



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:51 PM GMT

PDB ID : 1VGV  
Title : Crystal structure of UDP-N-acetylglucosamine\_2 epimerase  
Authors : Structural GenomiX  
Deposited on : 2003-11-03  
Resolution : 2.31 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<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

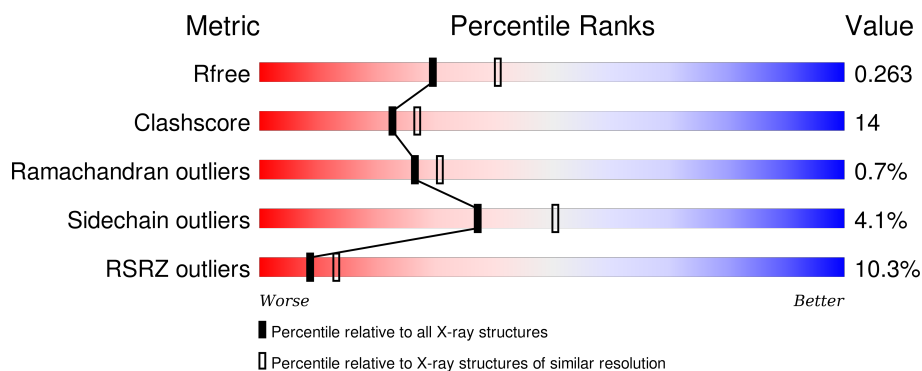
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.31 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	4425 (2.34-2.30)
Clashscore	102246	5057 (2.34-2.30)
Ramachandran outliers	100387	5008 (2.34-2.30)
Sidechain outliers	100360	5007 (2.34-2.30)
RSRZ outliers	91569	4432 (2.34-2.30)

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	384	<div> <div>5%</div> <div>72%</div> <div>24%</div> <div>..</div> </div>
1	B	384	<div> <div>10%</div> <div>68%</div> <div>28%</div> <div>..</div> </div>
1	C	384	<div> <div>12%</div> <div>63%</div> <div>30%</div> <div>..</div> </div>
1	D	384	<div> <div>13%</div> <div>67%</div> <div>29%</div> <div>..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UD1	B	385	X	-	-	-
2	UD1	C	385	X	-	-	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12241 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-N-acetylglucosamine 2-epimerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	376	Total	C	N	O	S	Se	0	1	0
			2966	1883	519	550	4	10			
1	B	372	Total	C	N	O	S	Se	0	4	0
			2958	1877	520	548	4	9			
1	C	367	Total	C	N	O	S	Se	0	1	0
			2902	1842	511	536	4	9			
1	D	374	Total	C	N	O	S	Se	0	0	0
			2928	1855	514	545	4	10			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	cloning artifact	UNP P27828
A	16	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	42	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	61	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	143	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	185	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	207	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	280	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	307	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	349	MSE	MET	MODIFIED RESIDUE	UNP P27828
A	377	GLY	-	cloning artifact	UNP P27828
A	378	SER	-	cloning artifact	UNP P27828
A	379	HIS	-	cloning artifact	UNP P27828
A	380	HIS	-	cloning artifact	UNP P27828
A	381	HIS	-	cloning artifact	UNP P27828
A	382	HIS	-	cloning artifact	UNP P27828
A	383	HIS	-	cloning artifact	UNP P27828
A	384	HIS	-	cloning artifact	UNP P27828
B	1	MSE	-	cloning artifact	UNP P27828
B	16	MSE	MET	MODIFIED RESIDUE	UNP P27828
B	42	MSE	MET	MODIFIED RESIDUE	UNP P27828

