



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:56 PM GMT

PDB ID : 4JZW  
Title : Crystal structure of CD4-mimetic miniprotein M48U1 in complex with HIV-1 YU2 gp120 in P212121 space group  
Authors : Acharya, P.; Kwong, P.D.  
Deposited on : 2013-04-03  
Resolution : 1.78 Å(reported)

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

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

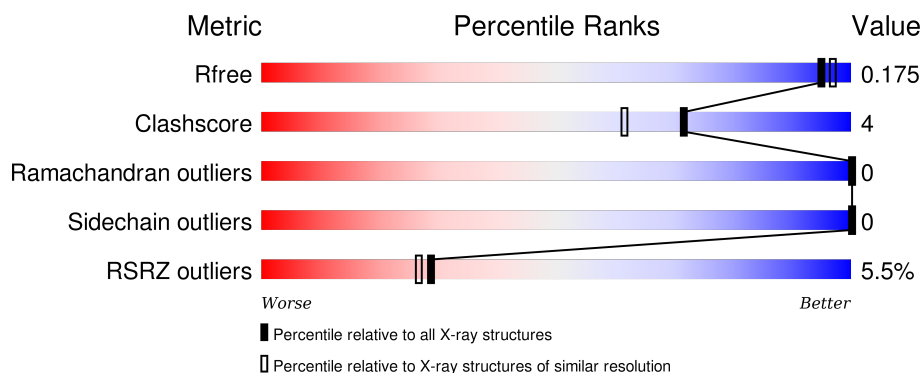
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.78 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	6655 (1.80-1.76)
Clashscore	102246	7658 (1.80-1.76)
Ramachandran outliers	100387	7570 (1.80-1.76)
Sidechain outliers	100360	7569 (1.80-1.76)
RSRZ outliers	91569	6671 (1.80-1.76)

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	376	<div> <div>4%</div> <div>83% 6% 11%</div> </div>
1	G	376	<div> <div>5%</div> <div>82% 8% 10%</div> </div>
2	M	28	<div> <div>11%</div> <div>96% •</div> </div>
2	R	28	<div> <div>14%</div> <div>96% •</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	503	-	-	-	X
3	NAG	A	504	-	-	-	X
3	NAG	A	507	-	-	-	X
3	NAG	A	514	-	-	-	X
3	NAG	G	501	-	-	-	X
3	NAG	G	504	-	-	-	X
3	NAG	G	505	-	-	-	X
3	NAG	G	508	-	-	-	X
4	IPA	A	512	-	-	-	X
4	IPA	A	515	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7061 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 HIV-1 YU2 gp120 glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	14	0
			2678	1681	466	511	20			
1	G	339	Total	C	N	O	S	1	21	0
			2718	1702	467	524	25			

- Molecule 2 is a protein called CD4-MIMETIC MINIPROTEIN M48U1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	28	Total	C	N	O	S	0	0	1
			209	133	38	32	6			
2	R	28	Total	C	N	O	S	0	3	1
			222	144	39	33	6			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		

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



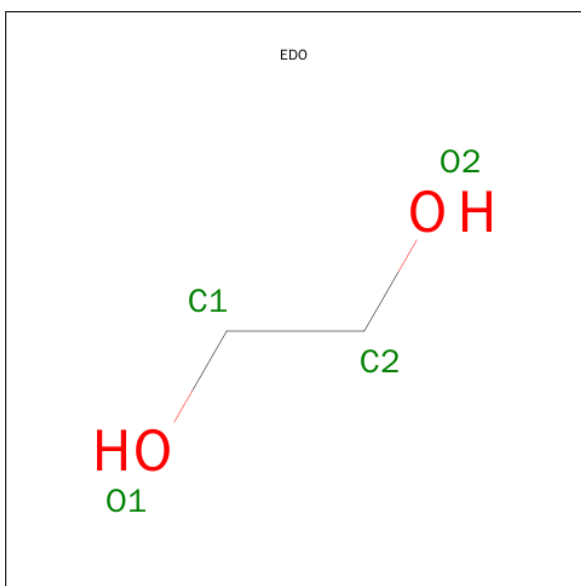
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	3	1		
4	A	1	Total	C	O	0	0
			4	3	1		
4	A	1	Total	C	O	0	0
			4	3	1		
4	G	1	Total	C	O	0	0
			4	3	1		
4	G	1	Total	C	O	0	0
			4	3	1		
4	G	1	Total	C	O	0	0
			4	3	1		
4	A	1	Total	C	O	0	0
			4	3	1		
4	A	1	Total	C	O	0	0
			4	3	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	450	Total 450	O 450	0	0
7	G	441	Total 441	O 441	0	0
7	M	22	Total 22	O 22	0	0
7	R	23	Total 23	O 23	0	0





