



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:05 PM GMT

PDB ID : 1RYW  
Title : C115S MurA liganded with reaction products  
Authors : Eschenburg, S.; Schonbrunn, E.  
Deposited on : 2003-12-22  
Resolution : 2.30 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.

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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

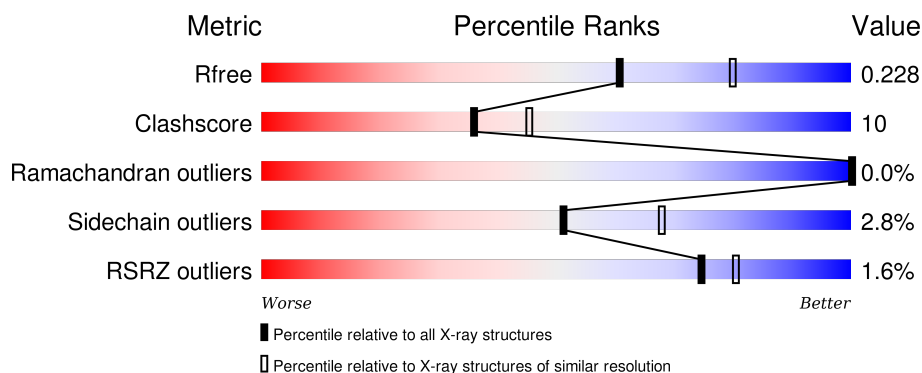
# 1 Overall quality at a glance ⓘ

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	419	<div> <div></div> <div>80%20%</div> </div>
1	B	419	<div> <div></div> <div>82%18%</div> </div>
1	C	419	<div> <div></div> <div>82%18%</div> </div>
1	D	419	<div> <div>2%</div> <div>79%21%</div> </div>
1	E	419	<div> <div></div> <div>83%17%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	419	
1	G	419	
1	H	419	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	A	2461	-	-	-	X
2	PO4	B	3461	-	-	-	X
2	PO4	D	5461	-	-	-	X
2	PO4	F	7461	-	-	-	X
2	PO4	G	8461	-	-	-	X
2	PO4	G	8462	-	-	-	X
4	GOL	A	2471	-	-	-	X
4	GOL	B	3471	-	-	-	X
4	GOL	B	3472	-	-	-	X
4	GOL	C	4471	-	-	-	X
4	GOL	C	4474	-	-	-	X
4	GOL	D	5471	-	-	-	X
4	GOL	E	6471	-	-	-	X
4	GOL	E	8472	-	-	-	X
4	GOL	F	7471	-	-	-	X
4	GOL	G	8471	-	-	-	X
4	GOL	H	9471	-	-	-	X
4	GOL	H	9472	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 27527 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 1-carboxyvinyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total	C	N	O	S	0	6	0
			3173	1996	560	603	14			
1	B	419	Total	C	N	O	S	0	0	0
			3143	1976	554	600	13			
1	C	419	Total	C	N	O	S	0	0	0
			3143	1976	554	600	13			
1	D	419	Total	C	N	O	S	0	1	0
			3145	1977	554	601	13			
1	E	419	Total	C	N	O	S	0	2	0
			3149	1979	555	602	13			
1	F	419	Total	C	N	O	S	0	1	0
			3150	1980	557	600	13			
1	G	419	Total	C	N	O	S	0	2	0
			3155	1983	557	602	13			
1	H	419	Total	C	N	O	S	0	2	0
			3154	1983	557	600	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	IAS	ASN	ENGINEERED	UNP P33038
A	115	SER	CYS	ENGINEERED	UNP P33038
B	67	IAS	ASN	ENGINEERED	UNP P33038
B	115	SER	CYS	ENGINEERED	UNP P33038
C	67	IAS	ASN	ENGINEERED	UNP P33038
C	115	SER	CYS	ENGINEERED	UNP P33038
D	67	IAS	ASN	ENGINEERED	UNP P33038
D	115	SER	CYS	ENGINEERED	UNP P33038
E	67	IAS	ASN	ENGINEERED	UNP P33038
E	115	SER	CYS	ENGINEERED	UNP P33038
F	67	IAS	ASN	ENGINEERED	UNP P33038
F	115	SER	CYS	ENGINEERED	UNP P33038
G	67	IAS	ASN	ENGINEERED	UNP P33038

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Chain	Residue	Modelled	Actual	Comment	Reference
G	115	SER	CYS	ENGINEERED	UNP P33038
H	67	IAS	ASN	ENGINEERED	UNP P33038
H	115	SER	CYS	ENGINEERED	UNP P33038

