



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2021 – 10:18 AM EDT

PDB ID : 1KVR  
Title : UDP-GALACTOSE 4-EPIMERASE COMPLEXED WITH UDP-PHENOL  
Authors : Thoden, J.B.; Gulick, A.M.; Holden, H.M.  
Deposited on : 1997-03-07  
Resolution : 1.90 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](mailto: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.

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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)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

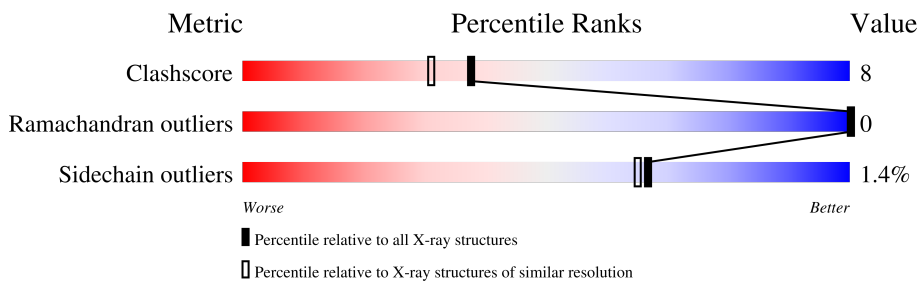
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	338	 77% 19% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	PEG	A	411	-	-	X	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3241 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 UDP-GALACTOSE 4-EPIMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	338	2625	1656	463	494	12	0	0	0

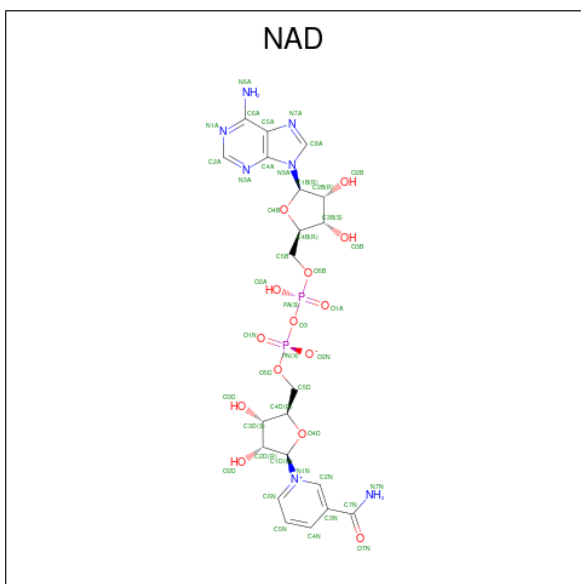
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	124	ALA	SER	engineered mutation	UNP P09147

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

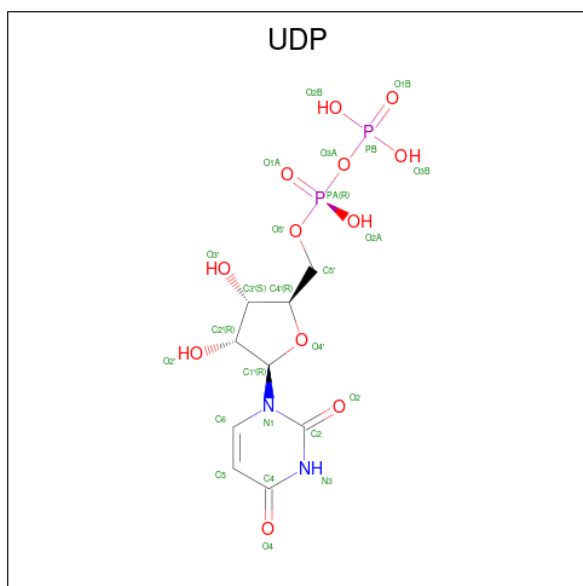
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Na	0	0
			4	4		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>7</sub>O<sub>14</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
3	A	1	44	21	7	14	2	0	0

- Molecule 4 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula:  $C_9H_{14}N_2O_{12}P_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
4	A	1	25	9	2	12	2	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is water.

