



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2021 – 08:10 am BST

PDB ID : 7NNG
Title : Crystal structure of the SARS-CoV-2 helicase in complex with Z2327226104
Authors : Newman, J.A.; Yosaatmadja, Y.; Douangamath, A.; Bountra, C.; Gileadi, O.
Deposited on : 2021-02-24
Resolution : 2.38 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

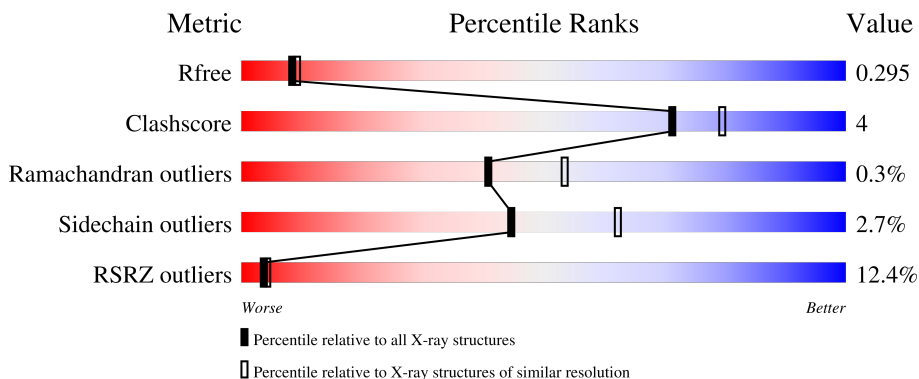
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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	601	 17% (Poor fit), 85% (0-3 outliers), 10% (1 outlier), 5% (2+ outliers)
1	B	601	 6% (Poor fit), 86% (0-3 outliers), 11% (1 outlier)

2 Entry composition [i](#)

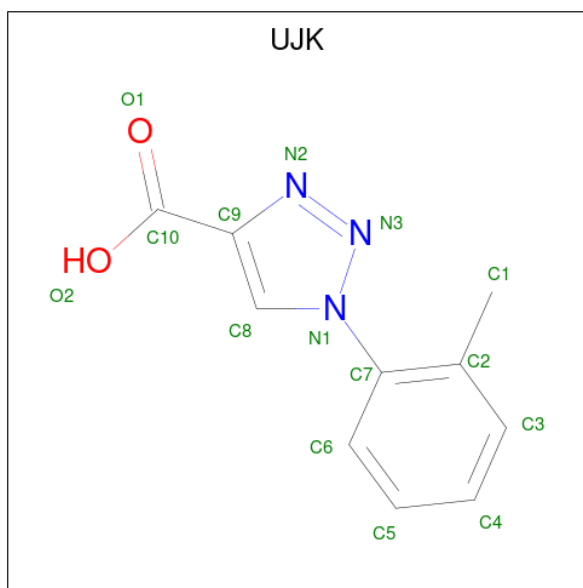
There are 5 unique types of molecules in this entry. The entry contains 9114 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SARS-CoV-2 helicase NSP13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	585	Total 4508	C 2875	N 750	O 848	S 35	0	1	0
1	A	572	Total 4417	C 2816	N 737	O 832	S 32	0	0	0

- Molecule 2 is 1-(2-methylphenyl)-1,2,3-triazole-4-carboxylic acid (three-letter code: UJK) (formula: C₁₀H₉N₃O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	B	1	Total 15	C 10	N 3	O 2	0	0
2	A	1	Total 15	C 10	N 3	O 2	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Zn	0	0
			3	3		
3	A	3	Total	Zn	0	0
			3	3		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		
4	A	1	Total	O	P	0	0
			5	4	1		
4	A	1	Total	O	P	0	0
			5	4	1		

