



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 29, 2025 – 11:26 AM EDT

PDB ID : 2ACV / pdb\_00002acv  
Title : Crystal Structure of Medicago truncatula UGT71G1  
Authors : Shao, H.; He, X.; Achnine, L.; Blount, J.W.; Dixon, R.A.; Wang, X.  
Deposited on : 2005-07-19  
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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

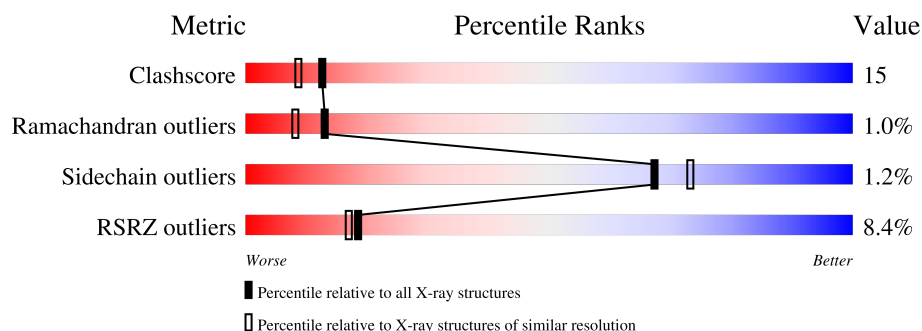
# 1 Overall quality at a glance

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))
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (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  $\geq 3$ , 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  $\leq 5\%$ . 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	463	<div> <div>6%</div> <div> <div></div> <div>71%</div> <div>26%</div> <div>.</div> </div> </div>
1	B	463	<div> <div>11%</div> <div> <div></div> <div>69%</div> <div>27%</div> <div>..</div> </div> </div>

## 2 Entry composition [i](#)

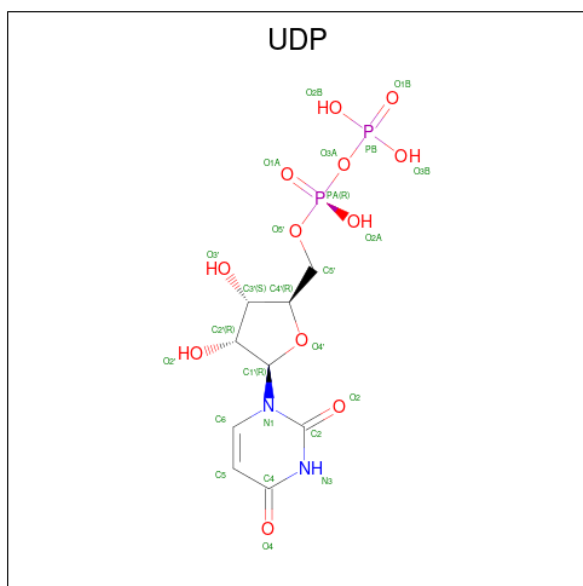
There are 3 unique types of molecules in this entry. The entry contains 7982 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 triterpene UDP-glucosyl transferase UGT71G1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	461	Total	C	N	O	S	0	0	0
			3621	2346	586	672	17			
1	B	456	Total	C	N	O	S	0	0	0
			3583	2324	580	663	16			

- Molecule 2 is URIDINE-5'-DIPHOSPHATE (CCD ID: UDP) (formula:  $C_9H_{14}N_2O_{12}P_2$ ).

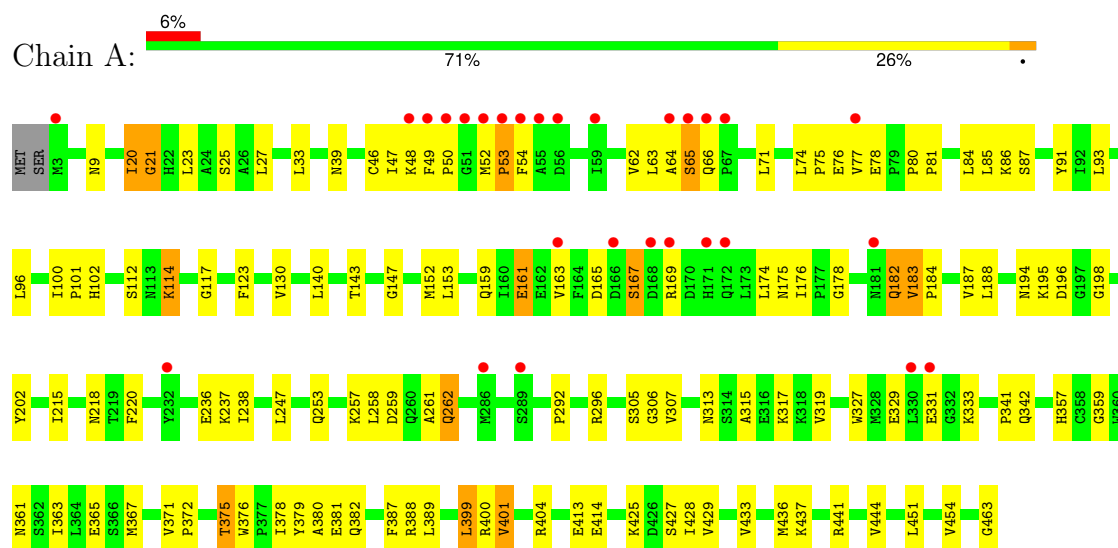


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	396	Total 396	O 396	0	0
3	B	332	Total 332	O 332	0	0