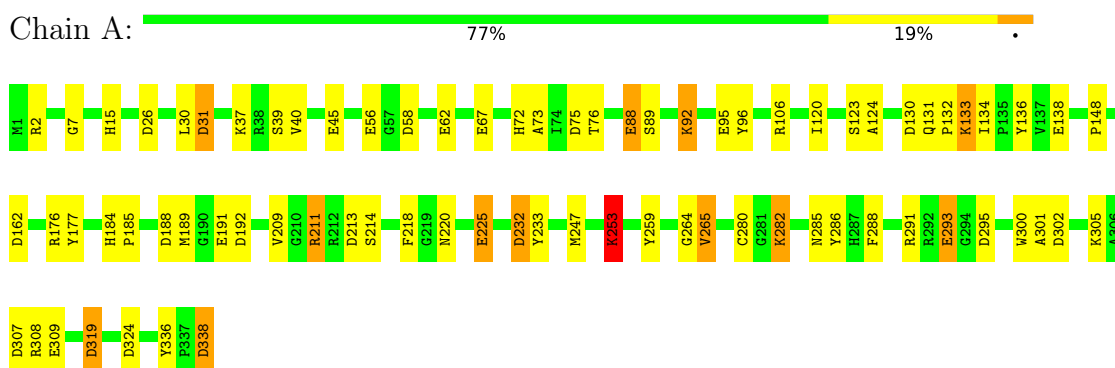
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	532	Total	O	0	0
			532	532		

### 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. 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. 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.

Note EDS was not executed.

- Molecule 1: UDP-GALACTOSE 4-EPIMERASE



## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.50Å 83.50Å 108.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-1.90)	Depositor
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	TNT	Depositor
R, $R_{free}$	0.179 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	3241	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

## 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: UDP, NA, NAD, PEG, EDO

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	1.04	16/2691 (0.6%)	1.43	39/3662 (1.1%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	253	LYS	CE-NZ	-9.96	1.24	1.49
1	A	88	GLU	CD-OE2	-9.24	1.15	1.25
1	A	92	LYS	CE-NZ	-9.13	1.26	1.49
1	A	88	GLU	CD-OE1	7.81	1.34	1.25
1	A	56	GLU	CD-OE1	-7.23	1.17	1.25
1	A	138	GLU	CD-OE1	7.08	1.33	1.25
1	A	225	GLU	CD-OE2	6.81	1.33	1.25
1	A	62	GLU	CD-OE2	-6.79	1.18	1.25
1	A	67	GLU	CD-OE1	6.77	1.33	1.25
1	A	309	GLU	CD-OE1	6.17	1.32	1.25
1	A	56	GLU	CD-OE2	6.12	1.32	1.25
1	A	95	GLU	CD-OE1	6.07	1.32	1.25
1	A	293	GLU	CD-OE2	6.01	1.32	1.25
1	A	191	GLU	CD-OE1	5.88	1.32	1.25
1	A	62	GLU	CD-OE1	5.28	1.31	1.25
1	A	45	GLU	CD-OE1	5.02	1.31	1.25

