



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2022 – 03:18 PM JST

PDB ID : 6LWH
Title : Crystal structure of human NEIL1(P2G, E3Q, K242) bound to duplex DNA containing dihydrothymine (DHT)
Authors : Liu, M.H.; Zhang, J.; Zhu, C.X.; Zhang, X.X.; Gao, Y.Q.; Yi, C.Q.
Deposited on : 2020-02-07
Resolution : 2.78 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:

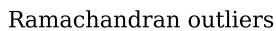
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.28.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.28.1

i

X-RAY DIFFRACTION

A.

Metric	Percentile Banks	Value
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R _{free}
Clashscore
Ramachandran outliers
Sidechain outliers
RSRZ outliers

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.

1	A	295	<div> <div></div> <div>80%</div> <div>9%</div> <div>10%</div> </div>
1	D	295	<div> <div></div> <div>78%</div> <div>11%</div> <div>10%</div> </div>
1	G	295	<div> <div></div> <div>9%</div> <div>72%</div> <div>5%</div> <div>22%</div> </div>
2	B	13	<div> <div></div> <div>85%</div> <div>15%</div> </div>
2	E	13	<div> <div></div> <div>85%</div> <div>15%</div> </div>
2	H	13	<div> <div></div> <div>85%</div> <div>15%</div> </div>

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Mol	Chain	Length	Quality of chain
3	C	13	 62%38%
3	F	13	 85%15%
3	I	13	 8%62%38%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7515 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 Endonuclease 8-like 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			2108	1347	384	367	10			
1	D	266	Total	C	N	O	S	0	0	0
			2108	1347	385	366	10			
1	G	231	Total	C	N	O	S	0	0	0
			1565	956	304	296	9			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLY	PRO	engineered mutation	UNP Q96FI4
A	3	GLN	GLU	engineered mutation	UNP Q96FI4
D	2	GLY	PRO	engineered mutation	UNP Q96FI4
D	3	GLN	GLU	engineered mutation	UNP Q96FI4
G	2	GLY	PRO	engineered mutation	UNP Q96FI4
G	3	GLN	GLU	engineered mutation	UNP Q96FI4

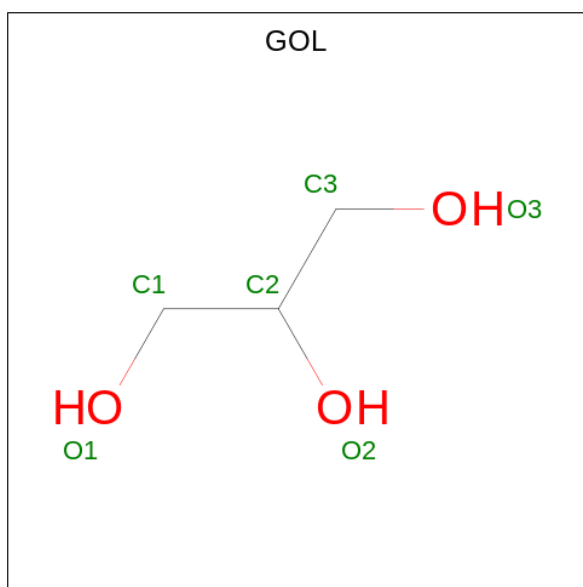
- Molecule 2 is a DNA chain called DNA (5'-D(*CP*GP*TP*CP*CP*AP*(TDH)P*GP*TP*CP*TP*AP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	13	Total	C	N	O	P	0	0	0
			258	125	43	78	12			
2	E	13	Total	C	N	O	P	0	0	0
			258	125	43	78	12			
2	H	13	Total	C	N	O	P	0	0	0
			258	125	43	78	12			

- Molecule 3 is a DNA chain called DNA (5'-D(*TP*AP*GP*AP*CP*CP*TP*GP*GP*AP*CP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	P	0	0	0
			267	127	53	75	12			
3	F	13	Total	C	N	O	P	0	0	0
			267	127	53	75	12			
3	I	13	Total	C	N	O	P	0	0	0
			267	127	53	75	12			