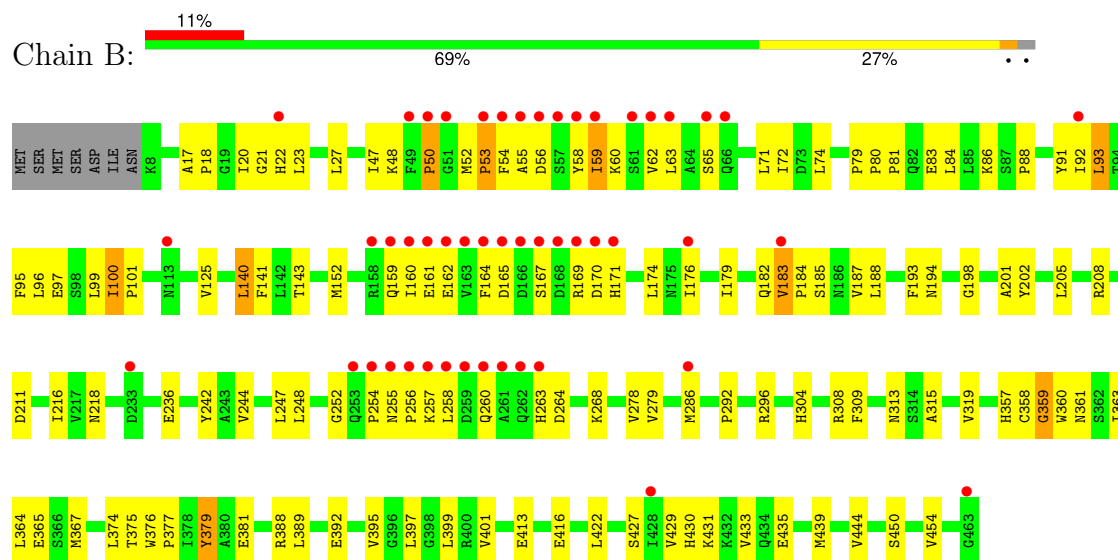
### 3 Residue-property plots [i](#)

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 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: triterpene UDP-glucosyl transferase UGT71G1



- Molecule 1: triterpene UDP-glucosyl transferase UGT71G1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.71Å 90.59Å 101.79Å 90.00° 102.57° 90.00°	Depositor
Resolution (Å)	66.94 – 2.00 66.94 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.8 (66.94-2.00) 94.6 (66.94-2.00)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.13 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.187 , 0.229 0.190 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.3	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 49.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7982	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: UDP

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	0.38	0/3708	0.96	15/5025 (0.3%)
1	B	0.39	0/3670	0.94	13/4974 (0.3%)
All	All	0.39	0/7378	0.95	28/9999 (0.3%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	399	LEU	N-CA-C	-11.85	96.92	112.68
1	A	399	LEU	N-CA-C	-10.38	98.87	112.68
1	A	359	GLY	N-CA-C	-9.22	100.25	112.14
1	B	359	GLY	N-CA-C	-8.84	100.73	112.14
1	B	444	VAL	N-CA-C	7.75	119.83	111.77
1	B	183	VAL	N-CA-C	7.67	115.51	107.76
1	A	444	VAL	N-CA-C	7.62	119.46	112.29
1	A	342	GLN	N-CA-C	7.38	119.96	111.11
1	B	278	VAL	N-CA-C	7.24	118.72	108.36
1	B	375	THR	N-CA-C	7.16	120.71	109.96
1	A	375	THR	N-CA-C	6.93	120.36	109.96
1	B	401	VAL	N-CA-C	-6.82	106.84	113.53
1	B	182	GLN	N-CA-C	-6.33	100.92	110.28
1	A	182	GLN	N-CA-C	-6.19	100.68	109.96
1	B	374	LEU	N-CA-C	-6.06	98.64	108.52
1	A	401	VAL	N-CA-C	-5.91	107.50	113.47
1	A	21	GLY	N-CA-C	-5.90	106.89	113.79
1	A	341	PRO	N-CA-C	-5.89	100.22	112.36
1	A	20	ILE	N-CA-C	-5.72	102.19	109.80
1	B	360	TRP	N-CA-C	5.68	117.47	111.28
1	A	86	LYS	N-CA-C	-5.66	106.08	112.87
1	A	183	VAL	N-CA-C	5.64	113.45	107.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	178	GLY	N-CA-C	-5.58	107.61	113.58
1	B	379	TYR	N-CA-C	5.46	115.49	108.34
1	A	380	ALA	CB-CA-C	-5.34	110.40	116.54
1	A	117	GLY	N-CA-C	5.23	118.05	111.09
1	B	100	ILE	CB-CA-C	-5.09	108.86	113.70
1	B	309	PHE	N-CA-C	5.07	116.77	108.76

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	3621	0	3634	103	0
1	B	3583	0	3599	116	0
2	A	25	0	11	0	0
2	B	25	0	11	0	0
3	A	396	0	0	8	0
3	B	332	0	0	4	0
All	All	7982	0	7255	217	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 15.

