



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:39 PM UTC

PDB ID : 3PJG / pdb_00003pjpg
Title : Crystal structure of UDP-glucose dehydrogenase from *Klebsiella pneumoniae* complexed with product UDP-glucuronic acid
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Deposited on : 2010-11-10
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

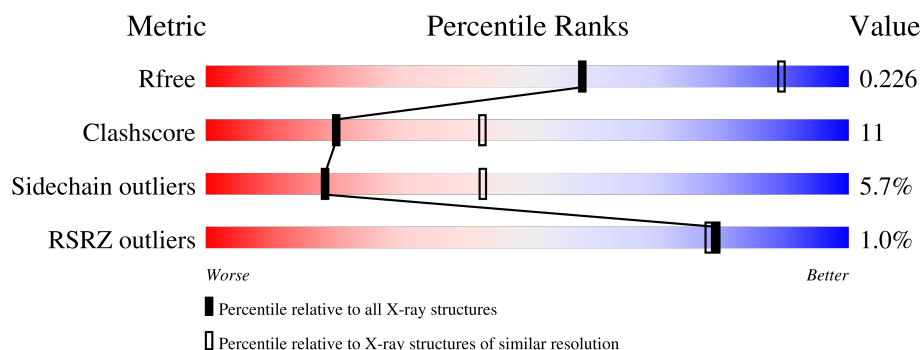
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	424	64% 24% • 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3322 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-glucose 6-dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	0	0
			3076	1950	527	590	9			

There are 36 discrepancies between the modelled and reference sequences:

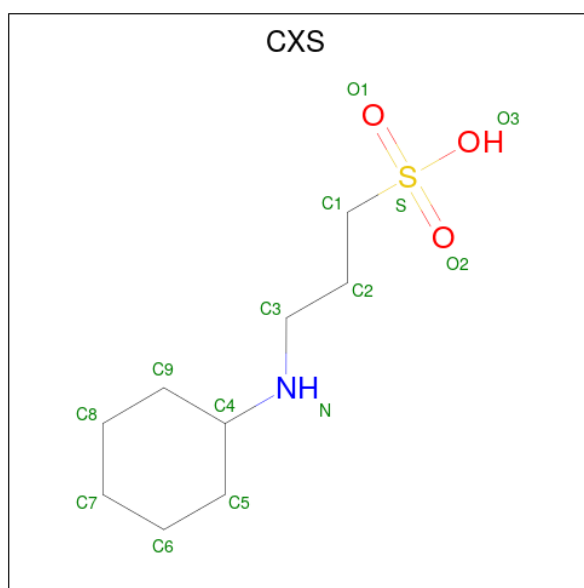
Chain	Residue	Modelled	Actual	Comment	Reference
A	964	MET	-	expression tag	UNP C4XAX5
A	965	GLY	-	expression tag	UNP C4XAX5
A	966	SER	-	expression tag	UNP C4XAX5
A	967	SER	-	expression tag	UNP C4XAX5
A	968	HIS	-	expression tag	UNP C4XAX5
A	969	HIS	-	expression tag	UNP C4XAX5
A	970	HIS	-	expression tag	UNP C4XAX5
A	971	HIS	-	expression tag	UNP C4XAX5
A	972	HIS	-	expression tag	UNP C4XAX5
A	973	HIS	-	expression tag	UNP C4XAX5
A	974	SER	-	expression tag	UNP C4XAX5
A	975	SER	-	expression tag	UNP C4XAX5
A	976	GLY	-	expression tag	UNP C4XAX5
A	977	LEU	-	expression tag	UNP C4XAX5
A	978	VAL	-	expression tag	UNP C4XAX5
A	979	PRO	-	expression tag	UNP C4XAX5
A	980	ARG	-	expression tag	UNP C4XAX5
A	981	GLY	-	expression tag	UNP C4XAX5
A	982	SER	-	expression tag	UNP C4XAX5
A	983	HIS	-	expression tag	UNP C4XAX5
A	984	MET	-	expression tag	UNP C4XAX5
A	985	ALA	-	expression tag	UNP C4XAX5
A	986	SER	-	expression tag	UNP C4XAX5
A	987	MET	-	expression tag	UNP C4XAX5
A	988	THR	-	expression tag	UNP C4XAX5
A	989	GLY	-	expression tag	UNP C4XAX5
A	990	GLY	-	expression tag	UNP C4XAX5

