



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:31 PM GMT

PDB ID : 3TYG  
Title : Crystal structure of broad and potent HIV-1 neutralizing antibody PGT128 in complex with a glycosylated engineered gp120 outer domain with miniV3 (eODmV3)  
Authors : Pejchal, R.; Huang, P.S.; Schief, W.R.; Stanfield, R.L.; Wilson, I.A.  
Deposited on : 2011-09-25  
Resolution : 3.25 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

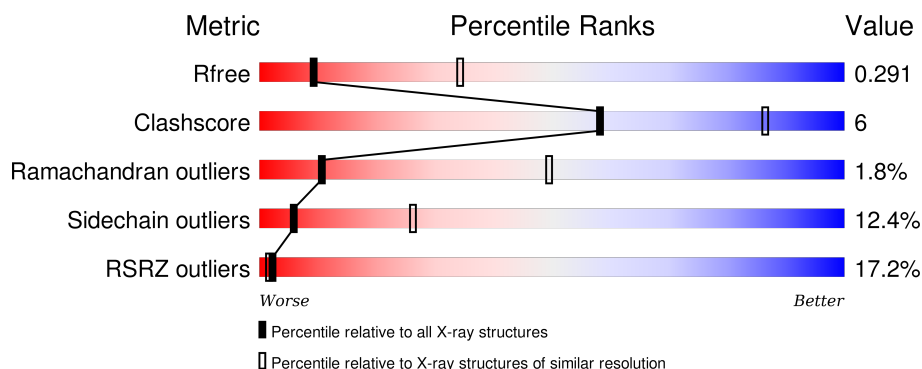
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.25 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	1624 (3.32-3.20)
Clashscore	102246	1806 (3.32-3.20)
Ramachandran outliers	100387	1773 (3.32-3.20)
Sidechain outliers	100360	1771 (3.32-3.20)
RSRZ outliers	91569	1632 (3.32-3.20)

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	199	<div> <div>30%</div> <div> <div>64%</div> <div>16%</div> <div>•</div> <div>17%</div> </div> </div>
2	L	211	<div> <div>6%</div> <div> <div>74%</div> <div>21%</div> <div>• •</div> </div> </div>
3	H	239	<div> <div>13%</div> <div> <div>75%</div> <div>20%</div> <div>• •</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4715 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 Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	0	0	0
			1239	761	220	251	7			

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	PRO	-	LINKER	UNP P04578
A	10	ALA	-	LINKER	UNP P04578
A	11	PRO	-	LINKER	UNP P04578
A	12	PRO	-	LINKER	UNP P04578
A	13	PRO	-	LINKER	UNP P04578
A	14	HIS	-	LINKER	UNP P04578
A	23	ILE	LEU	ENGINEERED MUTATION	UNP P04578
A	48	ILE	-	LINKER	UNP P04578
A	49	ALA	-	LINKER	UNP P04578
A	50	ARG	-	LINKER	UNP P04578
A	51	CYS	-	LINKER	UNP P04578
A	52	GLN	-	LINKER	UNP P04578
A	53	ILE	-	LINKER	UNP P04578
A	54	ALA	-	LINKER	UNP P04578
A	55	GLY	-	LINKER	UNP P04578
A	56	THR	-	LINKER	UNP P04578
A	86	SER	THR	ENGINEERED MUTATION	UNP P04578
A	88	CYS	ILE	ENGINEERED MUTATION	UNP P04578
A	108	PRO	LYS	ENGINEERED MUTATION	UNP Q75760
A	175	ASP	ASN	ENGINEERED MUTATION	UNP P04578
A	191	GLY	-	EXPRESSION TAG	UNP P04578
A	192	THR	-	EXPRESSION TAG	UNP P04578
A	193	LYS	-	EXPRESSION TAG	UNP P04578
A	194	HIS	-	EXPRESSION TAG	UNP P04578
A	195	HIS	-	EXPRESSION TAG	UNP P04578
A	196	HIS	-	EXPRESSION TAG	UNP P04578
A	197	HIS	-	EXPRESSION TAG	UNP P04578

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Chain	Residue	Modelled	Actual	Comment	Reference
A	198	HIS	-	EXPRESSION TAG	UNP P04578
A	199	HIS	-	EXPRESSION TAG	UNP P04578

- Molecule 2 is a protein called PGT128 light chain, Ig lambda-2 chain C regions.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	207	Total	C	N	O	S	0	0	0
			1527	958	254	311	4			

- Molecule 3 is a protein called PGT128 heavy chain, Ig gamma-1 chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	234	Total	C	N	O	S	0	0	0
			1750	1115	293	336	6			