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	66	Total	O	0	0
			66	66		
5	B	13	Total	O	0	0
			13	13		
5	C	6	Total	O	0	0
			6	6		
5	D	54	Total	O	0	0
			54	54		
5	E	4	Total	O	0	0
			4	4		

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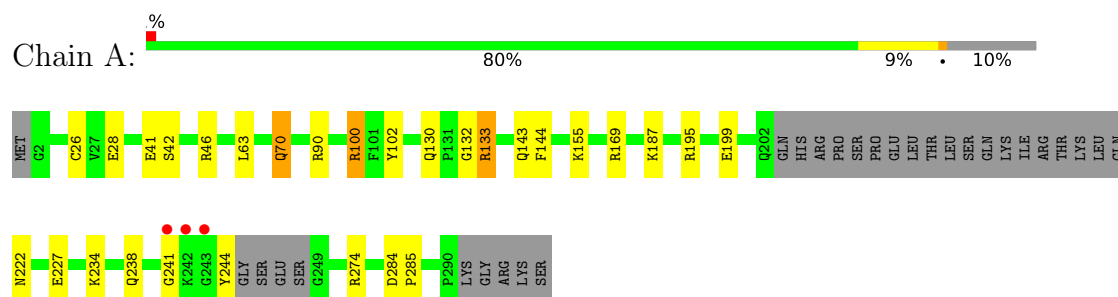
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	3	Total 3	O 3	0	0
5	G	3	Total 3	O 3	0	0
5	H	2	Total 2	O 2	0	0
5	I	2	Total 2	O 2	0	0

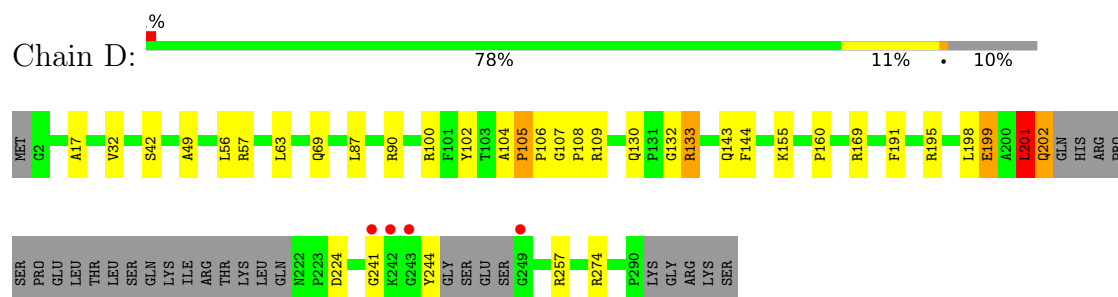
3 Residue-property plots

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.