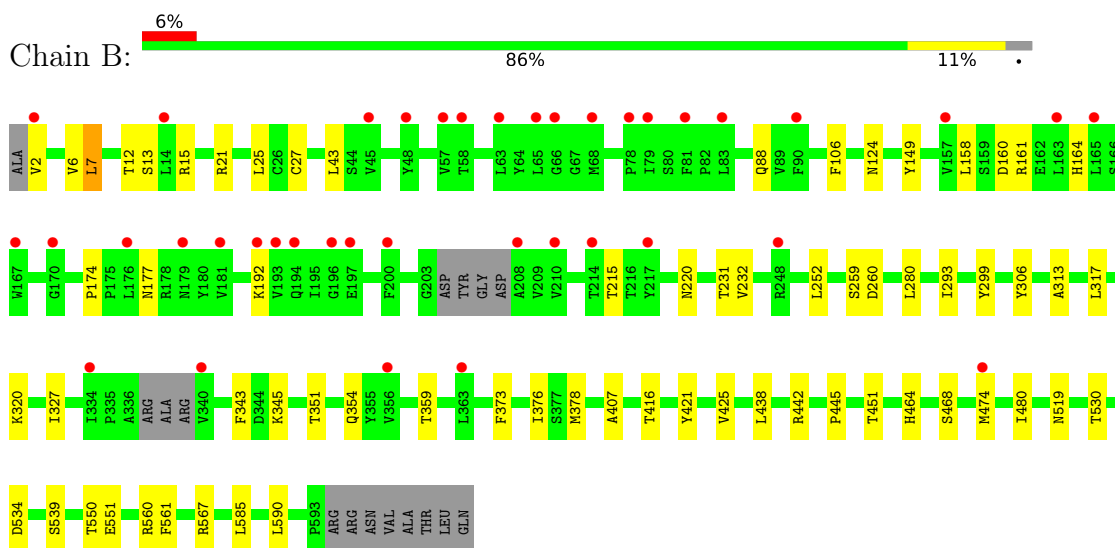
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	75	Total	O	0	0
			75	75		
5	A	58	Total	O	0	0
			58	58		

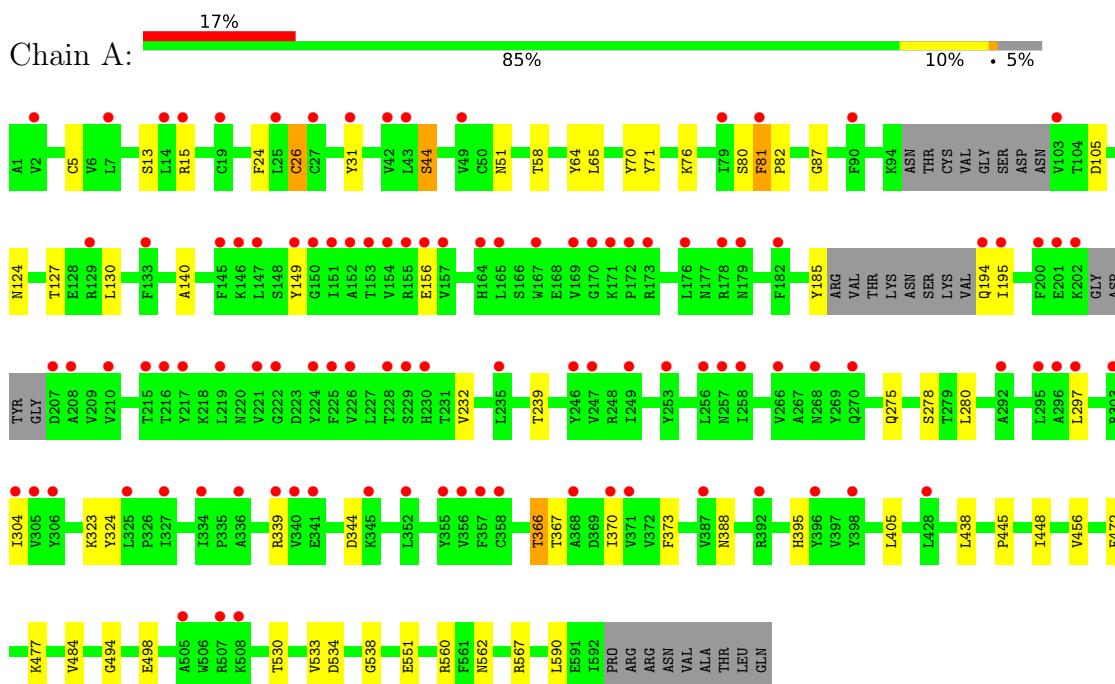
3 Residue-property plots

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: SARS-CoV-2 helicase NSP13



• Molecule 1: SARS-CoV-2 helicase NSP13



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.20Å 70.35Å 85.50Å 103.16° 96.10° 112.04°	Depositor
Resolution (Å)	81.35 – 2.38 81.35 – 2.38	Depositor EDS
% Data completeness (in resolution range)	87.5 (81.35-2.38) 87.6 (81.35-2.38)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.37Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.245 , 0.295 0.245 , 0.295	Depositor DCC
R_{free} test set	2174 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	53.2	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9114	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.75% 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: UJK, PO4, ZN

