



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2016 – 04:38 PM EST

PDB ID : 4QGT
Title : The Crystal Structure of Human IgG Fc Domain with Enhanced Aromatic Sequon
Authors : Kong, L.; Connelly, S.C.; Wilson, I.A.
Deposited on : 2014-05-25
Resolution : 2.99 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028320
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) : rb-20028320

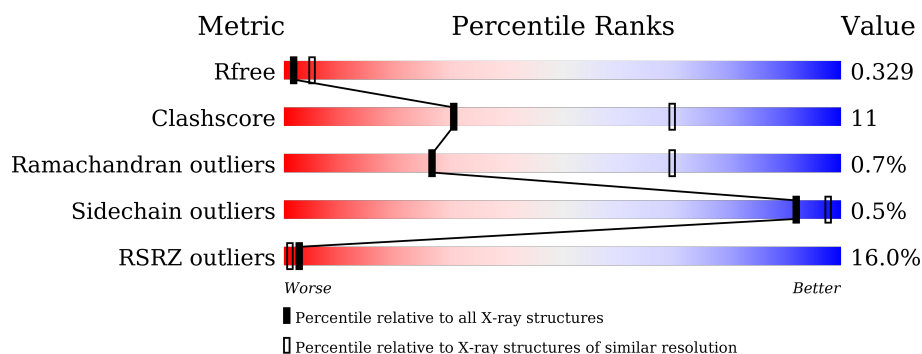
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	A	233	<div> <div>16%</div> <div> <div></div> <div>63%</div> <div>24%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	233	<div> <div>12%</div> <div> <div></div> <div>71%</div> <div>18%</div> <div></div> <div>11%</div> </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3463 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 Hepatitis B virus receptor binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1637	1044	274	312	7			
1	B	207	Total	C	N	O	S	0	0	0
			1654	1054	278	315	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	215	PHE	-	EXPRESSION TAG	UNP Q6PYX1
A	295	PHE	GLN	ENGINEERED MUTATION	UNP Q6PYX1
A	296	ALA	TYR	ENGINEERED MUTATION	UNP Q6PYX1
B	215	PHE	-	EXPRESSION TAG	UNP Q6PYX1
B	295	PHE	GLN	ENGINEERED MUTATION	UNP Q6PYX1
B	296	ALA	TYR	ENGINEERED MUTATION	UNP Q6PYX1

- Molecule 2 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	5	Total	C	N	O	0	0
			64	36	3	25		

- Molecule 3 is a polymer of unknown type called SUGAR (8-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	8	Total	C	N	O	0	0
			99	56	4	39		

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



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

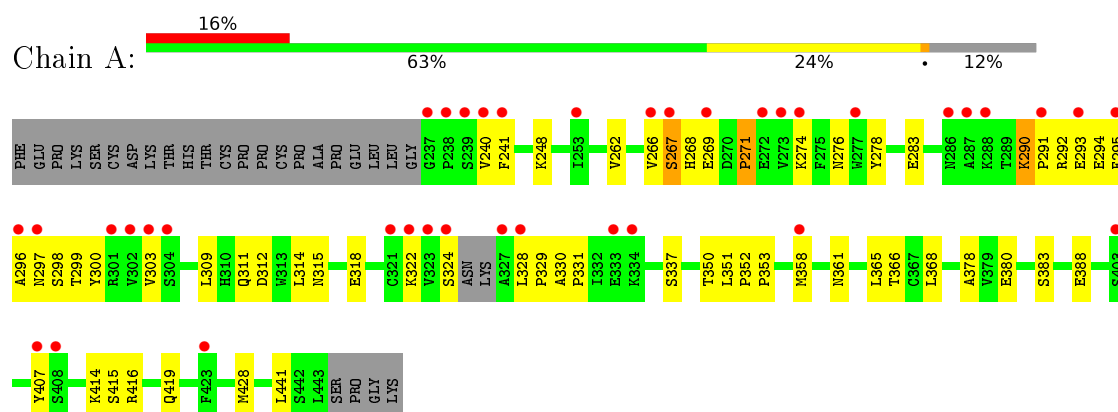
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	O	0	0
			2	2		
5	B	1	Total	O	0	0
			1	1		

