



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:43 PM GMT

PDB ID : 1Q3G  
Title : MurA (Asp305Ala) liganded with tetrahedral reaction intermediate  
Authors : Eschenburg, S.; Kabsch, W.; Healy, M.L.; Schonbrunn, E.  
Deposited on : 2003-07-29  
Resolution : 2.65 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

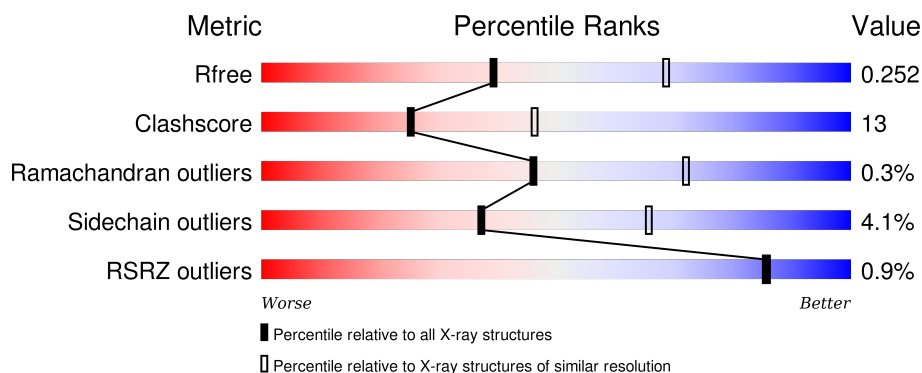
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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.





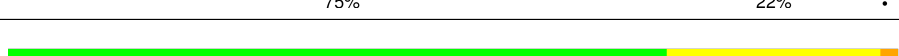

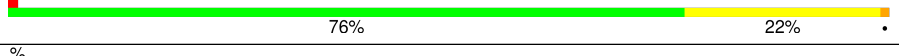
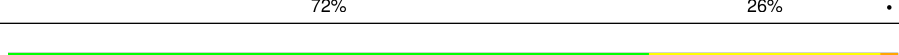
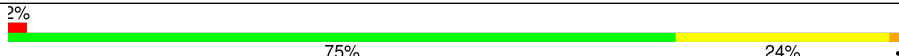
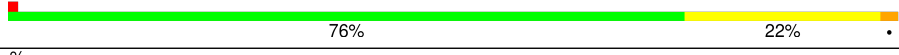
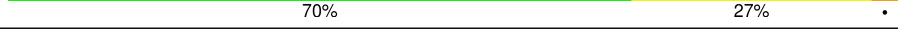
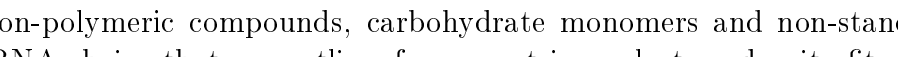

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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 style="width: 100%; height: 10px; background: linear-gradient(to right, red 10%, orange 10%, yellow 10%, green 72%, green 26%, orange 2%, red 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>72%</span> <span>26%</span> </div> </div>
1	B	419	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 10%, orange 10%, yellow 10%, green 74%, green 25%, orange 2%, red 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>74%</span> <span>25%</span> </div> </div>
1	C	419	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 79%, green 19%, orange 2%, red 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>79%</span> <span>19%</span> </div> </div>
1	D	419	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 10%, orange 10%, yellow 10%, green 73%, green 26%, orange 2%, red 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>73%</span> <span>26%</span> </div> </div>
1	E	419	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 77%, green 22%, orange 2%, red 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>77%</span> <span>22%</span> </div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	419	
1	G	419	
1	H	419	
1	I	419	
1	J	419	
1	K	419	
1	L	419	
1	W	419	
1	X	419	
1	Y	419	
1	Z	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
3	EDO	A	1470	-	-	-	X
3	EDO	B	1471	-	-	-	X
3	EDO	C	1472	-	-	-	X
3	EDO	D	1473	-	-	-	X
3	EDO	E	1474	-	-	-	X
3	EDO	F	1475	-	-	-	X
3	EDO	G	1476	-	-	-	X
3	EDO	H	1477	-	-	-	X
3	EDO	K	1480	-	-	-	X
3	EDO	L	1481	-	-	-	X
3	EDO	W	1482	-	-	-	X
3	EDO	X	1483	-	-	-	X
3	EDO	Y	1484	-	-	-	X
3	EDO	Z	1485	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 52519 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.

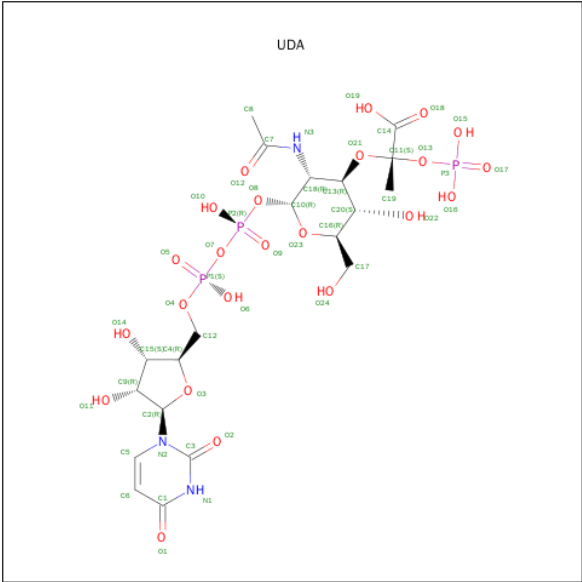
- Molecule 1 is a protein called UDP-N-acetylglucosamine 1-carboxyvinyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	B	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	C	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	D	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	E	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	F	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	G	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	H	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	I	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	J	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	K	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	L	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	W	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	X	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	Y	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			
1	Z	419	Total	C	N	O	S	0	0	0
			3140	1975	554	597	14			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	IAS	ASN	ENGINEERED	UNP P33038
A	305	ALA	ASP	ENGINEERED	UNP P33038
B	67	IAS	ASN	ENGINEERED	UNP P33038
B	305	ALA	ASP	ENGINEERED	UNP P33038
C	67	IAS	ASN	ENGINEERED	UNP P33038
C	305	ALA	ASP	ENGINEERED	UNP P33038
D	67	IAS	ASN	ENGINEERED	UNP P33038
D	305	ALA	ASP	ENGINEERED	UNP P33038
E	67	IAS	ASN	ENGINEERED	UNP P33038
E	305	ALA	ASP	ENGINEERED	UNP P33038
F	67	IAS	ASN	ENGINEERED	UNP P33038
F	305	ALA	ASP	ENGINEERED	UNP P33038
G	67	IAS	ASN	ENGINEERED	UNP P33038
G	305	ALA	ASP	ENGINEERED	UNP P33038
H	67	IAS	ASN	ENGINEERED	UNP P33038
H	305	ALA	ASP	ENGINEERED	UNP P33038
I	67	IAS	ASN	ENGINEERED	UNP P33038
I	305	ALA	ASP	ENGINEERED	UNP P33038
J	67	IAS	ASN	ENGINEERED	UNP P33038
J	305	ALA	ASP	ENGINEERED	UNP P33038
K	67	IAS	ASN	ENGINEERED	UNP P33038
K	305	ALA	ASP	ENGINEERED	UNP P33038
L	67	IAS	ASN	ENGINEERED	UNP P33038
L	305	ALA	ASP	ENGINEERED	UNP P33038
W	67	IAS	ASN	ENGINEERED	UNP P33038
W	305	ALA	ASP	ENGINEERED	UNP P33038
X	67	IAS	ASN	ENGINEERED	UNP P33038
X	305	ALA	ASP	ENGINEERED	UNP P33038
Y	67	IAS	ASN	ENGINEERED	UNP P33038
Y	305	ALA	ASP	ENGINEERED	UNP P33038
Z	67	IAS	ASN	ENGINEERED	UNP P33038
Z	305	ALA	ASP	ENGINEERED	UNP P33038

