Full wwPDB X-ray Structure Validation Report (i)

May 25, 2020 – 04:38 pm BST

PDB ID	:	5HUV
Title	:	Structure of Candida albicans trehalose-6-phosphate synthase E341R/E346R in complex with UDP-glucose
Authors	:	Miao, Y.; Brennan, R.G.
Deposited on	:	2016-01-27
Resolution	:	2.00 Å(reported)

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

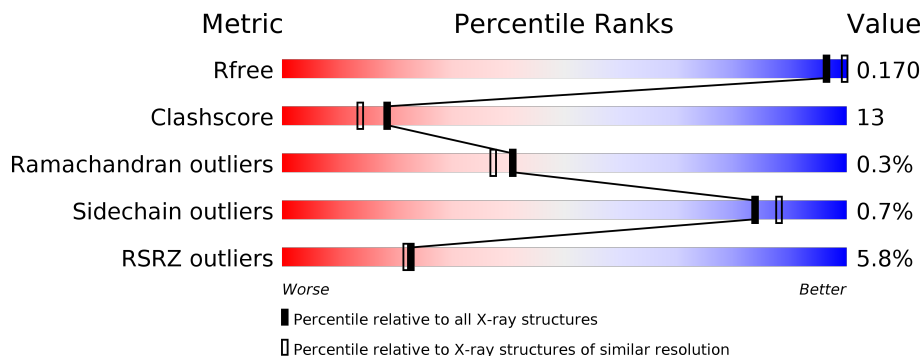|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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	Percentile Ranks	Value
Rfree		0.170
Clashscore		13
Ramachandran outliers		0.3%
Sidechain outliers		0.7%
RSRZ outliers		5.8%

Worse ◼ Percentile relative to all X-ray structures

Better ◻ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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 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 <=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	478	3% 77% 20% ··
1	B	478	8% 73% 23% ··

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8364 atoms, of which 44 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 Alpha,alpha-trehalose-phosphate synthase [UDP-forming].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	469	Total 3776	C 2442	N 626	O 697	S 11	0	0	0
1	B	464	Total 3737	C 2418	N 620	O 688	S 11	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	341	ARG	GLU	engineered mutation	UNP Q92410
A	346	ARG	GLU	engineered mutation	UNP Q92410
B	341	ARG	GLU	engineered mutation	UNP Q92410
B	346	ARG	GLU	engineered mutation	UNP Q92410

- Molecule 2 is URIDINE-5'-DIPHOSPHATE-GLUCOSE (three-letter code: UPG) (formula: $C_{15}H_{24}N_2O_{17}P_2$).
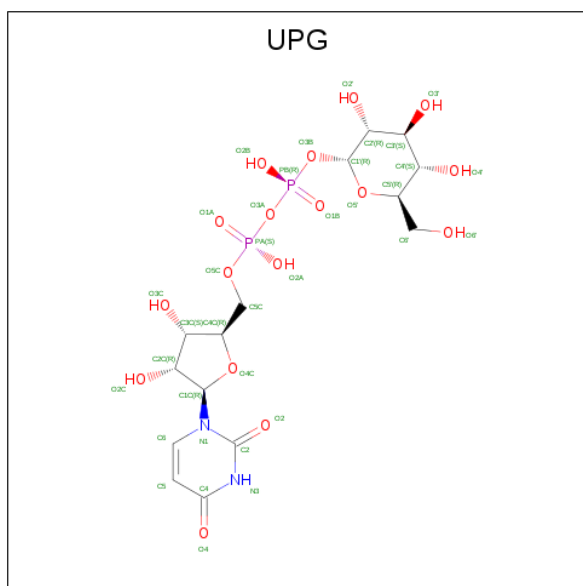
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			58	15	22	2	17	2		
2	B	1	Total	C	H	N	O	P	0	0
			58	15	22	2	17	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	354	Total	O	0	0
			354	354		
3	B	381	Total	O	0	0
			381	381		

