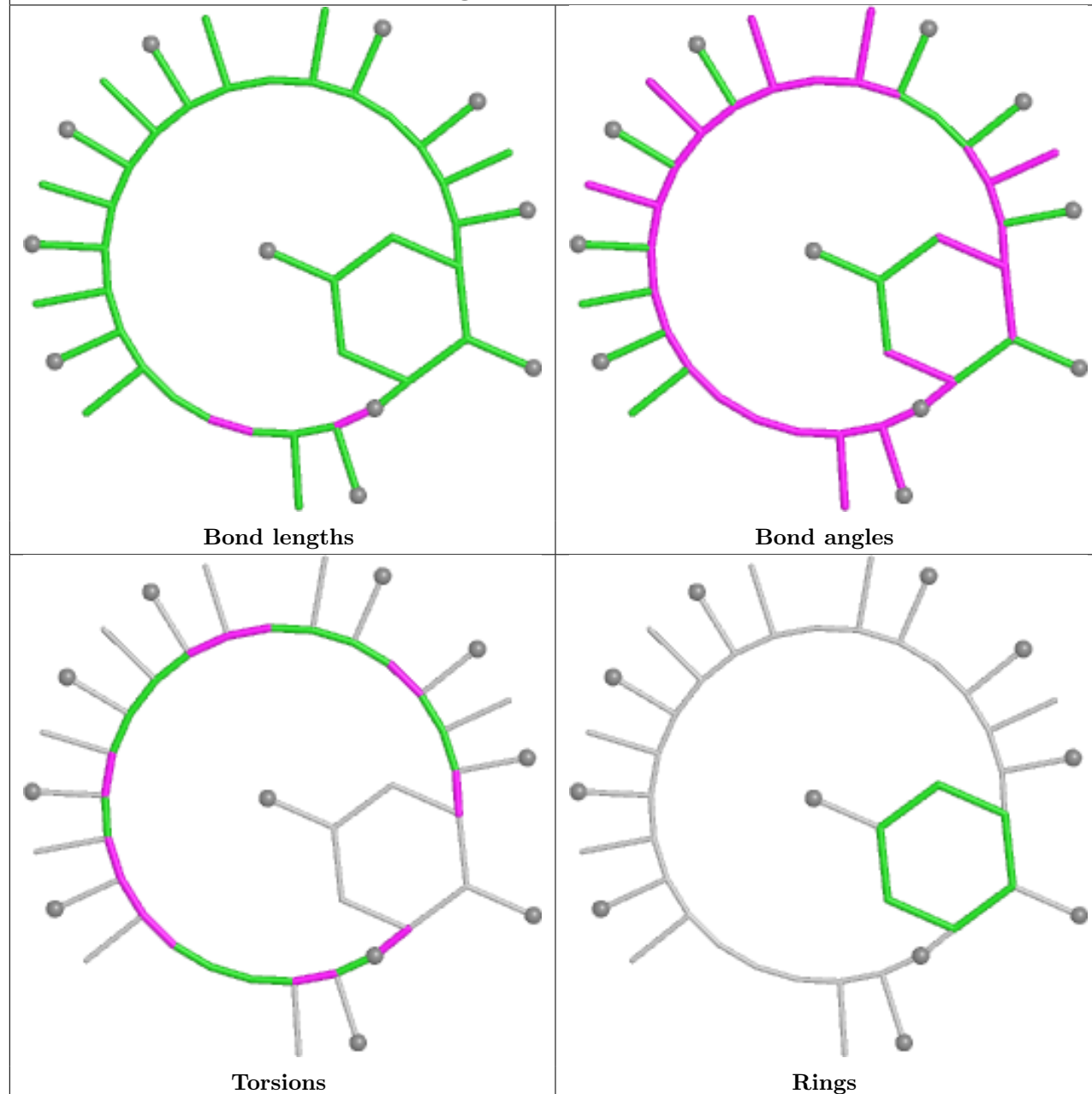
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	UT3	2	0
4	A	402	AMP	2	0

