



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 7, 2017 – 07:46 PM EDT

PDB ID : 4WI7
Title : Structural mapping of the human IgG1 binding site for FcRn: hu3S193 Fc mutation H435A
Authors : Farrugia, W.; Burvenich, I.J.G.; Scott, A.M.; Ramsland, P.A.
Deposited on : unknown
Resolution : 1.90 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029824

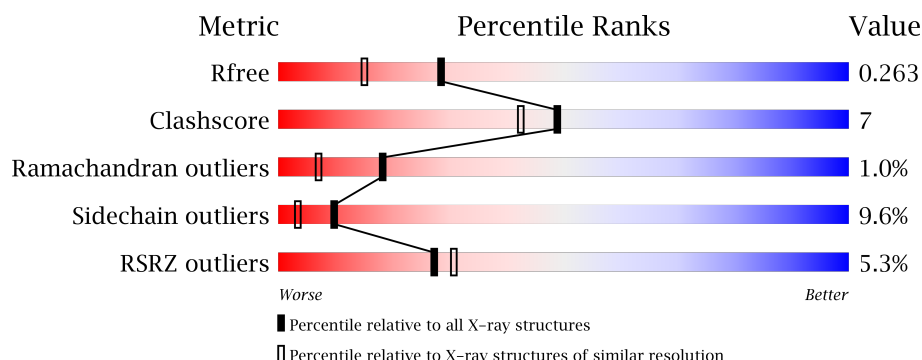
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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	208	<div> <div>4%</div> <div>78%</div> <div>17%</div> <div>.</div> </div>
1	B	208	<div> <div>6%</div> <div>80%</div> <div>15%</div> <div>5%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	502	-	-	-	X
2	NAG	B	507	-	-	-	X
6	EDO	A	509	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3712 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 Ig gamma-1 chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1659	1056	278	319	6			
1	B	208	Total	C	N	O	S	0	0	0
			1659	1056	278	319	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	435	ALA	HIS	engineered mutation	UNP P01857
B	435	ALA	HIS	engineered mutation	UNP P01857

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C₈H₁₅NO₆).



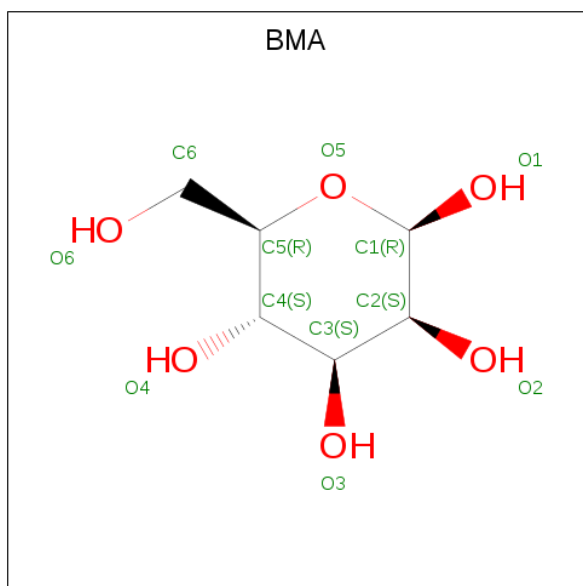
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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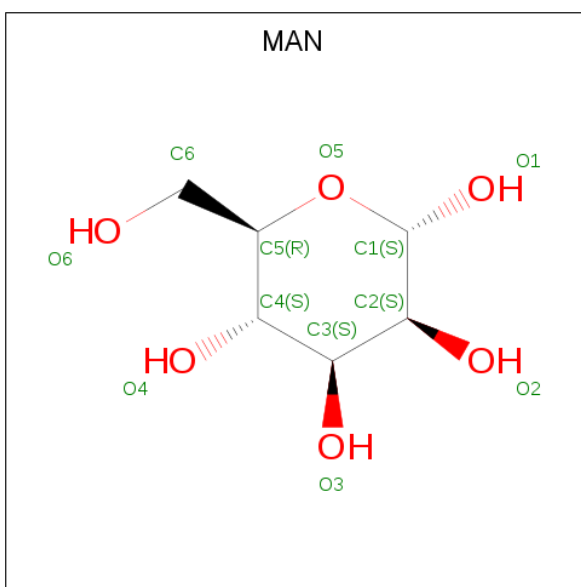
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula: C₆H₁₂O₆).