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	0.24	0/4517	0.42	0/6156
1	B	0.24	0/4610	0.43	0/6283
All	All	0.24	0/9127	0.42	0/12439

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	4417	0	4321	30	0
1	B	4508	0	4424	32	0
2	A	15	0	0	0	0
2	B	15	0	0	1	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	10	0	0	0	0
4	B	10	0	0	0	0
5	A	58	0	0	2	0
5	B	75	0	0	3	0
All	All	9114	0	8745	62	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 4.

All (62) 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:445:PRO:HD2	1:A:448:ILE:HD12	1.73	0.70
1:B:293:ILE:HG13	1:B:320:LYS:HB3	1.76	0.67
1:A:5:CYS:HB2	1:A:26:CYS:HB3	1.80	0.63
1:B:474[B]:MET:HG2	1:B:590:LEU:HB2	1.80	0.63
1:B:534:ASP:OD2	5:B:801:HOH:O	2.16	0.62
1:B:6:VAL:HG23	1:B:7:LEU:HD23	1.83	0.61
1:B:306:TYR:HB3	1:B:317:LEU:HD13	1.84	0.59
1:B:124:ASN:HD22	1:B:421:TYR:HA	1.71	0.56
1:A:339:ARG:NH2	5:A:808:HOH:O	2.40	0.55
1:B:21:ARG:NH2	1:B:232:VAL:O	2.40	0.54
1:B:480:ILE:HD13	1:B:550:THR:HG22	1.90	0.54
1:A:140:ALA:HA	1:A:232:VAL:HG21	1.90	0.53
1:A:65:LEU:N	1:A:81:PHE:O	2.40	0.53
1:B:445:PRO:HB3	1:B:468:SER:HB3	1.90	0.53
1:B:560:ARG:NE	5:B:801:HOH:O	2.33	0.53
1:A:127:THR:HG22	1:A:130:LEU:HB2	1.91	0.52
1:B:158:LEU:HD13	1:B:164:HIS:HB2	1.92	0.51
1:B:519:ASN:HB3	1:B:530:THR:HB	1.92	0.51
1:B:12:THR:HG21	1:B:25:LEU:O	2.11	0.50
1:A:477:LYS:NZ	1:A:551:GLU:OE2	2.44	0.50
1:B:280:LEU:HD11	1:B:438:LEU:HG	1.94	0.49
1:B:442:ARG:HA	1:B:464:HIS:HB3	1.95	0.49
1:A:280:LEU:HD11	1:A:438:LEU:HG	1.93	0.48
1:B:15:ARG:N	1:B:43:LEU:O	2.37	0.48
1:A:13:SER:O	1:A:44:SER:HA	2.15	0.47
1:A:472:PHE:HB3	1:A:590:LEU:HG	1.96	0.47
1:B:7:LEU:HD21	1:B:106:PHE:HB2	1.96	0.46
1:A:297:LEU:HD11	1:A:324:TYR:HB3	1.96	0.46
1:B:451:THR:HG21	1:B:585:LEU:HD23	1.97	0.46
1:B:2:VAL:HG22	1:B:13:SER:HB2	1.98	0.46
1:B:313:ALA:O	5:B:802:HOH:O	2.21	0.46
1:A:304:ILE:HG12	1:A:370:ILE:HB	1.98	0.46
1:B:27:CYS:HB3	1:B:88:GLN:HB3	1.97	0.46
1:B:320:LYS:NZ	2:B:701:UJK:N2	2.64	0.46
1:A:533:VAL:HG11	1:A:560:ARG:HG3	1.97	0.46
1:A:456:VAL:HG21	1:A:562:ASN:ND2	2.31	0.45
1:A:494:GLY:O	1:A:498:GLU:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:TYR:HB3	1:B:174:PRO:HD3	1.99	0.44
1:A:64:TYR:HA	1:A:82:PRO:HA	1.99	0.44
1:B:149:TYR:CD2	1:B:174:PRO:HB3	2.53	0.43
1:A:64:TYR:N	1:A:71:TYR:O	2.47	0.43
1:A:124:ASN:ND2	5:A:813:HOH:O	2.50	0.43
1:B:378:MET:O	1:B:407:ALA:HB2	2.19	0.43
1:A:366:THR:OG1	1:A:367:THR:N	2.51	0.43
1:B:539:SER:O	1:B:567:ARG:HD3	2.19	0.43
1:A:5:CYS:HA	1:A:24:PHE:O	2.19	0.43
1:B:252:LEU:HB3	1:B:299:TYR:CD1	2.53	0.42
1:A:76:LYS:HD2	1:A:80:SER:OG	2.19	0.42
1:A:275:GLN:O	1:A:395:HIS:ND1	2.47	0.42
1:B:343:PHE:CZ	1:B:345:LYS:HB2	2.53	0.42
1:A:239:THR:O	1:A:388:ASN:ND2	2.53	0.42
1:A:15:ARG:HD3	1:A:24:PHE:CE1	2.55	0.41
1:A:405:LEU:HD21	1:A:560:ARG:HB2	2.02	0.41
1:B:376:ILE:HG12	1:B:425:VAL:HG11	2.02	0.41
1:A:31:TYR:CD2	1:A:87:GLY:HA2	2.55	0.41
1:A:538:GLY:H	1:A:567:ARG:NH1	2.17	0.41
1:B:561:PHE:HZ	1:B:585:LEU:HD11	1.86	0.41
1:A:405:LEU:HD13	1:A:534:ASP:OD1	2.21	0.41
1:A:185:TYR:HE2	1:A:194:GLN:HG3	1.86	0.41
1:B:260:ASP:N	1:B:260:ASP:OD1	2.52	0.40
1:B:160:ASP:OD2	1:B:161:ARG:N	2.54	0.40
1:A:185:TYR:CE2	1:A:194:GLN:HG3	2.56	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	564/601 (94%)	532 (94%)	29 (5%)	3 (0%)	29 39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	580/601 (96%)	539 (93%)	40 (7%)	1 (0%)	47	61
All	All	1144/1202 (95%)	1071 (94%)	69 (6%)	4 (0%)	41	53

