



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 01:55 AM UTC

PDB ID : 7UKZ / pdb_00007ukz
Title : CDK11 in complex with small molecule inhibitor OTS964
Authors : Kelso, S.; Sicheri, F.
Deposited on : 2022-04-03
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

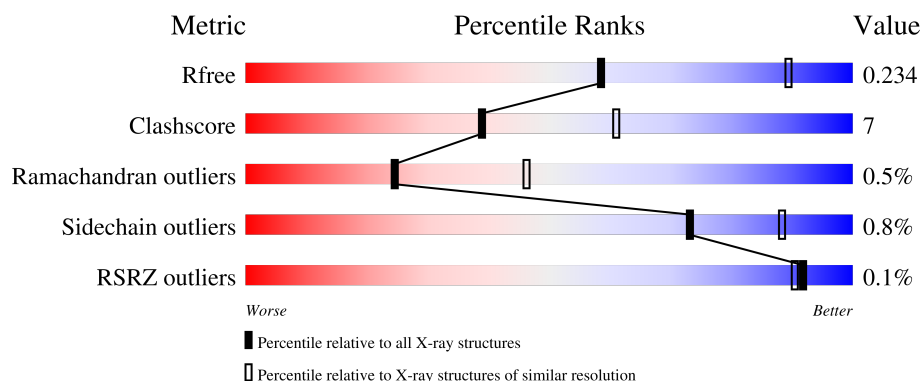
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

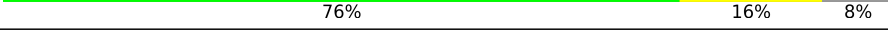
The reported resolution of this entry is 2.60 Å.

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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 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	319	 78%14%7%
1	B	319	 79%13%7%
1	C	319	 80%12%8%
1	D	319	 76%16%8%
1	E	319	 76%17%6%

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Mol	Chain	Length	Quality of chain
1	F	319	 A horizontal bar chart showing the quality of the chain. The bar is divided into three segments: green (73%), yellow (19%), and grey (8%). The percentages are labeled below the segments.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13429 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 Cyclin-dependent kinase 11B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	P	S	2	0	0
			2247	1453	371	410	1	12			
1	B	296	Total	C	N	O	P	S	4	0	0
			2177	1397	365	404	1	10			
1	C	294	Total	C	N	O	P	S	5	0	0
			2185	1417	359	397	1	11			
1	D	294	Total	C	N	O	P	S	3	0	0
			2170	1409	357	392	1	11			
1	E	299	Total	C	N	O	P	S	6	0	0
			2254	1455	373	413	1	12			
1	F	295	Total	C	N	O	P	S	12	0	0
			2198	1430	352	404	1	11			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68	GLY	-	expression tag	UNP P21127
A	69	ALA	-	expression tag	UNP P21127
A	70	MET	-	expression tag	UNP P21127
A	71	GLY	-	expression tag	UNP P21127
A	381	LYS	-	expression tag	UNP P21127
A	382	LEU	-	expression tag	UNP P21127
A	383	VAL	-	expression tag	UNP P21127
A	384	GLU	-	expression tag	UNP P21127
A	385	LYS	-	expression tag	UNP P21127
A	386	TYR	-	expression tag	UNP P21127
B	68	GLY	-	expression tag	UNP P21127
B	69	ALA	-	expression tag	UNP P21127
B	70	MET	-	expression tag	UNP P21127
B	71	GLY	-	expression tag	UNP P21127
B	381	LYS	-	expression tag	UNP P21127
B	382	LEU	-	expression tag	UNP P21127
B	383	VAL	-	expression tag	UNP P21127

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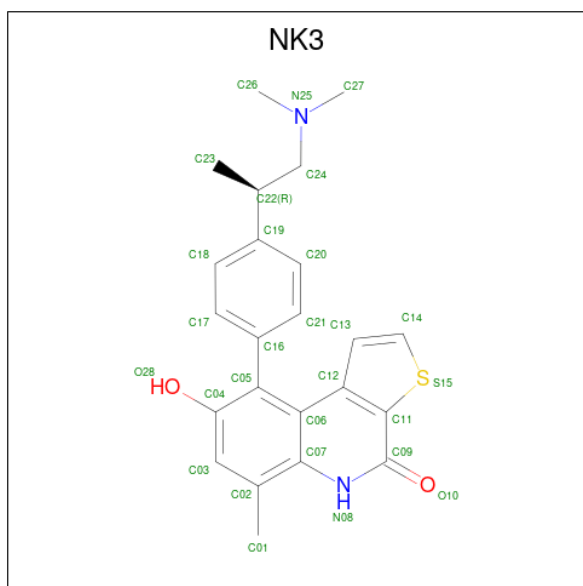
Chain	Residue	Modelled	Actual	Comment	Reference
B	384	GLU	-	expression tag	UNP P21127
B	385	LYS	-	expression tag	UNP P21127
B	386	TYR	-	expression tag	UNP P21127
C	68	GLY	-	expression tag	UNP P21127
C	69	ALA	-	expression tag	UNP P21127
C	70	MET	-	expression tag	UNP P21127
C	71	GLY	-	expression tag	UNP P21127
C	381	LYS	-	expression tag	UNP P21127
C	382	LEU	-	expression tag	UNP P21127
C	383	VAL	-	expression tag	UNP P21127
C	384	GLU	-	expression tag	UNP P21127
C	385	LYS	-	expression tag	UNP P21127
C	386	TYR	-	expression tag	UNP P21127
D	68	GLY	-	expression tag	UNP P21127
D	69	ALA	-	expression tag	UNP P21127
D	70	MET	-	expression tag	UNP P21127
D	71	GLY	-	expression tag	UNP P21127
D	381	LYS	-	expression tag	UNP P21127
D	382	LEU	-	expression tag	UNP P21127
D	383	VAL	-	expression tag	UNP P21127
D	384	GLU	-	expression tag	UNP P21127
D	385	LYS	-	expression tag	UNP P21127
D	386	TYR	-	expression tag	UNP P21127
E	68	GLY	-	expression tag	UNP P21127
E	69	ALA	-	expression tag	UNP P21127
E	70	MET	-	expression tag	UNP P21127
E	71	GLY	-	expression tag	UNP P21127
E	381	LYS	-	expression tag	UNP P21127
E	382	LEU	-	expression tag	UNP P21127
E	383	VAL	-	expression tag	UNP P21127
E	384	GLU	-	expression tag	UNP P21127
E	385	LYS	-	expression tag	UNP P21127
E	386	TYR	-	expression tag	UNP P21127
F	68	GLY	-	expression tag	UNP P21127
F	69	ALA	-	expression tag	UNP P21127
F	70	MET	-	expression tag	UNP P21127
F	71	GLY	-	expression tag	UNP P21127
F	381	LYS	-	expression tag	UNP P21127
F	382	LEU	-	expression tag	UNP P21127
F	383	VAL	-	expression tag	UNP P21127
F	384	GLU	-	expression tag	UNP P21127
F	385	LYS	-	expression tag	UNP P21127