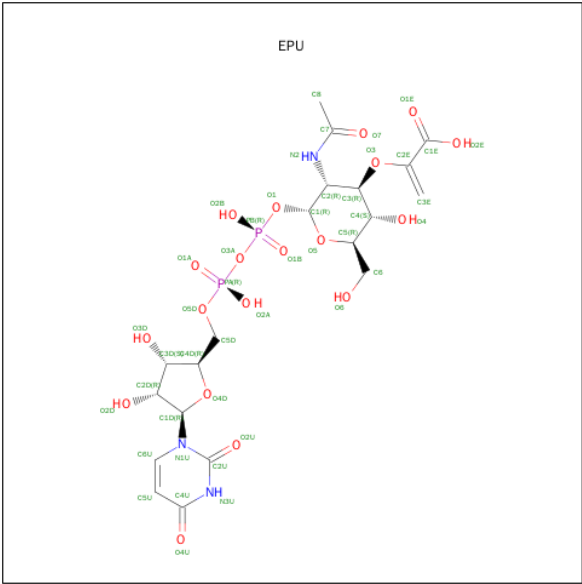
- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	G	1	Total	O	P	0	0
			5	4	1		
2	G	1	Total	O	P	0	0
			5	4	1		
2	H	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is URIDINE-DIPHOSPHATE-2(N-ACETYLGUCOSAMINYL) BUTYRIC

ACID (three-letter code: EPU) (formula: C<sub>20</sub>H<sub>29</sub>N<sub>3</sub>O<sub>19</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	20	3	19	2		
3	B	1	Total	C	N	O	P	0	0
			44	20	3	19	2		
3	C	1	Total	C	N	O	P	0	0
			44	20	3	19	2		
3	D	1	Total	C	N	O	P	0	0
			44	20	3	19	2		
3	E	1	Total	C	N	O	P	0	0
			44	20	3	19	2		
3	F	1	Total	C	N	O	P	0	0
			44	20	3	19	2		
3	G	1	Total	C	N	O	P	0	0
			44	20	3	19	2		
3	H	1	Total	C	N	O	P	0	0
			44	20	3	19	2		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

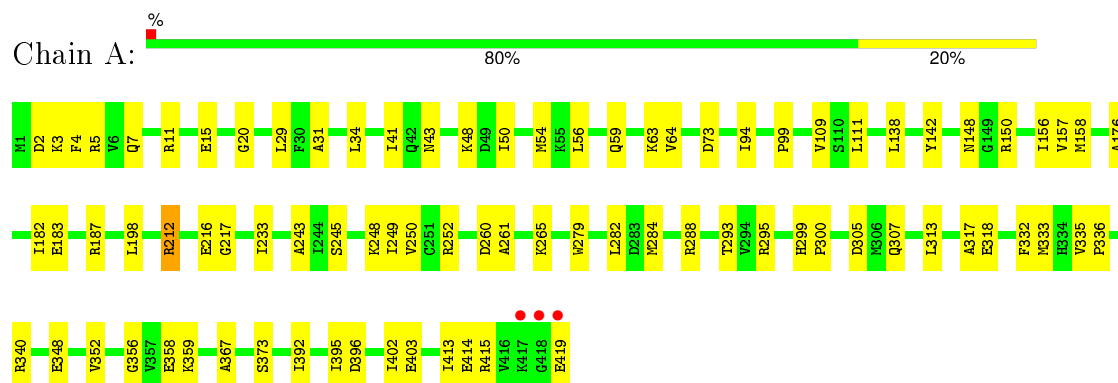
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	284	Total	O	0	0
			284	284		
5	B	253	Total	O	0	0
			253	253		
5	C	272	Total	O	0	0
			272	272		
5	D	208	Total	O	0	0
			208	208		
5	E	214	Total	O	0	0
			214	214		
5	F	136	Total	O	0	0
			136	136		
5	G	237	Total	O	0	0
			237	237		
5	H	212	Total	O	0	0
			212	212		



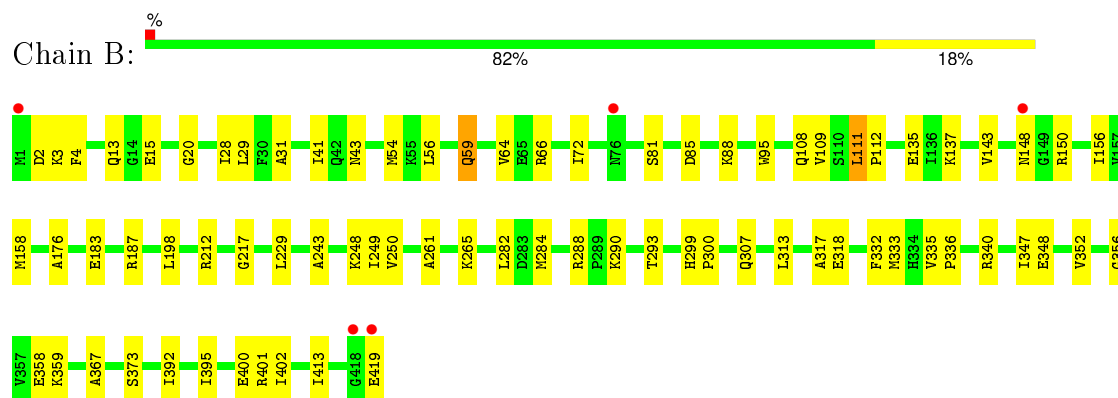
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