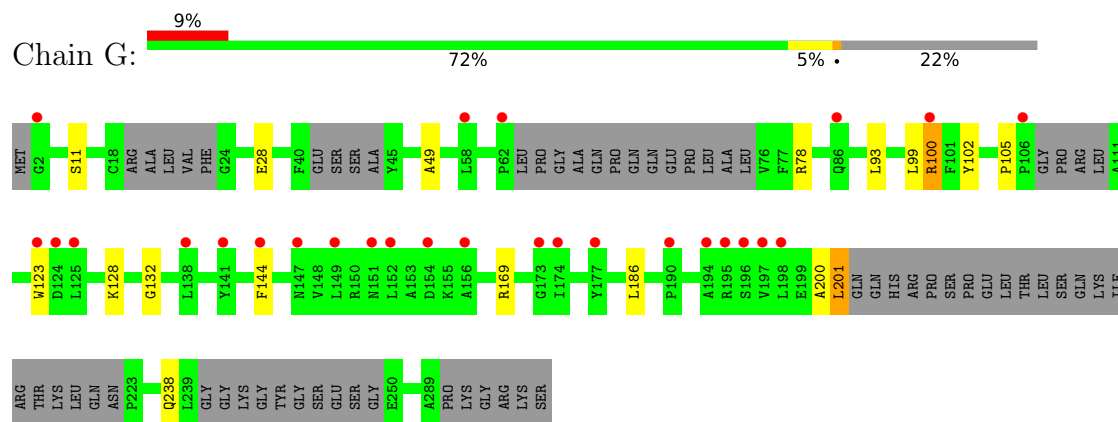
- Molecule 1: Endonuclease 8-like 1



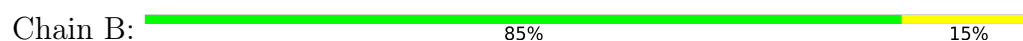
- Molecule 1: Endonuclease 8-like 1



- Molecule 1: Endonuclease 8-like 1

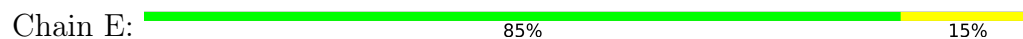


- Molecule 2: DNA (5'-D(*CP*GP*TP*CP*CP*AP*(TDH)P*GP*TP*CP*TP*AP*C)-3')

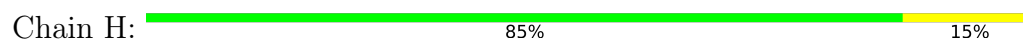




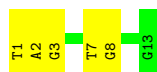
- Molecule 2: DNA (5'-D(*CP*GP*TP*CP*CP*AP*(TDH)P*GP*TP*CP*TP*AP*C)-3')



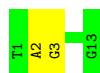
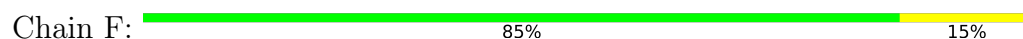
- Molecule 2: DNA (5'-D(*CP*GP*TP*CP*CP*AP*(TDH)P*GP*TP*CP*TP*AP*C)-3')



- Molecule 3: DNA (5'-D(*TP*AP*GP*AP*CP*CP*TP*GP*GP*AP*CP*GP*G)-3')



- Molecule 3: DNA (5'-D(*TP*AP*GP*AP*CP*CP*TP*GP*GP*AP*CP*GP*G)-3')



- Molecule 3: DNA (5'-D(*TP*AP*GP*AP*CP*CP*TP*GP*GP*AP*CP*GP*G)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.59Å 109.01Å 168.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.41 – 2.78 49.36 – 2.78	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.41-2.78) 99.8 (49.36-2.78)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.200 , 0.242 0.206 , 0.239	Depositor DCC
R_{free} test set	1766 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	64.9	Xtriage
Anisotropy	0.656	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 60.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7515	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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: QBT, GOL

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	0.77	0/2163	0.89	1/2923 (0.0%)
1	D	0.74	0/2165	0.90	3/2927 (0.1%)
1	G	0.72	0/1598	0.81	0/2138
2	B	0.58	0/264	0.86	1/402 (0.2%)
2	E	0.62	0/264	1.24	2/402 (0.5%)
2	H	0.49	0/264	0.93	2/402 (0.5%)
3	C	0.70	2/300 (0.7%)	0.87	0/462
3	F	0.68	0/300	0.83	0/462
3	I	0.58	1/300 (0.3%)	0.79	0/462
All	All	0.72	3/7618 (0.0%)	0.88	9/10580 (0.1%)

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	D	0	1
1	G	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	7	DT	O3'-P	-6.04	1.53	1.61
3	C	8	DG	O3'-P	-5.19	1.54	1.61
3	I	6	DC	O3'-P	-5.15	1.54	1.61