- Molecule 1: HIV-1 YU2 gp120 glycoprotein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.65Å 78.01Å 163.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.66 – 1.78 24.66 – 1.78	Depositor EDS
% Data completeness (in resolution range)	82.7 (24.66-1.78) 77.6 (24.66-1.78)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.81 (at 1.78Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.164 , 0.209 0.177 , 0.175	Depositor DCC
$R_{free}$ test set	3267 reflections (5.68%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.5	Xtriage
Anisotropy	0.386	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 49.3	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	3 of 64795 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7061	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	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 91.39 % 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 1.5236e-08. 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: IPA, DPR, EDO, MPT, SO4, NH2, U2X, NAG

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	0.43	0/2797	0.56	0/3796
1	G	0.43	0/2879	0.56	0/3908
2	M	0.38	0/176	0.63	0/231
2	R	0.42	0/199	0.50	0/261
All	All	0.43	0/6051	0.56	0/8196

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	2678	0	2611	19	0
1	G	2718	0	2643	25	0
2	M	209	0	212	1	0
2	R	222	0	237	1	0
3	A	140	0	130	5	0
3	G	112	0	104	2	0
4	A	20	0	40	1	0
4	G	12	0	24	2	0
5	A	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	5	0	0	1	0
6	G	4	0	6	0	0
7	A	450	0	0	11	0
7	G	441	0	0	10	0
7	M	22	0	0	1	0
7	R	23	0	0	0	0
All	All	7061	0	6007	52	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 4.

