



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 1, 2022 – 01:43 PM EDT

PDB ID : 5RLF
Title : PanDDA analysis group deposition – Crystal Structure of SARS-CoV-2 heli-
case in complex with Z235341991
Authors : Newman, J.A.; Yosaatmadja, Y.; Douangamath, A.; Aimon, A.; Powell, A.J.;
Dias, A.; Fearon, D.; Dunnett, L.; Brandao-Neto, J.; Krojer, T.; Skyner, R.;
Gorrie-Stone, T.; Thompson, W.; von Delft, F.; Arrowsmith, C.H.; Edwards,
A.; Bountra, C.; Gileadi, O.
Deposited on : 2020-09-16
Resolution : 2.23 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](#) ①) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.29
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.29

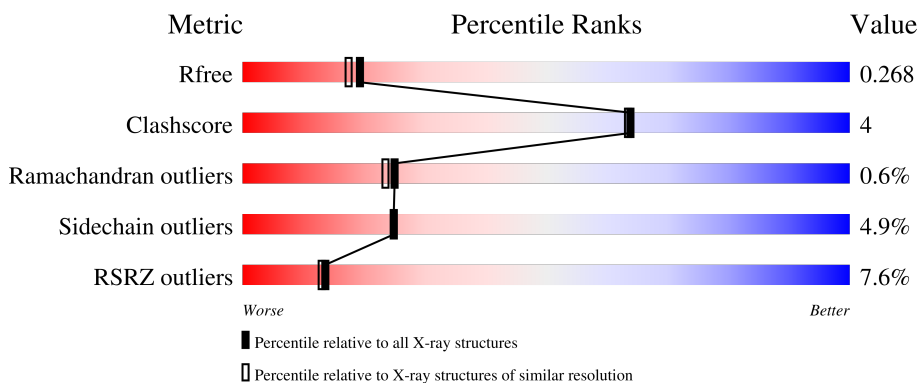
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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	<div style="display: flex; align-items: center;"> <div style="width: 13%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 81%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 13%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 10px;">13% 81% 13% • 5%</p>
1	B	601	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 86%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 11%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 10px;">2% 86% 11% •</p>

2 Entry composition [i](#)

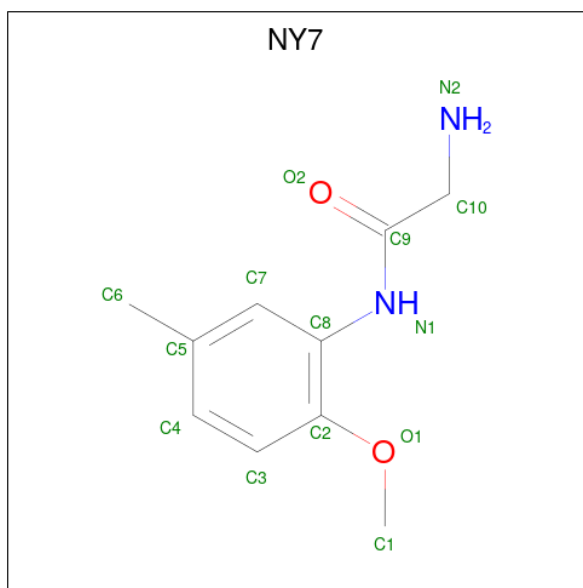
There are 5 unique types of molecules in this entry. The entry contains 9418 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Helicase.

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

- Molecule 2 is N-(2-methoxy-5-methylphenyl)glycinamide (three-letter code: NY7) (formula: $C_{10}H_{14}N_2O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total 14	C 10	N 2	O 2	0	0

