



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:51 PM UTC

PDB ID : 4D11 / pdb\_00004d11  
Title : GalNAc-T2 crystal soaked with UDP-5SGalNAc, mEA2 peptide and manganese (Lower resolution dataset)  
Authors : Lira-Navarrete, E.; Iglesias-Fernandez, J.; Zandberg, W.F.; Companon, I.; Kong, Y.; Corzana, F.; Pinto, B.M.; Clausen, H.; Peregrina, J.M.; Vocadlo, D.; Rovira, C.; Hurtado-Guerrero, R.  
Deposited on : 2014-05-01  
Resolution : 2.85 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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](#) ①) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (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

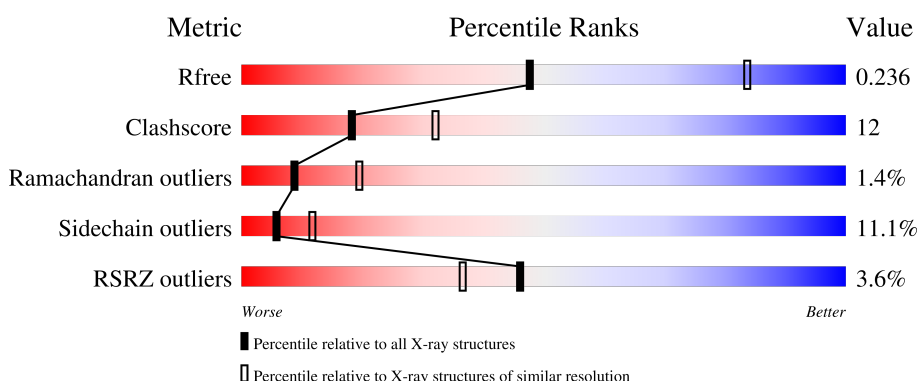
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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.



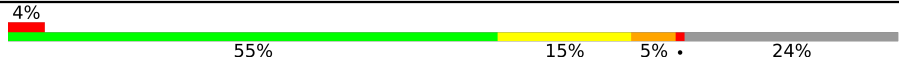





Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	571	
1	B	571	
1	D	571	
1	E	571	
1	F	571	

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Mol	Chain	Length	Quality of chain
2	C	571	 <p>4% 55% 15% 5% 24%</p>
3	L	6	 <p>50% 17% 17% 17%</p>
3	O	6	 <p>50% 33% 17%</p>
3	P	6	 <p>67% 33%</p>
3	X	6	 <p>33% 50% 33% 17%</p>
3	Z	6	 <p>17% 67% 17% 17%</p>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 21829 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 POLYPEPTIDE GALNAC-TRANSFERASE T2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	491	Total 3938	C 2477	N 715	O 722	S 24	20	0	0
1	B	482	Total 3877	C 2441	N 703	O 710	S 23	20	1	0
1	D	487	Total 3916	C 2465	N 711	O 716	S 24	20	0	0
1	E	487	Total 3917	C 2465	N 711	O 717	S 24	20	0	0
1	F	276	Total 2246	C 1419	N 406	O 407	S 14	8	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	516	ASP	ASN	engineered mutation	UNP Q10471
B	516	ASP	ASN	engineered mutation	UNP Q10471
D	516	ASP	ASN	engineered mutation	UNP Q10471
E	516	ASP	ASN	engineered mutation	UNP Q10471
F	516	ASP	ASN	engineered mutation	UNP Q10471

- Molecule 2 is a protein called POLYPEPTIDE GALNAC-TRANSFERASE T2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	436	Total 3560	C 2249	N 646	O 644	S 21	20	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	74	SER	GLY	conflict	UNP Q10471
C	516	ASP	ASN	engineered mutation	UNP Q10471

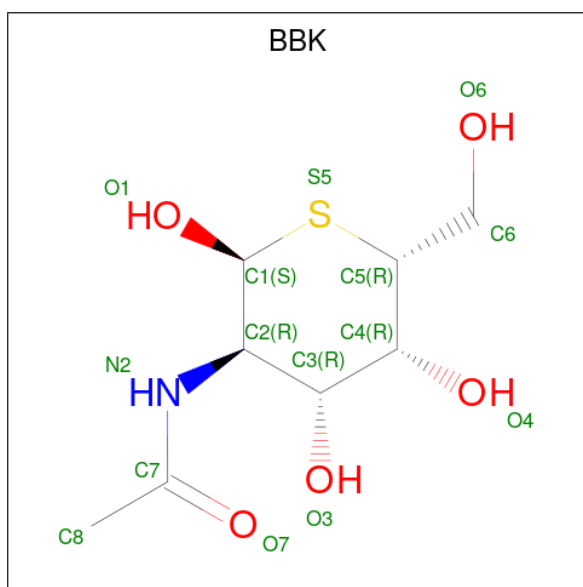
- Molecule 3 is a protein called PEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	6	Total	C	N	O	S	0	0	1
			32	18	6	7	1			
3	O	6	Total	C	N	O	S	0	0	1
			32	18	6	7	1			
3	P	6	Total	C	N	O	S	0	0	1
			32	18	6	7	1			
3	X	6	Total	C	N	O	S	0	0	1
			32	18	6	7	1			
3	Z	5	Total	C	N	O	S	0	0	0
			31	18	5	7	1			

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

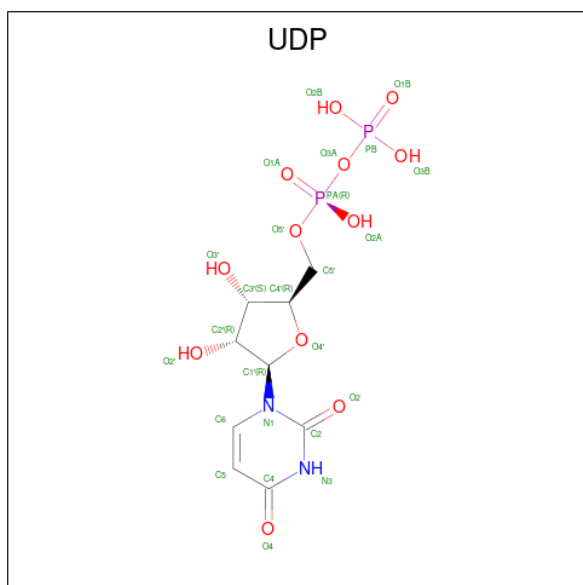
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mn	0	0
			1	1		
4	B	1	Total	Mn	0	0
			1	1		
4	C	1	Total	Mn	0	0
			1	1		
4	D	1	Total	Mn	0	0
			1	1		
4	E	1	Total	Mn	0	0
			1	1		
4	F	1	Total	Mn	0	0
			1	1		

- Molecule 5 is 2-acetamido-2-deoxy-5-thio-alpha-D-galactopyranose (CCD ID: BBK) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	A	1	Total	C	N	O	S	0	0
			15	8	1	5	1		
5	B	1	Total	C	N	O	S	0	0
			15	8	1	5	1		
5	D	1	Total	C	N	O	S	0	0
			15	8	1	5	1		
5	E	1	Total	C	N	O	S	0	0
			15	8	1	5	1		

- Molecule 6 is URIDINE-5'-DIPHOSPHATE (CCD ID: UDP) (formula:  $C_9H_{14}N_2O_{12}P_2$ ).

