



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2019 – 02:02 PM EDT

PDB ID : 6CXG
Title : anti-HIV-1 Fab 2G12 in complex with glycopeptide 10V1S
Authors : Stanfield, R.L.; Wilson, I.A.
Deposited on : 2018-04-03
Resolution : 2.30 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

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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : rb-20031633
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031633

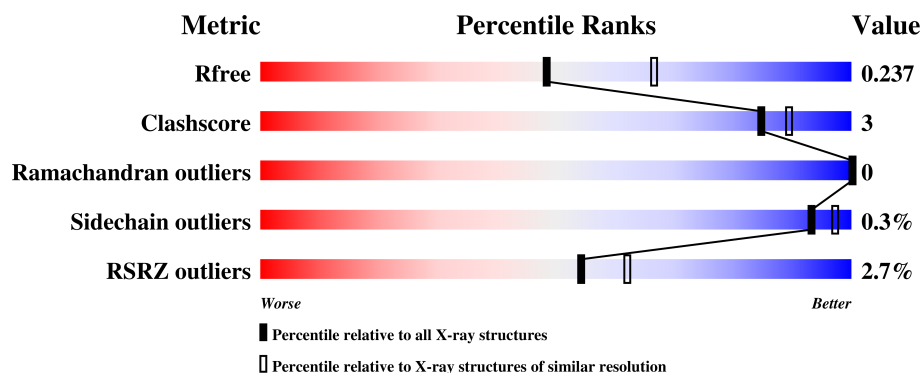
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	K	213	<div> <div style="width: 98%;"></div> <div>98%</div> </div>
1	L	213	<div> <div style="width: 93%;"></div> <div>93%</div> <div style="width: 7%;"></div> <div>7%</div> </div>
2	H	224	<div> <div style="width: 2%;"></div> <div style="width: 89%;"></div> <div style="width: 8%;"></div> <div>8%</div> </div>
2	M	224	<div> <div style="width: 2%;"></div> <div style="width: 97%;"></div> <div style="width: 1%;"></div> <div>97%</div> </div>
3	A	40	<div> <div style="width: 3%;"></div> <div style="width: 38%;"></div> <div style="width: 60%;"></div> <div>38%</div> <div>60%</div> </div>

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Mol	Chain	Length	Quality of chain
3	C	40	<div><div><div></div><div></div><div></div></div><div>28%33%65%</div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7504 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 anti-HIV-1 Fab 2G12 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	213	Total	C	N	O	S	0	0	0
			1632	1026	274	327	5			
1	K	213	Total	C	N	O	S	0	1	0
			1638	1030	274	329	5			

- Molecule 2 is a protein called anti-HIV-1 Fab 2g12 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	219	Total	C	N	O	S	0	0	0
			1641	1034	280	320	7			
2	M	224	Total	C	N	O	S	0	0	0
			1675	1053	286	329	7			

- Molecule 3 is a protein called 10V1S glycopeptide.

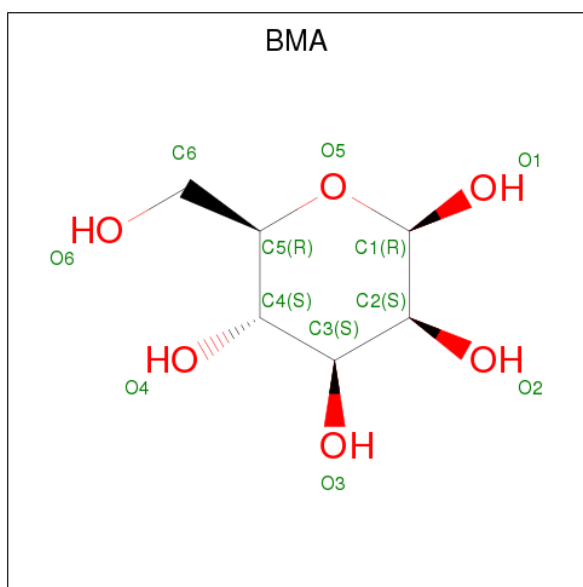
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	A	16	Total	C	N	O	0	0	0
			158	107	28	23			
3	C	14	Total	C	N	O	0	0	0
			143	99	25	19			