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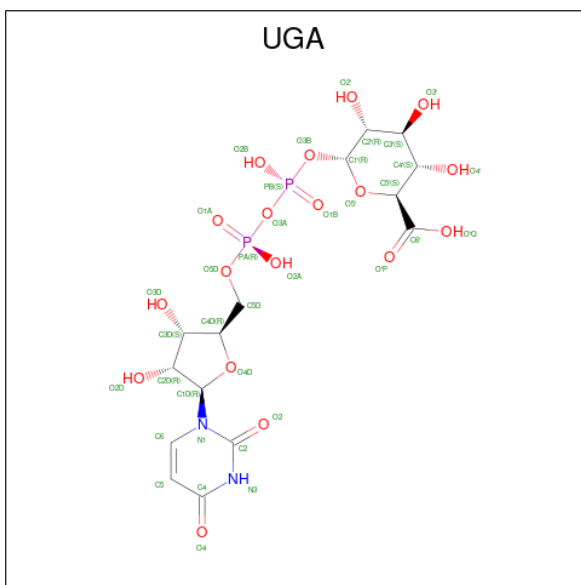
Chain	Residue	Modelled	Actual	Comment	Reference
A	991	GLN	-	expression tag	UNP C4XAX5
A	992	GLN	-	expression tag	UNP C4XAX5
A	993	MET	-	expression tag	UNP C4XAX5
A	994	GLY	-	expression tag	UNP C4XAX5
A	995	ARG	-	expression tag	UNP C4XAX5
A	996	GLY	-	expression tag	UNP C4XAX5
A	997	SER	-	expression tag	UNP C4XAX5
A	998	GLU	-	expression tag	UNP C4XAX5
A	999	PHE	-	expression tag	UNP C4XAX5

- Molecule 2 is 3-CYCLOHEXYL-1-PROPYLSULFONIC ACID (CCD ID: CXS) (formula: $C_9H_{19}NO_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			14	9	1	3	1		

- Molecule 3 is URIDINE-5'-DIPHOSPHATE-GLUCURONIC ACID (CCD ID: UGA) (formula: $C_{15}H_{22}N_2O_{18}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 37	C 15	N 2	O 18	P 2	0	0
3	A	1	Total 37	C 15	N 2	O 18	P 2	0	0

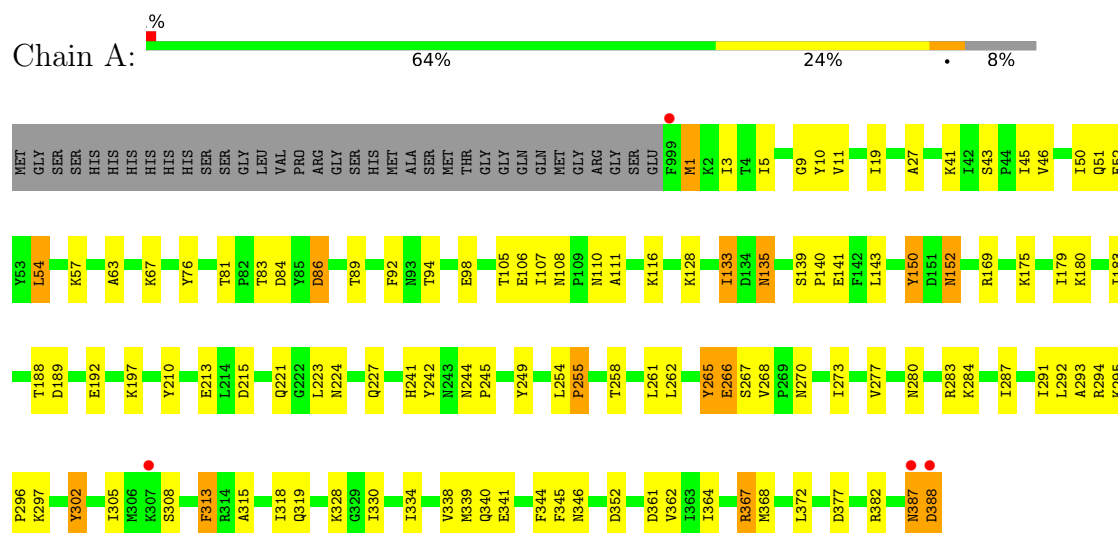
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	158	Total O 158 158	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: UDP-glucose 6-dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, α , β , γ	133.40Å 133.40Å 187.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.70 30.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.2 (30.00-2.70) 96.1 (30.00-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.68 (at 2.72Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.185 , 0.226 0.186 , 0.226	Depositor DCC
R_{free} test set	1286 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	44.4	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3322	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 3.53% 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: UGA, CXS

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	1.13	4/3129 (0.1%)	1.34	26/4236 (0.6%)

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	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	258	THR	CA-CB	5.46	1.62	1.53
1	A	1	MET	SD-CE	5.33	1.92	1.79
1	A	111	ALA	CA-CB	-5.09	1.45	1.53
1	A	188	THR	CA-CB	5.02	1.62	1.53