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

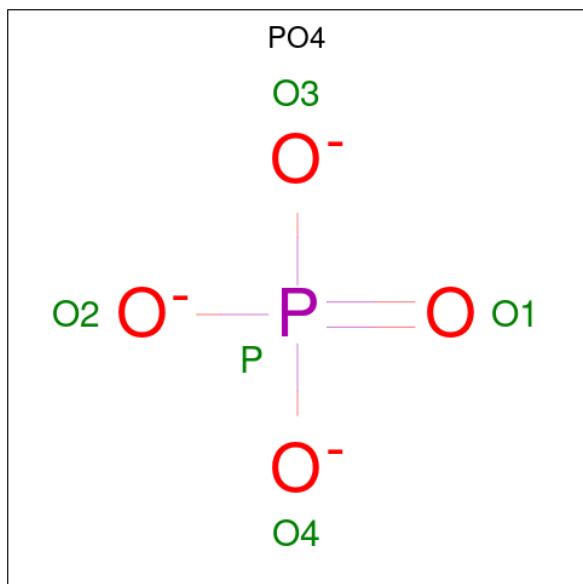
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	A	3	Total 3	Zn 3	0	0

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

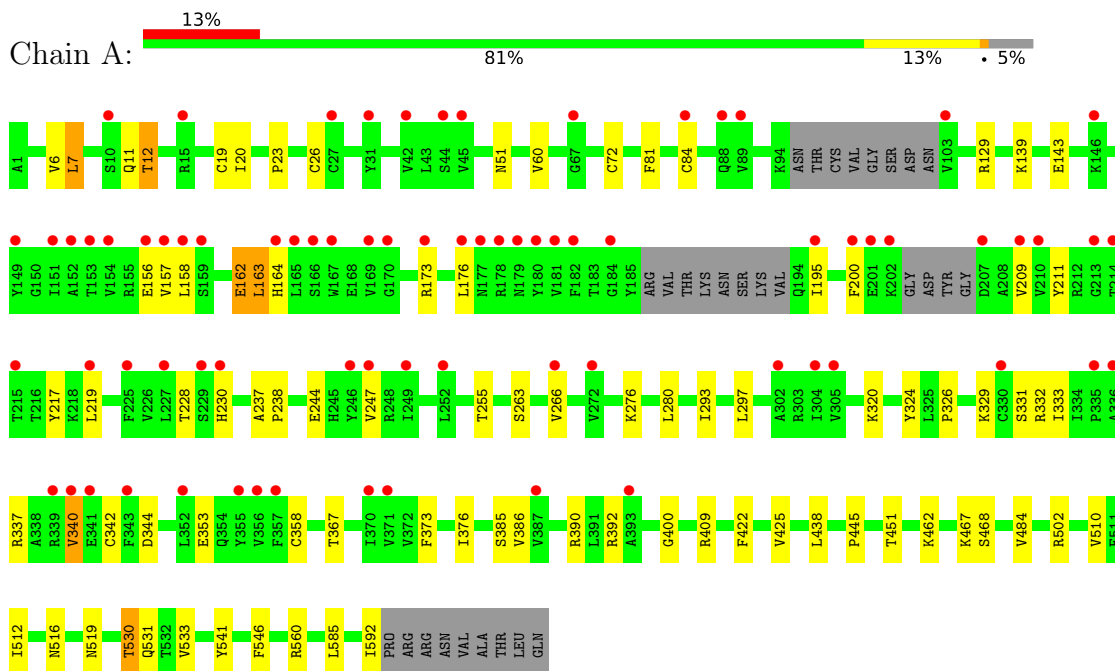
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	202	Total	O	0	0
			202	202		
5	B	251	Total	O	0	0
			251	251		