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	188	ASP	CB-CG-OD1	-9.52	109.73	118.30
1	A	233	TYR	CB-CG-CD1	-9.15	115.51	121.00
1	A	26	ASP	CB-CG-OD1	-9.12	110.09	118.30
1	A	211	ARG	NE-CZ-NH1	9.03	124.82	120.30
1	A	233	TYR	CB-CG-CD2	8.29	125.97	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	319	ASP	CB-CG-OD1	8.17	125.66	118.30
1	A	31	ASP	CB-CG-OD2	7.68	125.21	118.30
1	A	307	ASP	CB-CG-OD2	7.67	125.20	118.30
1	A	307	ASP	CB-CG-OD1	-7.57	111.49	118.30
1	A	286	TYR	CB-CG-CD1	7.26	125.36	121.00
1	A	265	VAL	CB-CA-C	-7.12	97.87	111.40
1	A	295	ASP	CB-CG-OD1	7.04	124.64	118.30
1	A	319	ASP	CB-CG-OD2	-6.70	112.27	118.30
1	A	136	TYR	CB-CG-CD1	6.57	124.94	121.00
1	A	213	ASP	CB-CG-OD1	6.42	124.08	118.30
1	A	295	ASP	CB-CG-OD2	-6.38	112.56	118.30
1	A	291	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	A	136	TYR	CB-CG-CD2	-6.36	117.18	121.00
1	A	75	ASP	CB-CG-OD1	-6.27	112.66	118.30
1	A	162	ASP	CB-CG-OD1	-6.20	112.72	118.30
1	A	302	ASP	CB-CG-OD1	-6.17	112.75	118.30
1	A	96	TYR	CA-CB-CG	-5.98	102.04	113.40
1	A	106	ARG	NE-CZ-NH2	-5.97	117.31	120.30
1	A	188	ASP	CB-CG-OD2	5.79	123.51	118.30
1	A	162	ASP	CB-CG-OD2	5.75	123.47	118.30
1	A	232	ASP	CB-CG-OD1	-5.65	113.22	118.30
1	A	302	ASP	N-CA-C	-5.58	95.93	111.00
1	A	338	ASP	CB-CG-OD1	-5.52	113.33	118.30
1	A	176	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	76	THR	CA-CB-CG2	-5.49	104.72	112.40
1	A	58	ASP	CB-CG-OD2	-5.47	113.38	118.30
1	A	302	ASP	CB-CG-OD2	5.43	123.18	118.30
1	A	177	TYR	CB-CG-CD2	-5.32	117.81	121.00
1	A	192	ASP	CB-CG-OD1	5.32	123.09	118.30
1	A	58	ASP	CB-CG-OD1	5.25	123.03	118.30
1	A	130	ASP	CB-CG-OD2	5.21	122.98	118.30
1	A	324	ASP	CB-CG-OD2	-5.17	113.65	118.30
1	A	308	ARG	N-CA-CB	-5.15	101.33	110.60
1	A	286	TYR	CB-CG-CD2	-5.12	117.93	121.00

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	2625	0	2557	41	0
2	A	4	0	0	0	0
3	A	44	0	26	0	0
4	A	25	0	11	1	0
5	A	4	0	6	0	0
6	A	7	0	10	6	0
7	A	532	0	0	7	4
All	All	3241	0	2610	41	4

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 8.

All (41) 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:131:GLN:OE1	1:A:132:PRO:HD2	1.71	0.90
1:A:293:GLU:O	7:A:890:HOH:O	1.98	0.80
1:A:293:GLU:OE1	7:A:767:HOH:O	2.00	0.78
1:A:37:LYS:HE2	1:A:338:ASP:OD1	1.93	0.68
1:A:319:ASP:OD1	7:A:927:HOH:O	2.11	0.68
1:A:30:LEU:C	1:A:30:LEU:HD13	2.17	0.64
1:A:253:LYS:HD2	6:A:411:PEG:H41	1.80	0.64
1:A:253:LYS:HZ2	6:A:411:PEG:H22	1.64	0.62
1:A:214:SER:HB2	1:A:285:ASN:ND2	2.17	0.60
1:A:15:HIS:HA	1:A:189:MET:HE1	1.84	0.59
1:A:253:LYS:CD	6:A:411:PEG:H41	2.33	0.59
1:A:253:LYS:HZ2	6:A:411:PEG:C2	2.15	0.58
1:A:88:GLU:HG2	1:A:92:LYS:HE3	1.86	0.57
1:A:88:GLU:CG	1:A:92:LYS:HE3	2.34	0.57
1:A:220:ASN:HB3	1:A:288:PHE:CD1	2.41	0.55
1:A:225:GLU:CD	7:A:715:HOH:O	2.45	0.55
1:A:88:GLU:HG3	1:A:92:LYS:CE	2.40	0.52
1:A:89:SER:O	1:A:148:PRO:HG2	2.11	0.51
1:A:88:GLU:CG	1:A:92:LYS:CE	2.90	0.50
1:A:184:HIS:CG	1:A:185:PRO:HD2	2.47	0.49
1:A:88:GLU:HG3	1:A:92:LYS:HE2	1.97	0.47
1:A:264:GLY:HA2	1:A:301:ALA:O	2.14	0.46
1:A:253:LYS:HZ2	6:A:411:PEG:H41	1.80	0.46
1:A:293:GLU:HB3	7:A:890:HOH:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:ILE:HD12	1:A:300:TRP:CZ3	2.52	0.45
1:A:259:TYR:CE1	1:A:305:LYS:HE2	2.51	0.45
1:A:72:HIS:O	1:A:73:ALA:C	2.53	0.45
1:A:280:CYS:SG	1:A:282:LYS:HG2	2.57	0.45
1:A:253:LYS:NZ	6:A:411:PEG:C2	2.79	0.45
1:A:7:GLY:HA2	1:A:31:ASP:OD2	2.17	0.45
1:A:2:ARG:HD3	1:A:73:ALA:O	2.18	0.44
1:A:232:ASP:HB2	1:A:300:TRP:CB	2.48	0.43
1:A:265:VAL:HG23	1:A:265:VAL:O	2.19	0.43
1:A:120:ILE:HD11	1:A:247:MET:HA	2.01	0.43
1:A:123:SER:OG	1:A:124:ALA:N	2.52	0.42
1:A:37:LYS:O	1:A:40:VAL:HG12	2.20	0.42
1:A:211:ARG:NH2	7:A:673:HOH:O	2.44	0.42
1:A:211:ARG:O	1:A:211:ARG:HG3	2.18	0.42
1:A:39:SER:OG	1:A:336:TYR:HB3	2.21	0.41
1:A:218:PHE:CE2	4:A:341:UDP:C4	3.09	0.41
1:A:133:LYS:HD2	7:A:599:HOH:O	2.22	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:876:HOH:O	7:A:911:HOH:O[2_654]	1.15	1.05
7:A:885:HOH:O	7:A:926:HOH:O[3_655]	1.36	0.84
7:A:944:HOH:O	7:A:944:HOH:O[4_556]	1.66	0.54
7:A:942:HOH:O	7:A:942:HOH:O[5_555]	2.13	0.07

