



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:34 PM GMT

PDB ID : 4M2B
Title : Crystal structure of L281D mutant of udp-glucose pyrophosphorylase from leishmania major in complex with udp-glc
Authors : Fuehring, J.; Routier, F.H.; Lamerz, A.-C.; Baruch, P.; Gerardy-Schahn, R.; Fedorov, R.
Deposited on : 2013-08-05
Resolution : 2.20 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

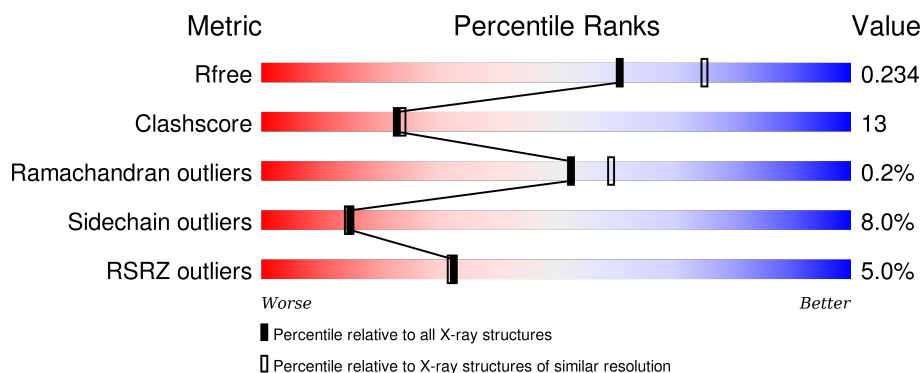
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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. 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	505	<div> <div>5%</div> <div>71%</div> <div>20%</div> <div>...</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4159 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

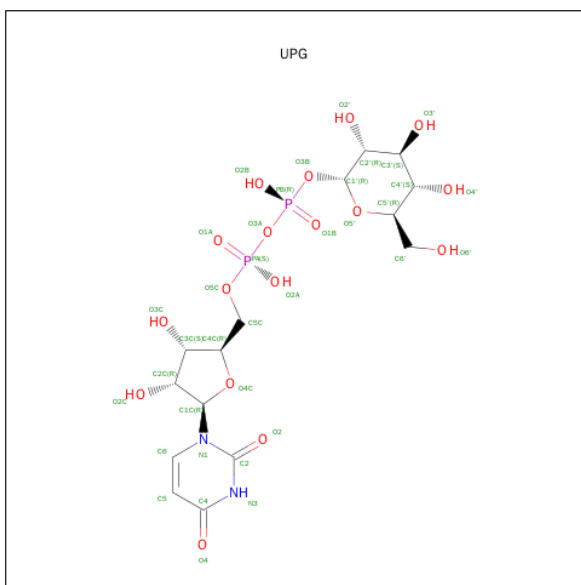
- Molecule 1 is a protein called UDP-glucose pyrophosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	483	Total	C	N	O	S	0	0	0
			3730	2349	636	719	26			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	ASP	LEU	ENGINEERED MUTATION	UNP Q4QDU3
A	495	MET	-	EXPRESSION TAG	UNP Q4QDU3
A	496	ARG	-	EXPRESSION TAG	UNP Q4QDU3
A	497	PRO	-	EXPRESSION TAG	UNP Q4QDU3
A	498	LEU	-	EXPRESSION TAG	UNP Q4QDU3
A	499	GLU	-	EXPRESSION TAG	UNP Q4QDU3
A	500	HIS	-	EXPRESSION TAG	UNP Q4QDU3
A	501	HIS	-	EXPRESSION TAG	UNP Q4QDU3
A	502	HIS	-	EXPRESSION TAG	UNP Q4QDU3
A	503	HIS	-	EXPRESSION TAG	UNP Q4QDU3
A	504	HIS	-	EXPRESSION TAG	UNP Q4QDU3
A	505	HIS	-	EXPRESSION TAG	UNP Q4QDU3

- Molecule 2 is URIDINE-5'-DIPHOSPHATE-GLUCOSE (three-letter code: UPG) (formula: C₁₅H₂₄N₂O₁₇P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			36	15	2	17	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	393	Total O 393 393	0	0

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

Chain A:

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	78.79 Å 86.90 Å 138.23 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.40 – 2.20 23.42 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (23.40-2.20) 98.1 (23.42-2.20)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.50 (at 2.19 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.175 , 0.242 0.172 , 0.234	Depositor DCC
R_{free} test set	1203 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 54.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 23985 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4159	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	1.51	11/3800 (0.3%)	0.97	7/5147 (0.1%)