- Molecule 4 is a polymer of unknown type called SUGAR (10-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	10	Total	C	N	O	0	0
			116	64	2	50		

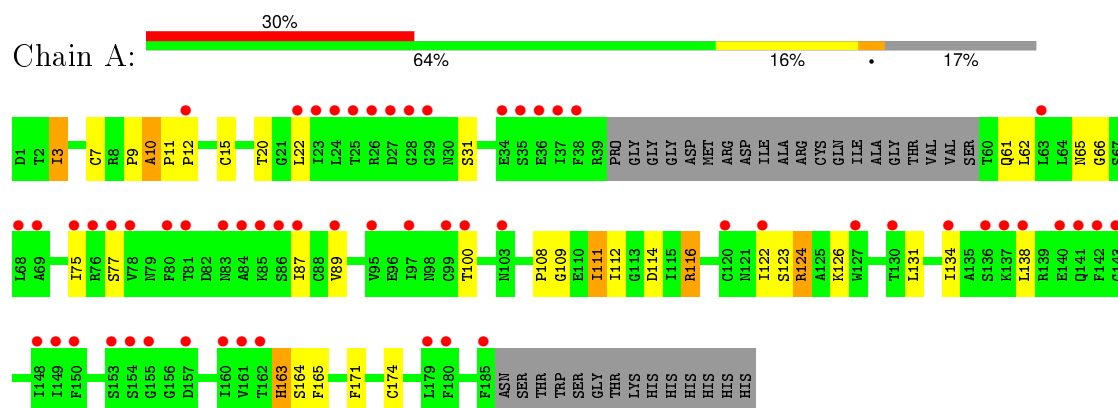
- Molecule 5 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	7	Total	C	N	O	0	0
			83	46	2	35		

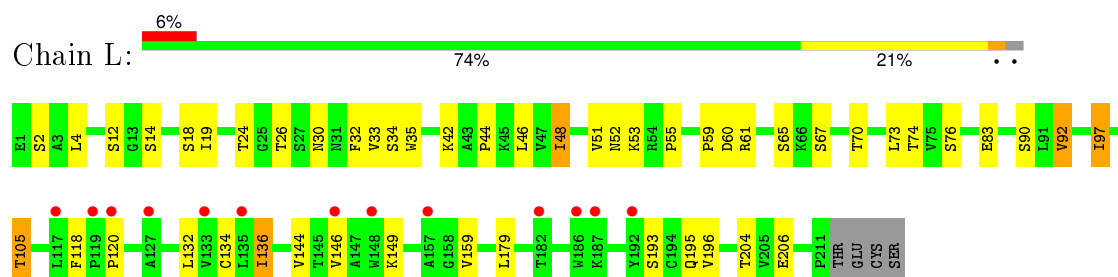
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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.

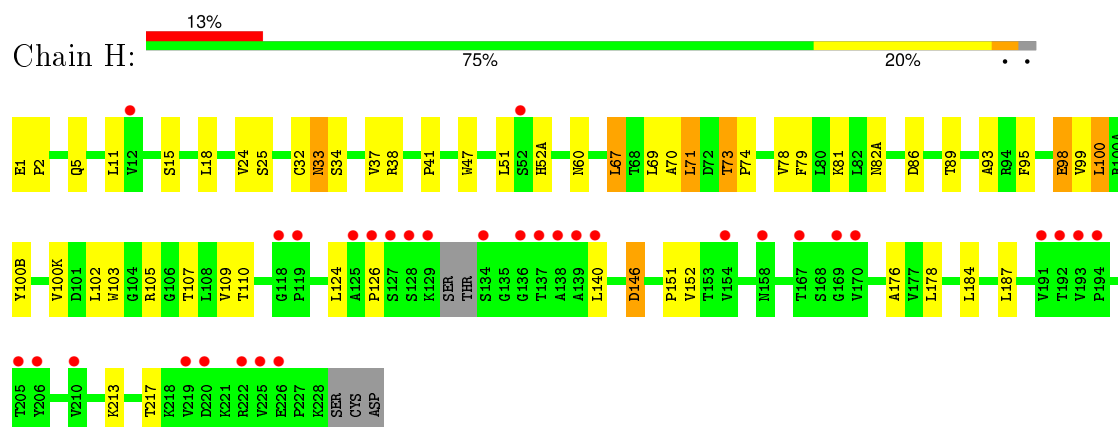
- Molecule 1: Envelope glycoprotein gp160