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	484	VAL
1	B	354	GLN
1	A	44	SER
1	A	195	ILE

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	485/523 (93%)	471 (97%)	14 (3%)	42	60
1	B	498/523 (95%)	485 (97%)	13 (3%)	46	64
All	All	983/1046 (94%)	956 (97%)	27 (3%)	44	62

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

Mol	Chain	Res	Type
1	B	7	LEU
1	B	177	ASN
1	B	192	LYS
1	B	215	THR
1	B	220	ASN
1	B	231	THR
1	B	259	SER
1	B	327	ILE
1	B	351	THR
1	B	359	THR
1	B	373	PHE
1	B	416	THR

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Mol	Chain	Res	Type
1	B	551	GLU
1	A	26	CYS
1	A	51	ASN
1	A	58	THR
1	A	70	TYR
1	A	81	PHE
1	A	105	ASP
1	A	149	TYR
1	A	156	GLU
1	A	278	SER
1	A	323	LYS
1	A	344	ASP
1	A	366	THR
1	A	373	PHE
1	A	530	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	51	ASN
1	B	88	GLN
1	B	164	HIS
1	B	179	ASN
1	B	268	ASN
1	B	275	GLN
1	B	404	GLN
1	A	11	GLN
1	A	88	GLN
1	A	404	GLN
1	A	531	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	UJK	A	701	-	9,16,16	0.63	0	7,22,22	1.03	1 (14%)
4	PO4	B	706	-	4,4,4	0.94	0	6,6,6	0.42	0
4	PO4	B	705	-	4,4,4	0.98	0	6,6,6	0.42	0
4	PO4	A	706	-	4,4,4	0.89	0	6,6,6	0.46	0
4	PO4	A	705	-	4,4,4	0.96	0	6,6,6	0.43	0
2	UJK	B	701	-	9,16,16	0.62	0	7,22,22	1.09	1 (14%)

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	UJK	A	701	-	-	2/4/8/8	0/2/2/2
2	UJK	B	701	-	-	2/4/8/8	0/2/2/2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	701	UJK	C2-C7-N1	2.45	120.45	118.20
2	A	701	UJK	C2-C7-N1	2.26	120.27	118.20

There are no chirality outliers.

