



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:49 am BST

PDB ID : 3OH1
Title : Protein structure of USP from L. major bound to URIDINE-5'-DIPHOSPHATE-Galacturonic acid
Authors : Dickmanns, A.; Damerow, S.; Neumann, P.; Schulz, E.-C.; Lamerz, A.; Routier, F.; Ficner, R.
Deposited on : 2010-08-17
Resolution : 2.18 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

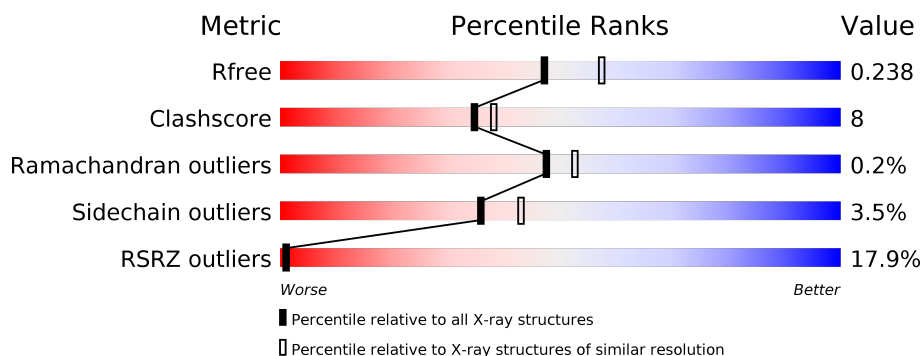
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 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}	130704	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

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 on 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	641	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4819 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.

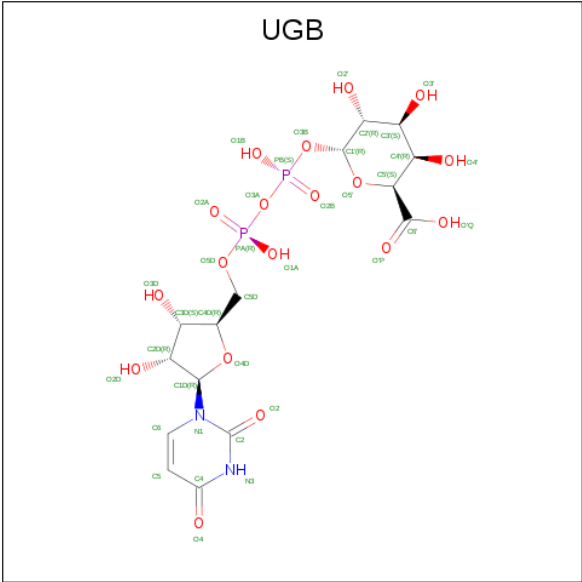
- Molecule 1 is a protein called UDP-sugar pyrophosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	0	4	0
			4551	2891	787	854	19			

There are 11 discrepancies between the modelled and reference sequences:

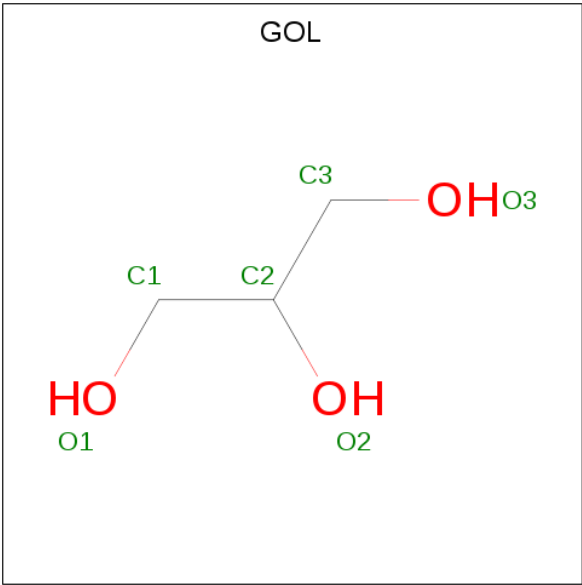
Chain	Residue	Modelled	Actual	Comment	Reference
A	631	MET	-	EXPRESSION TAG	UNP D3G6S4
A	632	ARG	-	EXPRESSION TAG	UNP D3G6S4
A	633	ARG	-	EXPRESSION TAG	UNP D3G6S4
A	634	LEU	-	EXPRESSION TAG	UNP D3G6S4
A	635	GLU	-	EXPRESSION TAG	UNP D3G6S4
A	636	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	637	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	638	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	639	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	640	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	641	HIS	-	EXPRESSION TAG	UNP D3G6S4