*Continued on next page...*

*Continued from previous page...*

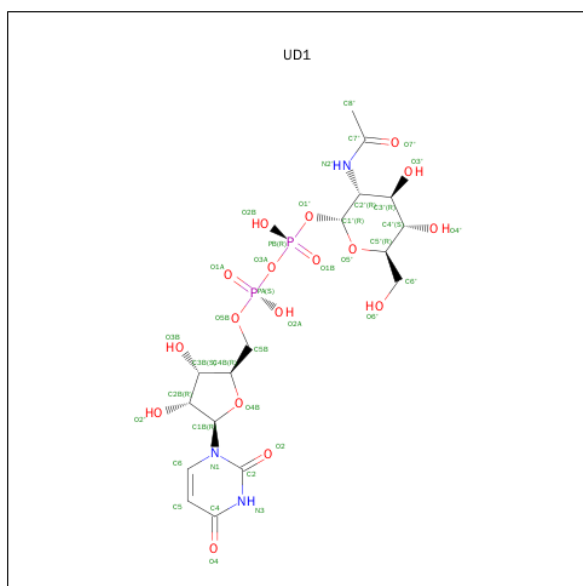
Chain	Residue	Modelled	Actual	Comment	Reference
B	61	MSE	MET	MODIFIED RESIDUE	UNP P27828
B	143	MSE	MET	MODIFIED RESIDUE	UNP P27828
B	185	MSE	MET	MODIFIED RESIDUE	UNP P27828
B	207	MSE	MET	MODIFIED RESIDUE	UNP P27828
B	280	MSE	MET	MODIFIED RESIDUE	UNP P27828
B	307	MSE	MET	MODIFIED RESIDUE	UNP P27828
B	349	MSE	MET	MODIFIED RESIDUE	UNP P27828
B	377	GLY	-	cloning artifact	UNP P27828
B	378	SER	-	cloning artifact	UNP P27828
B	379	HIS	-	cloning artifact	UNP P27828
B	380	HIS	-	cloning artifact	UNP P27828
B	381	HIS	-	cloning artifact	UNP P27828
B	382	HIS	-	cloning artifact	UNP P27828
B	383	HIS	-	cloning artifact	UNP P27828
B	384	HIS	-	cloning artifact	UNP P27828
C	1	MSE	-	cloning artifact	UNP P27828
C	16	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	42	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	61	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	143	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	185	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	207	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	280	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	307	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	349	MSE	MET	MODIFIED RESIDUE	UNP P27828
C	377	GLY	-	cloning artifact	UNP P27828
C	378	SER	-	cloning artifact	UNP P27828
C	379	HIS	-	cloning artifact	UNP P27828
C	380	HIS	-	cloning artifact	UNP P27828
C	381	HIS	-	cloning artifact	UNP P27828
C	382	HIS	-	cloning artifact	UNP P27828
C	383	HIS	-	cloning artifact	UNP P27828
C	384	HIS	-	cloning artifact	UNP P27828
D	1	MSE	-	cloning artifact	UNP P27828
D	16	MSE	MET	MODIFIED RESIDUE	UNP P27828
D	42	MSE	MET	MODIFIED RESIDUE	UNP P27828
D	61	MSE	MET	MODIFIED RESIDUE	UNP P27828
D	143	MSE	MET	MODIFIED RESIDUE	UNP P27828
D	185	MSE	MET	MODIFIED RESIDUE	UNP P27828
D	207	MSE	MET	MODIFIED RESIDUE	UNP P27828
D	280	MSE	MET	MODIFIED RESIDUE	UNP P27828
D	307	MSE	MET	MODIFIED RESIDUE	UNP P27828

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
D	349	MSE	MET	MODIFIED RESIDUE	UNP P27828
D	377	GLY	-	cloning artifact	UNP P27828
D	378	SER	-	cloning artifact	UNP P27828
D	379	HIS	-	cloning artifact	UNP P27828
D	380	HIS	-	cloning artifact	UNP P27828
D	381	HIS	-	cloning artifact	UNP P27828
D	382	HIS	-	cloning artifact	UNP P27828
D	383	HIS	-	cloning artifact	UNP P27828
D	384	HIS	-	cloning artifact	UNP P27828

- Molecule 2 is URIDINE-DIPHOSPHATE-N-ACETYLGLUCOSAMINE (three-letter code: UD1) (formula:  $C_{17}H_{27}N_3O_{17}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
2	C	1	Total	C	N	O	P	0	0
			39	17	3	17	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	134	Total	O	0	0
			134	134		
3	B	95	Total	O	0	0
			95	95		