## 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	336/338 (99%)	329 (98%)	7 (2%)	0	<a href="#">100</a> <a href="#">100</a>

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	281/281 (100%)	277 (99%)	4 (1%)	67 65

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	133	LYS
1	A	209	VAL
1	A	253	LYS
1	A	282	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	158	GLN
1	A	274	ASN
1	A	285	ASN
1	A	323	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	NAD	A	340	-	42,48,48	1.81	7 (16%)	50,73,73	1.85	8 (16%)
6	PEG	A	411	-	6,6,6	0.69	0	5,5,5	1.31	0
4	UDP	A	341	-	20,26,26	2.03	5 (25%)	25,40,40	1.23	3 (12%)
5	EDO	A	410	-	3,3,3	0.66	0	2,2,2	0.40	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
3	NAD	A	340	-	-	7/26/62/62	0/5/5/5
6	PEG	A	411	-	-	1/4/4/4	-
4	UDP	A	341	-	-	2/14/32/32	0/2/2/2
5	EDO	A	410	-	-	0/1/1/1	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	340	NAD	C5N-C4N	5.84	1.51	1.38
4	A	341	UDP	C6-N1	5.66	1.42	1.35
3	A	340	NAD	C4N-C3N	5.55	1.48	1.39
3	A	340	NAD	C2N-C3N	4.80	1.46	1.39
4	A	341	UDP	C4-N3	4.16	1.40	1.33
4	A	341	UDP	PB-O3B	2.92	1.66	1.54
4	A	341	UDP	C6-C5	-2.49	1.32	1.38
3	A	340	NAD	C7N-N7N	2.34	1.37	1.33
4	A	341	UDP	C3'-C4'	-2.27	1.47	1.53
3	A	340	NAD	O4D-C1D	-2.18	1.38	1.41
3	A	340	NAD	C6N-C5N	-2.15	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	340	NAD	C6N-N1N	2.03	1.40	1.35