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	8	DG	O5'-P-OP1	-17.03	90.27	110.70
2	H	8	DG	O5'-P-OP1	-9.59	97.07	105.70
2	E	8	DG	O5'-P-OP2	7.64	119.87	110.70
1	D	133	ARG	NE-CZ-NH1	6.89	123.75	120.30
2	H	8	DG	O5'-P-OP2	6.04	117.95	110.70
2	B	8	DG	O5'-P-OP2	-5.92	100.38	105.70
1	A	133	ARG	CG-CD-NE	-5.74	99.75	111.80
1	D	133	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	D	201	LEU	CA-CB-CG	5.18	127.21	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	105	PRO	Peptide
1	G	105	PRO	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	2108	0	2082	14	0
1	D	2108	0	2083	28	0
1	G	1565	0	1285	13	0
2	B	258	0	151	0	0
2	E	258	0	151	0	0
2	H	258	0	151	0	0
3	C	267	0	147	2	0
3	F	267	0	147	1	0
3	I	267	0	147	3	0
4	A	6	0	8	0	0
5	A	66	0	0	1	0
5	B	13	0	0	0	0
5	C	6	0	0	0	0
5	D	54	0	0	0	0
5	E	4	0	0	0	0
5	F	3	0	0	0	0
5	G	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	H	2	0	0	0	0
5	I	2	0	0	0	0
All	All	7515	0	6352	57	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 (57) 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:222:ASN:N	1:A:222:ASN:C	2.29	0.85
1:D:201:LEU:HD11	1:D:224:ASP:CG	2.01	0.80
1:A:143:GLN:NE2	5:A:401:HOH:O	1.85	0.73
1:D:130:GLN:NE2	1:D:133:ARG:HH11	1.89	0.69
1:A:41:GLU:O	1:A:70:GLN:NE2	2.29	0.65
1:D:106:PRO:HG2	1:G:186:LEU:HD23	1.80	0.64
1:A:195:ARG:O	1:A:199:GLU:HB2	1.99	0.61
1:D:107:GLY:O	1:D:109:ARG:HD2	2.02	0.59
1:A:28:GLU:OE1	1:A:100:ARG:NH2	2.36	0.59
1:D:106:PRO:CG	1:G:186:LEU:HD23	2.34	0.57
1:D:143:GLN:NE2	1:D:143:GLN:HA	2.17	0.57
1:G:99:LEU:HD13	1:G:123:TRP:CZ2	2.41	0.56
1:A:234:LYS:O	1:A:238:GLN:HG2	2.08	0.54
1:G:11:SER:HB2	1:G:49:ALA:HB1	1.88	0.53
1:D:201:LEU:CD1	1:D:224:ASP:OD2	2.57	0.53
3:C:2:DA:H2''	3:C:3:DG:OP2	2.09	0.52
1:G:93:LEU:HD13	1:G:100:ARG:HD3	1.93	0.51
1:D:130:GLN:NE2	1:D:133:ARG:NH1	2.59	0.50
1:A:26:CYS:SG	1:A:41:GLU:HG3	2.51	0.50
1:D:106:PRO:HG3	1:G:186:LEU:CD2	2.43	0.49
1:A:241:GLY:O	1:A:244:TYR:HB2	2.14	0.48
1:D:132:GLY:O	1:D:169:ARG:HG2	2.15	0.47
1:D:201:LEU:HD11	1:D:224:ASP:OD2	2.14	0.47
3:I:2:DA:H2''	3:I:3:DG:OP2	2.14	0.47
1:D:130:GLN:HE22	1:D:133:ARG:NH1	2.13	0.47
3:F:2:DA:H2''	3:F:3:DG:OP2	2.15	0.47
1:G:200:ALA:O	1:G:201:LEU:HD23	2.15	0.47
1:D:198:LEU:O	1:D:201:LEU:HB2	2.15	0.45
1:A:130:GLN:NE2	1:A:133:ARG:HE	2.15	0.45
1:A:132:GLY:O	1:A:169:ARG:HG2	2.17	0.44
1:D:201:LEU:CD1	1:D:224:ASP:CG	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:132:GLY:O	1:G:169:ARG:HG2	2.17	0.44
1:A:46:ARG:HG3	1:A:63:LEU:HD21	1.97	0.44
1:G:93:LEU:HD13	1:G:100:ARG:CD	2.48	0.44
1:G:28:GLU:HB3	1:G:100:ARG:HG3	2.00	0.44
1:D:104:ALA:HB1	1:D:105:PRO:CD	2.48	0.43
1:A:284:ASP:HA	1:A:285:PRO:HD2	1.93	0.43
1:D:105:PRO:HA	1:D:106:PRO:HA	1.54	0.43
1:A:90:ARG:NH1	1:A:102:TYR:HB3	2.33	0.43
1:A:222:ASN:C	1:A:222:ASN:CB	2.86	0.43
1:G:93:LEU:CD1	1:G:100:ARG:CD	2.97	0.43
1:D:90:ARG:NH1	1:D:102:TYR:HB3	2.34	0.42
1:D:202:GLN:HE21	1:D:202:GLN:HB3	1.46	0.42
1:D:107:GLY:O	1:D:108:PRO:C	2.56	0.42
1:D:241:GLY:O	1:D:244:TYR:HB2	2.20	0.42
1:D:49:ALA:HA	1:D:57:ARG:O	2.19	0.42
1:G:28:GLU:OE1	1:G:102:TYR:OH	2.25	0.42
3:C:1:DT:C4	3:I:13:DG:C6	3.07	0.41
1:D:17:ALA:HB1	1:D:87:LEU:HD22	2.01	0.41
1:D:143:GLN:HA	1:D:143:GLN:HE21	1.85	0.41
1:D:195:ARG:O	1:D:199:GLU:HB2	2.20	0.41
1:D:160:PRO:HB3	1:D:191:PHE:HA	2.03	0.40
1:G:93:LEU:CD1	1:G:100:ARG:HD3	2.50	0.40
1:D:104:ALA:HA	1:D:105:PRO:HD3	1.86	0.40
1:D:56:LEU:C	1:D:56:LEU:HD23	2.41	0.40
1:D:130:GLN:HE22	1:D:133:ARG:HH11	1.61	0.40
3:I:12:DG:H1'	3:I:13:DG:H5'	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	260/295 (88%)	249 (96%)	11 (4%)	0	100	100
1	D	260/295 (88%)	247 (95%)	13 (5%)	0	100	100
1	G	217/295 (74%)	204 (94%)	13 (6%)	0	100	100
All	All	737/885 (83%)	700 (95%)	37 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	219/247 (89%)	211 (96%)	8 (4%)	34	65
1	D	219/247 (89%)	207 (94%)	12 (6%)	21	49
1	G	130/247 (53%)	124 (95%)	6 (5%)	27	57
All	All	568/741 (77%)	542 (95%)	26 (5%)	27	57