- Molecule 2 is 3'-1-CARBOXY-1-PHOSPHONOXY-ETHOXY-URIDINE-DIPHOSPHAT E-N-ACETYLGLUCOSAMINE (three-letter code: UDA) (formula: C<sub>20</sub>H<sub>32</sub>N<sub>3</sub>O<sub>23</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	B	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	C	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	D	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	E	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	F	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	G	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	H	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	I	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	J	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	K	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	L	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	W	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	X	1	Total	C	N	O	P	0	0
			49	20	3	23	3		

Continued on next page...

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	Y	1	Total	C	N	O	P	0	0
			49	20	3	23	3		
2	Z	1	Total	C	N	O	P	0	0
			49	20	3	23	3		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	J	1	Total	C	O	0	0
			4	2	2		
3	K	1	Total	C	O	0	0
			4	2	2		
3	L	1	Total	C	O	0	0
			4	2	2		
3	W	1	Total	C	O	0	0
			4	2	2		
3	X	1	Total	C	O	0	0
			4	2	2		
3	Y	1	Total	C	O	0	0
			4	2	2		
3	Z	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	93	Total	O	0	0
			93	93		
4	B	100	Total	O	0	0
			100	100		
4	C	124	Total	O	0	0
			124	124		
4	D	123	Total	O	0	0
			123	123		
4	E	116	Total	O	0	0
			116	116		
4	F	106	Total	O	0	0
			106	106		
4	G	136	Total	O	0	0
			136	136		
4	H	111	Total	O	0	0
			111	111		
4	I	76	Total	O	0	0
			76	76		
4	J	76	Total	O	0	0
			76	76		
4	K	67	Total	O	0	0
			67	67		
4	L	68	Total	O	0	0
			68	68		

*Continued on next page...*



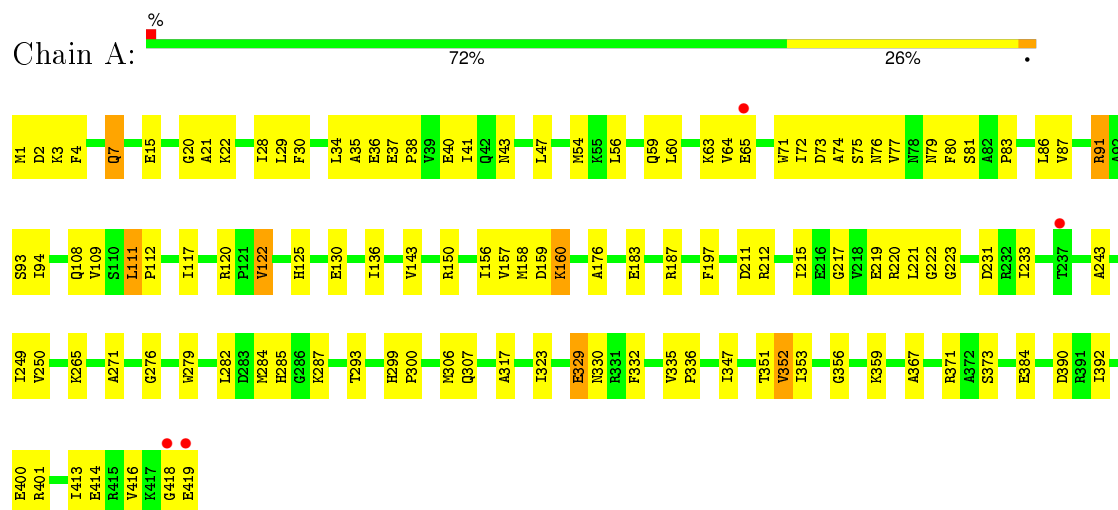
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	W	70	Total 70	O 70	0	0
4	X	52	Total 52	O 52	0	0
4	Y	67	Total 67	O 67	0	0
4	Z	46	Total 46	O 46	0	0

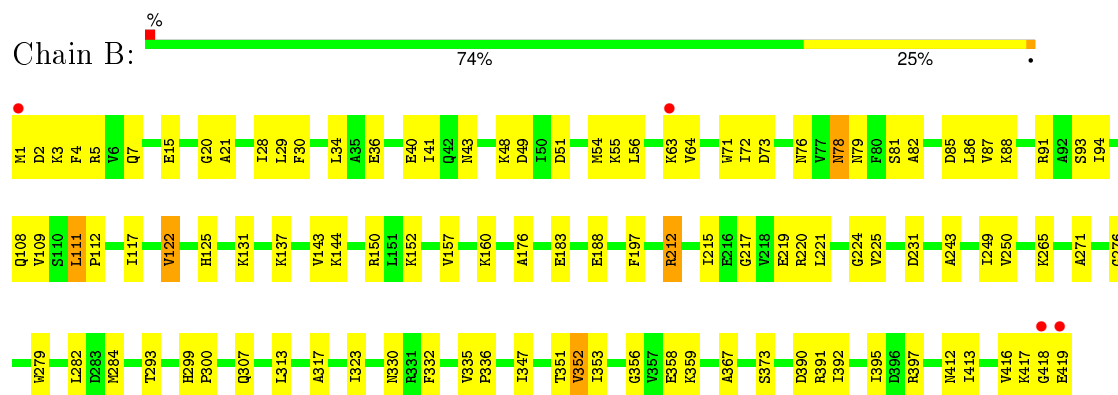
### 3 Residue-property plots

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.