All (4) torsion outliers are listed below:

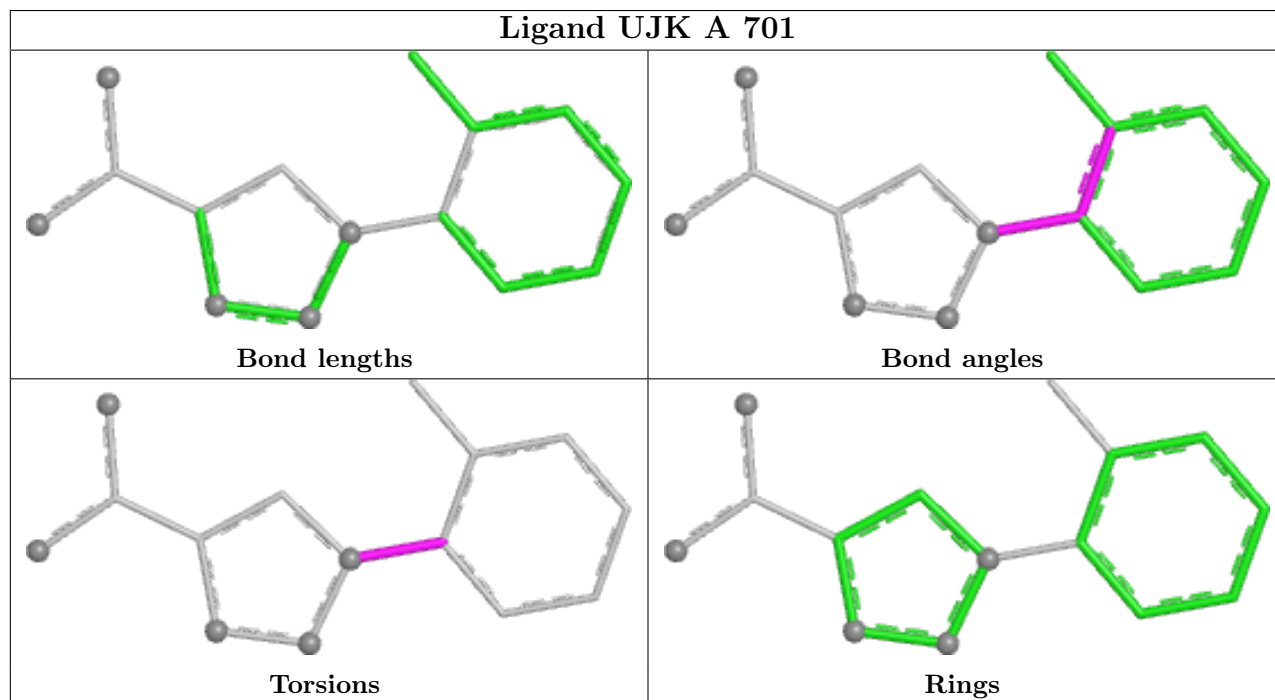
Mol	Chain	Res	Type	Atoms
2	B	701	UJK	C6-C7-N1-C8
2	A	701	UJK	C6-C7-N1-C8
2	B	701	UJK	C2-C7-N1-C8
2	A	701	UJK	C2-C7-N1-C8

