Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:55 PM UTC

PDB ID	:	7UEV / pdb_00007uev
Title	:	PANK3 complex structure with compound PZ-4200
Authors	:	White, S.W.; Yun, M.; Lee, R.E.
Deposited on	:	2022-03-22
Resolution	:	1.80 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:

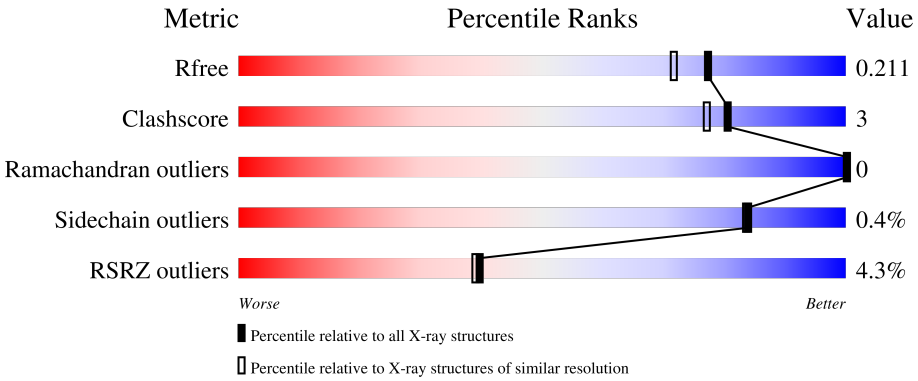
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 <=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	380	4% 87% 5% 7%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 2909 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.

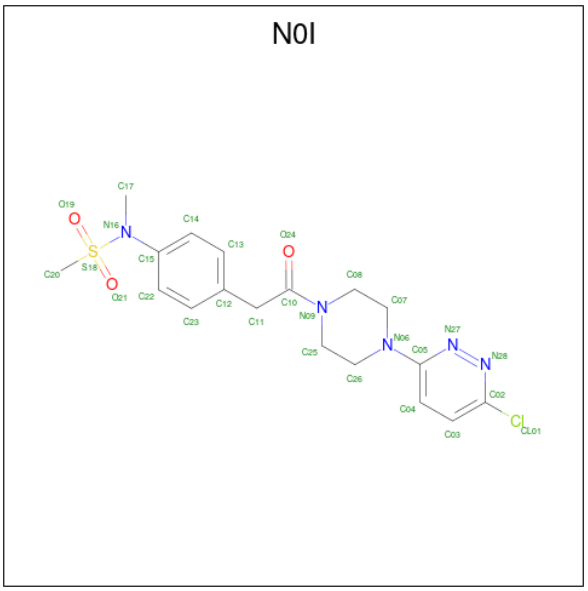
- Molecule 1 is a protein called Pantothenate kinase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	1	0
			2712	1738	454	506	14			

There are 21 discrepancies between the modelled and reference sequences:

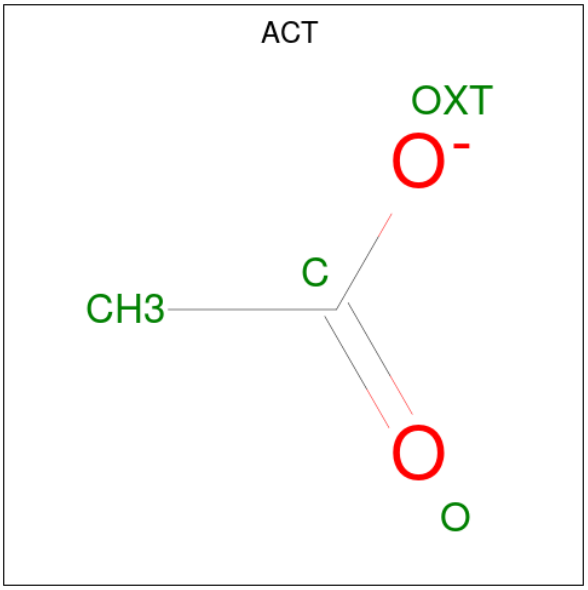
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP Q9H999
A	-6	GLY	-	expression tag	UNP Q9H999
A	-5	SER	-	expression tag	UNP Q9H999
A	-4	SER	-	expression tag	UNP Q9H999
A	-3	HIS	-	expression tag	UNP Q9H999
A	-2	HIS	-	expression tag	UNP Q9H999
A	-1	HIS	-	expression tag	UNP Q9H999
A	0	HIS	-	expression tag	UNP Q9H999
A	1	HIS	-	expression tag	UNP Q9H999
A	2	HIS	-	expression tag	UNP Q9H999
A	3	SER	-	expression tag	UNP Q9H999
A	4	SER	-	expression tag	UNP Q9H999
A	5	GLY	-	expression tag	UNP Q9H999
A	6	LEU	-	expression tag	UNP Q9H999
A	7	VAL	-	expression tag	UNP Q9H999
A	8	PRO	-	expression tag	UNP Q9H999
A	9	ARG	-	expression tag	UNP Q9H999
A	10	GLY	-	expression tag	UNP Q9H999
A	11	SER	-	expression tag	UNP Q9H999
A	371	ASP	-	expression tag	UNP Q9H999
A	372	ASP	-	expression tag	UNP Q9H999