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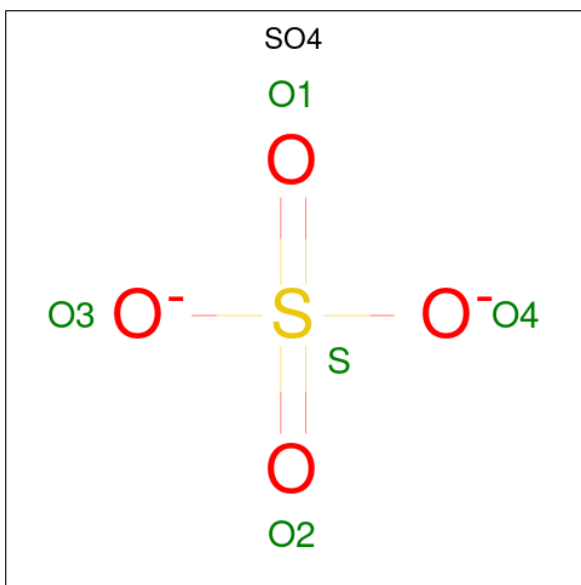
Chain	Residue	Modelled	Actual	Comment	Reference
F	386	TYR	-	expression tag	UNP P21127

- Molecule 2 is OTS964 (CCD ID: NK3) (formula: $C_{23}H_{24}N_2O_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			28	23	2	2	1		
2	B	1	Total	C	N	O	S	0	0
			28	23	2	2	1		
2	C	1	Total	C	N	O	S	0	0
			28	23	2	2	1		
2	D	1	Total	C	N	O	S	0	0
			28	23	2	2	1		
2	E	1	Total	C	N	O	S	0	0
			28	23	2	2	1		
2	F	1	Total	C	N	O	S	0	0
			28	23	2	2	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).

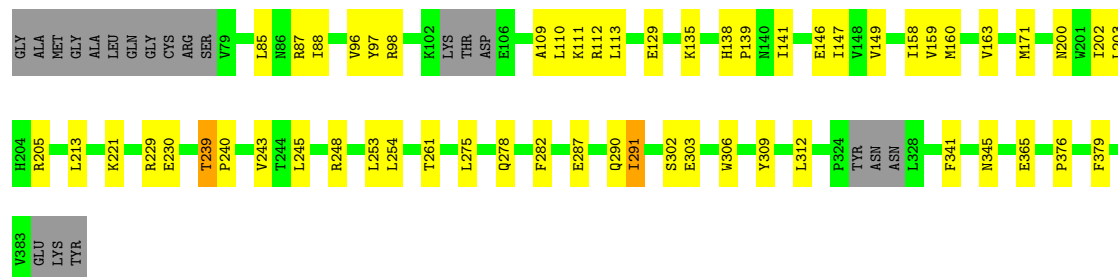


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		



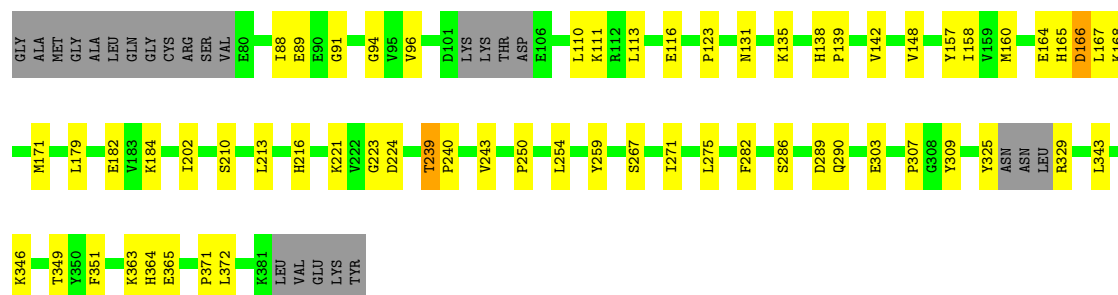
• Molecule 1: Cyclin-dependent kinase 11B

Chain E: 76% 17% 6%



• Molecule 1: Cyclin-dependent kinase 11B

Chain F: 73% 19% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	146.68Å 146.68Å 230.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	127.03 – 2.60 127.03 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (127.03-2.60) 100.0 (127.03-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.20.1	Depositor
R, R_{free}	0.222 , 0.236 0.223 , 0.234	Depositor DCC
R_{free} test set	4315 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	76.2	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 69.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.309 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.650 for h,-h-k,-l	Depositor
Outliers	0 of 86274 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13429	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.36% 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, TPO, NK3

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	0.09	0/2288	0.24	0/3108
1	B	0.12	0/2217	0.27	0/3021
1	C	0.08	0/2226	0.24	0/3033
1	D	0.10	0/2209	0.27	0/3007
1	E	0.11	0/2296	0.27	0/3124
1	F	0.10	0/2242	0.27	0/3057
All	All	0.10	0/13478	0.26	0/18350

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	2247	0	2103	27	0
1	B	2177	0	1958	24	0
1	C	2185	0	2003	23	0
1	D	2170	0	1987	32	0
1	E	2254	0	2093	32	0
1	F	2198	0	2006	44	0
2	A	28	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	28	0	0	0	0
2	C	28	0	0	0	0
2	D	28	0	0	0	0
2	E	28	0	0	0	0
2	F	28	0	0	1	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
All	All	13429	0	12150	174	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 7.

