



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 8, 2021 – 11:32 AM EST

PDB ID : 7MX7
Title : PRMT5:MEP50 complexed with inhibitor PF-06939999
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Deposited on : 2021-05-18
Resolution : 2.49 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 : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

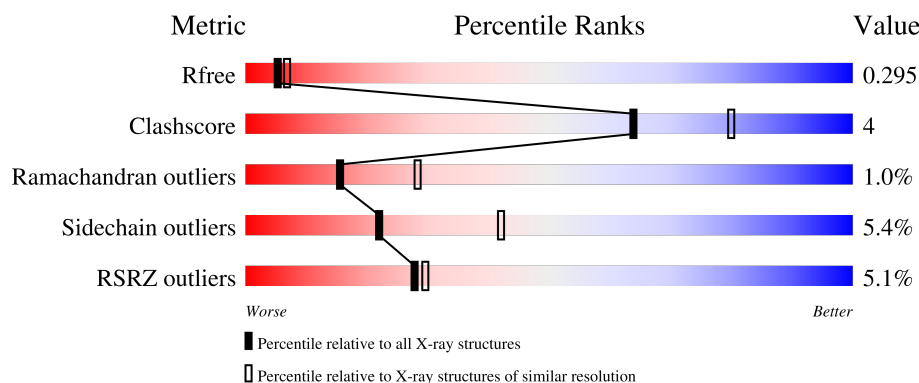
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	637	
2	B	366	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7629 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 Protein arginine N-methyltransferase 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	621	Total	C	N	O	S	0	1	0
			5031	3217	865	924	25			

- Molecule 2 is a protein called Methylosome protein 50.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	307	Total	C	N	O	S	0	0	0
			2317	1454	396	453	14			

There are 25 discrepancies between the modelled and reference sequences:

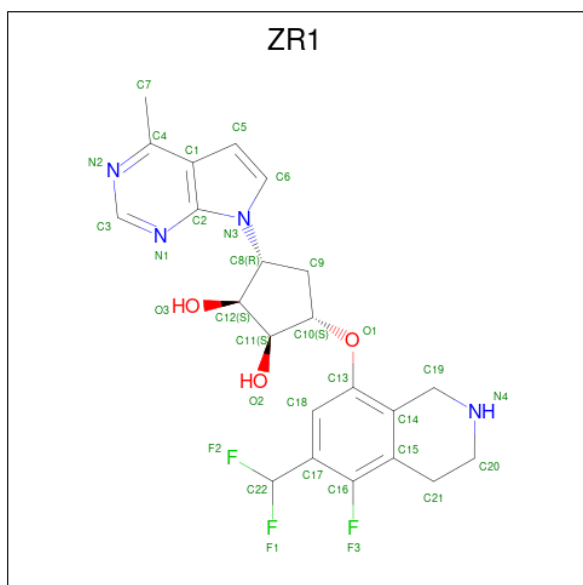
Chain	Residue	Modelled	Actual	Comment	Reference
B	-23	MET	-	expression tag	UNP Q9BQA1
B	-22	ALA	-	expression tag	UNP Q9BQA1
B	-21	SER	-	expression tag	UNP Q9BQA1
B	-20	HIS	-	expression tag	UNP Q9BQA1
B	-19	HIS	-	expression tag	UNP Q9BQA1
B	-18	HIS	-	expression tag	UNP Q9BQA1
B	-17	HIS	-	expression tag	UNP Q9BQA1
B	-16	HIS	-	expression tag	UNP Q9BQA1
B	-15	HIS	-	expression tag	UNP Q9BQA1
B	-14	ASP	-	expression tag	UNP Q9BQA1
B	-13	TYR	-	expression tag	UNP Q9BQA1
B	-12	ASP	-	expression tag	UNP Q9BQA1
B	-11	GLY	-	expression tag	UNP Q9BQA1
B	-10	ALA	-	expression tag	UNP Q9BQA1
B	-9	THR	-	expression tag	UNP Q9BQA1
B	-8	THR	-	expression tag	UNP Q9BQA1
B	-7	GLU	-	expression tag	UNP Q9BQA1
B	-6	ASN	-	expression tag	UNP Q9BQA1
B	-5	LEU	-	expression tag	UNP Q9BQA1
B	-4	TYR	-	expression tag	UNP Q9BQA1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	PHE	-	expression tag	UNP Q9BQA1
B	-2	GLN	-	expression tag	UNP Q9BQA1
B	-1	GLY	-	expression tag	UNP Q9BQA1
B	0	SER	-	expression tag	UNP Q9BQA1
B	1	LEU	-	expression tag	UNP Q9BQA1