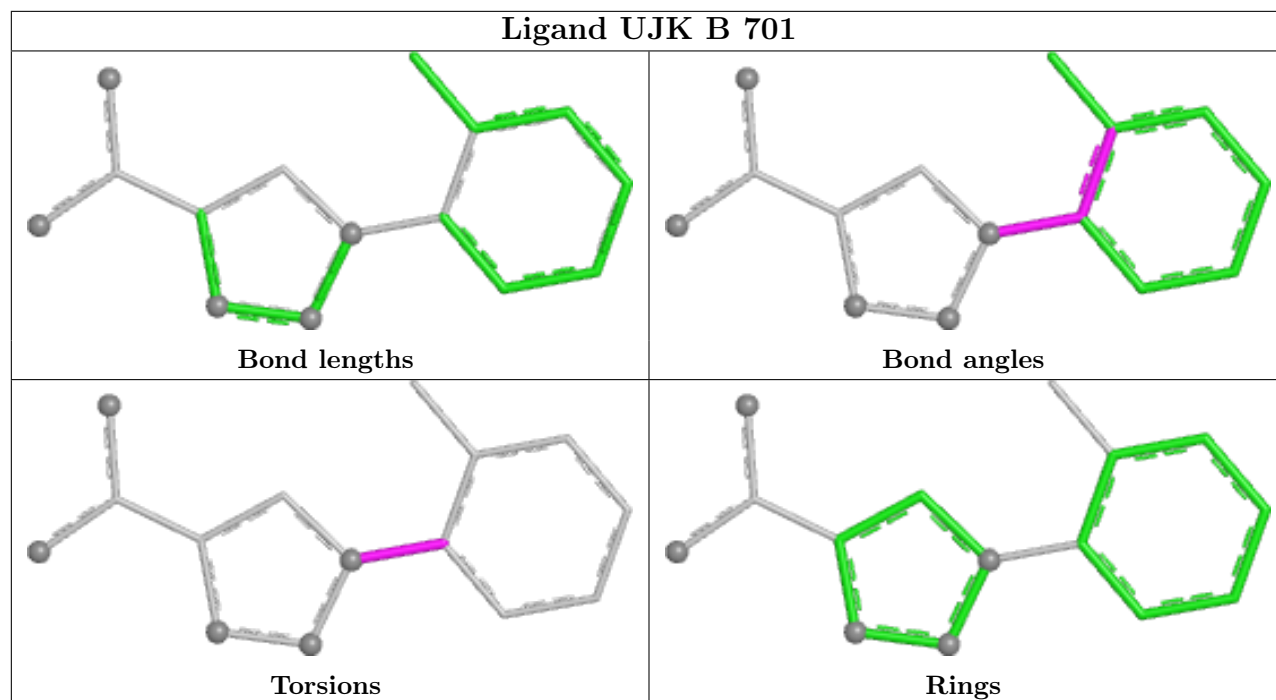
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	UJK	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.





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	572/601 (95%)	1.11	104 (18%) 1 1	37, 70, 133, 155	0
1	B	585/601 (97%)	0.56	39 (6%) 17 19	33, 56, 98, 123	0
All	All	1157/1202 (96%)	0.83	143 (12%) 4 4	33, 63, 121, 155	0

All (143) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	167	TRP	12.1
1	A	149	TYR	10.4
1	A	154	VAL	10.2
1	A	200	PHE	9.5
1	A	202	LYS	9.2
1	A	228	THR	7.9
1	A	182	PHE	7.2
1	B	217	TYR	7.0
1	A	225	PHE	6.7
1	A	334	ILE	6.7
1	A	179	ASN	6.5
1	A	170	GLY	6.3
1	A	171	LYS	6.2
1	A	215	THR	5.8
1	A	176	LEU	5.6
1	A	352	LEU	5.6
1	A	169	VAL	5.6
1	A	229	SER	5.2
1	B	163	LEU	5.2
1	A	370	ILE	5.2
1	A	178	ARG	5.0
1	A	304	ILE	5.0
1	A	221	VAL	5.0
1	A	296	ALA	4.9

