



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 03:33 PM BST

PDB ID : 1HZH
Title : CRYSTAL STRUCTURE OF THE INTACT HUMAN IGG B12 WITH BROAD AND POTENT ACTIVITY AGAINST PRIMARY HIV-1 ISOLATES: A TEMPLATE FOR HIV VACCINE DESIGN
Authors : Sapphire, E.O.; Burton, D.R.; Wilson, I.A.
Deposited on : 2001-01-24
Resolution : 2.70 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

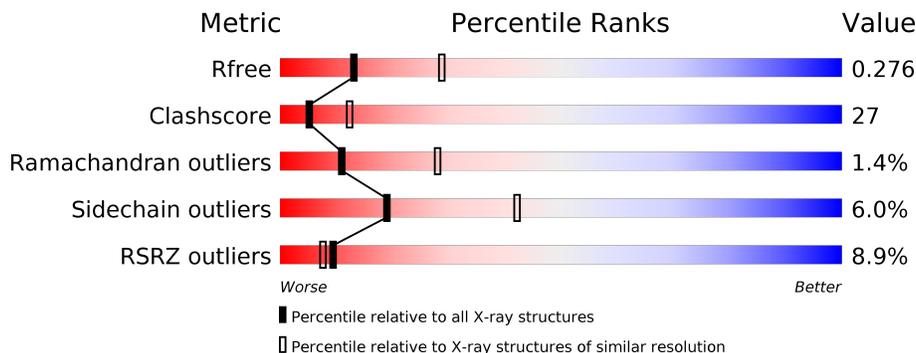
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	H	457	<div style="display: flex; align-items: center;"> <div style="width: 12%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 50%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 45%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">12% 50% 45% 5%</p>
1	K	457	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 62%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 32%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">8% 62% 32% . .</p>
2	L	215	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 58%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 40%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">4% 58% 40% .</p>
2	M	215	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 48%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 48%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">8% 48% 48% .</p>
3	A	9	<div style="display: flex; align-items: center;"> <div style="width: 33%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 33%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 33%; height: 10px; background-color: orange; margin-right: 5px;"></div> </div> <p style="font-size: small; margin-top: 5px;">33% 33% 33%</p>
4	B	9	<div style="display: flex; align-items: center;"> <div style="width: 44%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 33%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 22%; height: 10px; background-color: orange; margin-right: 5px;"></div> </div> <p style="font-size: small; margin-top: 5px;">44% 33% 22%</p>

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	GAL	A	6	-	-	-	X
4	GAL	B	6	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10647 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 IMMUNOGLOBULIN HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	457	3553	2252	600	685	16	0	0	0
1	K	444	3466	2202	583	665	16	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	225	ALA	VAL	conflict	UNP P0DOX5
K	225	ALA	VAL	conflict	UNP P0DOX5

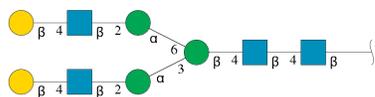
- Molecule 2 is a protein called IMMUNOGLOBULIN LIGHT CHAIN, Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	215	1668	1036	297	330	5	0	0	0
2	M	215	1668	1036	297	330	5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

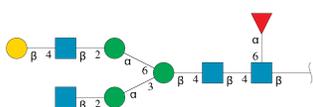
Chain	Residue	Modelled	Actual	Comment	Reference
L	202	ARG	SER	conflict	UNP Q8TCD0
M	202	ARG	SER	conflict	UNP Q8TCD0

- Molecule 3 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	A	9	111	62	4	45	0	0	0

- Molecule 4 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	B	9	110	62	4	44	0	0	0