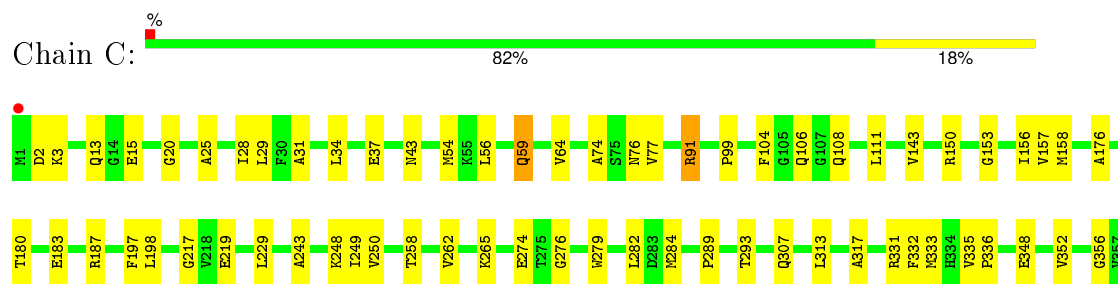
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

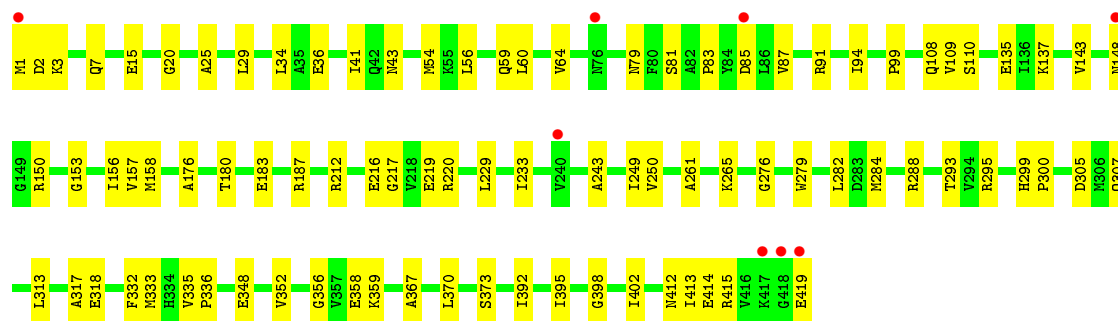
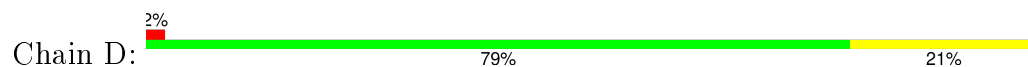


- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

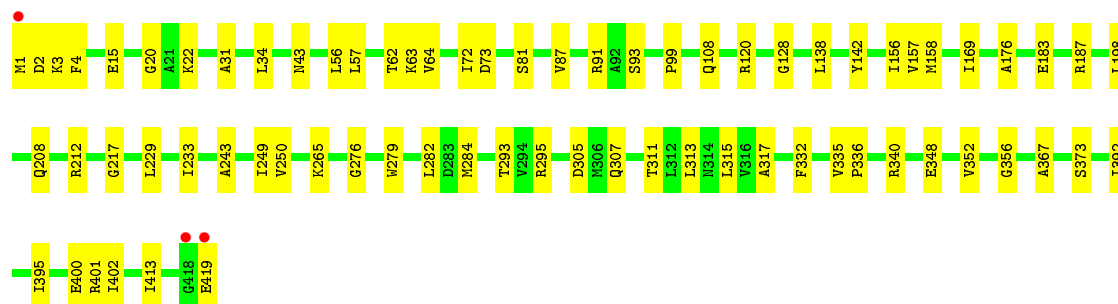
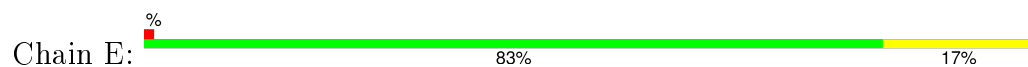