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Mol	Chain	Res	Type	RSRZ
1	B	45	VAL	4.9
1	A	152	ALA	4.9
1	A	339	ARG	4.8
1	A	157	VAL	4.8
1	A	156	GLU	4.8
1	A	165	LEU	4.7
1	B	2	VAL	4.6
1	B	340	VAL	4.6
1	A	258	ILE	4.5
1	A	195	ILE	4.5
1	A	256	LEU	4.4
1	A	153	THR	4.4
1	A	246	TYR	4.4
1	A	146	LYS	4.3
1	A	305	VAL	4.3
1	B	193	VAL	4.2
1	B	57	VAL	4.2
1	A	217	TYR	4.2
1	A	387	VAL	4.0
1	A	216	THR	4.0
1	B	179	ASN	4.0
1	A	371	VAL	3.8
1	A	210	VAL	3.7
1	A	219	LEU	3.7
1	A	247	VAL	3.7
1	A	79	ILE	3.6
1	A	297	LEU	3.6
1	A	507	ARG	3.6
1	A	90	PHE	3.6
1	A	345	LYS	3.5
1	A	194	GLN	3.5
1	B	167	TRP	3.4
1	A	207	ASP	3.4
1	A	266	VAL	3.3
1	A	151	ILE	3.3
1	A	230	HIS	3.3
1	A	398	TYR	3.2
1	A	257	ASN	3.2
1	B	63	LEU	3.2
1	A	14	LEU	3.2
1	A	249	ILE	3.2
1	A	224	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	355	TYR	3.1
1	A	49	VAL	3.1
1	A	164	HIS	3.1
1	A	81	PHE	3.1
1	A	133	PHE	3.1
1	B	200	PHE	3.1
1	A	325	LEU	3.0
1	A	103	VAL	3.0
1	A	396	TYR	2.9
1	A	428	LEU	2.9
1	A	42	VAL	2.9
1	B	165	LEU	2.9
1	B	208	ALA	2.9
1	A	340	VAL	2.8
1	A	357	PHE	2.8
1	A	295	LEU	2.8
1	A	7	LEU	2.7
1	A	208	ALA	2.7
1	A	147	LEU	2.7
1	A	253	TYR	2.7
1	B	81	PHE	2.6
1	B	90	PHE	2.6
1	B	176	LEU	2.6
1	B	68	MET	2.6
1	A	172	PRO	2.6
1	B	334	ILE	2.6
1	A	173	ARG	2.6
1	B	14	LEU	2.6
1	A	292	ALA	2.6
1	A	356	VAL	2.6
1	A	31	TYR	2.6
1	B	214	THR	2.5
1	A	358	CYS	2.5
1	A	268	ASN	2.5
1	A	327	ILE	2.5
1	B	181	VAL	2.5
1	B	58	THR	2.5
1	A	2	VAL	2.5
1	B	197	GLU	2.5
1	A	303	ARG	2.4
1	A	19	CYS	2.4
1	B	363	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	508	LYS	2.4
1	A	43	LEU	2.4
1	A	129	ARG	2.3
1	A	201	GLU	2.3
1	A	145	PHE	2.3
1	A	505	ALA	2.3
1	B	196	GLY	2.3
1	B	66	GLY	2.3
1	B	79	ILE	2.3
1	A	25	LEU	2.2
1	A	222	GLY	2.2
1	B	48	TYR	2.2
1	A	306	TYR	2.2
1	A	392	ARG	2.2
1	A	270	GLN	2.2
1	A	150	GLY	2.2
1	B	210	VAL	2.2
1	B	192	LYS	2.2
1	A	226	VAL	2.1
1	B	65	LEU	2.1
1	B	78	PRO	2.1
1	B	170	GLY	2.1
1	A	341	GLU	2.1
1	A	336	ALA	2.1
1	B	356	VAL	2.1
1	A	235	LEU	2.1
1	B	248	ARG	2.1
1	A	15	ARG	2.0
1	A	155	ARG	2.0
1	A	368	ALA	2.0
1	B	157	VAL	2.0
1	B	83	LEU	2.0
1	B	474[A]	MET	2.0
1	B	194	GLN	2.0
1	A	27	CYS	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 monosaccharides in this entry.