The worst 5 of 174 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:D:363:LYS:HB3	1:F:363:LYS:HD2	1.68	0.75
1:F:171:MET:HE1	1:F:275:LEU:HA	1.69	0.75
1:C:349:THR:O	1:C:355:ARG:NH1	2.20	0.73
1:C:282:PHE:O	1:C:290:GLN:NE2	2.22	0.73
1:F:135:LYS:HB2	1:F:202:ILE:HD11	1.70	0.73

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	287/319 (90%)	279 (97%)	7 (2%)	1 (0%)	36 58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	289/319 (91%)	280 (97%)	8 (3%)	1 (0%)	36	58
1	C	285/319 (89%)	272 (95%)	11 (4%)	2 (1%)	18	38
1	D	283/319 (89%)	274 (97%)	8 (3%)	1 (0%)	30	51
1	E	292/319 (92%)	280 (96%)	10 (3%)	2 (1%)	18	38
1	F	288/319 (90%)	276 (96%)	10 (4%)	2 (1%)	18	38
All	All	1724/1914 (90%)	1661 (96%)	54 (3%)	9 (0%)	24	46

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	243	VAL
1	F	243	VAL
1	A	243	VAL
1	B	243	VAL
1	C	243	VAL

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	217/281 (77%)	216 (100%)	1 (0%)	81	92
1	B	200/281 (71%)	198 (99%)	2 (1%)	68	86
1	C	204/281 (73%)	204 (100%)	0	100	100
1	D	201/281 (72%)	198 (98%)	3 (2%)	57	80
1	E	217/281 (77%)	215 (99%)	2 (1%)	70	87
1	F	208/281 (74%)	206 (99%)	2 (1%)	68	86
All	All	1247/1686 (74%)	1237 (99%)	10 (1%)	73	88

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	291	ILE

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Mol	Chain	Res	Type
1	F	160	MET
1	F	166	ASP
1	D	167	LEU
1	D	170	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	339	GLN
1	F	165	HIS
1	E	339	GLN
1	D	211	ASN
1	F	86	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues 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
1	TPO	A	239	1	8,10,11	1.65	1 (12%)	10,14,16	1.76	1 (10%)
1	TPO	D	239	1	8,10,11	1.65	1 (12%)	10,14,16	1.99	1 (10%)
1	TPO	C	239	1	8,10,11	1.64	1 (12%)	10,14,16	1.94	1 (10%)
1	TPO	E	239	1	8,10,11	1.10	0	10,14,16	2.04	1 (10%)
1	TPO	F	239	1	8,10,11	1.65	1 (12%)	10,14,16	1.84	1 (10%)
1	TPO	B	239	1	8,10,11	1.65	1 (12%)	10,14,16	1.94	1 (10%)

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
1	TPO	A	239	1	-	4/9/11/13	-
1	TPO	D	239	1	-	1/9/11/13	-
1	TPO	C	239	1	-	4/9/11/13	-
1	TPO	E	239	1	-	1/9/11/13	-
1	TPO	F	239	1	-	2/9/11/13	-
1	TPO	B	239	1	-	3/9/11/13	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	239	TPO	P-O1P	3.55	1.61	1.50
1	D	239	TPO	P-O1P	3.53	1.61	1.50
1	C	239	TPO	P-O1P	3.51	1.61	1.50
1	F	239	TPO	P-O1P	3.49	1.61	1.50
1	A	239	TPO	P-O1P	3.48	1.61	1.50

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	239	TPO	P-OG1-CB	-5.72	107.79	123.33
1	C	239	TPO	P-OG1-CB	-5.58	108.17	123.33
1	D	239	TPO	P-OG1-CB	-5.57	108.18	123.33
1	B	239	TPO	P-OG1-CB	-5.43	108.58	123.33
1	F	239	TPO	P-OG1-CB	-5.07	109.55	123.33

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	239	TPO	N-CA-CB-OG1
1	A	239	TPO	C-CA-CB-CG2
1	C	239	TPO	C-CA-CB-CG2
1	F	239	TPO	C-CA-CB-CG2
1	B	239	TPO	CB-OG1-P-O2P

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	239	TPO	1	0
1	C	239	TPO	1	0
1	E	239	TPO	1	0
1	F	239	TPO	2	0
1	B	239	TPO	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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
2	NK3	B	401	-	31,31,31	1.86	8 (25%)	36,46,46	2.14	9 (25%)
3	SO4	C	402	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	E	402	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	D	402	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	B	402	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	F	402	-	4,4,4	0.24	0	6,6,6	0.08	0
2	NK3	D	401	-	31,31,31	1.86	8 (25%)	36,46,46	2.14	9 (25%)
2	NK3	A	401	-	31,31,31	1.86	8 (25%)	36,46,46	2.15	9 (25%)
2	NK3	F	401	-	31,31,31	1.88	8 (25%)	36,46,46	2.17	9 (25%)
3	SO4	A	402	-	4,4,4	0.24	0	6,6,6	0.08	0
2	NK3	C	401	-	31,31,31	1.88	8 (25%)	36,46,46	2.16	9 (25%)
2	NK3	E	401	-	31,31,31	1.87	8 (25%)	36,46,46	2.13	9 (25%)

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
2	NK3	B	401	-	-	4/12/12/12	0/4/4/4
2	NK3	D	401	-	-	2/12/12/12	0/4/4/4
2	NK3	A	401	-	-	3/12/12/12	0/4/4/4
2	NK3	F	401	-	-	1/12/12/12	0/4/4/4
2	NK3	C	401	-	-	3/12/12/12	0/4/4/4
2	NK3	E	401	-	-	0/12/12/12	0/4/4/4

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	401	NK3	C24-C22	4.86	1.57	1.53
2	F	401	NK3	C24-C22	4.78	1.57	1.53
2	B	401	NK3	C24-C22	4.78	1.57	1.53
2	D	401	NK3	C24-C22	4.78	1.57	1.53
2	C	401	NK3	C24-C22	4.75	1.57	1.53

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	401	NK3	C13-C12-C11	-6.06	106.61	111.69
2	C	401	NK3	C13-C12-C11	-6.05	106.62	111.69
2	A	401	NK3	C13-C12-C11	-6.01	106.65	111.69
2	D	401	NK3	C13-C12-C11	-5.99	106.67	111.69
2	B	401	NK3	C13-C12-C11	-5.96	106.70	111.69