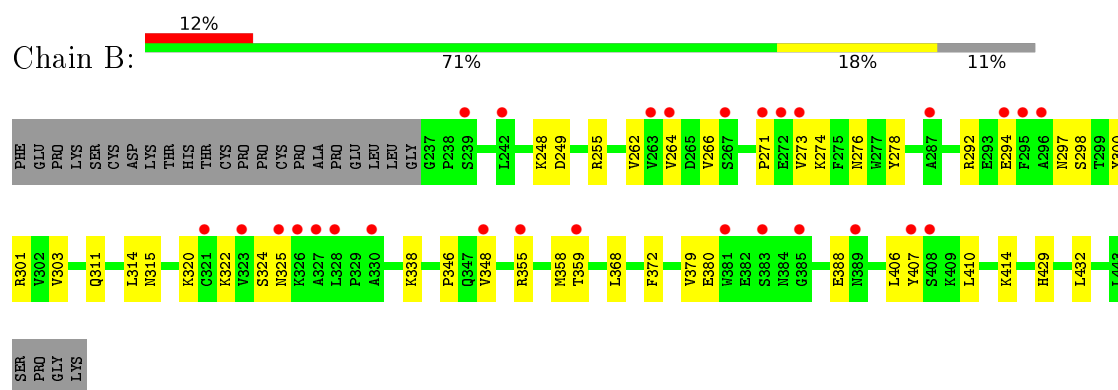
3 Residue-property plots [i](#)

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: Hepatitis B virus receptor binding protein



- Molecule 1: Hepatitis B virus receptor binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	154.07Å 49.19Å 75.54Å 90.00° 104.21° 90.00°	Depositor
Resolution (Å)	46.85 – 2.99 46.85 – 2.99	Depositor EDS
% Data completeness (in resolution range)	87.9 (46.85-2.99) 88.0 (46.85-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.298 , 0.326 0.302 , 0.329	Depositor DCC
R_{free} test set	517 reflections (5.17%)	DCC
Wilson B-factor (Å ²)	69.3	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	3463	wwPDB-VP
Average B, all atoms (Å ²)	77.0	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 48.10 % 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 9.0296e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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, GOL, 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	A	0.26	0/1682	0.45	0/2290
1	B	0.22	0/1700	0.40	0/2315
All	All	0.24	0/3382	0.42	0/4605

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1637	0	1603	44	0
1	B	1654	0	1621	31	0
2	A	64	0	55	3	0
3	B	99	0	85	1	0
4	B	6	0	8	0	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
All	All	3463	0	3372	75	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 11.