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	340	NAD	C5N-C4N-C3N	-6.16	113.05	120.34
3	A	340	NAD	C3N-C7N-N7N	5.91	124.85	117.75
3	A	340	NAD	C6N-N1N-C2N	-4.70	117.68	121.97
3	A	340	NAD	O7N-C7N-C3N	-4.00	114.84	119.63
3	A	340	NAD	C5A-C6A-N6A	3.63	125.88	120.35
4	A	341	UDP	C5-C4-N3	-3.51	115.59	123.31
4	A	341	UDP	O4'-C1'-C2'	-2.75	102.90	106.93
3	A	340	NAD	C4A-C5A-N7A	2.53	112.04	109.40
3	A	340	NAD	C5N-C6N-N1N	2.45	123.91	120.40
3	A	340	NAD	C3N-C2N-N1N	2.03	122.41	120.43
4	A	341	UDP	O2'-C2'-C1'	-2.01	103.42	110.85

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	340	NAD	C5D-O5D-PN-O2N
3	A	340	NAD	O4D-C1D-N1N-C2N
4	A	341	UDP	C2'-C1'-N1-C6
4	A	341	UDP	PB-O3A-PA-O5'
3	A	340	NAD	C5D-O5D-PN-O3
3	A	340	NAD	PA-O3-PN-O2N
6	A	411	PEG	O2-C3-C4-O4
3	A	340	NAD	C5B-O5B-PA-O3
3	A	340	NAD	O4B-C4B-C5B-O5B
3	A	340	NAD	C5D-O5D-PN-O1N

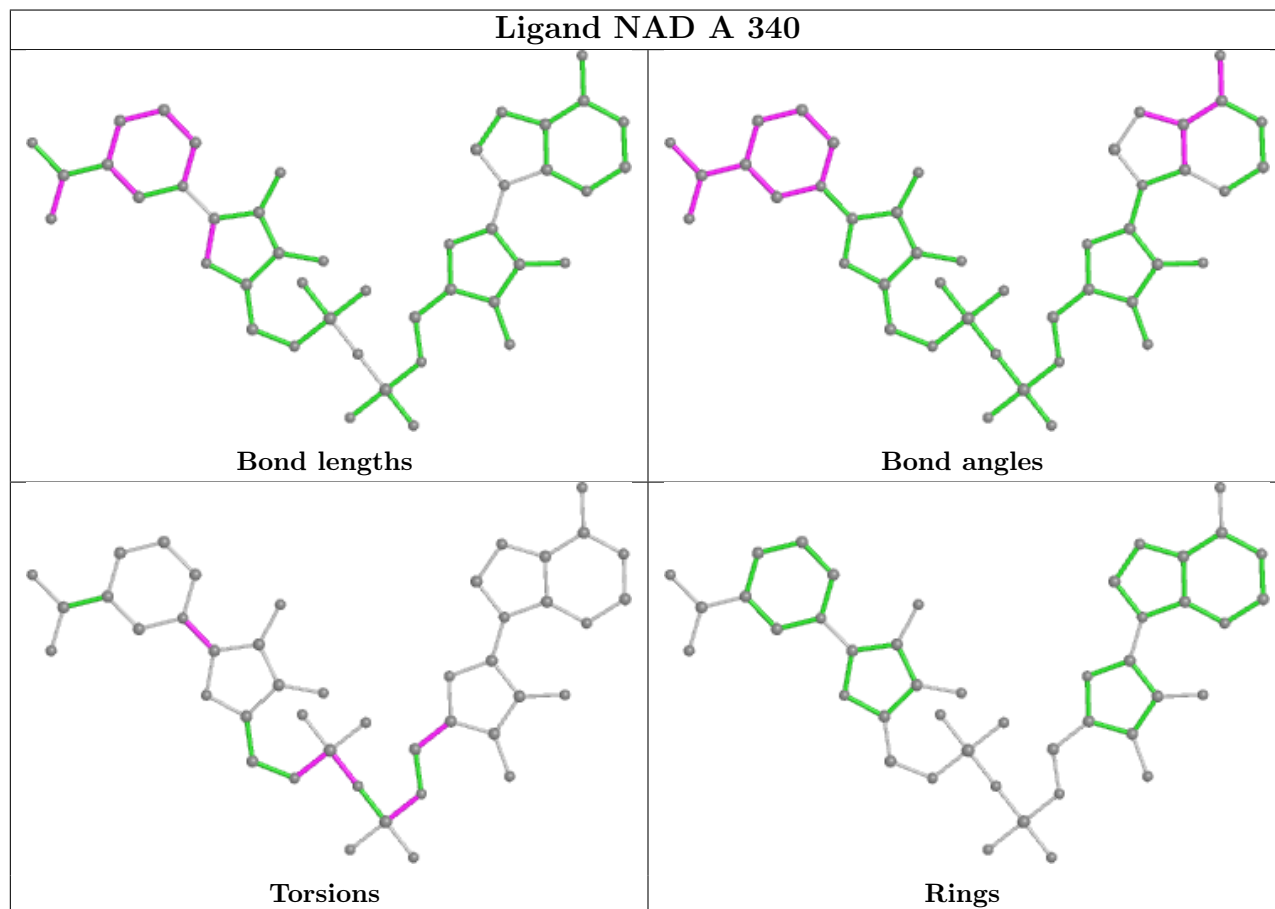
There are no ring outliers.