3 Residue-property plots ⓘ

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: Alpha,alpha-trehalose-phosphate synthase [UDP-forming]
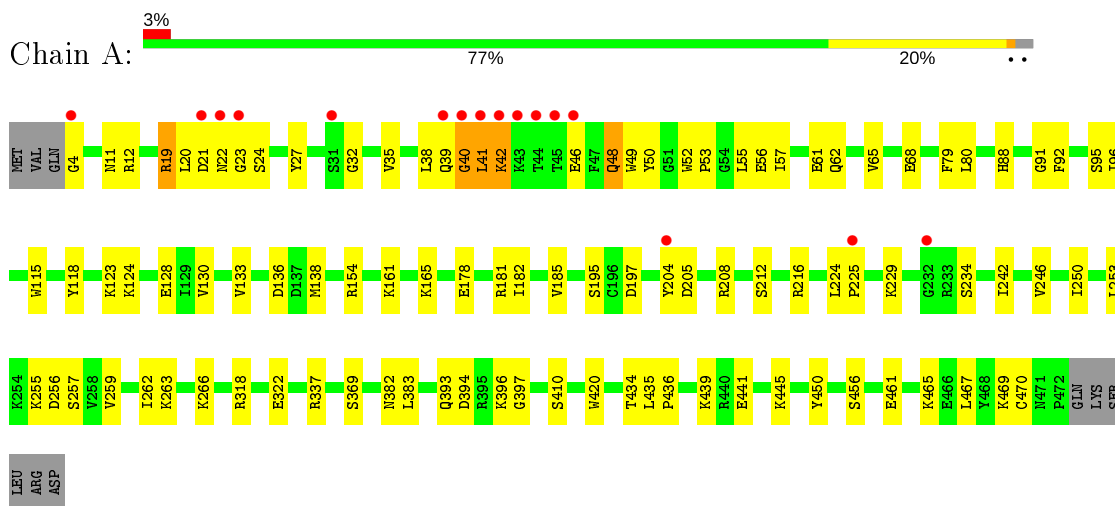
• Molecule 1: Alpha,alpha-trehalose-phosphate synthase [UDP-forming]
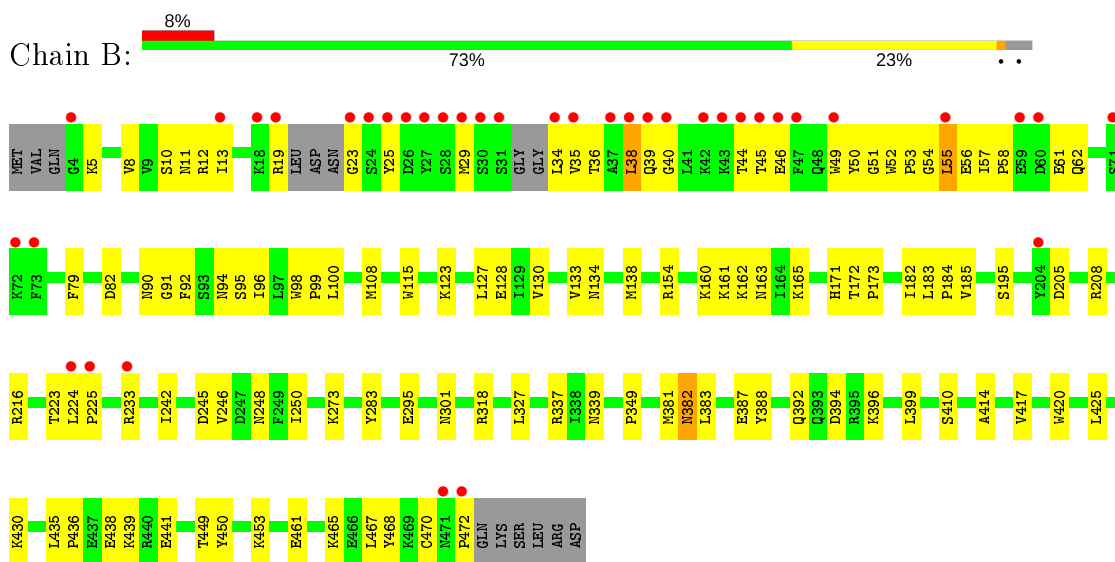
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α, β, γ	98.64Å 98.64Å 186.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.32 – 2.00 49.32 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.32-2.00) 98.7 (49.32-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	4.59 (at 2.00Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.145 , 0.171 0.144 , 0.170	Depositor DCC
R_{free} test set	2017 reflections (2.93%)	wwPDB-VP
Wilson B-factor (Å^2)	22.2	Xtriage
Anisotropy	0.241	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 29.6	EDS
L-test for twinning [2]	$<|L|> = 0.42$, $<L^2> = 0.24$	Xtriage
Estimated twinning fraction	0.268 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.270 for h,-h-k,-l	Depositor
Outliers	0 of 68942 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8364	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $<|L|>$, $<L^2>$ 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: UPG

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	0/3868	0.53	1/5239 (0.0%)
1	B	0.39	0/3826	0.54	0/5179
All	All	0.38	0/7694	0.54	1/10418 (0.0%)

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	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	40	GLY	N-CA-C	-5.47	99.43	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	42	LYS	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	3776	0	3768	83	2
1	B	3737	0	3732	118	1
2	A	36	22	21	1	0
2	B	36	22	21	0	0
3	A	354	0	0	24	2
3	B	381	0	0	32	2
All	All	8320	44	7542	199	4