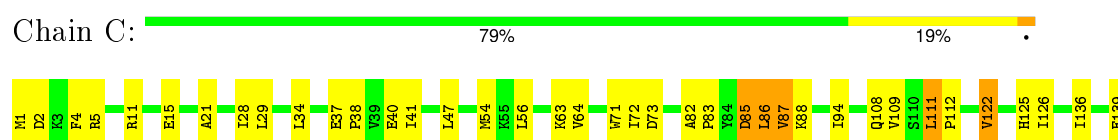
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

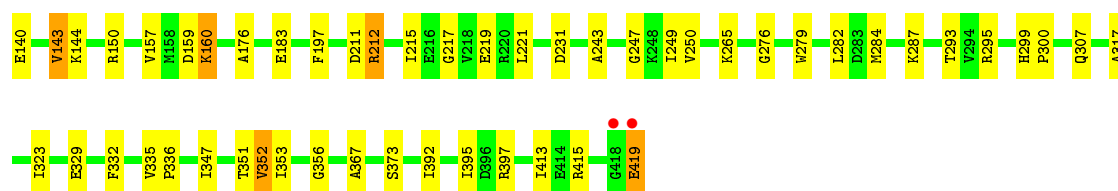


- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

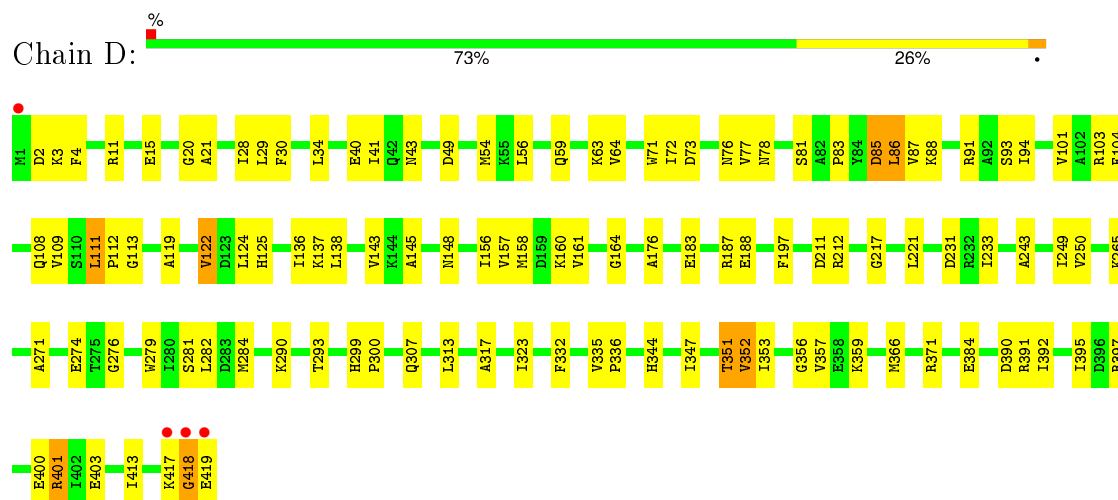


- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

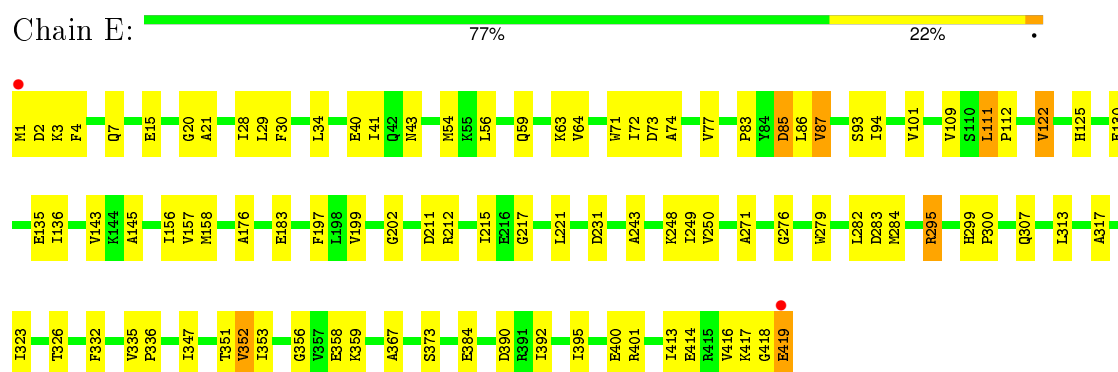




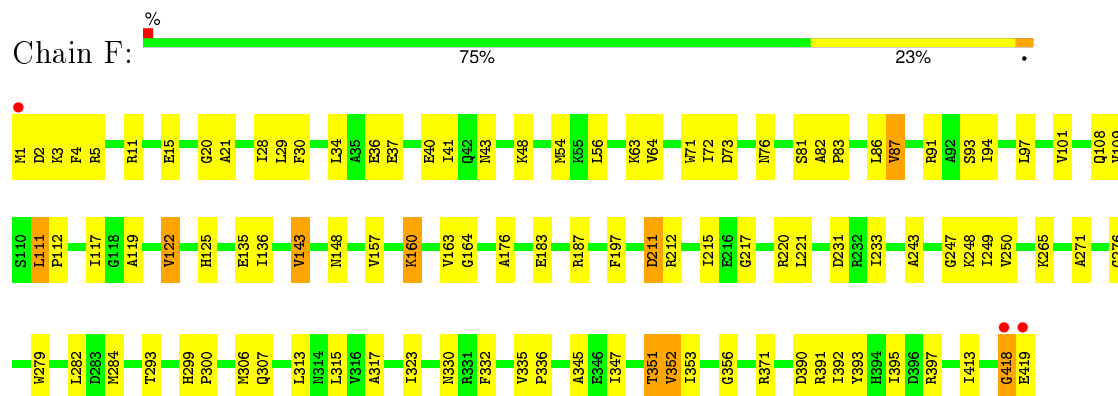
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



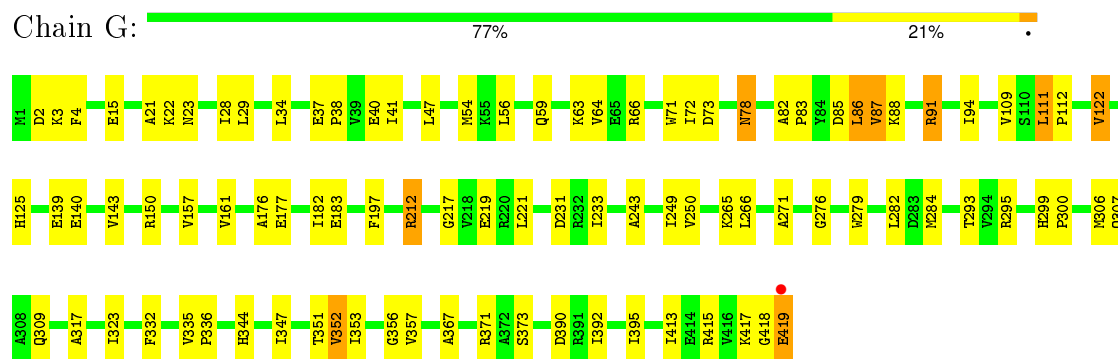
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



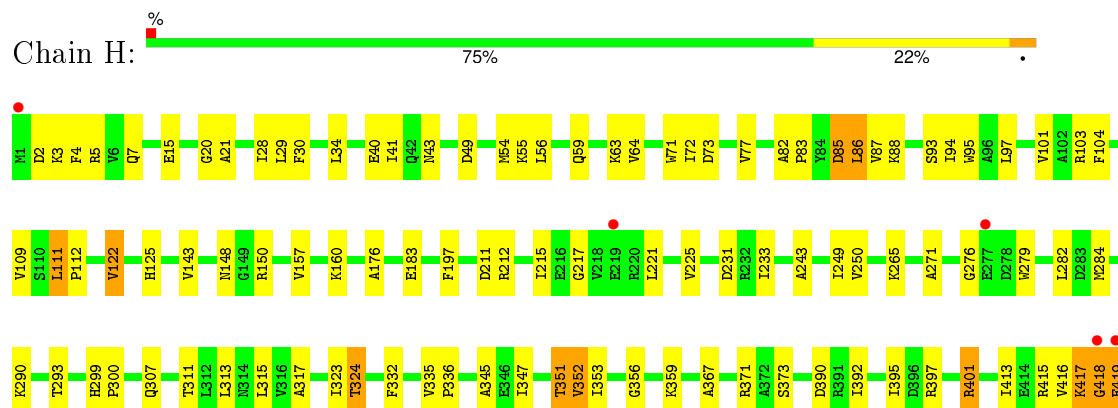
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