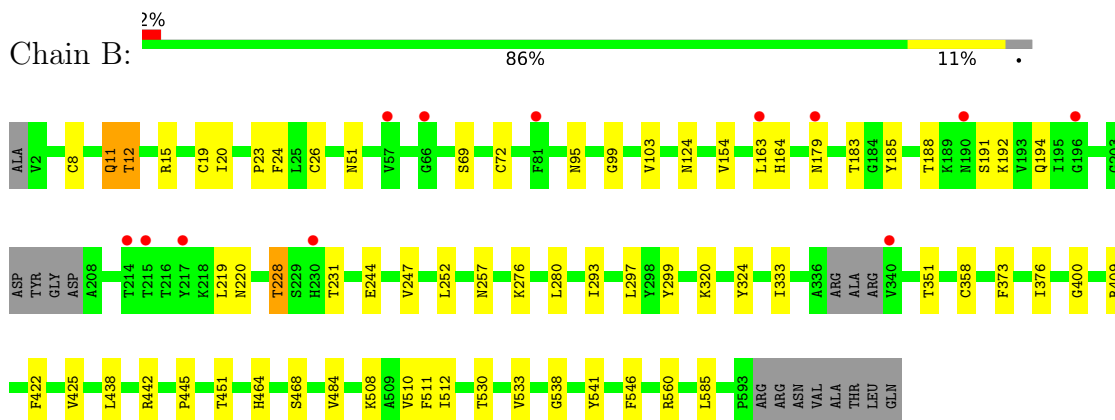
3 Residue-property plots [i](#)

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: Helicase



• Molecule 1: Helicase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.27Å 70.42Å 86.16Å 102.99° 96.42° 112.18°	Depositor
Resolution (Å)	81.93 – 2.23 81.93 – 2.23	Depositor EDS
% Data completeness (in resolution range)	96.9 (81.93-2.23) 96.9 (81.93-2.23)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.22Å)	Xtriage
Refinement program	BUSTER 2.10.3 (20-MAY-2020)	Depositor
R, R_{free}	0.161 , 0.254 0.178 , 0.268	Depositor DCC
R_{free} test set	2995 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å ²)	44.9	Xtriage
Anisotropy	0.410	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 61.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9418	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% 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: PO4, ZN, NY7

