



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:18 PM UTC

PDB ID : 6LWB / pdb_00006lwb
Title : Crystal structure of human NEIL1(P2G, E3Q, R242) bound to duplex DNA containing 5-hydroxyuracil (5-OHU)
Authors : Liu, M.H.; Zhang, J.; Zhu, C.X.; Zhang, X.X.; Gao, Y.Q.; Yi, C.Q.
Deposited on : 2020-02-07
Resolution : 2.55 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
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

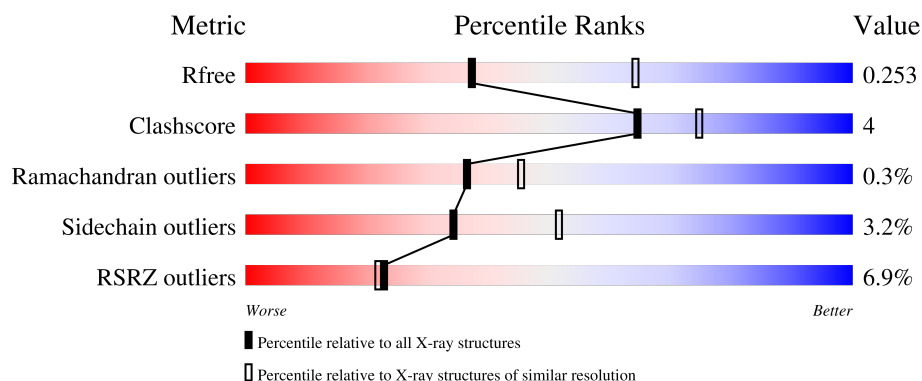
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	295	81% 8% 10%
1	D	295	3% 79% 9% 12%
1	G	295	15% 70% 7% 23%
2	B	13	92% 8%
2	E	13	85% 15%

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Mol	Chain	Length	Quality of chain
2	H	13	 85% 8% 8%
3	C	13	 77% 23%
3	F	13	 54% 31% 15%
3	I	13	 69% 31%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7570 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	265	Total	C	N	O	S	0	0	0
			2106	1345	385	366	10			
1	D	261	Total	C	N	O	S	0	0	0
			2055	1312	378	355	10			
1	G	228	Total	C	N	O	S	0	0	0
			1574	975	301	290	8			

There are 9 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
A	242	ARG	LYS	variant	UNP Q96FI4
D	2	GLY	PRO	engineered mutation	UNP Q96FI4
D	3	GLN	GLU	engineered mutation	UNP Q96FI4
D	242	ARG	LYS	variant	UNP Q96FI4
G	2	GLY	PRO	engineered mutation	UNP Q96FI4
G	3	GLN	GLU	engineered mutation	UNP Q96FI4
G	242	ARG	LYS	variant	UNP Q96FI4

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*GP*TP*CP*CP*AP*(OHU)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	124	43	79	12			
2	E	13	Total	C	N	O	P	0	0	0
			258	124	43	79	12			
2	H	13	Total	C	N	O	P	0	0	0
			258	124	43	79	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 267	C 127	N 53	O 75	P 12	0	0	0
3	F	13	Total 267	C 127	N 53	O 75	P 12	0	0	0
3	I	13	Total 267	C 127	N 53	O 75	P 12	0	0	0

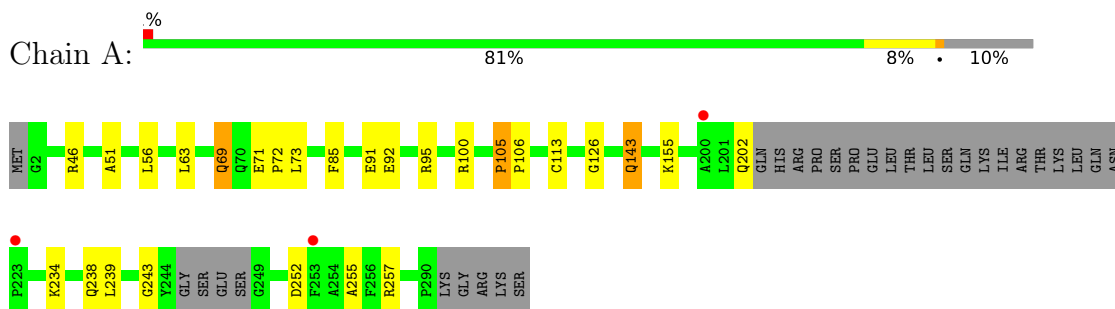
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	132	Total 132	O 132	0	0
4	B	16	Total 16	O 16	0	0
4	C	4	Total 4	O 4	0	0
4	D	76	Total 76	O 76	0	0
4	E	11	Total 11	O 11	0	0
4	F	8	Total 8	O 8	0	0
4	G	10	Total 10	O 10	0	0
4	H	1	Total 1	O 1	0	0
4	I	2	Total 2	O 2	0	0