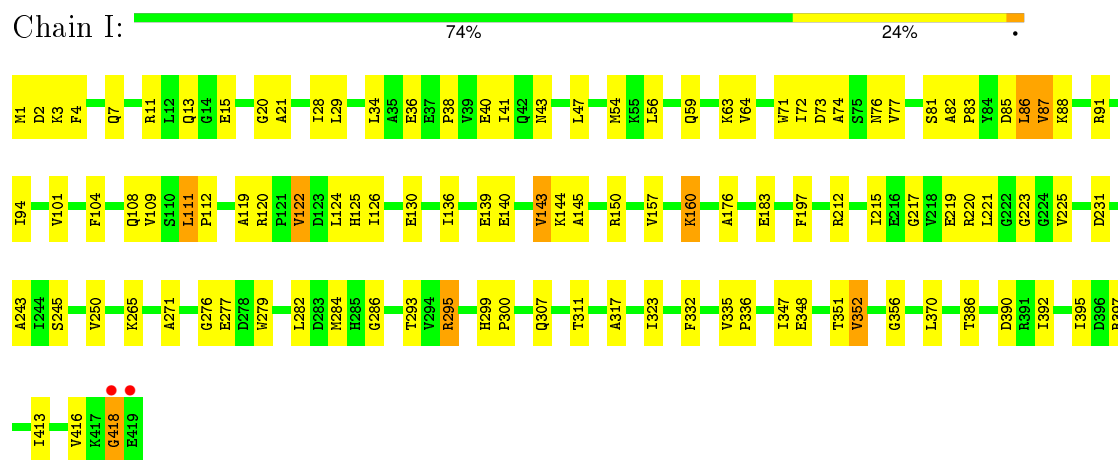
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



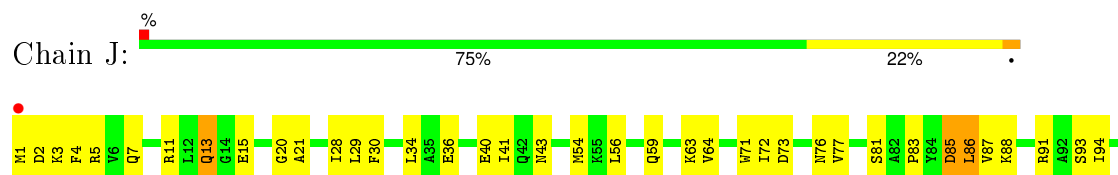
- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

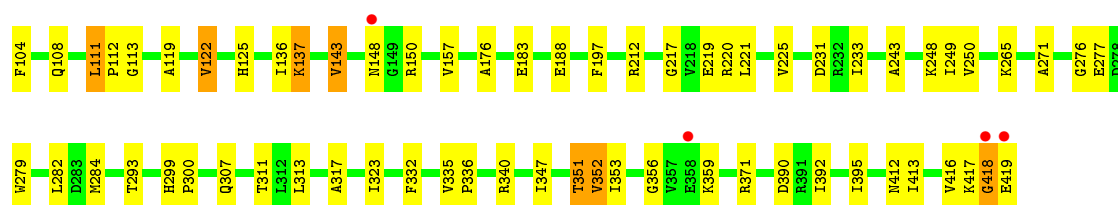


- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

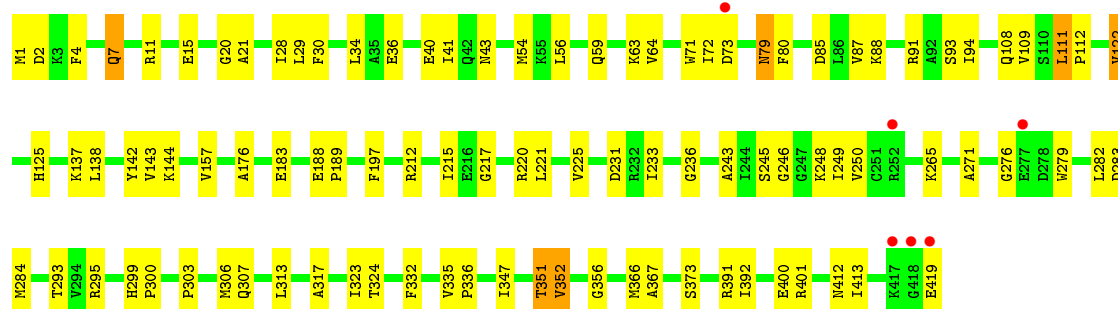
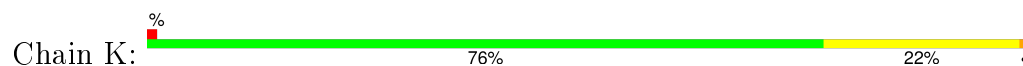


- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

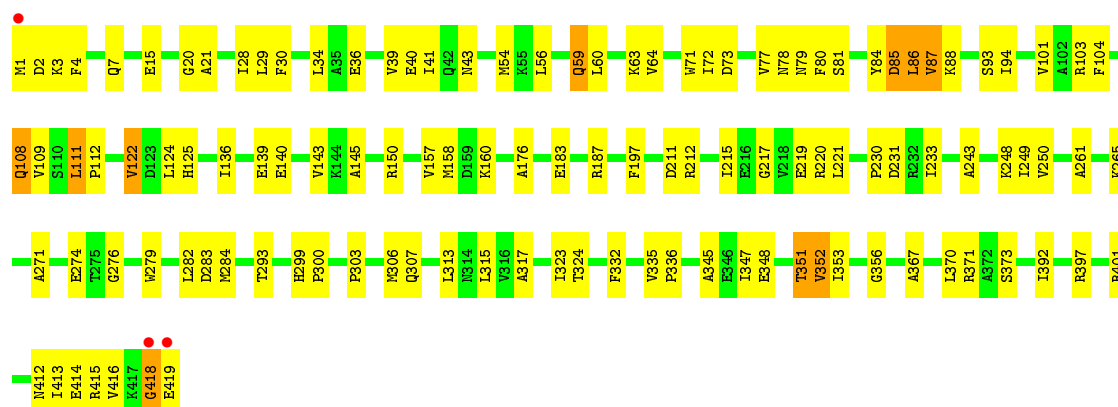




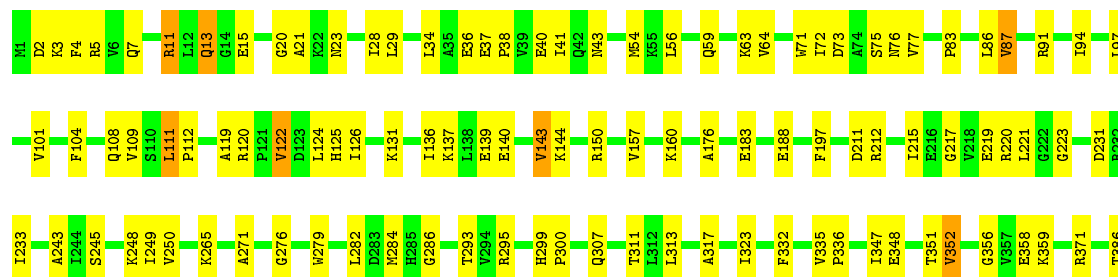
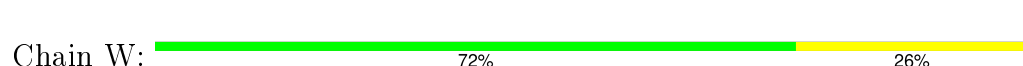
• Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

