



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:50 AM GMT

PDB ID : 2OEG  
Title : Open and Closed Structures of the UDP-Glucose Pyrophosphorylase from  
Leishmania major  
Authors : Steiner, T.  
Deposited on : 2006-12-29  
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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

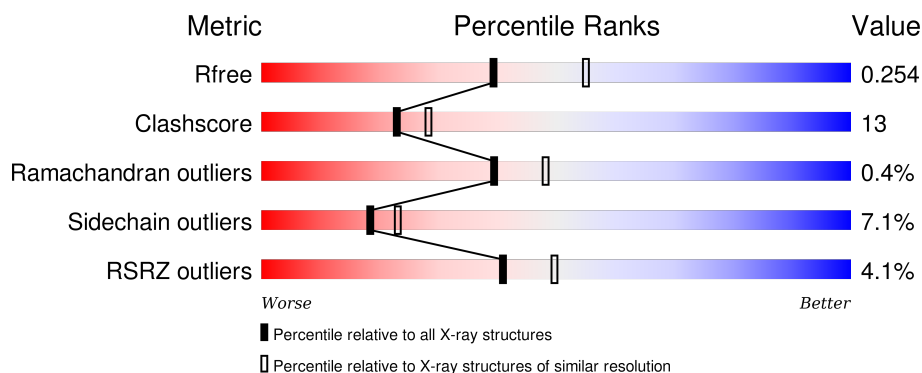
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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  $\geq 3$ , 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>4%</div> <div>74%</div> <div>19%</div> <div>• 5%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3982 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 UTP-glucose-1-phosphate uridylyltransferase 2, putative.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	482	Total	C	N	O	S	Se	0	0	0
			3721	2345	634	716	10	16			

There are 29 discrepancies between the modelled and reference sequences:

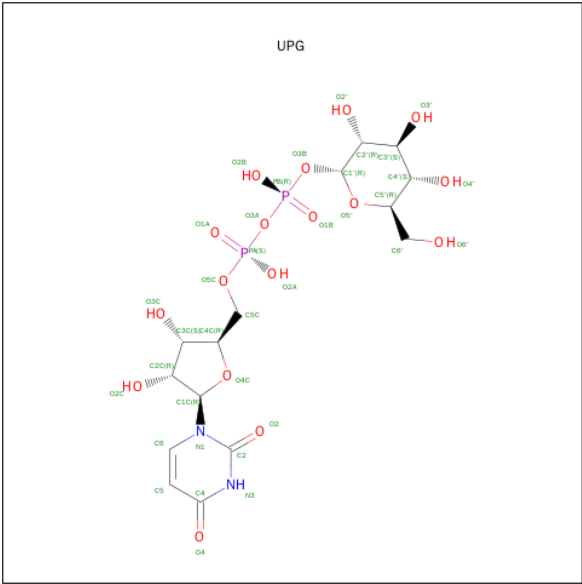
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	5	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	19	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	38	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	53	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	89	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	128	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	130	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	161	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	215	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	235	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	244	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	293	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	321	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	356	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	362	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	423	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	424	MSE	MET	MODIFIED RESIDUE	UNP Q4QDU3
A	495	MSE	-	CLONING ARTIFACT	UNP Q4QDU3
A	496	ARG	-	CLONING ARTIFACT	UNP Q4QDU3
A	497	PRO	-	CLONING ARTIFACT	UNP Q4QDU3
A	498	LEU	-	CLONING ARTIFACT	UNP Q4QDU3
A	499	GLU	-	CLONING ARTIFACT	UNP Q4QDU3
A	500	HIS	-	CLONING ARTIFACT	UNP Q4QDU3
A	501	HIS	-	CLONING ARTIFACT	UNP Q4QDU3
A	502	HIS	-	CLONING ARTIFACT	UNP Q4QDU3
A	503	HIS	-	CLONING ARTIFACT	UNP Q4QDU3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	504	HIS	-	CLONING ARTIFACT	UNP Q4QDU3
A	505	HIS	-	CLONING ARTIFACT	UNP Q4QDU3

- Molecule 2 is URIDINE-5'-DIPHOSPHATE-GLUCOSE (three-letter code: UPG) (formula: C<sub>15</sub>H<sub>24</sub>N<sub>2</sub>O<sub>17</sub>P<sub>2</sub>).