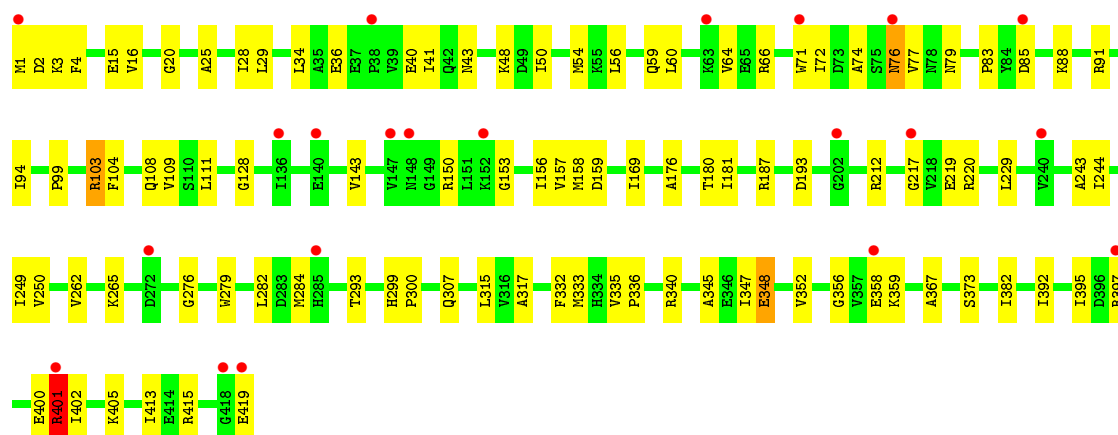
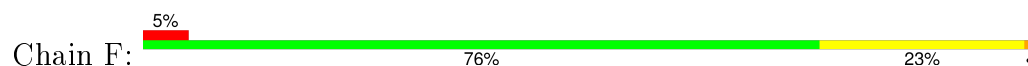
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



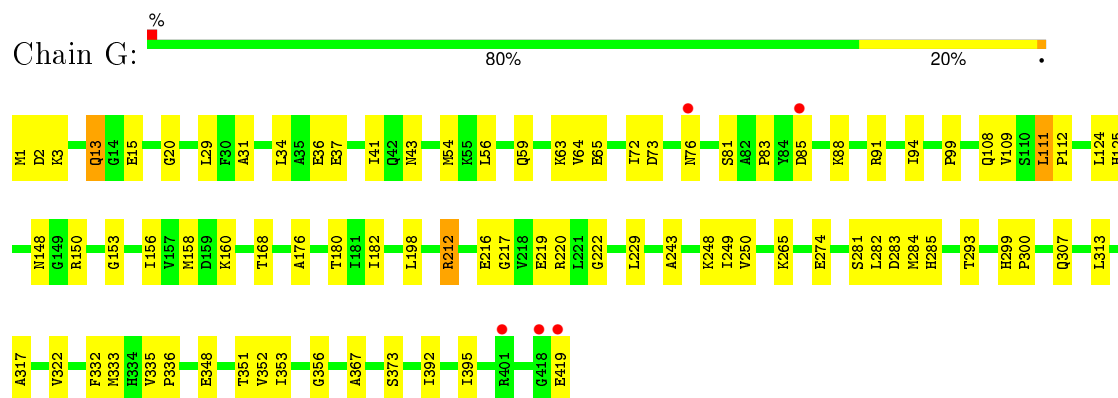
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



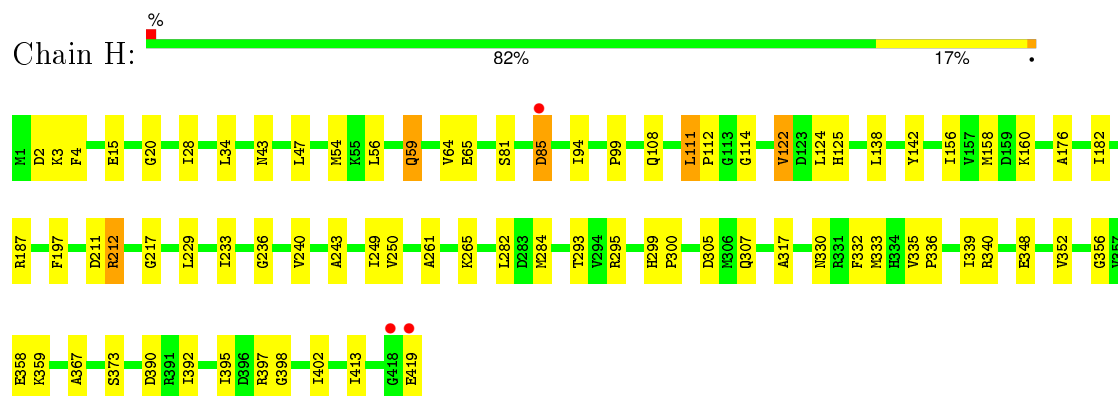
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.87Å 153.73Å 135.09Å 90.00° 104.17° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 29.92 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.0 (20.00-2.30) 98.9 (29.92-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.60 (at 2.31Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.178 , 0.225 0.183 , 0.228	Depositor DCC
$R_{free}$ test set	2798 reflections (2.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.1	Xtriage
Anisotropy	0.513	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 140045 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	27527	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	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 24.52 % 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 3.7730e-03. 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: GOL, PO4, EPU, IAS