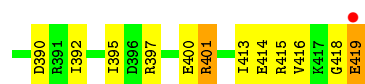


• Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

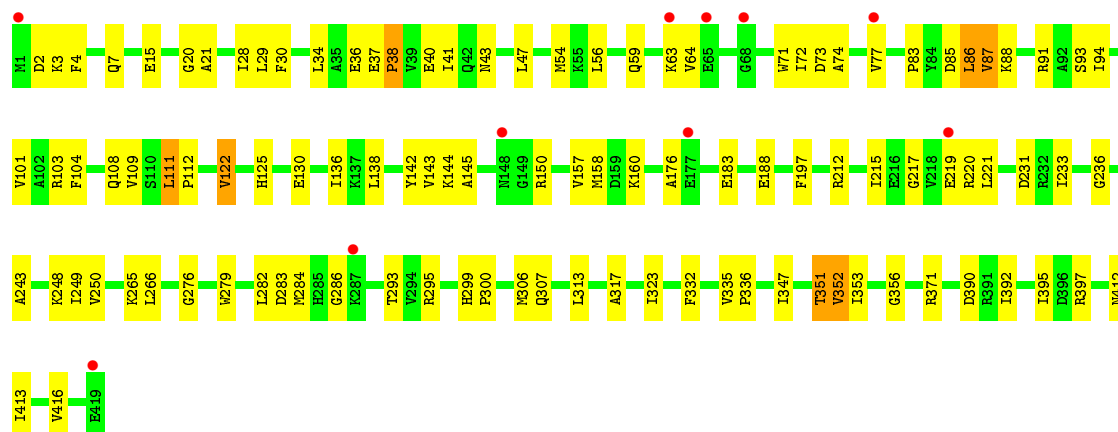
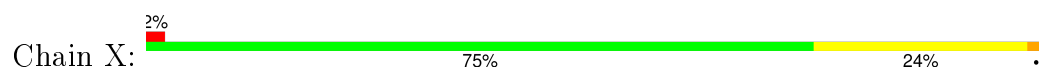


• Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

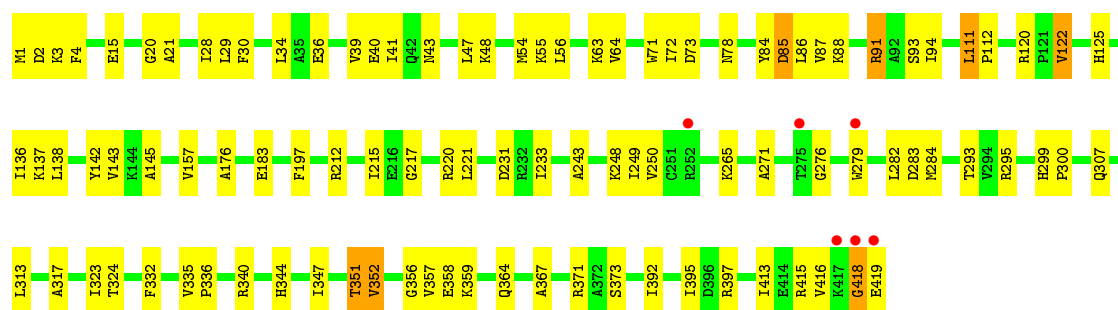
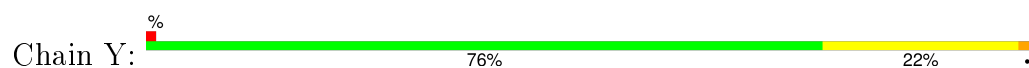




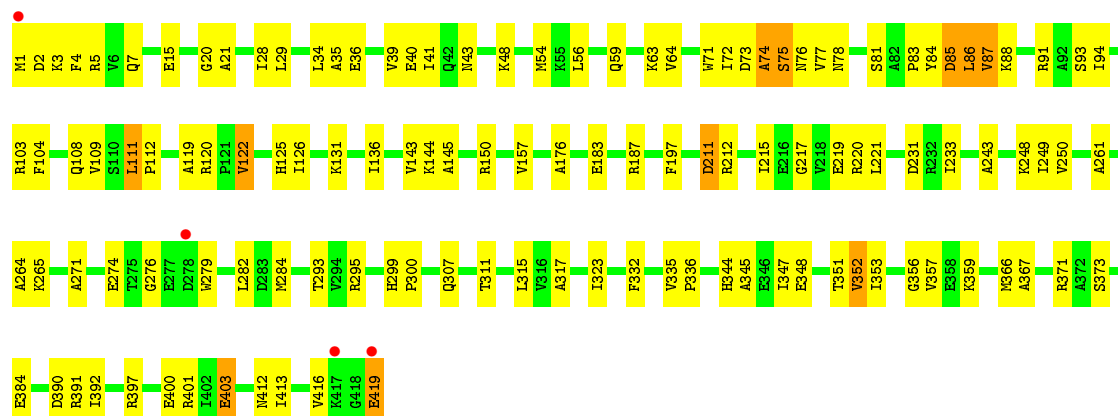
• Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



• 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, $\alpha$ , $\beta$ , $\gamma$	139.46Å 153.93Å 167.48Å 90.00° 112.95° 90.00°	Depositor
Resolution (Å)	20.00 – 2.65 29.94 – 2.65	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.65) 98.7 (29.94-2.65)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.78 (at 2.64Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.217 , 0.253 0.216 , 0.252	Depositor DCC
$R_{free}$ test set	3716 reflections (2.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.4	Xtriage
Anisotropy	0.360	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 47.7	EDS
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	4 of 186059 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	52519	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	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 45.13 % 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 1.3816e-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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UDA, EDO, 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	0.36	0/3176	0.60	0/4301
1	B	0.36	0/3176	0.60	0/4301
1	C	0.38	0/3176	0.60	0/4301
1	D	0.36	0/3176	0.60	0/4301
1	E	0.37	0/3176	0.60	0/4301
1	F	0.37	0/3176	0.60	0/4301
1	G	0.38	0/3176	0.61	0/4301
1	H	0.36	0/3176	0.59	0/4301
1	I	0.36	0/3176	0.61	0/4301
1	J	0.35	0/3176	0.59	0/4301
1	K	0.36	0/3176	0.60	0/4301
1	L	0.36	0/3176	0.60	0/4301
1	W	0.36	0/3176	0.60	0/4301
1	X	0.35	0/3176	0.60	0/4301
1	Y	0.36	0/3176	0.60	0/4301
1	Z	0.36	0/3176	0.59	0/4301
All	All	0.36	0/50816	0.60	0/68816

