



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:37 PM UTC

PDB ID : 2OD7 / pdb_00002od7
Title : Crystal Structure of yHst2 bound to the intermediate analogue ADP-HPD,
and and aceylated H4 peptide
Authors : Marmorstein, R.Q.; Sanders, B.D.
Deposited on : 2006-12-21
Resolution : 2.00 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

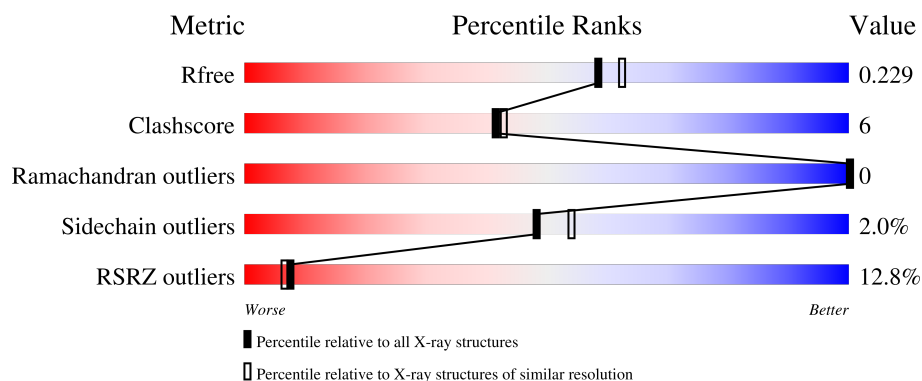
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	308	
2	B	14	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2515 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 NAD-dependent deacetylase HST2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2286	1478	377	419	12			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP P53686
A	-12	ARG	-	cloning artifact	UNP P53686
A	-11	GLY	-	cloning artifact	UNP P53686
A	-10	SER	-	cloning artifact	UNP P53686
A	-9	HIS	-	expression tag	UNP P53686
A	-8	HIS	-	expression tag	UNP P53686
A	-7	HIS	-	expression tag	UNP P53686
A	-6	HIS	-	expression tag	UNP P53686
A	-5	HIS	-	expression tag	UNP P53686
A	-4	HIS	-	expression tag	UNP P53686
A	-3	GLY	-	cloning artifact	UNP P53686
A	-2	MET	-	cloning artifact	UNP P53686
A	-1	ALA	-	cloning artifact	UNP P53686
A	0	SER	-	cloning artifact	UNP P53686

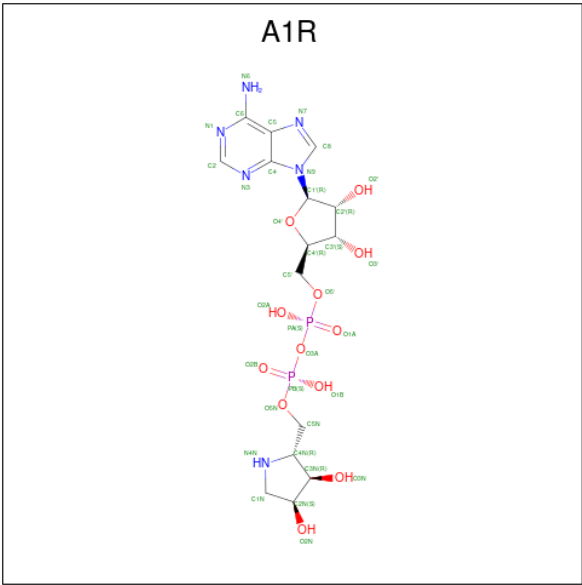
- Molecule 2 is a protein called Acetylated histone H4 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	8	Total	C	N	O	0	0	0
			60	36	15	9			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is 5'-O-[(S)-{[(S)-{[(2R,3R,4S)-3,4-DIHYDROXYPYRROLIDIN-2-YL]MET HOXY}(HYDROXY)PHOSPHORYL]OXY}(HYDROXY)PHOSPHORYL]ADENOSINE (CCD ID: A1R) (formula: C₁₅H₂₄N₆O₁₂P₂).