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	0.51	0/4517	0.65	0/6156
1	B	0.53	0/4610	0.65	0/6283
All	All	0.52	0/9127	0.65	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	4322	47	0
1	B	4508	0	4425	28	0
2	A	14	0	0	0	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	1	0
5	A	202	0	0	4	0
5	B	251	0	0	2	0
All	All	9418	0	8747	75	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 (75) 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:158:LEU:HD21	1:A:164:HIS:CE1	2.15	0.81
1:A:331:SER:HB2	1:A:353:GLU:HG3	1.68	0.75
1:A:326:PRO:HG2	1:A:329:LYS:NZ	2.08	0.68
1:A:386:VAL:HG13	1:A:390:ARG:HE	1.58	0.67
1:A:326:PRO:HB2	1:A:329:LYS:HZ3	1.62	0.65
1:A:238:PRO:HG3	5:A:990:HOH:O	1.97	0.65
1:A:158:LEU:HD11	1:A:164:HIS:CE1	2.34	0.63
1:A:519:ASN:HB3	1:A:530:THR:CG2	2.30	0.61
1:A:6:VAL:O	1:A:6:VAL:HG23	2.01	0.61
1:B:511:PHE:HB3	1:B:530:THR:HG22	1.83	0.61
1:B:510:VAL:HG21	1:B:541:TYR:CD1	2.38	0.58
1:A:519:ASN:HB3	1:A:530:THR:HG23	1.85	0.56
1:A:326:PRO:HG2	1:A:329:LYS:HZ1	1.71	0.56
1:A:158:LEU:HD21	1:A:164:HIS:HE1	1.69	0.55
1:B:333:ILE:HB	1:B:358:CYS:HB2	1.90	0.54
1:A:510:VAL:HG21	1:A:541:TYR:CD1	2.43	0.53
1:A:333:ILE:HB	1:A:358:CYS:HB2	1.89	0.53
1:A:244:GLU:HB2	1:A:276:LYS:HB2	1.91	0.53
1:A:326:PRO:CG	1:A:329:LYS:HZ3	2.22	0.53
1:A:326:PRO:CB	1:A:329:LYS:HZ3	2.21	0.53
1:A:139:LYS:O	1:A:143:GLU:HG2	2.09	0.52
1:A:445:PRO:HB3	1:A:468:SER:HB3	1.91	0.52
1:B:8:CYS:SG	1:B:99:GLY:O	2.68	0.52
1:B:445:PRO:HB3	1:B:468:SER:HB3	1.91	0.51
1:B:451:THR:HG21	1:B:585:LEU:HD23	1.93	0.50
1:A:326:PRO:HG2	1:A:329:LYS:HZ3	1.75	0.49
1:A:158:LEU:HD21	1:A:164:HIS:ND1	2.26	0.49
1:B:15:ARG:HG3	1:B:24:PHE:CD2	2.46	0.49
1:B:442:ARG:HH11	1:B:464:HIS:CE1	2.30	0.49
1:A:293:ILE:HG13	1:A:320:LYS:HB3	1.94	0.49
1:B:244:GLU:HB2	1:B:276:LYS:HB2	1.94	0.49
1:A:19:CYS:HB2	1:A:23:PRO:HD2	1.95	0.49
1:A:332:ARG:CZ	1:A:342:CYS:SG	3.01	0.49
1:A:326:PRO:HB2	1:A:329:LYS:NZ	2.26	0.48
1:B:293:ILE:HG13	1:B:320:LYS:HB3	1.94	0.48
1:A:462:LYS:NZ	5:A:803:HOH:O	2.46	0.48
1:B:19:CYS:HB2	1:B:23:PRO:HD2	1.95	0.48
1:A:451:THR:HG21	1:A:585:LEU:HD23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:LEU:HD22	1:A:200:PHE:HB2	1.96	0.47
1:B:252:LEU:HB3	1:B:299:TYR:CD1	2.50	0.46
1:B:12:THR:OG1	1:B:26:CYS:HA	2.16	0.46
1:A:367:THR:HG22	1:A:392:ARG:HB3	1.98	0.46
1:A:409:ARG:NH2	1:A:422:PHE:O	2.47	0.46
1:B:538:GLY:HA2	4:B:705:PO4:O1	2.16	0.46
1:A:263:SER:HA	1:A:266:VAL:HG13	1.97	0.45
1:B:276:LYS:NZ	5:B:811:HOH:O	2.49	0.45
1:B:508:LYS:HD2	5:B:873:HOH:O	2.15	0.45
1:B:183:THR:OG1	1:B:228:THR:OG1	2.26	0.45
1:B:185:TYR:CE2	1:B:194:GLN:HG2	2.52	0.45
1:A:6:VAL:HA	1:A:129:ARG:HD2	1.98	0.45
1:A:280:LEU:HD11	1:A:438:LEU:HG	1.98	0.45
1:A:519:ASN:HB3	1:A:530:THR:HG21	1.98	0.45
1:A:533:VAL:HG11	1:A:560:ARG:HG3	1.98	0.44
1:A:512:ILE:O	1:A:546:PHE:HA	2.17	0.44
1:A:467:LYS:NZ	5:A:812:HOH:O	2.51	0.44
1:B:533:VAL:HG11	1:B:560:ARG:HG3	2.00	0.44
1:B:376:ILE:HG22	1:B:400:GLY:HA3	2.00	0.43
1:A:12:THR:OG1	1:A:26:CYS:HA	2.18	0.43
1:B:409:ARG:NH2	1:B:422:PHE:O	2.51	0.43
1:A:6:VAL:O	1:A:6:VAL:CG2	2.67	0.43
1:A:60:VAL:HG13	1:A:84:CYS:SG	2.59	0.43
1:A:297:LEU:HD11	1:A:324:TYR:HB3	2.01	0.42
1:B:183:THR:HG1	1:B:228:THR:HG1	1.56	0.42
1:B:376:ILE:HG12	1:B:425:VAL:HG11	2.01	0.42
1:A:516:ASN:ND2	5:A:814:HOH:O	2.52	0.42
1:B:154:VAL:HG22	1:B:163:LEU:HD13	2.01	0.42
1:B:297:LEU:HD11	1:B:324:TYR:HB3	2.02	0.42
1:A:376:ILE:HG22	1:A:400:GLY:HA3	2.01	0.41
1:B:512:ILE:O	1:B:546:PHE:HA	2.20	0.41
1:A:237:ALA:O	1:A:385:SER:OG	2.36	0.41
1:B:376:ILE:HD12	1:B:376:ILE:HA	1.92	0.41
1:A:163:LEU:HG	1:A:211:TYR:HB3	2.03	0.41
1:A:376:ILE:HG12	1:A:425:VAL:HG11	2.02	0.41
1:A:158:LEU:HB2	1:A:162:GLU:HB2	2.03	0.41
1:B:280:LEU:HD11	1:B:438:LEU:HG	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	564/601 (94%)	537 (95%)	21 (4%)	6 (1%)	14	9
1	B	580/601 (96%)	554 (96%)	25 (4%)	1 (0%)	47	53
All	All	1144/1202 (95%)	1091 (95%)	46 (4%)	7 (1%)	25	23