- Molecule 2 is N-(4-{2-[4-(6-chloropyridazin-3-yl)piperazin-1-yl]-2-oxoethyl}phenyl)-N-methylmethanesulfonamide (CCD ID: N0I) (formula: $C_{18}H_{22}ClN_5O_3S$) (labeled as "Ligand of Interest" by depositor).



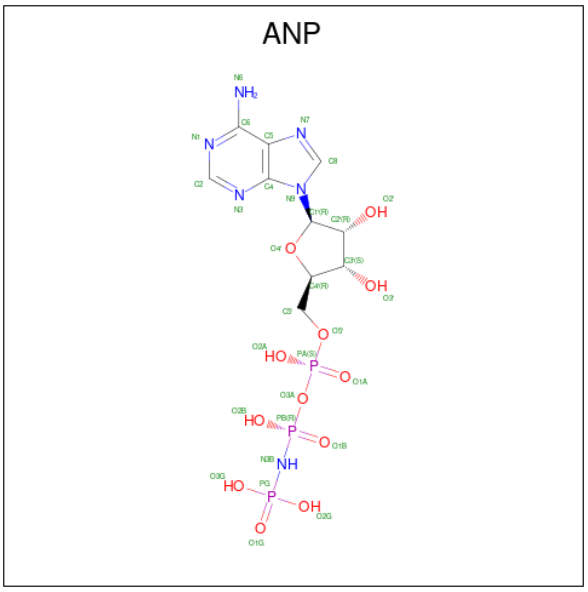
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0	1
			33	20	1	5	5	2		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).

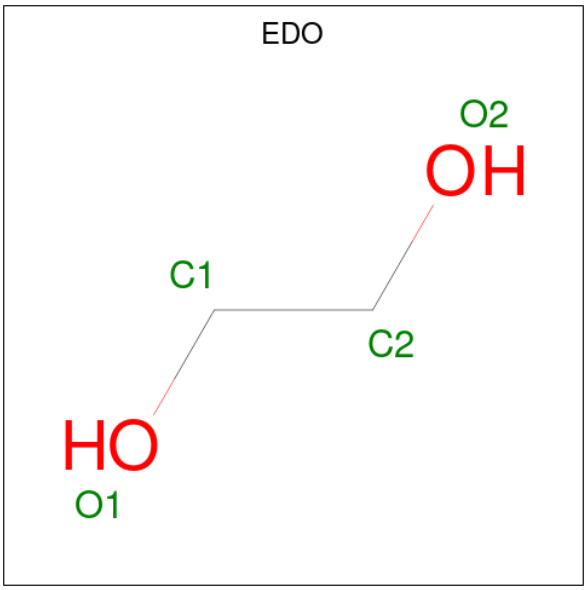


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Cl 1 1	0	0

- Molecule 8 is water.