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	267	SER	N-CA-C	-10.65	100.34	113.97
1	A	270	ASN	N-CA-C	7.98	120.69	111.11
1	A	313	PHE	N-CA-C	-7.08	104.63	113.55
1	A	1	MET	N-CA-C	6.80	120.75	109.46
1	A	179	ILE	N-CA-C	-6.78	105.14	111.45
1	A	268	VAL	N-CA-C	6.67	115.24	107.84
1	A	265	TYR	CA-C-N	-6.33	116.92	126.86
1	A	265	TYR	C-N-CA	-6.33	116.92	126.86
1	A	315	ALA	CA-C-N	-6.10	114.51	123.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	ALA	C-N-CA	-6.10	114.51	123.05
1	A	9	GLY	N-CA-C	-5.74	103.80	112.41
1	A	265	TYR	N-CA-C	-5.57	102.78	110.35
1	A	255	PRO	N-CA-C	-5.38	102.66	111.15
1	A	5	ILE	CB-CA-C	-5.28	103.74	110.98
1	A	330	ILE	CA-C-N	-5.28	114.48	119.76
1	A	330	ILE	C-N-CA	-5.28	114.48	119.76
1	A	330	ILE	CB-CA-C	-5.28	106.03	110.94
1	A	294	ARG	N-CA-C	-5.26	106.88	113.15
1	A	297	LYS	N-CA-C	-5.15	106.68	113.12
1	A	86	ASP	CA-C-N	-5.14	114.41	120.12
1	A	86	ASP	C-N-CA	-5.14	114.41	120.12
1	A	81	THR	CA-C-N	5.13	125.37	119.83
1	A	81	THR	C-N-CA	5.13	125.37	119.83
1	A	107	ILE	N-CA-C	5.09	118.27	111.44
1	A	352	ASP	N-CA-C	5.09	117.05	108.96
1	A	128	LYS	N-CA-C	-5.02	105.94	111.71

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	TYR	Sidechain
1	A	302	TYR	Sidechain

5.2 Too-close contacts [i](#)

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	3076	0	3088	71	0
2	A	14	0	19	4	0
3	A	74	0	39	1	0
4	A	158	0	0	4	0
All	All	3322	0	3146	71	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 11.