- Molecule 3 is (1S,2S,3S,5R)-3-{[6-(difluoromethyl)-5-fluoro-1,2,3,4-tetrahydroisoquinolin-8-yl]oxy}-5-(4-methyl-7H-pyrrolo[2,3-d]pyrimidin-7-yl)cyclopentane-1,2-diol (three-letter code: ZR1) (formula: C₂₂H₂₃F₃N₄O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			32	22	3	4	3		

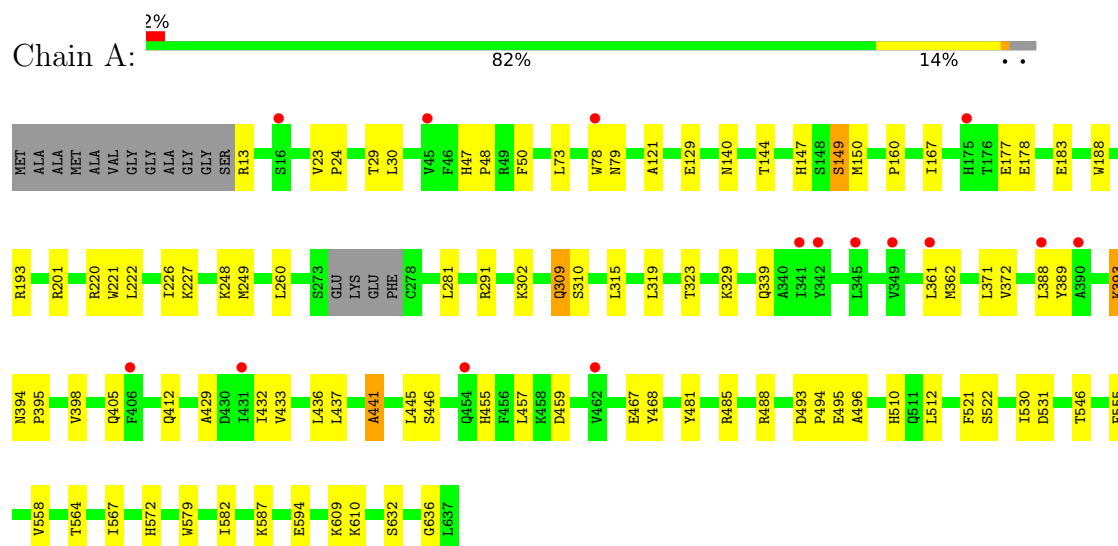
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	197	Total	O	0	0
			197	197		
4	B	52	Total	O	0	0
			52	52		