All (75) 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:297:ASN:HD21	2:A:501:NAG:C1	1.02	1.54
1:A:297:ASN:ND2	2:A:501:NAG:C1	1.87	1.37
1:B:358:MET:O	1:B:414:LYS:NZ	1.62	1.32
1:A:358:MET:O	1:A:414:LYS:NZ	1.94	1.00
1:A:268:HIS:O	1:A:269:GLU:HB2	1.81	0.81
1:A:296:ALA:HB3	1:A:299:THR:O	1.81	0.80
1:A:296:ALA:HB3	1:A:299:THR:C	2.01	0.80
1:B:266:VAL:CG1	1:B:300:TYR:O	2.36	0.74
1:B:271:PRO:HB3	1:B:292:ARG:HH12	1.53	0.73
1:A:294:GLU:HG2	1:A:300:TYR:H	1.54	0.73
1:B:266:VAL:HG12	1:B:300:TYR:O	1.90	0.72
1:B:276:ASN:HB2	1:B:322:LYS:HB3	1.72	0.72
1:A:388:GLU:OE1	1:A:416:ARG:NH2	2.24	0.71
1:A:297:ASN:OD1	1:A:298:SER:N	2.24	0.70
1:A:383:SER:HB2	1:A:388:GLU:OE2	1.92	0.70
1:B:346:PRO:HB3	1:B:372:PHE:HB3	1.74	0.68
1:A:361:ASN:HA	1:A:414:LYS:HE2	1.76	0.67
1:A:268:HIS:O	1:A:269:GLU:CB	2.43	0.66
1:B:294:GLU:HB2	1:B:300:TYR:HE1	1.62	0.64
1:A:291:PRO:HB3	1:A:300:TYR:CZ	2.35	0.61
1:A:266:VAL:O	1:A:267:SER:CB	2.49	0.60
1:A:248:LYS:NZ	1:A:380:GLU:OE2	2.26	0.60
1:B:294:GLU:CB	1:B:300:TYR:HE1	2.16	0.59
1:B:314:LEU:O	1:B:338:LYS:NZ	2.36	0.58
1:B:274:LYS:HB3	1:B:324:SER:HB2	1.87	0.56
1:A:383:SER:CB	1:A:388:GLU:OE2	2.54	0.56
1:A:378:ALA:HB3	1:A:428:MET:HB2	1.89	0.55
1:A:351:LEU:HB2	1:A:366:THR:HB	1.90	0.54
1:B:368:LEU:HD13	1:B:407:TYR:CZ	2.43	0.53
1:B:248:LYS:NZ	1:B:380:GLU:OE2	2.31	0.53
1:A:266:VAL:O	1:A:267:SER:HB3	2.08	0.52
1:A:297:ASN:CG	1:A:298:SER:H	2.12	0.52
1:B:266:VAL:HG13	1:B:300:TYR:O	2.10	0.52
1:A:291:PRO:HB3	1:A:300:TYR:OH	2.11	0.51
1:B:294:GLU:CG	1:B:300:TYR:HE1	2.24	0.51
1:A:368:LEU:HD13	1:A:407:TYR:CZ	2.45	0.51
1:A:353:PRO:HD3	1:A:365:LEU:HD23	1.94	0.50
1:B:429:HIS:H	1:B:432:LEU:HD12	1.77	0.50
1:B:355:ARG:HA	1:B:358:MET:HG2	1.95	0.49
1:A:291:PRO:O	1:A:292:ARG:HB2	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:273:VAL:HG12	1:B:325:ASN:HD22	1.77	0.49
1:A:295:PHE:H	1:A:300:TYR:HB3	1.78	0.49
1:A:352:PRO:HG3	1:A:441:LEU:HD11	1.95	0.49
1:A:328:LEU:HD12	1:A:329:PRO:HD2	1.95	0.48
1:A:241:PHE:HE1	2:A:503:BMA:H2	1.80	0.47
1:A:309:LEU:HB2	1:A:312:ASP:HB2	1.95	0.47
1:B:388:GLU:HG3	1:B:410:LEU:HD11	1.97	0.47
1:B:294:GLU:HG3	1:B:300:TYR:CE1	2.50	0.46
1:A:240:VAL:C	1:A:241:PHE:HD2	2.19	0.46
1:B:274:LYS:NZ	1:B:276:ASN:OD1	2.49	0.46
1:B:262:VAL:HG22	1:B:303:VAL:HG13	1.97	0.46
1:A:318:GLU:HA	1:A:337:SER:HB3	1.98	0.45
1:B:249:ASP:OD1	1:B:255:ARG:NH2	2.45	0.45
1:B:264:VAL:HG12	1:B:301:ARG:HG3	1.98	0.45
1:A:350:THR:HB	1:A:441:LEU:HD22	1.99	0.44
1:A:278:TYR:HA	1:A:283:GLU:HA	1.99	0.44
1:A:295:PHE:CD2	1:A:295:PHE:O	2.70	0.44
1:A:297:ASN:N	1:A:297:ASN:OD1	2.51	0.44
1:B:294:GLU:CG	1:B:300:TYR:CE1	3.02	0.43
1:A:290:LYS:HB2	1:A:291:PRO:HD3	2.00	0.43
1:A:271:PRO:HB2	1:A:293:GLU:HG2	2.01	0.43
1:A:311:GLN:O	1:A:315:ASN:N	2.47	0.42
1:B:379:VAL:HG21	1:B:406:LEU:HD11	2.02	0.42
1:B:311:GLN:O	1:B:315:ASN:N	2.48	0.42
1:A:276:ASN:HB2	1:A:322:LYS:HB3	2.02	0.41
1:A:274:LYS:HE2	1:A:324:SER:HB2	2.01	0.41
1:A:330:ALA:HA	1:A:331:PRO:HD3	1.90	0.41
1:A:415:SER:O	1:A:419:GLN:HG2	2.21	0.41
1:B:338:LYS:HB3	1:B:338:LYS:HE2	1.84	0.41
1:B:297:ASN:OD1	3:B:508:FUC:H61	2.21	0.41
1:B:294:GLU:HB2	1:B:300:TYR:CE1	2.49	0.40
1:B:359:THR:HG22	1:B:359:THR:O	2.22	0.40
1:A:262:VAL:HA	1:A:303:VAL:HG22	2.03	0.40
1:A:311:GLN:HA	1:A:314:LEU:HB2	2.04	0.40
1:B:278:TYR:HB2	1:B:320:LYS:HB3	2.03	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	201/233 (86%)	188 (94%)	10 (5%)	3 (2%)	13	50
1	B	205/233 (88%)	199 (97%)	6 (3%)	0	100	100
All	All	406/466 (87%)	387 (95%)	16 (4%)	3 (1%)	26	70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	267	SER
1	A	290	LYS
1	A	271	PRO