All (71) 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:1:MET:HE1	1:A:169:ARG:HD2	1.48	0.95
1:A:135:ASN:H	1:A:135:ASN:HD22	1.21	0.85
1:A:319:GLN:HE21	3:A:902:UGA:H61	1.40	0.84
1:A:338:VAL:HG13	2:A:900:CXS:H72	1.61	0.81
1:A:135:ASN:H	1:A:135:ASN:ND2	1.84	0.75
1:A:265:TYR:O	1:A:266:GLU:CB	2.38	0.72
1:A:135:ASN:HD22	1:A:135:ASN:N	1.78	0.70
1:A:43:SER:HB3	1:A:51:GLN:HG2	1.76	0.68
1:A:265:TYR:O	1:A:266:GLU:HB3	1.93	0.67
1:A:141:GLU:OE2	1:A:143:LEU:HD23	1.98	0.63
1:A:339:MET:HE1	1:A:344:PHE:CD1	2.33	0.63
1:A:367:ARG:NH1	1:A:388:ASP:O	2.31	0.63
1:A:10:TYR:HB3	1:A:45:ILE:HD12	1.81	0.62
1:A:245:PRO:O	1:A:367:ARG:NH2	2.35	0.60
1:A:141:GLU:HG3	1:A:143:LEU:HG	1.84	0.59
1:A:296:PRO:HB3	1:A:362:VAL:CG2	2.35	0.56
1:A:296:PRO:HB3	1:A:362:VAL:HG21	1.88	0.54
1:A:313:PHE:HB2	2:A:900:CXS:O3	2.08	0.53
1:A:180:LYS:HD3	1:A:183:ILE:HD12	1.90	0.53
1:A:291:ILE:HD13	1:A:364:ILE:HG21	1.91	0.53
1:A:302:TYR:CD2	1:A:372:LEU:HD11	2.45	0.52
1:A:261:LEU:HD13	1:A:273:ILE:CG2	2.40	0.52
1:A:261:LEU:HD13	1:A:273:ILE:HG21	1.92	0.52
1:A:338:VAL:CG1	2:A:900:CXS:H72	2.37	0.51
1:A:387:ASN:O	1:A:388:ASP:O	2.29	0.50
1:A:368:MET:CE	4:A:1064:HOH:O	2.60	0.50
1:A:116:LYS:HE2	1:A:139:SER:OG	2.11	0.49
1:A:221:GLN:HB3	1:A:223:LEU:HG	1.95	0.48
1:A:108:ASN:C	1:A:110:ASN:H	2.22	0.47
1:A:140:PRO:HB3	1:A:197:LYS:HB2	1.97	0.47
1:A:143:LEU:C	1:A:143:LEU:HD12	2.39	0.47
1:A:345:PHE:O	1:A:346:ASN:HB2	2.14	0.47
1:A:180:LYS:HD3	1:A:183:ILE:CD1	2.45	0.47
1:A:265:TYR:O	1:A:266:GLU:CG	2.64	0.46
1:A:338:VAL:O	2:A:900:CXS:H82	2.16	0.46
1:A:224:ASN:CG	1:A:227:GLN:HG3	2.41	0.45
1:A:86:ASP:OD1	1:A:89:THR:N	2.33	0.45
1:A:340:GLN:HG3	1:A:341:GLU:N	2.30	0.45
1:A:280:ASN:O	1:A:284:LYS:HG3	2.16	0.45
1:A:254:LEU:O	1:A:255:PRO:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:LEU:HD13	1:A:328:LYS:HG3	1.99	0.45
1:A:1:MET:HE1	1:A:169:ARG:CD	2.34	0.43
1:A:344:PHE:O	1:A:345:PHE:C	2.59	0.43
1:A:50:ILE:O	1:A:54:LEU:HB2	2.18	0.43
1:A:283:ARG:O	1:A:287:ILE:HG12	2.18	0.43
1:A:57:LYS:NZ	4:A:1107:HOH:O	2.52	0.43
1:A:215:ASP:CG	1:A:382:ARG:HH21	2.27	0.43
1:A:92:PHE:HD1	1:A:94:THR:HG23	1.84	0.43
1:A:266:GLU:HB2	4:A:1132:HOH:O	2.18	0.43
1:A:133:ILE:H	1:A:133:ILE:HG12	1.74	0.42
1:A:41:LYS:HE2	4:A:1105:HOH:O	2.19	0.42
1:A:210:TYR:CD2	1:A:210:TYR:C	2.97	0.42
1:A:388:ASP:OD2	1:A:388:ASP:N	2.52	0.42
1:A:3:ILE:HG13	1:A:19:ILE:HG21	2.01	0.42
1:A:46:VAL:HA	1:A:51:GLN:OE1	2.20	0.42
1:A:141:GLU:CD	1:A:143:LEU:HD23	2.44	0.42
1:A:293:ALA:C	1:A:295:LYS:H	2.28	0.42
1:A:27:ALA:O	1:A:63:ALA:HA	2.20	0.41
1:A:76:TYR:OH	1:A:169:ARG:HB3	2.20	0.41
1:A:11:VAL:HG13	1:A:141:GLU:HG2	2.01	0.41
1:A:83:THR:O	1:A:84:ASP:HB2	2.20	0.41
1:A:334:ILE:CD1	1:A:344:PHE:HB3	2.51	0.41
1:A:318:ILE:HD11	1:A:364:ILE:HG13	2.02	0.41
1:A:67:LYS:HE2	1:A:67:LYS:HB3	1.95	0.41
1:A:241:HIS:O	1:A:242:TYR:C	2.63	0.41
1:A:150:TYR:C	1:A:150:TYR:CD1	2.98	0.41
1:A:152:ASN:HD22	1:A:152:ASN:HA	1.54	0.41
1:A:305:ILE:HG23	1:A:313:PHE:HE1	1.85	0.41
1:A:189:ASP:HB2	1:A:192:GLU:OE1	2.21	0.40
1:A:244:ASN:HA	1:A:245:PRO:HD3	1.94	0.40
1:A:249:TYR:CD1	1:A:249:TYR:C	2.99	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

There are no protein backbone outliers to report in this entry.

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	335/362 (92%)	316 (94%)	19 (6%)	18	43

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	GLU
1	A	54	LEU
1	A	98	GLU
1	A	105	THR
1	A	106	GLU
1	A	133	ILE
1	A	135	ASN
1	A	152	ASN
1	A	175	LYS
1	A	213	GLU
1	A	262	LEU
1	A	266	GLU
1	A	277	VAL
1	A	308	SER
1	A	361	ASP
1	A	367	ARG
1	A	377	ASP
1	A	387	ASN
1	A	388	ASP

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	90	ASN
1	A	135	ASN
1	A	152	ASN
1	A	319	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

3 ligands 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	CXS	A	900	-	14,14,14	1.34	1 (7%)	18,18,18	1.05	1 (5%)
3	UGA	A	902	-	38,39,39	1.16	4 (10%)	56,60,60	1.52	10 (17%)
3	UGA	A	901	-	38,39,39	1.39	4 (10%)	56,60,60	1.49	9 (16%)