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

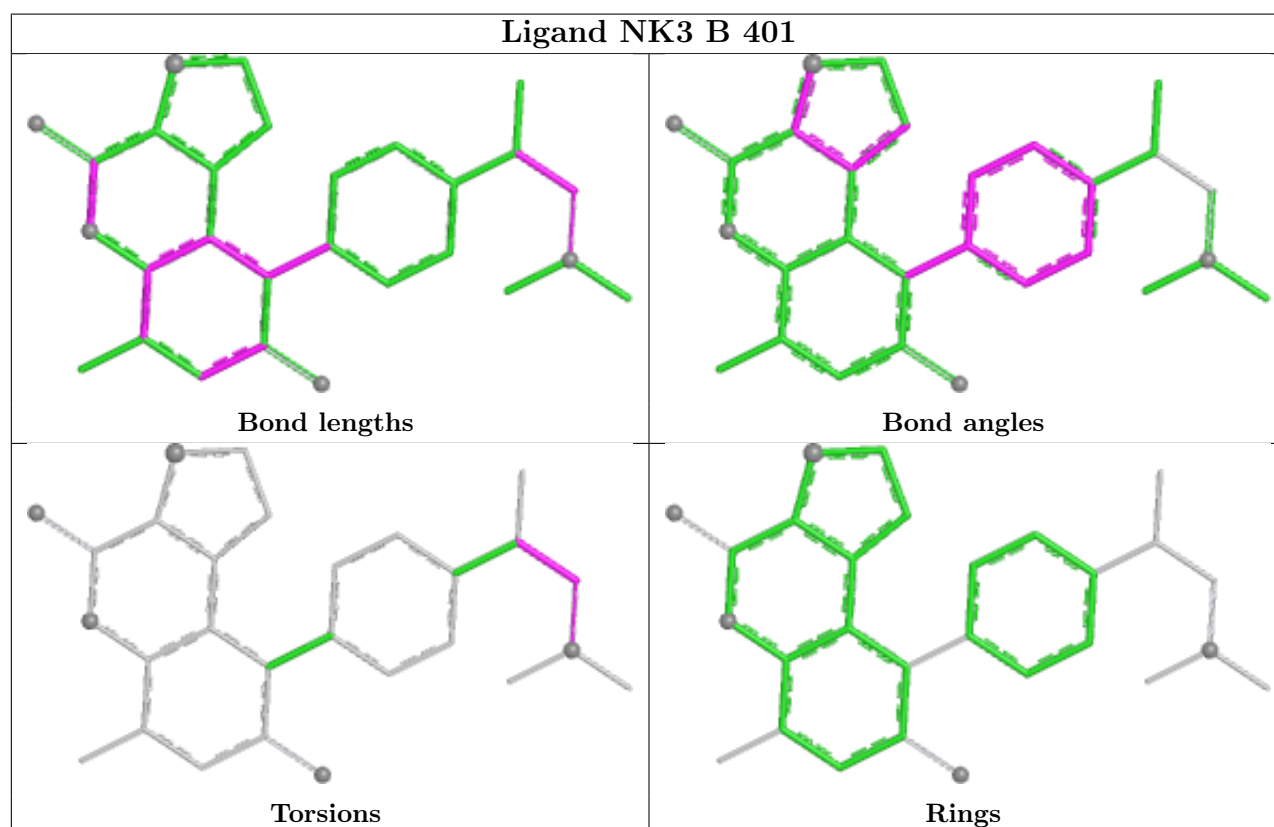
Mol	Chain	Res	Type	Atoms
2	A	401	NK3	C19-C22-C24-N25
2	A	401	NK3	C23-C22-C24-N25
2	B	401	NK3	C19-C22-C24-N25
2	B	401	NK3	C23-C22-C24-N25
2	C	401	NK3	C19-C22-C24-N25

There are no ring outliers.

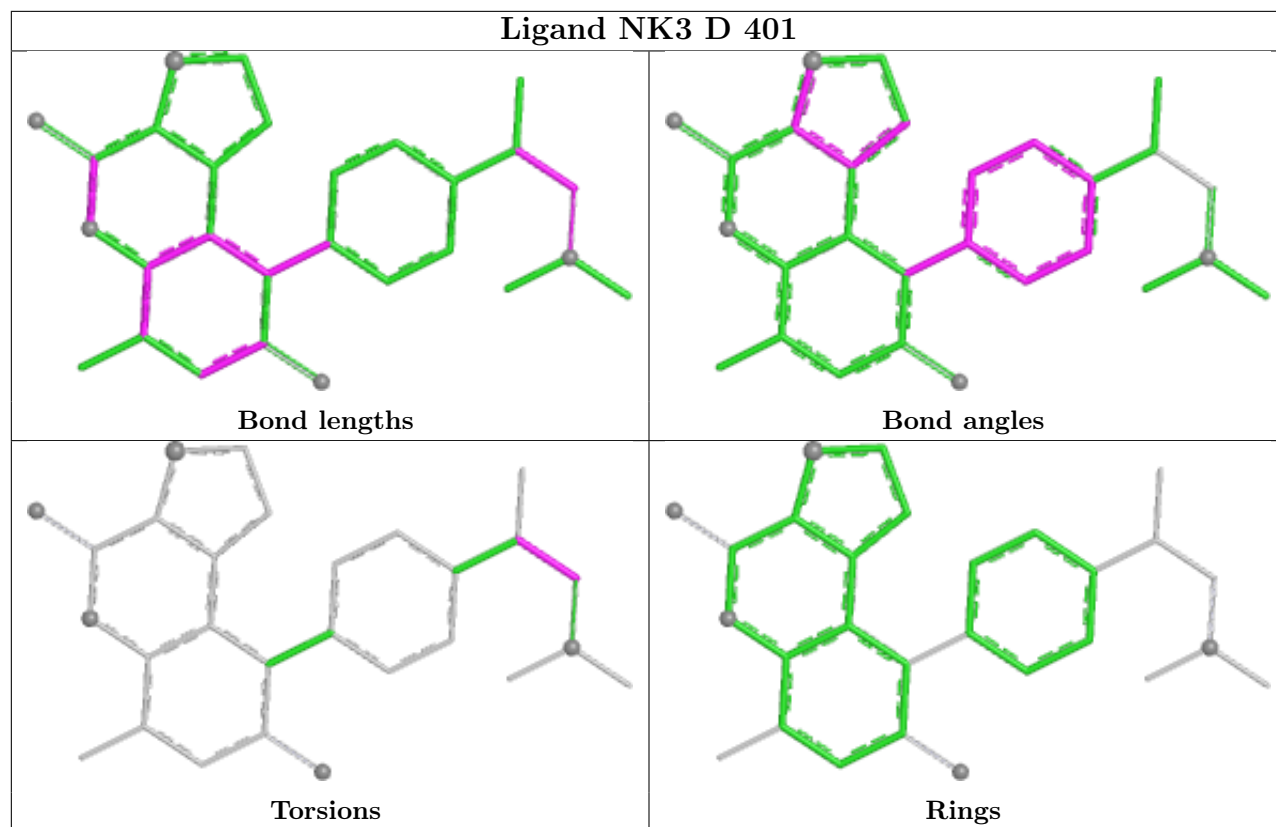
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	401	NK3	1	0