- Molecule 2 is (2S,3R,4S,5R,6R)-6-[[[(2R,3S,4R,5R)-5-(2,4-dioxypyrimidin-1-yl)-3,4-dihydroxy-oxolan-2-yl]methoxy-hydroxy-phosphoryl]oxy-hydroxy-phosphoryl]oxy-3,4,5-trihydroxy-oxane-2-carboxylic acid (three-letter code: UGB) (formula: C₁₅H₂₂N₂O₁₈P₂).



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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

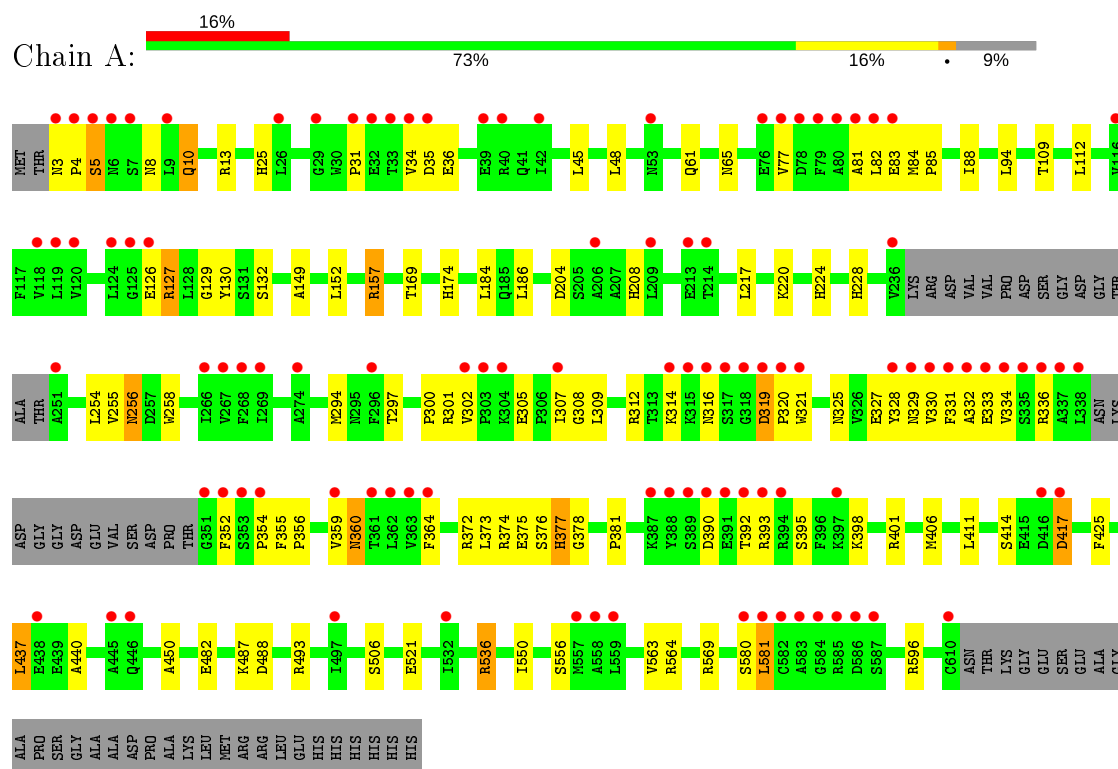
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	219	Total 219	O 219	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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-sugar pyrophosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	108.23Å 122.32Å 61.22Å 90.00° 105.42° 90.00°	Depositor
Resolution (Å)	29.51 – 2.18 29.51 – 2.18	Depositor EDS
% Data completeness (in resolution range)	94.2 (29.51-2.18) 94.2 (29.51-2.18)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.6.1 _357	Depositor
R, R_{free}	0.200 , 0.243 0.194 , 0.238	Depositor DCC
R_{free} test set	1840 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4819	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, UGB

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	0.61	0/4646	0.67	2/6314 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	596	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	A	596	ARG	NE-CZ-NH1	5.58	123.09	120.30

There are no chirality outliers.