*Continued on next page...*

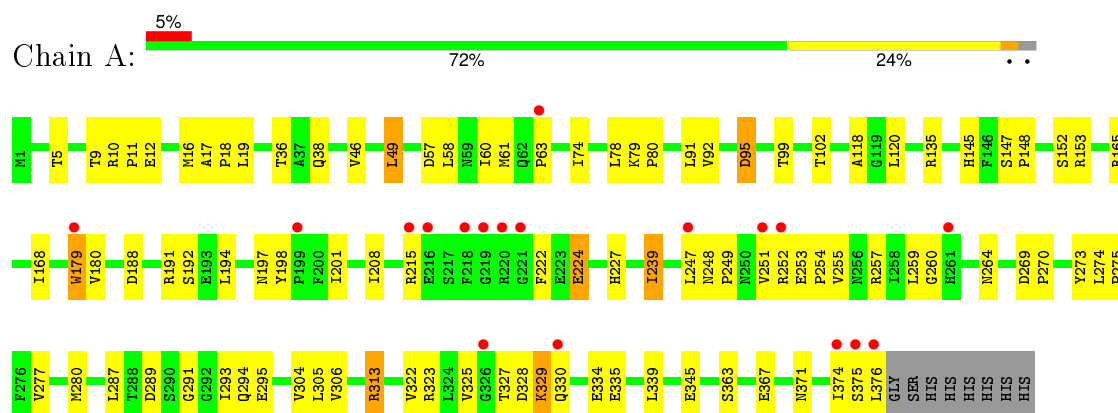
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	84	Total	O	0	0
			84	84		
3	D	96	Total	O	0	0
			96	96		

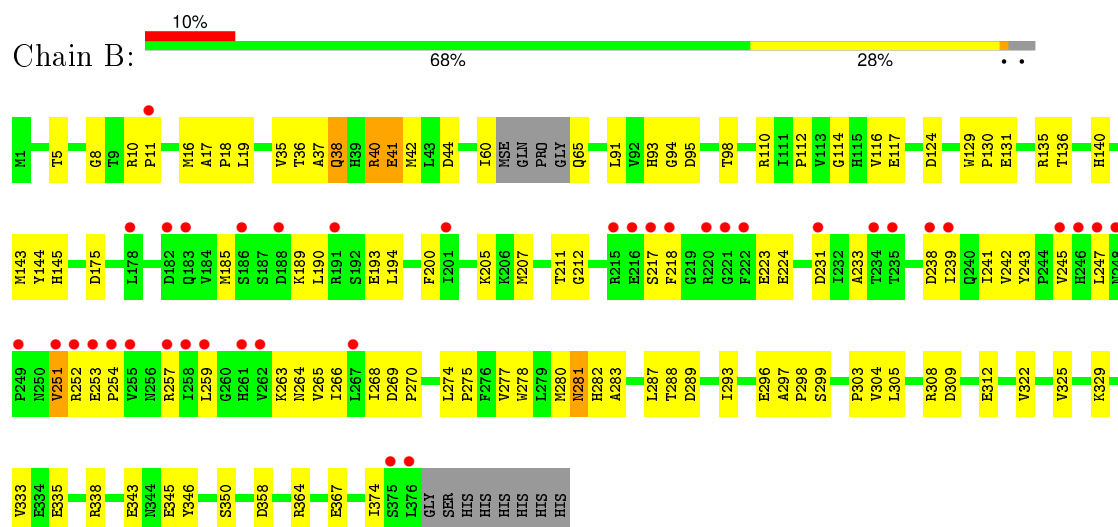
### 3 Residue-property plots

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 ( $\text{RSRZ} > 2$ ). 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.

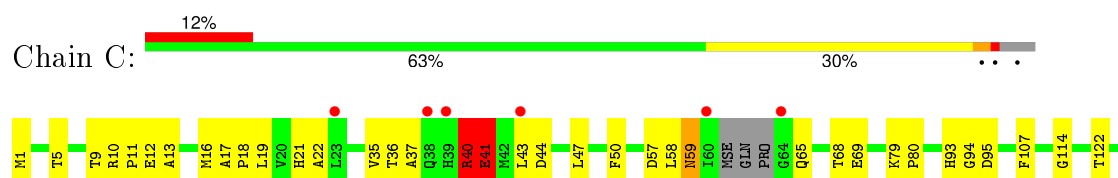
#### • Molecule 1: UDP-N-acetylglucosamine 2-epimerase