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	4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	185	GLU	CD-OE2	-6.95	1.18	1.25
1	A	209	GLU	CD-OE1	-6.44	1.18	1.25
1	A	245	GLU	CD-OE1	-6.44	1.18	1.25
1	A	26	GLU	CD-OE1	-6.29	1.18	1.25
1	A	284	GLU	CD-OE1	-5.71	1.19	1.25
1	A	311	TRP	NE1-CE2	-5.71	1.30	1.37
1	A	159	GLU	CD-OE2	-5.57	1.19	1.25
1	A	26	GLU	CD-OE2	-5.50	1.19	1.25
1	A	245	GLU	CD-OE2	-5.46	1.19	1.25
1	A	157	GLU	CD-OE1	-5.38	1.19	1.25
1	A	365	SER	CB-OG	-5.20	1.35	1.42

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	263	THR	N-CA-C	8.82	134.81	111.00
1	A	469	SER	CB-CA-C	-8.41	94.12	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	ASP	CB-CA-C	8.28	126.97	110.40
1	A	270	ASP	N-CA-C	-8.14	89.01	111.00
1	A	373	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	A	401	LEU	CA-CB-CG	5.66	128.32	115.30
1	A	470	ALA	N-CA-CB	5.04	117.15	110.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	272	GLN	Peptide
1	A	273	PRO	Peptide
1	A	274	ASP	Peptide
1	A	7	SER	Peptide

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	3730	0	3713	101	0
2	A	36	0	22	2	0
3	A	393	0	0	18	0
All	All	4159	0	3735	101	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 13.