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	484	VAL
1	B	11	GLN
1	A	219	LEU
1	A	195	ILE
1	A	228	THR
1	A	340	VAL

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%)	460 (95%)	25 (5%)	23	22
1	B	498/523 (95%)	475 (95%)	23 (5%)	27	28
All	All	983/1046 (94%)	935 (95%)	48 (5%)	25	25

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	11	GLN
1	A	12	THR
1	A	20	ILE
1	A	51	ASN
1	A	72	CYS
1	A	81	PHE
1	A	156	GLU
1	A	157	VAL
1	A	162	GLU
1	A	163	LEU
1	A	173	ARG
1	A	209	VAL
1	A	217	TYR
1	A	230	HIS
1	A	247	VAL
1	A	255	THR
1	A	337	ARG
1	A	340	VAL
1	A	344	ASP
1	A	373	PHE
1	A	502	ARG
1	A	530	THR
1	A	531	GLN
1	A	592	ILE
1	B	11	GLN
1	B	12	THR
1	B	20	ILE
1	B	51	ASN
1	B	69	SER
1	B	72	CYS
1	B	95	ASN
1	B	103	VAL
1	B	124	ASN
1	B	164	HIS
1	B	179	ASN
1	B	188	THR
1	B	191	SER
1	B	192	LYS
1	B	219	LEU
1	B	220	ASN
1	B	228	THR
1	B	231	THR

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Mol	Chain	Res	Type
1	B	247	VAL
1	B	257	ASN
1	B	351	THR
1	B	373	PHE
1	B	484	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	164	HIS
1	A	245	HIS
1	A	404	GLN
1	B	179	ASN
1	B	268	ASN
1	B	464	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 6 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
4	PO4	A	705	-	4,4,4	2.52	1 (25%)	6,6,6	0.70	0
4	PO4	B	704	-	4,4,4	2.49	2 (50%)	6,6,6	0.77	0
4	PO4	A	706	-	4,4,4	2.54	3 (75%)	6,6,6	0.70	0
4	PO4	B	705	-	4,4,4	2.48	1 (25%)	6,6,6	0.86	0
2	NY7	A	701	-	13,14,14	0.29	0	16,18,18	0.59	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
2	NY7	A	701	-	-	2/8/8/8	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	705	PO4	P-O1	4.23	1.60	1.50
4	A	705	PO4	P-O1	4.22	1.60	1.50
4	A	706	PO4	P-O1	4.10	1.60	1.50
4	B	704	PO4	P-O1	4.06	1.60	1.50
4	B	704	PO4	P-O4	2.05	1.60	1.54
4	A	706	PO4	P-O4	2.04	1.60	1.54
4	A	706	PO4	P-O3	2.00	1.60	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