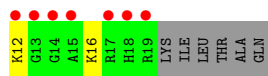


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	35	15	6	12	2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	131	Total	O	0	0
			131	131		
5	B	2	Total	O	0	0
			2	2		

- Molecule 1: NAD-dependent deacetylase HST2



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	106.76 Å 106.76 Å 67.69 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.92 – 2.00 41.92 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.4 (41.92-2.00) 91.4 (41.92-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.99 (at 2.00 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.234 0.217 , 0.229	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.586	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2515	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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: ZN, A1R, ALY

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	2.20	74/2345 (3.2%)	1.58	23/3178 (0.7%)
2	B	0.34	0/47	0.77	0/58
All	All	2.18	74/2392 (3.1%)	1.57	23/3236 (0.7%)

All (74) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	112	VAL	CA-CB	10.97	1.68	1.54
1	A	75	ASP	CA-C	9.84	1.65	1.52
1	A	216	GLN	CA-C	9.82	1.64	1.52
1	A	146	CYS	CA-C	8.80	1.64	1.52
1	A	150	TYR	CA-C	8.33	1.60	1.52
1	A	273	PHE	N-CA	7.94	1.55	1.46
1	A	235	PRO	C-O	-7.81	1.14	1.24
1	A	65	ALA	C-O	7.69	1.33	1.24
1	A	139	ALA	CA-CB	7.66	1.67	1.53
1	A	266	VAL	CA-C	7.63	1.61	1.52
1	A	122	ARG	C-O	7.54	1.32	1.24
1	A	28	ILE	CA-CB	-7.50	1.45	1.54
1	A	172	VAL	CA-C	7.25	1.61	1.52
1	A	50	GLY	C-O	7.07	1.32	1.23
1	A	33	ALA	CA-CB	6.93	1.65	1.53
1	A	132	ILE	CA-CB	6.56	1.62	1.54
1	A	34	GLY	CA-C	6.56	1.59	1.52
1	A	286	ASP	CA-C	6.50	1.61	1.52
1	A	142	HIS	CA-CB	6.49	1.65	1.53
1	A	142	HIS	CA-C	6.44	1.60	1.52
1	A	279	GLU	C-O	-6.33	1.16	1.24
1	A	203	LEU	CA-C	6.32	1.60	1.52
1	A	81	THR	C-O	-6.29	1.16	1.24
1	A	228	VAL	CA-CB	6.28	1.62	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	274	ALA	CA-CB	6.24	1.63	1.53
1	A	193	SER	N-CA	6.21	1.53	1.46
1	A	279	GLU	CA-C	6.18	1.60	1.52
1	A	156	LYS	C-O	6.13	1.31	1.24
1	A	101	LYS	C-O	6.11	1.31	1.24
1	A	45	ARG	C-O	6.09	1.32	1.24
1	A	84	LYS	N-CA	-6.08	1.38	1.46
1	A	137	SER	C-O	6.07	1.30	1.23
1	A	166	ASP	CA-CB	6.04	1.61	1.53
1	A	37	THR	CA-CB	5.98	1.62	1.53
1	A	72	PHE	CA-C	5.97	1.60	1.52
1	A	241	LYS	CG-CD	5.95	1.70	1.52
1	A	80	TYR	CA-C	5.91	1.60	1.52
1	A	102	LEU	CA-C	5.87	1.60	1.52
1	A	81	THR	CA-C	5.83	1.60	1.52
1	A	99	LEU	N-CA	5.83	1.53	1.46
1	A	271	ASP	CA-C	5.77	1.60	1.52
1	A	166	ASP	CB-CG	5.68	1.66	1.52
1	A	31	VAL	C-O	5.66	1.29	1.23
1	A	219	VAL	CA-CB	-5.66	1.47	1.54
1	A	28	ILE	CA-C	5.64	1.59	1.52
1	A	251	THR	CA-CB	5.63	1.60	1.53
1	A	131	ILE	CA-CB	5.58	1.60	1.54
1	A	92	ARG	CB-CG	5.57	1.69	1.52
1	A	143	CYS	C-O	5.56	1.30	1.24
1	A	178	LYS	CA-C	5.56	1.57	1.52
1	A	7	SER	C-O	5.53	1.30	1.23
1	A	271	ASP	N-CA	-5.52	1.39	1.46
1	A	37	THR	CA-C	-5.51	1.45	1.52
1	A	110	LYS	CA-C	5.50	1.59	1.52
1	A	-1	ALA	C-O	5.49	1.30	1.23
1	A	60	LEU	CG-CD2	5.47	1.70	1.52
1	A	165	LYS	CA-C	5.46	1.59	1.52
1	A	71	PHE	CA-CB	5.43	1.61	1.53
1	A	225	SER	C-O	5.38	1.31	1.24
1	A	35	ILE	CA-CB	5.38	1.62	1.54
1	A	264	LEU	CA-C	5.38	1.59	1.52
1	A	262	THR	CA-C	5.36	1.60	1.52
1	A	24	ASN	N-CA	5.33	1.52	1.46
1	A	26	LYS	N-CA	5.28	1.52	1.45
1	A	75	ASP	C-O	-5.23	1.17	1.24
1	A	162	HIS	C-O	5.21	1.29	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	241	LYS	CB-CG	5.16	1.68	1.52
1	A	36	SER	CA-C	5.14	1.59	1.52
1	A	171	ASP	C-O	-5.13	1.17	1.24
1	A	137	SER	CA-C	5.08	1.59	1.52
1	A	37	THR	CB-OG1	-5.06	1.35	1.43
1	A	269	TYR	C-O	5.04	1.30	1.23
1	A	215	GLN	C-O	5.01	1.33	1.23
1	A	132	ILE	C-O	5.01	1.29	1.24