There are no planarity outliers.

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	4551	0	4531	76	0
2	A	37	0	19	2	0
3	A	12	0	16	0	0
4	A	219	0	0	0	0
All	All	4819	0	4566	76	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 8.

All (76) 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:126:GLU:O	1:A:129:GLY:N	2.07	0.87
1:A:157:ARG:HD2	1:A:506:SER:HA	1.62	0.81
1:A:316:ASN:O	1:A:319:ASP:HB2	1.82	0.79
1:A:10:GLN:HG2	1:A:34:VAL:HG23	1.65	0.77
1:A:204:ASP:OD1	1:A:208:HIS:HD2	1.69	0.74
1:A:157:ARG:HH12	1:A:556:SER:HB3	1.52	0.73
1:A:83:GLU:HG2	1:A:84:MET:N	2.02	0.73
1:A:381:PRO:HG2	1:A:411:LEU:HD12	1.71	0.73
1:A:319:ASP:OD1	1:A:320:PRO:HD2	1.92	0.69
1:A:301:ARG:O	1:A:352:PHE:HB3	1.92	0.69
1:A:390:ASP:HB3	1:A:392:THR:H	1.59	0.66
1:A:330:VAL:O	1:A:334:VAL:HG23	1.97	0.65
1:A:329:ASN:O	1:A:333:GLU:HG3	1.97	0.63
1:A:84:MET:HE1	1:A:354:PRO:CB	2.29	0.63
1:A:25:HIS:CE1	1:A:208:HIS:HB3	2.35	0.62
1:A:308:GLY:HA3	1:A:325:ASN:HD21	1.65	0.61
1:A:256:ASN:ND2	1:A:374:ARG:HH21	1.99	0.60
1:A:332:ALA:O	1:A:336:ARG:HG3	2.03	0.59
1:A:328:TYR:O	1:A:331:PHE:N	2.37	0.58
1:A:329:ASN:OD1	1:A:330:VAL:HG23	2.05	0.57
1:A:61:GLN:HE21	1:A:65:ASN:ND2	2.02	0.57
1:A:152:LEU:HD12	1:A:186:LEU:HD13	1.87	0.57
1:A:581:LEU:N	1:A:581:LEU:HD23	2.20	0.57
1:A:580:SER:HB2	1:A:581:LEU:HD23	1.85	0.56
1:A:81:ALA:HB3	1:A:314:LYS:CB	2.36	0.55
1:A:521:GLU:H	1:A:521:GLU:CD	2.10	0.55
1:A:440:ALA:HB1	1:A:450:ALA:HB1	1.87	0.54
1:A:327:GLU:CD	1:A:328:TYR:H	2.10	0.53
1:A:3:ASN:N	1:A:4:PRO:HD3	2.21	0.53
1:A:414:SER:OG	1:A:417:ASP:OD2	2.27	0.53
1:A:3:ASN:N	1:A:4:PRO:CD	2.72	0.52
1:A:302:VAL:HG22	1:A:305:GLU:OE2	2.08	0.52
1:A:255:VAL:HG23	1:A:256:ASN:HD22	1.75	0.52
1:A:376:SER:O	1:A:377:HIS:HB2	2.10	0.51
1:A:61:GLN:HE21	1:A:65:ASN:HD21	1.59	0.51
1:A:312:ARG:HG2	1:A:321:TRP:CE3	2.45	0.50
1:A:81:ALA:HB3	1:A:314:LYS:HB2	1.92	0.50
1:A:5:SER:HB3	1:A:8:ASN:ND2	2.26	0.50
1:A:48:LEU:HG	1:A:217:LEU:HD11	1.95	0.49