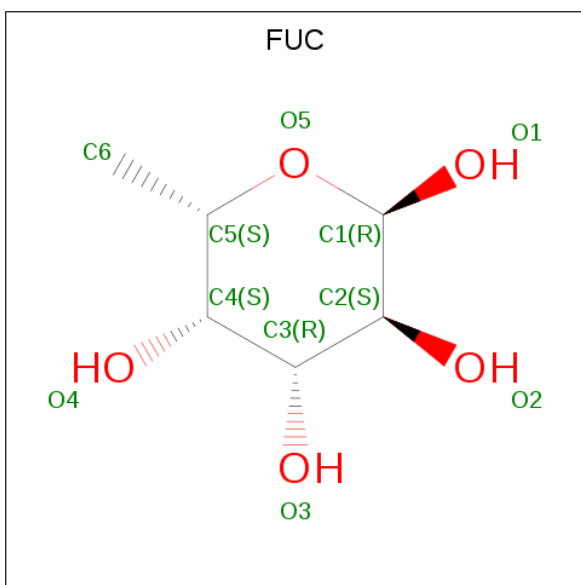
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		
3	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



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

- Molecule 5 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: $C_6H_{12}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		
5	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

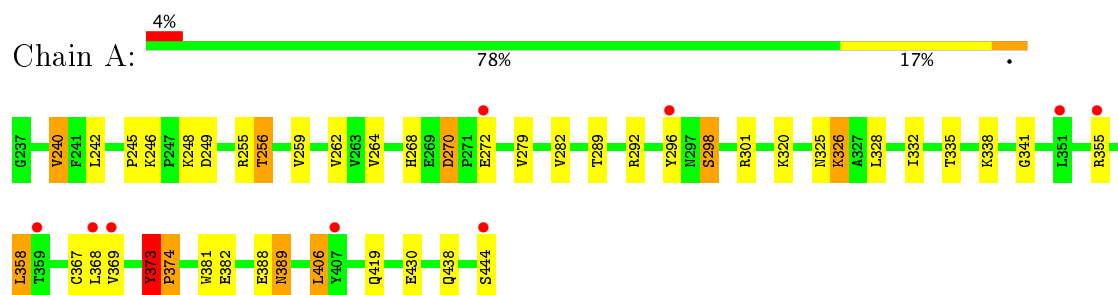
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	98	Total	O	0	0
			98	98		
7	B	90	Total	O	0	0
			90	90		

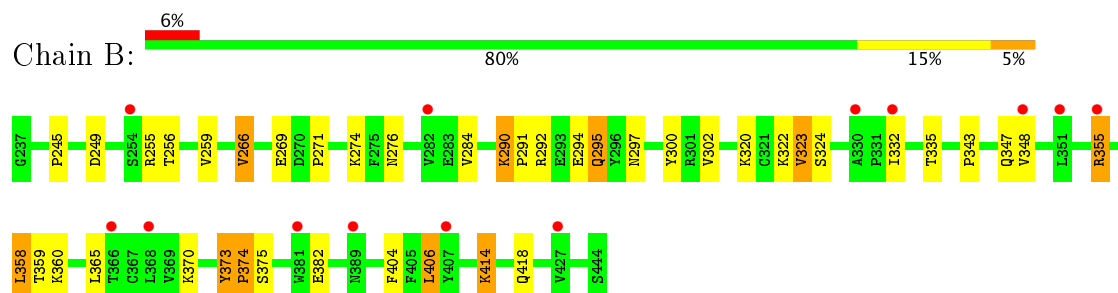
3 Residue-property plots

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: Ig gamma-1 chain C region



- Molecule 1: Ig gamma-1 chain C region



GLOBAL-STATISTICS INFOmissingINFO

4 Model quality

4.1 Standard geometry

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

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	0.55	0/1704	0.76	3/2322 (0.1%)
1	B	0.54	0/1704	0.69	3/2322 (0.1%)
All	All	0.54	0/3408	0.73	6/4644 (0.1%)

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	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	373	TYR	C-N-CD	-14.64	88.38	120.60
1	B	373	TYR	C-N-CD	-9.11	100.55	120.60
1	B	406	LEU	CA-CB-CG	7.45	132.42	115.30
1	A	373	TYR	C-N-CA	6.05	147.43	122.00
1	A	406	LEU	CA-CB-CG	5.79	128.62	115.30
1	B	406	LEU	CB-CG-CD2	5.29	120.00	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	373	TYR	Peptide
1	B	373	TYR	Peptide