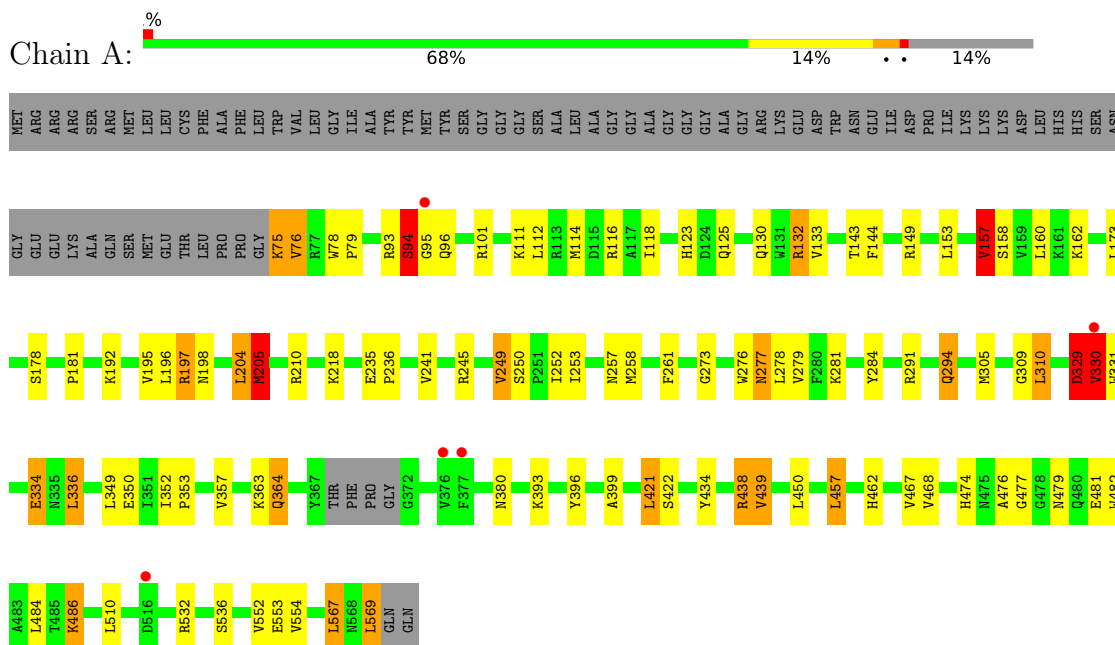


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
6	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
6	C	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
6	D	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
6	E	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
6	F	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

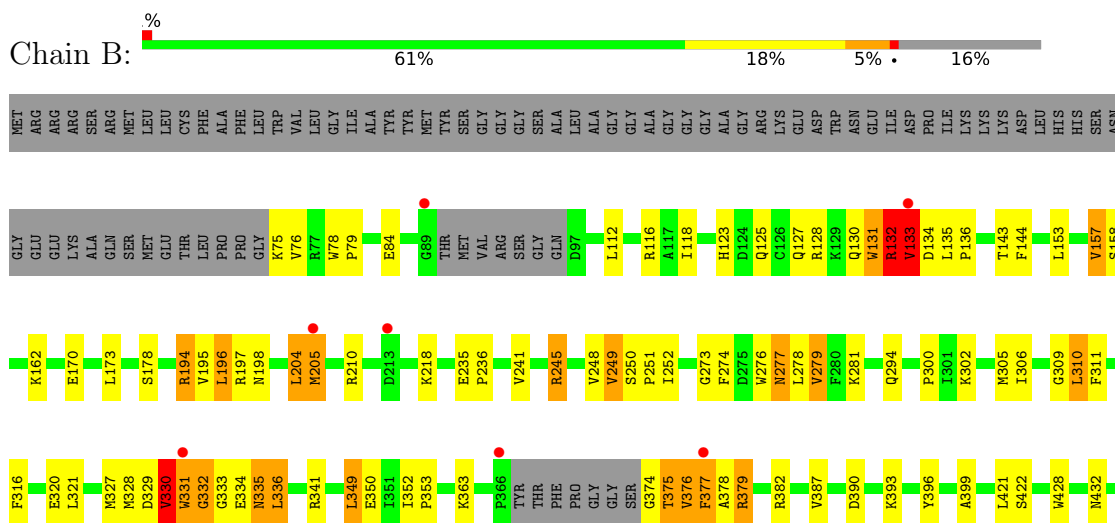
### 3 Residue-property plots [i](#)

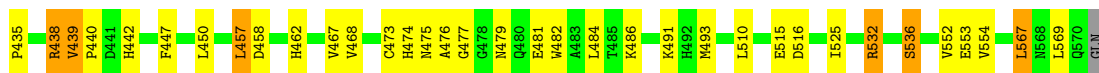
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: POLYPEPTIDE GALNAC-TRANSFERASE T2

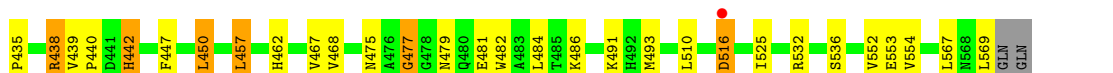
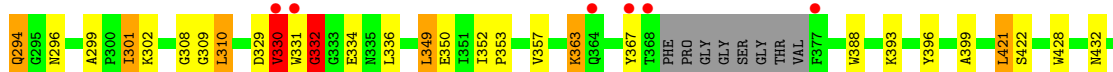
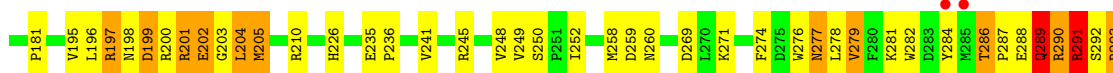


#### • Molecule 1: POLYPEPTIDE GALNAC-TRANSFERASE T2





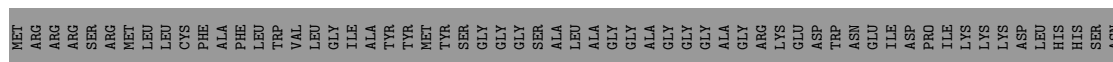
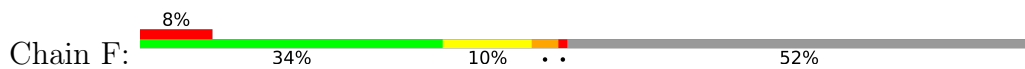
● Molecule 1: POLYPEPTIDE GALNAC-TRANSFERASE T2