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	L	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		
4	K	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



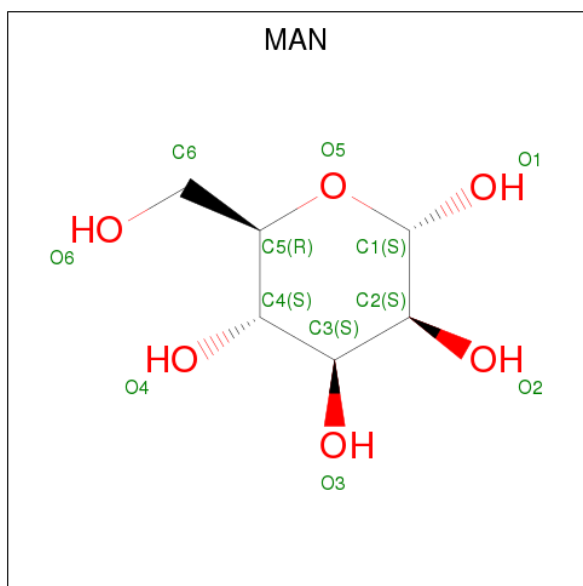
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	C	1	Total	C	O	0	0
			11	6	5		
6	C	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total C O 11 6 5	0	0
6	C	1	Total C O 11 6 5	0	0
6	C	1	Total C O 11 6 5	0	0
6	C	1	Total C O 11 6 5	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	84	Total O 84 84	0	0
7	H	107	Total O 107 107	0	0
7	K	114	Total O 114 114	0	0
7	M	93	Total O 93 93	0	0
7	A	17	Total O 17 17	0	0
7	C	8	Total O 8 8	0	0

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 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.

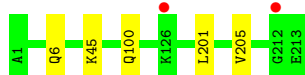
- Molecule 1: anti-HIV-1 Fab 2G12 light chain

Chain L: 




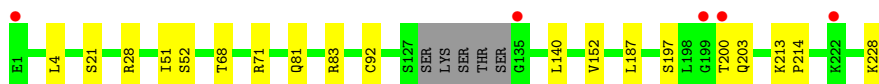
- Molecule 1: anti-HIV-1 Fab 2G12 light chain

Chain K: 



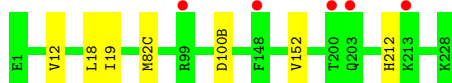
- Molecule 2: anti-HIV-1 Fab 2g12 heavy chain

Chain H: 



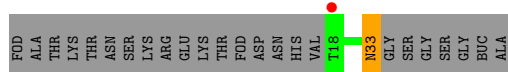
- Molecule 2: anti-HIV-1 Fab 2g12 heavy chain

Chain M: 

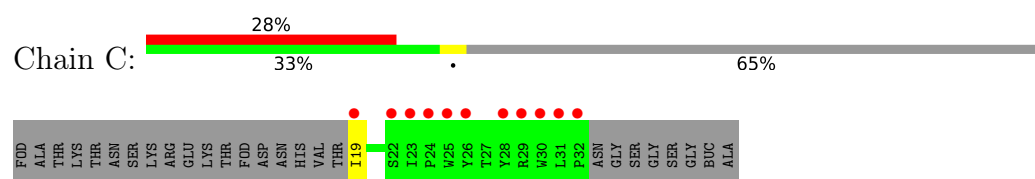


- Molecule 3: 10V1S glycopeptide

Chain A: 



- Molecule 3: 10V1S glycopeptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	45.22Å 131.18Å 169.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.38 – 2.30 43.69 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (42.38-2.30) 99.3 (43.69-2.30)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.197 , 0.237 0.197 , 0.237	Depositor DCC
R_{free} test set	2230 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	26.8	Xtriage
Anisotropy	0.473	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7504	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FOD, GOL, 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	K	0.31	0/1677	0.55	0/2277
1	L	0.48	0/1668	0.59	0/2265
2	H	0.37	0/1679	0.60	0/2286
2	M	0.38	0/1714	0.58	0/2334
3	A	0.57	0/146	0.60	0/200
3	C	0.27	0/131	0.46	0/179
All	All	0.39	0/7015	0.58	0/9541

