



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:28 PM UTC

PDB ID : 5TUS / pdb_00005tus
Title : Potent competitive inhibition of human ribonucleotide reductase by a novel non-nucleoside small molecule
Authors : Mohammed, F.A.; Alam, I.; Dealwis, C.G.
Deposited on : 2016-11-07
Resolution : 2.66 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

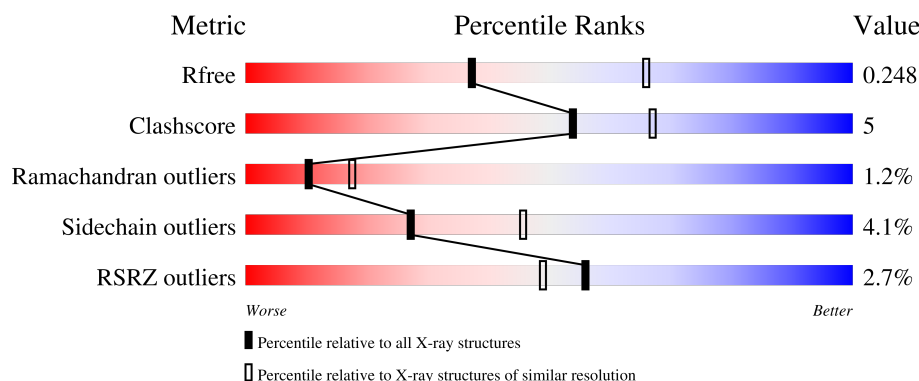
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.66 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	792	
1	B	792	

2 Entry composition [i](#)

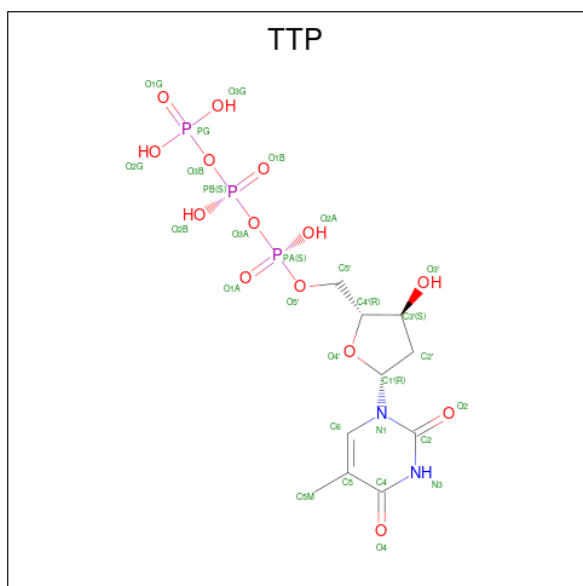
There are 5 unique types of molecules in this entry. The entry contains 11713 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ribonucleoside-diphosphate reductase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	720	Total	C	N	O	S	0	0	0
			5752	3674	964	1081	33			
1	B	731	Total	C	N	O	S	0	0	0
			5845	3729	986	1096	34			

- Molecule 2 is THYMIDINE-5'-TRIPHOSPHATE (CCD ID: TTP) (formula: $C_{10}H_{17}N_2O_{14}P_3$).

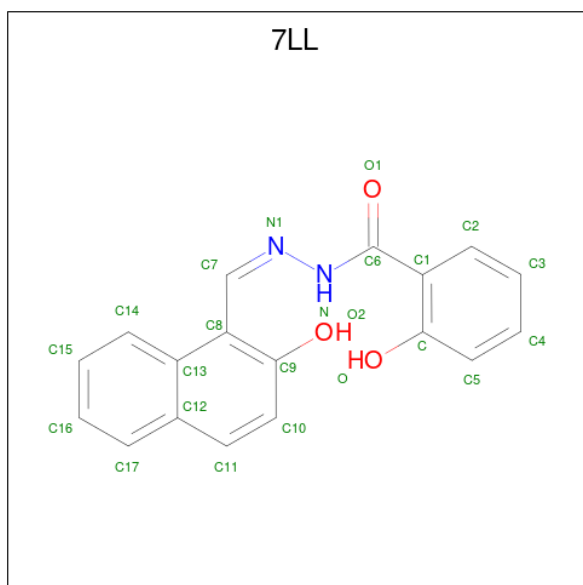


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
2	B	1	Total	C	N	O	P	0	0
			29	10	2	14	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0

- Molecule 4 is 2-hydroxy-N'-[(Z)-(2-hydroxynaphthalen-1-yl)methylidene]benzohydrazide (CCD ID: 7LL) (formula: C₁₈H₁₄N₂O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N O 23 18 2 3	0	0

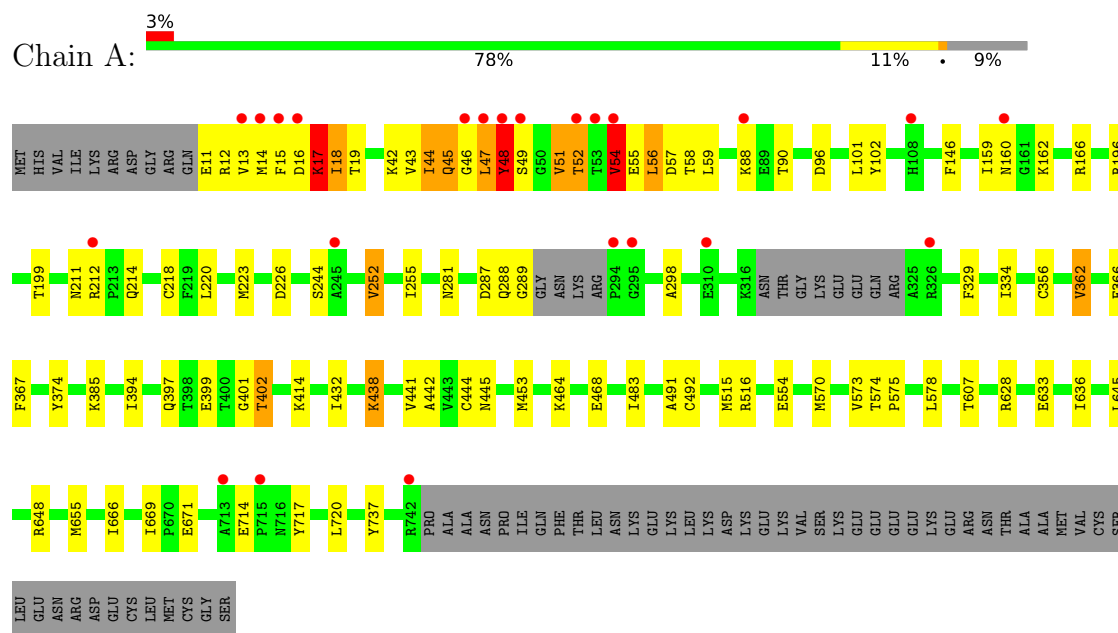
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	28	Total O 28 28	0	0
5	B	5	Total O 5 5	0	0