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	190/215 (88%)	190 (100%)	0	100	100
1	B	192/215 (89%)	190 (99%)	2 (1%)	82	95
All	All	382/430 (89%)	380 (100%)	2 (0%)	92	98

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

Mol	Chain	Res	Type
1	B	298	SER
1	B	348	VAL

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

13 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	$\# Z > 2$
2	NAG	A	501	2	14,14,15	0.71	0	15,19,21	1.23	0
2	NAG	A	502	2	14,14,15	0.73	0	15,19,21	0.88	0
2	BMA	A	503	2	11,11,12	0.61	0	15,15,17	1.57	3 (20%)
2	MAN	A	504	2	11,11,12	0.78	0	15,15,17	1.29	1 (6%)
2	NAG	A	505	2	14,14,15	0.90	0	15,19,21	1.35	2 (13%)
3	NAG	B	501	1,3	14,14,15	0.69	0	15,19,21	1.23	0
3	NAG	B	502	3	14,14,15	0.73	0	15,19,21	0.89	0
3	BMA	B	503	3	11,11,12	0.60	0	15,15,17	1.58	3 (20%)
3	MAN	B	504	3	11,11,12	0.60	0	15,15,17	1.38	1 (6%)
3	NAG	B	505	3	14,14,15	0.46	0	15,19,21	0.98	1 (6%)
3	MAN	B	506	3	11,11,12	0.79	0	15,15,17	1.29	1 (6%)
3	NAG	B	507	3	14,14,15	0.90	0	15,19,21	1.34	2 (13%)
3	FUC	B	508	3	10,10,11	0.58	0	13,14,16	1.23	1 (7%)

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	NAG	A	501	2	-	0/6/23/26	0/1/1/1
2	NAG	A	502	2	-	0/6/23/26	0/1/1/1
2	BMA	A	503	2	-	0/2/19/22	0/1/1/1
2	MAN	A	504	2	-	0/2/19/22	0/1/1/1
2	NAG	A	505	2	-	0/6/23/26	0/1/1/1
3	NAG	B	501	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	502	3	-	0/6/23/26	0/1/1/1
3	BMA	B	503	3	-	0/2/19/22	0/1/1/1
3	MAN	B	504	3	-	0/2/19/22	0/1/1/1
3	NAG	B	505	3	-	0/6/23/26	0/1/1/1
3	MAN	B	506	3	-	0/2/19/22	0/1/1/1
3	NAG	B	507	3	-	0/6/23/26	0/1/1/1
3	FUC	B	508	3	-	0/0/17/20	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	503	BMA	O3-C3-C4	-3.42	102.64	110.36
2	A	503	BMA	O3-C3-C4	-3.42	102.65	110.36
2	A	503	BMA	O6-C6-C5	-2.76	102.09	111.30
3	B	503	BMA	O6-C6-C5	-2.74	102.14	111.30
2	A	505	NAG	O5-C5-C4	-2.57	105.87	110.13
3	B	507	NAG	O5-C5-C4	-2.53	105.95	110.13
3	B	508	FUC	O2-C2-C1	2.35	113.94	109.23
2	A	503	BMA	C1-O5-C5	2.75	116.18	112.14
3	B	503	BMA	C1-O5-C5	2.77	116.21	112.14
3	B	505	NAG	C1-O5-C5	2.96	116.49	112.14
3	B	507	NAG	O4-C4-C3	3.35	117.91	110.36
2	A	505	NAG	O4-C4-C3	3.36	117.94	110.36
3	B	504	MAN	C1-O5-C5	3.47	117.25	112.14
2	A	504	MAN	C1-O5-C5	4.20	118.31	112.14
3	B	506	MAN	C1-O5-C5	4.20	118.32	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	NAG	2	0
2	A	503	BMA	1	0
3	B	508	FUC	1	0