All (217) 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:B:218:ASN:HD21	1:B:247:LEU:H	1.11	0.96
1:B:435:GLU:HG2	1:B:439:MET:HE2	1.50	0.92
1:B:194:ASN:HD22	1:B:198:GLY:H	1.18	0.91
1:B:363:ILE:HD12	1:B:389:LEU:HD11	1.53	0.90
1:B:47:ILE:HD11	1:B:74:LEU:HD22	1.57	0.87
1:B:363:ILE:HG22	1:B:367:MET:HE2	1.55	0.86
1:B:23:LEU:O	1:B:27:LEU:HD23	1.75	0.86
1:B:140:LEU:O	1:B:216:ILE:HG22	1.77	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:ASP:HA	1:B:59:ILE:HD13	1.56	0.84
1:A:363:ILE:HD12	1:A:389:LEU:HD11	1.61	0.81
1:B:176:ILE:CD1	1:B:179:ILE:HD12	2.12	0.80
1:B:260:GLN:HB3	1:B:263:HIS:HB3	1.62	0.79
1:B:141:PHE:HA	1:B:216:ILE:HG23	1.63	0.78
1:B:176:ILE:HD11	1:B:179:ILE:HD12	1.66	0.78
1:A:413:GLU:OE2	1:B:296:ARG:NH2	2.17	0.78
1:B:313:ASN:HD22	1:B:315:ALA:H	1.32	0.77
1:B:159:GLN:HG2	1:B:160:ILE:H	1.50	0.77
1:A:218:ASN:HD21	1:A:247:LEU:H	1.30	0.76
1:B:141:PHE:HA	1:B:216:ILE:CG2	2.16	0.76
1:A:80:PRO:HG2	1:A:91:TYR:CE1	2.22	0.74
1:B:264:ASP:O	1:B:268:LYS:HG2	1.88	0.72
1:A:152:MET:HE2	1:A:152:MET:HA	1.70	0.72
1:B:20:ILE:HD12	1:B:21:GLY:N	2.03	0.72
1:B:429:VAL:O	1:B:433:VAL:HG23	1.90	0.71
1:B:364:LEU:HA	1:B:367:MET:HE3	1.73	0.71
1:A:400:ARG:HH12	1:A:414:GLU:CD	1.98	0.70
1:B:169:ARG:HD2	1:B:169:ARG:O	1.92	0.70
1:B:58:TYR:HA	1:B:255:ASN:HD21	1.60	0.66
1:A:20:ILE:HB	1:A:54:PHE:CE2	2.29	0.66
1:A:112:SER:OG	1:A:114:LYS:HG2	1.96	0.65
1:A:259:ASP:OD1	1:A:262:GLN:HB2	1.96	0.65
1:A:425:LYS:O	1:A:425:LYS:HD3	1.97	0.65
1:B:216:ILE:HD11	1:B:244:VAL:CG2	2.26	0.65
1:B:100:ILE:HB	1:B:101:PRO:HD3	1.79	0.64
1:B:80:PRO:HG2	1:B:91:TYR:CE1	2.33	0.64
1:A:159:GLN:HB3	1:A:161:GLU:OE2	1.97	0.64
1:A:49:PHE:CD1	1:A:50:PRO:HD2	2.32	0.64
1:A:296:ARG:NH2	1:B:413:GLU:OE2	2.25	0.64
1:A:262:GLN:C	1:A:262:GLN:HE21	2.06	0.64
1:B:47:ILE:CD1	1:B:74:LEU:HD22	2.26	0.64
1:B:364:LEU:HD23	1:B:367:MET:CE	2.27	0.63
1:A:47:ILE:HG12	1:A:74:LEU:HD12	1.80	0.63
1:A:75:PRO:HB2	1:A:102:HIS:CD2	2.35	0.62
1:A:331:GLU:HB2	3:A:1148:HOH:O	1.98	0.62
1:B:279:VAL:HG12	1:B:308:ARG:O	1.98	0.62
1:B:431:LYS:HD2	1:B:431:LYS:N	2.14	0.62
1:A:378:ILE:H	1:A:382:GLN:HE21	1.48	0.61
1:B:194:ASN:ND2	1:B:198:GLY:H	1.95	0.61
1:B:23:LEU:HD21	1:B:59:ILE:HG13	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:LYS:C	1:B:258:LEU:HD22	2.26	0.61
1:A:194:ASN:ND2	1:A:196:ASP:H	1.99	0.61
1:A:153:LEU:HD13	1:A:238:ILE:HD13	1.83	0.60
1:A:367:MET:HE3	1:A:436:MET:HG3	1.83	0.60
1:A:363:ILE:CD1	1:A:389:LEU:HD11	2.31	0.60
1:B:216:ILE:HD11	1:B:244:VAL:CG1	2.31	0.60
1:B:427:SER:OG	1:B:429:VAL:HG22	2.01	0.60
1:B:83:GLU:O	1:B:86:LYS:HG3	2.01	0.60
1:A:194:ASN:HB3	1:A:198:GLY:HA3	1.84	0.59
1:B:431:LYS:HD2	1:B:431:LYS:H	1.67	0.59
1:B:159:GLN:NE2	1:B:161:GLU:HG2	2.16	0.59
1:A:400:ARG:NH1	1:A:414:GLU:OE1	2.36	0.58
1:B:176:ILE:HD13	1:B:183:VAL:HG11	1.84	0.58
1:B:93:LEU:O	1:B:97:GLU:HG3	2.04	0.58
1:A:220:PHE:CZ	1:A:367:MET:HE1	2.39	0.58
1:A:194:ASN:ND2	1:A:198:GLY:H	2.02	0.58
1:A:428:ILE:HG23	3:A:1265:HOH:O	2.03	0.58
1:A:75:PRO:HB2	1:A:102:HIS:HD2	1.69	0.57
1:A:48:LYS:HG2	1:A:76:GLU:OE2	2.05	0.57
1:B:364:LEU:HD23	1:B:367:MET:HE1	1.86	0.57
1:A:367:MET:HE3	1:A:436:MET:CG	2.35	0.57
1:B:255:ASN:HA	1:B:257:LYS:N	2.20	0.57
1:B:174:LEU:HB2	1:B:183:VAL:CG1	2.36	0.56