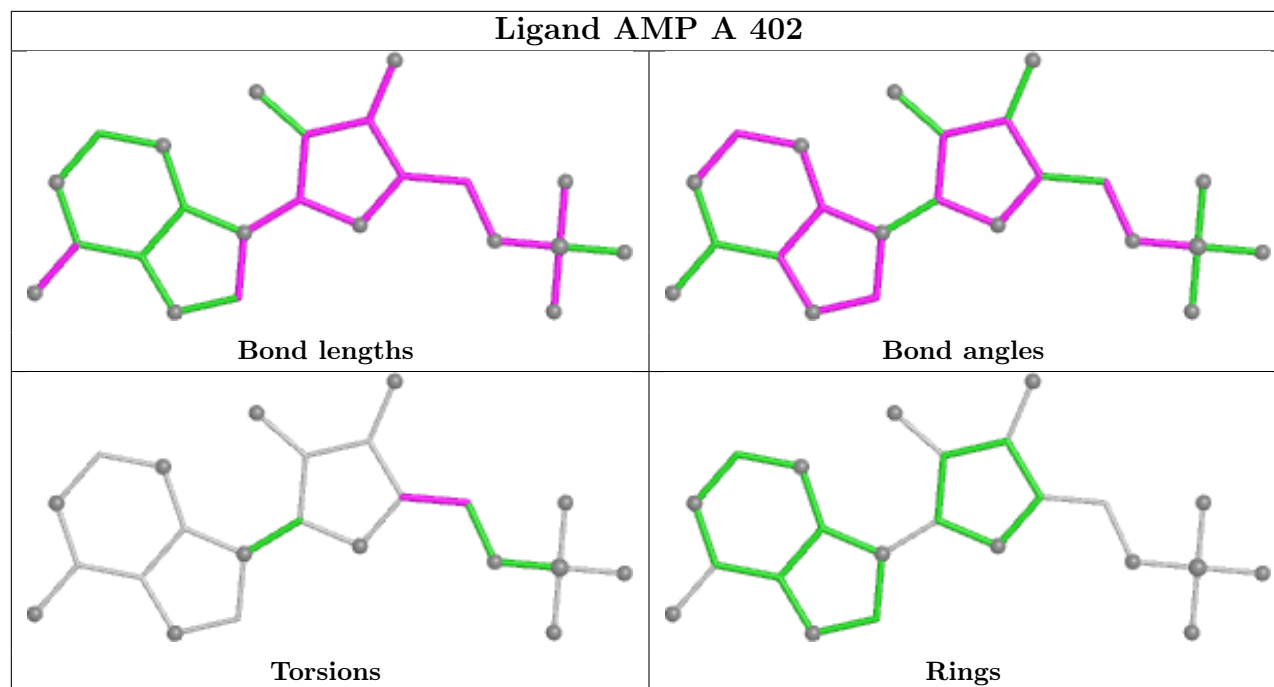
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand UT3 A 401



Ligand UT3 C 401





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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	323/342 (94%)	-0.20	7 (2%) 62 58	13, 31, 54, 72	0
1	C	321/342 (93%)	-0.38	0 100 100	13, 25, 42, 56	0
2	B	254/256 (99%)	-0.32	2 (0%) 82 80	12, 26, 50, 73	0
2	D	253/256 (98%)	-0.00	5 (1%) 65 60	18, 34, 64, 80	0
All	All	1151/1196 (96%)	-0.24	14 (1%) 76 73	12, 28, 54, 80	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	278	GLY	3.2
2	D	572	ASP	2.6
2	D	496	ILE	2.6
1	A	70	GLU	2.5
1	A	16	LEU	2.5
1	A	279	ALA	2.5
2	B	496	ILE	2.4
2	D	360	ALA	2.3
1	A	280	GLY	2.2
2	D	349	VAL	2.1
1	A	52	ARG	2.1
1	A	54	ARG	2.1
2	B	403	ALA	2.0
2	D	569	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