5.6 Ligand geometry

1 ligand is 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	GOL	B	509	-	5,5,5	0.36	0	5,5,5	0.22	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
4	GOL	B	509	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 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	A	205/233 (87%)	1.06	38 (18%)	2 1	31, 67, 130, 143	0
1	B	207/233 (88%)	1.01	28 (13%)	4 1	31, 66, 106, 127	0
All	All	412/466 (88%)	1.04	66 (16%)	3 1	31, 67, 123, 143	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	303	VAL	8.6
1	B	271	PRO	7.3
1	A	297	ASN	7.2
1	B	327	ALA	6.9
1	B	273	VAL	6.6
1	B	272	GLU	6.5
1	B	325	ASN	6.2
1	B	326	LYS	5.6
1	A	408	SER	4.7
1	A	324	SER	4.5
1	A	240	VAL	4.5
1	A	266	VAL	4.5
1	A	302	VAL	4.4
1	A	273	VAL	4.0
1	A	328	LEU	3.7
1	A	238	PRO	3.7
1	A	269	GLU	3.7
1	A	288	LYS	3.7
1	A	403	SER	3.6
1	A	334	LYS	3.6
1	A	296	ALA	3.6
1	A	407	TYR	3.5
1	B	239	SER	3.5
1	B	323	VAL	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	385	GLY	3.2
1	B	294	GLU	3.1
1	A	423	PHE	3.1
1	A	301	ARG	3.0
1	A	333	GLU	3.0
1	B	381	TRP	2.9
1	A	267	SER	2.8
1	A	277	TRP	2.8
1	B	355	ARG	2.8
1	B	295	PHE	2.8
1	B	389	ASN	2.7
1	B	267	SER	2.6
1	A	241	PHE	2.6
1	A	287	ALA	2.6
1	A	327	ALA	2.6
1	A	304	SER	2.6
1	A	323	VAL	2.5
1	B	330	ALA	2.5
1	B	407	TYR	2.5
1	A	321	CYS	2.5
1	A	322	LYS	2.5
1	B	264	VAL	2.5
1	B	263	VAL	2.5
1	A	358	MET	2.4
1	B	321	CYS	2.4
1	B	328	LEU	2.4
1	A	239	SER	2.4
1	B	383	SER	2.4
1	A	293	GLU	2.3
1	B	287	ALA	2.3
1	A	291	PRO	2.3
1	B	296	ALA	2.3
1	A	274	LYS	2.2
1	B	348	VAL	2.2
1	B	359	THR	2.1
1	A	253	ILE	2.1
1	A	237	GLY	2.1
1	B	408	SER	2.1
1	A	272	GLU	2.1
1	B	242	LEU	2.0
1	A	286	ASN	2.0
1	A	295	PHE	2.0

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. 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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	B	507	14/15	0.82	0.31	1.49	66,90,109,110	0
2	NAG	A	505	14/15	0.82	0.30	1.01	81,105,130,142	0
3	NAG	B	502	14/15	0.91	0.17	-1.45	89,99,103,104	0
2	BMA	A	503	11/12	0.66	0.34	-	194,302,322,324	0
3	NAG	B	505	14/15	0.76	0.24	-	104,111,116,120	0
2	NAG	A	501	14/15	0.64	0.46	-	280,327,380,388	0
3	BMA	B	503	11/12	0.82	0.17	-	80,100,108,110	0
3	NAG	B	501	14/15	0.84	0.17	-	87,98,103,109	0
2	MAN	A	504	11/12	0.87	0.21	-	123,146,164,167	0
3	MAN	B	504	11/12	0.72	0.22	-	107,111,116,116	0
3	FUC	B	508	10/11	0.60	0.32	-	87,99,110,115	0
2	NAG	A	502	14/15	0.49	0.43	-	249,308,346,366	0
3	MAN	B	506	11/12	0.92	0.17	-	90,95,98,103	0

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. 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, 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	LLDF	B-factors(Å ²)	Q<0.9
4	GOL	B	509	6/6	0.68	0.42	-	61,83,85,92	0

6.5 Other polymers [i](#)

There are no such residues in this entry.