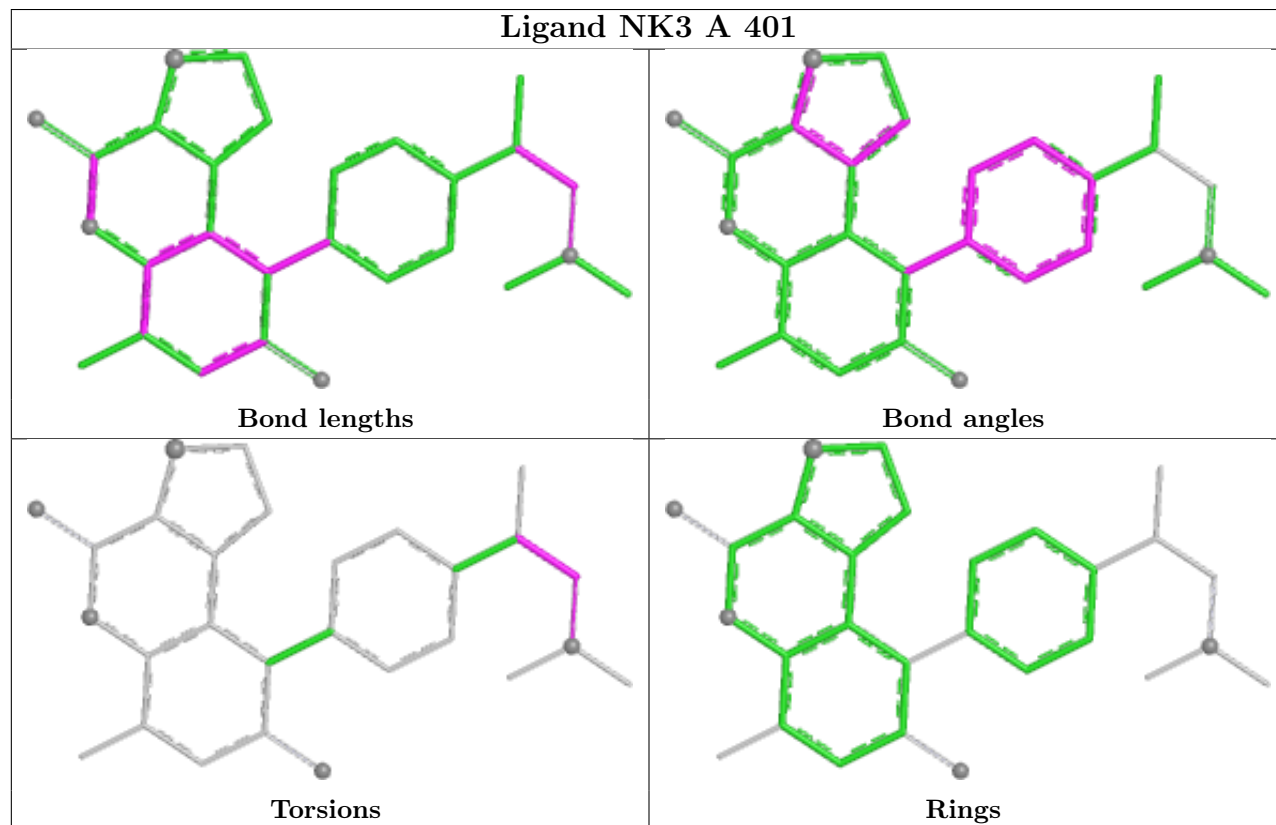
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