1:A:85:LEU:C	1:A:87:SER:H	2.13	0.56
1:B:159:GLN:HG2	1:B:160:ILE:N	2.21	0.56
1:A:451:LEU:O	1:A:454:VAL:HG12	2.05	0.56
1:A:176:ILE:CD1	1:A:183:VAL:HG11	2.35	0.56
1:B:361:ASN:O	1:B:365:GLU:HG3	2.06	0.55
1:A:21:GLY:HA2	1:A:361:ASN:ND2	2.22	0.55
1:B:218:ASN:HD21	1:B:247:LEU:N	1.93	0.54
1:B:59:ILE:N	1:B:59:ILE:HD12	2.21	0.54
1:A:379:TYR:H	1:A:382:GLN:NE2	2.05	0.54
1:A:85:LEU:C	1:A:87:SER:N	2.63	0.54
1:B:88:PRO:O	1:B:92:ILE:HG12	2.08	0.53
1:A:81:PRO:HG2	1:A:84:LEU:HG	1.90	0.53
1:B:388:ARG:NH1	1:B:392:GLU:OE1	2.42	0.53
1:A:23:LEU:O	1:A:27:LEU:HD23	2.07	0.53
1:A:313:ASN:HD22	1:A:315:ALA:H	1.55	0.53
1:B:363:ILE:CD1	1:B:389:LEU:HD11	2.31	0.53
1:A:236:GLU:CD	1:A:236:GLU:H	2.18	0.52
1:B:258:LEU:HD22	1:B:258:LEU:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:LEU:HB2	1:A:183:VAL:HG13	1.91	0.52
1:A:387:PHE:HA	1:A:401:VAL:HG21	1.92	0.52
1:A:153:LEU:HD13	1:A:238:ILE:CD1	2.40	0.51
1:A:262:GLN:HE21	1:A:262:GLN:CA	2.23	0.51
1:A:372:PRO:HG3	3:A:1071:HOH:O	2.10	0.51
1:B:71:LEU:HD13	1:B:72:ILE:N	2.25	0.51
1:B:357:HIS:HA	1:B:376:TRP:O	2.11	0.51
1:A:23:LEU:HD22	1:A:27:LEU:HD21	1.92	0.51
1:A:48:LYS:HE2	1:A:49:PHE:O	2.10	0.51
1:A:100:ILE:HB	1:A:101:PRO:HD3	1.93	0.51
1:B:255:ASN:HA	1:B:256:PRO:C	2.35	0.51
1:B:218:ASN:ND2	1:B:247:LEU:H	1.93	0.51
1:B:174:LEU:HB2	1:B:183:VAL:HG13	1.93	0.50
1:B:248:LEU:HD22	1:B:365:GLU:HG2	1.93	0.50
1:A:93:LEU:C	1:A:93:LEU:HD23	2.36	0.50
1:A:184:PRO:O	1:A:187:VAL:HG22	2.12	0.50
1:A:258:LEU:HD12	1:A:262:GLN:HB3	1.94	0.49
1:A:313:ASN:ND2	1:A:315:ALA:H	2.09	0.49
1:A:49:PHE:CG	1:A:50:PRO:HD2	2.48	0.49
1:A:257:LYS:HE3	3:A:1046:HOH:O	2.12	0.49
1:B:152:MET:HE1	1:B:202:TYR:CD1	2.48	0.49
1:B:304:HIS:HD2	1:B:416:GLU:OE1	1.95	0.49
1:B:52:MET:HE2	1:B:54:PHE:CE1	2.48	0.49
1:B:93:LEU:HD12	1:B:201:ALA:HA	1.94	0.48
1:A:400:ARG:HG2	1:A:400:ARG:HH11	1.77	0.48
1:A:27:LEU:HD12	1:A:63:LEU:HD21	1.94	0.48
1:B:208:ARG:NH1	1:B:211:ASP:OD2	2.46	0.48
1:B:97:GLU:O	1:B:100:ILE:HG12	2.13	0.48
1:B:357:HIS:HD2	3:B:907:HOH:O	1.95	0.48
1:B:167:SER:C	1:B:169:ARG:H	2.21	0.48
1:A:77:VAL:HG12	1:A:78:GLU:N	2.28	0.48
1:B:50:PRO:HB3	1:B:79:PRO:HB3	1.94	0.48
1:B:152:MET:HA	1:B:152:MET:HE2	1.96	0.47
1:B:184:PRO:O	1:B:187:VAL:HG22	2.14	0.47
1:A:152:MET:HE1	1:A:202:TYR:CD2	2.49	0.47
1:A:237:LYS:O	1:A:237:LYS:HG2	2.14	0.47
1:B:143:THR:HB	3:B:1132:HOH:O	2.15	0.47
1:B:169:ARG:HG2	1:B:193:PHE:CZ	2.50	0.47
1:B:20:ILE:HD12	1:B:20:ILE:C	2.40	0.46
1:B:56:ASP:HA	1:B:59:ILE:CD1	2.38	0.46
1:A:259:ASP:OD2	1:A:261:ALA:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:170:ASP:HB3	1:B:171:HIS:CE1	2.51	0.46
1:B:260:GLN:HB3	1:B:263:HIS:CB	2.40	0.46
1:A:375:THR:O	1:A:399:LEU:HB3	2.16	0.46
1:A:64:ALA:O	1:A:65:SER:HB3	2.16	0.46
1:A:463:GLY:HA3	3:A:1262:HOH:O	2.15	0.46
1:B:216:ILE:HD11	1:B:244:VAL:HG21	1.97	0.46
1:A:357:HIS:HA	1:A:376:TRP:O	2.16	0.46
1:A:307:VAL:HG12	3:A:1229:HOH:O	2.15	0.46
1:B:59:ILE:HD12	1:B:59:ILE:H	1.81	0.46
1:A:451:LEU:HA	1:A:454:VAL:HG12	1.98	0.45
1:A:220:PHE:HZ	1:A:367:MET:HE1	1.80	0.45
1:B:236:GLU:HG2	3:B:1102:HOH:O	2.15	0.45
1:B:194:ASN:HB3	1:B:198:GLY:HA3	1.97	0.45
1:A:194:ASN:HD22	1:A:198:GLY:H	1.63	0.45
1:B:308:ARG:NE	3:B:994:HOH:O	2.41	0.45
1:A:25:SER:OG	1:A:143:THR:HG22	2.17	0.45