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	3140	0	3217	90	0
1	B	3140	0	3217	77	0
1	C	3140	0	3217	68	0
1	D	3140	0	3217	83	0
1	E	3140	0	3217	81	0
1	F	3140	0	3217	79	0
1	G	3140	0	3217	72	0
1	H	3140	0	3217	88	0
1	I	3140	0	3217	91	0
1	J	3140	0	3217	81	0
1	K	3140	0	3217	78	0
1	L	3140	0	3217	95	0
1	W	3140	0	3217	101	0
1	X	3140	0	3217	84	0
1	Y	3140	0	3217	82	0
1	Z	3140	0	3217	101	0
2	A	49	0	28	1	0
2	B	49	0	28	0	0
2	C	49	0	28	1	0
2	D	49	0	28	0	0
2	E	49	0	28	0	0
2	F	49	0	28	0	0
2	G	49	0	28	0	0
2	H	49	0	28	0	0
2	I	49	0	28	2	0
2	J	49	0	28	0	0
2	K	49	0	28	0	0
2	L	49	0	28	0	0
2	W	49	0	28	1	0
2	X	49	0	28	0	0
2	Y	49	0	28	1	0
2	Z	49	0	28	1	0
3	A	4	0	6	0	0
3	B	4	0	6	1	0
3	C	4	0	6	0	0
3	D	4	0	6	3	0
3	E	4	0	6	0	0
3	F	4	0	6	2	0
3	G	4	0	6	0	0
3	H	4	0	6	0	0
3	I	4	0	6	0	0
3	J	4	0	6	0	0
3	K	4	0	6	0	0

Continued on next page...

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	4	0	6	0	0
3	W	4	0	6	0	0
3	X	4	0	6	1	0
3	Y	4	0	6	0	0
3	Z	4	0	6	0	0
4	A	93	0	0	2	0
4	B	100	0	0	2	0
4	C	124	0	0	1	0
4	D	123	0	0	7	0
4	E	116	0	0	0	0
4	F	106	0	0	5	0
4	G	136	0	0	5	0
4	H	111	0	0	5	0
4	I	76	0	0	0	0
4	J	76	0	0	3	0
4	K	67	0	0	2	0
4	L	68	0	0	1	0
4	W	70	0	0	2	0
4	X	52	0	0	3	0
4	Y	67	0	0	3	0
4	Z	46	0	0	2	0
All	All	52519	0	52016	1303	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.

The worst 5 of 1303 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:233:ILE:HG23	1:G:306:MET:HE3	1.41	0.99
1:W:5:ARG:HH12	1:W:7:GLN:HE21	1.13	0.95
1:E:1:MET:HB3	1:E:419:GLU:HA	1.49	0.91
1:H:401:ARG:HB3	1:H:401:ARG:NH1	1.85	0.90
1:D:401:ARG:HB3	1:D:401:ARG:HH11	1.35	0.89

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	415/419 (99%)	402 (97%)	11 (3%)	2 (0%)	34	59
1	B	415/419 (99%)	403 (97%)	12 (3%)	0	100	100
1	C	415/419 (99%)	404 (97%)	10 (2%)	1 (0%)	52	77
1	D	415/419 (99%)	400 (96%)	14 (3%)	1 (0%)	52	77
1	E	415/419 (99%)	404 (97%)	11 (3%)	0	100	100
1	F	415/419 (99%)	402 (97%)	12 (3%)	1 (0%)	52	77
1	G	415/419 (99%)	402 (97%)	13 (3%)	0	100	100
1	H	415/419 (99%)	405 (98%)	8 (2%)	2 (0%)	34	59
1	I	415/419 (99%)	402 (97%)	11 (3%)	2 (0%)	34	59
1	J	415/419 (99%)	403 (97%)	11 (3%)	1 (0%)	52	77
1	K	415/419 (99%)	401 (97%)	14 (3%)	0	100	100
1	L	415/419 (99%)	400 (96%)	13 (3%)	2 (0%)	34	59
1	W	415/419 (99%)	402 (97%)	13 (3%)	0	100	100
1	X	415/419 (99%)	403 (97%)	11 (3%)	1 (0%)	52	77
1	Y	415/419 (99%)	402 (97%)	11 (3%)	2 (0%)	34	59
1	Z	415/419 (99%)	403 (97%)	9 (2%)	3 (1%)	26	51
All	All	6640/6704 (99%)	6438 (97%)	184 (3%)	18 (0%)	46	72

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	SER
1	F	418	GLY
1	L	418	GLY
1	A	160	LYS
1	C	160	LYS

### 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	328/328 (100%)	315 (96%)	13 (4%)	38	66
1	B	328/328 (100%)	315 (96%)	13 (4%)	38	66
1	C	328/328 (100%)	315 (96%)	13 (4%)	38	66
1	D	328/328 (100%)	309 (94%)	19 (6%)	25	48
1	E	328/328 (100%)	316 (96%)	12 (4%)	41	69
1	F	328/328 (100%)	314 (96%)	14 (4%)	35	63
1	G	328/328 (100%)	317 (97%)	11 (3%)	44	72
1	H	328/328 (100%)	314 (96%)	14 (4%)	35	63
1	I	328/328 (100%)	315 (96%)	13 (4%)	38	66
1	J	328/328 (100%)	313 (95%)	15 (5%)	33	61
1	K	328/328 (100%)	316 (96%)	12 (4%)	41	69
1	L	328/328 (100%)	311 (95%)	17 (5%)	29	54
1	W	328/328 (100%)	313 (95%)	15 (5%)	33	61
1	X	328/328 (100%)	319 (97%)	9 (3%)	52	80
1	Y	328/328 (100%)	317 (97%)	11 (3%)	44	72
1	Z	328/328 (100%)	313 (95%)	15 (5%)	33	61
All	All	5248/5248 (100%)	5032 (96%)	216 (4%)	37	66

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	87	VAL
1	I	351	THR
1	Y	351	THR
1	H	148	ASN
1	I	13	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	344	HIS
1	J	13	GLN
1	Y	330	ASN
1	I	7	GLN
1	I	330	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

16 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	0.52	0	1,8,10	1.39	0
1	IAS	B	67	1	4,7,8	0.56	0	1,8,10	1.25	0
1	IAS	C	67	1	4,7,8	0.54	0	1,8,10	1.41	0
1	IAS	D	67	1	4,7,8	0.48	0	1,8,10	1.36	0
1	IAS	E	67	1	4,7,8	0.54	0	1,8,10	1.33	0
1	IAS	F	67	1	4,7,8	0.52	0	1,8,10	1.25	0
1	IAS	G	67	1	4,7,8	0.58	0	1,8,10	1.50	0
1	IAS	H	67	1	4,7,8	0.59	0	1,8,10	1.22	0
1	IAS	I	67	1	4,7,8	0.68	0	1,8,10	1.17	0
1	IAS	J	67	1	4,7,8	0.60	0	1,8,10	1.32	0
1	IAS	K	67	1	4,7,8	0.53	0	1,8,10	1.25	0
1	IAS	L	67	1	4,7,8	0.51	0	1,8,10	1.45	0
1	IAS	W	67	1	4,7,8	0.71	0	1,8,10	1.18	0
1	IAS	X	67	1	4,7,8	0.59	0	1,8,10	1.30	0
1	IAS	Y	67	1	4,7,8	0.56	0	1,8,10	1.33	0
1	IAS	Z	67	1	4,7,8	0.55	0	1,8,10	1.37	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
1	IAS	I	67	1	-	0/3/7/8	0/0/0/0
1	IAS	J	67	1	-	0/3/7/8	0/0/0/0
1	IAS	K	67	1	-	0/3/7/8	0/0/0/0
1	IAS	L	67	1	-	0/3/7/8	0/0/0/0
1	IAS	W	67	1	-	0/3/7/8	0/0/0/0
1	IAS	X	67	1	-	0/3/7/8	0/0/0/0
1	IAS	Y	67	1	-	0/3/7/8	0/0/0/0
1	IAS	Z	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](#)