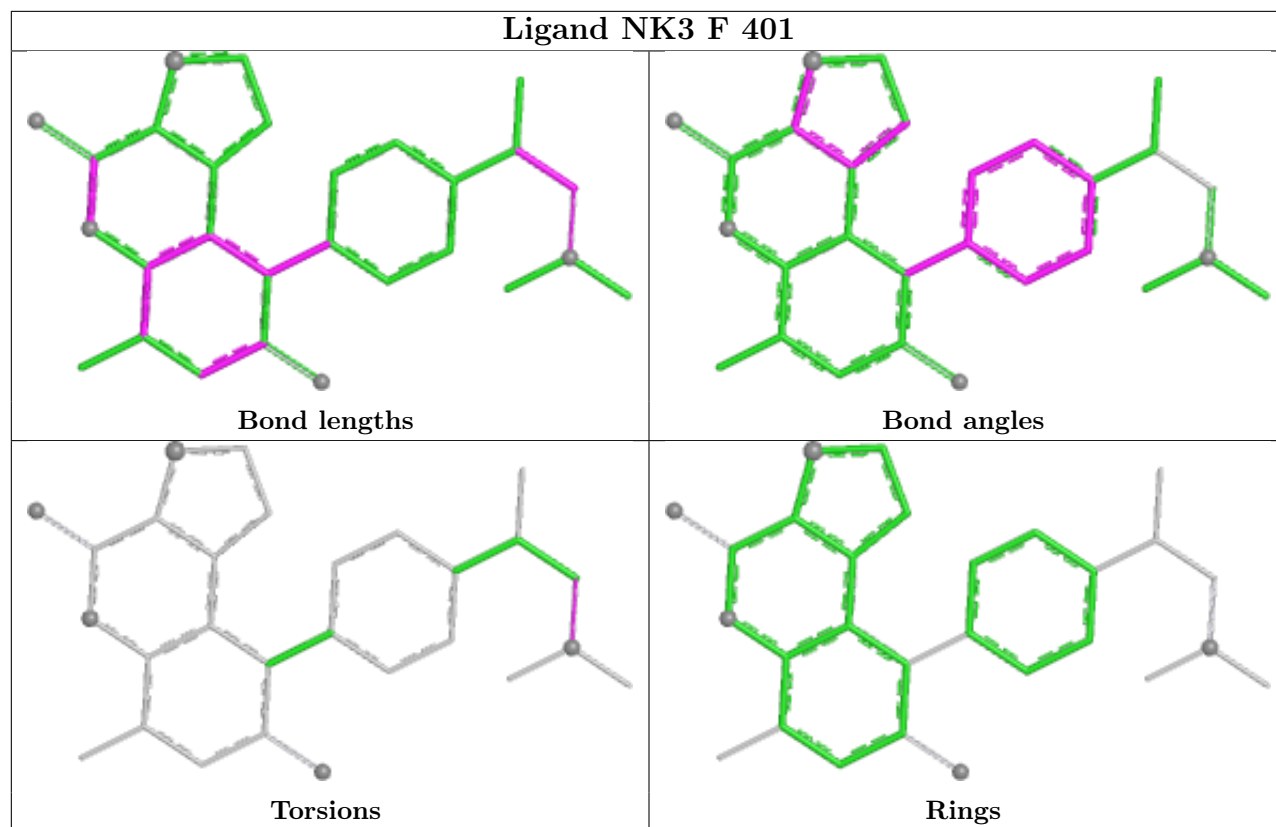
Ligand NK3 D 401



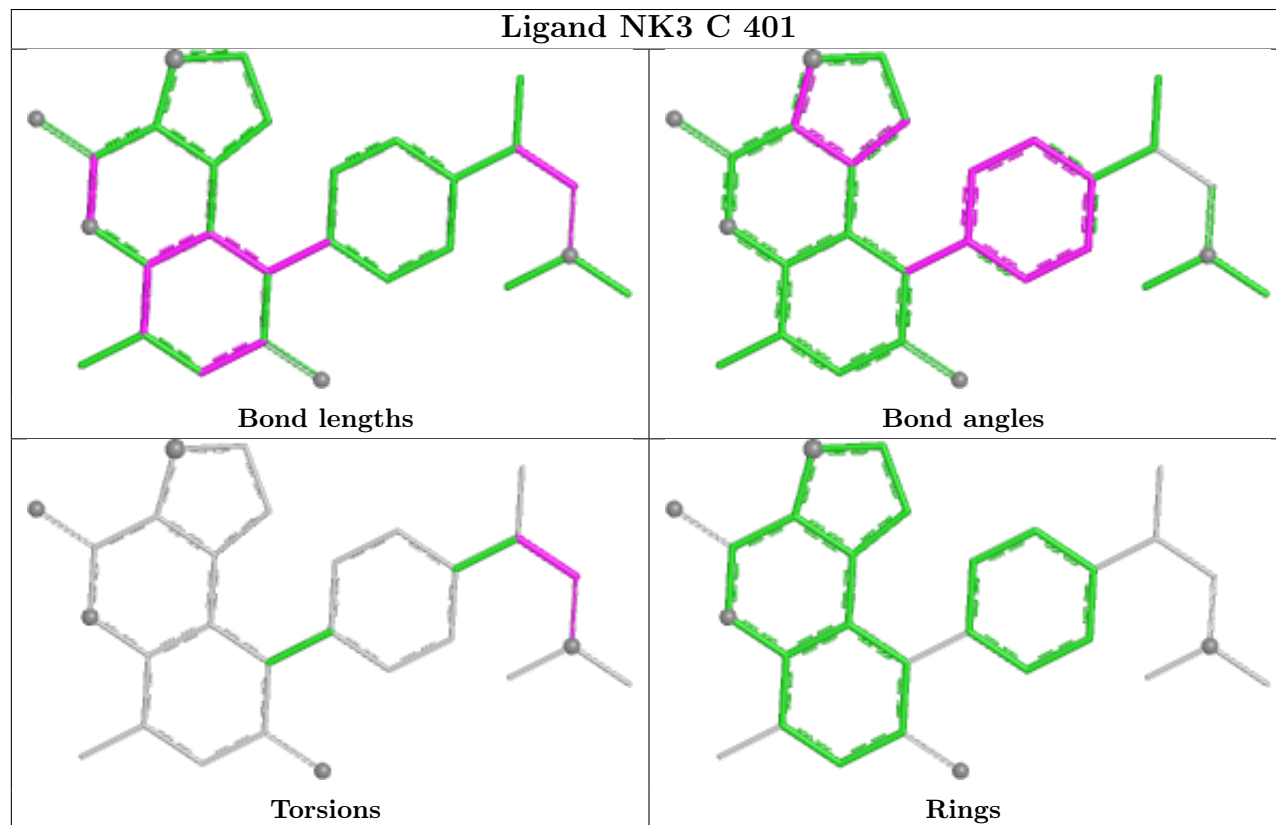
Ligand NK3 A 401

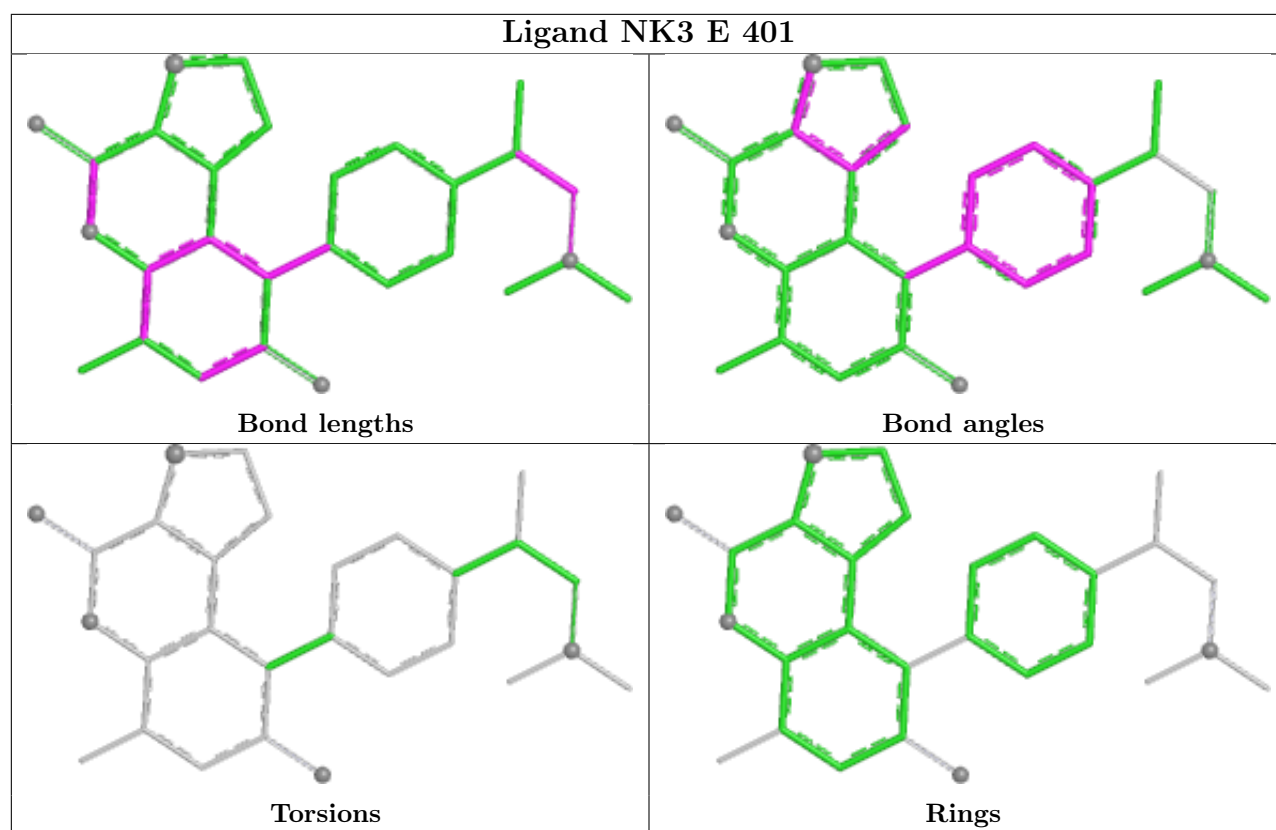


Ligand NK3 F 401



Ligand NK3 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	295/319 (92%)	-0.72	0	100 100	52, 68, 96, 121	1 (0%)
1	B	295/319 (92%)	-0.58	0	100 100	50, 74, 102, 120	1 (0%)
1	C	293/319 (91%)	-0.74	0	100 100	45, 67, 94, 110	2 (0%)
1	D	293/319 (91%)	-0.60	2 (0%)	84 82	52, 73, 101, 124	2 (0%)
1	E	298/319 (93%)	-0.66	0	100 100	51, 73, 97, 106	3 (1%)
1	F	294/319 (92%)	-0.70	0	100 100	55, 77, 102, 115	6 (2%)
All	All	1768/1914 (92%)	-0.67	2 (0%)	92 90	45, 73, 99, 124	15 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	92	THR	2.3
1	D	118	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	A	239	11/12	0.99	0.04	62,72,85,87	0
1	TPO	B	239	11/12	0.99	0.05	57,64,69,85	0
1	TPO	C	239	11/12	0.99	0.04	56,65,77,78	0
1	TPO	D	239	11/12	0.99	0.04	71,80,90,104	0
1	TPO	E	239	11/12	0.99	0.05	54,66,76,81	0