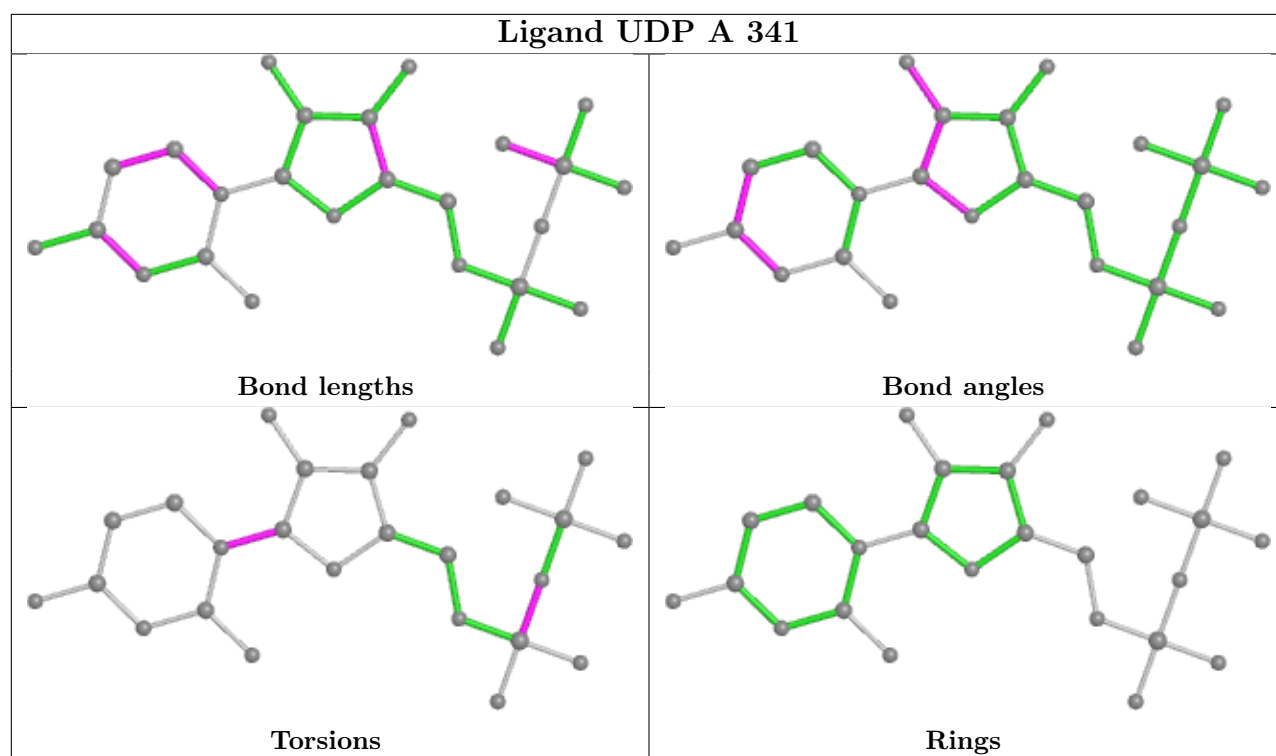
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	411	PEG	6	0
4	A	341	UDP	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

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.