1:A:84:MET:HE1	1:A:354:PRO:C	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:ASN:N	1:A:256:ASN:HD22	2.12	0.47
1:A:84:MET:HE1	1:A:354:PRO:HB2	1.97	0.46
1:A:305:GLU:HB3	1:A:307:ILE:HG22	1.96	0.46
1:A:309:LEU:HD12	1:A:309:LEU:N	2.31	0.46
1:A:354:PRO:HB2	1:A:355:PHE:CD1	2.51	0.45
1:A:393:ARG:C	1:A:395:SER:H	2.20	0.45
1:A:294:MET:HG3	1:A:364:PHE:CE1	2.52	0.45
1:A:77:VAL:HG13	1:A:77:VAL:O	2.17	0.45
1:A:82:LEU:HA	1:A:82:LEU:HD12	1.64	0.45
1:A:536:ARG:HD2	1:A:556:SER:O	2.16	0.44
1:A:130:TYR:CE1	1:A:132:SER:HB2	2.52	0.44
1:A:220:LYS:HZ1	1:A:398:LYS:HE3	1.82	0.44
1:A:487:LYS:O	1:A:488:ASP:HB2	2.17	0.44
1:A:297:THR:O	1:A:359:VAL:HG22	2.18	0.43
1:A:85:PRO:HB2	1:A:88:ILE:HD11	2.00	0.43
1:A:13:ARG:HB2	1:A:45:LEU:HD21	1.99	0.43
1:A:373:LEU:HD12	1:A:378:GLY:HA2	2.00	0.43
1:A:256:ASN:HD21	1:A:374:ARG:HH21	1.66	0.43
1:A:169:THR:OG1	1:A:174:HIS:HD2	2.03	0.42
1:A:94:LEU:HD12	1:A:94:LEU:C	2.40	0.42
1:A:355:PHE:HA	1:A:356:PRO:HD3	1.82	0.42
1:A:550:ILE:HD13	1:A:563:VAL:HG21	2.02	0.42
1:A:360:ASN:ND2	2:A:642:UGB:H2'	2.35	0.42
1:A:254:LEU:HG	1:A:258:TRP:CZ2	2.53	0.42
1:A:220:LYS:NZ	1:A:398:LYS:HE3	2.35	0.42
1:A:109:THR:HA	1:A:112:LEU:HD12	2.02	0.42
1:A:307:ILE:HD11	2:A:642:UGB:O'P	2.20	0.42
1:A:482:GLU:HG3	1:A:493:ARG:HB2	2.02	0.41
1:A:224:HIS:CE1	1:A:406:MET:H	2.39	0.41
1:A:437:LEU:HA	1:A:437:LEU:HD12	1.90	0.41
1:A:300:PRO:HD3	1:A:425:PHE:O	2.21	0.41
1:A:31:PRO:CB	1:A:36:GLU:HB2	2.51	0.41
1:A:149:ALA:HB2	1:A:184:LEU:HD13	2.02	0.41
1:A:327:GLU:CD	1:A:328:TYR:N	2.74	0.40
1:A:228:HIS:O	1:A:373:LEU:HD11	2.21	0.40
1:A:372:ARG:NE	1:A:372:ARG:HA	2.37	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	580/641 (90%)	560 (97%)	19 (3%)	1 (0%)	47	52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	127	ARG

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	493/536 (92%)	476 (97%)	17 (3%)	37	44

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	SER
1	A	10	GLN
1	A	35	ASP
1	A	127	ARG
1	A	157	ARG
1	A	256	ASN
1	A	319	ASP
1	A	360	ASN
1	A	375	GLU
1	A	377	HIS