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	THR	OG1-CB-CG2	-8.78	91.74	109.30
1	A	151	PRO	O-C-N	7.85	124.92	121.31
1	A	165	LYS	N-CA-C	7.52	118.53	108.38
1	A	46	SER	CA-C-O	6.58	124.19	119.32
1	A	46	SER	N-CA-C	6.50	118.28	109.24
1	A	138	PHE	N-CA-C	6.08	120.42	113.19
1	A	153	GLN	N-CA-C	5.83	118.42	111.71
1	A	272	GLU	N-CA-C	-5.78	104.35	111.40
1	A	77	LEU	O-C-N	5.77	125.61	120.48
1	A	69	VAL	N-CA-C	5.76	115.95	110.42
1	A	199	ASP	N-CA-C	-5.66	105.10	112.23
1	A	89	GLY	CA-C-O	5.56	125.14	118.97
1	A	252	VAL	CA-C-N	5.47	128.91	120.00
1	A	252	VAL	C-N-CA	5.47	128.91	120.00
1	A	260	ARG	NE-CZ-NH1	-5.43	116.07	121.50
1	A	0	SER	N-CA-C	5.43	118.11	109.81
1	A	192	PHE	N-CA-C	-5.34	105.10	111.03
1	A	130	LEU	N-CA-C	5.27	119.71	113.28
1	A	171	ASP	CB-CG-OD2	5.20	130.36	118.40
1	A	79	PHE	N-CA-C	-5.16	105.73	111.36
1	A	112	VAL	N-CA-C	5.13	115.24	107.75
1	A	215	GLN	O-C-N	-5.11	114.82	123.00
1	A	13	ARG	N-CA-C	5.02	117.13	111.11

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	2286	0	2263	30	0
2	B	60	0	58	6	0
3	A	1	0	0	0	0
4	A	35	0	22	0	0
5	A	131	0	0	1	0
5	B	2	0	0	0	0
All	All	2515	0	2343	30	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 6.