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	0.37	0/3233	0.62	0/4376
1	B	0.36	0/3179	0.61	0/4305
1	C	0.36	0/3179	0.61	0/4305
1	D	0.35	0/3185	0.59	0/4313
1	E	0.36	0/3193	0.61	0/4324
1	F	0.34	0/3190	0.60	0/4319
1	G	0.36	0/3199	0.61	0/4332
1	H	0.35	0/3198	0.62	0/4329
All	All	0.36	0/25556	0.61	0/34603

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 [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	3173	0	3253	70	0
1	B	3143	0	3216	56	0
1	C	3143	0	3216	58	0
1	D	3145	0	3217	61	0
1	E	3149	0	3219	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3150	0	3225	75	0
1	G	3155	0	3227	67	0
1	H	3154	0	3230	56	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	1	0
2	F	5	0	0	0	0
2	G	10	0	0	0	0
2	H	5	0	0	1	0
3	A	44	0	26	2	0
3	B	44	0	26	2	0
3	C	44	0	26	2	0
3	D	44	0	26	1	0
3	E	44	0	26	3	0
3	F	44	0	26	1	0
3	G	44	0	26	1	0
3	H	44	0	26	3	0
4	A	12	0	16	5	0
4	B	12	0	16	3	0
4	C	30	0	40	7	0
4	D	12	0	16	1	0
4	E	12	0	16	2	0
4	F	6	0	8	1	0
4	G	6	0	8	2	0
4	H	12	0	16	3	0
5	A	284	0	0	7	0
5	B	253	0	0	3	0
5	C	272	0	0	4	0
5	D	208	0	0	3	0
5	E	214	0	0	2	0
5	F	136	0	0	1	0
5	G	237	0	0	7	0
5	H	212	0	0	3	0
All	All	27527	0	26147	498	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 10.

The worst 5 of 498 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:G:81:SER:HB2	1:G:108:GLN:HE21	1.40	0.86
1:B:54:MET:HE3	1:B:66:ARG:HB3	1.57	0.85
1:G:13:GLN:HG2	1:G:248:LYS:H	1.41	0.84
1:A:150:ARG:HD3	5:A:1069:HOH:O	1.78	0.83
1:C:54:MET:HG2	1:C:64:VAL:HG11	1.60	0.83

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	421/419 (100%)	413 (98%)	8 (2%)	0	100	100
1	B	415/419 (99%)	404 (97%)	11 (3%)	0	100	100
1	C	415/419 (99%)	407 (98%)	8 (2%)	0	100	100
1	D	416/419 (99%)	405 (97%)	11 (3%)	0	100	100
1	E	417/419 (100%)	408 (98%)	9 (2%)	0	100	100
1	F	416/419 (99%)	399 (96%)	16 (4%)	1 (0%)	52	64
1	G	417/419 (100%)	409 (98%)	8 (2%)	0	100	100
1	H	417/419 (100%)	408 (98%)	9 (2%)	0	100	100
All	All	3334/3352 (100%)	3253 (98%)	80 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	401	ARG

### 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	335/329 (102%)	325 (97%)	10 (3%)	48	65
1	B	329/329 (100%)	322 (98%)	7 (2%)	61	78
1	C	329/329 (100%)	317 (96%)	12 (4%)	42	57
1	D	330/329 (100%)	321 (97%)	9 (3%)	52	70
1	E	331/329 (101%)	326 (98%)	5 (2%)	72	85
1	F	330/329 (100%)	318 (96%)	12 (4%)	42	57
1	G	331/329 (101%)	321 (97%)	10 (3%)	48	65
1	H	331/329 (101%)	320 (97%)	11 (3%)	45	61
All	All	2646/2632 (100%)	2570 (97%)	76 (3%)	51	66

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	187	ARG
1	E	348	GLU
1	H	187	ARG
1	D	229	LEU
1	E	91	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	148	ASN
1	E	330	ASN
1	H	148	ASN
1	D	344	HIS
1	F	7	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.