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (199) 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:13:ILE:HA	1:B:49:TRP:CZ3	2.03	0.93
1:A:128:GLU:OE1	3:A:601:HOH:O	1.90	0.90
1:B:205:ASP:OD1	1:B:208:ARG:NH1	2.04	0.89
1:A:88:HIS:O	3:A:602:HOH:O	1.90	0.89
1:A:22:ASN:N	1:A:23:GLY:HA2	1.88	0.89
1:A:234:SER:O	3:A:603:HOH:O	1.90	0.89
1:B:23:GLY:O	3:B:601:HOH:O	1.93	0.86
1:A:19:ARG:NH2	1:A:61:GLU:OE2	2.09	0.86
1:A:369:SER:O	3:A:604:HOH:O	1.95	0.85
1:B:49:TRP:CH2	1:B:51:GLY:HA3	2.15	0.81
1:B:273:LYS:NZ	3:B:602:HOH:O	1.94	0.81
1:A:204:TYR:CE2	1:A:208:ARG:HD2	2.17	0.80
1:B:295:GLU:OE1	3:B:603:HOH:O	1.99	0.79
1:B:13:ILE:HA	1:B:49:TRP:CH2	2.18	0.79
1:A:92:PHE:HB3	3:A:602:HOH:O	1.84	0.78
1:B:223:THR:OG1	3:B:604:HOH:O	2.00	0.78
1:A:435:LEU:HD12	1:A:436:PRO:HD2	1.66	0.78
1:A:394:ASP:O	3:A:605:HOH:O	2.02	0.78
1:A:42:LYS:NZ	3:A:606:HOH:O	2.04	0.78
1:B:337:ARG:NH2	3:B:603:HOH:O	2.17	0.77
1:B:108:MET:SD	3:B:923:HOH:O	2.41	0.77
1:B:13:ILE:HG22	1:B:49:TRP:HZ3	1.50	0.76
1:B:82:ASP:OD2	3:B:605:HOH:O	2.03	0.76
1:A:439:LYS:NZ	3:A:612:HOH:O	2.16	0.76
1:B:13:ILE:HG22	1:B:49:TRP:CZ3	2.21	0.75
1:A:456:SER:OG	3:A:607:HOH:O	2.04	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:ASP:HB3	1:B:248:ASN:ND2	2.03	0.73
1:B:467:LEU:O	3:B:606:HOH:O	2.08	0.72
1:B:224:LEU:HB3	1:B:225:PRO:HD2	1.72	0.72
1:A:322:GLU:OE1	3:A:608:HOH:O	2.08	0.70
1:B:128:GLU:OE1	3:B:607:HOH:O	2.09	0.70
1:A:318:ARG:NH1	3:A:618:HOH:O	2.25	0.70
1:B:134:ASN:ND2	3:B:616:HOH:O	2.26	0.69
1:B:34:LEU:O	1:B:38:LEU:HD22	1.92	0.69
1:B:100:LEU:HD13	3:B:923:HOH:O	1.92	0.68
1:B:13:ILE:CD1	1:B:53:PRO:HA	2.24	0.67
1:A:397:GLY:HA3	3:A:604:HOH:O	1.95	0.67
1:B:44:THR:OG1	3:B:608:HOH:O	2.13	0.66
1:A:229:LYS:NZ	3:A:621:HOH:O	2.28	0.66
1:B:19:ARG:HA	1:B:25:TYR:CZ	2.30	0.65
1:A:118:TYR:HD1	3:A:602:HOH:O	1.79	0.65
1:B:39:GLN:N	1:B:40:GLY:HA3	2.12	0.65
1:A:56:GLU:OE1	3:A:611:HOH:O	2.14	0.65
1:B:13:ILE:CG2	1:B:49:TRP:HZ3	2.09	0.65
1:B:19:ARG:HG3	1:B:25:TYR:CE2	2.32	0.65
1:B:35:VAL:HA	1:B:38:LEU:CD2	2.27	0.65
1:B:49:TRP:HH2	1:B:51:GLY:HA3	1.63	0.64
1:B:45:THR:HG22	1:B:46:GLU:N	2.12	0.64
1:A:19:ARG:HH12	1:A:23:GLY:HA3	1.64	0.63
1:B:46:GLU:OE1	1:B:46:GLU:N	2.32	0.62
1:A:12:ARG:HD2	3:A:815:HOH:O	1.97	0.62
1:A:39:GLN:N	1:A:40:GLY:HA3	2.14	0.62
1:A:204:TYR:CD2	1:A:208:ARG:HD2	2.35	0.61
1:A:123:LYS:HE3	3:A:680:HOH:O	2.00	0.61
1:B:435:LEU:HD12	1:B:436:PRO:HD2	1.83	0.60
1:B:163:ASN:OD1	1:B:472:PRO:HG2	2.02	0.60
1:B:461:GLU:HB3	1:B:465:LYS:HE3	1.83	0.59
1:B:470:CYS:N	3:B:606:HOH:O	2.27	0.59
1:A:393:GLN:O	1:A:396:LYS:NZ	2.33	0.59
1:B:11:ASN:OD1	3:B:609:HOH:O	2.17	0.59
1:A:205:ASP:HB2	3:A:742:HOH:O	2.02	0.58
1:A:4:GLY:HA3	1:A:136:ASP:O	2.02	0.58
1:B:29:MET:HE3	1:B:35:VAL:HG21	1.84	0.58
1:B:449:THR:OG1	3:B:610:HOH:O	2.17	0.58
1:B:10:SER:HG	1:B:49:TRP:HZ2	1.52	0.58
1:A:11:ASN:ND2	3:A:628:HOH:O	2.37	0.58
1:B:138:MET:HG2	1:B:165:LYS:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:GLU:O	1:A:465:LYS:HG2	2.04	0.57