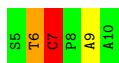
● Molecule 1: POLYPEPTIDE GALNAC-TRANSFERASE T2



● Molecule 1: POLYPEPTIDE GALNAC-TRANSFERASE T2







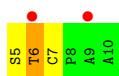
## ● Molecule 3: PEPTIDE



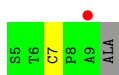
## ● Molecule 3: PEPTIDE



## ● Molecule 3: PEPTIDE



## ● Molecule 3: PEPTIDE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.77Å 120.90Å 249.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	249.61 – 2.85 124.80 – 2.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (249.61-2.85) 100.0 (124.80-2.85)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.98 (at 2.86Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.216 , 0.235 0.219 , 0.236	Depositor DCC
$R_{free}$ test set	2285 reflections (2.75%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	64.9	Xtrriage
Anisotropy	0.339	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 64.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.018 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	21829	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.04% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UDP, BBK, MN

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	1.29	10/4027 (0.2%)	1.34	20/5443 (0.4%)
1	B	1.39	9/3967 (0.2%)	1.37	27/5361 (0.5%)
1	D	1.43	14/4005 (0.3%)	1.35	18/5413 (0.3%)
1	E	1.36	5/4006 (0.1%)	1.35	23/5415 (0.4%)
1	F	1.20	4/2297 (0.2%)	1.34	14/3104 (0.5%)
2	C	1.22	4/3639 (0.1%)	1.35	20/4909 (0.4%)
3	L	0.75	0/32	1.37	2/44 (4.5%)
3	O	0.96	0/32	1.42	0/44
3	P	1.19	0/32	1.40	0/44
3	X	0.94	0/32	1.31	0/44
3	Z	1.10	0/31	1.16	0/42
All	All	1.33	46/22100 (0.2%)	1.35	124/29863 (0.4%)

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	D	0	1
2	C	0	1
All	All	0	2

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	202	GLU	C-N	-32.61	0.73	1.33
1	B	75	LYS	CB-CG	-30.62	0.60	1.52
1	D	486	LYS	CB-CG	-23.07	0.83	1.52
1	E	75	LYS	CB-CG	-22.92	0.83	1.52
2	C	75	LYS	CB-CG	-22.88	0.83	1.52

The worst 5 of 124 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	D	75	LYS	CB-CG-CD	20.91	159.39	111.30
1	B	84	GLU	CA-CB-CG	14.47	143.04	114.10
1	B	84	GLU	CB-CG-CD	12.33	133.57	112.60
2	C	75	LYS	CB-CG-CD	12.16	139.28	111.30
1	A	294	GLN	CA-CB-CG	11.92	137.95	114.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	127	GLN	Peptide
1	D	332	GLY	Peptide

## 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	3938	0	3863	45	0
1	B	3877	0	3804	102	0
1	D	3916	0	3842	87	0
1	E	3917	0	3843	79	0
1	F	2246	0	2214	91	0
2	C	3560	0	3495	112	0
3	L	32	0	28	4	0
3	O	32	0	28	2	0
3	P	32	0	28	0	0
3	X	32	0	28	8	0
3	Z	31	0	28	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	A	15	0	14	4	0
5	B	15	0	15	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	15	0	15	1	0
5	E	15	0	15	1	0
6	A	25	0	11	0	0
6	B	25	0	11	0	0
6	C	25	0	11	0	0
6	D	25	0	11	0	0
6	E	25	0	11	1	0
6	F	25	0	11	0	0
All	All	21829	0	21326	518	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 12.

The worst 5 of 518 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:F:328:MET:SD	1:F:334:GLU:CB	2.07	1.42
1:D:202:GLU:C	1:D:203:GLY:CA	1.92	1.40
1:D:202:GLU:CA	1:D:203:GLY:N	1.92	1.30
1:F:328:MET:SD	1:F:334:GLU:HB2	1.68	1.29
1:B:329:ASP:HB2	1:B:379:ARG:NH2	1.47	1.28

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	487/571 (85%)	461 (95%)	24 (5%)	2 (0%)	30	48
1	B	477/571 (84%)	445 (93%)	26 (6%)	6 (1%)	9	21
1	D	483/571 (85%)	449 (93%)	28 (6%)	6 (1%)	10	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	483/571 (85%)	457 (95%)	21 (4%)	5 (1%)	12	25
1	F	272/571 (48%)	252 (93%)	15 (6%)	5 (2%)	6	15
2	C	422/571 (74%)	387 (92%)	27 (6%)	8 (2%)	6	14
3	L	4/6 (67%)	1 (25%)	1 (25%)	2 (50%)	0	0
3	O	4/6 (67%)	2 (50%)	2 (50%)	0	100	100
3	P	4/6 (67%)	3 (75%)	0	1 (25%)	0	0
3	X	4/6 (67%)	1 (25%)	2 (50%)	1 (25%)	0	0
3	Z	3/6 (50%)	3 (100%)	0	0	100	100
All	All	2643/3456 (76%)	2461 (93%)	146 (6%)	36 (1%)	9	19

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	330	VAL
1	A	477	GLY
1	B	132	ARG
1	B	477	GLY
2	C	365	HIS

### 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	425/485 (88%)	381 (90%)	44 (10%)	7	14
1	B	418/485 (86%)	375 (90%)	43 (10%)	7	14
1	D	423/485 (87%)	376 (89%)	47 (11%)	6	12
1	E	423/485 (87%)	378 (89%)	45 (11%)	6	13
1	F	244/485 (50%)	213 (87%)	31 (13%)	4	8
2	C	385/486 (79%)	339 (88%)	46 (12%)	5	10
3	L	4/4 (100%)	4 (100%)	0	100	100
3	O	4/4 (100%)	2 (50%)	2 (50%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	P	4/4 (100%)	3 (75%)	1 (25%)	0	0
3	X	4/4 (100%)	4 (100%)	0	100	100
3	Z	4/4 (100%)	3 (75%)	1 (25%)	0	0
All	All	2338/2931 (80%)	2078 (89%)	260 (11%)	6	12

5 of 260 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	130	GLN
1	F	196	LEU
2	C	196	LEU
2	C	157	VAL
1	F	241	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	412	GLN
1	E	405	ASN
1	D	462	HIS
1	E	127	GLN
1	E	524	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 oligosaccharides in this entry.