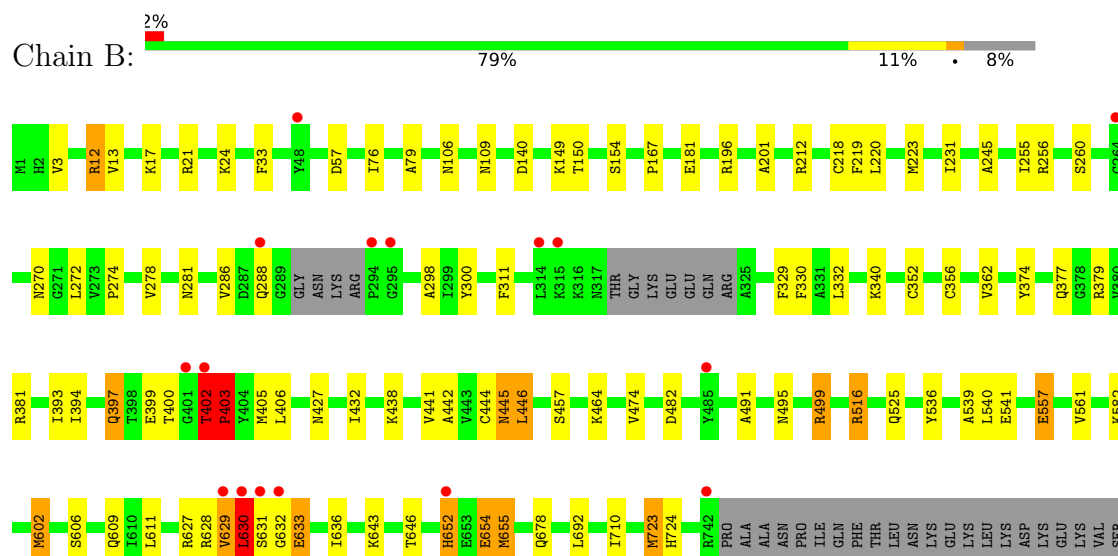
3 Residue-property plots

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: Ribonucleoside-diphosphate reductase large subunit



- Molecule 1: Ribonucleoside-diphosphate reductase large subunit



LYS
GLU
GLU
GLU
GLU
LYS
GLU
ARG
ASN
THR
ALA
ALA
MET
VAL
CYS
SER
LEU
GLU
ASN
ARG
ASP
GLU
CYS
LEU
MET
CYS
GLY
SER

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.52Å 114.28Å 220.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	110.18 – 2.66 110.18 – 2.66	Depositor EDS
% Data completeness (in resolution range)	98.7 (110.18-2.66) 98.6 (110.18-2.66)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.199 , 0.250 0.205 , 0.248	Depositor DCC
R_{free} test set	1998 reflections (3.89%)	wwPDB-VP
Wilson B-factor (Å ²)	58.0	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 28.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11713	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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: TTP, MG, 7LL

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	0.97	0/5877	1.08	13/7962 (0.2%)
1	B	0.94	0/5971	1.06	12/8086 (0.1%)
All	All	0.95	0/11848	1.07	25/16048 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	629	VAL	CB-CA-C	-9.80	95.22	111.29
1	A	46	GLY	N-CA-C	-8.98	103.53	114.66
1	B	402	THR	C-N-CD	-8.88	88.61	125.00
1	B	629	VAL	N-CA-C	8.71	127.46	109.34
1	B	630	LEU	N-CA-C	-8.45	100.30	110.44
1	A	45	GLN	N-CA-C	-8.21	102.16	113.56
1	A	49	SER	N-CA-C	-6.93	104.45	113.12
1	B	499	ARG	CA-C-N	-6.64	113.80	120.31
1	B	499	ARG	C-N-CA	-6.64	113.80	120.31
1	A	48	TYR	N-CA-C	6.59	124.84	110.80
1	A	578	LEU	N-CA-C	6.58	118.46	111.28
1	A	402	THR	C-N-CD	-6.07	107.24	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	629	VAL	N-CA-CB	-6.06	101.23	111.23
1	A	554	GLU	N-CA-C	6.03	118.63	111.33
1	B	400	THR	CB-CA-C	-5.77	99.95	109.99
1	A	334	ILE	N-CA-C	5.73	114.82	108.05
1	B	402	THR	N-CA-C	5.68	122.38	109.81
1	B	403	PRO	CA-N-CD	-5.68	104.04	112.00
1	A	438	LYS	N-CA-C	-5.30	105.59	111.36
1	A	52	THR	N-CA-C	5.19	115.14	108.34
1	A	648	ARG	N-CA-C	-5.12	106.35	112.59
1	A	96	ASP	N-CA-C	5.11	116.85	111.28
1	B	446	LEU	N-CA-C	5.11	117.58	109.50
1	B	278	VAL	CB-CA-C	-5.05	105.32	112.14
1	A	102	TYR	N-CA-C	5.00	116.42	111.07

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	402	THR	Peptide
1	B	402	THR	Peptide

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	5752	0	5728	55	1
1	B	5845	0	5827	60	1
2	A	29	0	13	1	0
2	B	29	0	13	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	23	0	0	2	0
5	A	28	0	0	4	0
5	B	5	0	0	0	0
All	All	11713	0	11581	115	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 5.