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	CXS	A	900	-	-	6/8/16/16	0/1/1/1
3	UGA	A	902	-	-	2/25/61/61	0/3/3/3
3	UGA	A	901	-	-	5/25/61/61	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	901	UGA	PB-O3A	4.76	1.64	1.59
2	A	900	CXS	C1-S	4.29	1.83	1.77
3	A	901	UGA	PA-O3A	3.47	1.63	1.59
3	A	901	UGA	PB-O3B	2.79	1.67	1.59
3	A	902	UGA	C5'-C6'	2.42	1.58	1.53
3	A	902	UGA	O4D-C1D	2.08	1.46	1.42
3	A	902	UGA	PA-O3A	2.06	1.61	1.59
3	A	902	UGA	O'Q-C6'	2.06	1.37	1.30
3	A	901	UGA	O4D-C1D	2.02	1.46	1.42

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	901	UGA	C4-N3-C2	-5.08	120.31	126.61
3	A	902	UGA	N3-C2-N1	4.24	120.41	114.89
3	A	902	UGA	C4-N3-C2	-4.06	121.57	126.61
3	A	902	UGA	PB-O3B-C1'	-3.91	105.28	121.21
3	A	901	UGA	N3-C2-N1	3.73	119.75	114.89
3	A	902	UGA	C5-C4-N3	3.33	119.46	114.80
3	A	901	UGA	C5-C4-N3	3.04	119.06	114.80
3	A	901	UGA	O4-C4-C5	-2.90	120.17	125.16
3	A	902	UGA	O4-C4-C5	-2.82	120.29	125.16
3	A	901	UGA	O'Q-C6'-C5'	2.62	123.11	113.64
3	A	901	UGA	O3A-PA-O1A	-2.55	103.02	110.70
3	A	902	UGA	O'Q-C6'-O'P	-2.37	118.71	124.08
2	A	900	CXS	C3-N-C4	-2.32	109.72	114.18
3	A	902	UGA	C3D-C2D-C1D	2.25	105.72	101.46
3	A	902	UGA	O3A-PA-O1A	2.18	117.27	110.70
3	A	901	UGA	O'Q-C6'-O'P	-2.12	119.27	124.08
3	A	901	UGA	O2A-PA-O3A	2.10	112.94	107.27
3	A	902	UGA	O3'-C3'-C2'	-2.02	105.62	110.38
3	A	902	UGA	O2B-PB-O3A	2.01	112.72	107.27
3	A	901	UGA	O2-C2-N1	-2.01	120.18	122.80

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	900	CXS	C2-C1-S-O3
2	A	900	CXS	C1-C2-C3-N
3	A	901	UGA	C4'-C5'-C6'-O'P
3	A	901	UGA	C4'-C5'-C6'-O'Q