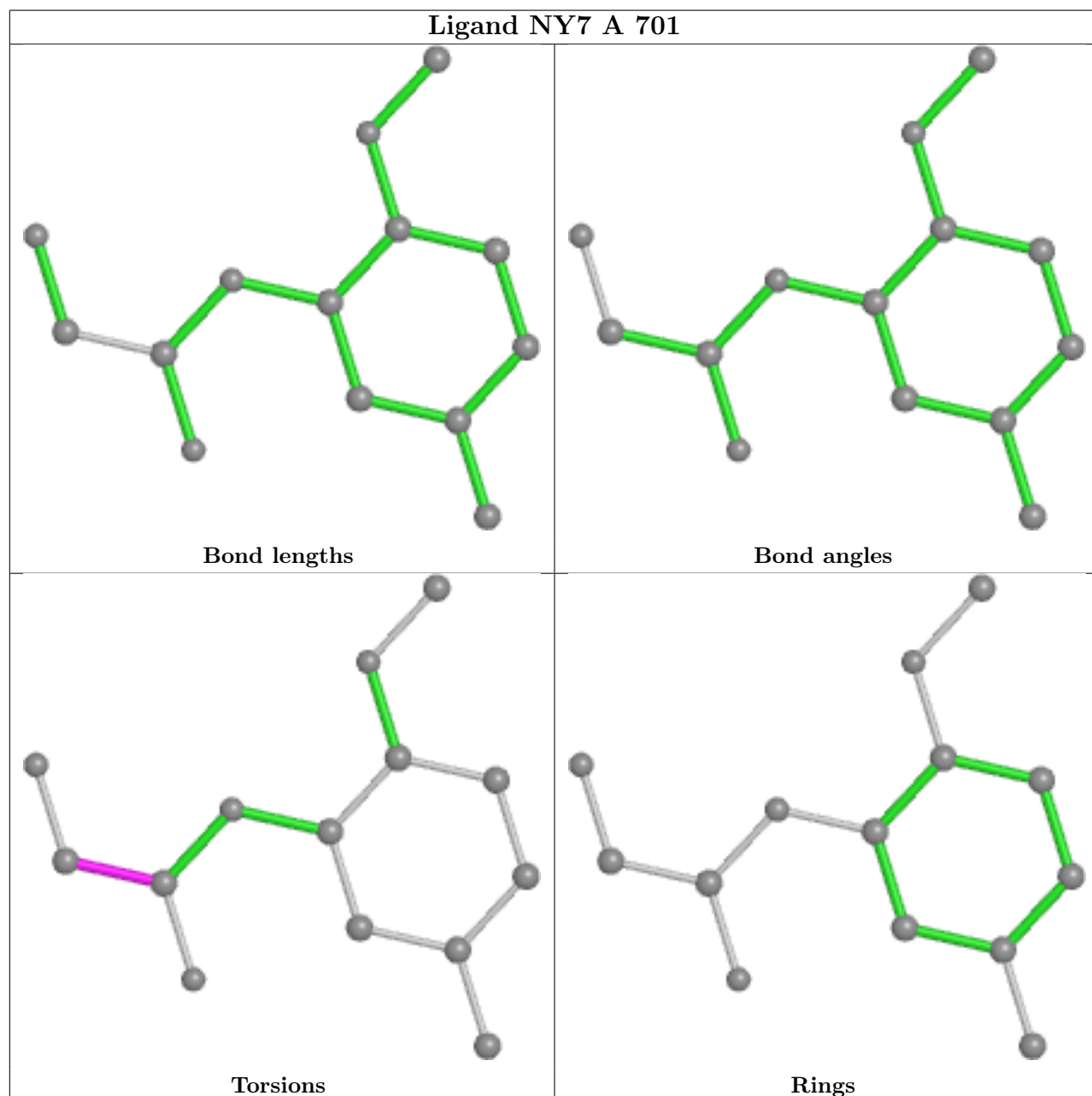
Mol	Chain	Res	Type	Atoms
2	A	701	NY7	N2-C10-C9-N1
2	A	701	NY7	N2-C10-C9-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	705	PO4	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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	572/601 (95%)	0.49	76 (13%) 3 2	41, 88, 153, 183	0
1	B	585/601 (97%)	-0.18	12 (2%) 63 65	39, 61, 117, 158	0
All	All	1157/1202 (96%)	0.15	88 (7%) 13 13	39, 72, 145, 183	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	149	TYR	7.7
1	A	167	TRP	7.0
1	A	181	VAL	6.7
1	A	229	SER	6.4
1	A	247	VAL	6.4
1	A	178	ARG	6.4
1	A	170	GLY	6.3
1	A	184	GLY	5.9
1	A	225	PHE	5.8
1	A	154	VAL	5.8
1	B	217	TYR	5.6
1	A	169	VAL	5.5
1	A	152	ALA	5.4
1	A	165	LEU	5.3
1	A	176	LEU	5.3
1	B	340	VAL	5.0
1	A	352	LEU	5.0
1	A	202	LYS	4.7
1	A	103	VAL	4.6
1	B	66	GLY	4.6
1	A	339	ARG	4.3
1	A	200	PHE	4.2
1	A	305	VAL	4.2
1	B	57	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	207	ASP	3.9
1	B	214	THR	3.8
1	A	177	ASN	3.8
1	A	182	PHE	3.8
1	A	45	VAL	3.8
1	A	210	VAL	3.7
1	A	266	VAL	3.5