1:A:176:ILE:HD12	1:A:183:VAL:HG11	1.99	0.45
1:A:9:ASN:HB2	3:A:1018:HOH:O	2.17	0.44
1:B:59:ILE:CD1	1:B:59:ILE:H	2.30	0.44
1:B:364:LEU:HA	1:B:367:MET:CE	2.46	0.44
1:A:65:SER:O	1:A:66:GLN:HG2	2.17	0.44
1:B:450:SER:O	1:B:454:VAL:HG23	2.17	0.44
1:A:147:GLY:HA3	1:A:388:ARG:NH1	2.32	0.44
1:A:306:GLY:O	1:A:333:LYS:HE2	2.18	0.44
1:A:429:VAL:O	1:A:433:VAL:HG23	2.17	0.44
1:B:397:LEU:HD12	1:B:422:LEU:HA	2.00	0.44
1:B:52:MET:HA	1:B:53:PRO:HD3	1.84	0.44
1:B:80:PRO:HB2	1:B:84:LEU:HD12	1.99	0.44
1:B:216:ILE:HD11	1:B:244:VAL:HG22	2.00	0.44
1:B:60:LYS:HA	1:B:63:LEU:HB2	2.00	0.44
1:B:176:ILE:HG13	1:B:179:ILE:HB	1.99	0.44
1:B:286:MET:HG2	1:B:379:TYR:OH	2.18	0.44
1:B:216:ILE:HD12	1:B:242:TYR:O	2.18	0.43
1:A:96:LEU:HD12	1:A:123:PHE:HB3	2.00	0.43
1:B:18:PRO:HD3	1:B:96:LEU:HD21	2.00	0.43
1:B:58:TYR:O	1:B:62:VAL:HG22	2.18	0.43
1:B:364:LEU:HD23	1:B:367:MET:HE3	2.00	0.43
1:B:174:LEU:HD11	1:B:188:LEU:HD11	1.99	0.43
1:B:63:LEU:HG	1:B:65:SER:N	2.34	0.43
1:A:292:PRO:HA	1:A:319:VAL:HG11	2.00	0.43
1:A:361:ASN:O	1:A:365:GLU:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:VAL:HG12	1:B:205:LEU:HD22	2.01	0.43
1:B:252:GLY:O	1:B:254:PRO:HD3	2.18	0.43
1:B:50:PRO:HD3	1:B:95:PHE:CE2	2.54	0.43
1:A:46:CYS:SG	1:A:71:LEU:HB2	2.58	0.43
1:A:218:ASN:ND2	1:A:247:LEU:H	2.07	0.43
1:B:174:LEU:CD1	1:B:188:LEU:HD11	2.49	0.43
1:B:357:HIS:O	1:B:377:PRO:HA	2.19	0.43
1:A:114:LYS:NZ	1:A:114:LYS:HB3	2.34	0.42
1:A:174:LEU:CD1	1:A:188:LEU:HD11	2.49	0.42
1:A:52:MET:HA	1:A:53:PRO:HD3	1.75	0.42
1:B:427:SER:HB3	1:B:430:HIS:ND1	2.35	0.42
1:A:236:GLU:CD	1:A:236:GLU:N	2.77	0.42
1:A:327:TRP:NE1	1:A:331:GLU:HG3	2.35	0.42
1:A:175:ASN:OD1	1:A:182:GLN:HG2	2.20	0.42
1:B:359:GLY:O	1:B:363:ILE:HG12	2.19	0.42
1:A:425:LYS:HD3	1:A:425:LYS:C	2.44	0.42
1:A:100:ILE:HG23	1:A:130:VAL:CG2	2.50	0.42
1:A:165:ASP:OD1	1:A:167:SER:HB3	2.20	0.42
1:B:292:PRO:HA	1:B:319:VAL:HG11	2.00	0.41
1:A:62:VAL:CG2	1:A:253:GLN:HG3	2.50	0.41
1:B:86:LYS:HE2	1:B:86:LYS:HB3	1.89	0.41
1:B:358:CYS:HA	1:B:363:ILE:HD11	2.03	0.41
1:B:304:HIS:HD2	1:B:416:GLU:CD	2.27	0.41
1:B:183:VAL:HG13	1:B:183:VAL:O	2.21	0.41
1:B:389:LEU:HD22	1:B:395:VAL:HG23	2.03	0.41
1:A:23:LEU:HD22	1:A:27:LEU:CD2	2.51	0.41
1:A:140:LEU:HD23	1:A:215:ILE:HG23	2.03	0.41
1:A:317:LYS:HG2	3:A:1194:HOH:O	2.20	0.41
1:A:371:VAL:HA	1:A:372:PRO:HD3	1.94	0.41
1:A:427:SER:OG	1:A:429:VAL:HG22	2.21	0.41
1:B:17:ALA:HB3	1:B:22:HIS:CD2	2.56	0.41
1:B:81:PRO:HG2	1:B:84:LEU:HG	2.03	0.41
1:B:162:GLU:O	1:B:162:GLU:HG3	2.21	0.41
1:B:169:ARG:HB3	1:B:185:SER:OG	2.21	0.41
1:B:248:LEU:HD22	1:B:365:GLU:CG	2.51	0.41
1:A:169:ARG:NH2	1:A:404:ARG:HD2	2.36	0.41
1:A:437:LYS:O	1:A:441:ARG:HG2	2.21	0.41
1:B:20:ILE:HG23	1:B:54:PHE:HB3	2.03	0.41
1:A:305:SER:OG	1:A:307:VAL:HG22	2.21	0.40
1:B:48:LYS:HD2	1:B:48:LYS:N	2.36	0.40
1:A:194:ASN:ND2	1:A:196:ASP:N	2.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:ARG:NH1	1:A:400:ARG:HG2	2.37	0.40
1:A:9:ASN:HD22	1:A:39:ASN:HB3	1.85	0.40
1:A:163:VAL:HG11	1:A:195:LYS:HG2	2.04	0.40
1:A:220:PHE:HZ	1:A:367:MET:CE	2.34	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	459/463 (99%)	446 (97%)	10 (2%)	3 (1%)	19	14
1	B	454/463 (98%)	429 (94%)	19 (4%)	6 (1%)	10	5
All	All	913/926 (99%)	875 (96%)	29 (3%)	9 (1%)	13	8