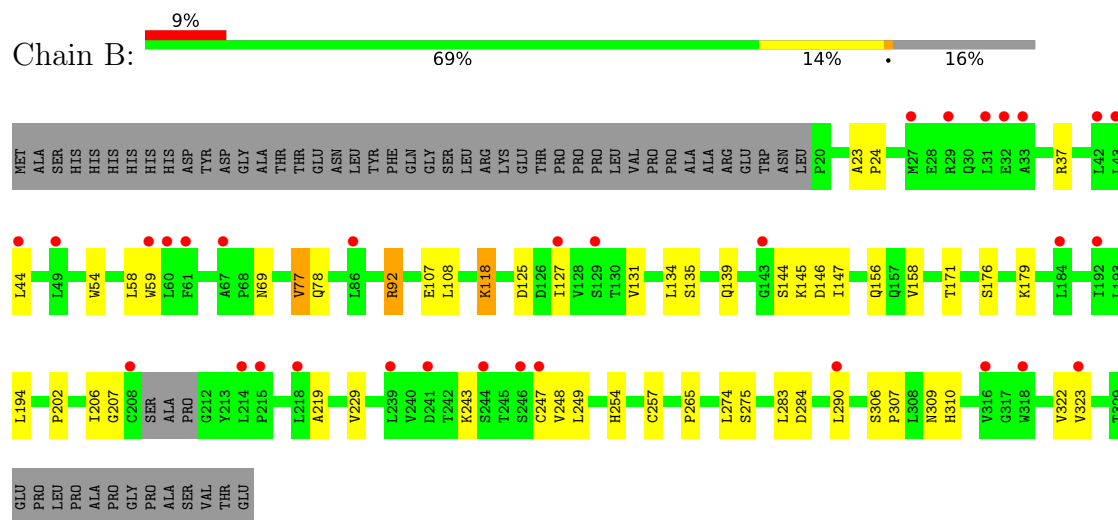
3 Residue-property plots [i](#)

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: Protein arginine N-methyltransferase 5



- Molecule 2: Methylosome protein 50



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	101.60Å 137.48Å 178.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.13 – 2.49 89.13 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.9 (89.13-2.49) 99.9 (89.13-2.49)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.48Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.222 , 0.279 0.225 , 0.295	Depositor DCC
R_{free} test set	2198 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	52.4	Xtriage
Anisotropy	1.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 66.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7629	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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: ZR1

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	0.46	0/5171	0.65	0/7034
2	B	0.43	0/2372	0.69	0/3239
All	All	0.45	0/7543	0.66	0/10273