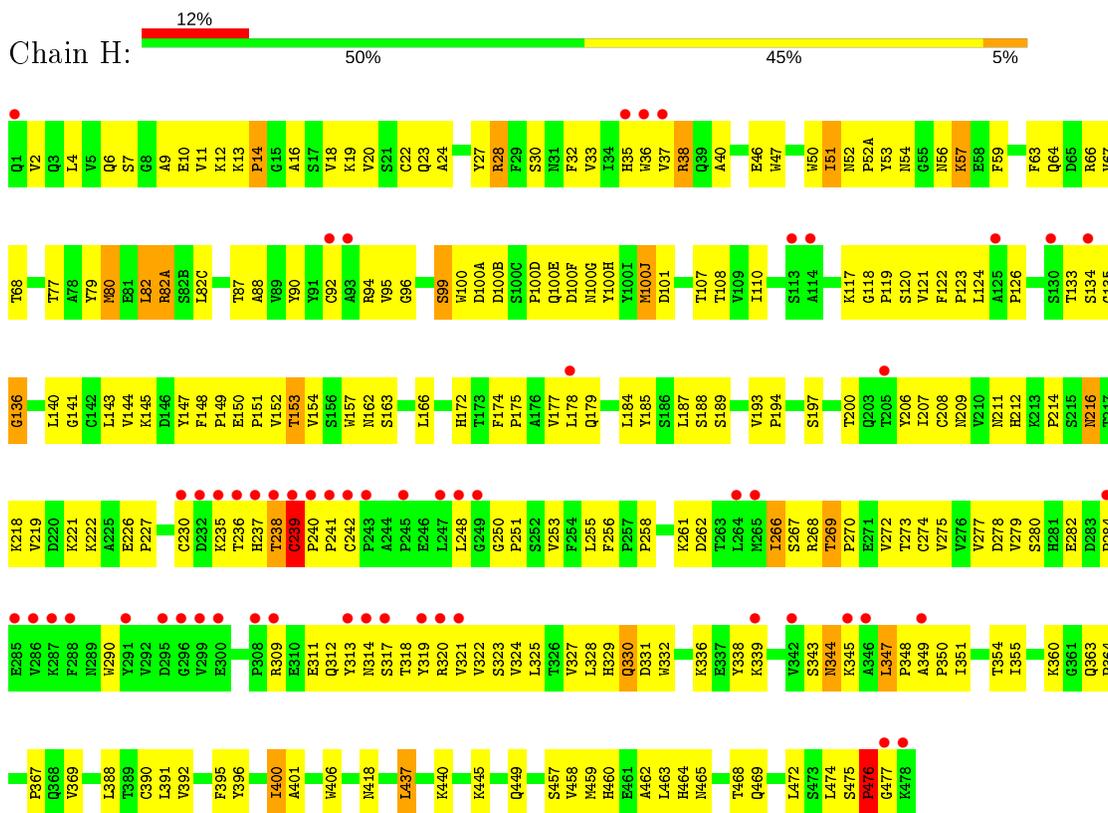
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	15	Total	O	0	0
			15	15		
5	K	38	Total	O	0	0
			38	38		
5	L	6	Total	O	0	0
			6	6		
5	M	12	Total	O	0	0
			12	12		

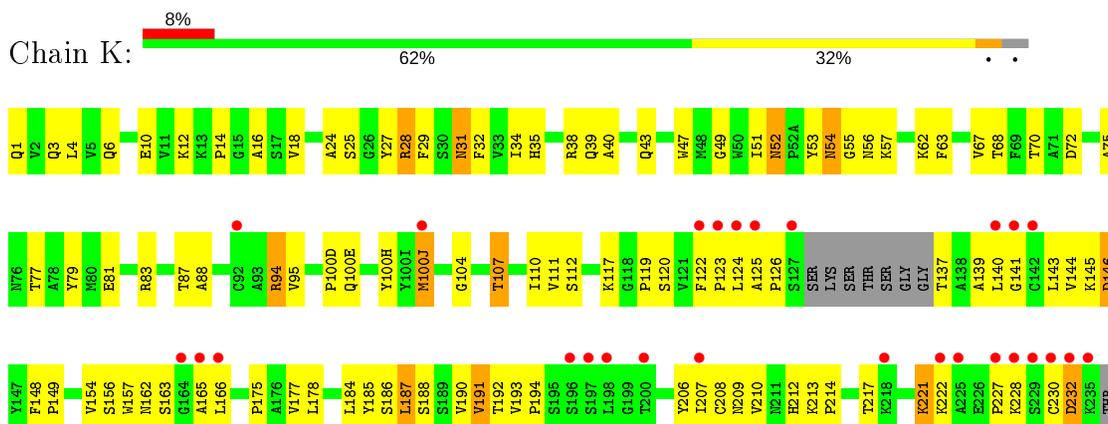
3 Residue-property plots [i](#)