32 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	UDA	A	1450	-	37,51,51	2.26	14 (37%)	51,79,79	2.56	13 (25%)
3	EDO	A	1470	-	3,3,3	0.56	0	2,2,2	0.19	0
2	UDA	B	1451	-	37,51,51	2.31	14 (37%)	51,79,79	2.51	13 (25%)
3	EDO	B	1471	-	3,3,3	0.49	0	2,2,2	0.07	0
2	UDA	C	1452	-	37,51,51	2.19	14 (37%)	51,79,79	2.56	13 (25%)
3	EDO	C	1472	-	3,3,3	0.51	0	2,2,2	0.09	0
2	UDA	D	1453	-	37,51,51	2.30	14 (37%)	51,79,79	2.54	12 (23%)
3	EDO	D	1473	-	3,3,3	0.82	0	2,2,2	0.53	0
2	UDA	E	1454	-	37,51,51	2.25	12 (32%)	51,79,79	2.54	16 (31%)
3	EDO	E	1474	-	3,3,3	0.40	0	2,2,2	0.10	0
2	UDA	F	1455	-	37,51,51	2.28	14 (37%)	51,79,79	2.55	13 (25%)
3	EDO	F	1475	-	3,3,3	0.78	0	2,2,2	0.21	0
2	UDA	G	1456	-	37,51,51	2.30	16 (43%)	51,79,79	2.56	13 (25%)
3	EDO	G	1476	-	3,3,3	0.56	0	2,2,2	0.18	0
2	UDA	H	1457	-	37,51,51	2.37	14 (37%)	51,79,79	2.56	13 (25%)
3	EDO	H	1477	-	3,3,3	0.42	0	2,2,2	0.04	0
2	UDA	I	1458	-	37,51,51	2.16	12 (32%)	51,79,79	2.50	13 (25%)
3	EDO	I	1478	-	3,3,3	0.58	0	2,2,2	0.20	0
2	UDA	J	1459	-	37,51,51	2.30	14 (37%)	51,79,79	2.56	11 (21%)
3	EDO	J	1479	-	3,3,3	0.60	0	2,2,2	0.23	0
2	UDA	K	1460	-	37,51,51	2.23	14 (37%)	51,79,79	2.55	14 (27%)
3	EDO	K	1480	-	3,3,3	0.42	0	2,2,2	0.04	0
2	UDA	L	1461	-	37,51,51	2.31	15 (40%)	51,79,79	2.53	11 (21%)
3	EDO	L	1481	-	3,3,3	0.57	0	2,2,2	0.13	0
2	UDA	W	1462	-	37,51,51	2.24	13 (35%)	51,79,79	2.52	13 (25%)
3	EDO	W	1482	-	3,3,3	0.52	0	2,2,2	0.19	0
2	UDA	X	1463	-	37,51,51	2.30	14 (37%)	51,79,79	2.59	14 (27%)
3	EDO	X	1483	-	3,3,3	0.48	0	2,2,2	0.11	0
2	UDA	Y	1464	-	37,51,51	2.28	13 (35%)	51,79,79	2.51	12 (23%)
3	EDO	Y	1484	-	3,3,3	0.46	0	2,2,2	0.10	0
2	UDA	Z	1465	-	37,51,51	2.19	14 (37%)	51,79,79	2.50	11 (21%)
3	EDO	Z	1485	-	3,3,3	0.60	0	2,2,2	0.21	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
2	UDA	A	1450	-	-	0/27/80/80	0/3/3/3
3	EDO	A	1470	-	-	0/1/1/1	0/0/0/0
2	UDA	B	1451	-	-	0/27/80/80	0/3/3/3
3	EDO	B	1471	-	-	0/1/1/1	0/0/0/0
2	UDA	C	1452	-	-	0/27/80/80	0/3/3/3
3	EDO	C	1472	-	-	0/1/1/1	0/0/0/0
2	UDA	D	1453	-	-	0/27/80/80	0/3/3/3
3	EDO	D	1473	-	-	0/1/1/1	0/0/0/0
2	UDA	E	1454	-	-	0/27/80/80	0/3/3/3
3	EDO	E	1474	-	-	0/1/1/1	0/0/0/0
2	UDA	F	1455	-	-	0/27/80/80	0/3/3/3
3	EDO	F	1475	-	-	0/1/1/1	0/0/0/0
2	UDA	G	1456	-	-	0/27/80/80	0/3/3/3
3	EDO	G	1476	-	-	0/1/1/1	0/0/0/0
2	UDA	H	1457	-	-	0/27/80/80	0/3/3/3
3	EDO	H	1477	-	-	0/1/1/1	0/0/0/0
2	UDA	I	1458	-	-	0/27/80/80	0/3/3/3
3	EDO	I	1478	-	-	0/1/1/1	0/0/0/0
2	UDA	J	1459	-	-	0/27/80/80	0/3/3/3
3	EDO	J	1479	-	-	0/1/1/1	0/0/0/0
2	UDA	K	1460	-	-	0/27/80/80	0/3/3/3
3	EDO	K	1480	-	-	0/1/1/1	0/0/0/0
2	UDA	L	1461	-	-	0/27/80/80	0/3/3/3
3	EDO	L	1481	-	-	0/1/1/1	0/0/0/0
2	UDA	W	1462	-	-	0/27/80/80	0/3/3/3
3	EDO	W	1482	-	-	0/1/1/1	0/0/0/0
2	UDA	X	1463	-	-	0/27/80/80	0/3/3/3
3	EDO	X	1483	-	-	0/1/1/1	0/0/0/0
2	UDA	Y	1464	-	-	0/27/80/80	0/3/3/3
3	EDO	Y	1484	-	-	0/1/1/1	0/0/0/0
2	UDA	Z	1465	-	-	0/27/80/80	0/3/3/3
3	EDO	Z	1485	-	-	0/1/1/1	0/0/0/0

The worst 5 of 221 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	1461	UDA	P3-O15	-3.39	1.42	1.54
2	K	1460	UDA	P3-O15	-3.34	1.42	1.54
2	G	1456	UDA	P3-O15	-3.33	1.42	1.54
2	E	1454	UDA	P3-O15	-3.27	1.43	1.54
2	C	1452	UDA	P3-O15	-3.26	1.43	1.54