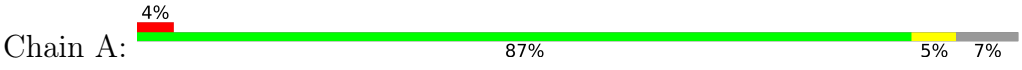
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	123	Total O 123 123	0	0

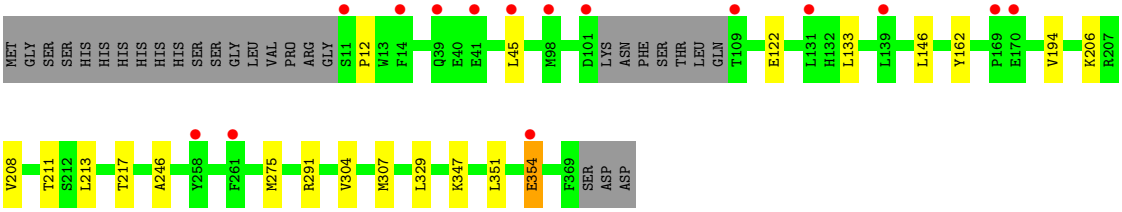
3 Residue-property plots (i)

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: Pantothenate kinase 3

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	98.23Å 98.23Å 69.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.03 – 1.80 40.03 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.03-1.80) 96.8 (40.03-1.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.27 (at 1.81Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.176 , 0.211 0.178 , 0.211	Depositor DCC
R_{free} test set	1774 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	26.8	Xtriage
Anisotropy	0.274	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 45.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	2909	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ANP, MG, ACT, N0I, CL, 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	A	0.42	0/2769	0.60	0/3742

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

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	2712	0	2677	13	0
2	A	33	0	0	0	0
3	A	4	0	3	1	0
4	A	31	0	13	0	0
5	A	1	0	0	0	0
6	A	4	0	6	0	0
7	A	1	0	0	0	0
8	A	123	0	0	1	0
All	All	2909	0	2699	14	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 (14) 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:351:LEU:O	1:A:354:GLU:HG2	1.95	0.66
1:A:213:LEU:HD23	1:A:217:THR:HG21	1.91	0.53
1:A:194:VAL:HB	1:A:211:THR:CG2	2.44	0.48
1:A:162:TYR:CD2	1:A:347:LYS:HE2	2.50	0.47
1:A:122:GLU:HG3	1:A:133:LEU:HD23	1.96	0.47
1:A:275:MET:HA	1:A:275:MET:HE2	1.98	0.46
1:A:12:PRO:HD3	1:A:45:LEU:HD12	1.99	0.44
1:A:246:ALA:HA	1:A:275:MET:HE3	1.99	0.43
1:A:291:ARG:NE	1:A:329:LEU:HD21	2.34	0.43
1:A:304:VAL:HA	1:A:307:MET:HE3	2.02	0.42
3:A:402:ACT:H3	8:A:530:HOH:O	2.20	0.41
1:A:206:LYS:HE2	1:A:208:VAL:HA	2.03	0.40
1:A:146:LEU:HD23	1:A:146:LEU:C	2.46	0.40
1:A:194:VAL:HB	1:A:211:THR:HG22	2.04	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	349/380 (92%)	343 (98%)	6 (2%)	0	100 100

There are no Ramachandran outliers to report.

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	286/320 (89%)	285 (100%)	1 (0%)	86 86

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	354	GLU

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

Mol	Chain	Res	Type
1	A	134	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)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	$\#\|Z\|>2$
2	N0I	A	401[B]	-	29,30,30	1.81	9 (31%)	40,43,43	2.32	8 (20%)
2	N0I	A	401[A]	-	29,30,30	1.84	9 (31%)	40,43,43	2.53	8 (20%)
4	ANP	A	403	5	33,33,33	1.16	5 (15%)	45,52,52	2.02	11 (24%)
6	EDO	A	405	-	3,3,3	0.47	0	2,2,2	0.48	0
3	ACT	A	402	-	3,3,3	1.08	0	3,3,3	1.80	2 (66%)