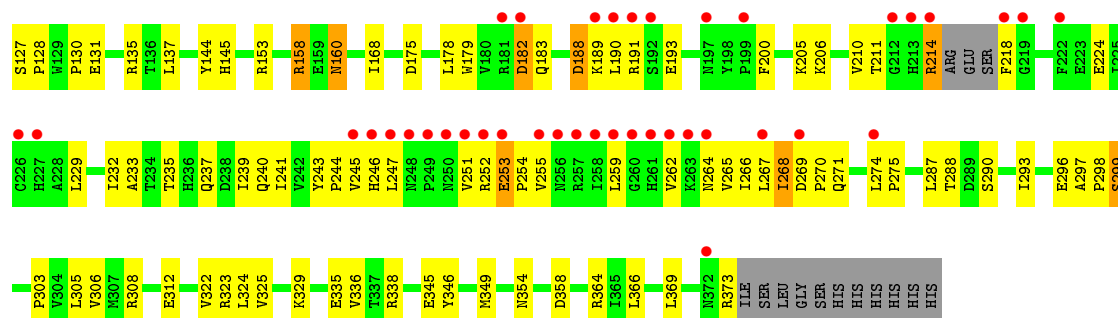
#### • Molecule 1: UDP-N-acetylglucosamine 2-epimerase



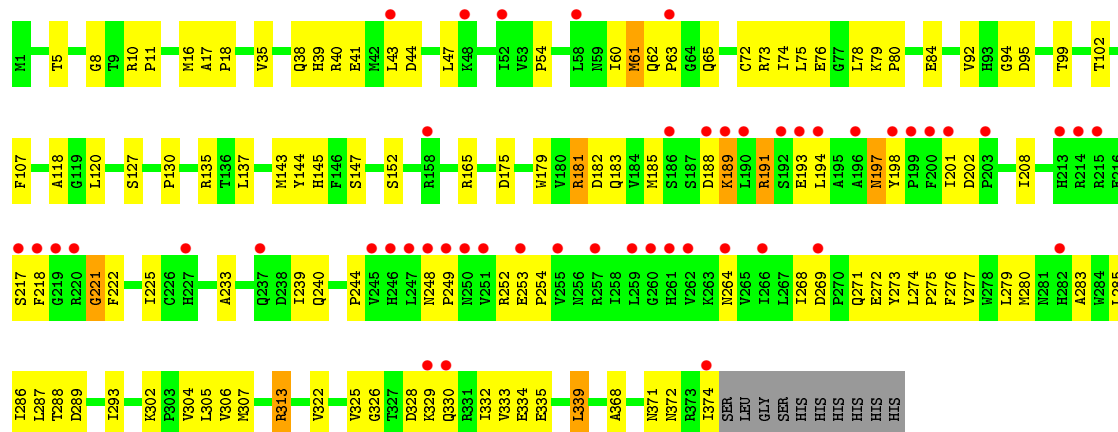
#### • Molecule 1: UDP-N-acetylglucosamine 2-epimerase







• Molecule 1: UDP-N-acetylglucosamine 2-epimerase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.36 Å 94.48 Å 100.73 Å 90.00° 109.29° 90.00°	Depositor
Resolution (Å)	42.47 – 2.31 42.47 – 2.31	Depositor EDS
% Data completeness (in resolution range)	(Not available) (42.47-2.31) 92.4 (42.47-2.31)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.11 (at 2.32 Å)	Xtriage
Refinement program	REFMAC 4	Depositor
R, $R_{free}$	0.249 , 0.295 0.226 , 0.263	Depositor DCC
$R_{free}$ test set	3261 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.3	Xtriage
Anisotropy	0.381	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 53.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 64548 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12241	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.52 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.1310e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: UD1

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	0.46	0/3024	0.93	1/4100 (0.0%)
1	B	0.45	0/3028	0.91	2/4104 (0.0%)
1	C	0.43	0/2959	0.90	6/4010 (0.1%)
1	D	0.46	0/2981	0.93	5/4043 (0.1%)
All	All	0.45	0/11992	0.92	14/16257 (0.1%)

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	313	ARG	CD-NE-CZ	14.71	144.19	123.60
1	C	40	ARG	NE-CZ-NH2	9.80	125.20	120.30
1	C	40	ARG	NE-CZ-NH1	-8.94	115.83	120.30
1	D	313	ARG	NE-CZ-NH1	8.35	124.48	120.30
1	C	158	ARG	CD-NE-CZ	8.10	134.94	123.60

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	2966	0	2983	68	0
1	B	2958	0	2968	80	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2902	0	2913	96	0
1	D	2928	0	2924	77	0
2	B	39	0	25	4	0
2	C	39	0	25	3	0
3	A	134	0	0	8	0
3	B	95	0	0	3	0
3	C	84	0	0	4	0
3	D	96	0	0	3	0
All	All	12241	0	11838	323	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 14.