1:B:10:SER:OG	1:B:49:TRP:HZ2	1.87	0.57
1:B:90:ASN:HA	1:B:94:ASN:HB2	1.84	0.57
1:A:224:LEU:HB3	1:A:225:PRO:HD2	1.86	0.57
1:B:160:LYS:NZ	3:B:625:HOH:O	2.29	0.56
1:A:62:GLN:HB3	1:A:79:PHE:CE2	2.39	0.56
1:A:434:THR:OG1	3:A:613:HOH:O	2.17	0.56
1:B:130:VAL:O	1:B:133:VAL:HG12	2.06	0.56
1:B:35:VAL:HA	1:B:38:LEU:HD23	1.88	0.56
1:A:38:LEU:O	1:A:41:LEU:N	2.39	0.56
1:B:318:ARG:NH2	3:B:630:HOH:O	2.39	0.55
1:A:21:ASP:C	1:A:23:GLY:HA2	2.27	0.55
1:A:259:VAL:O	1:A:263:LYS:HG3	2.07	0.55
1:B:461:GLU:O	1:B:465:LYS:HG3	2.07	0.55
1:A:410:SER:HB3	1:A:450:TYR:CZ	2.43	0.54
1:B:34:LEU:HG	1:B:38:LEU:HD21	1.88	0.54
1:B:56:GLU:HG3	1:B:82:ASP:CG	2.27	0.54
1:B:396:LYS:HE2	1:B:441:GLU:OE1	2.07	0.54
1:A:255:LYS:HE2	1:A:257:SER:OG	2.08	0.54
1:B:161:LYS:C	1:B:162:LYS:HD2	2.27	0.54
1:B:52:TRP:CD1	1:B:53:PRO:HD2	2.43	0.54
1:B:13:ILE:HD11	1:B:53:PRO:HA	1.88	0.53
1:A:337:ARG:HG2	1:A:337:ARG:HH11	1.73	0.53
1:A:337:ARG:HG2	1:A:337:ARG:NH1	2.22	0.53
1:A:80:LEU:CD2	1:A:124:LYS:HD2	2.39	0.53
1:B:13:ILE:CG2	1:B:49:TRP:CZ3	2.88	0.53
1:B:337:ARG:HG2	1:B:337:ARG:HH11	1.73	0.53
1:A:20:LEU:O	1:A:21:ASP:HB3	2.09	0.53
1:A:22:ASN:N	1:A:23:GLY:CA	2.69	0.52
1:A:138:MET:HG2	1:A:165:LYS:HB2	1.89	0.52
1:B:233:ARG:NE	3:B:617:HOH:O	2.27	0.52
1:B:19:ARG:HA	1:B:25:TYR:CE2	2.45	0.52
1:B:161:LYS:NZ	3:B:616:HOH:O	2.43	0.52
1:B:19:ARG:HG3	1:B:25:TYR:HE2	1.73	0.51
1:A:465:LYS:O	1:A:469:LYS:HG3	2.10	0.51
1:B:208:ARG:NH2	3:B:622:HOH:O	2.32	0.51
1:B:13:ILE:CA	1:B:49:TRP:CZ3	2.86	0.51
1:A:80:LEU:HD23	1:A:124:LYS:HD2	1.93	0.51
1:A:259:VAL:HG12	1:A:263:LYS:HE2	1.93	0.50
1:A:46:GLU:OE1	1:A:46:GLU:N	2.45	0.50
1:B:301:ASN:OD1	1:B:430:LYS:HE2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:VAL:HG13	1:A:161:LYS:HE3	1.93	0.50
1:B:57:ILE:HD12	1:B:79:PHE:CE1	2.47	0.50
1:B:39:GLN:NE2	3:B:639:HOH:O	2.44	0.50
1:A:19:ARG:CG	1:A:19:ARG:HH11	2.25	0.49
1:A:212:SER:OG	1:A:216:ARG:NH1	2.44	0.49
1:B:49:TRP:CZ3	1:B:50:TYR:C	2.86	0.49
1:B:92:PHE:CD1	1:B:96:ILE:HD12	2.47	0.49
1:B:399:LEU:HD23	1:B:414:ALA:HB2	1.94	0.49
1:B:246:VAL:O	1:B:250:ILE:HG12	2.12	0.49
1:B:57:ILE:HD12	1:B:79:PHE:HE1	1.76	0.49
1:B:417:VAL:HG21	1:B:425:LEU:HD13	1.94	0.49
2:A:501:UPG:O2'	2:A:501:UPG:O2B	2.15	0.48
1:B:208:ARG:NE	3:B:622:HOH:O	2.28	0.48
1:B:383:LEU:O	1:B:387:GLU:HG3	2.13	0.48
1:B:12:ARG:C	1:B:49:TRP:CH2	2.87	0.48
1:A:204:TYR:O	1:A:208:ARG:HG3	2.13	0.48
1:B:45:THR:CG2	1:B:46:GLU:N	2.76	0.48
1:A:115:TRP:CE2	1:A:185:VAL:HG11	2.49	0.48
1:B:115:TRP:CE2	1:B:185:VAL:HG11	2.49	0.48
1:B:171:HIS:HB3	3:B:614:HOH:O	2.14	0.48
1:B:439:LYS:HE3	3:B:846:HOH:O	2.13	0.48
1:B:337:ARG:HG2	1:B:337:ARG:NH1	2.28	0.47
1:A:178:GLU:OE1	1:A:181:ARG:NH1	2.47	0.47
1:A:22:ASN:HB3	1:A:24:SER:N	2.30	0.47
1:B:339:ASN:OD1	1:B:349:PRO:HD2	2.15	0.47
1:B:394:ASP:OD2	3:B:612:HOH:O	2.20	0.47
1:B:438:GLU:H	1:B:438:GLU:CD	2.18	0.47
1:B:35:VAL:HA	1:B:38:LEU:HD22	1.97	0.47