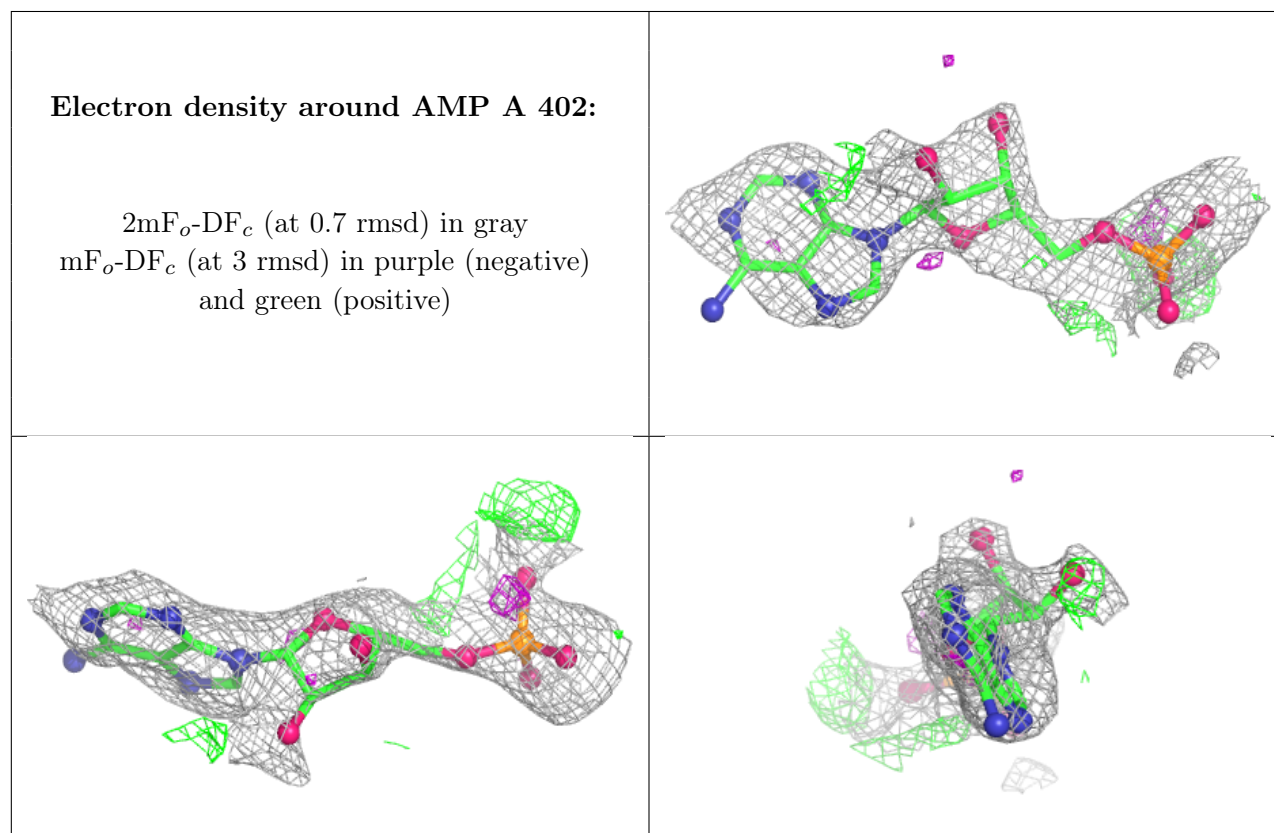
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

