



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 30, 2025 – 04:24 pm BST

PDB ID : 9R40 / pdb_00009r40
Title : HaloTag bound to compound MRC71
Authors : Luptak, J.
Deposited on : 2025-05-06
Resolution : 2.04 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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

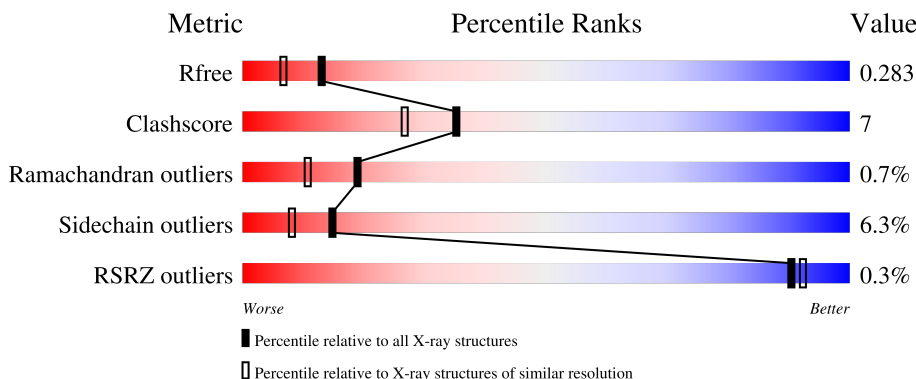
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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}	164625	2096 (2.04-2.04)
Clashscore	180529	2229 (2.04-2.04)
Ramachandran outliers	177936	2217 (2.04-2.04)
Sidechain outliers	177891	2217 (2.04-2.04)
RSRZ outliers	164620	2096 (2.04-2.04)

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	306	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4844 atoms, of which 2385 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 Haloalkane dehalogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	293	Total	C	H	N	O	S	49	2	0
			4680	1537	2321	395	418	9			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	MET	-	initiating methionine	UNP P0A3G3
A	17	ALA	-	expression tag	UNP P0A3G3
A	18	HIS	-	expression tag	UNP P0A3G3
A	19	HIS	-	expression tag	UNP P0A3G3
A	20	HIS	-	expression tag	UNP P0A3G3
A	21	HIS	-	expression tag	UNP P0A3G3
A	22	HIS	-	expression tag	UNP P0A3G3
A	23	HIS	-	expression tag	UNP P0A3G3
A	24	MET	-	expression tag	UNP P0A3G3
A	26	ALA	SER	conflict	UNP P0A3G3
A	71	VAL	LEU	conflict	UNP P0A3G3
A	82	THR	SER	conflict	UNP P0A3G3
A	102	GLY	ASP	conflict	UNP P0A3G3
A	111	PHE	TYR	conflict	UNP P0A3G3
A	112	MET	LEU	conflict	UNP P0A3G3
A	152	PHE	CYS	conflict	UNP P0A3G3
A	179	THR	ALA	conflict	UNP P0A3G3
A	184	LYS	GLU	conflict	UNP P0A3G3
A	191	VAL	ALA	conflict	UNP P0A3G3
A	196	THR	ALA	conflict	UNP P0A3G3
A	199	MET	LYS	conflict	UNP P0A3G3
A	200	GLY	CYS	conflict	UNP P0A3G3
A	219	ASN	LYS	conflict	UNP P0A3G3
A	248	GLU	ALA	conflict	UNP P0A3G3
A	251	ASP	ASN	conflict	UNP P0A3G3
A	281	LYS	GLU	conflict	UNP P0A3G3
A	288	ALA	THR	conflict	UNP P0A3G3

Continued on next page...

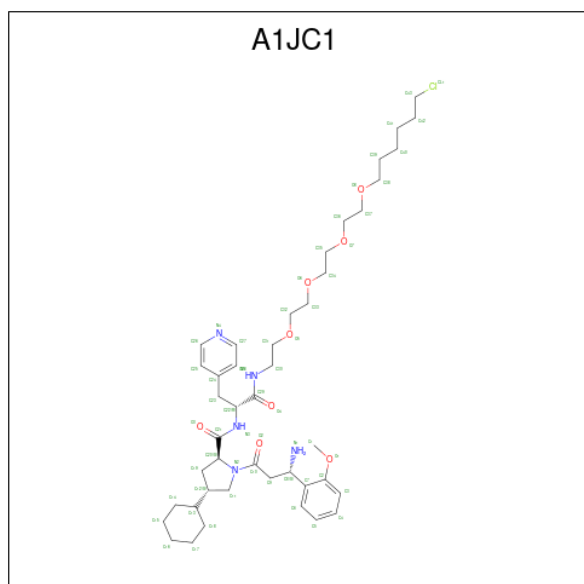
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	296	ASN	HIS	conflict	UNP P0A3G3
A	297	LEU	TYR	conflict	UNP P0A3G3
A	315	SER	PRO	conflict	UNP P0A3G3
A	316	THR	ALA	conflict	UNP P0A3G3
A	318	GLU	-	expression tag	UNP P0A3G3
A	319	ILE	-	expression tag	UNP P0A3G3
A	320	SER	-	expression tag	UNP P0A3G3
A	321	GLY	-	expression tag	UNP P0A3G3