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	K	1638	0	1600	3	0
1	L	1632	0	1594	9	0
2	H	1641	0	1612	16	0
2	M	1675	0	1648	5	0
3	A	158	0	135	1	0
3	C	143	0	122	1	0
4	K	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	12	0	16	2	0
5	A	11	0	8	2	0
5	C	11	0	8	0	0
6	A	88	0	74	2	0
6	C	66	0	56	2	0
7	A	17	0	0	0	0
7	C	8	0	0	0	0
7	H	107	0	0	1	0
7	K	114	0	0	1	0
7	L	84	0	0	0	0
7	M	93	0	0	0	0
All	All	7504	0	6881	35	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 3.

All (35) 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)
5:A:101:BMA:H62	6:A:102:MAN:H3	1.69	0.71
1:L:33:LEU:HD22	1:L:71:PHE:CG	2.36	0.61
1:K:6:GLN:O	1:K:100:GLN:NE2	2.34	0.60
2:H:51:ILE:O	2:H:51:ILE:HG23	2.01	0.60
2:M:100(B):ASP:OD1	6:C:103:MAN:O6	2.21	0.59
2:H:51:ILE:HG12	2:H:71:ARG:HD2	1.86	0.57
2:H:21:SER:HB3	2:M:19:ILE:HD13	1.87	0.56
5:A:101:BMA:H62	6:A:102:MAN:C3	2.35	0.54
2:H:140:LEU:C	2:H:140:LEU:HD12	2.31	0.51
1:L:212:GLY:O	1:L:213:GLU:HB2	2.11	0.50
2:H:197:SER:HA	2:H:200:THR:HG22	1.93	0.50
1:L:149:LYS:NZ	1:L:195:GLU:OE2	2.39	0.50
1:L:197:THR:HG23	4:L:302:GOL:C3	2.42	0.50
6:C:106:MAN:H4	6:C:107:MAN:H2	1.92	0.49
2:M:12:VAL:HG21	2:M:82(C):MET:HE1	1.95	0.49
1:L:203:SER:HB2	1:L:204:PRO:CD	2.43	0.48
2:H:200:THR:CG2	2:H:203:GLN:H	2.26	0.48
2:H:200:THR:CG2	2:H:203:GLN:N	2.77	0.47
2:H:83:ARG:NH1	7:H:304:HOH:O	2.41	0.47
1:L:94:TYR:CE1	2:H:52:SER:HB3	2.49	0.47
1:L:37:GLN:HB2	1:L:47:LEU:HD11	1.97	0.47
3:A:33:ASN:OD1	3:A:33:ASN:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:152:VAL:HG23	2:H:187:LEU:HD21	1.98	0.46
2:H:200:THR:HG23	2:H:203:GLN:N	2.31	0.45
2:H:68:THR:HG22	2:H:81:GLN:HB2	1.99	0.43
2:M:152:VAL:HG12	2:M:212:HIS:CD2	2.54	0.43
1:L:24:ARG:NH1	1:L:70:GLU:HG2	2.34	0.43
1:K:45:LYS:NZ	7:K:412:HOH:O	2.51	0.42
1:L:197:THR:HG23	4:L:302:GOL:H32	2.01	0.42
1:K:201:LEU:HD13	1:K:205:VAL:HG23	2.02	0.41
2:H:213:LYS:N	2:H:214:PRO:CD	2.83	0.41
2:H:187:LEU:C	2:H:187:LEU:HD12	2.41	0.41
2:M:18:LEU:HB3	2:M:82(C):MET:CE	2.51	0.41
2:H:4:LEU:HD23	2:H:92:CYS:SG	2.61	0.41
2:H:28:ARG:HH22	3:C:19:ILE:HD12	1.86	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	K	212/213 (100%)	204 (96%)	8 (4%)	0	100	100
1	L	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
2	H	215/224 (96%)	203 (94%)	12 (6%)	0	100	100
2	M	222/224 (99%)	217 (98%)	5 (2%)	0	100	100
3	A	13/40 (32%)	13 (100%)	0	0	100	100
3	C	11/40 (28%)	11 (100%)	0	0	100	100
All	All	884/954 (93%)	852 (96%)	32 (4%)	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	K	184/183 (100%)	184 (100%)	0	100	100
1	L	183/183 (100%)	183 (100%)	0	100	100
2	H	184/189 (97%)	183 (100%)	1 (0%)	90	96
2	M	189/189 (100%)	189 (100%)	0	100	100
3	A	15/31 (48%)	14 (93%)	1 (7%)	18	23
3	C	13/31 (42%)	13 (100%)	0	100	100
All	All	768/806 (95%)	766 (100%)	2 (0%)	93	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	228	LYS
3	A	33	ASN