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
6	EDO	A	405	-	-	0/1/1/1	-
2	N0I	A	401[B]	-	-	2/22/32/32	0/3/3/3
2	N0I	A	401[A]	-	-	3/22/32/32	0/3/3/3
4	ANP	A	403	5	-	4/18/38/38	0/3/3/3

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401[A]	N0I	C10-N09	4.61	1.44	1.35
2	A	401[B]	N0I	C10-N09	4.61	1.44	1.35
2	A	401[A]	N0I	S18-N16	3.84	1.70	1.64
2	A	401[A]	N0I	C08-N09	-3.55	1.40	1.47
2	A	401[B]	N0I	C08-N09	-3.55	1.40	1.47
2	A	401[B]	N0I	S18-N16	2.91	1.69	1.64
2	A	401[A]	N0I	C25-N09	-2.88	1.41	1.47
2	A	401[B]	N0I	C25-N09	-2.88	1.41	1.47
2	A	401[B]	N0I	C20-S18	2.72	1.81	1.75
2	A	401[A]	N0I	O21-S18	2.57	1.47	1.43
2	A	401[B]	N0I	O19-S18	2.51	1.47	1.43
2	A	401[B]	N0I	O21-S18	2.48	1.47	1.43
2	A	401[A]	N0I	C07-N06	2.48	1.51	1.46
2	A	401[B]	N0I	C07-N06	2.48	1.51	1.46
4	A	403	ANP	PG-O2G	-2.44	1.50	1.56
2	A	401[A]	N0I	C05-N06	2.35	1.43	1.37
2	A	401[B]	N0I	C05-N06	2.35	1.43	1.37
4	A	403	ANP	PG-O1G	2.32	1.49	1.46
4	A	403	ANP	PB-O2B	-2.29	1.50	1.56
4	A	403	ANP	C6-N6	2.25	1.39	1.34
2	A	401[A]	N0I	C20-S18	2.22	1.80	1.75

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401[A]	N0I	O19-S18	2.21	1.46	1.43
4	A	403	ANP	PB-O1B	2.17	1.49	1.46

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401[A]	N0I	O21-S18-O19	-11.16	101.77	118.46
2	A	401[B]	N0I	O21-S18-O19	-10.38	102.94	118.46
4	A	403	ANP	O1G-PG-N3B	-7.59	100.59	111.77
4	A	403	ANP	C5-C4-N3	-5.19	119.57	126.72
2	A	401[B]	N0I	O21-S18-C20	4.66	114.69	108.30
2	A	401[A]	N0I	O21-S18-N16	4.60	112.40	107.14
2	A	401[A]	N0I	O19-S18-N16	4.58	112.38	107.14
4	A	403	ANP	N3-C4-N9	4.26	134.41	127.17
2	A	401[A]	N0I	O19-S18-C20	4.21	114.07	108.30
2	A	401[B]	N0I	O19-S18-N16	3.46	111.10	107.14
4	A	403	ANP	C5-N7-C8	3.33	108.68	103.45
2	A	401[A]	N0I	C12-C11-C10	-3.05	107.31	112.64
2	A	401[B]	N0I	C12-C11-C10	-3.05	107.31	112.64
4	A	403	ANP	N9-C8-N7	-3.00	109.68	113.94
2	A	401[A]	N0I	C23-C12-C13	2.83	122.44	118.23
2	A	401[B]	N0I	C23-C12-C13	2.83	122.44	118.23
2	A	401[A]	N0I	C02-N28-N27	2.74	120.47	118.42
2	A	401[B]	N0I	C02-N28-N27	2.74	120.47	118.42
4	A	403	ANP	O2B-PB-O3A	2.62	113.40	104.64
4	A	403	ANP	C4-C5-N7	-2.58	107.63	110.58
4	A	403	ANP	C2-N3-C4	2.43	117.78	111.83
3	A	402	ACT	OXT-C-O	2.35	130.74	122.03
2	A	401[B]	N0I	C20-S18-N16	2.29	109.63	106.82
4	A	403	ANP	O2G-PG-O1G	-2.20	107.92	113.45
4	A	403	ANP	C4-N9-C8	2.17	108.02	105.74
4	A	403	ANP	O3'-C3'-C4'	-2.15	104.90	111.08
3	A	402	ACT	O-C-CH3	-2.06	114.07	122.53
2	A	401[A]	N0I	C03-C04-C05	-2.05	114.81	117.65
2	A	401[B]	N0I	C03-C04-C05	-2.05	114.81	117.65

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401[A]	N0I	C17-N16-S18-O21
2	A	401[B]	N0I	C15-N16-S18-O21

Continued on next page...