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	SER
1	A	70	GLN
1	A	100	ARG
1	A	144	PHE
1	A	155	LYS
1	A	187	LYS
1	A	227	GLU
1	A	274	ARG
1	D	32	VAL
1	D	42	SER
1	D	63	LEU
1	D	69	GLN
1	D	100	ARG
1	D	144	PHE
1	D	155	LYS

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Mol	Chain	Res	Type
1	D	199	GLU
1	D	201	LEU
1	D	202	GLN
1	D	257	ARG
1	D	274	ARG
1	G	78	ARG
1	G	100	ARG
1	G	128	LYS
1	G	144	PHE
1	G	201	LEU
1	G	238	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	130	GLN
1	D	70	GLN
1	D	130	GLN
1	D	143	GLN
1	D	202	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues are 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	$\# Z > 2$
2	QBT	E	7	2	17,21,22	1.20	2 (11%)	22,30,33	1.41	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	QBT	H	7	2	17,21,22	1.19	1 (5%)	22,30,33	1.43	3 (13%)
2	QBT	B	7	2	17,21,22	1.33	2 (11%)	22,30,33	1.57	5 (22%)

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	QBT	E	7	2	-	6/7/37/38	0/2/2/2
2	QBT	H	7	2	-	4/7/37/38	0/2/2/2
2	QBT	B	7	2	-	5/7/37/38	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	7	QBT	C2-N3	-3.57	1.31	1.38
2	H	7	QBT	C2-N3	-3.06	1.32	1.38
2	E	7	QBT	C2-N3	-2.72	1.33	1.38
2	B	7	QBT	C4-N3	-2.55	1.32	1.37
2	E	7	QBT	C4-N3	-2.47	1.33	1.37