All (30) 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:104:GLN:HE22	1:A:127:LYS:H	1.24	0.86
1:A:36:SER:HB3	1:A:41:ILE:HD12	1.58	0.84
1:A:158:LYS:NZ	1:A:165:LYS:O	2.14	0.80
1:A:27:VAL:HG11	1:A:220:ILE:HD12	1.77	0.67
1:A:158:LYS:CE	1:A:166:ASP:O	2.47	0.62
1:A:190:ASP:HA	2:B:12:LYS:NZ	2.15	0.61
1:A:28:ILE:HD11	1:A:110:LYS:HG3	1.84	0.59
1:A:104:GLN:NE2	1:A:127:LYS:H	1.99	0.58
1:A:104:GLN:HE22	1:A:127:LYS:N	2.01	0.56
1:A:158:LYS:NZ	1:A:166:ASP:O	2.38	0.56
1:A:243:LYS:NZ	1:A:262:THR:O	2.36	0.56
1:A:288:GLU:O	1:A:292:THR:HG23	2.06	0.55
1:A:193:SER:CB	2:B:12:LYS:HG3	2.37	0.54
1:A:153:GLN:NE2	1:A:153:GLN:H	2.07	0.53
1:A:28:ILE:HD11	1:A:110:LYS:CG	2.40	0.52
1:A:193:SER:HB2	2:B:12:LYS:NZ	2.27	0.50
1:A:18:HIS:CD2	1:A:18:HIS:C	2.90	0.50
1:A:36:SER:HB3	1:A:41:ILE:CD1	2.37	0.50
1:A:119:THR:HG21	5:A:1027:HOH:O	2.12	0.48
1:A:190:ASP:OD2	2:B:12:LYS:HE2	2.13	0.48
1:A:110:LYS:HE2	1:A:202:TRP:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:GLN:H	1:A:153:GLN:HE21	1.64	0.46
1:A:47:PRO:O	1:A:53:HIS:NE2	2.48	0.45
1:A:193:SER:OG	2:B:12:LYS:HG3	2.16	0.45
1:A:54:ASN:OD1	1:A:57:ARG:NH2	2.49	0.45
1:A:147:GLY:O	1:A:148:LYS:C	2.60	0.44
1:A:193:SER:HB2	2:B:12:LYS:HZ2	1.82	0.44
1:A:27:VAL:CG1	1:A:220:ILE:HD12	2.48	0.42
1:A:118:ASP:O	1:A:119:THR:OG1	2.32	0.41
1:A:104:GLN:HE21	1:A:130:LEU:HD12	1.86	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	285/308 (92%)	277 (97%)	8 (3%)	0	100	100
2	B	5/14 (36%)	5 (100%)	0	0	100	100
All	All	290/322 (90%)	282 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	252/271 (93%)	247 (98%)	5 (2%)	48	54
2	B	3/9 (33%)	3 (100%)	0	100	100
All	All	255/280 (91%)	250 (98%)	5 (2%)	48	54

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	PRO
1	A	153	GLN
1	A	218	LEU
1	A	224	THR
1	A	243	LYS

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	18	HIS
1	A	104	GLN
1	A	123	GLN
1	A	153	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	$\# Z > 2$
2	ALY	B	16	2	10,11,12	1.42	2 (20%)	7,12,14	2.13	1 (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
2	ALY	B	16	2	-	0/9/10/12	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	16	ALY	OH-CH	3.20	1.30	1.23
2	B	16	ALY	CH-NZ	2.63	1.41	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	16	ALY	CE-NZ-CH	-5.21	114.87	122.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
4	A1R	A	1001	-	38,38,38	3.60	13 (34%)	50,58,58	3.15	17 (34%)

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	A1R	A	1001	-	-	4/22/51/51	0/4/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1001	A1R	C1N-C2N	-11.24	1.38	1.53
4	A	1001	A1R	PB-O3A	-9.29	1.49	1.59
4	A	1001	A1R	C2-N3	7.08	1.46	1.33
4	A	1001	A1R	C5N-C4N	-5.68	1.41	1.51
4	A	1001	A1R	C4-N3	5.67	1.45	1.34
4	A	1001	A1R	PA-O3A	-5.61	1.53	1.59
4	A	1001	A1R	C2N-C3N	-5.30	1.44	1.53
4	A	1001	A1R	C2-N1	4.74	1.42	1.33
4	A	1001	A1R	C6-N1	3.55	1.45	1.35
4	A	1001	A1R	C5-C6	3.32	1.50	1.41
4	A	1001	A1R	C6-N6	3.17	1.42	1.34
4	A	1001	A1R	PB-O2B	-2.95	1.40	1.50
4	A	1001	A1R	O5N-C5N	-2.41	1.35	1.44