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	5031	0	4925	41	0
2	B	2317	0	2233	22	0
3	A	32	0	0	1	0
4	A	197	0	0	2	0
4	B	52	0	0	0	0
All	All	7629	0	7158	61	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 (61) 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:147:HIS:HD2	1:A:201:ARG:HH12	1.09	0.92
1:A:147:HIS:CD2	1:A:201:ARG:HH12	1.89	0.90
1:A:319:LEU:HD22	1:A:323:THR:HG21	1.67	0.77
2:B:23:ALA:HB1	2:B:24:PRO:HD2	1.74	0.69
1:A:144:THR:O	1:A:147:HIS:HE1	1.78	0.66
2:B:194:LEU:HB2	2:B:206:ILE:HD11	1.77	0.65
2:B:219:ALA:HB3	2:B:229:VAL:HG23	1.80	0.64
1:A:441:ALA:HB2	1:A:555:PHE:HB2	1.81	0.61
2:B:127:ILE:HB	2:B:145:LYS:HD2	1.84	0.59
2:B:107:GLU:HB2	2:B:118:LYS:HD3	1.84	0.59
1:A:495:GLU:HB3	1:A:587:LYS:HE2	1.84	0.59
2:B:254:HIS:CD2	2:B:275:SER:HB2	2.41	0.56
2:B:176:SER:HB3	2:B:179:LYS:O	2.06	0.55
2:B:219:ALA:HB3	2:B:229:VAL:CG2	2.37	0.55
2:B:284:ASP:HB3	2:B:290:LEU:HD11	1.89	0.55
1:A:24:PRO:HA	2:B:54:TRP:HB2	1.88	0.54
1:A:567:ILE:HG21	1:A:579:TRP:HB2	1.90	0.53
2:B:58:LEU:HB2	2:B:77:VAL:HG12	1.91	0.52
1:A:488:ARG:HD2	1:A:494:PRO:HA	1.90	0.52
1:A:47:HIS:HB3	1:A:50:PHE:HB2	1.91	0.51
2:B:322:VAL:HG12	2:B:322:VAL:O	2.11	0.51
2:B:44:LEU:HB2	2:B:59:TRP:HB2	1.92	0.51
1:A:140:ASN:HB3	4:A:974:HOH:O	2.11	0.50
1:A:610:LYS:HD3	1:A:636:GLY:HA2	1.93	0.50
1:A:160:PRO:HD2	4:A:899:HOH:O	2.11	0.50
1:A:144:THR:O	1:A:147:HIS:CE1	2.62	0.49
2:B:265:PRO:HB2	2:B:310:HIS:CE1	2.46	0.49
1:A:558:VAL:HA	1:A:564:THR:HG22	1.95	0.49
2:B:306:SER:HB3	2:B:309:ASN:O	2.13	0.49
1:A:222:LEU:HB3	1:A:510:HIS:HB2	1.94	0.49
1:A:468:TYR:CE1	1:A:521:PHE:HB2	2.48	0.47
1:A:467:GLU:HG3	1:A:522:SER:HB3	1.96	0.47
2:B:37:ARG:O	2:B:307:PRO:HG3	2.14	0.47
1:A:372:VAL:HG13	1:A:388:LEU:HD13	1.96	0.47
1:A:167:ILE:HB	2:B:202:PRO:HD2	1.97	0.46
2:B:156:GLN:HB3	2:B:158:VAL:HG22	1.98	0.46
1:A:394:ASN:O	1:A:398:VAL:HG23	2.17	0.45
1:A:493:ASP:HB3	1:A:496:ALA:HB2	1.99	0.45
1:A:23:VAL:HG22	1:A:29:THR:HG21	1.99	0.45
1:A:73:LEU:HB2	1:A:78:TRP:CE2	2.52	0.45
1:A:395:PRO:HA	1:A:398:VAL:HB	1.99	0.44
1:A:393:LYS:HE3	3:A:701:ZR1:O3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:92:ARG:HG3	2:B:108:LEU:HB2	1.99	0.43
1:A:129:GLU:HA	1:A:188:TRP:CD1	2.54	0.43
1:A:221:TRP:HB3	1:A:226:ILE:HD11	2.00	0.43
2:B:144:SER:HB3	2:B:146:ASP:OD1	2.19	0.43
1:A:567:ILE:HA	1:A:572:HIS:CD2	2.54	0.42
1:A:149:SER:H	1:A:201:ARG:NH1	2.18	0.42
1:A:362:MET:SD	1:A:429:ALA:HB2	2.60	0.42
1:A:436:LEU:O	1:A:446:SER:HB2	2.20	0.42
1:A:362:MET:HG2	1:A:389:TYR:HB2	2.02	0.42
2:B:134:LEU:HD12	2:B:139:GLN:HB3	2.02	0.41
1:A:512:LEU:HD13	1:A:546:THR:HG21	2.03	0.41
1:A:315:LEU:HD23	1:A:445:LEU:HD12	2.03	0.41
1:A:432:ILE:HG12	1:A:457:LEU:HD13	2.02	0.41
1:A:481:TYR:CE2	1:A:485:ARG:HD2	2.56	0.41
2:B:134:LEU:HD12	2:B:139:GLN:CB	2.50	0.41
1:A:121:ALA:HA	1:A:150:MET:O	2.20	0.40
1:A:309:GLN:HE21	1:A:309:GLN:HB2	1.72	0.40
1:A:437:LEU:HD21	1:A:468:TYR:CD2	2.57	0.40
1:A:371:LEU:HD13	1:A:433:VAL:HG12	2.04	0.40

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	618/637 (97%)	585 (95%)	29 (5%)	4 (1%)	25	43
2	B	303/366 (83%)	279 (92%)	19 (6%)	5 (2%)	9	16
All	All	921/1003 (92%)	864 (94%)	48 (5%)	9 (1%)	15	28