6.4 Ligands [i](#)

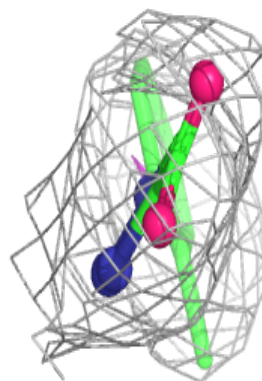
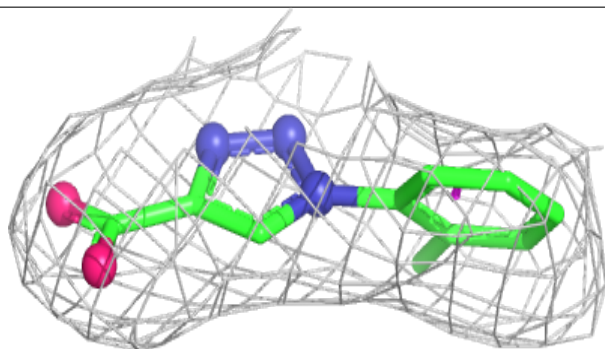
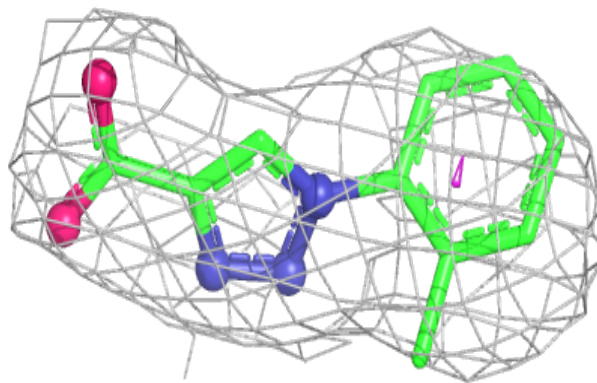
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ZN	B	703	1/1	0.79	0.09	90,90,90,90	0
3	ZN	A	702	1/1	0.79	0.13	71,71,71,71	0
3	ZN	A	704	1/1	0.81	0.11	102,102,102,102	0
3	ZN	B	704	1/1	0.89	0.09	102,102,102,102	0
4	PO4	B	705	5/5	0.89	0.15	47,49,62,63	0
2	UJK	B	701	15/15	0.90	0.15	41,53,64,82	0
2	UJK	A	701	15/15	0.91	0.15	53,61,70,74	0
3	ZN	B	702	1/1	0.94	0.11	56,56,56,56	0
3	ZN	A	703	1/1	0.94	0.15	68,68,68,68	0
4	PO4	B	706	5/5	0.96	0.13	37,39,53,54	0
4	PO4	A	706	5/5	0.96	0.16	37,44,60,62	0
4	PO4	A	705	5/5	0.97	0.15	40,47,54,60	0

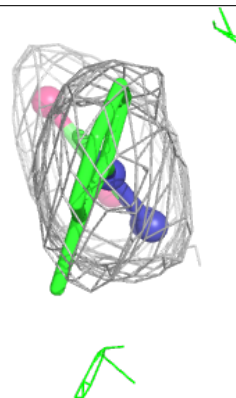
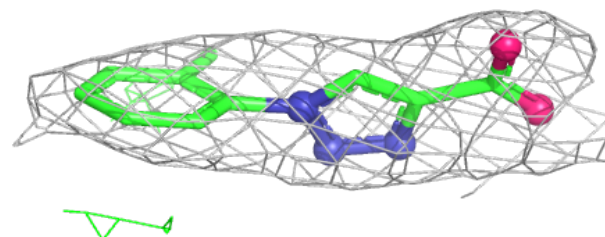
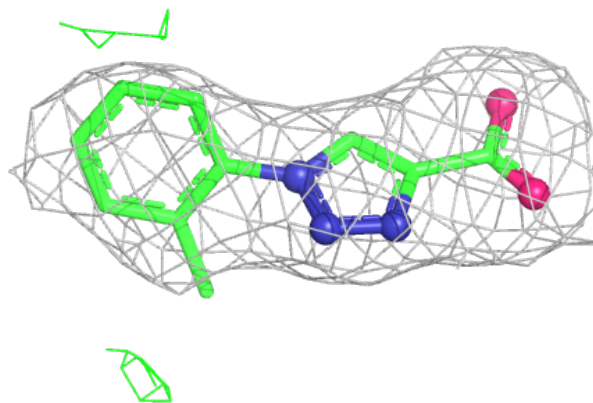
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around UJK B 701:

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

**Electron density around UJK A 701:**

$2mF_o-DF_c$ (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.