## 5.6 Ligand geometry

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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
6	UDP	D	1571	4	25,26,26	1.37	1 (4%)	38,40,40	1.80	6 (15%)
5	BBK	E	1571	-	13,15,15	9.42	4 (30%)	14,21,21	1.52	2 (14%)
6	UDP	B	1573	4	25,26,26	1.36	3 (12%)	38,40,40	1.90	7 (18%)
5	BBK	B	1572	-	13,15,15	9.00	4 (30%)	14,21,21	1.67	2 (14%)
6	UDP	E	1572	4	25,26,26	1.41	3 (12%)	38,40,40	1.85	5 (13%)
6	UDP	C	1571	4	25,26,26	1.49	3 (12%)	38,40,40	1.83	6 (15%)
5	BBK	A	1571	-	13,15,15	9.13	2 (15%)	14,21,21	1.45	4 (28%)
5	BBK	D	1572	-	13,15,15	9.16	4 (30%)	14,21,21	1.57	3 (21%)
6	UDP	A	1572	4	25,26,26	1.31	3 (12%)	38,40,40	1.88	9 (23%)
6	UDP	F	1364	4	25,26,26	1.27	3 (12%)	38,40,40	1.65	5 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	UDP	D	1571	4	-	9/16/32/32	0/2/2/2
5	BBK	E	1571	-	-	0/6/26/26	0/1/1/1
6	UDP	B	1573	4	-	7/16/32/32	0/2/2/2
5	BBK	B	1572	-	-	5/6/26/26	0/1/1/1
6	UDP	E	1572	4	-	10/16/32/32	0/2/2/2
6	UDP	C	1571	4	-	10/16/32/32	0/2/2/2
5	BBK	A	1571	-	-	2/6/26/26	0/1/1/1
5	BBK	D	1572	-	-	2/6/26/26	0/1/1/1
6	UDP	A	1572	4	-	8/16/32/32	0/2/2/2
6	UDP	F	1364	4	-	10/16/32/32	0/2/2/2

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	1571	BBK	C5-S5	-26.71	1.43	1.82
5	A	1571	BBK	C5-S5	-25.99	1.44	1.82
5	D	1572	BBK	C5-S5	-25.86	1.44	1.82
5	B	1572	BBK	C5-S5	-25.38	1.45	1.82
5	E	1571	BBK	C1-S5	-20.58	1.43	1.83

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1572	UDP	C4-N3-C2	-5.95	119.22	126.61
6	D	1571	UDP	C4-N3-C2	-5.67	119.57	126.61
6	C	1571	UDP	C4-N3-C2	-5.60	119.66	126.61
6	A	1572	UDP	C4-N3-C2	-5.43	119.88	126.61
6	B	1573	UDP	C4-N3-C2	-5.28	120.05	126.61

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1571	BBK	C4-C5-C6-O6
5	A	1571	BBK	S5-C5-C6-O6
5	B	1572	BBK	C4-C5-C6-O6
5	B	1572	BBK	S5-C5-C6-O6
5	D	1572	BBK	C4-C5-C6-O6

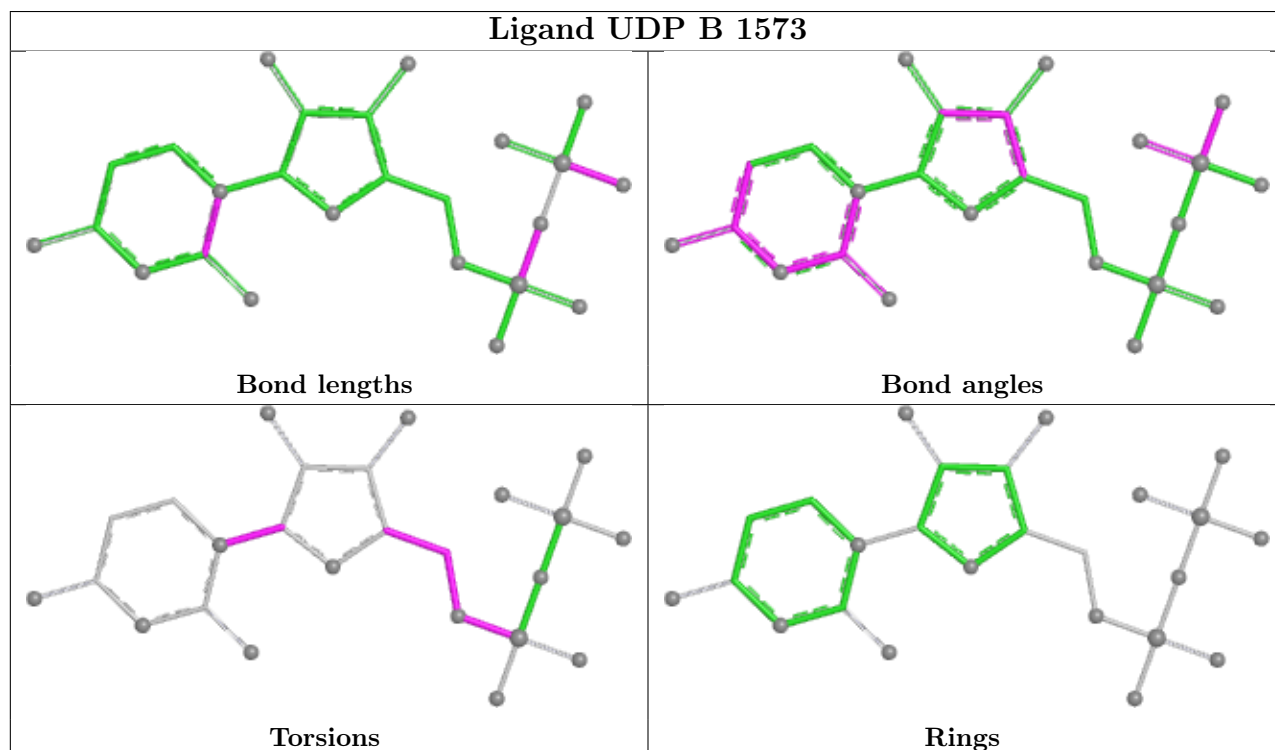
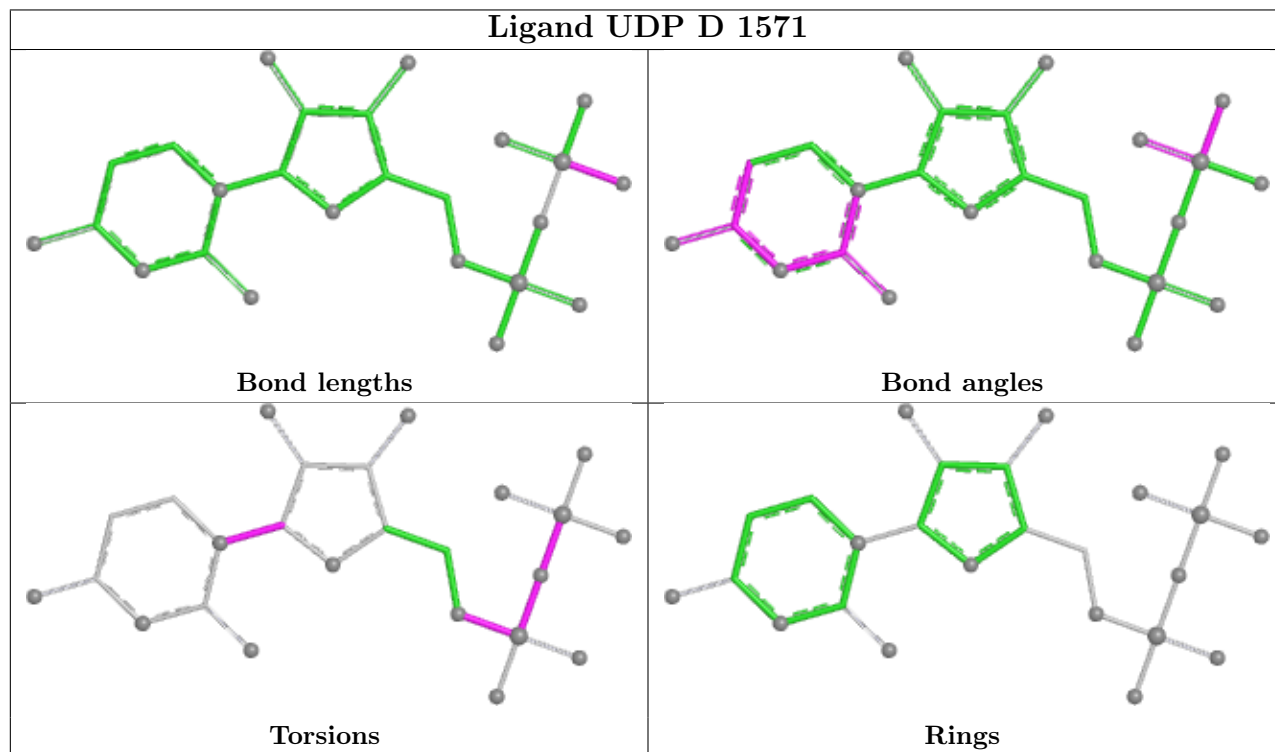
There are no ring outliers.