The worst 5 of 323 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:C:37:ALA:HB2	1:C:43:LEU:HD23	1.35	1.07
1:C:253:GLU:H	1:C:254:PRO:HD2	1.28	0.96
1:A:208:ILE:HD12	1:A:239:ILE:HD13	1.47	0.96
1:B:16:MSE:HE1	1:B:93:HIS:HB2	1.46	0.95
1:D:233:ALA:HB1	1:D:264:ASN:HB2	1.50	0.92

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	375/384 (98%)	362 (96%)	12 (3%)	1 (0%)	46 56
1	B	372/384 (97%)	353 (95%)	18 (5%)	1 (0%)	46 56
1	C	362/384 (94%)	341 (94%)	17 (5%)	4 (1%)	17 18

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	372/384 (97%)	347 (93%)	21 (6%)	4 (1%)	17	18
All	All	1481/1536 (96%)	1403 (95%)	68 (5%)	10 (1%)	26	31

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	41	GLU
1	A	61	MSE
1	D	61	MSE
1	D	217	SER
1	B	41	GLU

### 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	326/324 (101%)	315 (97%)	11 (3%)	44	59
1	B	326/324 (101%)	311 (95%)	15 (5%)	33	44
1	C	318/324 (98%)	306 (96%)	12 (4%)	40	54
1	D	318/324 (98%)	302 (95%)	16 (5%)	30	41
All	All	1288/1296 (99%)	1234 (96%)	54 (4%)	37	49

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	350	SER
1	C	175	ASP
1	D	252	ARG
1	B	367	GLU
1	C	41	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	281	ASN
1	C	45	GLN
1	D	240	GLN
1	B	282	HIS
1	C	145	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](#)

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	UD1	B	385	-	32,41,41	1.63	5 (15%)	46,62,62	2.71	13 (28%)
2	UD1	C	385	-	32,41,41	1.61	5 (15%)	46,62,62	2.95	11 (23%)

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	UD1	B	385	-	1/1/12/13	2/22/63/63	0/3/3/3
2	UD1	C	385	-	1/1/12/13	2/22/63/63	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	385	UD1	PB-O1'	-4.05	1.49	1.60
2	B	385	UD1	PB-O1'	-3.83	1.50	1.60
2	B	385	UD1	C4-N3	2.75	1.38	1.33
2	B	385	UD1	O5'-C1'	2.88	1.49	1.41
2	C	385	UD1	C4-N3	2.94	1.38	1.33

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	385	UD1	O5'-C1'-O1'	-8.78	99.79	111.36
2	B	385	UD1	O5'-C1'-O1'	-6.56	102.70	111.36
2	C	385	UD1	C5-C4-N3	-3.38	114.44	123.12
2	B	385	UD1	C2'-N2'-C7'	-3.11	115.12	123.10
2	C	385	UD1	C3'-C4'-C5'	-3.08	104.83	110.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	385	UD1	C2'
2	C	385	UD1	C2'

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	385	UD1	C8'-C7'-N2'-C2'
2	C	385	UD1	C8'-C7'-N2'-C2'
2	C	385	UD1	O7'-C7'-N2'-C2'
2	B	385	UD1	O7'-C7'-N2'-C2'

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	385	UD1	4	0
2	C	385	UD1	3	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	366/384 (95%)	0.45	18 (4%) 33 42	18, 32, 59, 71	0
1	B	363/384 (94%)	0.81	38 (10%) 8 12	19, 35, 71, 86	0
1	C	358/384 (93%)	0.87	45 (12%) 5 8	21, 43, 82, 90	0
1	D	364/384 (94%)	0.80	49 (13%) 4 7	18, 37, 81, 91	0
All	All	1451/1536 (94%)	0.73	150 (10%) 9 13	18, 37, 73, 91	0

The worst 5 of 150 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	247	LEU	9.2
1	B	376	LEU	7.3
1	B	251	VAL	6.3
1	C	251	VAL	5.8
1	B	247	LEU	5.8

### 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, 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	UD1	C	385	39/39	0.89	0.19	0.68	46,51,54,54	0
2	UD1	B	385	39/39	0.91	0.16	-0.50	41,45,50,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.