Continued from previous page...

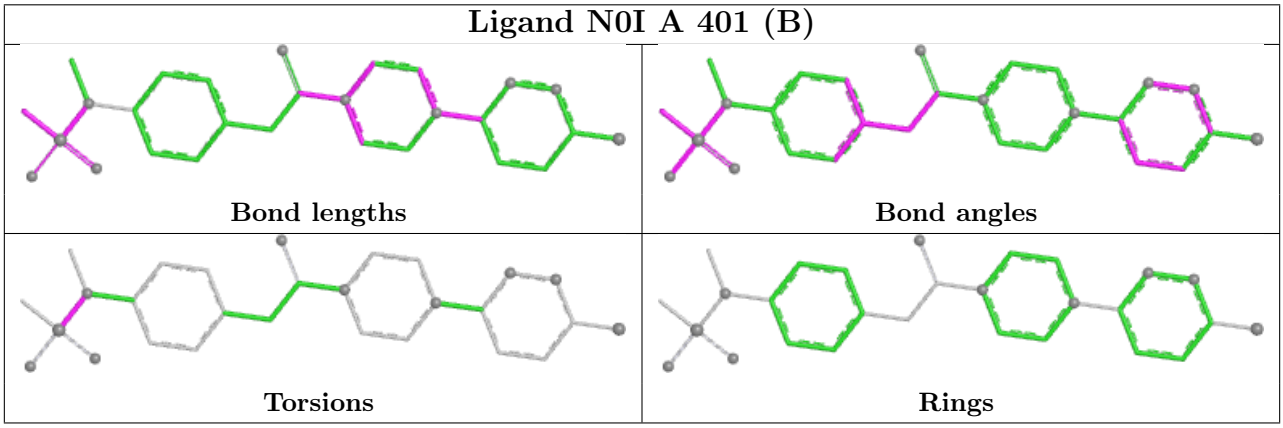
Mol	Chain	Res	Type	Atoms
4	A	403	ANP	PB-N3B-PG-O1G
4	A	403	ANP	C2'-C1'-N9-C4
4	A	403	ANP	C2'-C1'-N9-C8
2	A	401[A]	N0I	C14-C15-N16-C17
2	A	401[B]	N0I	C17-N16-S18-O21
2	A	401[A]	N0I	C15-N16-S18-O19
4	A	403	ANP	PB-O3A-PA-O2A

There are no ring outliers.

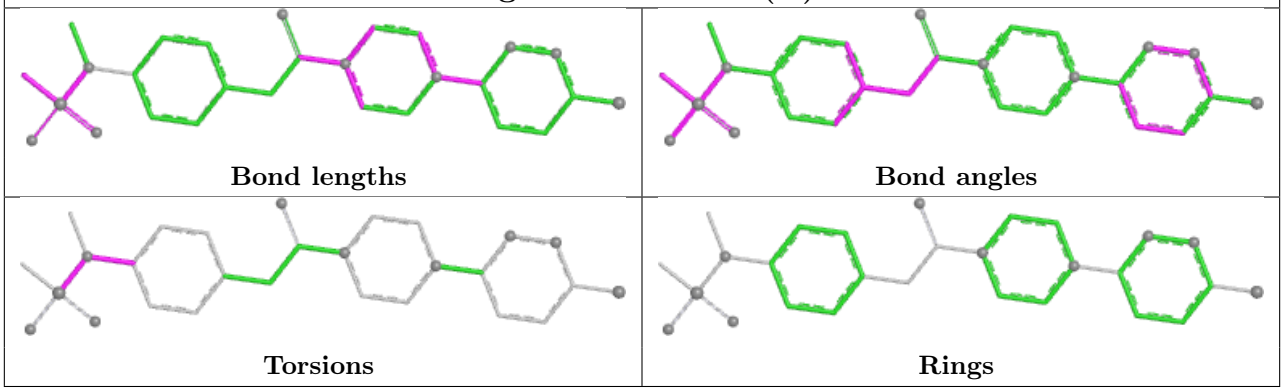
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	ACT	1	0