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0

- Molecule 3 is (2 {S},4 {S})-1-[(3 {S})-3-azanyl-3-(2-methoxyphenyl)propanoyl]- {N}-[(2 {R})-1-[2-[2-[2-(6-chloranylhexoxy)ethoxy]ethoxy]ethoxy]ethylamino]-1-oxidanylidene-3-pyridin-4-yl-propan-2-yl]-4-cyclohexyl-pyrrolidine-2-carboxamide (CCD ID: A1JC1) (formula: C₄₃H₆₆ClN₅O₈) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	
			120	43	64	5	8	

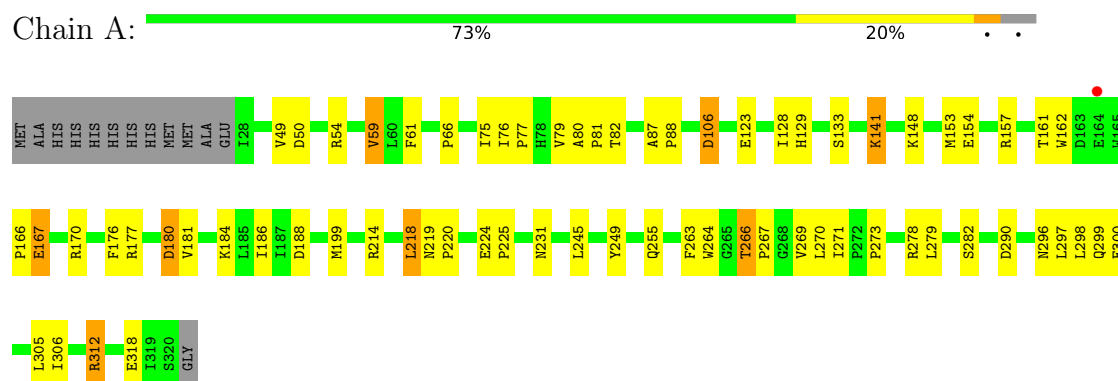
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	43	Total 43	O 43	0	0

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: Haloalkane dehalogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	62.80Å 62.80Å 163.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.68 – 2.04 58.61 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.6 (58.68-2.04) 98.8 (58.61-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.100)	Depositor
R, R_{free}	0.237 , 0.286 0.233 , 0.283	Depositor DCC
R_{free} test set	1053 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.800	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4844	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.29% 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: CL, A1JC1

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	0.61	0/2447	1.17	8/3347 (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

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	141	LYS	N-CA-CB	6.46	119.75	110.06
1	A	75	ILE	CA-C-N	5.99	124.01	120.24
1	A	75	ILE	C-N-CA	5.99	124.01	120.24
1	A	123	GLU	CB-CA-C	5.90	120.31	109.46
1	A	59	VAL	N-CA-CB	-5.41	104.65	111.46
1	A	106	ASP	CA-CB-CG	5.29	117.89	112.60
1	A	82	THR	CA-CB-OG1	-5.25	101.72	109.60
1	A	123	GLU	CB-CG-CD	5.22	121.48	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	278	ARG	Sidechain