All (52) 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)
3:A:503:NAG:H3	3:A:503:NAG:H83	1.59	0.84
1:G:54:CYS:O	7:G:1023:HOH:O	2.04	0.74
1:A:106[A]:GLU:OE2	7:A:851:HOH:O	2.04	0.73
1:A:351:GLU:OE1	7:A:860:HOH:O	2.06	0.72
1:A:394:ASN:O	7:A:928:HOH:O	2.12	0.68
4:A:516:IPA:H12	2:R:9:ARG:HE	1.60	0.66
1:G:356[A]:ASN:ND2	7:G:910:HOH:O	2.29	0.65
1:A:429:GLU:OE1	7:A:991:HOH:O	2.15	0.65
1:G:252:ARG:NH1	7:G:681:HOH:O	2.32	0.61
1:G:412:ARG:NH1	7:G:981:HOH:O	2.34	0.60
1:G:119:CYS:O	1:G:202[A]:THR:HG23	2.06	0.56
1:G:423:ILE:N	5:G:513:SO4:O2	2.39	0.55
3:A:503:NAG:H3	3:A:503:NAG:C8	2.33	0.55
1:G:394:ASN:ND2	3:G:507:NAG:O7	2.38	0.55
1:G:45:TRP:HB2	1:G:489[B]:VAL:CG1	2.36	0.55
1:A:325:ASP:N	7:A:918:HOH:O	2.39	0.55
2:M:7:GLN:OE1	7:M:204:HOH:O	2.19	0.53
1:A:97:LYS:NZ	7:A:1004:HOH:O	2.42	0.53
3:A:503:NAG:H2	7:A:997:HOH:O	2.10	0.52
1:G:446:SER:O	4:G:511:IPA:H31	2.10	0.51
1:G:45:TRP:HB2	1:G:489[B]:VAL:HG11	1.89	0.51
1:A:71[A]:THR:HG22	7:A:715:HOH:O	2.08	0.51
1:G:50:THR:O	1:G:103:GLN:NE2	2.38	0.50
3:A:503:NAG:H82	3:A:503:NAG:C1	2.41	0.50
1:G:71[A]:THR:HG22	7:G:660:HOH:O	2.12	0.50
1:A:46:LYS:NZ	7:A:1046:HOH:O	2.43	0.49
1:G:60:ALA:HA	1:G:71[A]:THR:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:ILE:N	5:A:513:SO4:O2	2.44	0.48
1:A:60:ALA:HA	1:A:71[A]:THR:HG21	1.95	0.47
1:A:287:GLN:NE2	7:A:759:HOH:O	2.41	0.47
3:G:508:NAG:HN2	4:G:511:IPA:H11	1.81	0.46
1:G:87[A]:GLU:OE2	7:G:986:HOH:O	2.21	0.46
1:G:68:VAL:O	1:G:71[A]:THR:OG1	2.30	0.46
1:A:396:THR:O	1:A:397:ARG:HB3	2.16	0.46
1:G:287:GLN:NE2	7:G:715:HOH:O	2.47	0.46
1:G:72:HIS:ND1	7:G:1003:HOH:O	2.34	0.45
1:G:88:ASN:ND2	7:G:934:HOH:O	2.49	0.44
1:G:239[A]:CYS:SG	1:G:242:VAL:HG22	2.58	0.44
1:G:332:ASN:ND2	7:G:919:HOH:O	2.51	0.44
1:A:333:LEU:CD2	1:A:416[A]:LEU:HD11	2.48	0.44
1:G:50:THR:OG1	1:G:51:THR:N	2.51	0.43
1:G:67:ASN:O	1:G:71[A]:THR:HG23	2.18	0.43
1:A:50:THR:O	1:A:103:GLN:NE2	2.41	0.43
1:A:67:ASN:O	1:A:71[A]:THR:HG23	2.19	0.42
1:A:339:GLU:OE2	7:A:977:HOH:O	2.22	0.42
1:G:45:TRP:CD1	1:G:489[B]:VAL:HG11	2.55	0.41
1:A:65:VAL:HB	1:A:115:SER:HB3	2.02	0.41
1:G:56:SER:C	1:G:77[B]:THR:HG23	2.41	0.40
1:A:84:VAL:HB	1:A:244[A]:THR:CG2	2.51	0.40
1:G:395:ASP:OD1	1:G:396:THR:N	2.55	0.40
3:A:503:NAG:C1	3:A:503:NAG:C8	2.99	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	341/376 (91%)	335 (98%)	6 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	353/376 (94%)	343 (97%)	10 (3%)	0	100	100
2	M	24/28 (86%)	23 (96%)	1 (4%)	0	100	100
2	R	27/28 (96%)	27 (100%)	0	0	100	100
All	All	745/808 (92%)	728 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	310/328 (94%)	310 (100%)	0	100	100
1	G	322/328 (98%)	322 (100%)	0	100	100
2	M	20/20 (100%)	20 (100%)	0	100	100
2	R	23/20 (115%)	23 (100%)	0	100	100
All	All	675/696 (97%)	675 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 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
2	DPR	M	21	2	6,7,8	0.56	0	7,8,10	1.17	0
2	U2X	M	23	2	19,20,21	1.63	3 (15%)	22,25,27	1.13	2 (9%)
2	DPR	R	21	2	6,7,8	0.62	0	7,8,10	1.30	0
2	U2X	R	23	2	19,20,21	1.58	3 (15%)	22,25,27	1.19	2 (9%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DPR	M	21	2	-	0/0/9/11	0/1/1/1
2	U2X	M	23	2	-	0/9/19/21	0/2/2/2
2	DPR	R	21	2	-	0/0/9/11	0/1/1/1
2	U2X	R	23	2	-	0/9/19/21	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	23	U2X	CB-CA	-2.66	1.48	1.53
2	R	23	U2X	CB-CA	-2.41	1.48	1.53
2	M	23	U2X	CE1-CD1	3.44	1.45	1.38
2	R	23	U2X	CE1-CD1	3.61	1.45	1.38
2	R	23	U2X	CE2-CD2	3.67	1.45	1.38
2	M	23	U2X	CE2-CD2	4.25	1.46	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	23	U2X	C1-C2-C3	-2.82	107.67	112.22
2	M	23	U2X	C1-C2-C3	-2.35	108.43	112.22
2	M	23	U2X	OH-C7-C3	2.80	114.42	107.97
2	R	23	U2X	OH-C7-C3	3.10	115.11	107.97

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](#)