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Mol	Chain	Res	Type
1	A	401	ARG
1	A	417	ASP
1	A	437	LEU
1	A	536	ARG
1	A	564	ARG
1	A	569	ARG
1	A	581	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	41	GLN
1	A	65	ASN
1	A	156	GLN
1	A	174	HIS
1	A	179	GLN
1	A	208	HIS
1	A	256	ASN
1	A	325	ASN
1	A	446	GLN
1	A	527	GLN
1	A	576	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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$
3	GOL	A	643	-	5,5,5	0.46	0	5,5,5	0.53	0
3	GOL	A	644	-	5,5,5	0.50	0	5,5,5	0.29	0
2	UGB	A	642	-	29,39,39	1.86	7 (24%)	39,60,60	2.21	7 (17%)

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	GOL	A	643	-	-	3/4/4/4	-
3	GOL	A	644	-	-	2/4/4/4	-
2	UGB	A	642	-	-	4/19/61/61	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	642	UGB	O4-C4	4.14	1.35	1.24
2	A	642	UGB	C6-N1	3.68	1.40	1.35
2	A	642	UGB	C3'-C2'	2.75	1.59	1.52
2	A	642	UGB	C2D-C1D	2.61	1.57	1.53
2	A	642	UGB	C3D-C4D	2.38	1.59	1.53
2	A	642	UGB	C1'-C2'	2.09	1.58	1.52
2	A	642	UGB	C2-N3	2.08	1.42	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	642	UGB	O3A-PB-O3B	9.42	121.49	102.48
2	A	642	UGB	O3B-C1'-C2'	5.30	118.09	108.38
2	A	642	UGB	O5'-C1'-O3B	-3.10	107.31	111.36
2	A	642	UGB	O4D-C1D-C2D	2.98	111.28	106.93
2	A	642	UGB	O4D-C4D-C5D	2.91	118.96	109.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	642	UGB	O3B-PB-O2B	-2.91	98.55	109.47
2	A	642	UGB	O5D-C5D-C4D	2.64	118.08	108.99

There are no chirality outliers.

All (9) torsion outliers are listed below:

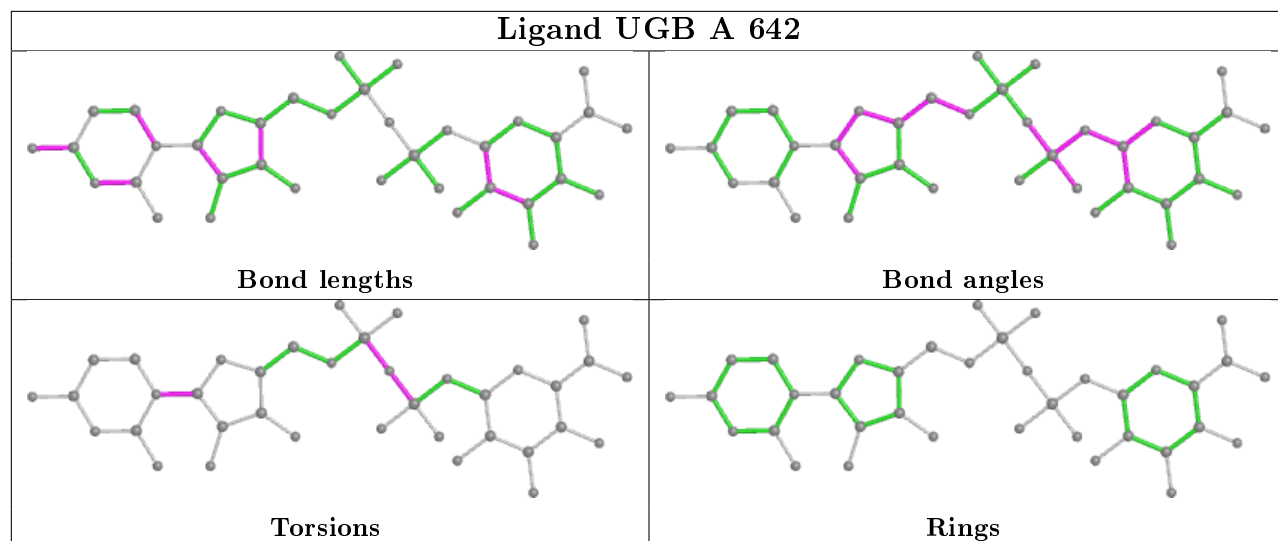
Mol	Chain	Res	Type	Atoms
3	A	643	GOL	C1-C2-C3-O3
3	A	644	GOL	O1-C1-C2-C3
2	A	642	UGB	O4D-C1D-N1-C6
3	A	643	GOL	O2-C2-C3-O3
3	A	644	GOL	O1-C1-C2-O2
2	A	642	UGB	PB-O3A-PA-O5D
2	A	642	UGB	PA-O3A-PB-O2B
3	A	643	GOL	O1-C1-C2-C3
2	A	642	UGB	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	642	UGB	2	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 ⓘ