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1001	A1R	C1N-C2N-C3N	9.54	113.42	103.40
4	A	1001	A1R	O2N-C2N-C1N	-8.66	90.68	110.90
4	A	1001	A1R	C5N-C4N-N4N	-8.43	93.96	111.44
4	A	1001	A1R	O2N-C2N-C3N	-7.81	96.06	111.43
4	A	1001	A1R	C5N-C4N-C3N	6.54	125.00	113.75
4	A	1001	A1R	O3N-C3N-C2N	6.04	126.28	111.97
4	A	1001	A1R	N3-C2-N1	-4.07	122.42	128.58
4	A	1001	A1R	O5N-PB-O2B	3.59	123.17	108.94
4	A	1001	A1R	O3A-PB-O2B	3.41	120.97	110.70
4	A	1001	A1R	C2'-C1'-N9	3.36	121.65	113.30
4	A	1001	A1R	C4-N9-C1'	-2.62	120.51	126.63
4	A	1001	A1R	PB-O5N-C5N	2.46	135.42	121.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1001	A1R	C1'-N9-C8	2.43	132.49	127.09
4	A	1001	A1R	O4'-C1'-N9	-2.37	103.53	108.09
4	A	1001	A1R	C3'-C2'-C1'	2.26	105.73	101.46
4	A	1001	A1R	O1B-PB-O2B	-2.25	101.96	112.44
4	A	1001	A1R	O2A-PA-O3A	-2.18	101.39	107.27

There are no chirality outliers.

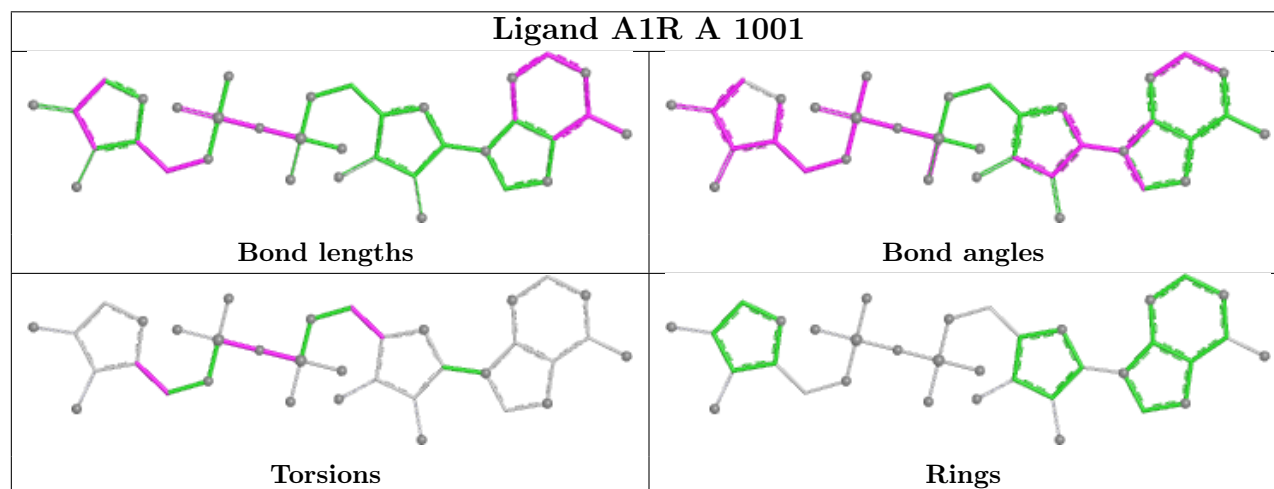
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1001	A1R	PB-O3A-PA-O5'
4	A	1001	A1R	PA-O3A-PB-O1B
4	A	1001	A1R	N4N-C4N-C5N-O5N
4	A	1001	A1R	O4'-C4'-C5'-O5'

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	16:ALY	C	17:ARG	N	1.15

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	289/308 (93%)	0.60	31 (10%)	11 10	17, 30, 56, 75	0
2	B	7/14 (50%)	4.29	7 (100%)	0 0	43, 52, 73, 109	0
All	All	296/322 (91%)	0.69	38 (12%)	7 6	17, 31, 58, 109	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	19	ARG	8.1
1	A	293	ALA	5.6
2	B	12	LYS	5.3
1	A	207	ILE	4.6
2	B	13	GLY	4.3
1	A	166	ASP	4.2
1	A	292	THR	4.1
1	A	205	GLU	3.5
2	B	14	GLY	3.4
1	A	13	ARG	3.4
1	A	10	MET	3.2
1	A	215	GLN	3.1
2	B	18	HIS	3.0
1	A	204	ARG	3.0
1	A	257	ALA	3.0
1	A	69	VAL	3.0
2	B	17	ARG	2.9
1	A	24	ASN	2.9
1	A	241	LYS	2.9
2	B	15	ALA	2.9
1	A	162	HIS	2.8
1	A	279	GLU	2.7
1	A	9	GLU	2.7
1	A	158	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	163	PRO	2.6
1	A	4	SER	2.5
1	A	28	ILE	2.3
1	A	250	GLU	2.3
1	A	21	SER	2.3
1	A	265	ILE	2.2
1	A	242	VAL	2.2
1	A	185	GLY	2.2
1	A	206	LYS	2.2
1	A	264	LEU	2.1
1	A	289	LYS	2.1
1	A	291	LEU	2.0
1	A	23	PRO	2.0
1	A	258	ASN	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($\text{\AA}^2$)	Q<0.9
2	ALY	B	16	12/13	0.92	0.10	22,26,32,33	0