1	A	180	TYR	3.5
1	A	357	PHE	3.4
1	A	340	VAL	3.4
1	A	27	CYS	3.3
1	A	227	LEU	3.3
1	A	215	THR	3.3
1	A	302	ALA	3.2
1	A	201	GLU	3.2
1	B	196	GLY	3.2
1	A	157	VAL	3.1
1	A	166	SER	3.0
1	A	371	VAL	3.0
1	A	15	ARG	3.0
1	A	304	ILE	3.0
1	A	164	HIS	3.0
1	A	10	SER	3.0
1	A	42	VAL	2.8
1	A	44	SER	2.8
1	A	341	GLU	2.7
1	A	335	PRO	2.7
1	A	158	LEU	2.7
1	A	195	ILE	2.6
1	A	156	GLU	2.6
1	B	190	ASN	2.6
1	A	209	VAL	2.6
1	A	67	GLY	2.6
1	A	153	THR	2.5
1	A	343	PHE	2.5
1	B	81	PHE	2.5
1	A	355	TYR	2.5
1	A	159	SER	2.5
1	A	213	GLY	2.4
1	A	249	ILE	2.4
1	A	393	ALA	2.4
1	A	173	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	356	VAL	2.4
1	A	179	ASN	2.4
1	A	89	VAL	2.3
1	A	84	CYS	2.3
1	A	31	TYR	2.3
1	A	272	VAL	2.3
1	A	387	VAL	2.3
1	A	252	LEU	2.2
1	A	219	LEU	2.2
1	A	370	ILE	2.2
1	A	88	GLN	2.2
1	A	246	TYR	2.2
1	B	163	LEU	2.2
1	A	146	LYS	2.1
1	A	330	CYS	2.1
1	A	214	THR	2.1
1	A	151	ILE	2.1
1	B	230	HIS	2.1
1	A	230	HIS	2.0
1	B	179	ASN	2.0
1	B	215	THR	2.0
1	A	336	ALA	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 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.