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	2359	2321	2310	34	0
2	A	1	0	0	0	0
3	A	56	64	0	0	0
4	A	43	0	0	0	0
All	All	2459	2385	2310	34	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (34) 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:157:ARG:NH1	1:A:270:LEU:O	2.10	0.84
1:A:167:GLU:HA	1:A:170:ARG:NH2	2.13	0.64
1:A:162:TRP:O	1:A:170:ARG:HD3	1.98	0.64
1:A:219:ASN:C	1:A:219:ASN:HD22	2.09	0.60
1:A:312:ARG:HG2	1:A:312:ARG:HH21	1.68	0.57
1:A:59:VAL:HG12	1:A:61:PHE:CE1	2.42	0.54
1:A:296:ASN:HD22	1:A:297:LEU:HD12	1.72	0.54
1:A:50:ASP:CG	1:A:54:ARG:HH22	2.15	0.53
1:A:153:MET:O	1:A:154:GLU:C	2.52	0.53
1:A:264:TRP:CZ2	1:A:290:ASP:HB2	2.44	0.52
1:A:177:ARG:HA	1:A:231:ASN:OD1	2.11	0.51
1:A:267:PRO:O	1:A:273:PRO:HD3	2.10	0.51
1:A:129:HIS:CD2	1:A:299:GLN:HE22	2.29	0.51
1:A:219:ASN:HD22	1:A:220:PRO:N	2.10	0.50
1:A:214:ARG:O	1:A:218:LEU:HD13	2.12	0.49
1:A:245:LEU:C	1:A:245:LEU:HD23	2.38	0.49
1:A:61:PHE:O	1:A:88:PRO:HD2	2.12	0.49
1:A:184:LYS:O	1:A:188:ASP:HB2	2.13	0.48
1:A:263:PHE:CE2	1:A:306:ILE:HA	2.48	0.48
1:A:49:VAL:HB	1:A:87:ALA:HB3	1.96	0.46
1:A:76:ILE:N	1:A:77:PRO:CD	2.79	0.45
1:A:166:PRO:O	1:A:167:GLU:C	2.60	0.45
1:A:176:PHE:CG	1:A:186:ILE:HD11	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:LEU:HA	1:A:282:SER:OG	2.17	0.44
1:A:128:ILE:HD12	1:A:133:SER:HA	2.00	0.44
1:A:300:GLU:HA	1:A:300:GLU:OE1	2.18	0.43
1:A:224:GLU:N	1:A:225:PRO:CD	2.82	0.43
1:A:80:ALA:N	1:A:81:PRO:CD	2.82	0.43
1:A:167:GLU:HA	1:A:170:ARG:HH21	1.83	0.43
1:A:270:LEU:O	1:A:271:ILE:HD13	2.18	0.42
1:A:318:GLU:HA	1:A:318:GLU:OE1	2.18	0.42
1:A:266:THR:HA	1:A:267:PRO:HA	1.86	0.42
1:A:157:ARG:HH11	1:A:157:ARG:HG2	1.84	0.42
1:A:79:VAL:C	1:A:81:PRO:HD2	2.46	0.41

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	293/306 (96%)	277 (94%)	14 (5%)	2 (1%)	19 11

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	ASP
1	A	269	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	255/263 (97%)	239 (94%)	16 (6%)	15 8

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	PRO
1	A	106	ASP
1	A	141	LYS
1	A	148	LYS
1	A	161	THR
1	A	167	GLU
1	A	180	ASP
1	A	181	VAL
1	A	199	MET
1	A	218	LEU
1	A	249	TYR
1	A	255	GLN
1	A	266	THR
1	A	298	LEU
1	A	305	LEU
1	A	312	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	HIS
1	A	129	HIS
1	A	219	ASN
1	A	296	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
3	A1JC1	A	402	1	59,59,60	0.26	0	67,74,75	1.00	2 (2%)

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	A1JC1	A	402	1	-	27/53/73/74	0/4/4/4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	A1JC1	O5-C31-C30	-6.12	86.62	109.67
3	A	402	A1JC1	C32-O5-C31	-3.72	97.16	113.29

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	A1JC1	C9-C10-N2-C11
3	A	402	A1JC1	C9-C10-N2-C20
3	A	402	A1JC1	O2-C10-N2-C11
3	A	402	A1JC1	O2-C10-N2-C20

Continued on next page...