All (115) 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:B:654:GLU:HG3	1:B:655:MET:H	1.06	1.12
1:A:17:LYS:HD3	1:A:18:ILE:N	1.71	1.04
1:A:575:PRO:HD3	5:A:1701:HOH:O	1.64	0.94
1:A:17:LYS:HD3	1:A:18:ILE:H	1.33	0.92
1:A:16:ASP:O	1:A:19:THR:N	2.02	0.92
1:B:223:MET:HE1	1:B:231:ILE:HA	1.56	0.88
1:B:446:LEU:HB3	1:B:602:MET:HE1	1.54	0.87
1:B:654:GLU:HG3	1:B:655:MET:N	1.90	0.86
1:B:652:HIS:HB2	1:B:654:GLU:HG2	1.58	0.84
1:B:654:GLU:CG	1:B:655:MET:H	1.89	0.82
1:B:218:CYS:HB2	1:B:444:CYS:SG	2.20	0.81
1:A:17:LYS:CD	1:A:18:ILE:H	1.92	0.81
1:A:492:CYS:SG	5:A:1727:HOH:O	2.39	0.80
1:A:56:LEU:O	1:A:59:LEU:N	2.15	0.79
1:B:652:HIS:CB	1:B:654:GLU:HG2	2.14	0.77
1:B:629:VAL:HG11	1:B:633:GLU:N	2.01	0.76
1:A:90:THR:HG21	1:A:166:ARG:HG3	1.72	0.72
1:A:56:LEU:O	1:A:57:ASP:C	2.33	0.71
1:B:630:LEU:HD12	1:B:630:LEU:C	2.19	0.68
1:A:218:CYS:HB3	1:A:444:CYS:SG	2.34	0.67
1:A:16:ASP:O	1:A:18:ILE:N	2.28	0.67
1:A:574:THR:HA	5:A:1701:HOH:O	1.96	0.66
1:A:573:VAL:O	5:A:1701:HOH:O	2.13	0.65
1:B:446:LEU:HB3	1:B:602:MET:CE	2.25	0.65
1:A:281:ASN:OD1	1:B:281:ASN:ND2	2.30	0.64
1:B:630:LEU:HD12	1:B:630:LEU:O	1.99	0.63
1:B:201:ALA:HA	4:B:1603:7LL:C16	2.31	0.61
1:B:557:GLU:H	1:B:557:GLU:CD	2.09	0.60
1:B:150:THR:OG1	1:B:609:GLN:OE1	2.14	0.60
1:A:223:MET:HG2	1:A:255:ILE:HD11	1.83	0.60
1:B:627:ARG:HG3	1:B:636:ILE:HD12	1.83	0.59
1:B:260:SER:OG	1:B:381:ARG:NH1	2.36	0.59
1:A:17:LYS:HD3	1:A:18:ILE:HB	1.84	0.58
1:B:330:PHE:O	1:B:403:PRO:HA	2.04	0.58
1:A:52:THR:HG23	1:A:54:VAL:HG12	1.85	0.57
1:B:629:VAL:CG1	1:B:633:GLU:N	2.66	0.57
1:A:17:LYS:HE2	1:A:18:ILE:HD12	1.87	0.56
1:A:287:ASP:C	1:A:289:GLY:H	2.15	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:405:MET:HG3	1:B:724:HIS:CE1	2.42	0.55
1:B:220:LEU:HD11	1:B:427:ASN:HB3	1.90	0.54
1:A:17:LYS:CD	1:A:18:ILE:HB	2.37	0.54
1:B:270:ASN:HB3	1:B:274:PRO:HG2	1.90	0.54
1:A:220:LEU:HB2	1:A:442:ALA:HB3	1.90	0.53
1:B:106:ASN:HD21	1:B:109:ASN:HB3	1.73	0.53
1:A:17:LYS:CD	1:A:18:ILE:N	2.53	0.53
1:A:362:VAL:HG22	1:A:366:GLU:HB3	1.91	0.53
1:A:199:THR:HG21	1:A:607:THR:HB	1.91	0.53
1:B:311:PHE:CZ	1:B:330:PHE:HD1	2.27	0.52
1:A:43:VAL:C	1:A:44:ILE:O	2.53	0.51
1:A:48:TYR:CD1	1:A:51:VAL:HB	2.46	0.51
1:A:101:LEU:HD23	1:A:159:ILE:HD11	1.92	0.51
1:B:652:HIS:HB3	1:B:654:GLU:HG2	1.93	0.50
1:A:56:LEU:O	1:A:58:THR:N	2.45	0.50
1:A:666:ILE:HA	1:A:669:ILE:HD12	1.94	0.50
1:B:402:THR:C	1:B:403:PRO:O	2.54	0.50
1:A:146:PHE:CE2	1:A:636:ILE:HD11	2.49	0.48
1:B:710:ILE:HG21	1:B:723:MET:SD	2.53	0.48
1:A:223:MET:HE2	1:A:252:VAL:HG23	1.95	0.48
1:B:219:PHE:C	1:B:220:LEU:HD12	2.38	0.48
1:B:220:LEU:HB2	1:B:442:ALA:HB3	1.94	0.48
1:A:214:GLN:HG2	1:A:244:SER:HB3	1.95	0.48
1:A:432:ILE:HG13	1:A:444:CYS:SG	2.54	0.48
1:A:394:ILE:HD11	1:A:717:TYR:HB3	1.96	0.48
1:B:482:ASP:OD2	1:B:499:ARG:NH2	2.47	0.48
1:B:393:ILE:O	1:B:397:GLN:HG3	2.14	0.47
1:B:394:ILE:HA	1:B:397:GLN:HG3	1.96	0.47
1:B:482:ASP:CG	1:B:499:ARG:HH22	2.24	0.46
1:B:17:LYS:O	1:B:21:ARG:HG3	2.16	0.46
1:B:377:GLN:OE1	1:B:379:ARG:NH1	2.49	0.45
1:B:432:ILE:HG13	1:B:444:CYS:SG	2.57	0.45
1:A:159:ILE:O	1:A:160:ASN:CB	2.62	0.45
1:B:140:ASP:OD2	1:B:167:PRO:HB2	2.17	0.45
1:A:226:ASP:OD2	2:A:1601:TTP:O3'	2.34	0.45
1:A:56:LEU:CD1	1:A:56:LEU:N	2.79	0.45
1:B:21:ARG:NH2	1:B:57:ASP:OD1	2.50	0.45
1:A:47:LEU:HB3	1:A:48:TYR:H	1.54	0.44
1:B:76:ILE:O	1:B:79:ALA:HB3	2.18	0.44
1:A:362:VAL:HG13	1:A:367:PHE:HA	2.00	0.44
1:B:196:ARG:HG2	1:B:611:LEU:HD22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ILE:O	1:A:45:GLN:CB	2.66	0.44
1:A:414:LYS:HG2	1:A:570:MET:HB3	1.99	0.43
1:A:397:GLN:O	1:A:401:GLY:HA2	2.18	0.43
1:B:474:VAL:HG21	1:B:539:ALA:HA	2.01	0.43
1:B:245:ALA:HB2	1:B:288:GLN:CD	2.43	0.43
1:B:300:TYR:HE2	1:B:406:LEU:HD13	1.84	0.43
1:B:629:VAL:HG13	1:B:633:GLU:HA	2.00	0.43
1:A:464:LYS:HE3	1:A:468:GLU:OE1	2.18	0.43
1:A:441:VAL:O	1:A:491:ALA:HA	2.19	0.43
1:A:15:PHE:O	1:A:15:PHE:CG	2.70	0.43
1:B:3:VAL:HG22	1:B:13:VAL:HG22	2.01	0.43
1:B:627:ARG:HG3	1:B:636:ILE:CD1	2.48	0.42
4:B:1603:7LL:O2	4:B:1603:7LL:N	2.53	0.42
1:A:287:ASP:C	1:A:289:GLY:N	2.78	0.42
1:B:256:ARG:HH22	2:B:1601:TTP:PG	2.42	0.42
1:A:159:ILE:O	1:A:160:ASN:HB3	2.20	0.42
1:A:515:MET:O	1:A:516:ARG:HB2	2.18	0.42
1:B:298:ALA:HA	1:B:329:PHE:O	2.19	0.42
1:A:356:CYS:HB3	1:A:374:TYR:CD1	2.54	0.42
1:A:483:ILE:O	1:A:483:ILE:HG22	2.20	0.42
1:B:33:PHE:CE2	1:B:646:THR:HB	2.54	0.41
1:A:42:LYS:O	1:A:44:ILE:O	2.37	0.41
1:A:146:PHE:CD2	1:A:636:ILE:HD11	2.56	0.41
1:A:298:ALA:HA	1:A:329:PHE:O	2.20	0.41
1:B:692:LEU:HD11	1:B:723:MET:HG2	2.02	0.41
1:A:453:MET:HE3	1:A:453:MET:HB3	1.95	0.41
1:B:445:ASN:HD21	1:B:495:ASN:HD21	1.68	0.41
1:B:255:ILE:HB	1:B:272:LEU:HD21	2.03	0.41
1:B:629:VAL:CG1	1:B:633:GLU:H	2.34	0.41
1:A:645:LEU:HD13	1:A:655:MET:CE	2.51	0.40
1:B:516:ARG:HD2	1:B:516:ARG:HA	1.84	0.40
1:B:536:TYR:CZ	1:B:540:LEU:HD11	2.56	0.40
1:B:356:CYS:HB3	1:B:374:TYR:CD1	2.56	0.40
1:B:441:VAL:O	1:B:491:ALA:HA	2.21	0.40
1:B:332:LEU:HG	1:B:403:PRO:HB2	2.03	0.40
1:B:106:ASN:ND2	1:B:109:ASN:HB3	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:GLU:OE1	1:B:12:ARG:NH2[3_554]	2.12	0.08