1:B:13:ILE:CA	1:B:49:TRP:CH2	2.95	0.47
1:A:19:ARG:HH12	1:A:23:GLY:CA	2.25	0.46
1:B:52:TRP:CZ3	1:B:54:GLY:HA2	2.51	0.46
1:B:162:LYS:HD2	1:B:162:LYS:N	2.31	0.46
1:B:52:TRP:CH2	1:B:54:GLY:HA2	2.50	0.46
1:A:154:ARG:NH2	1:A:197:ASP:OD2	2.48	0.46
1:A:246:VAL:O	1:A:250:ILE:HG12	2.16	0.46
1:A:32:GLY:O	1:A:35:VAL:HG12	2.16	0.45
1:A:48:GLN:HG3	1:A:50:TYR:CE1	2.52	0.45
1:A:182:ILE:HG23	1:B:420:TRP:CG	2.50	0.45
1:B:470:CYS:HB2	3:B:606:HOH:O	2.17	0.45
1:B:388:TYR:O	1:B:392:GLN:HG2	2.15	0.45
1:B:49:TRP:CZ3	1:B:51:GLY:N	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:LYS:HE3	3:B:778:HOH:O	2.15	0.45
1:A:420:TRP:CG	1:B:182:ILE:HG23	2.51	0.45
1:B:29:MET:CE	1:B:35:VAL:HG21	2.46	0.45
1:B:96:ILE:HA	1:B:108:MET:HG3	1.98	0.45
1:A:22:ASN:HB3	1:A:24:SER:H	1.82	0.45
1:B:165:LYS:NZ	3:B:606:HOH:O	2.49	0.45
1:A:61:GLU:HA	3:A:650:HOH:O	2.17	0.44
1:A:242:ILE:HG23	1:A:383:LEU:HD21	1.99	0.44
1:A:19:ARG:NH1	1:A:23:GLY:HA3	2.32	0.44
1:A:27:TYR:CE2	1:A:68:GLU:HG2	2.52	0.44
1:A:253:LEU:O	3:A:614:HOH:O	2.21	0.44
1:A:154:ARG:HG3	1:A:195:SER:HB3	1.99	0.44
1:A:439:LYS:HD3	1:A:439:LYS:HA	1.63	0.44
1:A:182:ILE:HG23	1:B:420:TRP:CD1	2.53	0.44
1:A:52:TRP:CD1	1:A:53:PRO:HD2	2.53	0.43
1:B:436:PRO:HA	3:B:874:HOH:O	2.18	0.43
1:B:39:GLN:HG2	1:B:245:ASP:OD1	2.18	0.43
1:B:410:SER:HB3	1:B:450:TYR:CZ	2.54	0.43
1:B:12:ARG:HG2	1:B:52:TRP:HE3	1.82	0.43
1:B:55:LEU:N	1:B:55:LEU:HD12	2.33	0.43
1:A:322:GLU:OE2	3:A:615:HOH:O	2.21	0.43
1:A:19:ARG:NH1	1:A:19:ARG:CG	2.80	0.43
1:B:453:LYS:HB2	3:B:711:HOH:O	2.17	0.43
1:B:216:ARG:HH11	1:B:216:ARG:HG3	1.84	0.42
1:A:91:GLY:O	1:A:95:SER:HB2	2.20	0.42
1:B:233:ARG:NH2	3:B:617:HOH:O	2.48	0.42
1:A:130:VAL:O	1:A:133:VAL:HG12	2.20	0.42
1:B:165:LYS:NZ	1:B:468:TYR:O	2.47	0.41
1:A:49:TRP:HD1	1:A:50:TYR:N	2.18	0.41
1:B:58:PRO:HG2	1:B:61:GLU:HB3	2.02	0.41
1:B:154:ARG:HG3	1:B:195:SER:HB3	2.02	0.41
1:B:381:MET:O	1:B:382:ASN:HB3	2.20	0.41
1:B:62:GLN:HB3	1:B:79:PHE:CE2	2.55	0.41
1:B:91:GLY:O	1:B:95:SER:HB2	2.20	0.41
1:A:57:ILE:HD12	1:A:65:VAL:HG21	2.01	0.41
1:B:283:TYR:N	1:B:327:LEU:HD22	2.35	0.41
1:B:8:VAL:HG12	1:B:49:TRP:CD1	2.55	0.41
1:A:262:ILE:CG2	1:A:266:LYS:HE3	2.51	0.41
1:B:12:ARG:O	1:B:49:TRP:CH2	2.74	0.41
1:B:242:ILE:HG23	1:B:383:LEU:HD21	2.03	0.41
1:A:92:PHE:O	1:A:96:ILE:HB	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:467:LEU:O	1:A:470:CYS:HB2	2.20	0.41
1:B:183:LEU:HD12	1:B:184:PRO:HD2	2.03	0.41
1:A:441:GLU:O	1:A:445:LYS:HG2	2.22	0.40
1:B:36:THR:HG22	3:B:696:HOH:O	2.22	0.40
1:A:208:ARG:NE	3:A:652:HOH:O	2.54	0.40
1:B:98:TRP:N	1:B:99:PRO:HD2	2.36	0.40
1:B:172:THR:HB	1:B:173:PRO:HD2	2.02	0.40
1:A:48:GLN:CG	1:A:50:TYR:CE1	3.04	0.40
1:B:127:LEU:O	1:B:130:VAL:HG12	2.22	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:GLU:OE1	1:A:469:LYS:NZ[4_695]	2.08	0.12
3:A:891:HOH:O	3:B:757:HOH:O[4_7105]	2.14	0.06
1:A:256:ASP:OD1	1:B:23:GLY:N[5_365]	2.18	0.02
3:A:643:HOH:O	3:B:654:HOH:O[5_465]	2.19	0.01