4.2 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	1659	0	1628	25	0
1	B	1659	0	1628	22	0
2	A	56	0	49	0	0
2	B	56	0	49	1	0
3	A	11	0	8	0	0
3	B	11	0	8	0	0
4	A	22	0	18	0	0
4	B	22	0	18	0	0
5	A	10	0	10	1	0
5	B	10	0	10	0	0
6	A	4	0	6	0	0
6	B	4	0	6	0	0
7	A	98	0	0	6	0
7	B	90	0	0	3	0
All	All	3712	0	3438	47	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 7.

All (47) 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:268:HIS:HE1	1:A:298:SER:HB2	1.51	0.76
1:A:388:GLU:OE2	7:A:697:HOH:O	2.03	0.74
1:B:245:PRO:HD3	1:B:259:VAL:HG12	1.75	0.69
1:A:389:ASN:O	7:A:601:HOH:O	2.11	0.69
1:B:347:GLN:OE1	7:B:677:HOH:O	2.13	0.67
1:B:290:LYS:HZ1	1:B:302:VAL:HA	1.63	0.64
1:B:360:LYS:O	1:B:414:LYS:NZ	2.31	0.62
1:A:268:HIS:CE1	1:A:298:SER:HB2	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:LYS:NZ	7:A:672:HOH:O	2.32	0.57
1:B:355:ARG:HA	1:B:358:LEU:HD22	1.87	0.57
1:A:438:GLN:OE1	7:A:602:HOH:O	2.18	0.56
1:B:266:VAL:HG22	1:B:300:TYR:HB2	1.87	0.56
1:A:373:TYR:CD2	1:A:374:PRO:HD3	2.41	0.56
1:A:264:VAL:HG12	1:A:301:ARG:HG3	1.88	0.55
1:A:270:ASP:OD2	1:A:270:ASP:N	2.40	0.54
1:A:272:GLU:O	1:A:325:ASN:ND2	2.40	0.53
1:B:347:GLN:NE2	7:B:687:HOH:O	2.39	0.52
1:B:249:ASP:OD1	1:B:255:ARG:NE	2.35	0.52
1:A:355:ARG:HA	1:A:358:LEU:HD22	1.95	0.48
1:B:274:LYS:HE3	1:B:276:ASN:OD1	2.13	0.48
1:B:297:ASN:HD22	2:B:501:NAG:H83	1.79	0.48
1:A:382:GLU:OE2	7:A:602:HOH:O	2.20	0.48
1:B:295:GLN:HA	7:B:618:HOH:O	2.13	0.48
1:B:343:PRO:HA	1:B:374:PRO:HD2	1.95	0.48
1:B:271:PRO:O	1:B:292:ARG:NH1	2.48	0.47
1:A:367:CYS:HB2	1:A:381:TRP:CZ2	2.50	0.47
1:A:374:PRO:HG2	1:A:430:GLU:CD	2.34	0.47
1:B:320:LYS:HB2	1:B:335:THR:HG22	1.97	0.46
1:B:274:LYS:HB3	1:B:324:SER:HB2	1.98	0.46
1:A:249:ASP:OD1	1:A:255:ARG:HD3	2.15	0.45
1:A:320:LYS:HB2	1:A:335:THR:HG22	1.98	0.45
1:B:375:SER:HB3	1:B:404:PHE:CE2	2.53	0.44
1:A:245:PRO:HD3	1:A:259:VAL:HG12	1.98	0.44
1:B:355:ARG:O	1:B:358:LEU:HB2	2.16	0.44
1:A:256:THR:HG23	7:A:628:HOH:O	2.18	0.44
1:A:296:TYR:HD1	5:A:508:FUC:H62	1.83	0.44
1:B:322:LYS:O	1:B:332:ILE:O	2.36	0.44
1:B:266:VAL:HG13	1:B:300:TYR:O	2.18	0.43
1:A:326:LYS:HB3	1:A:326:LYS:HE3	1.82	0.43
1:B:290:LYS:NZ	1:B:302:VAL:HA	2.32	0.43
1:A:341:GLY:HA3	1:A:373:TYR:CE2	2.54	0.42
1:A:268:HIS:CE1	1:A:298:SER:O	2.72	0.42
1:A:373:TYR:HD2	1:A:374:PRO:HD3	1.85	0.42
1:A:240:VAL:HG13	1:A:332:ILE:HG21	2.02	0.42
1:A:373:TYR:CD2	1:A:374:PRO:CD	3.04	0.41
1:B:290:LYS:HG2	1:B:291:PRO:O	2.20	0.41
1:B:274:LYS:O	1:B:323:VAL:HA	2.21	0.41

There are no symmetry-related clashes.