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	714/792 (90%)	671 (94%)	34 (5%)	9 (1%)	9	16
1	B	725/792 (92%)	693 (96%)	24 (3%)	8 (1%)	11	19
All	All	1439/1584 (91%)	1364 (95%)	58 (4%)	17 (1%)	10	17

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	288	GLN
1	B	403	PRO
1	B	633	GLU
1	B	654	GLU
1	B	655	MET
1	A	48	TYR
1	A	54	VAL
1	B	402	THR
1	A	12	ARG
1	A	737	TYR
1	B	631	SER
1	A	13	VAL
1	B	632	GLY
1	A	196	ARG
1	A	44	ILE
1	B	212	ARG

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	629/693 (91%)	606 (96%)	23 (4%)	30	50
1	B	639/693 (92%)	610 (96%)	29 (4%)	24	42
All	All	1268/1386 (92%)	1216 (96%)	52 (4%)	27	46

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	GLU
1	A	14	MET
1	A	17	LYS
1	A	18	ILE
1	A	47	LEU
1	A	51	VAL
1	A	54	VAL
1	A	55	GLU
1	A	56	LEU
1	A	88	LYS
1	A	162	LYS
1	A	211	ASN
1	A	212	ARG
1	A	252	VAL
1	A	362	VAL
1	A	385	LYS
1	A	438	LYS
1	A	445	ASN
1	A	628	ARG
1	A	633	GLU
1	A	671	GLU
1	A	714	GLU
1	A	720	LEU
1	B	12	ARG
1	B	24	LYS
1	B	149	LYS
1	B	154	SER