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

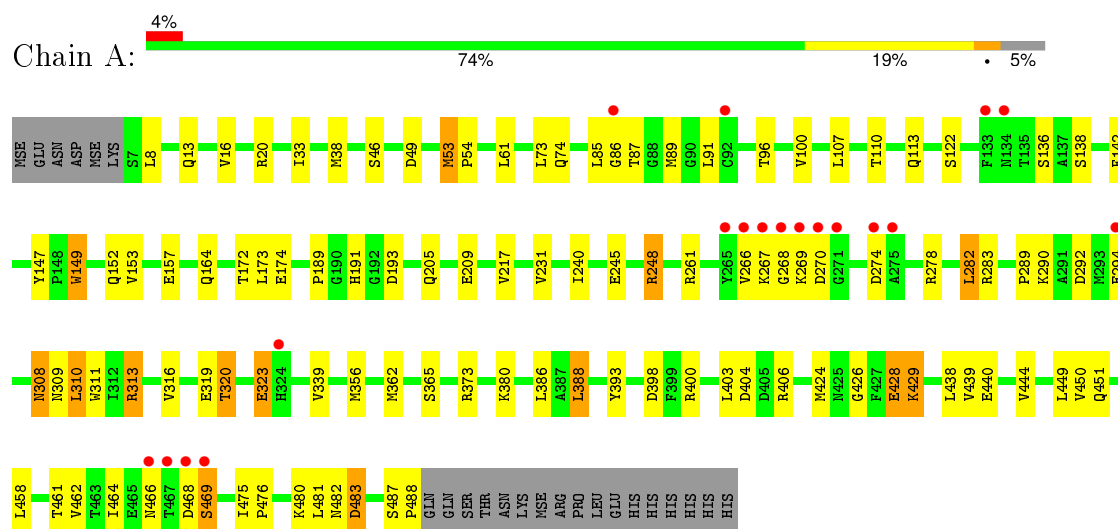
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	225	Total	0	0
			225 O		

### 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 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 ( $RSRZ > 2$ ). 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: UTP-glucose-1-phosphate uridylyltransferase 2, putative



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.25Å 89.93Å 137.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.30 19.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.3 (19.96-2.30) 97.4 (19.96-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	18.48 (at 2.30Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.210 , 0.255 0.210 , 0.254	Depositor DCC
$R_{free}$ test set	1065 reflections (4.88%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 38.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 21812 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3982	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.86% 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, 0.375 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	0.41	0/3775	0.67	0/5088