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	582/641 (90%)	0.77	104 (17%) 1 1	26, 51, 121, 170	4 (0%)

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	352	PHE	11.4
1	A	338	LEU	8.9
1	A	351	GLY	8.5
1	A	585	ARG	8.1
1	A	393	ARG	8.0
1	A	586	ASP	7.6
1	A	80	ALA	7.2
1	A	334	VAL	6.9
1	A	337	ALA	6.2
1	A	582	CYS	6.1
1	A	81	ALA	6.0
1	A	353	SER	5.9
1	A	584	GLY	5.6
1	A	332	ALA	5.6
1	A	303	PRO	5.6
1	A	328	TYR	5.4
1	A	251	ALA	5.4
1	A	392	THR	5.3
1	A	336	ARG	5.1
1	A	331	PHE	5.0
1	A	126	GLU	4.9
1	A	390	ASP	4.6
1	A	79	PHE	4.4
1	A	321	TRP	4.3
1	A	362	LEU	4.3
1	A	318	GLY	4.2
1	A	389	SER	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	34	VAL	4.1
1	A	6	ASN	4.1
1	A	82	LEU	4.0
1	A	268	PHE	4.0
1	A	581	LEU	3.9
1	A	317	SER	3.9
1	A	29	GLY	3.8
1	A	335	SER	3.8
1	A	269	ILE	3.7
1	A	214	THR	3.7
1	A	354	PRO	3.7
1	A	304	LYS	3.7
1	A	363	VAL	3.5
1	A	213	GLU	3.4
1	A	320	PRO	3.4
1	A	559	LEU	3.4
1	A	394	ARG	3.4
1	A	364	PHE	3.3
1	A	388	TYR	3.3
1	A	40	ARG	3.2
1	A	329	ASN	3.2
1	A	78	ASP	3.1
1	A	39	GLU	3.1
1	A	31	PRO	3.1
1	A	397	LYS	3.1
1	A	361	THR	3.1
1	A	558	ALA	3.0
1	A	5	SER	3.0
1	A	33	THR	3.0
1	A	319	ASP	3.0
1	A	7	SER	3.0
1	A	316	ASN	3.0
1	A	391	GLU	3.0
1	A	3	ASN	3.0
1	A	333	GLU	3.0
1	A	267[A]	VAL	2.9
1	A	35	ASP	2.9
1	A	446	GLN	2.9
1	A	445	ALA	2.8
1	A	125	GLY	2.8
1	A	77	VAL	2.7
1	A	557	MET	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	119	LEU	2.7
1	A	359	VAL	2.6
1	A	124	LEU	2.6
1	A	26	LEU	2.5
1	A	296	PHE	2.5
1	A	580	SER	2.5
1	A	387	LYS	2.5
1	A	438	GLU	2.4
1	A	314	LYS	2.4
1	A	4	PRO	2.4
1	A	587	SER	2.4
1	A	53	ASN	2.3
1	A	9	LEU	2.3
1	A	583	ALA	2.3
1	A	209	LEU	2.2
1	A	118	VAL	2.2
1	A	417	ASP	2.2
1	A	206	ALA	2.2
1	A	416	ASP	2.2
1	A	42	ILE	2.2
1	A	266	ILE	2.1
1	A	120	VAL	2.1
1	A	274	ALA	2.1
1	A	315	LYS	2.1
1	A	76	GLU	2.1
1	A	32	GLU	2.1
1	A	83	GLU	2.1
1	A	307	ILE	2.1
1	A	302	VAL	2.1
1	A	330	VAL	2.1
1	A	532[A]	ILE	2.0
1	A	236	VAL	2.0
1	A	610	CYS	2.0
1	A	116	VAL	2.0
1	A	497	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