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Mol	Chain	Res	Type
1	B	181	GLU
1	B	286	VAL
1	B	340	LYS
1	B	352	CYS
1	B	362	VAL
1	B	397	GLN
1	B	399	GLU
1	B	438	LYS
1	B	445	ASN
1	B	457	SER
1	B	464	LYS
1	B	516	ARG
1	B	525	GLN
1	B	541	GLU
1	B	557	GLU
1	B	561	VAL
1	B	582	LYS
1	B	602	MET
1	B	606	SER
1	B	628	ARG
1	B	630	LEU
1	B	643	LYS
1	B	652	HIS
1	B	678	GLN
1	B	723	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	ASN
1	A	266	ASN
1	A	418	GLN
1	B	2	HIS
1	B	38	GLN
1	B	268	ASN
1	B	345	ASN
1	B	495	ASN
1	B	530	GLN
1	B	614	ASN
1	B	635	GLN
1	B	663	ASN
1	B	730	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	TTP	B	1601	3	29,30,30	1.41	4 (13%)	43,47,47	1.71	7 (16%)
2	TTP	A	1601	3	29,30,30	1.51	6 (20%)	43,47,47	1.80	11 (25%)
4	7LL	B	1603	-	25,25,25	1.49	5 (20%)	34,34,34	2.23	10 (29%)

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	TTP	B	1601	3	-	4/22/34/34	0/2/2/2
2	TTP	A	1601	3	-	2/22/34/34	0/2/2/2
4	7LL	B	1603	-	-	4/10/10/10	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1601	TTP	PB-O3A	4.05	1.63	1.59
4	B	1603	7LL	N-N1	3.96	1.43	1.38
2	A	1601	TTP	PB-O3B	3.35	1.63	1.59
2	A	1601	TTP	PB-O3A	3.20	1.62	1.59
2	A	1601	TTP	C4-N3	-3.06	1.33	1.38
2	B	1601	TTP	PB-O3B	3.01	1.62	1.59
4	B	1603	7LL	C8-C7	2.64	1.50	1.44
2	A	1601	TTP	O2-C2	2.36	1.27	1.23
2	A	1601	TTP	C2-N1	2.34	1.42	1.38
2	B	1601	TTP	C4-N3	-2.23	1.34	1.38
4	B	1603	7LL	C16-C17	2.20	1.41	1.36
4	B	1603	7LL	C13-C12	-2.16	1.39	1.43
2	B	1601	TTP	C2-N1	2.10	1.41	1.38
4	B	1603	7LL	C17-C12	-2.07	1.37	1.42
2	A	1601	TTP	C6-N1	-2.02	1.34	1.38

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1603	7LL	C7-N1-N	6.90	128.14	115.97
2	B	1601	TTP	C5-C4-N3	4.67	119.38	115.32
4	B	1603	7LL	C8-C7-N1	4.60	130.06	121.42
2	B	1601	TTP	O4-C4-C5	-4.39	119.90	124.92
2	B	1601	TTP	C4-N3-C2	-4.21	121.82	127.34
4	B	1603	7LL	C9-C8-C7	3.86	124.03	120.05
2	A	1601	TTP	C5-C4-N3	3.67	118.52	115.32
2	A	1601	TTP	O4-C4-C5	-3.65	120.75	124.92
2	A	1601	TTP	O3G-PG-O3B	-3.63	92.45	104.64
4	B	1603	7LL	C16-C17-C12	3.58	125.45	120.48
2	A	1601	TTP	N3-C2-N1	3.35	119.25	114.89
2	A	1601	TTP	C5M-C5-C4	3.29	122.30	118.78
2	B	1601	TTP	N3-C2-N1	3.28	119.16	114.89
2	A	1601	TTP	C4-N3-C2	-3.24	123.09	127.34
2	A	1601	TTP	O3A-PB-O1B	-3.19	101.12	110.70
2	A	1601	TTP	O3G-PG-O2G	3.18	119.71	107.80
4	B	1603	7LL	C11-C12-C13	3.14	123.17	119.12
4	B	1603	7LL	O2-C9-C8	-3.09	118.64	122.39
2	B	1601	TTP	C5-C6-N1	-2.86	120.21	123.31
4	B	1603	7LL	C16-C15-C14	-2.82	116.62	120.40
4	B	1603	7LL	C15-C14-C13	2.82	124.72	120.91
4	B	1603	7LL	O1-C6-N	-2.54	118.82	122.66
2	B	1601	TTP	O3A-PB-O1B	-2.51	103.14	110.70
4	B	1603	7LL	C10-C11-C12	-2.46	117.16	120.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1601	TTP	O2B-PB-O3B	-2.39	100.81	107.27
2	B	1601	TTP	O3B-PG-O1G	-2.21	99.43	111.04
2	A	1601	TTP	O2B-PB-O1B	2.16	122.50	112.44
2	A	1601	TTP	C5M-C5-C6	-2.15	119.94	122.85

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1603	7LL	C6-N-N1-C7
4	B	1603	7LL	N1-C7-C8-C9
4	B	1603	7LL	N1-C7-C8-C13
4	B	1603	7LL	C8-C7-N1-N
2	B	1601	TTP	PG-O3B-PB-O1B
2	B	1601	TTP	PA-O3A-PB-O1B
2	B	1601	TTP	PA-O3A-PB-O2B
2	B	1601	TTP	PG-O3B-PB-O2B
2	A	1601	TTP	PG-O3B-PB-O1B
2	A	1601	TTP	PG-O3B-PB-O2B