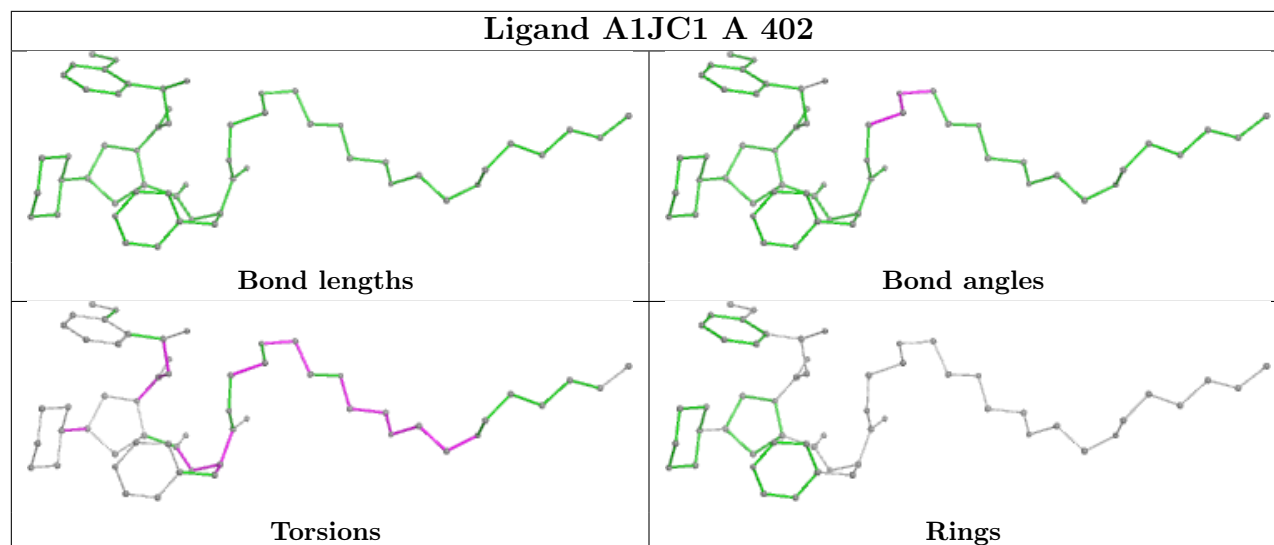
Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	A	402	A1JC1	C11-C12-C13-C14
3	A	402	A1JC1	C11-C12-C13-C18
3	A	402	A1JC1	C19-C12-C13-C14
3	A	402	A1JC1	C19-C12-C13-C18
3	A	402	A1JC1	C20-C21-N3-C22
3	A	402	A1JC1	O3-C21-N3-C22
3	A	402	A1JC1	C29-C22-N3-C21
3	A	402	A1JC1	N5-C30-C31-O5
3	A	402	A1JC1	C23-C22-C29-N5
3	A	402	A1JC1	C29-C22-C23-C24
3	A	402	A1JC1	C23-C22-C29-O4
3	A	402	A1JC1	O7-C36-C37-O8
3	A	402	A1JC1	O6-C34-C35-O7
3	A	402	A1JC1	C33-C32-O5-C31
3	A	402	A1JC1	N3-C22-C23-C24
3	A	402	A1JC1	N1-C8-C9-C10
3	A	402	A1JC1	O5-C32-C33-O6
3	A	402	A1JC1	O2-C10-C9-C8
3	A	402	A1JC1	N2-C10-C9-C8
3	A	402	A1JC1	C37-C36-O7-C35
3	A	402	A1JC1	C35-C34-O6-C33
3	A	402	A1JC1	C36-C37-O8-C38
3	A	402	A1JC1	C34-C35-O7-C36

There are no ring outliers.

No monomer is involved in short contacts.

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	293/306 (95%)	-0.23	1 (0%) 90 92	16, 36, 52, 66	28 (9%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	164	GLU	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](#)

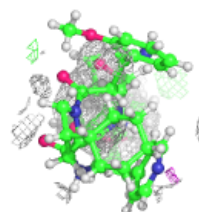
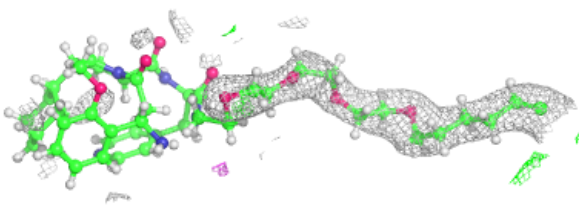
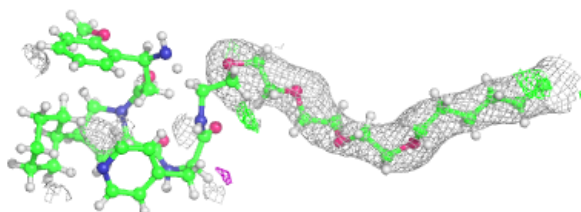
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	A1JC1	A	402	56/57	0.91	0.11	31,129,179,219	82
2	CL	A	401	1/1	0.98	0.04	32,32,32,32	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 A1JC1 A 402:

$2mF_o-DF_c$ (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.