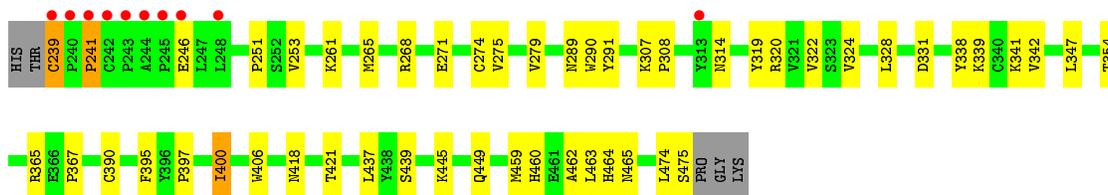
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: IMMUNOGLOBULIN HEAVY CHAIN

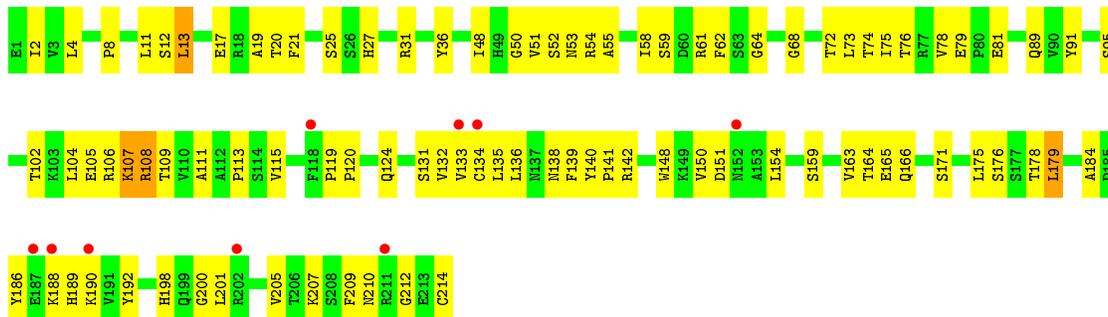


- Molecule 1: IMMUNOGLOBULIN HEAVY CHAIN

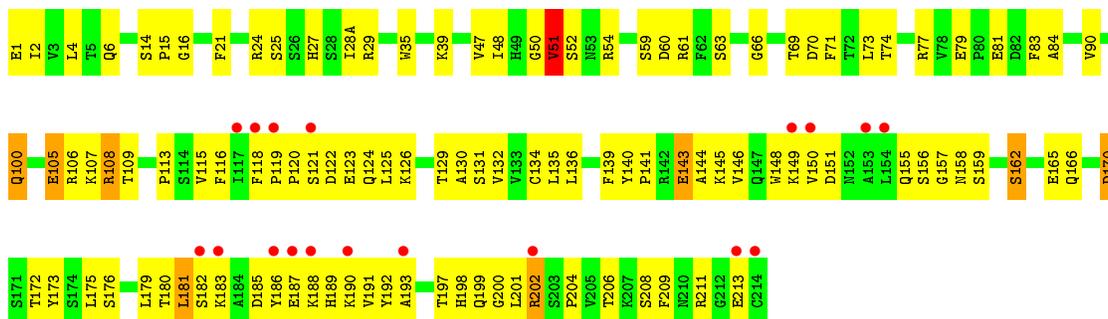




- Molecule 2: IMMUNOGLOBULIN LIGHT CHAIN, Uncharacterized protein



- Molecule 2: IMMUNOGLOBULIN LIGHT CHAIN, Uncharacterized protein



- Molecule 3: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:  44% 33% 22%

MG1	MG2	MG3	MG4	MG5	MG6	MG7	MG8	MG9
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4 Data and refinement statistics i

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	271.32Å 271.32Å 175.18Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.65 – 2.70 29.65 – 2.60	Depositor EDS
% Data completeness (in resolution range)	91.7 (29.65-2.70) 90.8 (29.65-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.61Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.229 , 0.273 0.233 , 0.276	Depositor DCC
R_{free} test set	6926 reflections (10.11%)	wwPDB-VP
Wilson B-factor (Å ²)	58.0	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 68.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for $-1/3^*h+1/3^*k+4/3^*l,-k,2/3^*h+1/3^*k+1/3^*l$ 0.012 for $-2/3^*h-1/3^*k-4/3^*l,-1/3^*h-2/3^*k+4/3^*l,-1/3^*h+1/3^*k+1/3^*l$ 0.006 for $-h,1/3^*h-1/3^*k-4/3^*l,-1/3^*h-2/3^*k+1/3^*l$	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10647	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: MAN, GAL, BMA, NAG, FUC