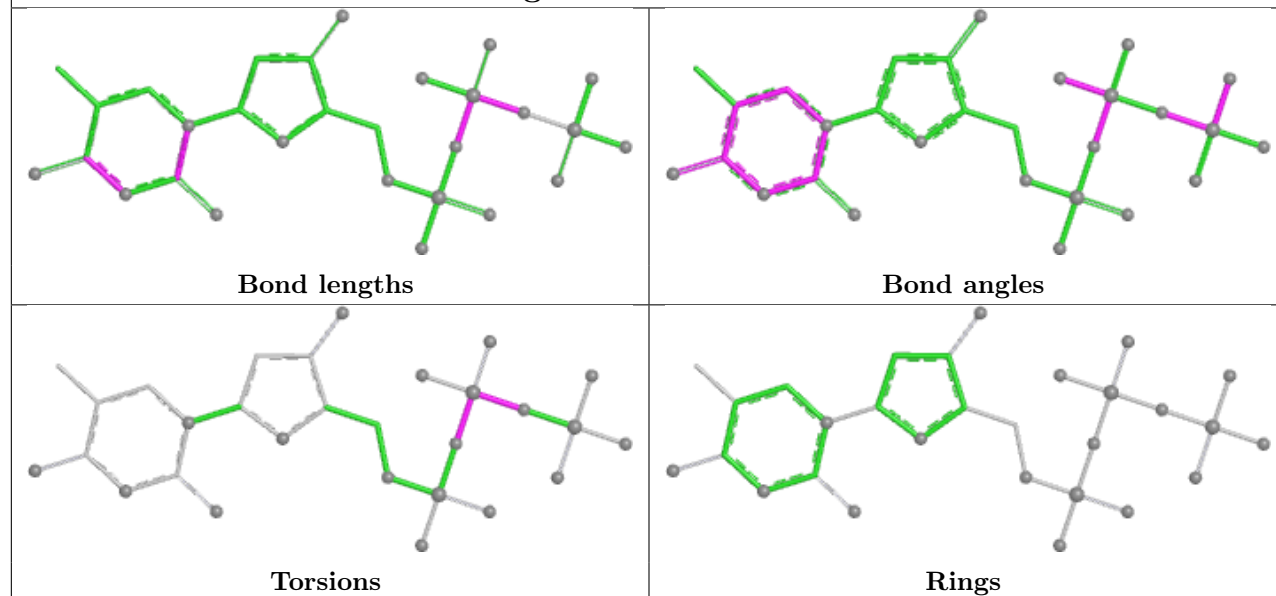
There are no ring outliers.

3 monomers are involved in 4 short contacts:

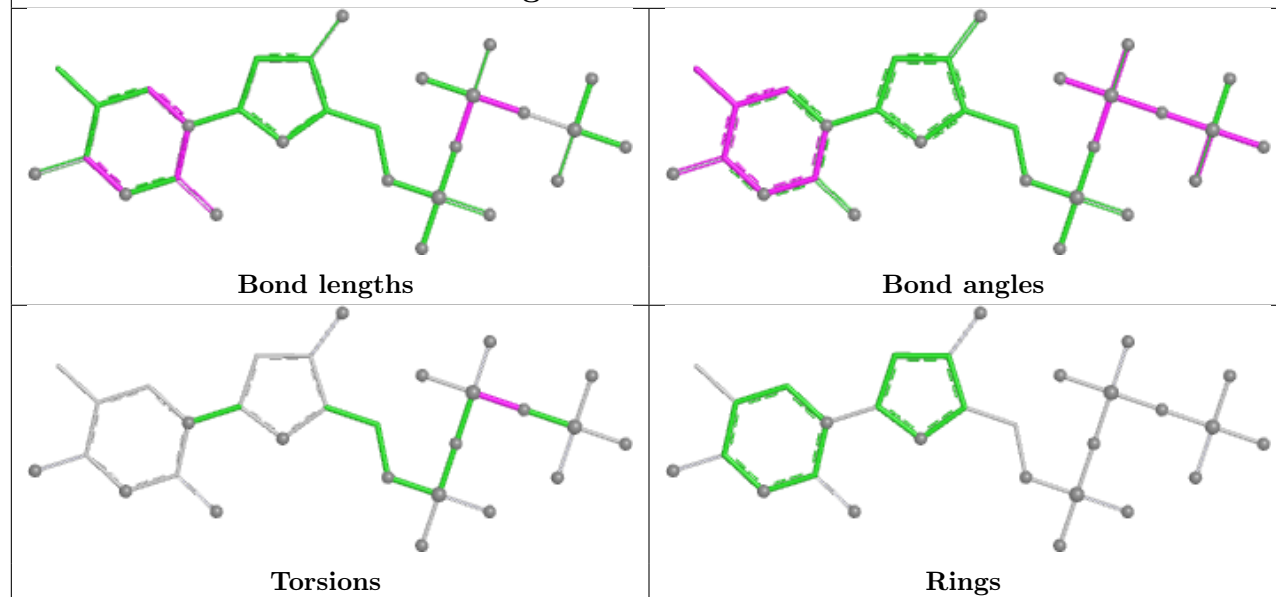
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1601	TTP	1	0
2	A	1601	TTP	1	0
4	B	1603	7LL	2	0