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](#)

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	FOD	A	20	3,5	18,19,20	1.48	1 (5%)	16,25,27	1.48	3 (18%)
3	FOD	C	20	3,5	18,19,20	1.50	1 (5%)	16,25,27	1.54	3 (18%)

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	FOD	A	20	3,5	-	0/5/21/23	0/2/2/2
3	FOD	C	20	3,5	-	0/5/21/23	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	20	FOD	O-C	5.34	1.41	1.19
3	C	20	FOD	O-C	5.52	1.42	1.19

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	20	FOD	O-C-CA	-3.66	114.91	124.96
3	C	20	FOD	O-C-CA	-3.45	115.48	124.96
3	A	20	FOD	C6-C5-N2	-2.31	107.96	111.41
3	C	20	FOD	C6-C5-N2	-2.24	108.05	111.41
3	A	20	FOD	C6-N4-C7	3.28	128.93	125.55
3	C	20	FOD	C6-N4-C7	3.44	129.09	125.55

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

19 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
5	BMA	A	101	3,6	11,11,12	1.27	1 (9%)	15,15,17	1.25	3 (20%)
6	MAN	A	102	5,6	11,11,12	1.48	2 (18%)	15,15,17	2.02	5 (33%)
6	MAN	A	103	6	11,11,12	0.55	0	15,15,17	1.21	1 (6%)
6	MAN	A	104	6	11,11,12	0.50	0	15,15,17	0.97	1 (6%)
6	MAN	A	105	6	11,11,12	0.57	0	15,15,17	1.24	1 (6%)
6	MAN	A	106	6	11,11,12	1.08	1 (9%)	15,15,17	1.61	2 (13%)
6	MAN	A	107	5,6	11,11,12	1.13	1 (9%)	15,15,17	0.84	0
6	MAN	A	108	6	11,11,12	0.69	0	15,15,17	1.45	1 (6%)
6	MAN	A	109	6	11,11,12	0.92	0	15,15,17	1.72	1 (6%)
5	BMA	C	101	3,6	11,11,12	1.19	1 (9%)	15,15,17	1.33	3 (20%)
6	MAN	C	102	5,6	11,11,12	1.00	1 (9%)	15,15,17	1.04	2 (13%)
6	MAN	C	103	6	11,11,12	0.67	0	15,15,17	1.23	2 (13%)
6	MAN	C	104	6	11,11,12	0.58	0	15,15,17	0.98	2 (13%)
6	MAN	C	105	6	11,11,12	0.72	0	15,15,17	0.92	1 (6%)
6	MAN	C	106	5,6	11,11,12	1.84	2 (18%)	15,15,17	1.50	2 (13%)
6	MAN	C	107	6	11,11,12	0.97	1 (9%)	15,15,17	1.27	2 (13%)
4	GOL	K	301	-	5,5,5	0.36	0	5,5,5	0.65	0
4	GOL	L	301	-	5,5,5	0.38	0	5,5,5	0.22	0
4	GOL	L	302	-	5,5,5	0.39	0	5,5,5	0.51	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BMA	A	101	3,6	-	0/2/19/22	0/1/1/1
6	MAN	A	102	5,6	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MAN	A	103	6	-	0/2/19/22	0/1/1/1
6	MAN	A	104	6	-	0/2/19/22	0/1/1/1
6	MAN	A	105	6	-	0/2/19/22	0/1/1/1
6	MAN	A	106	6	-	0/2/19/22	0/1/1/1
6	MAN	A	107	5,6	-	0/2/19/22	0/1/1/1