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	531	ASP
2	B	147	ILE
2	B	243	LYS
2	B	323	VAL
1	A	302	LYS
1	A	441	ALA
1	A	459	ASP
2	B	69	ASN
2	B	207	GLY

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	555/562 (99%)	525 (95%)	30 (5%)	22	42
2	B	260/310 (84%)	246 (95%)	14 (5%)	22	42
All	All	815/872 (94%)	771 (95%)	44 (5%)	22	42

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	30	LEU
1	A	48	PRO
1	A	79	ASN
1	A	149	SER
1	A	177	GLU
1	A	178	GLU
1	A	183	GLU
1	A	193	ARG
1	A	220	ARG
1	A	227	LYS
1	A	248	LYS
1	A	249	MET
1	A	260	LEU
1	A	281	LEU

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Mol	Chain	Res	Type
1	A	291	ARG
1	A	309	GLN
1	A	310	SER
1	A	329	LYS
1	A	339	GLN
1	A	361	LEU
1	A	393	LYS
1	A	405	GLN
1	A	412	GLN
1	A	455	HIS
1	A	530	ILE
1	A	582	ILE
1	A	594	GLU
1	A	609	LYS
1	A	632	SER
2	B	77	VAL
2	B	78	GLN
2	B	92	ARG
2	B	118	LYS
2	B	125	ASP
2	B	131	VAL
2	B	135	SER
2	B	171	THR
2	B	247	CYS
2	B	248	VAL
2	B	249	LEU
2	B	257	CYS
2	B	274	LEU
2	B	283	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN
1	A	147	HIS
1	A	216	HIS
1	A	270	ASN
1	A	309	GLN
1	A	339	GLN
1	A	381	GLN
1	A	405	GLN
2	B	254	HIS

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Mol	Chain	Res	Type
2	B	310	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z > 2$
3	ZR1	A	701	-	32,36,36	1.43	3 (9%)	34,54,54	1.16	5 (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
3	ZR1	A	701	-	-	2/6/35/35	0/5/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	701	ZR1	C19-N4	6.22	1.54	1.46
3	A	701	ZR1	C4-N2	2.83	1.34	1.32
3	A	701	ZR1	C17-C16	2.79	1.41	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	ZR1	F3-C16-C17	-3.03	116.44	119.56
3	A	701	ZR1	C7-C4-C1	2.60	123.27	121.11
3	A	701	ZR1	C1-C4-N2	-2.60	120.10	122.02
3	A	701	ZR1	C13-O1-C10	2.18	123.79	118.99
3	A	701	ZR1	C11-C12-C8	2.08	105.80	102.45

There are no chirality outliers.

All (2) torsion outliers are listed below:

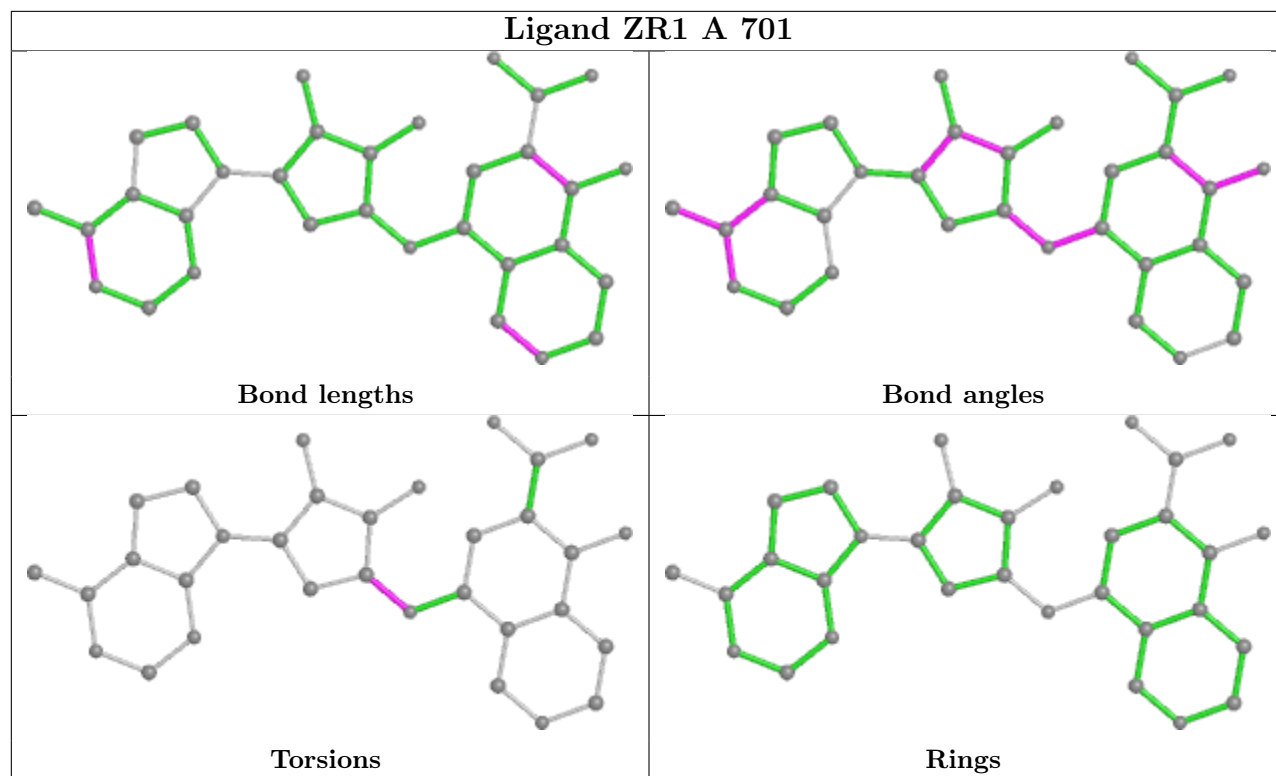
Mol	Chain	Res	Type	Atoms
3	A	701	ZR1	C9-C10-O1-C13
3	A	701	ZR1	C11-C10-O1-C13

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	701	ZR1	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	621/637 (97%)	0.49	15 (2%) 59 62	31, 63, 97, 117	0
2	B	307/366 (83%)	0.71	32 (10%) 6 6	59, 77, 105, 131	0
All	All	928/1003 (92%)	0.56	47 (5%) 28 29	31, 69, 101, 131	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	208	CYS	5.4
2	B	42	LEU	4.2
2	B	247	CYS	4.1
2	B	290	LEU	4.0
2	B	44	LEU	3.9
1	A	345	LEU	3.9
1	A	341	ILE	3.7
2	B	246	SER	3.6
2	B	218	LEU	3.6
1	A	361	LEU	3.3
2	B	244	SER	3.3
1	A	431	ILE	3.3
2	B	143	GLY	3.3
2	B	31	LEU	3.3
2	B	33	ALA	3.2
2	B	61	PHE	3.2
1	A	45	VAL	3.1
2	B	43	LEU	3.1
1	A	175	HIS	3.1
1	A	390	ALA	3.1
2	B	318	TRP	2.8
2	B	184	LEU	2.7
2	B	323	VAL	2.7
2	B	59	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	49	LEU	2.6
2	B	29	ARG	2.5
2	B	316	VAL	2.5
2	B	214	LEU	2.5
2	B	129	SER	2.5
2	B	239	LEU	2.5
2	B	60	LEU	2.4
1	A	454	GLN	2.4
1	A	388	LEU	2.3
1	A	349	VAL	2.3
2	B	67	ALA	2.2
1	A	78	TRP	2.2
1	A	462	VAL	2.2
2	B	127	ILE	2.2
1	A	342	TYR	2.1
2	B	32	GLU	2.1
2	B	192	ILE	2.1
2	B	241	ASP	2.1
1	A	406	PHE	2.1
2	B	27	MET	2.0
2	B	86	LEU	2.0
1	A	16	SER	2.0
2	B	215	PRO	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](#)