1	TPO	F	239	11/12	0.99	0.04	54,65,71,76	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

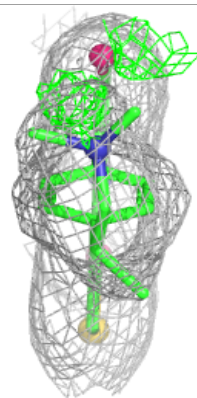
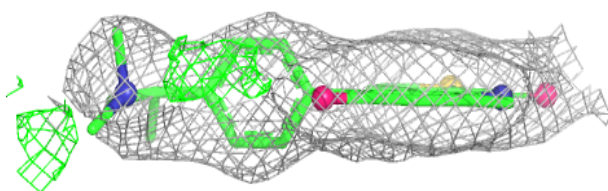
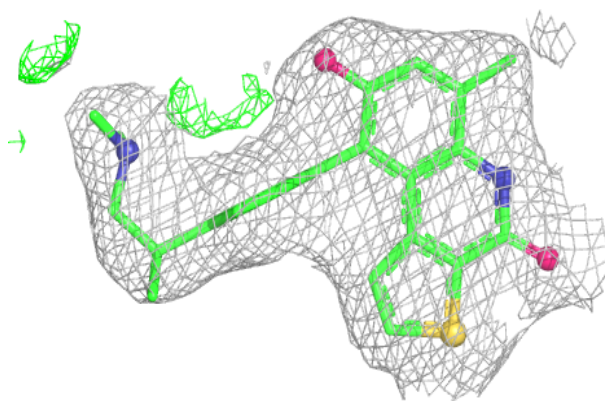
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NK3	D	401	28/28	0.98	0.07	57,66,69,90	0
3	SO4	B	402	5/5	0.98	0.04	62,64,65,68	0
3	SO4	C	402	5/5	0.98	0.06	61,61,72,100	0
3	SO4	D	402	5/5	0.98	0.05	71,73,76,84	0
3	SO4	E	402	5/5	0.98	0.04	70,71,72,81	0
3	SO4	F	402	5/5	0.98	0.04	70,71,74,91	0
3	SO4	A	402	5/5	0.99	0.04	54,61,61,99	0
2	NK3	B	401	28/28	0.99	0.07	60,72,80,86	0
2	NK3	C	401	28/28	0.99	0.07	62,71,88,94	0
2	NK3	A	401	28/28	0.99	0.05	53,65,73,76	0
2	NK3	E	401	28/28	0.99	0.06	57,67,75,78	0
2	NK3	F	401	28/28	0.99	0.06	67,77,86,89	0

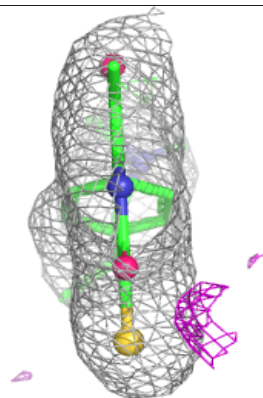
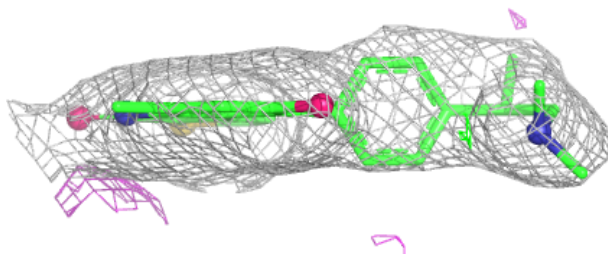
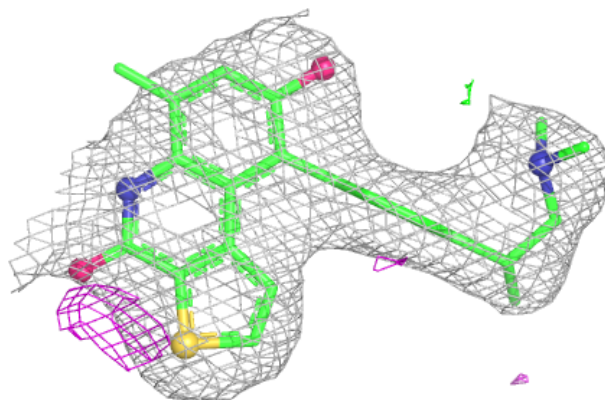
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NK3 D 401:

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

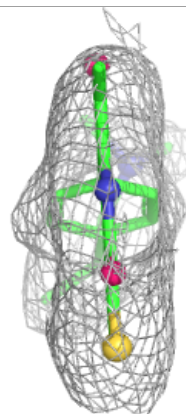
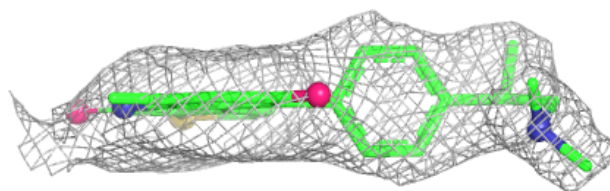
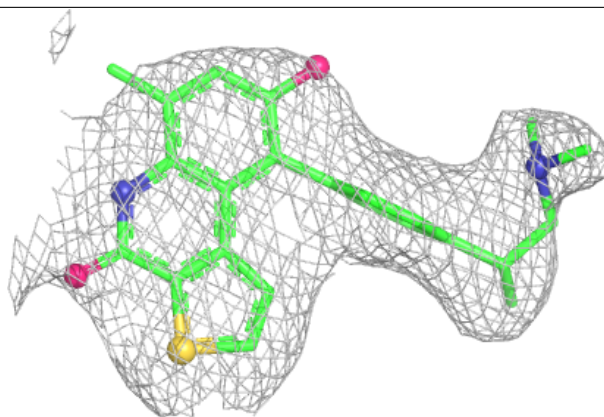
**Electron density around NK3 B 401:**

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

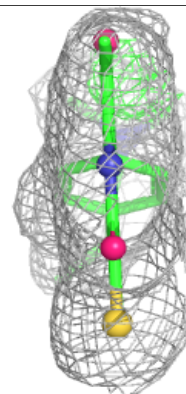
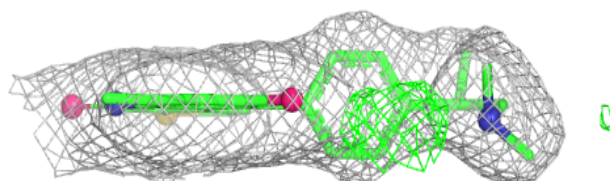
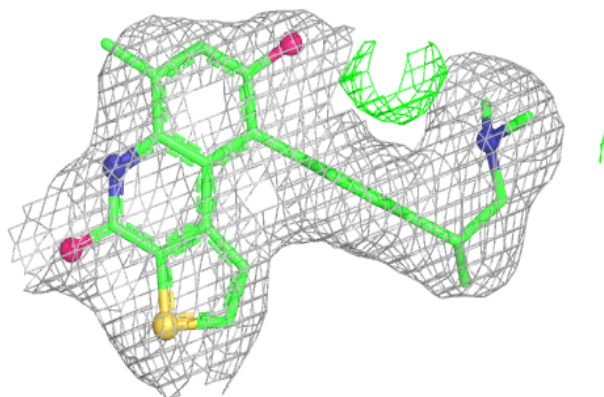


Electron density around NK3 C 401:

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

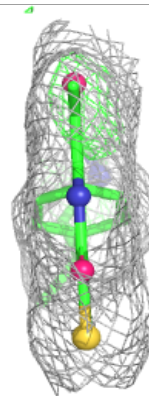
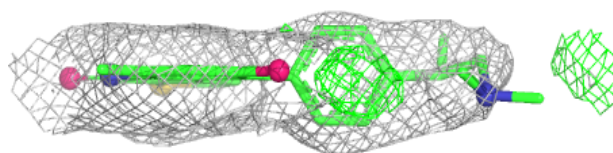
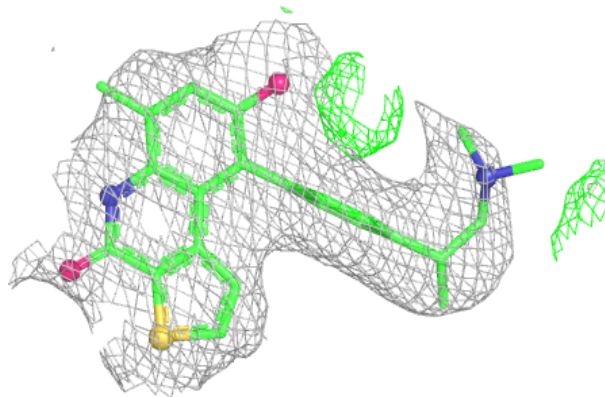
**Electron density around NK3 A 401:**

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

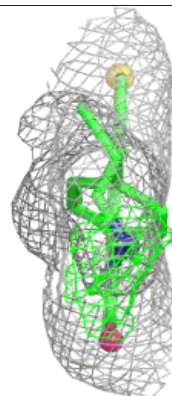
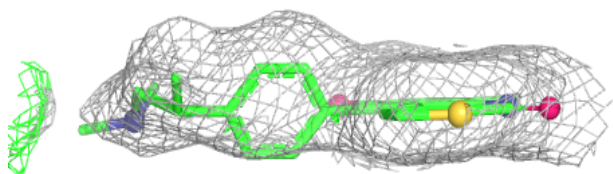
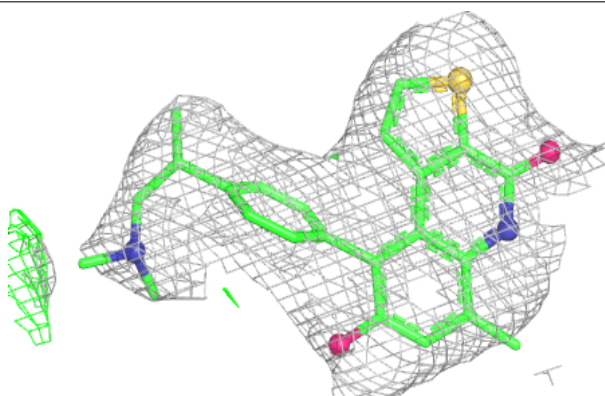


Electron density around NK3 E 401:

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

**Electron density around NK3 F 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 [i](#)

There are no such residues in this entry.