- Molecule 2: PGT128 light chain, Ig lambda-2 chain C regions



- Molecule 3: PGT128 heavy chain, Ig gamma-1 chain C region



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.79 Å 73.51 Å 241.45 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.70 – 3.25 49.70 – 3.07	Depositor EDS
% Data completeness (in resolution range)	89.9 (49.70-3.25) 79.0 (49.70-3.07)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.16	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 3.07 Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.207 , 0.257 0.232 , 0.291	Depositor DCC
$R_{free}$ test set	401 reflections (2.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.8	Xtriage
Anisotropy	1.366	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 110.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	2 of 13988 reflections (0.014%)	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4715	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: PCA, NAG, BMA, MAN

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	0/1259	0.70	0/1713
2	L	0.46	0/1558	0.71	0/2132
3	H	0.45	0/1794	0.70	0/2464
All	All	0.45	0/4611	0.70	0/6309

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	1239	0	1164	18	0
2	L	1527	0	1479	17	0
3	H	1750	0	1686	23	0
4	A	116	0	97	0	0
5	A	83	0	70	3	0
All	All	4715	0	4496	54	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 6.

The worst 5 of 54 close contacts within the same asymmetric unit are listed below, sorted by their

clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:CYS:HA	1:A:174:CYS:HB2	1.46	0.94
1:A:10:ALA:HB1	1:A:11:PRO:HA	1.48	0.93
5:A:302:BMA:O2	3:H:73:THR:HG21	1.90	0.72
2:L:30:ASN:HD22	2:L:32:PHE:H	1.39	0.70
1:A:7:CYS:HA	1:A:174:CYS:CB	2.23	0.66

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	161/199 (81%)	135 (84%)	20 (12%)	6 (4%)	4	28
2	L	205/211 (97%)	186 (91%)	18 (9%)	1 (0%)	34	75
3	H	230/239 (96%)	206 (90%)	20 (9%)	4 (2%)	11	50
All	All	596/649 (92%)	527 (88%)	58 (10%)	11 (2%)	11	49

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	PRO
1	A	15	CYS
1	A	116	ARG
1	A	163	HIS
3	H	146	ASP

### 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	139/175 (79%)	129 (93%)	10 (7%)	18	55
2	L	171/176 (97%)	143 (84%)	28 (16%)	3	14
3	H	192/202 (95%)	168 (88%)	24 (12%)	6	26
All	All	502/553 (91%)	440 (88%)	62 (12%)	6	26

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	97	ILE
2	L	179	LEU
3	H	152	VAL
2	L	136	ILE
2	L	204	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	L	30	ASN
2	L	195	GLN
3	H	179	GLN
3	H	209	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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
3	PCA	H	1	3	7,8,9	0.62	0	9,10,12	2.43	4 (44%)
2	PCA	L	1	2	7,8,9	1.27	1 (14%)	9,10,12	2.09	4 (44%)

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	PCA	H	1	3	-	0/0/11/13	0/1/1/1
2	PCA	L	1	2	-	0/0/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	1	PCA	CB-CG	2.25	1.58	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	1	PCA	O-C-CA	-3.02	117.46	125.44
3	H	1	PCA	CA-N-CD	-2.48	105.51	113.81
2	L	1	PCA	CA-N-CD	-2.34	105.95	113.81
2	L	1	PCA	O-C-CA	-2.31	119.33	125.44
2	L	1	PCA	OE-CD-CG	2.13	131.57	126.81

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1	PCA	1	0

## 5.5 Carbohydrates ⓘ

17 carbohydrates 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
4	NAG	A	200	1,4	14,14,15	0.30	0	15,19,21	0.81	1 (6%)
4	NAG	A	201	4	14,14,15	0.32	0	15,19,21	0.66	0
4	MAN	A	214	4	11,11,12	0.36	0	14,15,17	1.37	1 (7%)
4	MAN	A	215	4	11,11,12	0.33	0	14,15,17	0.81	0
4	BMA	A	232	4	11,11,12	0.41	0	14,15,17	0.65	0
4	MAN	A	233	4	11,11,12	0.42	0	14,15,17	1.16	1 (7%)
4	MAN	A	234	4	11,11,12	0.27	0	14,15,17	1.20	1 (7%)
4	MAN	A	235	4	11,11,12	0.33	0	14,15,17	0.98	2 (14%)
4	MAN	A	237	4	11,11,12	0.47	0	14,15,17	1.09	2 (14%)
4	MAN	A	238	4	11,11,12	0.48	0	14,15,17	1.27	1 (7%)
5	NAG	A	300	1,5	14,14,15	0.30	0	15,19,21	0.66	0
5	NAG	A	301	5	14,14,15	0.29	0	15,19,21	1.21	2 (13%)
5	BMA	A	302	5	11,11,12	0.42	0	14,15,17	1.30	2 (14%)
5	MAN	A	303	5	11,11,12	0.31	0	14,15,17	1.36	2 (14%)
5	MAN	A	304	5	11,11,12	0.42	0	14,15,17	0.96	1 (7%)
5	MAN	A	305	5	11,11,12	0.42	0	14,15,17	0.92	1 (7%)
5	MAN	A	307	5	11,11,12	0.45	0	14,15,17	0.88	2 (14%)