6.3 Carbohydrates [i](#)

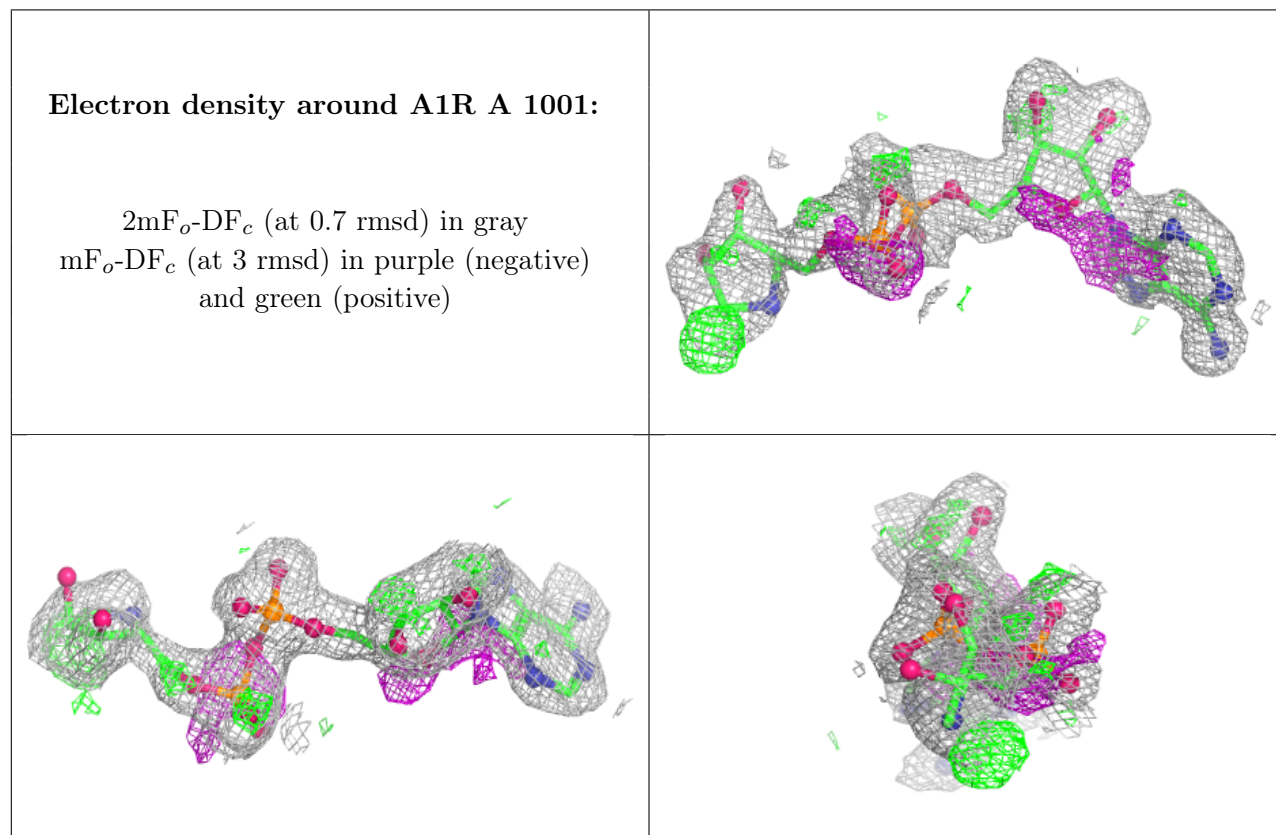
There are no oligosaccharides in this entry.

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	A1R	A	1001	35/35	0.86	0.17	35,39,52,58	0
3	ZN	A	701	1/1	0.99	0.04	26,26,26,26	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.