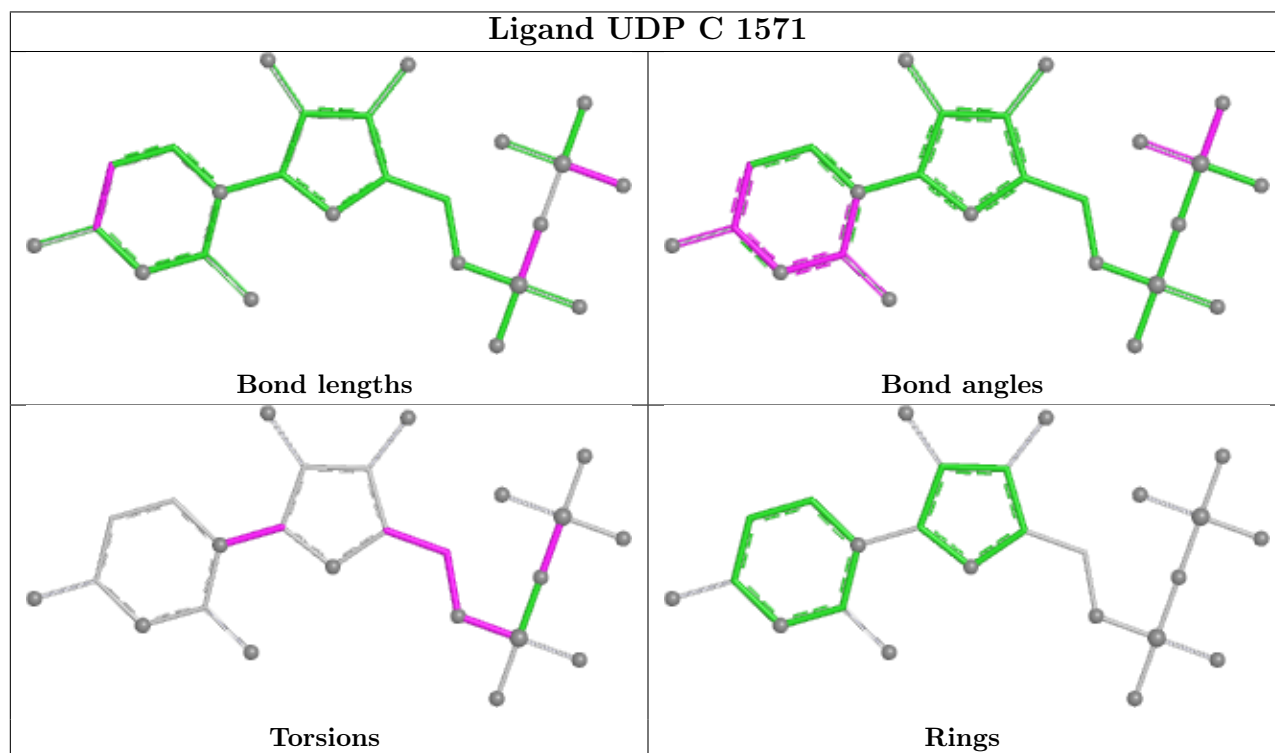
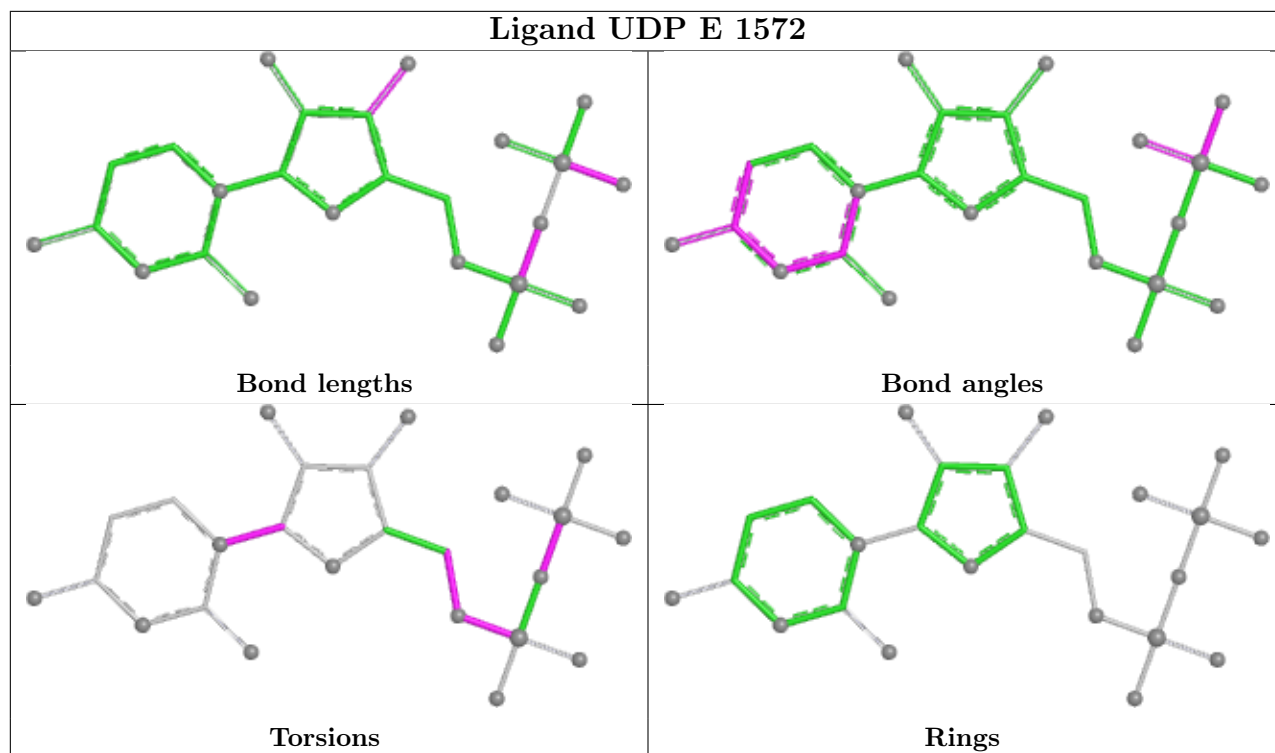
5 monomers are involved in 12 short contacts:

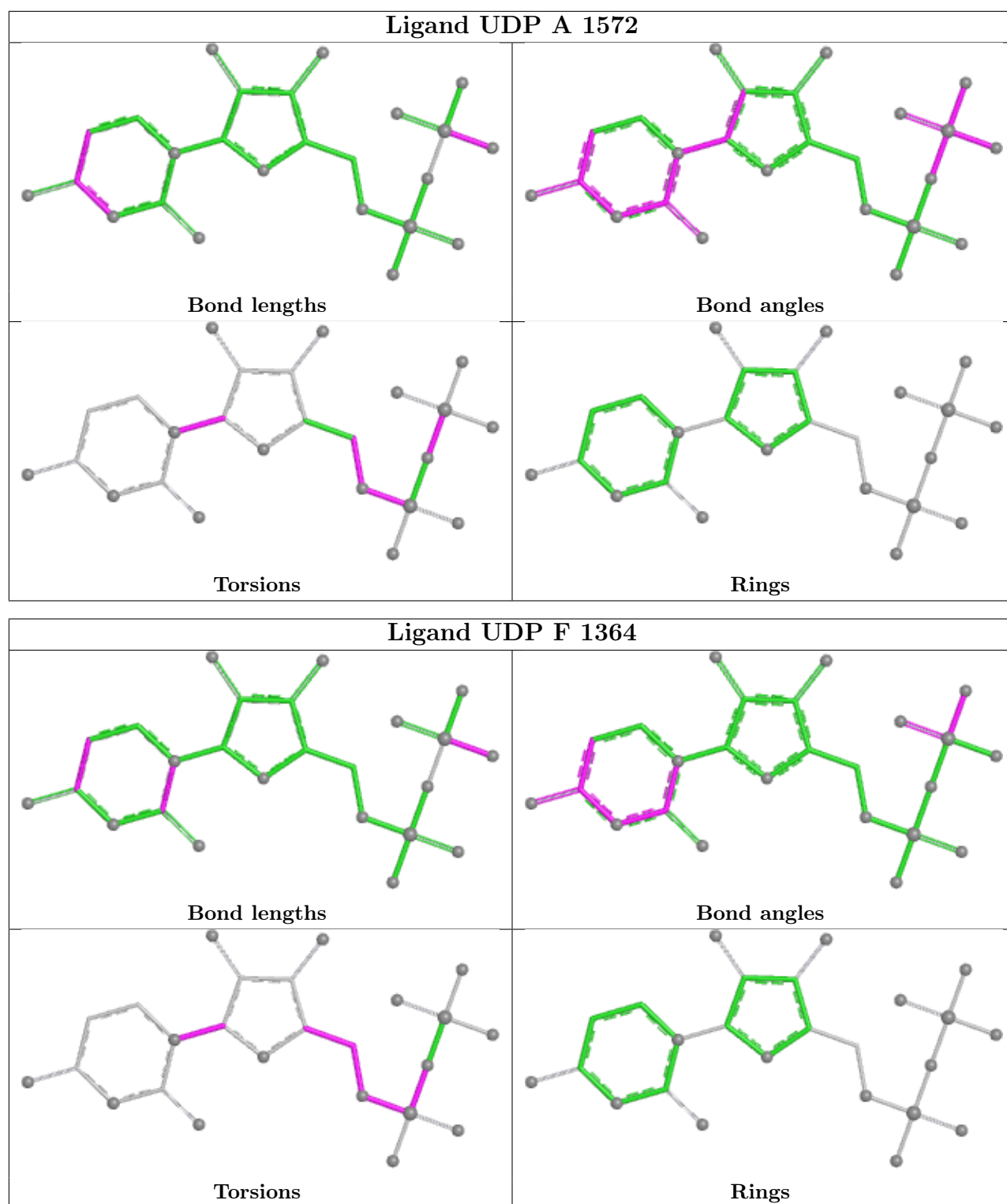
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	1571	BBK	1	0
5	B	1572	BBK	6	0
6	E	1572	UDP	1	0
5	A	1571	BBK	4	0
5	D	1572	BBK	1	0

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	202:GLU	C	203:GLY	N	0.73

## 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, 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	491/571 (85%)	-0.08	5 (1%) 79 74	28, 56, 96, 129	5 (1%)
1	B	482/571 (84%)	0.10	7 (1%) 72 65	16, 65, 115, 151	6 (1%)
1	D	487/571 (85%)	0.07	9 (1%) 67 61	29, 63, 110, 144	5 (1%)
1	E	487/571 (85%)	-0.01	5 (1%) 79 74	31, 57, 105, 159	5 (1%)
1	F	276/571 (48%)	1.15	46 (16%) 4 3	59, 112, 167, 187	2 (0%)
2	C	436/571 (76%)	0.45	20 (4%) 37 29	35, 89, 149, 182	5 (1%)
3	L	6/6 (100%)	0.97	0 100 100	86, 109, 116, 126	0
3	O	6/6 (100%)	1.74	3 (50%) 0 0	72, 94, 105, 110	0
3	P	6/6 (100%)	0.39	0 100 100	44, 72, 78, 90	0
3	X	6/6 (100%)	1.64	2 (33%) 1 1	91, 106, 118, 123	0
3	Z	5/6 (83%)	1.70	1 (20%) 3 3	72, 73, 88, 92	0
All	All	2688/3456 (77%)	0.22	98 (3%) 46 36	16, 66, 136, 187	28 (1%)