29 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	NAG	A	501	1	14,14,15	0.82	1 (7%)	15,19,21	0.67	1 (6%)
3	NAG	A	502	1	14,14,15	0.52	0	15,19,21	0.26	0
3	NAG	A	503	1	14,14,15	0.27	0	15,19,21	0.68	0
3	NAG	A	504	1	14,14,15	0.31	0	15,19,21	0.20	0
3	NAG	A	505	1	14,14,15	0.49	0	15,19,21	0.52	0
3	NAG	A	506	1	14,14,15	0.19	0	15,19,21	0.14	0
3	NAG	A	507	1	14,14,15	0.38	0	15,19,21	0.40	0
3	NAG	A	508	1	14,14,15	0.26	0	15,19,21	0.38	0
3	NAG	A	509	1	14,14,15	0.27	0	15,19,21	0.30	0
4	IPA	A	510	-	3,3,3	0.56	0	3,3,3	0.17	0
4	IPA	A	511	-	3,3,3	0.61	0	3,3,3	0.21	0
4	IPA	A	512	-	3,3,3	0.59	0	3,3,3	0.27	0
5	SO4	A	513	-	4,4,4	0.42	0	6,6,6	0.24	0
3	NAG	A	514	1	14,14,15	0.22	0	15,19,21	0.27	0
4	IPA	A	515	-	3,3,3	0.59	0	3,3,3	0.20	0
4	IPA	A	516	-	3,3,3	0.60	0	3,3,3	0.15	0
3	NAG	G	501	1	14,14,15	0.30	0	15,19,21	0.34	0
3	NAG	G	502	1	14,14,15	0.29	0	15,19,21	0.43	0
3	NAG	G	503	1	14,14,15	0.44	0	15,19,21	0.28	0
3	NAG	G	504	1	14,14,15	0.29	0	15,19,21	0.26	0
3	NAG	G	505	1	14,14,15	0.29	0	15,19,21	0.29	0
3	NAG	G	506	1	14,14,15	0.26	0	15,19,21	0.54	0
3	NAG	G	507	1	14,14,15	0.43	0	15,19,21	0.31	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	G	508	1	14,14,15	0.24	0	15,19,21	0.32	0
4	IPA	G	509	-	3,3,3	0.58	0	3,3,3	0.19	0
4	IPA	G	510	-	3,3,3	0.59	0	3,3,3	0.19	0
4	IPA	G	511	-	3,3,3	0.60	0	3,3,3	0.19	0
6	EDO	G	512	-	3,3,3	0.46	0	2,2,2	0.37	0
5	SO4	G	513	-	4,4,4	0.46	0	6,6,6	0.18	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	NAG	A	501	1	-	0/6/23/26	0/1/1/1
3	NAG	A	502	1	-	0/6/23/26	0/1/1/1
3	NAG	A	503	1	-	0/6/23/26	0/1/1/1
3	NAG	A	504	1	-	0/6/23/26	0/1/1/1
3	NAG	A	505	1	-	0/6/23/26	0/1/1/1
3	NAG	A	506	1	-	0/6/23/26	0/1/1/1
3	NAG	A	507	1	-	0/6/23/26	0/1/1/1
3	NAG	A	508	1	-	0/6/23/26	0/1/1/1
3	NAG	A	509	1	-	0/6/23/26	0/1/1/1
4	IPA	A	510	-	-	0/0/0/0	0/0/0/0
4	IPA	A	511	-	-	0/0/0/0	0/0/0/0
4	IPA	A	512	-	-	0/0/0/0	0/0/0/0
5	SO4	A	513	-	-	0/0/0/0	0/0/0/0
3	NAG	A	514	1	-	0/6/23/26	0/1/1/1
4	IPA	A	515	-	-	0/0/0/0	0/0/0/0
4	IPA	A	516	-	-	0/0/0/0	0/0/0/0
3	NAG	G	501	1	-	0/6/23/26	0/1/1/1
3	NAG	G	502	1	-	0/6/23/26	0/1/1/1
3	NAG	G	503	1	-	0/6/23/26	0/1/1/1
3	NAG	G	504	1	-	0/6/23/26	0/1/1/1
3	NAG	G	505	1	-	0/6/23/26	0/1/1/1
3	NAG	G	506	1	-	0/6/23/26	0/1/1/1
3	NAG	G	507	1	-	0/6/23/26	0/1/1/1
3	NAG	G	508	1	-	0/6/23/26	0/1/1/1
4	IPA	G	509	-	-	0/0/0/0	0/0/0/0
4	IPA	G	510	-	-	0/0/0/0	0/0/0/0
4	IPA	G	511	-	-	0/0/0/0	0/0/0/0
6	EDO	G	512	-	-	0/1/1/1	0/0/0/0
5	SO4	G	513	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	NAG	C1-C2	2.58	1.56	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	NAG	C1-O5-C5	2.29	115.15	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	NAG	5	0
5	A	513	SO4	1	0
4	A	516	IPA	1	0
3	G	507	NAG	1	0
3	G	508	NAG	1	0
4	G	511	IPA	2	0
5	G	513	SO4	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	336/376 (89%)	-0.05	15 (4%) 37 35	22, 31, 58, 110	0
1	G	339/376 (90%)	0.03	18 (5%) 30 28	22, 31, 59, 110	0
2	M	24/28 (85%)	0.35	3 (12%) 5 5	27, 52, 73, 84	0
2	R	24/28 (85%)	0.34	4 (16%) 2 2	25, 46, 60, 61	0
All	All	723/808 (89%)	0.01	40 (5%) 29 27	22, 32, 60, 110	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	410	THR	8.4
1	G	462	THR	6.7
1	A	397	ARG	6.4
1	G	397	ARG	6.3
1	G	44	VAL	5.9
1	G	463	ASN	5.1
1	G	356[A]	ASN	5.0
1	G	45	TRP	4.5
1	A	464	GLY	3.9
2	R	14	GLY	3.9
1	A	459	GLY	3.7
1	A	356	ASN	3.6
1	A	396	THR	3.4
1	G	411	GLY	3.4
1	A	301	ASN	3.3
1	A	44	VAL	3.3
1	G	464	GLY	3.1
1	A	45	TRP	3.0
2	M	5	PHE	3.0
1	G	396	THR	2.9
1	G	452	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
2	R	15	LEU	2.8
1	G	259	LEU	2.7
1	A	492	GLU	2.7
1	A	412	ARG	2.7
1	G	88	ASN	2.7
1	G	301	ASN	2.5
1	A	345	ILE	2.5
2	R	13	LEU	2.5
1	A	259	LEU	2.4
1	G	286	VAL	2.3
1	G	459	GLY	2.3
1	G	492	GLU	2.3
1	G	412	ARG	2.2
1	A	411	GLY	2.1
2	R	16[A]	LEU	2.1
1	A	453	LEU	2.1
2	M	13	LEU	2.0
1	A	72[A]	HIS	2.0
2	M	11	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
2	U2X	M	23	19/20	0.97	0.08	-	22,26,32,34	0
2	DPR	R	21	7/8	0.98	0.04	-	22,25,26,27	0
2	DPR	M	21	7/8	0.98	0.06	-	25,26,28,29	0
2	U2X	R	23	19/20	0.94	0.10	-	21,25,34,36	0