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	467/478 (98%)	457 (98%)	8 (2%)	2 (0%)	34	30
1	B	458/478 (96%)	446 (97%)	11 (2%)	1 (0%)	47	44
All	All	925/956 (97%)	903 (98%)	19 (2%)	3 (0%)	41	37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	LEU

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Mol	Chain	Res	Type
1	B	382	ASN
1	A	382	ASN

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	420/429 (98%)	417 (99%)	3 (1%)	84	88
1	B	416/429 (97%)	413 (99%)	3 (1%)	84	88
All	All	836/858 (97%)	830 (99%)	6 (1%)	84	88

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ARG
1	A	48	GLN
1	A	55	LEU
1	B	38	LEU
1	B	55	LEU
1	B	123	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

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	UPG	A	501	-	31,38,38	4.39	11 (35%)	41,58,58	1.86	7 (17%)
2	UPG	B	501	-	31,38,38	4.37	10 (32%)	41,58,58	1.91	8 (19%)

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	UPG	A	501	-	-	10/21/59/59	0/3/3/3
2	UPG	B	501	-	-	9/21/59/59	0/3/3/3

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	UPG	O4C-C1C	15.24	1.62	1.41
2	A	501	UPG	O4C-C1C	15.14	1.62	1.41
2	A	501	UPG	C2C-C1C	-13.07	1.33	1.53
2	B	501	UPG	C2C-C1C	-12.94	1.34	1.53
2	A	501	UPG	O4C-C4C	-6.33	1.30	1.45
2	B	501	UPG	O4C-C4C	-6.28	1.31	1.45
2	B	501	UPG	C4-N3	5.91	1.43	1.33
2	A	501	UPG	C4-N3	5.72	1.43	1.33
2	B	501	UPG	C6-N1	5.68	1.42	1.35
2	A	501	UPG	C6-N1	5.51	1.42	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	UPG	C6-C5	4.53	1.48	1.38
2	B	501	UPG	C6-C5	4.48	1.48	1.38
2	A	501	UPG	O3C-C3C	-4.46	1.32	1.43
2	B	501	UPG	O3C-C3C	-4.38	1.32	1.43
2	A	501	UPG	C2-N3	4.10	1.46	1.38
2	B	501	UPG	C2-N3	3.91	1.45	1.38
2	A	501	UPG	O5'-C1'	3.82	1.51	1.41
2	B	501	UPG	O5'-C1'	3.10	1.49	1.41
2	A	501	UPG	C3C-C4C	2.33	1.58	1.53
2	A	501	UPG	O5'-C5'	2.09	1.49	1.44
2	B	501	UPG	C3C-C4C	2.04	1.58	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	UPG	O3B-C1'-C2'	6.79	120.82	108.38
2	A	501	UPG	O3B-C1'-C2'	6.53	120.34	108.38
2	A	501	UPG	O3A-PB-O3B	4.52	111.59	102.48
2	B	501	UPG	O5'-C1'-O3B	-4.38	105.64	111.36
2	A	501	UPG	O4'-C4'-C3'	-4.16	100.73	110.35
2	B	501	UPG	O3A-PB-O3B	3.68	109.91	102.48
2	B	501	UPG	O4'-C4'-C3'	-3.24	102.86	110.35
2	B	501	UPG	O5'-C5'-C4'	3.17	115.45	109.69
2	A	501	UPG	C3'-C4'-C5'	3.09	115.75	110.24
2	B	501	UPG	O5'-C1'-C2'	-2.79	104.45	110.35
2	A	501	UPG	O5'-C1'-C2'	-2.77	104.49	110.35
2	A	501	UPG	O5'-C5'-C4'	2.57	114.37	109.69
2	B	501	UPG	C3'-C4'-C5'	2.19	114.14	110.24
2	A	501	UPG	O5'-C1'-O3B	-2.11	108.61	111.36
2	B	501	UPG	O5'-C5'-C6'	-2.02	101.42	106.44