All (101) 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:265:TYR:CA	1:A:276:GLU:HB3	1.72	1.18
1:A:265:TYR:HA	1:A:276:GLU:HB3	1.22	1.15
1:A:126:ARG:HD2	3:A:2259:HOH:O	1.48	1.14
1:A:469:SER:HA	3:A:2129:HOH:O	1.51	1.06
1:A:273:PRO:HA	1:A:274:ASP:HB2	1.40	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:GLN:HE21	1:A:273:PRO:HD3	1.24	1.01
1:A:162:GLN:HE22	2:A:1001:UPG:HN3	1.05	0.99
1:A:115:GLN:HG3	1:A:149:TRP:CZ2	1.98	0.97
1:A:265:TYR:HA	1:A:276:GLU:CB	1.96	0.95
1:A:152:GLN:O	1:A:153:VAL:HG22	1.72	0.90
1:A:273:PRO:CA	1:A:274:ASP:HB2	2.02	0.88
1:A:265:TYR:CB	1:A:276:GLU:HB3	2.02	0.88
1:A:126:ARG:HH21	1:A:210:GLN:HE22	1.23	0.86
1:A:265:TYR:HB3	1:A:276:GLU:HB3	1.63	0.80
1:A:126:ARG:HH21	1:A:210:GLN:NE2	1.82	0.77
1:A:262:GLN:O	1:A:262:GLN:CG	2.36	0.74
1:A:229:LYS:NZ	3:A:2205:HOH:O	2.20	0.74
1:A:472:ALA:HB3	3:A:2362:HOH:O	1.87	0.73
1:A:272:GLN:NE2	1:A:273:PRO:HD3	2.02	0.73
1:A:115:GLN:HG3	1:A:149:TRP:HZ2	1.52	0.73
1:A:46:SER:HB3	3:A:2195:HOH:O	1.91	0.69
1:A:91:LEU:HD22	3:A:2134:HOH:O	1.93	0.69
1:A:266:VAL:HG23	1:A:277:LYS:H	1.62	0.65
1:A:162:GLN:NE2	2:A:1001:UPG:HN3	1.87	0.62
1:A:410:HIS:HE1	3:A:2064:HOH:O	1.81	0.62
1:A:453:GLY:H	1:A:456:ASN:HD21	1.47	0.62
1:A:266:VAL:HG21	1:A:277:LYS:HB2	1.80	0.62
1:A:265:TYR:HA	1:A:276:GLU:CA	2.30	0.61
1:A:265:TYR:HB3	1:A:276:GLU:CB	2.31	0.61
1:A:152:GLN:O	1:A:153:VAL:CG2	2.48	0.60
1:A:261:ARG:HG3	1:A:278:ARG:HG3	1.83	0.59
1:A:265:TYR:HA	1:A:276:GLU:HA	1.85	0.58
1:A:262:GLN:O	1:A:262:GLN:HG3	2.05	0.56
1:A:22:ALA:C	1:A:23:LYS:HG2	2.26	0.56
1:A:7:SER:OG	1:A:8:LEU:N	2.39	0.55
1:A:213:ARG:HD2	1:A:315:PRO:HG3	1.87	0.55
1:A:265:TYR:HB3	1:A:276:GLU:CG	2.37	0.55
1:A:96:THR:HA	1:A:106:PHE:HB2	1.89	0.54
1:A:100:VAL:O	1:A:389:ARG:HG2	2.07	0.54
1:A:133:PHE:HE2	3:A:2351:HOH:O	1.90	0.53
1:A:371:VAL:HB	1:A:372:PRO:HD2	1.90	0.53
1:A:293:MET:O	1:A:297:GLN:HG3	2.07	0.53
1:A:319:GLU:HG3	3:A:2257:HOH:O	2.09	0.53
1:A:104:LYS:HE2	3:A:2184:HOH:O	2.09	0.52
1:A:278:ARG:NH2	3:A:2208:HOH:O	2.41	0.52
1:A:46:SER:CB	3:A:2195:HOH:O	2.52	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:THR:O	1:A:483:ASP:HA	2.09	0.52
1:A:222:ASN:ND2	1:A:377:ALA:H	2.07	0.52
1:A:126:ARG:NH2	1:A:210:GLN:NE2	2.55	0.51
1:A:264:VAL:O	1:A:276:GLU:HB2	2.10	0.51
1:A:395:VAL:HG22	1:A:401:LEU:HD22	1.91	0.51
1:A:152:GLN:HG2	1:A:153:VAL:HG13	1.92	0.51
1:A:265:TYR:HB3	1:A:276:GLU:HG2	1.91	0.51
1:A:261:ARG:CG	1:A:278:ARG:HG3	2.39	0.51
1:A:251:GLU:OE1	1:A:443:ARG:NH2	2.38	0.50
1:A:273:PRO:CB	1:A:274:ASP:HB2	2.42	0.49
1:A:91:LEU:CD2	1:A:98:LEU:HD11	2.42	0.49
1:A:300:ASN:ND2	3:A:2326:HOH:O	2.44	0.49
1:A:210:GLN:HE21	1:A:212:TYR:HE1	1.61	0.49
1:A:273:PRO:HA	1:A:274:ASP:CB	2.27	0.49
1:A:266:VAL:CG2	1:A:277:LYS:H	2.25	0.49
1:A:262:GLN:O	1:A:262:GLN:HG2	2.12	0.48
1:A:386:LEU:HB2	1:A:427:PHE:HE1	1.78	0.48
1:A:125:LEU:HD12	3:A:2244:HOH:O	2.13	0.48
1:A:7:SER:HA	1:A:8:LEU:HG	1.95	0.47
1:A:386:LEU:HB2	1:A:427:PHE:CE1	2.48	0.47
1:A:99:GLU:OE1	1:A:103:GLY:HA2	2.14	0.46
1:A:249:ARG:NE	3:A:2115:HOH:O	2.47	0.46
1:A:439:VAL:HG13	1:A:440:GLU:HG3	1.96	0.46
1:A:379:VAL:CG2	1:A:388:LEU:HD22	2.46	0.46
1:A:264:VAL:O	1:A:276:GLU:CB	2.64	0.46
1:A:226:THR:HB	1:A:400:ARG:HD3	1.97	0.46
1:A:245:GLU:HB2	1:A:309:ASN:HB2	1.97	0.46
1:A:412:PRO:HB3	1:A:441:CYS:O	2.16	0.45
1:A:386:LEU:HD23	1:A:414:VAL:HG11	1.98	0.45
1:A:291:ALA:HB3	3:A:2308:HOH:O	2.16	0.45
1:A:256:GLY:HA3	1:A:305:PHE:CZ	2.51	0.45
1:A:49:ASP:OD2	1:A:292:ASP:HB3	2.16	0.45
1:A:6:LYS:HB3	1:A:7:SER:H	1.37	0.45
1:A:265:TYR:O	1:A:265:TYR:HD1	2.00	0.45
1:A:115:GLN:CG	1:A:149:TRP:CZ2	2.86	0.44
1:A:314:LEU:N	1:A:315:PRO:HD2	2.32	0.44
1:A:265:TYR:N	1:A:276:GLU:HB3	2.27	0.44
1:A:343:ASN:HD22	1:A:343:ASN:C	2.20	0.43
1:A:146:ARG:HG2	3:A:2200:HOH:O	2.18	0.43
1:A:466:ASN:OD1	1:A:466:ASN:C	2.56	0.43
1:A:7:SER:HA	1:A:8:LEU:CG	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:LEU:CD1	1:A:98:LEU:HD11	2.49	0.43
1:A:261:ARG:NH1	1:A:278:ARG:HA	2.34	0.42
1:A:337:LYS:HG3	1:A:351:GLN:NE2	2.34	0.42
1:A:282:LEU:HD22	1:A:357:GLY:HA3	2.02	0.42
1:A:388:LEU:HA	1:A:393:TYR:CD1	2.56	0.41
1:A:38:MET:HA	1:A:38:MET:HE2	2.01	0.41
1:A:433:HIS:HE1	3:A:2171:HOH:O	2.04	0.41
1:A:107:LEU:HD23	1:A:142:PHE:CD2	2.55	0.41
1:A:192:GLY:HA3	1:A:354:THR:OG1	2.21	0.41
1:A:266:VAL:HG11	1:A:277:LYS:HZ1	1.86	0.41
1:A:463:THR:O	1:A:485:THR:HA	2.21	0.40
1:A:7:SER:HA	1:A:8:LEU:HA	1.89	0.40
1:A:235:MET:HG2	1:A:240:ILE:HB	2.04	0.40
1:A:25:ASN:ND2	1:A:28:CYS:H	2.20	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	481/505 (95%)	472 (98%)	8 (2%)	1 (0%)	52 59