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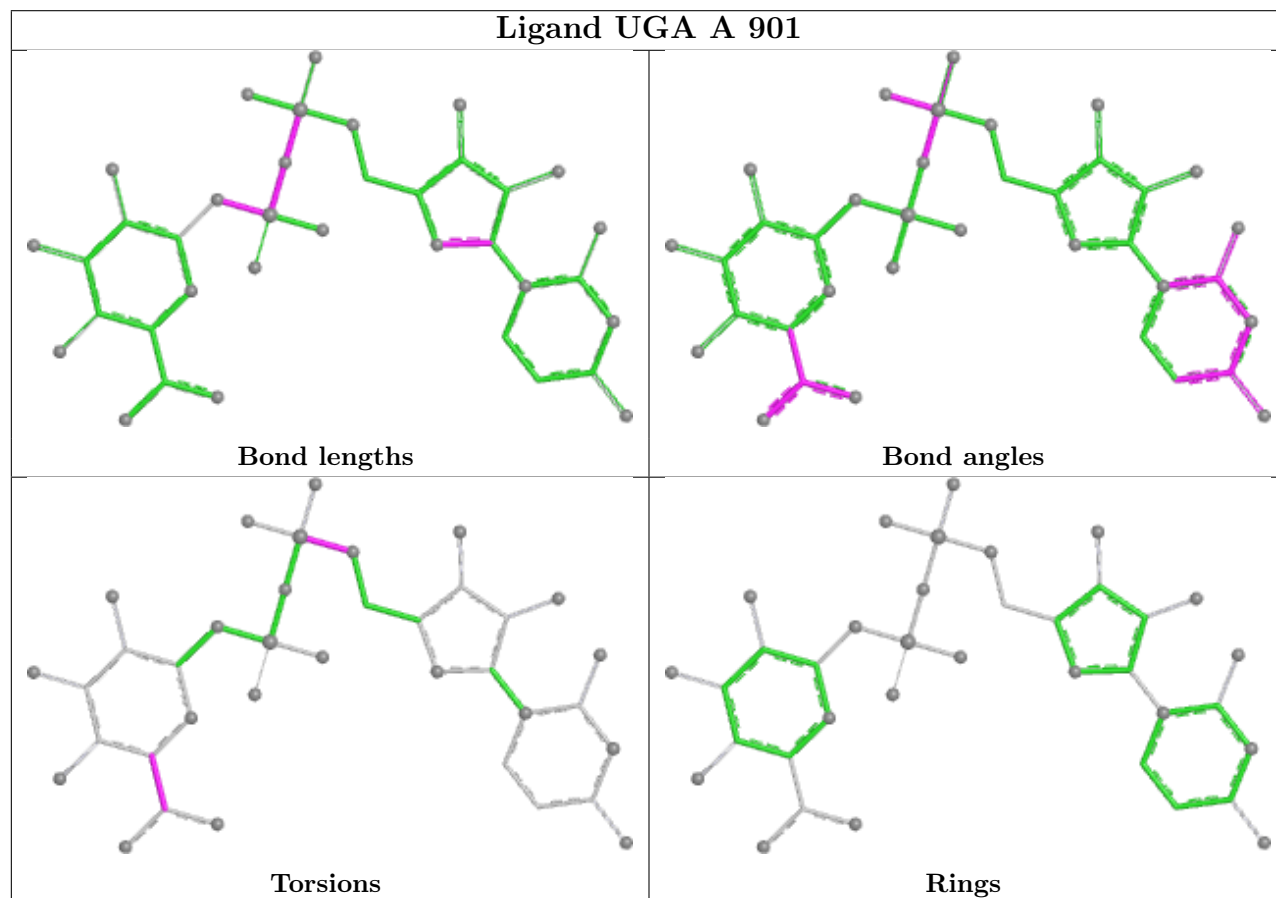
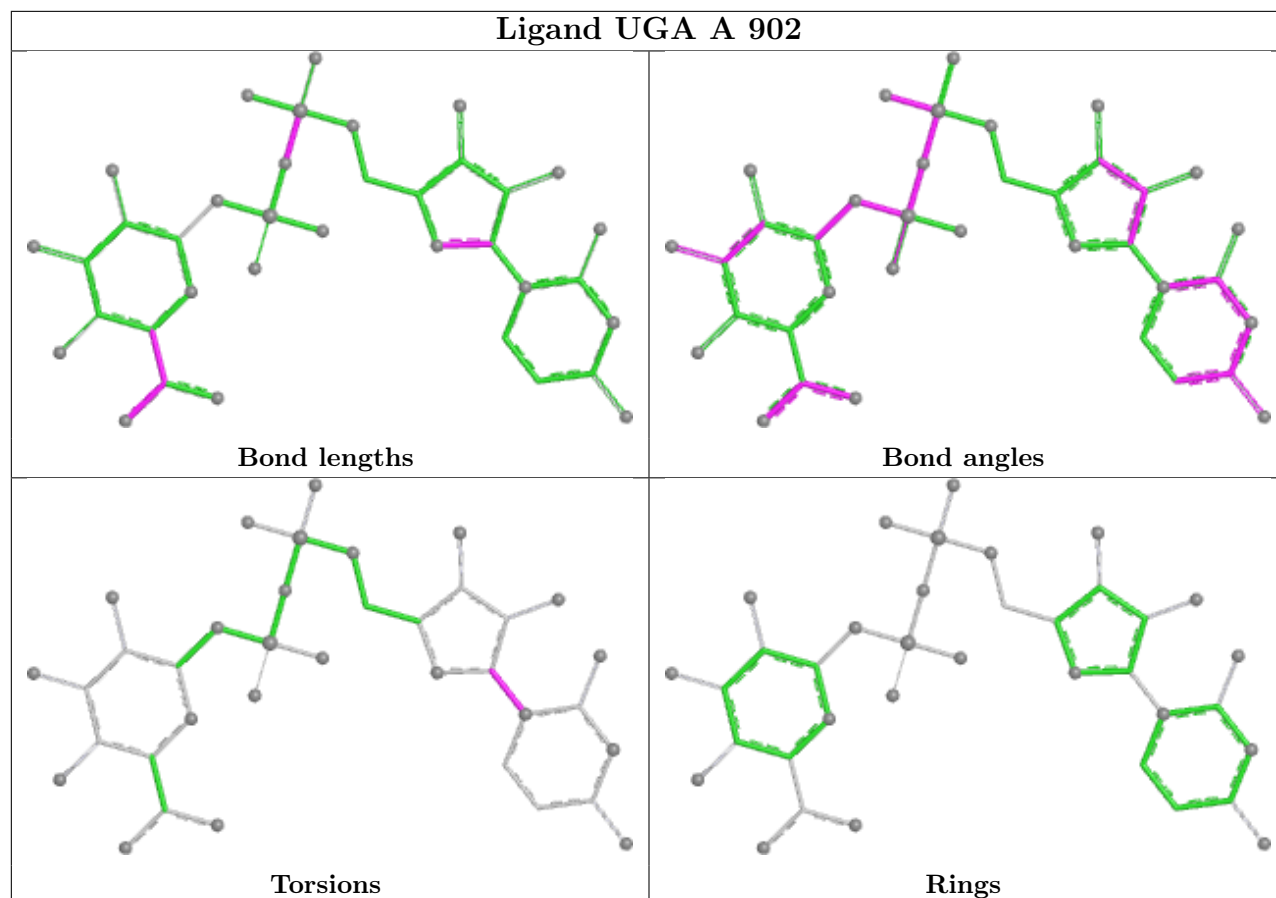
Mol	Chain	Res	Type	Atoms
3	A	901	UGA	C5D-O5D-PA-O3A
3	A	901	UGA	C5D-O5D-PA-O2A
2	A	900	CXS	S-C1-C2-C3
2	A	900	CXS	C2-C1-S-O1
2	A	900	CXS	C2-C1-S-O2
2	A	900	CXS	C2-C3-N-C4
3	A	901	UGA	C5D-O5D-PA-O1A
3	A	902	UGA	C2D-C1D-N1-C6
3	A	902	UGA	O4D-C1D-N1-C6