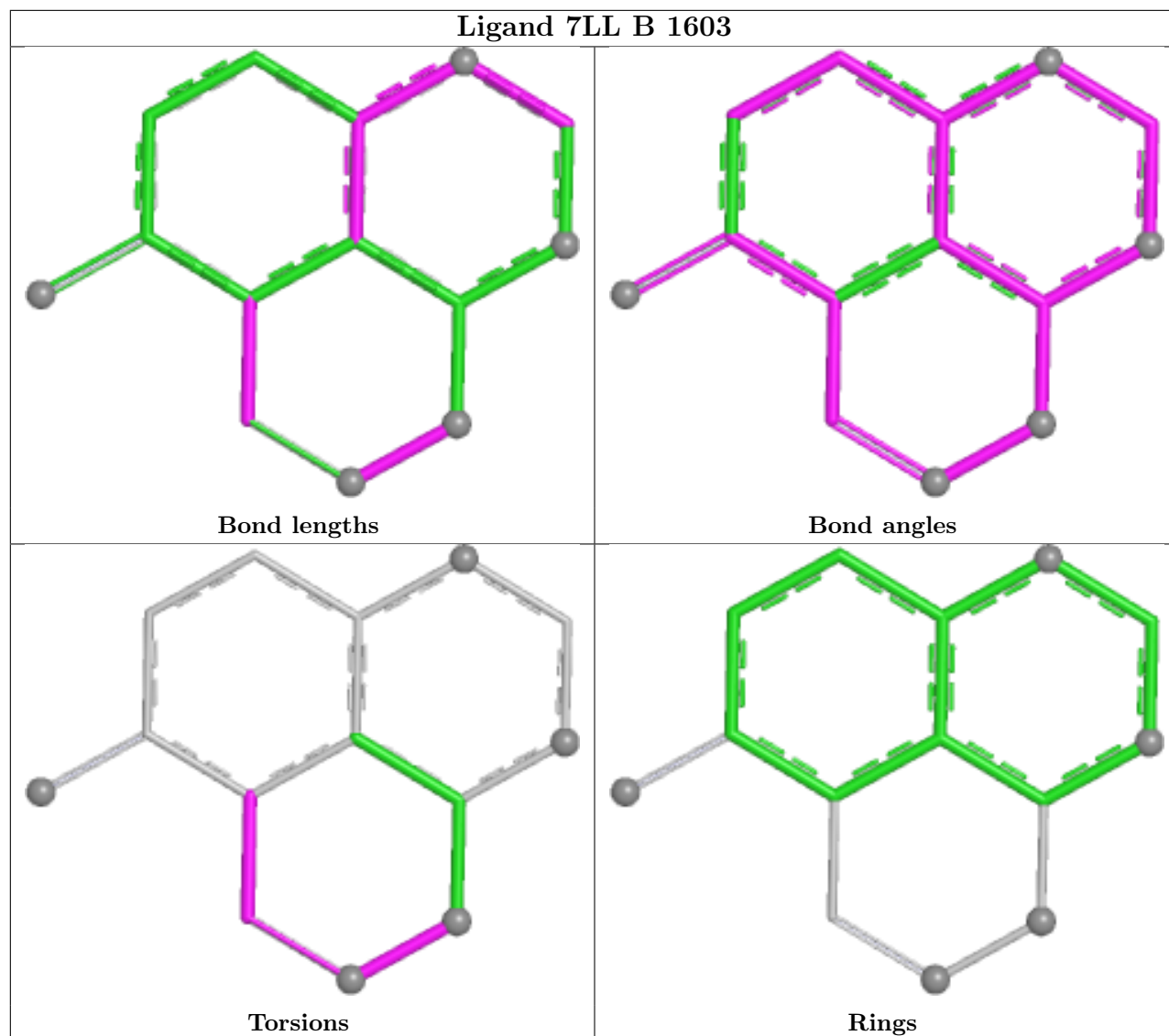
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand TTP B 1601



Ligand TTP A 1601





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	720/792 (90%)	-0.10	23 (3%)	50 42	36, 50, 86, 141	0
1	B	731/792 (92%)	-0.03	16 (2%)	62 56	40, 55, 85, 123	0
All	All	1451/1584 (91%)	-0.07	39 (2%)	56 49	36, 52, 86, 141	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	16	ASP	6.6
1	A	47	LEU	6.1
1	A	54	VAL	5.4
1	B	402	THR	5.0
1	A	294	PRO	4.9
1	A	53	THR	4.8
1	B	630	LEU	4.5
1	A	14	MET	3.8
1	B	314	LEU	3.8
1	B	629	VAL	3.7
1	A	108	HIS	3.6
1	A	212	ARG	3.4
1	A	715	PRO	3.2
1	A	245	ALA	3.1
1	B	742	ARG	3.0
1	B	485	TYR	3.0
1	B	401	GLY	2.9
1	A	13	VAL	2.9
1	A	742	ARG	2.8
1	A	15	PHE	2.8
1	B	295	GLY	2.8
1	A	48	TYR	2.7
1	B	631	SER	2.5
1	A	295	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	632	GLY	2.5
1	A	52	THR	2.5
1	B	315	LYS	2.4
1	A	88	LYS	2.4
1	A	46	GLY	2.4
1	B	288	GLN	2.3
1	A	326	ARG	2.3
1	B	264	GLY	2.2
1	A	160	ASN	2.2
1	A	49	SER	2.2
1	A	310	GLU	2.2
1	B	294	PRO	2.2
1	B	48	TYR	2.1
1	B	652	HIS	2.0
1	A	713	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 oligosaccharides in this entry.

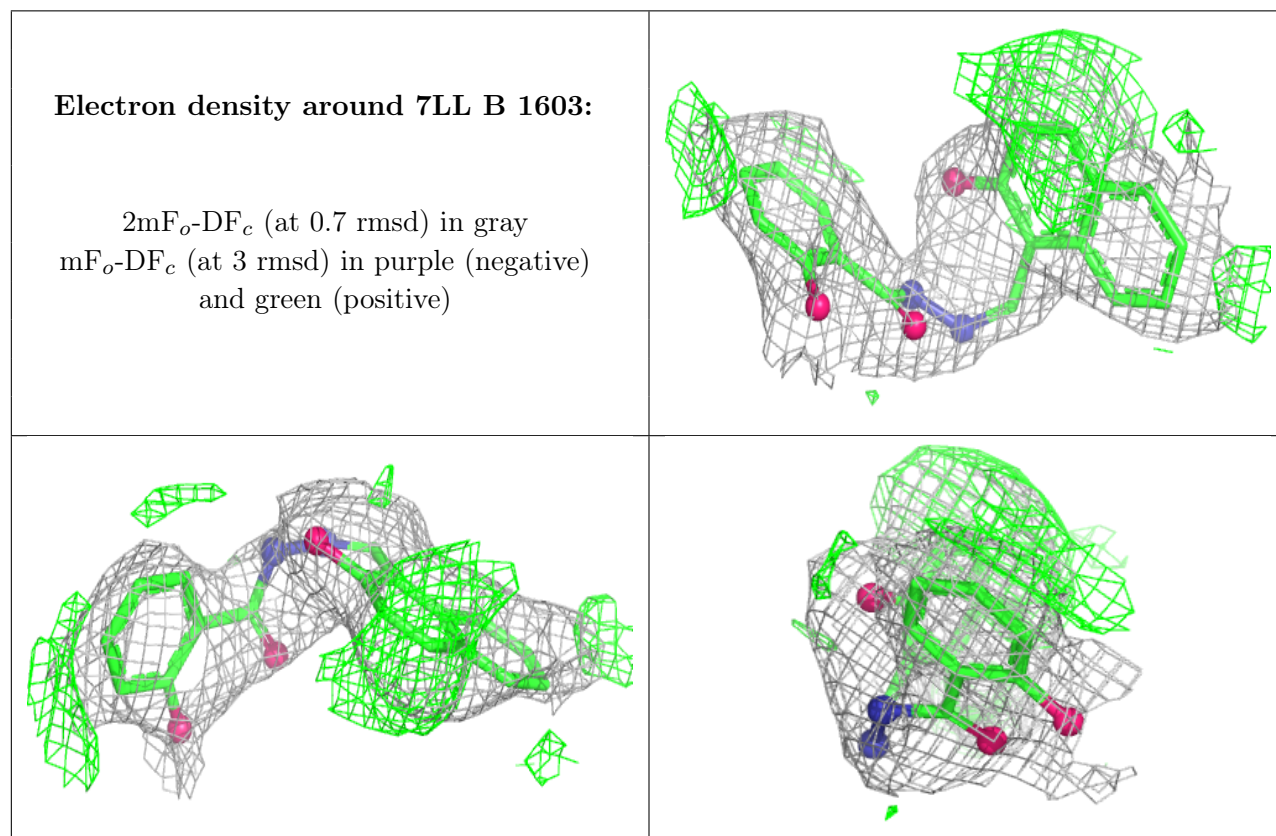
6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
4	7LL	B	1603	23/23	0.82	0.18	58,86,98,105	0
3	MG	A	1602	1/1	0.95	0.05	46,46,46,46	0
2	TTP	A	1601	29/29	0.96	0.06	43,49,72,80	0
2	TTP	B	1601	29/29	0.96	0.07	45,56,77,94	0
3	MG	B	1602	1/1	0.98	0.02	45,45,45,45	0