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3721	0	3707	100	0
2	A	36	0	22	12	0
3	A	225	0	0	12	0
All	All	3982	0	3729	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:308:ASN:ND2	2:A:5206:UPG:H2'	1.49	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:MSE:HE2	1:A:424:MSE:HE1	1.25	1.14
1:A:248:ARG:HG2	1:A:248:ARG:HH11	1.03	1.11
1:A:308:ASN:ND2	2:A:5206:UPG:C2'	2.27	0.97
1:A:310:LEU:HD22	1:A:356:MSE:HE3	1.45	0.96
1:A:74:GLN:HE22	1:A:122:SER:HB2	1.31	0.96
1:A:308:ASN:OD1	1:A:356:MSE:HE2	1.66	0.95
1:A:248:ARG:NH1	1:A:248:ARG:HG2	1.77	0.95
1:A:426:GLY:O	1:A:429:LYS:HD3	1.66	0.95
1:A:308:ASN:HD22	2:A:5206:UPG:H2'	1.33	0.92
1:A:316:VAL:O	1:A:320:THR:HG23	1.84	0.77
1:A:74:GLN:NE2	1:A:122:SER:HB2	2.00	0.77
1:A:189:PRO:HG2	1:A:193:ASP:HB2	1.66	0.76
1:A:308:ASN:HD22	2:A:5206:UPG:C1'	1.99	0.75
1:A:308:ASN:HD21	2:A:5206:UPG:H2'	1.55	0.72
1:A:308:ASN:HD22	2:A:5206:UPG:C2'	1.92	0.72
1:A:469:SER:HA	3:A:5324:HOH:O	1.91	0.69
1:A:89:MSE:HE2	1:A:424:MSE:CE	2.15	0.68
1:A:191:HIS:CD2	2:A:5206:UPG:H5C1	2.30	0.67
1:A:248:ARG:CG	1:A:248:ARG:HH11	1.93	0.66
1:A:310:LEU:HD22	1:A:356:MSE:CE	2.25	0.63
1:A:464:ILE:HD13	1:A:475:ILE:HD11	1.80	0.63
1:A:468:ASP:O	1:A:469:SER:HB2	2.00	0.62
1:A:268:GLY:O	1:A:269:LYS:HB2	2.00	0.61
1:A:245:GLU:HB2	1:A:309:ASN:HB2	1.85	0.58
1:A:189:PRO:HG2	1:A:193:ASP:CB	2.33	0.58
1:A:487:SER:HB2	1:A:488:PRO:HD2	1.86	0.57
1:A:450:VAL:HG12	1:A:451:GLN:N	2.20	0.57
1:A:248:ARG:NH1	3:A:5273:HOH:O	2.38	0.56
1:A:323:GLU:OE2	1:A:323:GLU:C	2.43	0.56
1:A:439:VAL:HG13	1:A:440:GLU:HG2	1.86	0.56
1:A:153:VAL:HB	1:A:157:GLU:HG2	1.88	0.56
1:A:86:GLY:HA3	1:A:91:LEU:HD12	1.89	0.55
1:A:248:ARG:NH1	1:A:248:ARG:CG	2.57	0.55
1:A:466:ASN:CG	1:A:468:ASP:OD1	2.45	0.55
1:A:278:ARG:HD2	3:A:5249:HOH:O	2.06	0.55
1:A:393:TYR:CZ	1:A:403:LEU:HD13	2.41	0.55
1:A:308:ASN:ND2	2:A:5206:UPG:C1'	2.63	0.55
1:A:400:ARG:HH11	1:A:400:ARG:HG3	1.71	0.55
1:A:310:LEU:CD2	1:A:356:MSE:HG2	2.36	0.54
1:A:380:LYS:HE3	2:A:5206:UPG:O6'	2.07	0.54
1:A:20:ARG:HH11	1:A:20:ARG:HG3	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:ILE:HD13	1:A:475:ILE:CD1	2.38	0.53
1:A:91:LEU:HD21	1:A:424:MSE:HE3	1.91	0.53
1:A:100:VAL:HG13	1:A:388:LEU:HD13	1.89	0.53
1:A:16:VAL:HG23	1:A:33:ILE:HD11	1.90	0.53
1:A:404:ASP:OD1	1:A:406:ARG:HG3	2.10	0.52
1:A:468:ASP:OD1	1:A:468:ASP:N	2.43	0.51
1:A:73:LEU:O	1:A:73:LEU:HD13	2.10	0.51
1:A:205:GLN:O	1:A:209:GLU:HG3	2.11	0.51
1:A:294:GLU:HB3	3:A:5317:HOH:O	2.11	0.51
1:A:400:ARG:NE	3:A:5240:HOH:O	2.42	0.50
1:A:461:THR:O	1:A:483:ASP:HA	2.11	0.50
1:A:96:THR:HG23	3:A:5259:HOH:O	2.11	0.50
1:A:429:LYS:HE3	1:A:449:LEU:HD11	1.94	0.49
1:A:450:VAL:CG1	1:A:451:GLN:N	2.75	0.49
1:A:38:MSE:HE3	3:A:5262:HOH:O	2.13	0.49
1:A:53:MSE:HE3	1:A:53:MSE:HA	1.94	0.49
1:A:310:LEU:HD23	1:A:356:MSE:HG2	1.94	0.49
1:A:444:VAL:HA	1:A:462:VAL:O	2.13	0.49
1:A:320:THR:HA	1:A:323:GLU:HG3	1.94	0.48
1:A:85:LEU:HB3	1:A:87:THR:HG23	1.94	0.48
1:A:400:ARG:NH2	3:A:5240:HOH:O	2.44	0.48
1:A:240:ILE:HG23	1:A:365:SER:O	2.14	0.48
1:A:316:VAL:HA	1:A:319:GLU:HG2	1.96	0.48
1:A:73:LEU:HD13	1:A:73:LEU:C	2.35	0.47
2:A:5206:UPG:H6	2:A:5206:UPG:H5C2	1.96	0.47
1:A:53:MSE:HG3	1:A:54:PRO:HD2	1.97	0.47
1:A:53:MSE:HE3	3:A:5417:HOH:O	2.14	0.47
1:A:53:MSE:HG3	1:A:54:PRO:CD	2.45	0.47
1:A:313:ARG:HG2	1:A:316:VAL:HG23	1.97	0.47
1:A:289:PRO:HG2	1:A:292:ASP:HB2	1.97	0.46
1:A:482:ASN:O	1:A:483:ASP:C	2.53	0.46
1:A:282:LEU:HD22	1:A:283:ARG:N	2.30	0.46
1:A:107:LEU:HD23	1:A:142:PHE:CD2	2.52	0.45
1:A:147:TYR:HD2	1:A:149:TRP:CZ3	2.35	0.45
1:A:458:LEU:HD23	1:A:458:LEU:N	2.31	0.45
1:A:191:HIS:HD2	2:A:5206:UPG:H5C1	1.79	0.44
1:A:172:THR:OG1	1:A:174:GLU:HG3	2.17	0.44
1:A:261:ARG:CZ	1:A:278:ARG:HG3	2.47	0.44
1:A:231:VAL:HG11	1:A:311:TRP:CE2	2.52	0.44
1:A:147:TYR:HD2	1:A:149:TRP:CH2	2.36	0.44
1:A:74:GLN:HE22	1:A:122:SER:CB	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:VAL:HG13	1:A:440:GLU:N	2.33	0.43
1:A:308:ASN:HD21	2:A:5206:UPG:C2'	2.17	0.43
1:A:89:MSE:CE	1:A:424:MSE:HE1	2.19	0.43
1:A:475:ILE:HA	1:A:476:PRO:HD3	1.87	0.42
1:A:282:LEU:CD2	1:A:283:ARG:N	2.83	0.42
1:A:110:THR:O	1:A:113:GLN:HB2	2.20	0.42
1:A:217:VAL:HG11	1:A:356:MSE:SE	2.69	0.42
1:A:136:SER:HB3	3:A:5412:HOH:O	2.21	0.41
1:A:308:ASN:OD1	1:A:356:MSE:CE	2.54	0.41
1:A:248:ARG:HA	1:A:248:ARG:HD3	1.71	0.41
1:A:398:ASP:OD1	1:A:400:ARG:NH1	2.53	0.41
1:A:172:THR:O	1:A:173:LEU:HB2	2.21	0.41
1:A:429:LYS:HE3	1:A:449:LEU:CD1	2.51	0.41
1:A:428:GLU:HG3	3:A:5269:HOH:O	2.20	0.41
1:A:107:LEU:HD12	1:A:107:LEU:HA	1.93	0.41
1:A:480:LYS:C	1:A:481:LEU:HD23	2.42	0.40
1:A:373:ARG:HD3	3:A:5365:HOH:O	2.21	0.40
1:A:468:ASP:O	1:A:469:SER:CB	2.67	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	480/505 (95%)	454 (95%)	24 (5%)	2 (0%)	39	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	483	ASP
1	A	469	SER