6	MAN	A	108	6	-	0/2/19/22	0/1/1/1
6	MAN	A	109	6	-	0/2/19/22	0/1/1/1
5	BMA	C	101	3,6	-	0/2/19/22	0/1/1/1
6	MAN	C	102	5,6	-	0/2/19/22	0/1/1/1
6	MAN	C	103	6	-	0/2/19/22	0/1/1/1
6	MAN	C	104	6	-	0/2/19/22	0/1/1/1
6	MAN	C	105	6	-	0/2/19/22	0/1/1/1
6	MAN	C	106	5,6	-	0/2/19/22	0/1/1/1
6	MAN	C	107	6	-	0/2/19/22	0/1/1/1
4	GOL	K	301	-	-	0/4/4/4	0/0/0/0
4	GOL	L	301	-	-	0/4/4/4	0/0/0/0
4	GOL	L	302	-	-	0/4/4/4	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	102	MAN	O5-C5	-3.50	1.36	1.43
5	A	101	BMA	O5-C1	-3.34	1.38	1.43
6	A	107	MAN	O5-C1	-2.53	1.39	1.43
6	A	102	MAN	O5-C1	-2.51	1.39	1.43
6	C	102	MAN	C2-C3	2.00	1.55	1.52
6	C	107	MAN	O5-C5	2.44	1.48	1.43
6	A	106	MAN	O5-C5	2.51	1.48	1.43
5	C	101	BMA	C2-C3	2.85	1.56	1.52
6	C	106	MAN	O2-C2	3.62	1.51	1.43
6	C	106	MAN	C2-C3	3.95	1.58	1.52

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	102	MAN	O5-C5-C6	-3.46	101.67	107.15
6	C	107	MAN	O2-C2-C3	-2.65	105.01	110.19
5	A	101	BMA	C6-C5-C4	-2.61	106.82	112.99
5	A	101	BMA	O3-C3-C4	-2.57	104.34	110.34
6	C	105	MAN	O2-C2-C3	-2.20	105.89	110.19
6	C	104	MAN	O2-C2-C3	-2.14	106.03	110.19
6	C	106	MAN	O2-C2-C1	-2.13	104.87	109.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	101	BMA	O2-C2-C3	-2.06	106.17	110.19
6	C	102	MAN	O2-C2-C3	-2.05	106.19	110.19
6	A	106	MAN	O2-C2-C3	-2.03	106.23	110.19
6	C	103	MAN	O2-C2-C3	-2.03	106.23	110.19
6	A	102	MAN	C6-C5-C4	2.02	117.77	112.99
5	A	101	BMA	C3-C4-C5	2.03	113.87	110.24
6	C	102	MAN	C1-O5-C5	2.15	115.15	112.19
6	A	102	MAN	C1-C2-C3	2.18	112.42	109.66
5	C	101	BMA	C1-C2-C3	2.22	112.47	109.66
6	C	104	MAN	C1-O5-C5	2.58	115.73	112.19
5	C	101	BMA	C1-O5-C5	2.72	115.93	112.19
6	C	107	MAN	C1-O5-C5	2.78	116.01	112.19
6	A	104	MAN	C1-O5-C5	2.81	116.06	112.19
6	A	102	MAN	O5-C1-C2	3.36	116.02	110.78
6	A	105	MAN	C1-O5-C5	3.37	116.82	112.19
6	C	103	MAN	C1-O5-C5	3.42	116.89	112.19
6	A	103	MAN	C1-O5-C5	3.57	117.09	112.19
6	C	106	MAN	O2-C2-C3	3.64	117.28	110.19
6	A	102	MAN	C1-O5-C5	4.60	118.52	112.19
6	A	108	MAN	C1-O5-C5	4.96	119.01	112.19
6	A	106	MAN	C1-O5-C5	5.54	119.81	112.19
6	A	109	MAN	C1-O5-C5	5.94	120.36	112.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	101	BMA	2	0
6	A	102	MAN	2	0
6	C	103	MAN	1	0
6	C	106	MAN	1	0
6	C	107	MAN	1	0
4	L	302	GOL	2	0