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	H	0.37	0/3654	0.62	0/4983
1	K	0.40	0/3563	0.64	0/4859
2	L	0.34	0/1704	0.60	0/2306
2	M	0.38	0/1704	0.63	0/2306
All	All	0.38	0/10625	0.62	0/14454

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	136	GLY	Mainchain

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	H	3553	0	3460	231	1
1	K	3466	0	3373	152	0
2	L	1668	0	1621	69	0
2	M	1668	0	1621	110	0
3	A	111	0	94	11	0
4	B	110	0	94	7	0
5	H	15	0	0	2	0
5	K	38	0	0	0	0
5	L	6	0	0	0	0
5	M	12	0	0	1	0
All	All	10647	0	10263	556	1

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 27.

The worst 5 of 556 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:K:261:LYS:HE2	1:K:265:MET:HE1	1.09	1.06
1:H:400:ILE:HD11	1:H:458:VAL:HG13	1.38	1.05
1:K:221:LYS:HE3	1:K:221:LYS:HA	1.39	1.04
2:M:1:GLU:HG3	2:M:2:ILE:H	1.18	1.03
2:M:100:GLN:NE2	2:M:100:GLN:H	1.56	1.03

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:136:GLY:CA	1:H:136:GLY:CA[4_557]	1.86	0.34

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	H	455/457 (100%)	400 (88%)	48 (10%)	7 (2%)	10	26
1	K	438/457 (96%)	402 (92%)	30 (7%)	6 (1%)	11	28
2	L	213/215 (99%)	193 (91%)	17 (8%)	3 (1%)	11	28
2	M	213/215 (99%)	195 (92%)	15 (7%)	3 (1%)	11	28
All	All	1319/1344 (98%)	1190 (90%)	110 (8%)	19 (1%)	11	28

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	99	SER
1	H	239	CYS
1	H	476	PRO
1	H	477	GLY
1	K	16	ALA

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	H	405/405 (100%)	376 (93%)	29 (7%)	14	34
1	K	395/405 (98%)	378 (96%)	17 (4%)	29	57
2	L	187/187 (100%)	179 (96%)	8 (4%)	29	57
2	M	187/187 (100%)	171 (91%)	16 (9%)	10	24
All	All	1174/1184 (99%)	1104 (94%)	70 (6%)	19	42

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	31	ASN
1	K	221	LYS
2	M	122	ASP
1	K	38	ARG
1	K	94	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	31	ASN
1	K	314	ASN
2	M	124	GLN
1	K	35	HIS
1	K	52	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

18 monosaccharides 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	1	3	14,14,15	0.45	0	17,19,21	0.86	0
3	NAG	A	2	3	14,14,15	0.37	0	17,19,21	0.85	1 (5%)
3	BMA	A	3	3	11,11,12	0.50	0	15,15,17	0.85	1 (6%)
3	MAN	A	4	3	11,11,12	0.57	0	15,15,17	0.70	0
3	NAG	A	5	3	14,14,15	0.65	0	17,19,21	0.83	1 (5%)
3	GAL	A	6	3	11,11,12	0.46	0	15,15,17	0.40	0
3	MAN	A	7	3	11,11,12	0.71	0	15,15,17	0.59	0
3	NAG	A	8	3	14,14,15	0.65	0	17,19,21	0.98	1 (5%)
3	GAL	A	9	3	11,11,12	0.57	0	15,15,17	0.33	0
4	NAG	B	1	4	14,14,15	0.43	0	17,19,21	1.00	1 (5%)
4	NAG	B	2	4	14,14,15	0.50	0	17,19,21	0.84	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BMA	B	3	4	11,11,12	0.69	0	15,15,17	0.64	0
4	MAN	B	4	4	11,11,12	0.82	0	15,15,17	0.64	0
4	NAG	B	5	4	14,14,15	0.53	0	17,19,21	1.00	1 (5%)
4	GAL	B	6	4	11,11,12	0.55	0	15,15,17	0.40	0
4	MAN	B	7	4	11,11,12	0.58	0	15,15,17	1.14	1 (6%)
4	NAG	B	8	4	14,14,15	0.56	0	17,19,21	0.66	0
4	FUC	B	9	4	10,10,11	0.60	0	14,14,16	0.41	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	1	3	-	0/6/23/26	0/1/1/1
3	NAG	A	2	3	-	2/6/23/26	0/1/1/1
3	BMA	A	3	3	-	0/2/19/22	0/1/1/1
3	MAN	A	4	3	-	0/2/19/22	0/1/1/1
3	NAG	A	5	3	-	0/6/23/26	0/1/1/1
3	GAL	A	6	3	-	2/2/19/22	0/1/1/1
3	MAN	A	7	3	-	2/2/19/22	0/1/1/1
3	NAG	A	8	3	-	2/6/23/26	0/1/1/1
3	GAL	A	9	3	-	2/2/19/22	0/1/1/1
4	NAG	B	1	4	-	4/6/23/26	0/1/1/1
4	NAG	B	2	4	-	1/6/23/26	0/1/1/1
4	BMA	B	3	4	-	0/2/19/22	0/1/1/1
4	MAN	B	4	4	-	0/2/19/22	0/1/1/1
4	NAG	B	5	4	-	2/6/23/26	0/1/1/1
4	GAL	B	6	4	-	0/2/19/22	0/1/1/1
4	MAN	B	7	4	-	2/2/19/22	0/1/1/1
4	NAG	B	8	4	-	3/6/23/26	0/1/1/1
4	FUC	B	9	4	-	-	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	8	NAG	C2-N2-C7	-2.87	118.82	122.90
4	B	5	NAG	C2-N2-C7	-2.74	119.00	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1	NAG	C2-N2-C7	-2.72	119.03	122.90
4	B	2	NAG	C2-N2-C7	-2.53	119.30	122.90
3	A	2	NAG	C2-N2-C7	-2.49	119.36	122.90