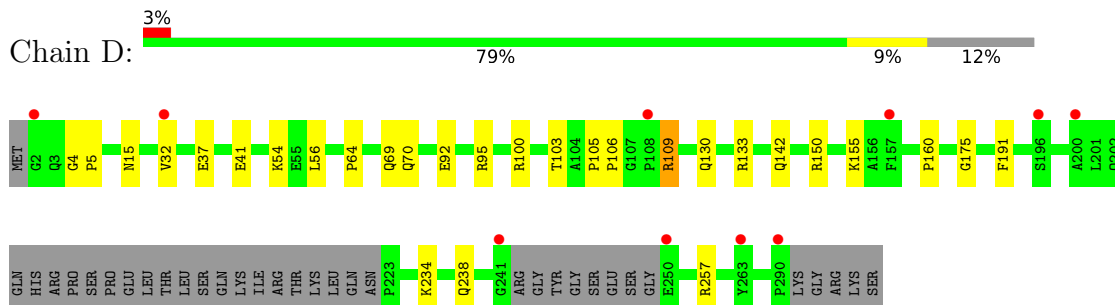
3 Residue-property plots

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.

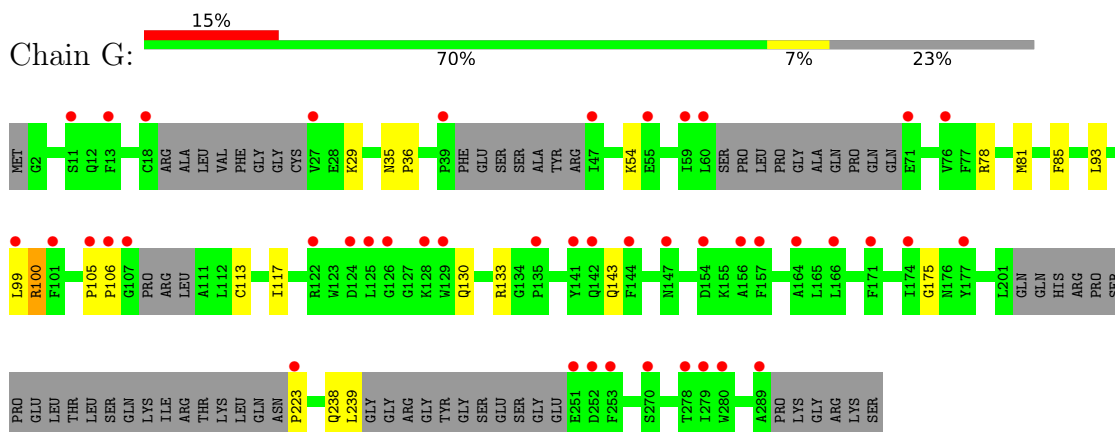
- Molecule 1: Endonuclease 8-like 1



- Molecule 1: Endonuclease 8-like 1



- Molecule 1: Endonuclease 8-like 1



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

Chain B:  92% 8%



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

Chain E:  85% 15%



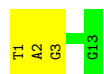
- Molecule 2: DNA (5'-D(*CP*GP*TP*CP*CP*AP*(OHU)P*GP*TP*CP*TP*AP*C)-3')

Chain H:  85% 8% 8%



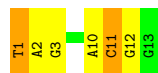
- Molecule 3: DNA (5'-D(*TP*AP*GP*AP*CP*CP*TP*GP*GP*AP*CP*GP*G)-3')

Chain C:  77% 23%



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

Chain F:  54% 31% 15%



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

Chain I:  69% 31%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.81Å 109.24Å 169.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.34 – 2.55 32.34 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.5 (32.34-2.55) 99.5 (32.34-2.55)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.54Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.210 , 0.253 0.212 , 0.253	Depositor DCC
R_{free} test set	2275 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	60.6	Xtriage
Anisotropy	0.459	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 60.4	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	0.95	EDS
Total number of atoms	7570	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: OHU

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	1.07	3/2163 (0.1%)	1.33	3/2923 (0.1%)
1	D	1.07	2/2110 (0.1%)	1.33	3/2852 (0.1%)
1	G	1.06	0/1607	1.34	0/2148
2	B	0.40	0/264	0.89	0/402
2	E	0.49	0/264	0.92	1/402 (0.2%)
2	H	0.38	0/264	0.83	0/402
3	C	0.48	0/300	0.81	0/462
3	F	0.52	0/300	1.02	3/462 (0.6%)
3	I	0.42	0/300	0.78	0/462
All	All	0.96	5/7572 (0.1%)	1.24	10/10515 (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	A	0	3
1	G	0	1
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	92	GLU	CD-OE1	7.44	1.39	1.25
1	D	150	ARG	NE-CZ	7.18	1.41	1.33
1	A	92	GLU	CD-OE1	6.57	1.37	1.25
1	A	91	GLU	CG-CD	5.97	1.67	1.52
1	A	92	GLU	CD-OE2	5.52	1.35	1.25

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	8	DG	O5'-P-OP1	-7.27	87.19	109.00
3	F	11	DC	C5'-C4'-C3'	-6.62	104.96	114.90
3	F	1	DT	C2'-C3'-O3'	6.51	121.27	111.50
1	A	105	PRO	CB-CA-C	-6.16	103.40	110.92
1	A	105	PRO	N-CA-C	5.78	117.75	110.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	105	PRO	Mainchain,Peptide
1	A	243	GLY	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	2106	0	2082	12	0
1	D	2055	0	2034	18	0
1	G	1574	0	1320	13	0
2	B	258	0	147	0	0
2	E	258	0	147	2	0
2	H	258	0	147	3	0
3	C	267	0	147	4	0
3	F	267	0	147	4	0
3	I	267	0	147	5	0
4	A	132	0	0	3	0
4	B	16	0	0	0	0
4	C	4	0	0	0	0
4	D	76	0	0	0	0
4	E	11	0	0	0	0
4	F	8	0	0	0	0
4	G	10	0	0	1	0
4	H	1	0	0	0	0
4	I	2	0	0	0	0
All	All	7570	0	6318	53	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.