The worst 5 of 98 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	264	VAL	6.0
3	X	9	ALA	4.3
1	E	377	PHE	4.2
1	D	377	PHE	4.2
2	C	98	PRO	3.9

### 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](#)

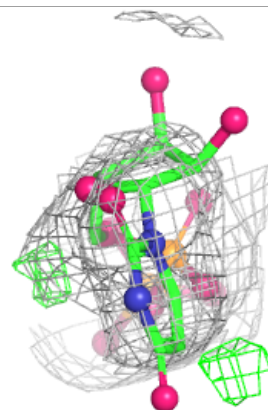
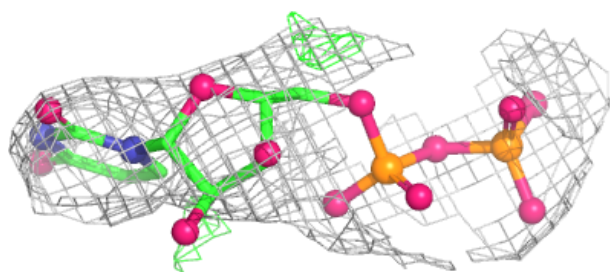
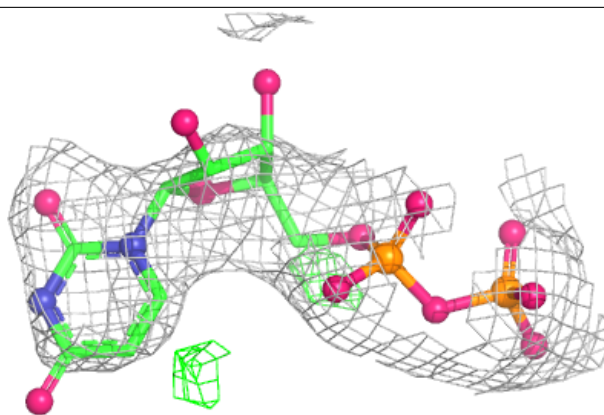
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	BBK	B	1572	15/15	0.77	0.18	66,81,110,110	0
5	BBK	D	1572	15/15	0.78	0.19	97,106,117,122	0
5	BBK	E	1571	15/15	0.80	0.17	67,86,120,144	0
5	BBK	A	1571	15/15	0.83	0.13	52,76,82,88	0
6	UDP	F	1364	25/25	0.83	0.11	107,134,151,177	0
6	UDP	C	1571	25/25	0.87	0.10	83,96,111,114	0
6	UDP	E	1572	25/25	0.90	0.10	69,78,89,97	0
6	UDP	B	1573	25/25	0.90	0.10	77,89,97,106	0
6	UDP	D	1571	25/25	0.92	0.11	64,98,118,128	0
6	UDP	A	1572	25/25	0.94	0.09	54,74,89,97	0
4	MN	E	1570	1/1	0.99	0.03	46,46,46,46	0
4	MN	F	1363	1/1	0.99	0.02	93,93,93,93	0
4	MN	B	1571	1/1	0.99	0.02	63,63,63,63	0
4	MN	A	1570	1/1	1.00	0.03	46,46,46,46	0
4	MN	C	1570	1/1	1.00	0.02	67,67,67,67	0
4	MN	D	1570	1/1	1.00	0.03	58,58,58,58	0

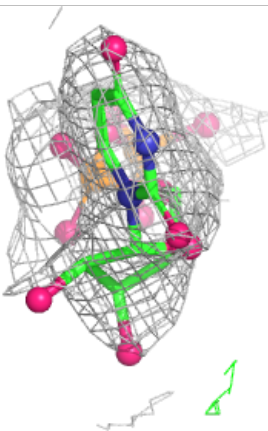
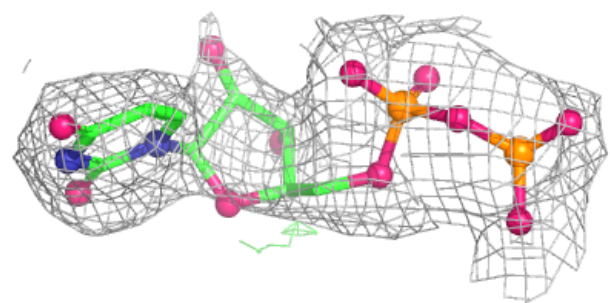
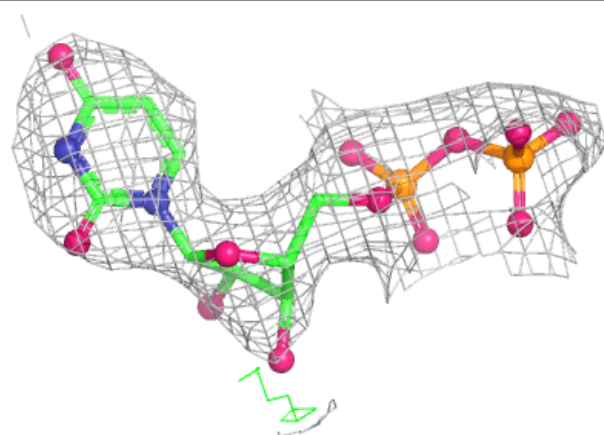
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around UDP F 1364:**