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

8 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	IAS	A	67	1	4,7,8	0.62	0	1,8,10	1.28	0
1	IAS	B	67	1	4,7,8	0.62	0	1,8,10	1.28	0
1	IAS	C	67	1	4,7,8	0.64	0	1,8,10	1.34	0
1	IAS	D	67	1	4,7,8	0.46	0	1,8,10	1.46	0
1	IAS	E	67	1	4,7,8	0.50	0	1,8,10	1.45	0
1	IAS	F	67	1	4,7,8	0.66	0	1,8,10	1.38	0
1	IAS	G	67	1	4,7,8	0.50	0	1,8,10	1.41	0
1	IAS	H	67	1	4,7,8	0.59	0	1,8,10	1.36	0

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
1	IAS	A	67	1	-	0/3/7/8	0/0/0/0
1	IAS	B	67	1	-	0/3/7/8	0/0/0/0
1	IAS	C	67	1	-	0/3/7/8	0/0/0/0
1	IAS	D	67	1	-	0/3/7/8	0/0/0/0
1	IAS	E	67	1	-	0/3/7/8	0/0/0/0
1	IAS	F	67	1	-	0/3/7/8	0/0/0/0
1	IAS	G	67	1	-	0/3/7/8	0/0/0/0
1	IAS	H	67	1	-	0/3/7/8	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

34 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	EPU	A	2450	-	34,46,46	2.11	14 (41%)	47,69,69	2.48	7 (14%)
2	PO4	A	2461	-	4,4,4	1.17	0	6,6,6	0.27	0
4	GOL	A	2471	-	5,5,5	0.49	0	5,5,5	0.31	0
4	GOL	A	2472	-	5,5,5	0.65	0	5,5,5	0.50	0
3	EPU	B	3450	-	34,46,46	2.23	14 (41%)	47,69,69	2.47	9 (19%)
2	PO4	B	3461	-	4,4,4	1.19	0	6,6,6	0.27	0
4	GOL	B	3471	-	5,5,5	0.38	0	5,5,5	0.31	0
4	GOL	B	3472	-	5,5,5	0.49	0	5,5,5	0.48	0
4	GOL	C	2473	-	5,5,5	0.38	0	5,5,5	0.52	0
4	GOL	C	3473	-	5,5,5	0.46	0	5,5,5	0.48	0
3	EPU	C	4450	-	34,46,46	2.22	14 (41%)	47,69,69	2.47	8 (17%)
2	PO4	C	4461	-	4,4,4	1.13	0	6,6,6	0.27	0
4	GOL	C	4471	-	5,5,5	0.37	0	5,5,5	0.32	0
4	GOL	C	4472	-	5,5,5	0.48	0	5,5,5	0.47	0
4	GOL	C	4474	-	5,5,5	0.40	0	5,5,5	0.42	0
3	EPU	D	5450	-	34,46,46	2.16	14 (41%)	47,69,69	2.47	9 (19%)
2	PO4	D	5461	-	4,4,4	1.14	0	6,6,6	0.27	0
4	GOL	D	5471	-	5,5,5	0.44	0	5,5,5	0.34	0
4	GOL	D	5472	-	5,5,5	0.46	0	5,5,5	0.56	0
3	EPU	E	6450	-	34,46,46	2.30	16 (47%)	47,69,69	2.52	9 (19%)
2	PO4	E	6461	-	4,4,4	1.12	0	6,6,6	0.27	0
4	GOL	E	6471	-	5,5,5	0.47	0	5,5,5	0.34	0
4	GOL	E	8472	-	5,5,5	0.43	0	5,5,5	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EPU	F	7450	-	34,46,46	2.19	14 (41%)	47,69,69	2.57	9 (19%)
2	PO4	F	7461	-	4,4,4	1.17	0	6,6,6	0.27	0
4	GOL	F	7471	-	5,5,5	0.45	0	5,5,5	0.36	0
3	EPU	G	8450	-	34,46,46	2.27	13 (38%)	47,69,69	2.44	9 (19%)
2	PO4	G	8461	-	4,4,4	1.14	0	6,6,6	0.27	0
2	PO4	G	8462	-	4,4,4	1.06	0	6,6,6	0.27	0
4	GOL	G	8471	-	5,5,5	0.41	0	5,5,5	0.28	0
3	EPU	H	9450	-	34,46,46	2.12	12 (35%)	47,69,69	2.44	9 (19%)
2	PO4	H	9461	-	4,4,4	1.19	0	6,6,6	0.27	0
4	GOL	H	9471	-	5,5,5	0.44	0	5,5,5	0.38	0
4	GOL	H	9472	-	5,5,5	0.42	0	5,5,5	0.51	0