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	VAL

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	410/432 (95%)	377 (92%)	33 (8%)	15	15

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	7	SER
1	A	23	LYS
1	A	46	SER
1	A	49	ASP
1	A	53	MET
1	A	55	VAL
1	A	56	ASP
1	A	63	SER
1	A	74	GLN
1	A	99	GLU
1	A	100	VAL
1	A	152	GLN
1	A	203	LYS
1	A	226	THR
1	A	254	LYS
1	A	261	ARG
1	A	263	THR
1	A	265	TYR
1	A	270	ASP
1	A	274	ASP
1	A	276	GLU
1	A	295	SER
1	A	303	SER
1	A	308	ASN
1	A	342	SER
1	A	343	ASN
1	A	364	GLU
1	A	367	SER
1	A	401	LEU
1	A	459	THR
1	A	469	SER
1	A	480	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	35	GLN
1	A	82	ASN
1	A	119	GLN
1	A	162	GLN
1	A	163	ASN
1	A	170	GLN
1	A	210	GLN
1	A	222	ASN
1	A	272	GLN
1	A	300	ASN
1	A	322	GLN
1	A	335	ASN
1	A	343	ASN
1	A	351	GLN
1	A	410	HIS
1	A	420	HIS
1	A	456	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	1001	-	29,38,38	0.88	1 (3%)	43,58,58	1.55	6 (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
2	UPG	A	1001	-	-	0/19/59/59	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	UPG	O5'-C1'	2.52	1.48	1.41

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	UPG	O5'-C1'-O3B	-2.65	107.87	111.36
2	A	1001	UPG	PB-O3A-PA	-2.45	125.84	132.73
2	A	1001	UPG	O2B-PB-O3B	-2.26	97.41	106.49
2	A	1001	UPG	O3C-C3C-C4C	-2.25	104.29	111.05
2	A	1001	UPG	C4C-O4C-C1C	2.23	112.17	109.72
2	A	1001	UPG	C4-N3-C2	6.88	120.96	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	UPG	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	483/505 (95%)	-0.10	24 (4%) 32 32	12, 24, 52, 133	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	272	GLN	20.3
1	A	273	PRO	14.4
1	A	274	ASP	13.0
1	A	268	GLY	10.8
1	A	275	ALA	10.3
1	A	269	LYS	8.9
1	A	266	VAL	8.6
1	A	265	TYR	8.2
1	A	271	GLY	7.3
1	A	469	SER	6.7
1	A	276	GLU	6.5
1	A	267	LYS	6.5
1	A	270	ASP	6.4
1	A	264	VAL	5.5
1	A	263	THR	5.3
1	A	468	ASP	5.1
1	A	7	SER	5.0
1	A	92	CYS	4.5
1	A	277	LYS	4.4
1	A	87	THR	3.0
1	A	6	LYS	3.0
1	A	470	ALA	2.9
1	A	467	THR	2.4
1	A	152	GLN	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	UPG	A	1001	36/36	0.98	0.07	-1.02	14,15,18,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.