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	7	QBT	C6-N1-C1'	-3.86	113.34	120.94
2	B	7	QBT	C6-N1-C1'	-3.85	113.37	120.94
2	H	7	QBT	C6-N1-C1'	-3.68	113.69	120.94
2	H	7	QBT	C4-N3-C2	-3.38	122.73	126.86
2	E	7	QBT	C4-N3-C2	-3.22	122.93	126.86
2	B	7	QBT	C4-N3-C2	-3.13	123.03	126.86
2	B	7	QBT	O4-C4-N3	-2.32	116.87	121.01
2	B	7	QBT	O4'-C1'-C2'	-2.12	102.24	106.25
2	B	7	QBT	C5M-C5-C6	-2.08	107.91	112.34
2	H	7	QBT	N3-C2-N1	2.03	118.80	116.65

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	7	QBT	O4'-C4'-C5'-O5'
2	B	7	QBT	C2'-C1'-N1-C6
2	B	7	QBT	O4'-C4'-C5'-O5'
2	E	7	QBT	C4'-C5'-O5'-P
2	E	7	QBT	C2'-C1'-N1-C6
2	B	7	QBT	C2'-C1'-N1-C2
2	H	7	QBT	O4'-C4'-C5'-O5'
2	B	7	QBT	O4'-C1'-N1-C2
2	B	7	QBT	C3'-C4'-C5'-O5'
2	H	7	QBT	C2'-C1'-N1-C6
2	E	7	QBT	O4'-C1'-N1-C2
2	H	7	QBT	C4'-C5'-O5'-P
2	E	7	QBT	C3'-C4'-C5'-O5'
2	E	7	QBT	C2'-C1'-N1-C2
2	H	7	QBT	O4'-C1'-N1-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
4	GOL	A	301	-	5,5,5	0.13	0	5,5,5	0.34	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
4	GOL	A	301	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