5.7 Other polymers ⓘ

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 ⓘ

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, 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	K	213/213 (100%)	-0.04	2 (0%) 84 87	15, 26, 46, 64	0
1	L	213/213 (100%)	-0.05	0 100 100	17, 33, 47, 64	0
2	H	219/224 (97%)	-0.00	5 (2%) 60 67	15, 30, 65, 80	0
2	M	224/224 (100%)	-0.08	5 (2%) 62 69	15, 30, 54, 69	0
3	A	15/40 (37%)	0.05	1 (6%) 18 23	23, 27, 58, 64	0
3	C	13/40 (32%)	3.60	11 (84%) 0 0	44, 57, 79, 83	0
All	All	897/954 (94%)	0.01	24 (2%) 54 62	15, 30, 56, 83	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	19	ILE	8.7
3	C	31	LEU	7.6
1	K	212	GLY	4.7
3	C	26	TYR	4.0
3	C	30	TRP	3.8
2	H	135	GLY	3.7
3	C	22	SER	3.7
3	C	25	TRP	3.6
2	H	200	THR	3.4
3	C	32	PRO	3.1
3	C	28	TYR	3.0
3	C	29	ARG	3.0
2	H	1	GLU	2.9
2	H	199	GLY	2.7
2	M	148	PHE	2.7
3	C	23	ILE	2.6
3	C	24	PRO	2.5
1	K	126	LYS	2.4
3	A	18	THR	2.4

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Mol	Chain	Res	Type	RSRZ
2	M	203	GLN	2.4
2	M	200	THR	2.3
2	H	222	LYS	2.2
2	M	213	LYS	2.2
2	M	99	ARG	2.1

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. 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	FOD	C	20	18/19	0.80	0.25	44,58,63,66	0
3	FOD	A	20	18/19	0.96	0.14	20,25,32,32	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
6	MAN	A	109	11/12	0.55	0.40	90,93,98,102	0
6	MAN	C	107	11/12	0.65	0.25	71,81,89,90	0
4	GOL	L	302	6/6	0.72	0.26	41,48,49,50	0
6	MAN	A	106	11/12	0.75	0.30	56,64,68,73	0
6	MAN	A	105	11/12	0.79	0.21	47,51,58,59	0
6	MAN	C	106	11/12	0.80	0.23	60,66,73,76	0
6	MAN	A	108	11/12	0.82	0.16	55,65,74,75	0
4	GOL	L	301	6/6	0.82	0.20	36,44,44,45	0
5	BMA	A	101	11/12	0.84	0.20	31,35,41,41	0
6	MAN	C	105	11/12	0.89	0.17	42,52,55,57	0
5	BMA	C	101	11/12	0.89	0.14	40,49,58,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GOL	K	301	6/6	0.90	0.17	29,35,43,44	0
6	MAN	A	107	11/12	0.92	0.14	46,49,54,57	0
6	MAN	C	102	11/12	0.93	0.13	28,32,38,48	0
6	MAN	C	103	11/12	0.95	0.10	19,24,32,35	0
6	MAN	A	102	11/12	0.95	0.13	23,26,34,41	0
6	MAN	C	104	11/12	0.97	0.12	16,19,22,25	0
6	MAN	A	104	11/12	0.97	0.15	14,17,21,22	0
6	MAN	A	103	11/12	0.97	0.13	17,18,24,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.