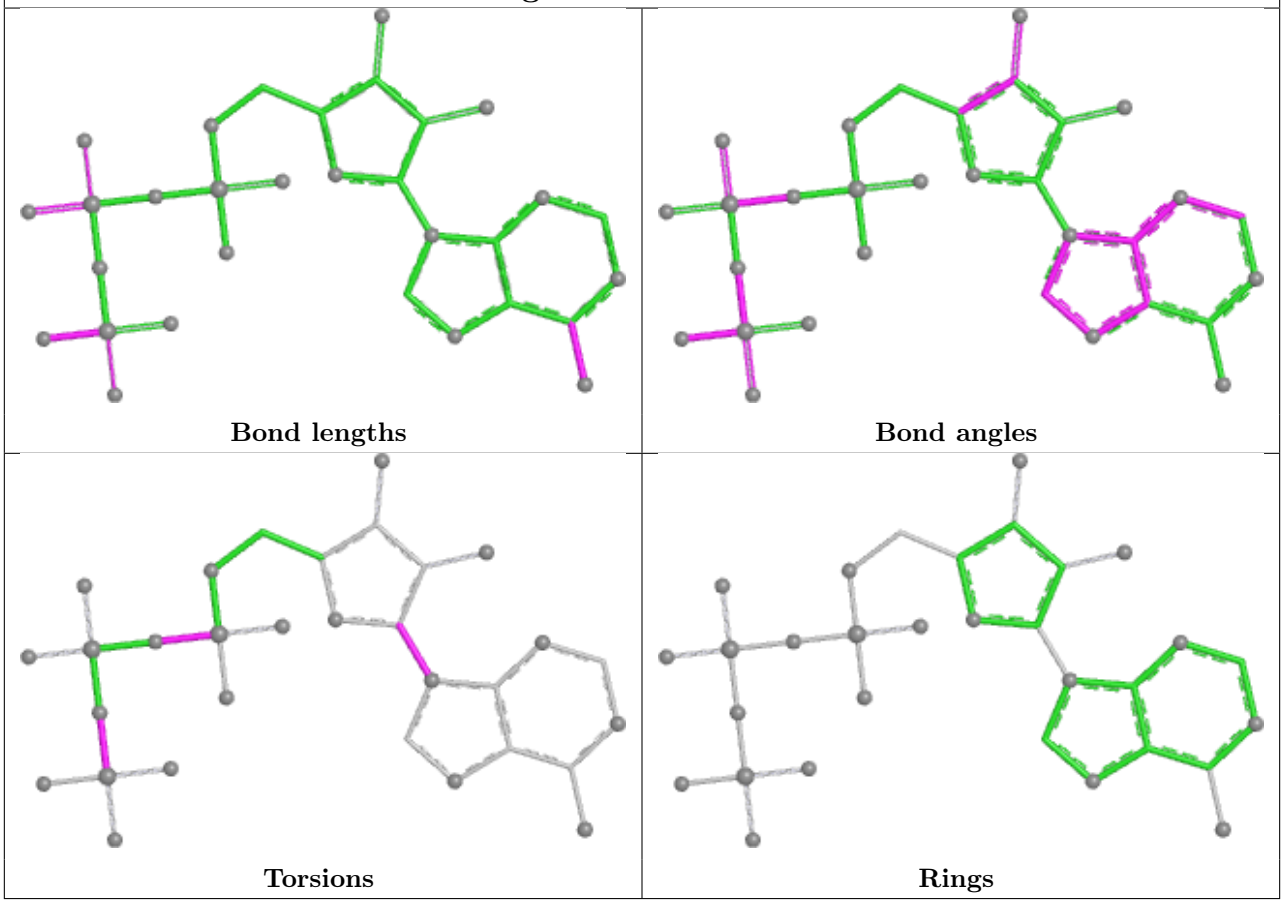
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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 N0I A 401 (A)