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
4	NAG	A	200	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	201	4	-	0/6/23/26	0/1/1/1
4	MAN	A	214	4	-	0/2/19/22	0/1/1/1
4	MAN	A	215	4	-	0/2/19/22	0/1/1/1
4	BMA	A	232	4	-	0/2/19/22	0/1/1/1
4	MAN	A	233	4	-	0/2/19/22	0/1/1/1
4	MAN	A	234	4	-	0/2/19/22	0/1/1/1
4	MAN	A	235	4	-	0/2/19/22	0/1/1/1
4	MAN	A	237	4	-	0/2/19/22	0/1/1/1
4	MAN	A	238	4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	300	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	301	5	-	0/6/23/26	0/1/1/1
5	BMA	A	302	5	-	0/2/19/22	0/1/1/1
5	MAN	A	303	5	-	0/2/19/22	0/1/1/1
5	MAN	A	304	5	-	0/2/19/22	0/1/1/1
5	MAN	A	305	5	-	0/2/19/22	0/1/1/1
5	MAN	A	307	5	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	237	MAN	O2-C2-C3	-2.42	105.24	110.12
5	A	303	MAN	O5-C1-C2	-2.36	107.03	110.86
5	A	301	NAG	C4-C3-C2	-2.23	107.77	111.23
5	A	307	MAN	C1-O5-C5	2.14	114.96	112.25
5	A	307	MAN	C1-C2-C3	2.15	112.08	109.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	300	NAG	1	0
5	A	302	BMA	1	0
5	A	304	MAN	1	0
5	A	307	MAN	1	0

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	165/199 (82%)	1.82	59 (35%) 0 1	72, 172, 206, 212	0
2	L	206/211 (97%)	0.43	13 (6%) 23 17	32, 76, 168, 183	0
3	H	233/239 (97%)	0.85	32 (13%) 4 3	42, 87, 181, 208	0
All	All	604/649 (93%)	0.97	104 (17%) 2 1	32, 130, 198, 212	0

The worst 5 of 104 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	37	ILE	14.7
3	H	128	SER	14.6
3	H	129	LYS	12.4
1	A	24	LEU	7.6
3	H	127	SER	7.3

### 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
3	PCA	H	1	8/9	0.89	0.28	-	89,92,94,94	0
2	PCA	L	1	8/9	0.89	0.22	-	76,78,81,83	0

### 6.3 Carbohydrates ⓘ

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
4	MAN	A	238	11/12	0.92	0.26	0.43	52,54,57,58	0
4	MAN	A	215	11/12	0.95	0.25	0.32	46,55,59,60	0
5	NAG	A	301	14/15	0.95	0.23	0.08	39,45,57,59	0
4	NAG	A	200	14/15	0.89	0.23	-0.19	87,95,101,102	0
5	NAG	A	300	14/15	0.94	0.21	-0.63	35,39,49,50	0
4	MAN	A	234	11/12	0.91	0.17	-	69,78,86,96	0
5	MAN	A	303	11/12	0.73	0.30	-	79,83,85,85	0
5	MAN	A	305	11/12	0.85	0.24	-	95,96,97,99	0
4	MAN	A	235	11/12	0.87	0.19	-	98,104,105,106	0
5	MAN	A	307	11/12	0.79	0.26	-	100,105,107,108	0
5	BMA	A	302	11/12	0.87	0.24	-	63,74,79,82	0
4	MAN	A	214	11/12	0.95	0.17	-	61,68,70,71	0
4	NAG	A	201	14/15	0.87	0.20	-	73,79,90,92	0
4	MAN	A	233	11/12	0.90	0.19	-	58,71,78,81	0
5	MAN	A	304	11/12	0.91	0.21	-	84,90,95,99	0
4	MAN	A	237	11/12	0.95	0.25	-	38,41,54,54	0
4	BMA	A	232	11/12	0.93	0.25	-	67,70,74,77	0

### 6.4 Ligands ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.