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	UPG	C2C-C1C-N1-C6
2	A	501	UPG	O4C-C1C-N1-C6
2	A	501	UPG	O4C-C4C-C5C-O5C
2	A	501	UPG	C1'-O3B-PB-O2B
2	A	501	UPG	C2'-C1'-O3B-PB
2	A	501	UPG	O5'-C1'-O3B-PB
2	B	501	UPG	PB-O3A-PA-O5C

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Mol	Chain	Res	Type	Atoms
2	B	501	UPG	C2'-C1'-O3B-PB
2	B	501	UPG	O5'-C1'-O3B-PB
2	B	501	UPG	C4'-C5'-C6'-O6'
2	B	501	UPG	O5'-C5'-C6'-O6'
2	B	501	UPG	O4C-C4C-C5C-O5C
2	A	501	UPG	C3C-C4C-C5C-O5C
2	B	501	UPG	C3C-C4C-C5C-O5C
2	A	501	UPG	C1'-O3B-PB-O3A
2	B	501	UPG	C1'-O3B-PB-O3A
2	A	501	UPG	PB-O3A-PA-O5C
2	A	501	UPG	PA-O3A-PB-O3B
2	B	501	UPG	PA-O3A-PB-O3B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	UPG	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 then 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.

Ligand UPG A 501

Bond lengths

Bond angles

Torsions

Rings

Ligand UPG B 501

Bond lengths

Bond angles

Torsions

Rings
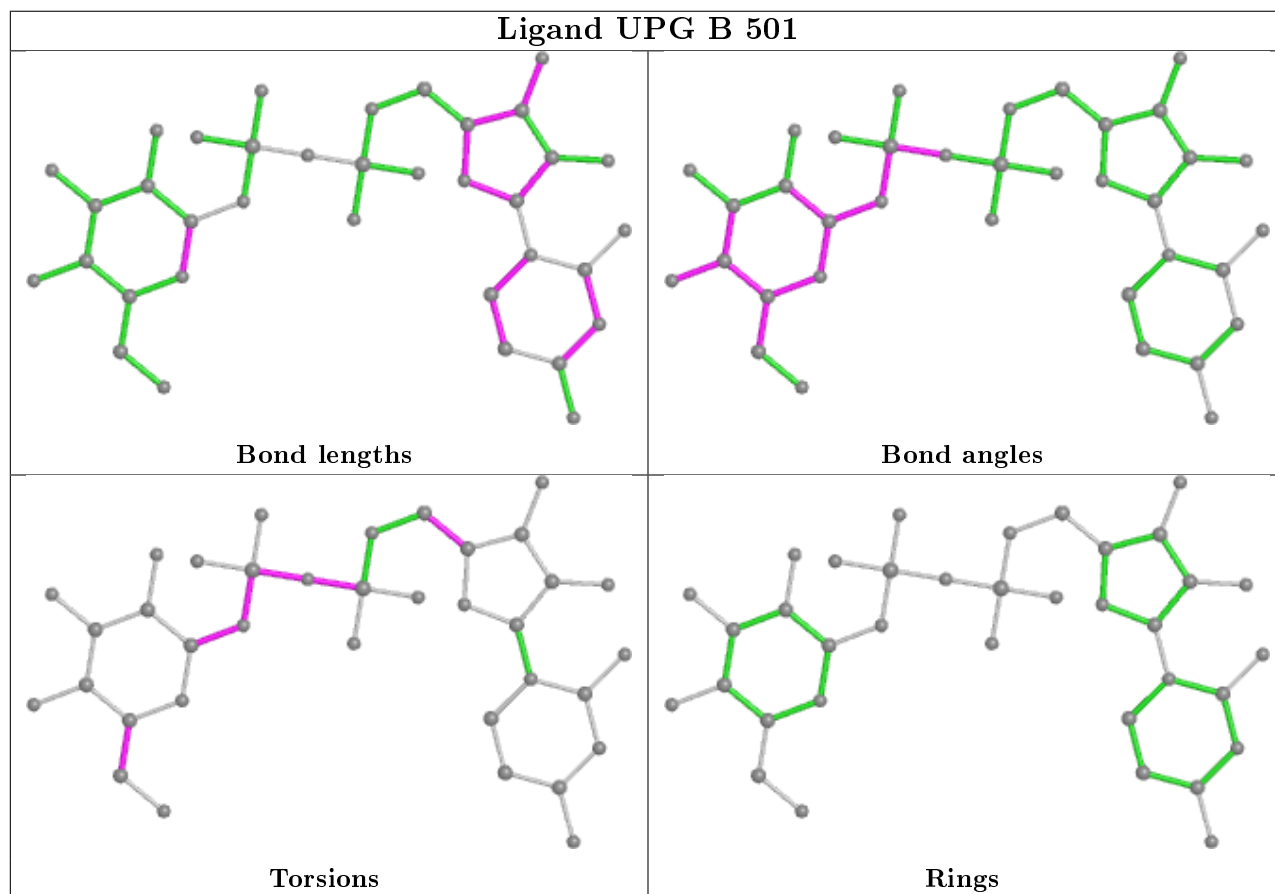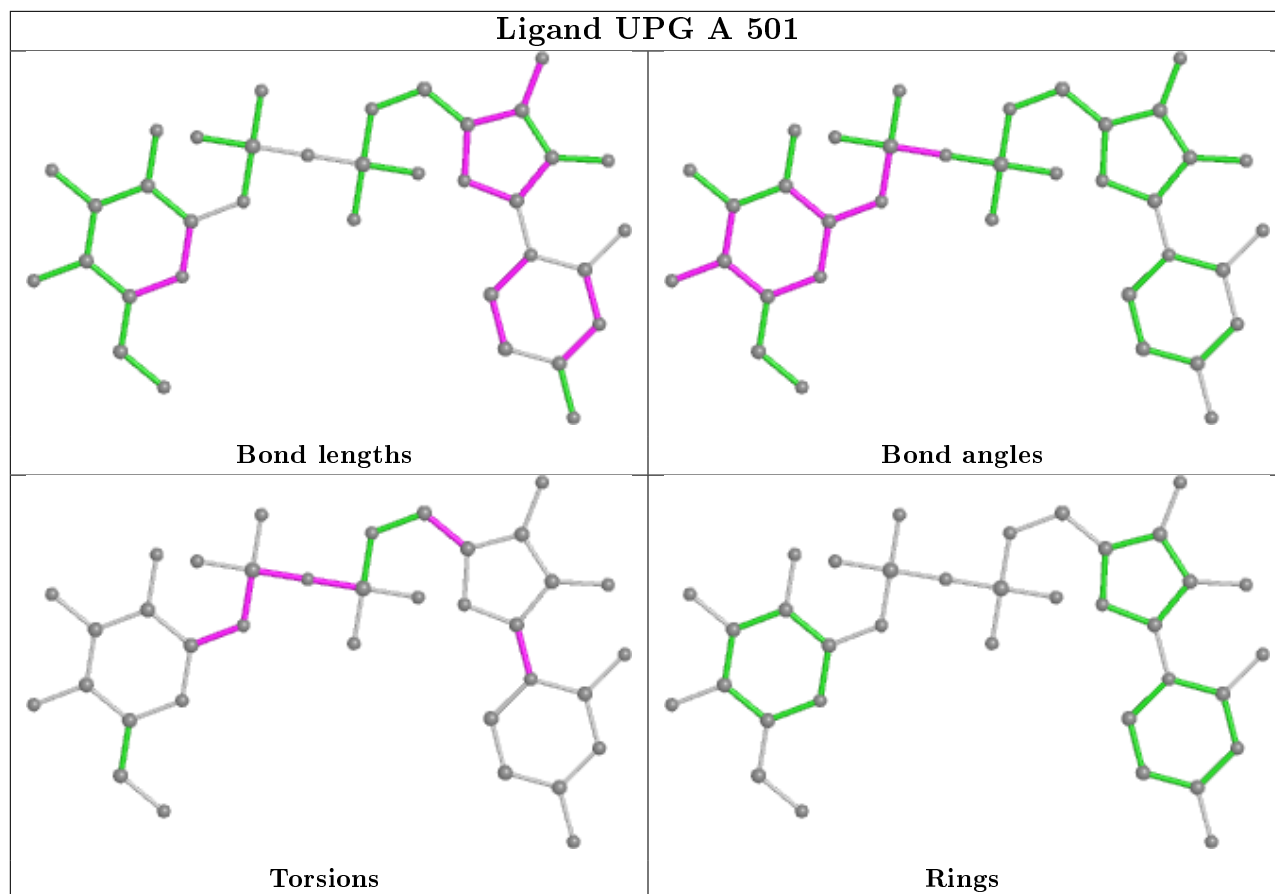
5.7 Other polymers (i)