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	EPU	A	2450	-	-	0/24/71/71	0/3/3/3
2	PO4	A	2461	-	-	0/0/0/0	0/0/0/0
4	GOL	A	2471	-	-	0/4/4/4	0/0/0/0
4	GOL	A	2472	-	-	0/4/4/4	0/0/0/0
3	EPU	B	3450	-	-	0/24/71/71	0/3/3/3
2	PO4	B	3461	-	-	0/0/0/0	0/0/0/0
4	GOL	B	3471	-	-	0/4/4/4	0/0/0/0
4	GOL	B	3472	-	-	0/4/4/4	0/0/0/0
4	GOL	C	2473	-	-	0/4/4/4	0/0/0/0
4	GOL	C	3473	-	-	0/4/4/4	0/0/0/0
3	EPU	C	4450	-	-	0/24/71/71	0/3/3/3
2	PO4	C	4461	-	-	0/0/0/0	0/0/0/0
4	GOL	C	4471	-	-	0/4/4/4	0/0/0/0
4	GOL	C	4472	-	-	0/4/4/4	0/0/0/0
4	GOL	C	4474	-	-	0/4/4/4	0/0/0/0
3	EPU	D	5450	-	-	0/24/71/71	0/3/3/3
2	PO4	D	5461	-	-	0/0/0/0	0/0/0/0
4	GOL	D	5471	-	-	0/4/4/4	0/0/0/0
4	GOL	D	5472	-	-	0/4/4/4	0/0/0/0
3	EPU	E	6450	-	-	0/24/71/71	0/3/3/3
2	PO4	E	6461	-	-	0/0/0/0	0/0/0/0
4	GOL	E	6471	-	-	0/4/4/4	0/0/0/0
4	GOL	E	8472	-	-	0/4/4/4	0/0/0/0
3	EPU	F	7450	-	-	0/24/71/71	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PO4	F	7461	-	-	0/0/0/0	0/0/0/0
4	GOL	F	7471	-	-	0/4/4/4	0/0/0/0
3	EPU	G	8450	-	-	0/24/71/71	0/3/3/3
2	PO4	G	8461	-	-	0/0/0/0	0/0/0/0
2	PO4	G	8462	-	-	0/0/0/0	0/0/0/0
4	GOL	G	8471	-	-	0/4/4/4	0/0/0/0
3	EPU	H	9450	-	-	0/24/71/71	0/3/3/3
2	PO4	H	9461	-	-	0/0/0/0	0/0/0/0
4	GOL	H	9471	-	-	0/4/4/4	0/0/0/0
4	GOL	H	9472	-	-	0/4/4/4	0/0/0/0

The worst 5 of 111 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	8450	EPU	PB-O1B	-2.66	1.41	1.51
3	E	6450	EPU	PB-O2B	-2.39	1.44	1.54
3	C	4450	EPU	PB-O1B	-2.34	1.42	1.51
3	F	7450	EPU	PB-O2B	-2.34	1.45	1.54
3	A	2450	EPU	PB-O1B	-2.34	1.42	1.51

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	9450	EPU	C2D-C3D-C4D	-3.25	95.94	102.61
3	E	6450	EPU	C5U-C4U-N3U	-3.25	114.79	123.12
3	G	8450	EPU	C2D-C3D-C4D	-3.25	95.94	102.61
3	F	7450	EPU	C5U-C4U-N3U	-3.22	114.86	123.12
3	F	7450	EPU	C2D-C3D-C4D	-3.22	96.00	102.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

22 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2450	EPU	2	0
4	A	2471	GOL	2	0
4	A	2472	GOL	3	0
3	B	3450	EPU	2	0
4	B	3471	GOL	3	0
4	C	2473	GOL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	3473	GOL	1	0
3	C	4450	EPU	2	0
4	C	4471	GOL	3	0
4	C	4474	GOL	2	0
3	D	5450	EPU	1	0
4	D	5471	GOL	1	0
3	E	6450	EPU	3	0
2	E	6461	PO4	1	0
4	E	6471	GOL	2	0
3	F	7450	EPU	1	0
4	F	7471	GOL	1	0
3	G	8450	EPU	1	0
4	G	8471	GOL	2	0
3	H	9450	EPU	3	0
2	H	9461	PO4	1	0
4	H	9471	GOL	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 ⓘ