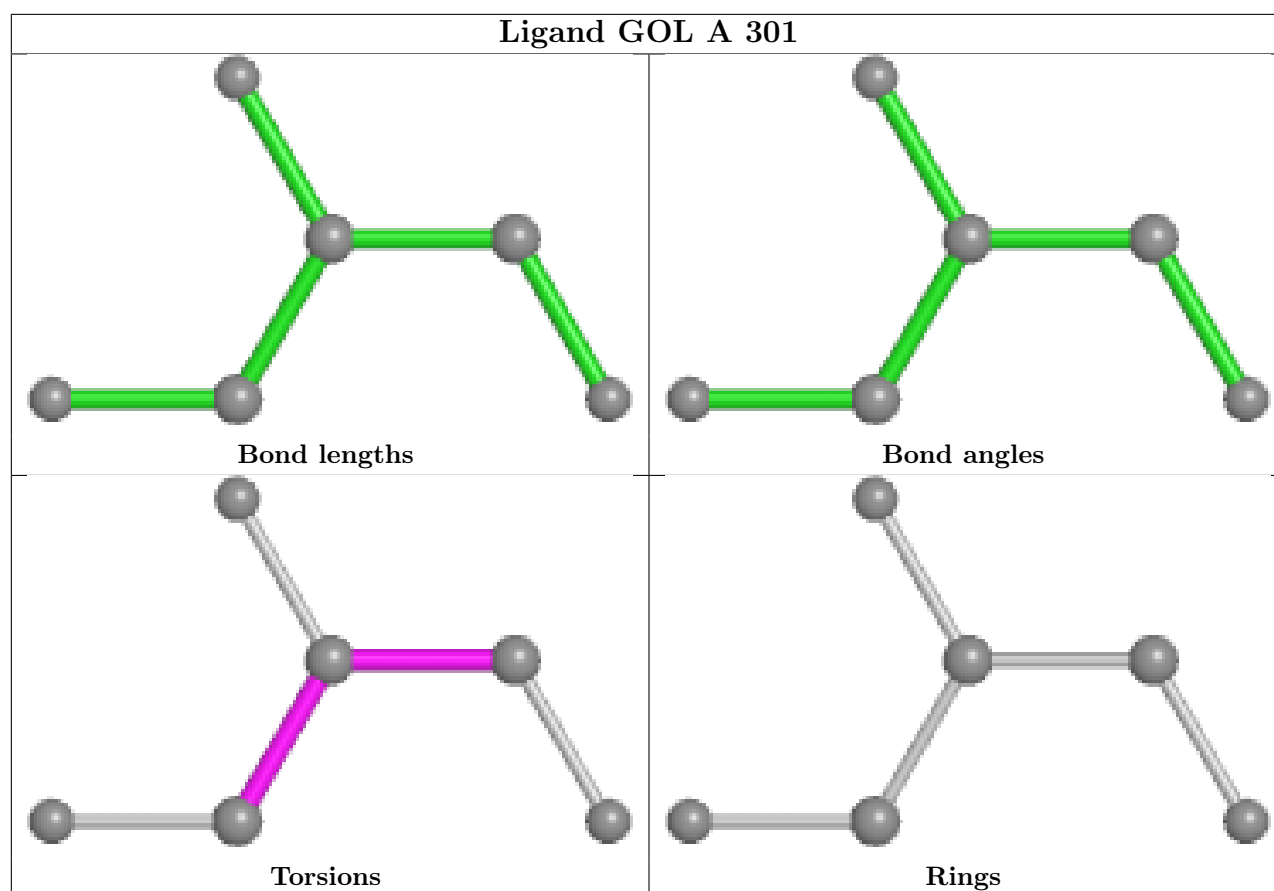
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	301	GOL	O1-C1-C2-O2
4	A	301	GOL	O1-C1-C2-C3
4	A	301	GOL	C1-C2-C3-O3
4	A	301	GOL	O2-C2-C3-O3

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 ⓘ

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	266/295 (90%)	0.07	3 (1%) 80 78	41, 62, 102, 137	0
1	D	266/295 (90%)	0.17	4 (1%) 73 71	41, 73, 125, 156	0
1	G	231/295 (78%)	0.67	27 (11%) 4 3	82, 114, 144, 173	0
2	B	12/13 (92%)	-0.34	0 100 100	64, 99, 147, 160	0
2	E	12/13 (92%)	-0.23	0 100 100	61, 89, 114, 132	0
2	H	12/13 (92%)	-0.04	0 100 100	92, 110, 132, 135	0
3	C	13/13 (100%)	-0.62	0 100 100	81, 98, 141, 157	0
3	F	13/13 (100%)	0.03	0 100 100	56, 92, 131, 147	0
3	I	13/13 (100%)	-0.03	1 (7%) 13 9	80, 115, 140, 143	0
All	All	838/963 (87%)	0.24	35 (4%) 36 30	41, 85, 139, 173	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	243	GLY	6.3
1	G	156	ALA	5.9
1	G	100	ARG	4.7
1	G	125	LEU	4.4
1	G	177	TYR	3.8
1	G	195	ARG	3.7
1	D	241	GLY	3.4
1	G	151	ASN	3.3
1	D	243	GLY	3.3
3	I	1	DT	3.3
1	A	242	LYS	3.2
1	G	173	GLY	3.1
1	G	138	LEU	3.1
1	G	147	ASN	3.0
1	D	242	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	G	196	SER	3.0
1	G	2	GLY	2.7
1	G	194	ALA	2.7
1	G	62	PRO	2.6
1	A	241	GLY	2.5
1	G	149	LEU	2.5
1	G	144	PHE	2.4
1	G	123	TRP	2.4
1	G	58	LEU	2.4
1	G	152	LEU	2.4
1	G	154	ASP	2.3
1	G	141	TYR	2.3
1	G	198	LEU	2.3
1	G	106	PRO	2.3
1	G	174	ILE	2.2
1	D	249	GLY	2.1
1	G	124	ASP	2.1
1	G	197	VAL	2.1
1	G	190	PRO	2.1
1	G	86	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	QBT	B	7	20/21	0.97	0.17	56,63,76,81	0
2	QBT	H	7	20/21	0.97	0.17	93,97,108,112	0
2	QBT	E	7	20/21	0.98	0.16	63,71,85,91	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