## 6.3 Carbohydrates [i](#)

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	NAG	G	508	14/15	0.91	0.30	21.43	45,57,72,76	0
3	NAG	G	501	14/15	0.90	0.20	7.40	49,56,66,67	0
3	NAG	A	503	14/15	0.88	0.16	4.69	59,67,74,74	0
4	IPA	A	515	4/4	0.83	0.39	3.61	80,80,82,84	0
3	NAG	A	507	14/15	0.93	0.15	3.01	48,58,68,72	0
3	NAG	G	504	14/15	0.80	0.26	2.97	57,66,82,90	0
3	NAG	A	504	14/15	0.89	0.19	2.67	50,58,63,69	0
3	NAG	A	514	14/15	0.90	0.15	2.65	59,65,68,69	0
3	NAG	G	505	14/15	0.94	0.14	2.43	49,53,71,75	0
4	IPA	A	512	4/4	0.94	0.19	2.00	41,46,46,47	0
3	NAG	A	506	14/15	0.81	0.21	1.96	51,60,79,90	0
4	IPA	A	510	4/4	0.96	0.11	1.29	37,41,41,49	0
5	SO4	G	513	5/5	0.97	0.14	0.91	26,30,31,45	5
4	IPA	G	510	4/4	0.95	0.09	0.88	36,42,44,47	0
4	IPA	G	509	4/4	0.93	0.13	0.57	32,36,39,46	0
3	NAG	G	502	14/15	0.94	0.09	0.37	29,35,44,45	0
3	NAG	G	503	14/15	0.95	0.07	-0.37	29,33,45,46	0
3	NAG	A	502	14/15	0.97	0.06	-0.63	30,33,47,53	0
3	NAG	A	505	14/15	0.97	0.07	-0.84	27,30,42,46	0
3	NAG	G	506	14/15	0.93	0.13	-	35,48,60,69	0
5	SO4	A	513	5/5	0.96	0.18	-	26,32,35,55	5
3	NAG	A	509	14/15	0.89	0.28	-	49,58,65,67	0
4	IPA	A	511	4/4	0.91	0.12	-	46,51,52,54	0
3	NAG	A	508	14/15	0.93	0.18	-	40,61,68,71	0
6	EDO	G	512	4/4	0.91	0.28	-	62,62,64,65	0
3	NAG	G	507	14/15	0.75	0.42	-	102,119,122,126	0
4	IPA	G	511	4/4	0.88	0.21	-	62,63,69,79	0
3	NAG	A	501	14/15	0.53	0.67	-	118,126,131,132	0
4	IPA	A	516	4/4	0.86	0.32	-	68,71,73,74	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.