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 (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	469/478 (98%)	-0.18	16 (3%)	45	44	13, 23, 44, 65	0
1	B	464/478 (97%)	0.06	38 (8%)	11	11	13, 23, 55, 80	0
All	All	933/956 (97%)	-0.06	54 (5%)	23	22	13, 23, 50, 80	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	23	GLY	9.2
1	B	45	THR	8.7
1	B	25	TYR	8.1
1	B	42	LYS	8.0
1	B	472	PRO	7.0
1	B	49	TRP	7.0
1	B	24	SER	6.8
1	B	4	GLY	5.3
1	B	39	GLN	5.1
1	B	19	ARG	5.0
1	B	47	PHE	4.8
1	B	224	LEU	4.8
1	B	26	ASP	4.6
1	B	60	ASP	4.4
1	B	27	TYR	4.3
1	B	204	TYR	4.3
1	B	29	MET	4.2
1	A	21	ASP	4.1
1	A	40	GLY	4.0
1	A	43	LYS	3.8
1	B	13	ILE	3.7
1	A	45	THR	3.6
1	A	46	GLU	3.6
1	B	18	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	35	VAL	3.5
1	A	225	PRO	3.4
1	B	225	PRO	3.4
1	B	40	GLY	3.4
1	B	43	LYS	3.3
1	B	37	ALA	3.3
1	A	39	GLN	3.3
1	B	38	LEU	3.1
1	B	46	GLU	3.1
1	B	72	LYS	3.1
1	A	44	THR	3.0
1	B	34	LEU	3.0
1	A	22	ASN	2.8
1	A	4	GLY	2.8
1	B	233	ARG	2.7
1	B	73	PHE	2.6
1	A	42	LYS	2.4
1	B	44	THR	2.3
1	B	59	GLU	2.3
1	B	71	SER	2.3
1	A	41	LEU	2.2
1	B	28	SER	2.2
1	A	23	GLY	2.2
1	A	31	SER	2.2
1	A	204	TYR	2.1
1	B	30	SER	2.1
1	B	55	LEU	2.1
1	A	232	GLY	2.0
1	B	31	SER	2.0
1	B	471	ASN	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.
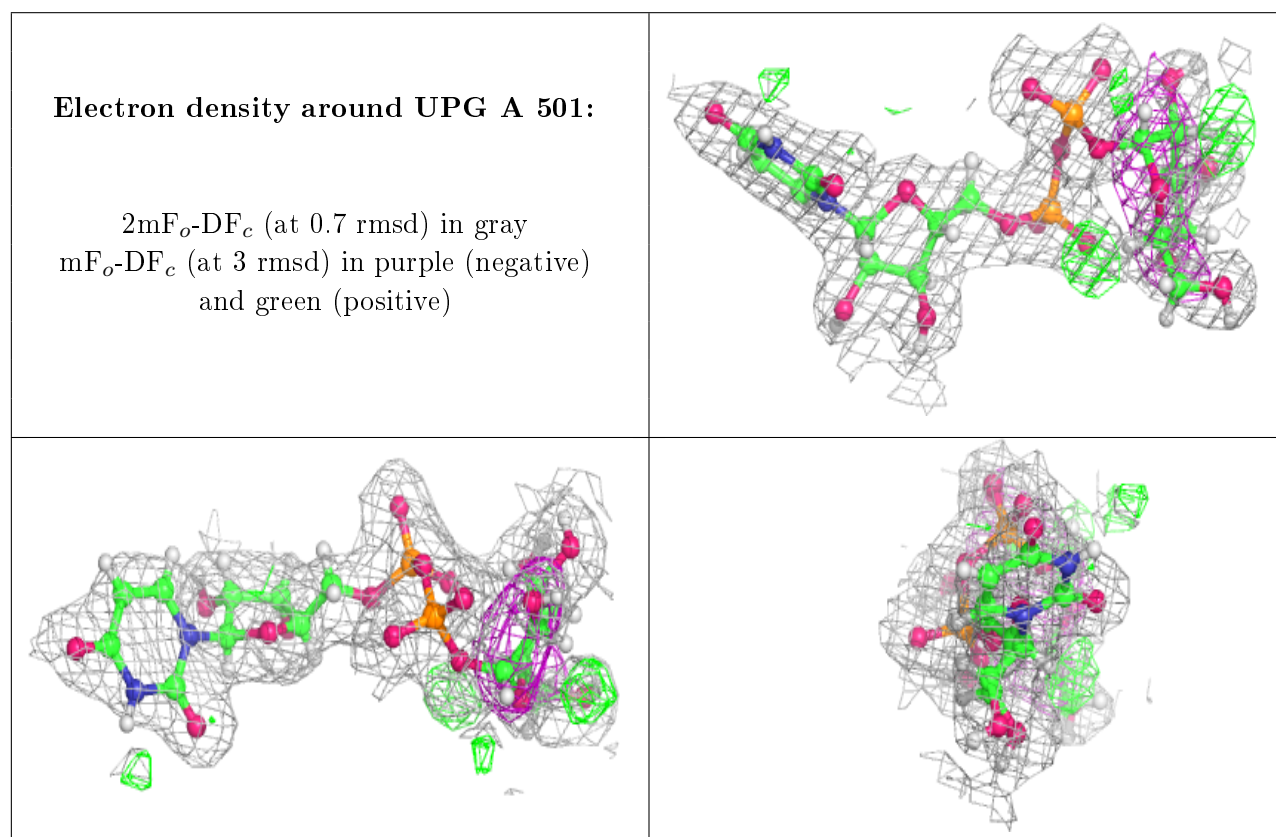
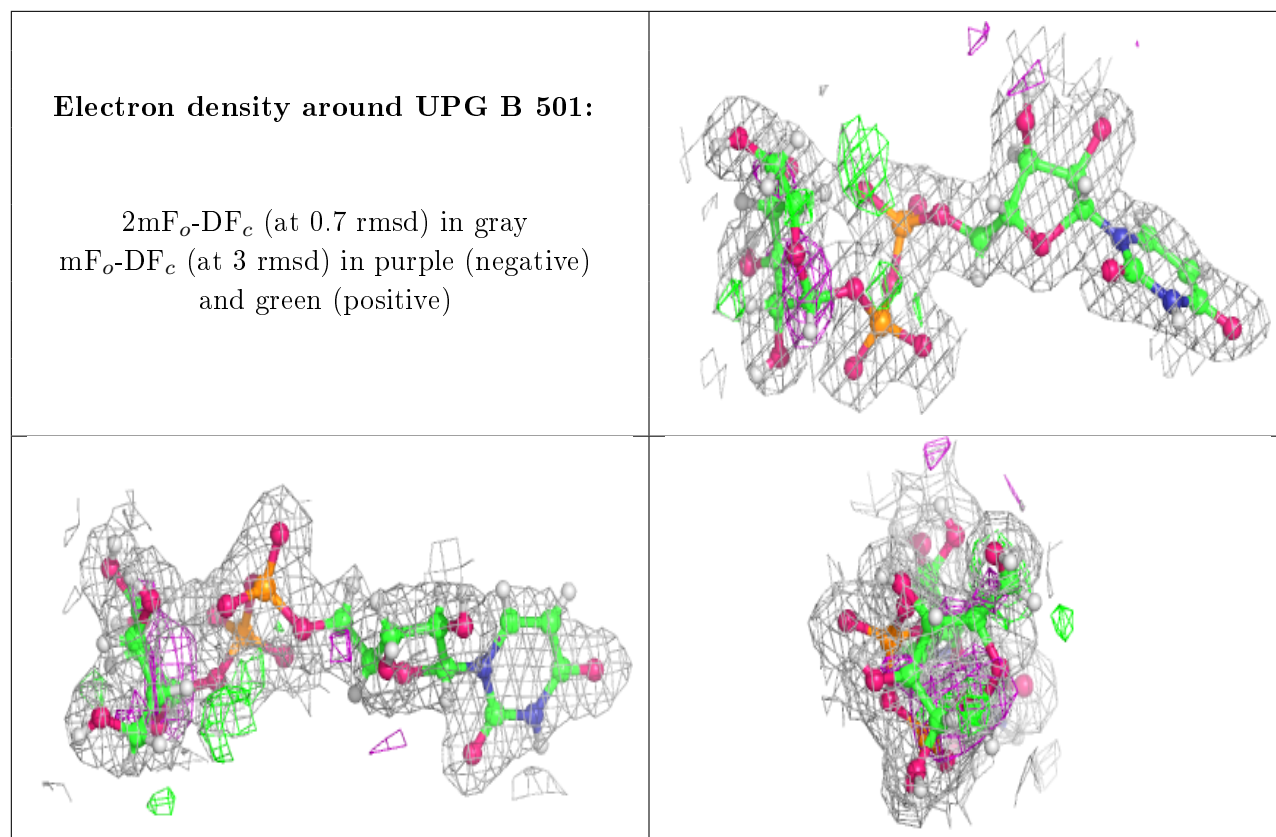## 6.3 Carbohydrates (i)

There are no 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
2	UPG	A	501	36/36	0.90	0.17	15,25,33,38	0
2	UPG	B	501	36/36	0.95	0.13	13,23,37,40	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 UPG A 501:

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

Electron density around UPG B 501:

$2mF_o$-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.