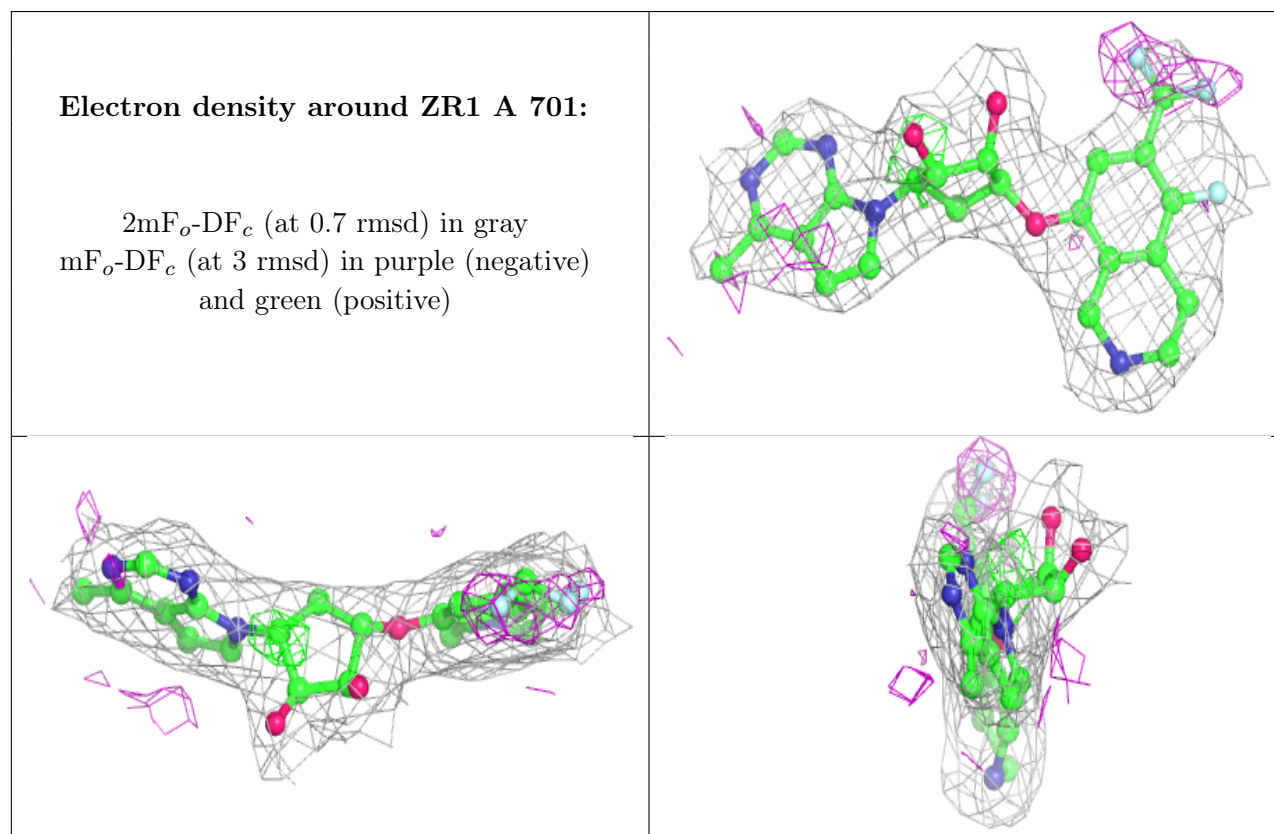
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ZR1	A	701	32/32	0.90	0.20	47,52,62,63	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 ⓘ

There are no such residues in this entry.