### 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	418/419 (99%)	-0.37	3 (0%) 89 92	7, 18, 33, 94	0
1	B	418/419 (99%)	-0.11	5 (1%) 81 85	10, 21, 38, 93	0
1	C	418/419 (99%)	-0.30	5 (1%) 81 85	9, 20, 35, 91	0
1	D	418/419 (99%)	-0.10	8 (1%) 70 76	10, 23, 40, 93	0
1	E	418/419 (99%)	-0.15	3 (0%) 89 92	12, 22, 36, 92	0
1	F	418/419 (99%)	0.32	21 (5%) 32 41	14, 29, 47, 95	0
1	G	418/419 (99%)	-0.14	5 (1%) 81 85	10, 22, 39, 94	0
1	H	418/419 (99%)	-0.22	3 (0%) 89 92	10, 21, 37, 92	0
All	All	3344/3352 (99%)	-0.13	53 (1%) 74 80	7, 22, 39, 95	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	418	GLY	9.5
1	F	419	GLU	9.0
1	A	419	GLU	7.7
1	H	419	GLU	7.2
1	A	418	GLY	6.7

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

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
1	IAS	B	67	8/9	0.93	0.15	-	23,26,29,35	0
1	IAS	D	67	8/9	0.95	0.17	-	24,27,29,31	0
1	IAS	F	67	8/9	0.81	0.30	-	34,36,38,41	0
1	IAS	H	67	8/9	0.96	0.13	-	18,22,24,24	0
1	IAS	A	67	8/9	0.97	0.09	-	13,16,17,18	0
1	IAS	C	67	8/9	0.96	0.14	-	20,21,28,28	0
1	IAS	E	67	8/9	0.96	0.19	-	22,26,28,34	0
1	IAS	G	67	8/9	0.97	0.14	-	21,23,25,28	0

## 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
4	GOL	A	2471	6/6	0.89	0.24	9.72	21,25,26,32	0
4	GOL	C	4474	6/6	0.90	0.21	6.10	32,39,41,43	0
4	GOL	G	8471	6/6	0.92	0.25	5.69	26,28,28,38	0
4	GOL	E	8472	6/6	0.82	0.34	4.72	51,56,59,61	0
4	GOL	E	6471	6/6	0.89	0.23	4.10	23,27,30,33	0
4	GOL	D	5471	6/6	0.90	0.26	3.90	24,29,34,38	0
4	GOL	H	9471	6/6	0.94	0.22	3.77	24,28,30,36	0
2	PO4	F	7461	5/5	0.91	0.21	3.59	64,65,66,70	0
4	GOL	B	3472	6/6	0.85	0.27	3.55	53,55,55,58	0
4	GOL	F	7471	6/6	0.86	0.26	3.37	38,40,41,44	0
4	GOL	C	4471	6/6	0.94	0.20	3.30	16,21,25,28	0
2	PO4	G	8462	5/5	0.74	0.22	3.27	91,92,93,93	0
2	PO4	G	8461	5/5	0.92	0.19	3.04	50,52,55,58	0
2	PO4	A	2461	5/5	0.96	0.18	2.86	34,35,41,46	0
4	GOL	B	3471	6/6	0.94	0.22	2.73	23,25,27,32	0
2	PO4	B	3461	5/5	0.94	0.18	2.51	46,48,51,52	0
2	PO4	D	5461	5/5	0.94	0.17	2.47	54,55,58,61	0
4	GOL	H	9472	6/6	0.86	0.29	2.22	40,47,50,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	E	6461	5/5	0.96	0.15	1.35	47,50,50,52	0
2	PO4	C	4461	5/5	0.96	0.15	0.55	42,45,48,50	0
2	PO4	H	9461	5/5	0.96	0.13	0.35	42,44,47,50	0
3	EPU	F	7450	44/44	0.96	0.13	0.14	14,21,27,29	0
3	EPU	A	2450	44/44	0.98	0.12	0.04	9,14,18,26	0
3	EPU	C	4450	44/44	0.97	0.12	-0.12	7,14,21,28	0
3	EPU	G	8450	44/44	0.97	0.12	-0.17	6,16,23,26	0
3	EPU	B	3450	44/44	0.97	0.11	-0.35	8,16,20,24	0
3	EPU	H	9450	44/44	0.98	0.11	-0.36	1,15,22,24	0
3	EPU	E	6450	44/44	0.98	0.11	-0.42	8,15,21,22	0
3	EPU	D	5450	44/44	0.98	0.10	-0.57	10,17,27,31	0
4	GOL	D	5472	6/6	0.88	0.30	-	44,46,47,47	0
4	GOL	C	2473	6/6	0.84	0.17	-	45,48,49,51	0
4	GOL	C	4472	6/6	0.79	0.34	-	47,52,56,57	0
4	GOL	A	2472	6/6	0.81	0.25	-	43,46,46,50	0
4	GOL	C	3473	6/6	0.82	0.22	-	54,56,60,66	0

## 6.5 Other polymers

There are no such residues in this entry.