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	409/413 (99%)	380 (93%)	29 (7%)	18	23

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	13	GLN
1	A	46	SER
1	A	49	ASP
1	A	53	MSE
1	A	61	LEU
1	A	138	SER
1	A	149	TRP
1	A	152	GLN
1	A	164	GLN
1	A	248	ARG
1	A	266	VAL
1	A	267	LYS
1	A	270	ASP
1	A	274	ASP
1	A	282	LEU
1	A	290	LYS
1	A	308	ASN
1	A	310	LEU
1	A	313	ARG
1	A	320	THR
1	A	323	GLU
1	A	339	VAL
1	A	362	MSE
1	A	386	LEU
1	A	388	LEU
1	A	428	GLU
1	A	429	LYS
1	A	438	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	74	GLN
1	A	120	HIS
1	A	297	GLN
1	A	308	ASN
1	A	322	GLN
1	A	451	GLN

### 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	5206	-	29,38,38	1.50	5 (17%)	43,58,58	2.56	4 (9%)

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	5206	-	-	0/19/59/59	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	5206	UPG	O5C-C5C	-2.31	1.35	1.44
2	A	5206	UPG	PA-O2A	-2.11	1.45	1.54
2	A	5206	UPG	O4C-C1C	2.81	1.44	1.41
2	A	5206	UPG	C4-N3	3.21	1.39	1.33
2	A	5206	UPG	C6-N1	3.99	1.41	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	A	5206	UPG	O3A-PA-O5C	-3.62	93.33	102.94
2	A	5206	UPG	C5-C4-N3	-3.40	114.41	123.12
2	A	5206	UPG	O6'-C6'-C5'	-2.55	102.92	111.33
2	A	5206	UPG	C4-N3-C2	14.66	128.66	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5206	UPG	12	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	466/505 (92%)	-0.02	19 (4%)	41 50	9, 26, 50, 74	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	265	TYR	4.9
1	A	274	ASP	4.1
1	A	268	GLY	4.0
1	A	92	CYS	3.9
1	A	468	ASP	3.9
1	A	133	PHE	3.4
1	A	467	THR	3.1
1	A	275	ALA	3.0
1	A	466	ASN	2.9
1	A	269	LYS	2.6
1	A	266	VAL	2.5
1	A	324	HIS	2.3
1	A	469	SER	2.3
1	A	267	LYS	2.2
1	A	134	ASN	2.2
1	A	271	GLY	2.2
1	A	294	GLU	2.1
1	A	270	ASP	2.1
1	A	86	GLY	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. 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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	UPG	A	5206	36/36	0.96	0.10	-0.73	11,16,23,25	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.