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	CXS	4	0
3	A	902	UGA	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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	389/424 (91%)	-0.46	4 (1%) 79 78	23, 39, 58, 87	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	999	PHE	5.1
1	A	307	LYS	4.1
1	A	388	ASP	2.8
1	A	387	ASN	2.5

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](#)

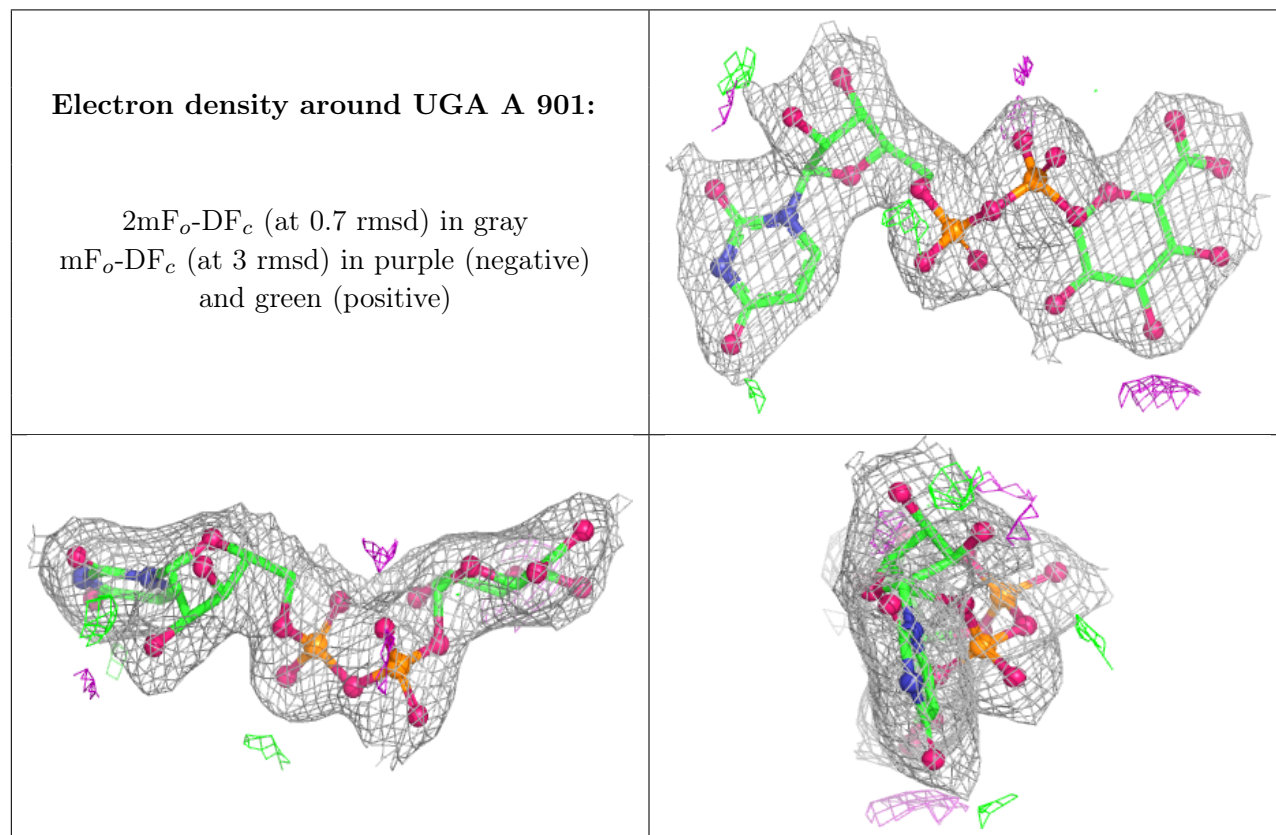
There are no oligosaccharides in this entry.