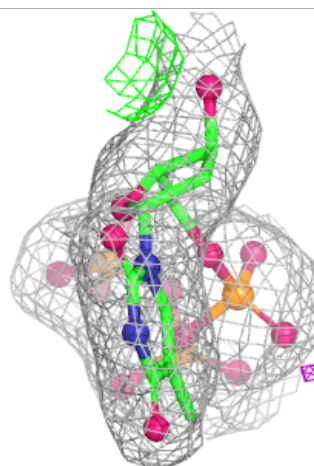
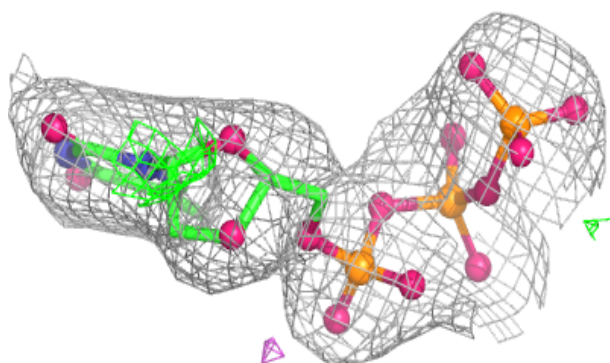
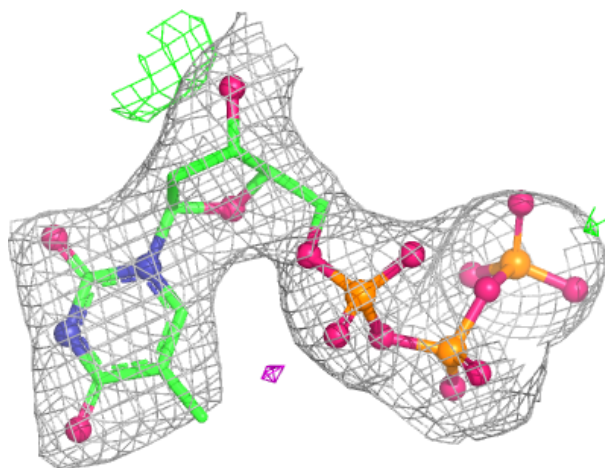
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



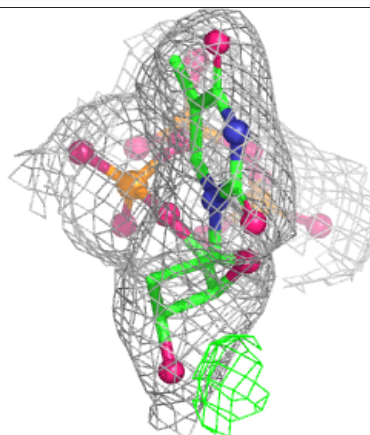
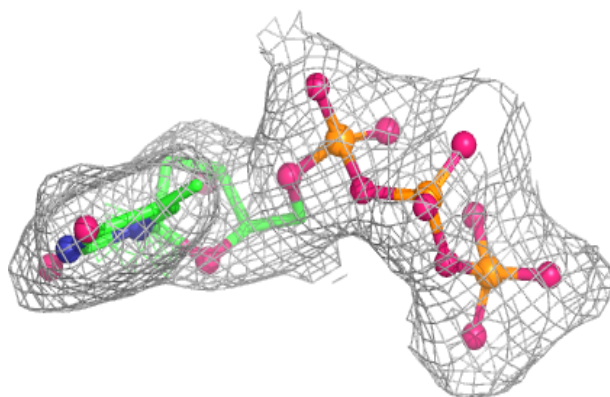
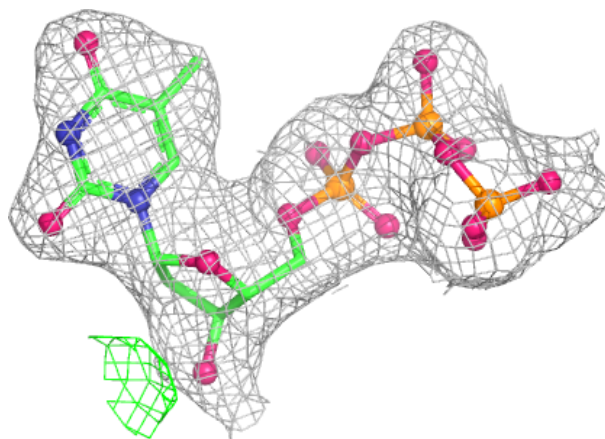
Electron density around TTP A 1601:

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



Electron density around TTP B 1601:

$2mF_o-DF_c$ (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.