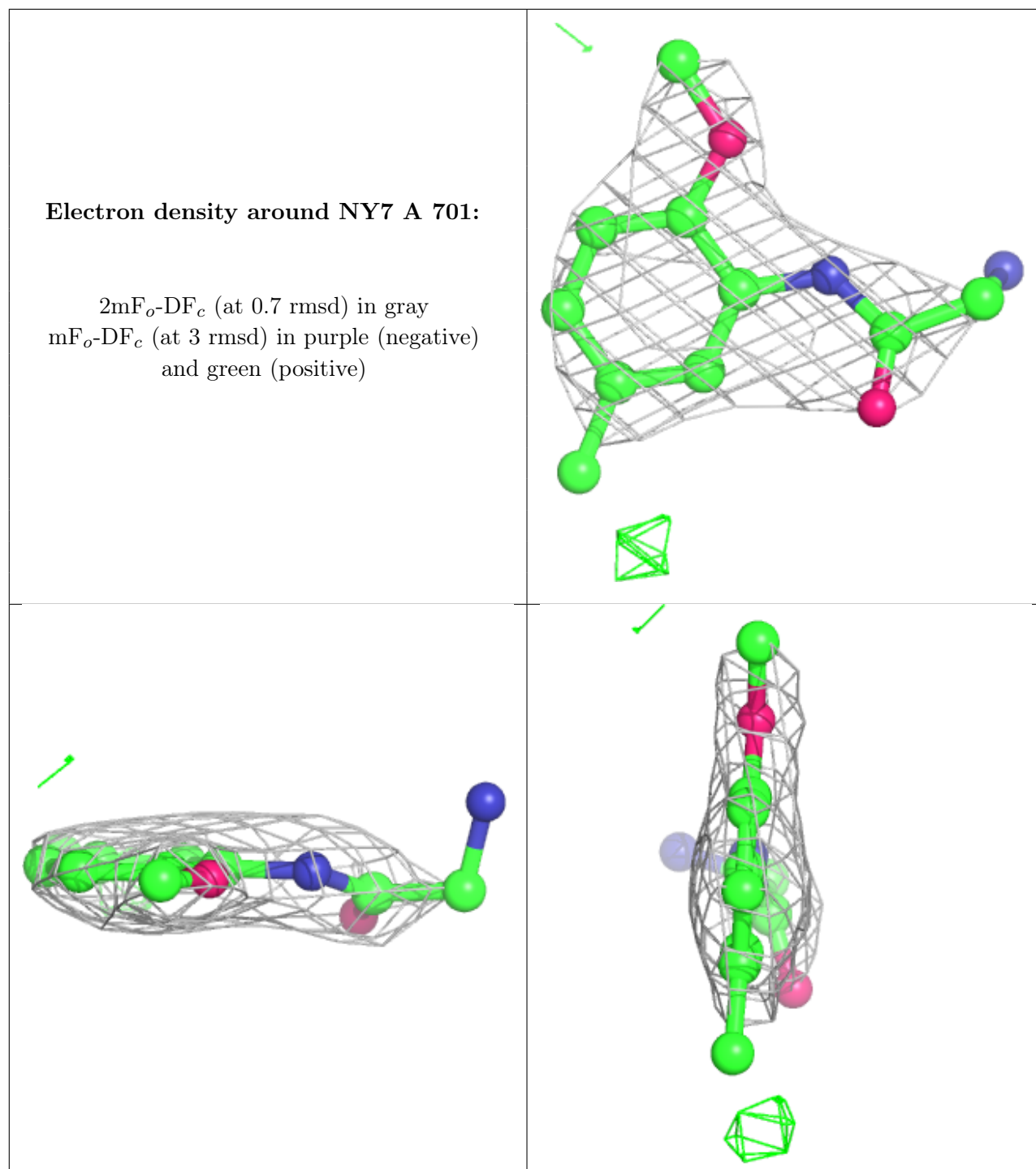
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NY7	A	701	14/14	0.93	0.25	54,56,61,63	14

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ZN	B	703	1/1	0.94	0.13	112,112,112,112	0
3	ZN	A	704	1/1	0.96	0.06	122,122,122,122	0
3	ZN	A	703	1/1	0.97	0.11	75,75,75,75	0
3	ZN	B	702	1/1	0.99	0.16	83,83,83,83	0
4	PO4	A	705	5/5	0.99	0.12	70,72,76,76	0
4	PO4	A	706	5/5	0.99	0.12	62,63,63,66	0
4	PO4	B	704	5/5	0.99	0.12	55,55,59,59	0
4	PO4	B	705	5/5	0.99	0.12	54,55,60,63	0
3	ZN	A	702	1/1	1.00	0.15	77,77,77,77	0
3	ZN	B	701	1/1	1.00	0.14	62,62,62,62	0

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



6.5 Other polymers [i](#)

There are no such residues in this entry.