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	53	PRO
1	B	55	ALA
1	A	167	SER
1	B	59	ILE
1	B	165	ASP
1	B	164	PHE
1	A	53	PRO
1	A	65	SER
1	B	50	PRO

### 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	403/405 (100%)	397 (98%)	6 (2%)	60	66
1	B	398/405 (98%)	394 (99%)	4 (1%)	73	78
All	All	801/810 (99%)	791 (99%)	10 (1%)	67	73

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LEU
1	A	114	LYS
1	A	161	GLU
1	A	262	GLN
1	A	329	GLU
1	A	381	GLU
1	B	93	LEU
1	B	99	LEU
1	B	140	LEU
1	B	381	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	39	ASN
1	A	66	GLN
1	A	68	GLN
1	A	194	ASN
1	A	218	ASN
1	A	253	GLN
1	A	262	GLN
1	A	313	ASN
1	A	382	GLN
1	B	9	ASN
1	B	22	HIS

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Mol	Chain	Res	Type
1	B	39	ASN
1	B	66	GLN
1	B	68	GLN
1	B	70	GLN
1	B	159	GLN
1	B	181	ASN
1	B	194	ASN
1	B	218	ASN
1	B	255	ASN
1	B	263	HIS
1	B	304	HIS
1	B	313	ASN
1	B	357	HIS

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 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	UDP	B	901	-	25,26,26	1.08	0	38,40,40	1.40	4 (10%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	UDP	A	900	-	25,26,26	1.08	0	38,40,40	1.41	4 (10%)

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	UDP	B	901	-	-	2/16/32/32	0/2/2/2
2	UDP	A	900	-	-	3/16/32/32	0/2/2/2

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	UDP	C4-N3-C2	-4.95	120.47	126.61
2	B	901	UDP	C4-N3-C2	-4.89	120.54	126.61
2	A	900	UDP	C5-C4-N3	3.93	120.31	114.80
2	B	901	UDP	C5-C4-N3	3.83	120.16	114.80
2	A	900	UDP	N3-C2-N1	3.29	119.18	114.89
2	B	901	UDP	N3-C2-N1	3.24	119.11	114.89
2	B	901	UDP	O4-C4-C5	-3.02	119.96	125.16
2	A	900	UDP	O4-C4-C5	-2.99	120.00	125.16

There are no chirality outliers.

All (5) torsion outliers are listed below:

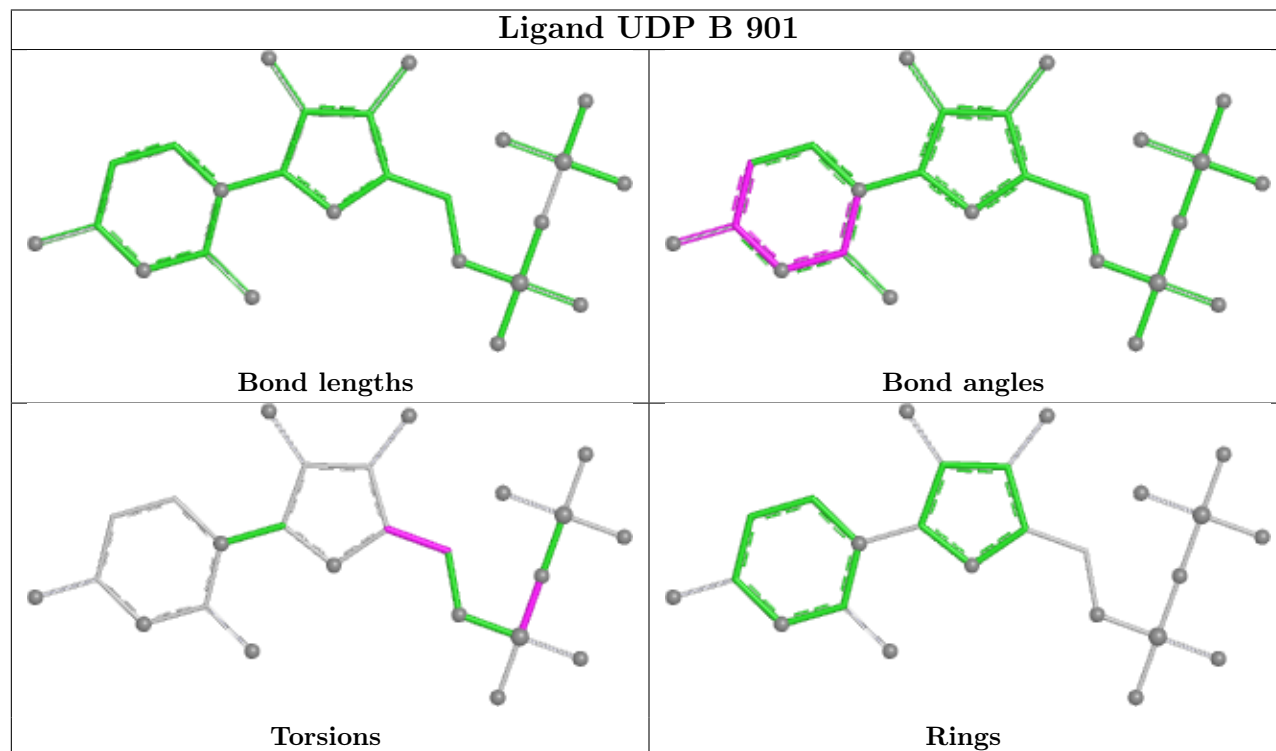
Mol	Chain	Res	Type	Atoms
2	A	900	UDP	PB-O3A-PA-O5'
2	A	900	UDP	O4'-C4'-C5'-O5'
2	A	900	UDP	C3'-C4'-C5'-O5'
2	B	901	UDP	PB-O3A-PA-O5'
2	B	901	UDP	O4'-C4'-C5'-O5'