Ligand ANP A 403



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, 95^{th} 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	352/380 (92%)	0.20	15 (4%) 40 39	15, 34, 63, 83	1 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	261	PHE	3.4
1	A	101	ASP	3.4
1	A	109	THR	3.1
1	A	14	PHE	3.0
1	A	39	GLN	2.9
1	A	41	GLU	2.7
1	A	258	TYR	2.7
1	A	139	LEU	2.7
1	A	354	GLU	2.4
1	A	169	PRO	2.4
1	A	131	LEU	2.3
1	A	45	LEU	2.3
1	A	170	GLU	2.3
1	A	11	SER	2.2
1	A	98	MET	2.2

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

There are no oligosaccharides in this entry.

6.4 Ligands (i)

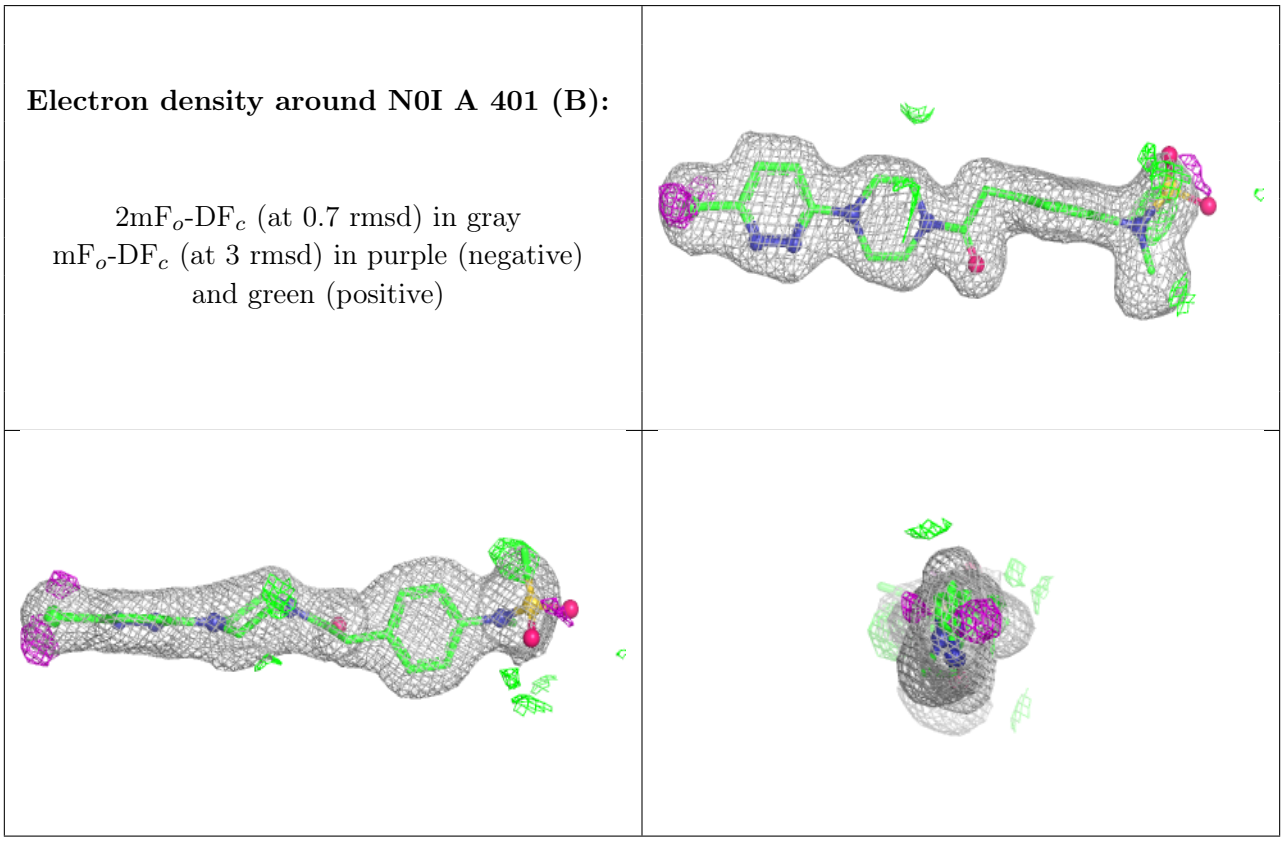
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	ACT	A	402	4/4	0.84	0.23	39,40,44,44	0
6	EDO	A	405	4/4	0.86	0.15	36,40,48,53	0
7	CL	A	406	1/1	0.93	0.09	63,63,63,63	0
2	N0I	A	401[B]	28/28	0.94	0.09	26,33,48,50	5
2	N0I	A	401[A]	28/28	0.94	0.09	26,33,51,52	5
5	MG	A	404	1/1	0.96	0.12	35,35,35,35	0
4	ANP	A	403	31/31	0.98	0.05	18,22,31,33	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.