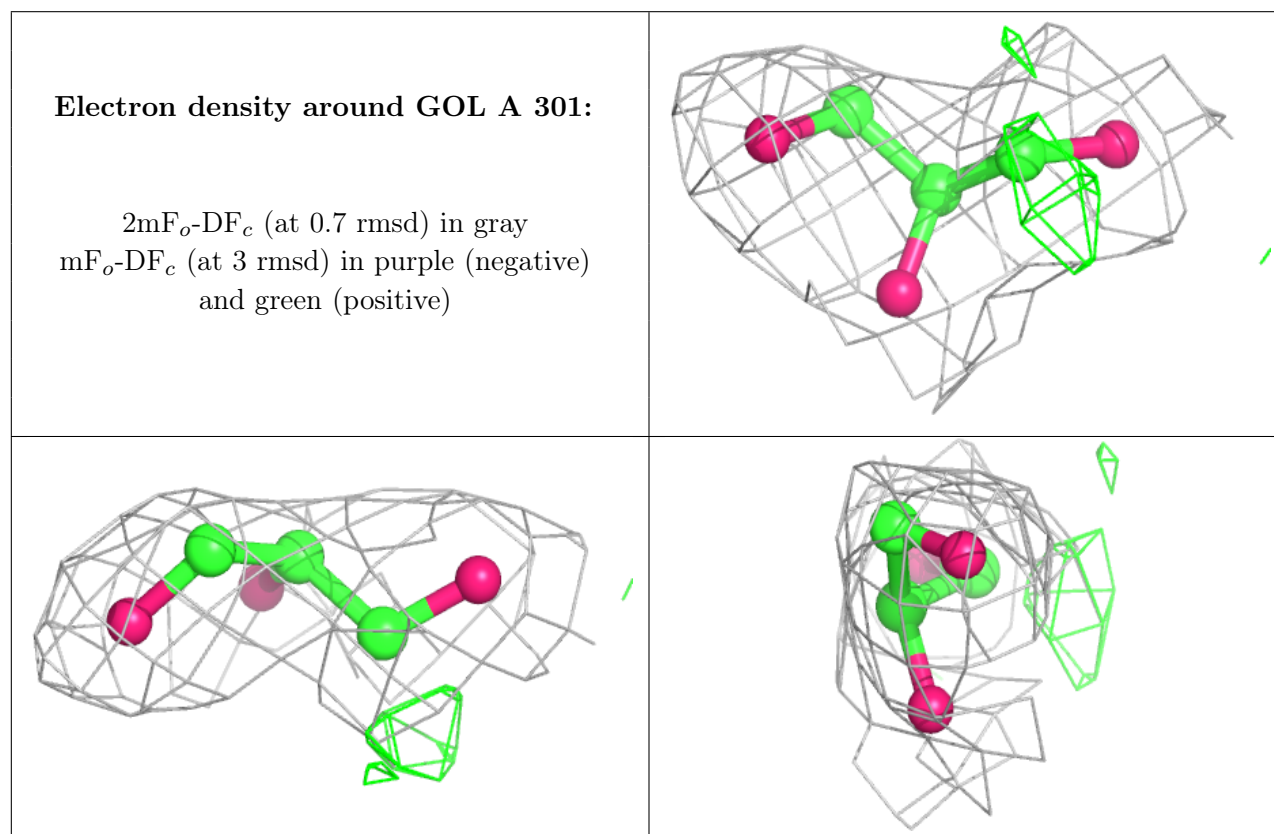
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	A	301	6/6	0.71	0.19	107,118,121,122	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.