The worst 5 of 53 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:D:109:ARG:HG3	1:D:109:ARG:HH11	1.32	0.95
1:D:109:ARG:N	1:D:109:ARG:HD2	1.92	0.82
1:A:143:GLN:NE2	4:A:301:HOH:O	1.70	0.80
1:G:78:ARG:NH1	1:G:130:GLN:OE1	2.16	0.79
1:D:109:ARG:HG3	1:D:109:ARG:NH1	1.95	0.77

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	259/295 (88%)	247 (95%)	11 (4%)	1 (0%)	30	39
1	D	255/295 (86%)	242 (95%)	13 (5%)	0	100	100
1	G	214/295 (72%)	203 (95%)	10 (5%)	1 (0%)	24	34
All	All	728/885 (82%)	692 (95%)	34 (5%)	2 (0%)	36	45

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	PRO
1	G	106	PRO

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	219/247 (89%)	213 (97%)	6 (3%)	39	58
1	D	213/247 (86%)	205 (96%)	8 (4%)	29	44
1	G	132/247 (53%)	128 (97%)	4 (3%)	36	53
All	All	564/741 (76%)	546 (97%)	18 (3%)	34	51

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	99	LEU
1	G	238	GLN
1	G	143	GLN
1	D	95	ARG
1	D	257	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	142	GLN
1	D	238	GLN
1	A	147	ASN
1	A	238	GLN
1	D	8	HIS

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	OHU	E	7	2	18,21,22	1.45	2 (11%)	23,30,33	1.88	5 (21%)
2	OHU	B	7	2	18,21,22	1.31	3 (16%)	23,30,33	2.12	9 (39%)
2	OHU	H	7	2	18,21,22	1.37	1 (5%)	23,30,33	1.84	3 (13%)

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	OHU	E	7	2	-	2/7/21/22	0/2/2/2
2	OHU	B	7	2	-	2/7/21/22	0/2/2/2
2	OHU	H	7	2	-	2/7/21/22	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	7	OHU	C2-N1	3.28	1.43	1.38
2	H	7	OHU	C2-N1	2.99	1.43	1.38
2	E	7	OHU	C6-C5	2.64	1.39	1.35
2	B	7	OHU	C2-N1	2.63	1.42	1.38
2	B	7	OHU	O2-C2	2.17	1.26	1.23

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	7	OHU	C4-N3-C2	-4.83	121.01	127.34
2	E	7	OHU	N3-C2-N1	4.55	120.81	114.89
2	H	7	OHU	C4-N3-C2	-4.48	121.47	127.34
2	B	7	OHU	C4-N3-C2	-4.43	121.53	127.34
2	B	7	OHU	O5-C5-C4	4.40	124.47	117.28

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	7	OHU	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	H	7	OHU	O4'-C4'-C5'-O5'
2	B	7	OHU	C3'-C4'-C5'-O5'
2	B	7	OHU	O4'-C4'-C5'-O5'
2	E	7	OHU	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	7	OHU	1	0
2	H	7	OHU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	265/295 (89%)	-0.05	3 (1%) 78 79	36, 60, 99, 132	0
1	D	261/295 (88%)	0.32	10 (3%) 44 45	39, 72, 126, 140	0
1	G	228/295 (77%)	1.22	44 (19%) 3 2	78, 112, 146, 157	0
2	B	12/13 (92%)	0.10	0 100 100	59, 95, 133, 140	0
2	E	12/13 (92%)	0.14	0 100 100	66, 92, 109, 127	0
2	H	12/13 (92%)	0.40	0 100 100	95, 113, 126, 132	0
3	C	13/13 (100%)	0.07	0 100 100	70, 96, 130, 149	0
3	F	13/13 (100%)	0.26	0 100 100	58, 94, 127, 143	0
3	I	13/13 (100%)	0.28	0 100 100	75, 117, 135, 138	0
All	All	829/963 (86%)	0.44	57 (6%) 23 22	36, 83, 135, 157	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	107	GLY	5.1
1	G	252	ASP	4.4
1	D	290	PRO	4.0
1	G	122	ARG	3.8
1	G	223	PRO	3.7

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($\text{\AA}^2$)	Q<0.9
2	OHU	H	7	20/21	0.87	0.11	96,112,127,130	0
2	OHU	E	7	20/21	0.94	0.10	73,84,105,108	0
2	OHU	B	7	20/21	0.95	0.09	59,72,104,107	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.