The worst 5 of 205 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1454	UDA	O15-P3-O17	-3.29	99.99	110.58
2	E	1454	UDA	C6-C1-N1	-3.04	115.33	123.12
2	J	1459	UDA	O15-P3-O17	-3.03	100.82	110.58
2	K	1460	UDA	C6-C1-N1	-3.02	115.37	123.12
2	A	1450	UDA	O15-P3-O17	-3.01	100.89	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1450	UDA	1	0
3	B	1471	EDO	1	0
2	C	1452	UDA	1	0
3	D	1473	EDO	3	0
3	F	1475	EDO	2	0
2	I	1458	UDA	2	0
2	W	1462	UDA	1	0
3	X	1483	EDO	1	0
2	Y	1464	UDA	1	0
2	Z	1465	UDA	1	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%)	-0.25	4 (0%) 84 84	18, 35, 58, 99	0
1	B	418/419 (99%)	-0.34	4 (0%) 84 84	20, 34, 52, 107	0
1	C	418/419 (99%)	-0.50	2 (0%) 91 92	19, 31, 47, 93	0
1	D	418/419 (99%)	-0.42	4 (0%) 84 84	18, 32, 50, 109	0
1	E	418/419 (99%)	-0.38	2 (0%) 91 92	18, 32, 50, 93	0
1	F	418/419 (99%)	-0.34	3 (0%) 89 89	20, 34, 50, 93	0
1	G	418/419 (99%)	-0.47	1 (0%) 95 96	18, 31, 47, 86	0
1	H	418/419 (99%)	-0.38	5 (1%) 81 80	18, 34, 53, 104	0
1	I	418/419 (99%)	-0.37	2 (0%) 91 92	20, 34, 52, 105	0
1	J	418/419 (99%)	-0.26	5 (1%) 81 80	22, 37, 56, 103	0
1	K	418/419 (99%)	-0.24	6 (1%) 78 76	20, 36, 53, 102	0
1	L	418/419 (99%)	-0.22	3 (0%) 89 89	22, 37, 58, 92	0
1	W	418/419 (99%)	-0.31	1 (0%) 95 96	22, 35, 54, 96	0
1	X	418/419 (99%)	-0.07	10 (2%) 62 60	22, 38, 61, 99	0
1	Y	418/419 (99%)	-0.19	6 (1%) 78 76	23, 37, 54, 99	0
1	Z	418/419 (99%)	-0.18	4 (0%) 84 84	22, 39, 61, 89	0
All	All	6688/6704 (99%)	-0.31	62 (0%) 85 86	18, 35, 54, 109	0

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	418	GLY	5.8
1	K	418	GLY	5.7
1	D	419	GLU	5.7
1	Y	418	GLY	5.6
1	F	418	GLY	5.6

## 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(Å <sup>2</sup> )	Q<0.9
1	IAS	G	67	8/9	0.95	0.11	-	30,33,39,39	0
1	IAS	A	67	8/9	0.88	0.22	-	45,47,49,51	0
1	IAS	L	67	8/9	0.92	0.23	-	44,46,48,52	0
1	IAS	C	67	8/9	0.95	0.10	-	31,35,37,37	0
1	IAS	H	67	8/9	0.93	0.20	-	30,41,46,51	0
1	IAS	J	67	8/9	0.88	0.26	-	43,46,48,50	0
1	IAS	Y	67	8/9	0.88	0.17	-	45,46,50,55	0
1	IAS	D	67	8/9	0.97	0.19	-	32,40,44,45	0
1	IAS	F	67	8/9	0.94	0.20	-	37,41,44,46	0
1	IAS	W	67	8/9	0.88	0.18	-	33,38,42,42	0
1	IAS	B	67	8/9	0.93	0.20	-	40,43,47,50	0
1	IAS	X	67	8/9	0.94	0.23	-	45,46,50,52	0
1	IAS	Z	67	8/9	0.91	0.24	-	47,48,51,53	0
1	IAS	I	67	8/9	0.88	0.23	-	37,40,41,44	0
1	IAS	K	67	8/9	0.92	0.19	-	43,48,51,56	0
1	IAS	E	67	8/9	0.86	0.25	-	40,44,47,49	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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(Å <sup>2</sup> )	Q<0.9
3	EDO	A	1470	4/4	0.85	0.48	7.39	36,36,42,42	0
3	EDO	D	1473	4/4	0.71	0.39	5.82	31,32,38,41	0
3	EDO	F	1475	4/4	0.73	0.33	5.58	32,35,37,38	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	B	1471	4/4	0.92	0.26	5.40	25,32,37,44	0
3	EDO	L	1481	4/4	0.88	0.34	5.29	42,42,50,53	0
3	EDO	W	1482	4/4	0.95	0.29	5.17	28,30,34,38	0
3	EDO	Z	1485	4/4	0.89	0.27	4.44	39,40,43,46	0
3	EDO	G	1476	4/4	0.95	0.27	3.73	23,26,30,38	0
3	EDO	K	1480	4/4	0.93	0.24	3.14	28,30,33,38	0
3	EDO	H	1477	4/4	0.95	0.24	2.97	26,28,29,31	0
3	EDO	C	1472	4/4	0.93	0.24	2.85	23,28,32,38	0
3	EDO	X	1483	4/4	0.94	0.22	2.63	41,45,45,47	0
3	EDO	E	1474	4/4	0.96	0.28	2.47	33,36,39,41	0
3	EDO	Y	1484	4/4	0.95	0.22	2.35	29,29,32,39	0
3	EDO	I	1478	4/4	0.98	0.16	1.01	30,31,34,40	0
2	UDA	C	1452	49/49	0.97	0.16	0.43	22,32,56,61	0
2	UDA	G	1456	49/49	0.97	0.16	0.24	11,30,59,65	0
2	UDA	H	1457	49/49	0.97	0.15	0.15	16,33,53,57	0
2	UDA	A	1450	49/49	0.96	0.15	0.12	20,32,56,63	0
2	UDA	E	1454	49/49	0.97	0.15	0.12	17,27,53,57	0
3	EDO	J	1479	4/4	0.97	0.16	0.10	28,30,31,32	0
2	UDA	D	1453	49/49	0.97	0.15	0.05	24,32,45,50	0
2	UDA	L	1461	49/49	0.96	0.15	0.02	24,38,57,58	0
2	UDA	J	1459	49/49	0.96	0.14	0.00	27,36,57,61	0
2	UDA	Z	1465	49/49	0.96	0.14	-0.02	25,38,61,66	0
2	UDA	X	1463	49/49	0.96	0.14	-0.12	30,41,57,60	0
2	UDA	B	1451	49/49	0.97	0.13	-0.16	23,34,54,57	0
2	UDA	K	1460	49/49	0.96	0.14	-0.17	24,30,54,58	0
2	UDA	W	1462	49/49	0.96	0.14	-0.24	19,40,51,56	0
2	UDA	I	1458	49/49	0.97	0.13	-0.28	16,35,51,55	0
2	UDA	Y	1464	49/49	0.97	0.12	-0.34	22,30,53,55	0
2	UDA	F	1455	49/49	0.97	0.12	-0.91	26,32,49,52	0

## 6.5 Other polymers

There are no such residues in this entry.