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

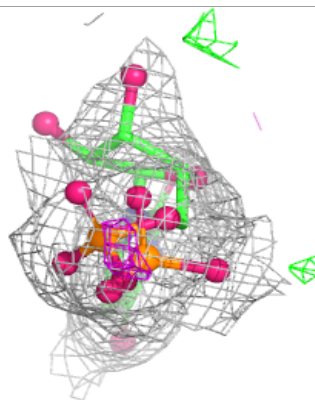
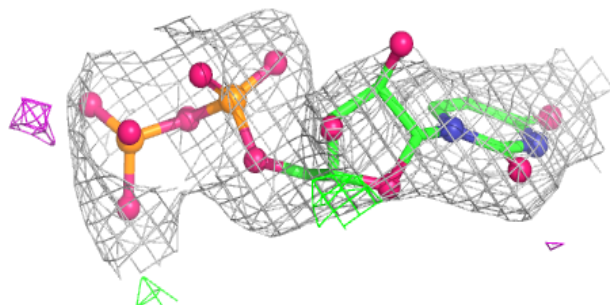
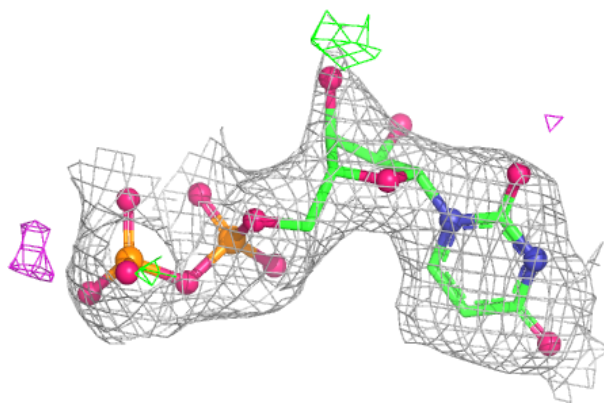
**Electron density around UDP C 1571:**

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

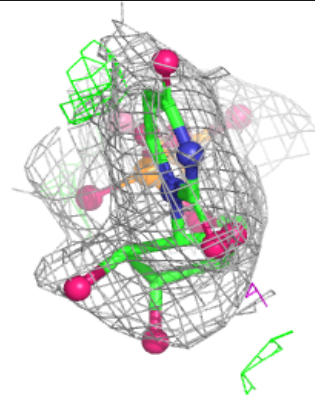
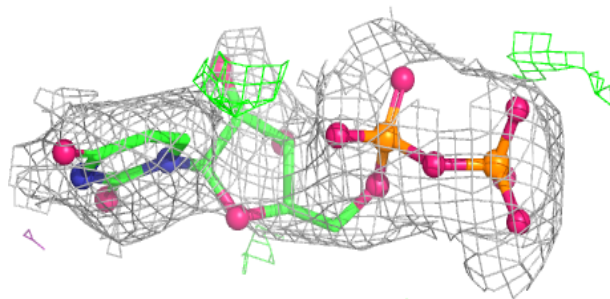
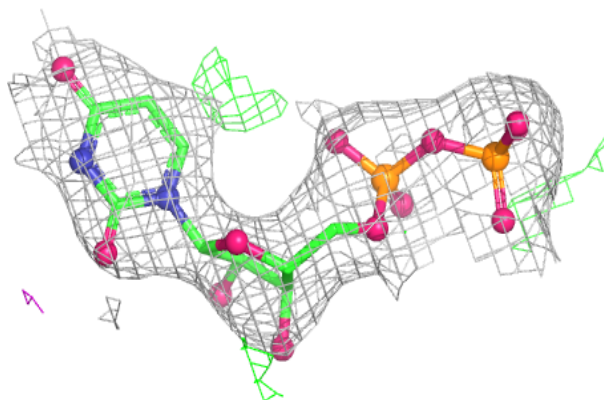


**Electron density around UDP E 1572:**

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

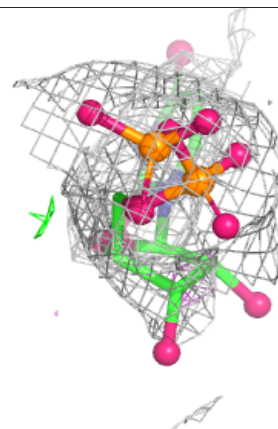
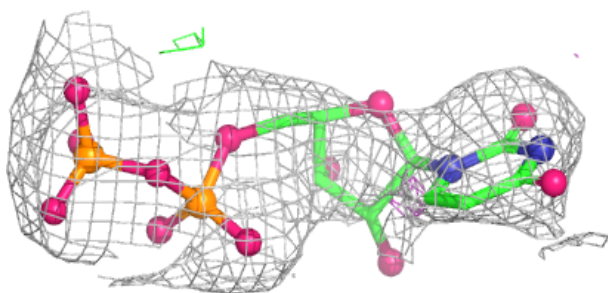
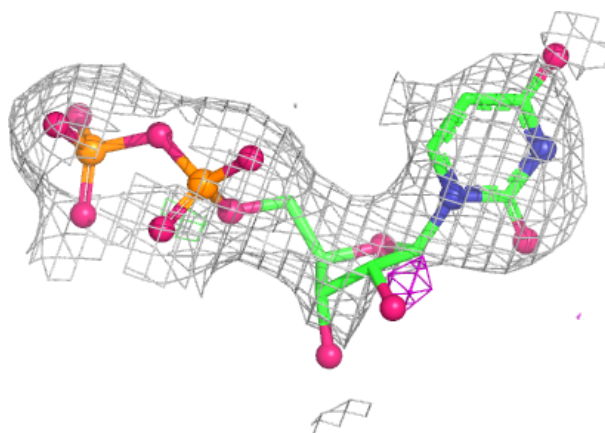
**Electron density around UDP B 1573:**

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

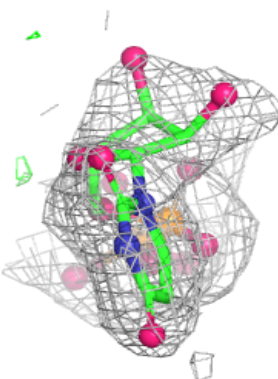
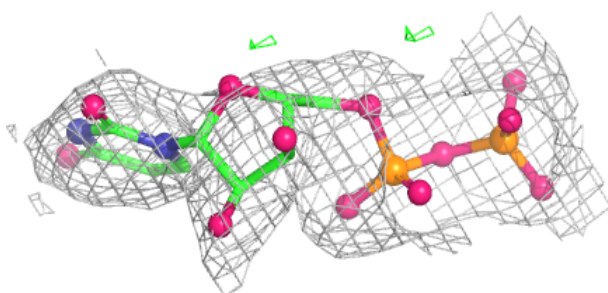
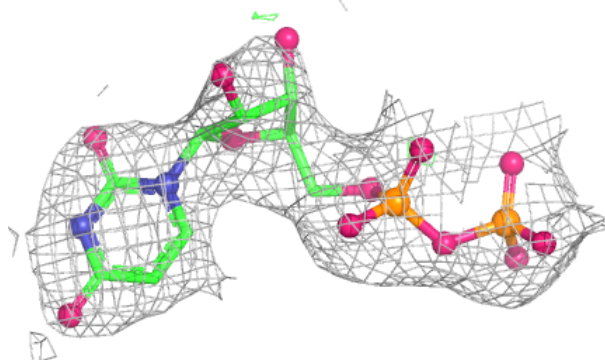


**Electron density around UDP D 1571:**

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

**Electron density around UDP A 1572:**

$2mF_o-DF_c$  (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.