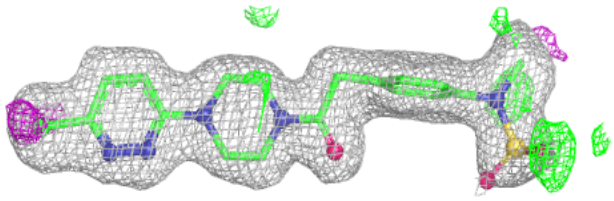
Electron density around N0I A 401 (B):

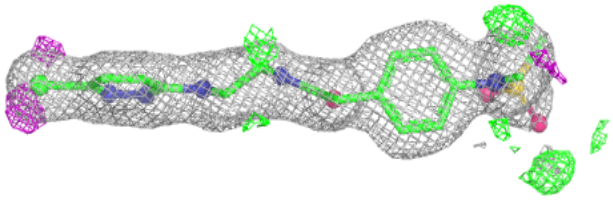
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

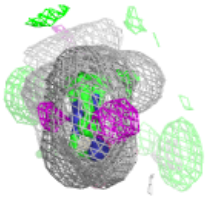


Electron density around N0I A 401 (A):

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

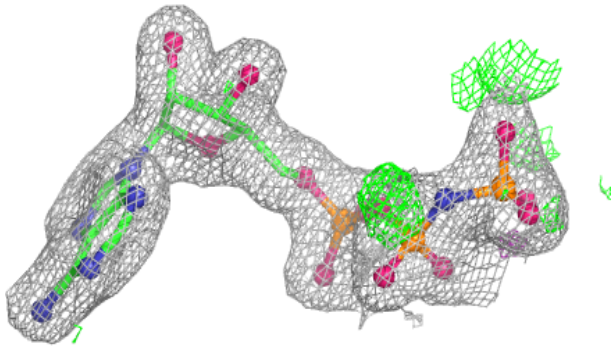


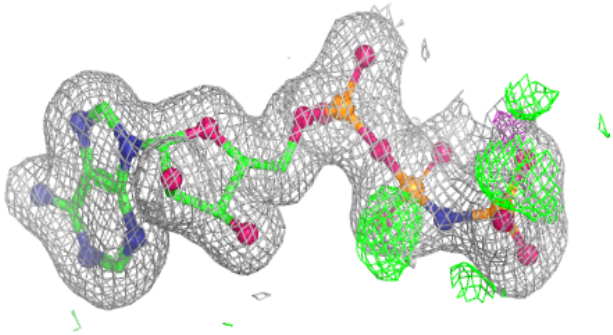


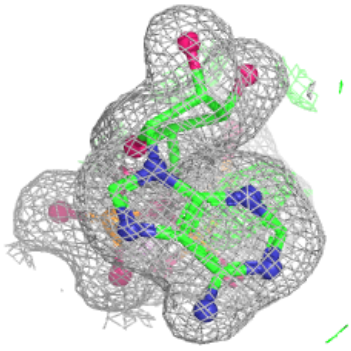


Electron density around ANP A 403:

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







6.5 Other polymers (i)

There are no such residues in this entry.