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	8	NAG	C3-C2-N2-C7
4	B	8	NAG	C8-C7-N2-C2
4	B	8	NAG	O7-C7-N2-C2
3	A	6	GAL	C4-C5-C6-O6
4	B	7	MAN	O5-C5-C6-O6

There are no ring outliers.

8 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	8	NAG	1	0
3	A	8	NAG	2	0
3	A	2	NAG	1	0
3	A	5	NAG	3	0
4	B	1	NAG	4	0
3	A	6	GAL	3	0
3	A	1	NAG	5	0
4	B	2	NAG	2	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 [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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 ²)	Q<0.9
1	H	457/457 (100%)	0.63	55 (12%) 4 3	29, 97, 181, 199	0
1	K	444/457 (97%)	0.24	37 (8%) 11 9	28, 67, 159, 197	0
2	L	215/215 (100%)	0.05	9 (4%) 36 35	43, 89, 146, 164	0
2	M	215/215 (100%)	0.19	18 (8%) 11 9	36, 77, 167, 193	0
All	All	1331/1344 (99%)	0.33	119 (8%) 9 7	28, 83, 167, 199	0

The worst 5 of 119 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	235	LYS	11.8
1	K	242	CYS	10.0
1	H	236	THR	7.6
1	H	241	PRO	7.5
1	H	238	THR	7.3

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å ²)	Q<0.9
3	GAL	A	6	11/12	0.41	0.52	198,198,198,198	0
4	GAL	B	6	11/12	0.58	0.44	168,168,168,168	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	A	2	14/15	0.70	0.34	168,168,168,168	0
3	BMA	A	3	11/12	0.74	0.15	130,130,130,130	0
3	NAG	A	1	14/15	0.74	0.26	90,146,146,146	0
3	NAG	A	5	14/15	0.76	0.28	172,172,172,172	0
3	GAL	A	9	11/12	0.77	0.34	151,151,151,151	0
3	NAG	A	8	14/15	0.78	0.21	136,136,136,136	0
4	FUC	B	9	10/11	0.78	0.34	133,133,133,133	0
3	MAN	A	7	11/12	0.82	0.20	164,164,164,164	0
4	NAG	B	8	14/15	0.83	0.30	157,157,157,157	0
4	NAG	B	1	14/15	0.86	0.15	95,95,95,95	0
3	MAN	A	4	11/12	0.87	0.28	191,191,191,191	0
4	NAG	B	5	14/15	0.89	0.16	110,110,110,110	0
4	MAN	B	7	11/12	0.90	0.16	154,154,154,154	0
4	BMA	B	3	11/12	0.91	0.10	77,77,77,77	0
4	MAN	B	4	11/12	0.92	0.17	97,97,97,97	0
4	NAG	B	2	14/15	0.92	0.15	84,84,84,84	0

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.