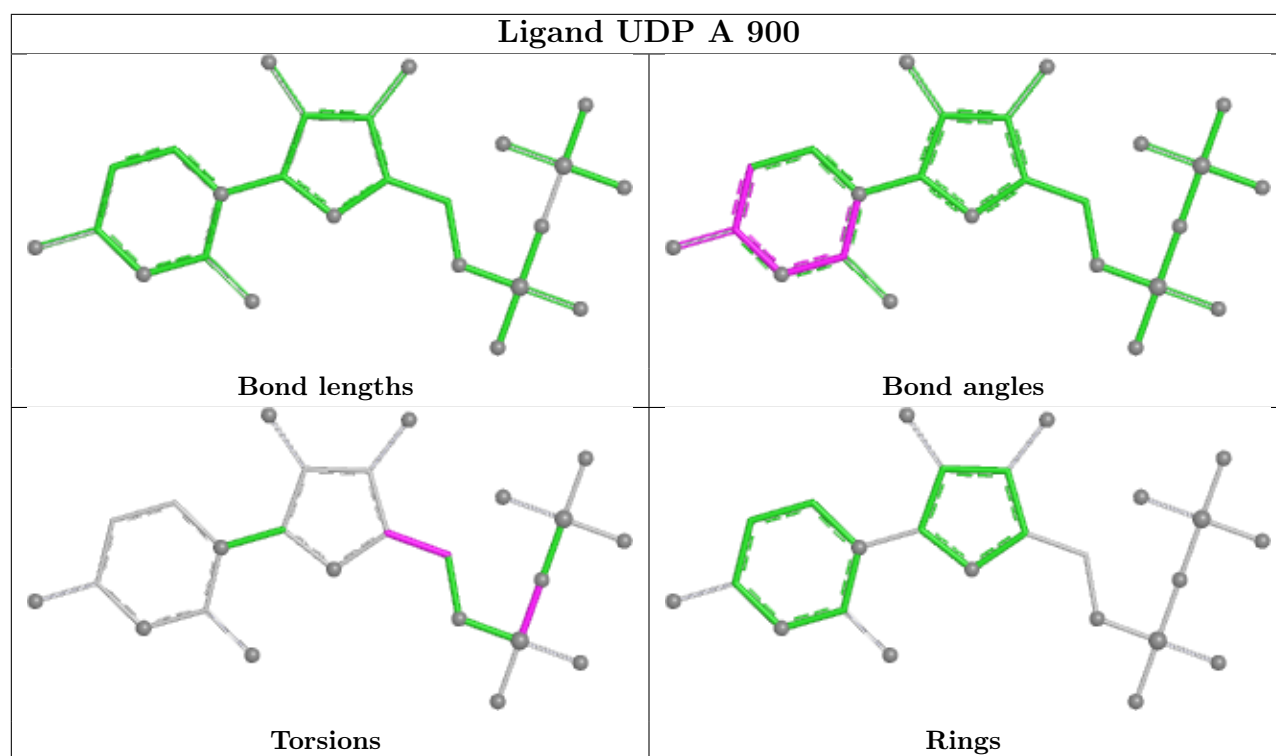
There are no ring outliers.

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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	461/463 (99%)	0.12	28 (6%)	28 26	14, 26, 51, 78	0
1	B	456/463 (98%)	0.29	49 (10%)	12 11	13, 25, 88, 103	0
All	All	917/926 (99%)	0.20	77 (8%)	18 17	13, 26, 69, 103	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	164	PHE	7.6
1	B	160	ILE	6.4
1	B	59	ILE	5.9
1	B	163	VAL	5.9
1	B	261	ALA	5.8
1	B	256	PRO	5.4
1	B	58	TYR	5.3
1	B	63	LEU	5.2
1	B	62	VAL	5.0
1	B	259	ASP	4.6
1	B	166	ASP	4.6
1	A	53	PRO	4.6
1	B	55	ALA	4.6
1	B	54	PHE	4.5
1	A	166	ASP	4.0
1	A	54	PHE	4.0
1	B	254	PRO	3.9
1	B	257	LYS	3.9
1	A	50	PRO	3.8
1	B	167	SER	3.7
1	A	49	PHE	3.7
1	B	169	ARG	3.7
1	B	258	LEU	3.5
1	B	260	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	53	PRO	3.2
1	B	50	PRO	3.2
1	A	67	PRO	3.1
1	B	428	ILE	3.1
1	B	253	GLN	3.1
1	B	158	ARG	3.1
1	B	255	ASN	3.0
1	A	55	ALA	3.0
1	A	66	GLN	2.9
1	A	3	MET	2.9
1	A	330	LEU	2.8
1	B	262	GLN	2.8
1	B	56	ASP	2.8
1	B	57	SER	2.8
1	A	52	MET	2.7
1	B	66	GLN	2.7
1	B	22	HIS	2.7
1	B	170	ASP	2.7
1	A	171	HIS	2.6
1	B	165	ASP	2.6
1	B	61	SER	2.6
1	B	65	SER	2.6
1	A	172	GLN	2.6
1	A	168	ASP	2.6
1	A	169	ARG	2.6
1	A	56	ASP	2.5
1	B	49	PHE	2.5
1	A	77	VAL	2.5
1	B	183	VAL	2.5
1	A	232	TYR	2.5
1	A	51	GLY	2.5
1	B	113	ASN	2.4
1	B	263	HIS	2.3
1	A	65	SER	2.3
1	B	161	GLU	2.3
1	B	168	ASP	2.3
1	B	159	GLN	2.3
1	B	162	GLU	2.3
1	A	289	SER	2.3
1	B	463	GLY	2.2
1	B	286	MET	2.2
1	A	64	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	181	ASN	2.2
1	B	176	ILE	2.2
1	A	48	LYS	2.2
1	A	331	GLU	2.1
1	A	59	ILE	2.1
1	A	163	VAL	2.1
1	B	171	HIS	2.1
1	B	51	GLY	2.1
1	B	92	ILE	2.1
1	B	233	ASP	2.0
1	A	286	MET	2.0