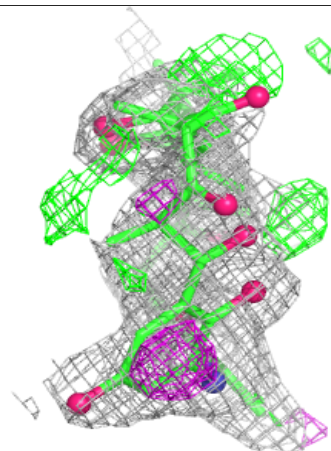
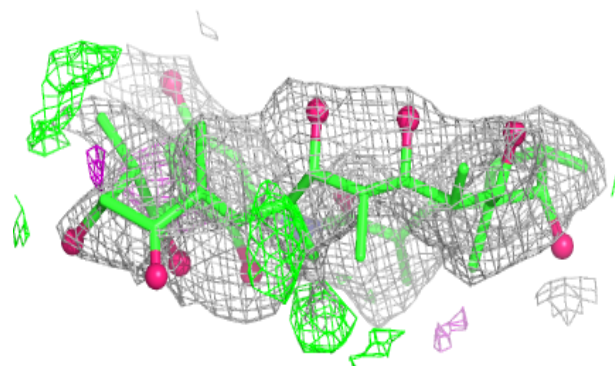
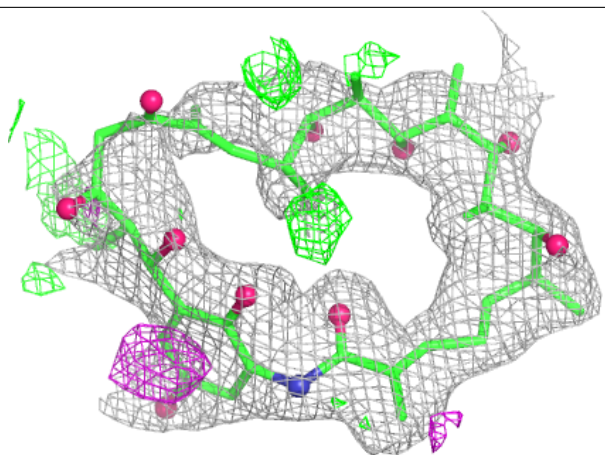
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	AMP	A	402	23/23	0.57	0.17	57,62,84,95	0
3	UT3	C	401	46/46	0.75	0.17	30,52,67,73	0
3	UT3	A	401	46/46	0.77	0.17	25,52,67,72	0
5	SO4	A	403	5/5	0.86	0.16	44,46,59,59	0
5	SO4	C	402	5/5	0.90	0.17	42,49,62,75	0

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.



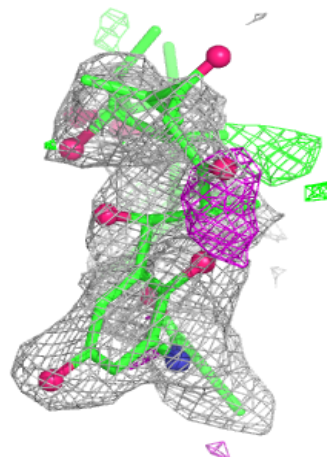
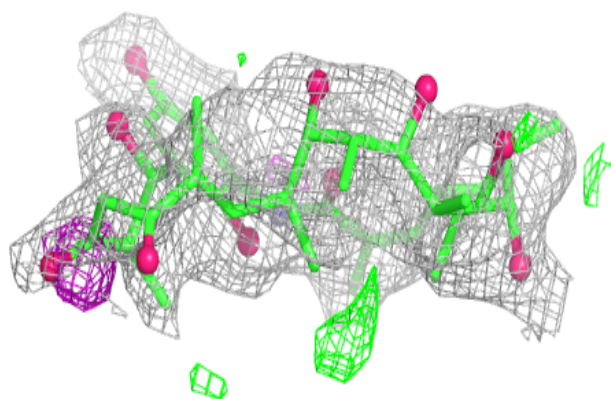
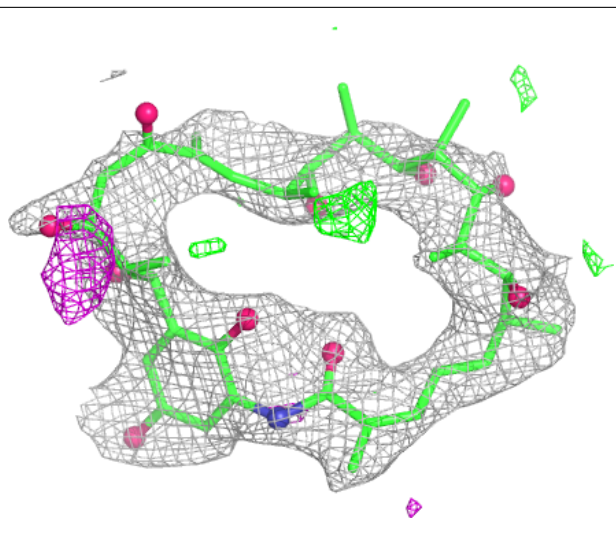
Electron density around UT3 C 401:

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



Electron density around UT3 A 401:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.