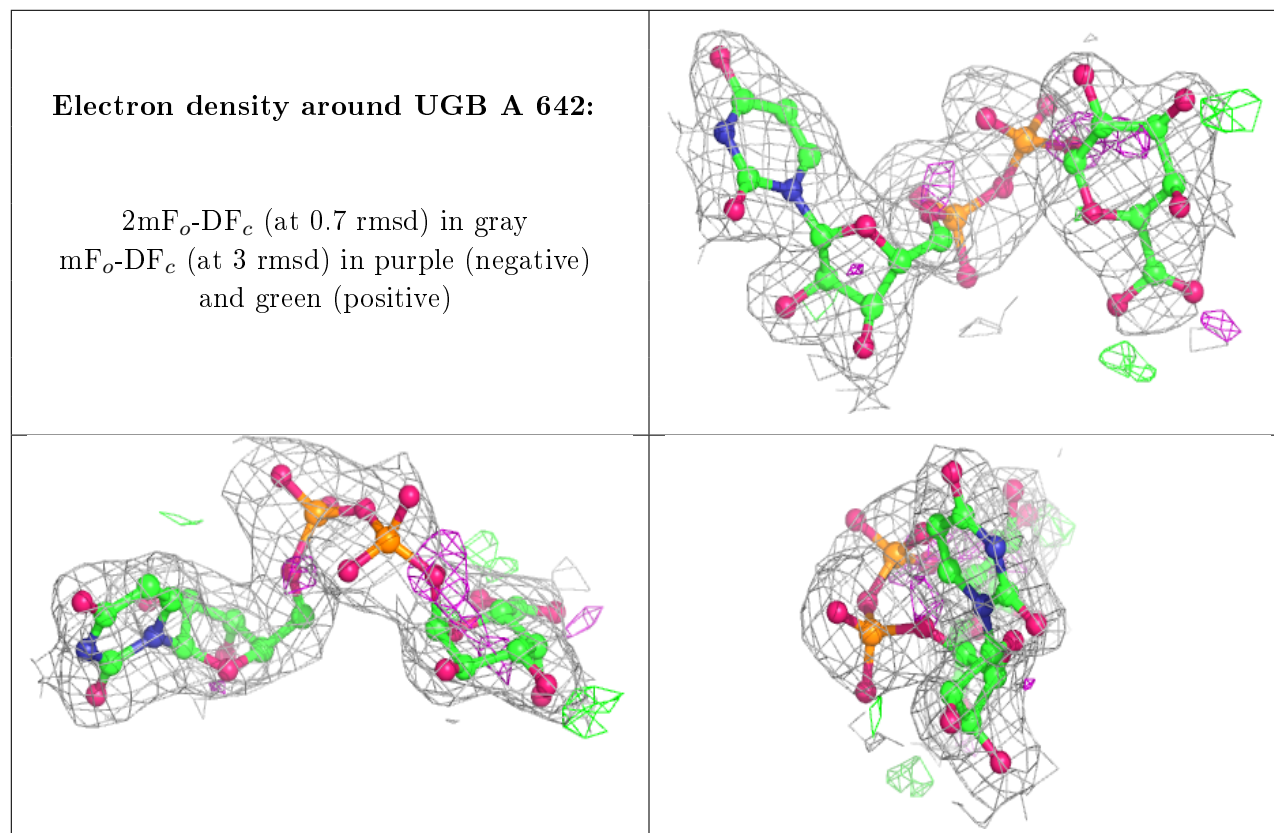
There are no carbohydrates in this entry.

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
3	GOL	A	643	6/6	0.68	0.37	76,79,80,81	0
3	GOL	A	644	6/6	0.91	0.22	65,69,70,71	0
2	UGB	A	642	37/37	0.93	0.14	38,61,156,257	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 ⓘ

There are no such residues in this entry.