## 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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

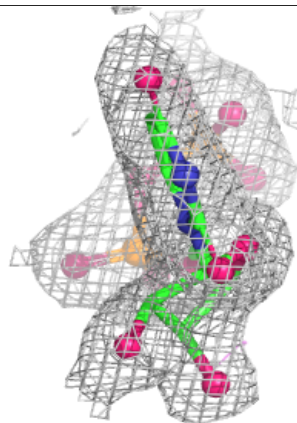
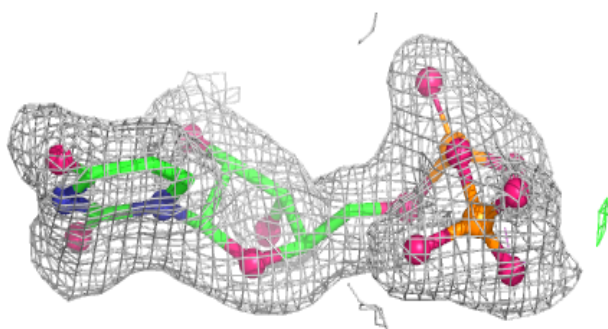
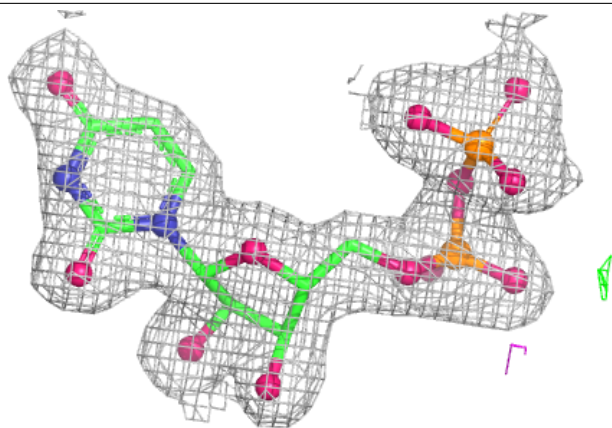
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

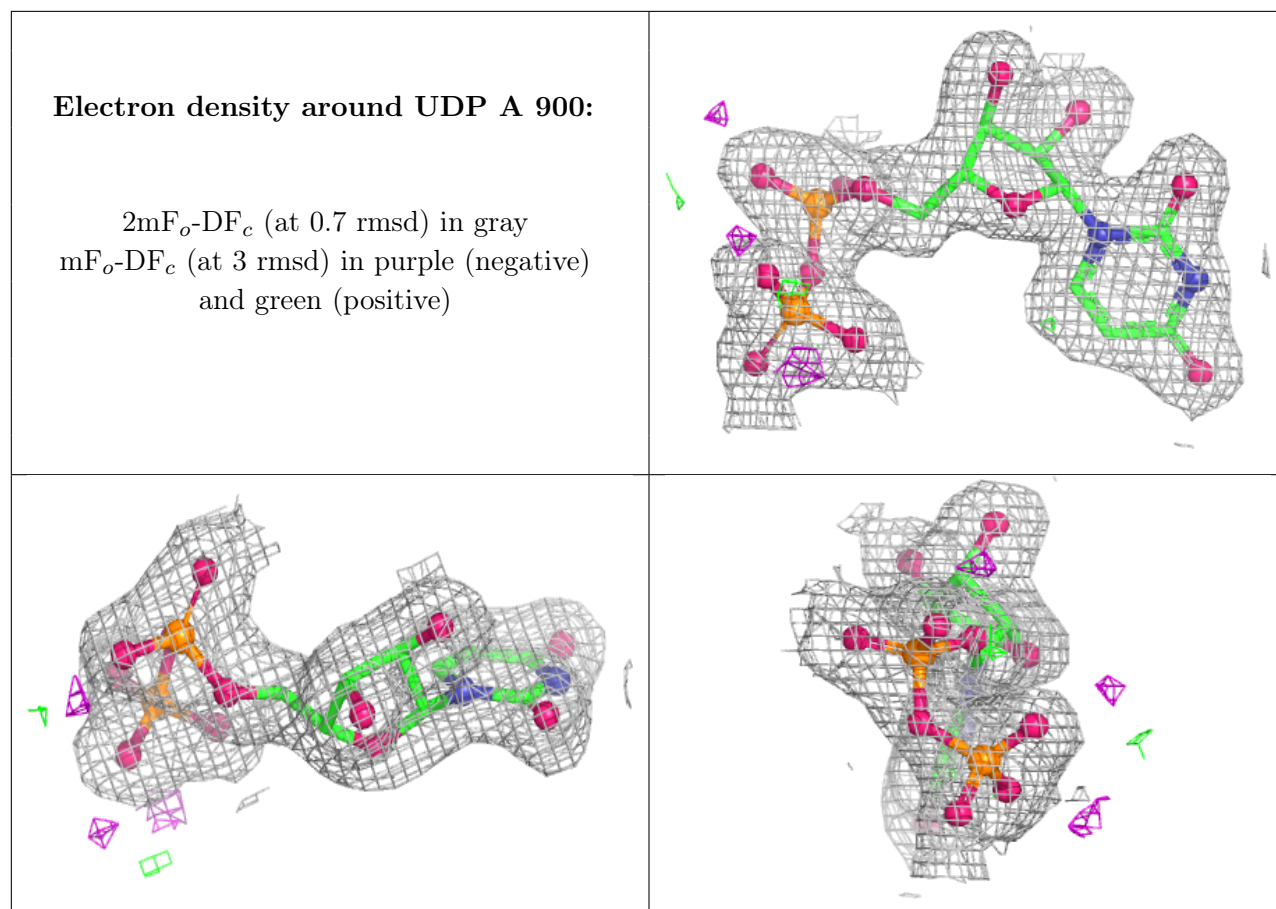
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	UDP	B	901	25/25	0.97	0.06	21,23,25,28	0
2	UDP	A	900	25/25	0.98	0.05	16,20,23,24	0

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.

**Electron density around UDP B 901:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers ⓘ

There are no such residues in this entry.