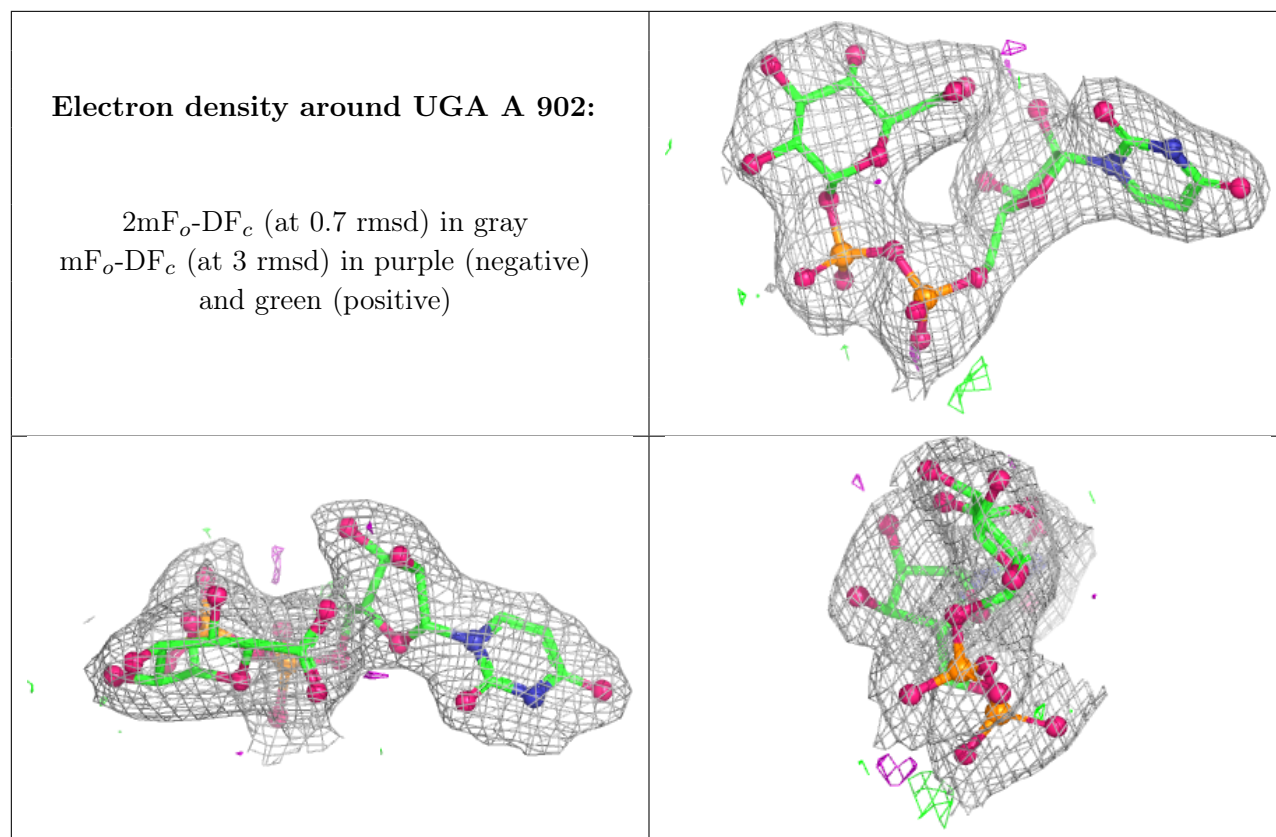
6.4 Ligands [i](#)

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
2	CXS	A	900	14/14	0.80	0.24	73,78,87,87	0
3	UGA	A	901	37/37	0.98	0.05	26,34,38,38	0
3	UGA	A	902	37/37	0.98	0.05	28,33,49,51	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.