4.3 Torsion angles

4.3.1 Protein backbone

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	206/208 (99%)	198 (96%)	7 (3%)	1 (0%)	32	20
1	B	206/208 (99%)	199 (97%)	4 (2%)	3 (2%)	12	3
All	All	412/416 (99%)	397 (96%)	11 (3%)	4 (1%)	18	7

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374	PRO
1	B	374	PRO
1	B	295	GLN
1	B	323	VAL

4.3.2 Protein sidechains

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	193/193 (100%)	172 (89%)	21 (11%)	7	2
1	B	193/193 (100%)	177 (92%)	16 (8%)	13	5
All	All	386/386 (100%)	349 (90%)	37 (10%)	10	3

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	240	VAL
1	A	242	LEU

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Mol	Chain	Res	Type
1	A	248	LYS
1	A	256	THR
1	A	262	VAL
1	A	270	ASP
1	A	279	VAL
1	A	282	VAL
1	A	289	THR
1	A	292	ARG
1	A	298	SER
1	A	326	LYS
1	A	328	LEU
1	A	338	LYS
1	A	358	LEU
1	A	368	LEU
1	A	369	VAL
1	A	389	ASN
1	A	406	LEU
1	A	419	GLN
1	A	444	SER
1	B	256	THR
1	B	266	VAL
1	B	269	GLU
1	B	284	VAL
1	B	290	LYS
1	B	294	GLU
1	B	348	VAL
1	B	355	ARG
1	B	358	LEU
1	B	359	THR
1	B	365	LEU
1	B	370	LYS
1	B	382	GLU
1	B	406	LEU
1	B	414	LYS
1	B	418	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	268	HIS

4.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

4.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

4.6 Ligand geometry ⓘ

18 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	$\# Z > 2$
2	NAG	A	501	1,2,5	14,14,15	0.57	0	15,19,21	0.96	1 (6%)
2	NAG	A	502	3,2	14,14,15	0.67	0	15,19,21	0.59	0
3	BMA	A	503	2,4	11,11,12	0.74	0	13,15,17	0.97	0
4	MAN	A	504	3,2	11,11,12	0.77	0	13,15,17	1.97	6 (46%)
2	NAG	A	505	4	14,14,15	0.61	0	15,19,21	1.22	2 (13%)
4	MAN	A	506	3,2	11,11,12	0.74	0	13,15,17	1.47	2 (15%)
2	NAG	A	507	4	14,14,15	0.58	0	15,19,21	1.12	1 (6%)
5	FUC	A	508	2	9,10,11	0.69	0	13,14,16	1.38	2 (15%)
6	EDO	A	509	-	3,3,3	0.48	0	2,2,2	0.34	0
2	NAG	B	501	1,2,5	14,14,15	0.55	0	15,19,21	1.42	1 (6%)
2	NAG	B	502	3,2	14,14,15	0.55	0	15,19,21	0.73	0
3	BMA	B	503	2,4	11,11,12	0.59	0	13,15,17	1.09	1 (7%)
4	MAN	B	504	3,2	11,11,12	0.76	0	13,15,17	1.83	4 (30%)
2	NAG	B	505	4	14,14,15	0.62	0	15,19,21	0.86	0
4	MAN	B	506	3,2	11,11,12	0.51	0	13,15,17	1.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	B	507	4	14,14,15	0.51	0	15,19,21	1.14	1 (6%)
5	FUC	B	508	2	9,10,11	0.66	0	13,14,16	2.18	5 (38%)
6	EDO	B	509	-	3,3,3	0.57	0	2,2,2	0.35	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
2	NAG	A	501	1,2,5	-	0/6/23/26	0/1/1/1
2	NAG	A	502	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	503	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	504	3,2	-	0/2/19/22	0/1/1/1
2	NAG	A	505	4	-	0/6/23/26	0/1/1/1
4	MAN	A	506	3,2	-	0/2/19/22	0/1/1/1
2	NAG	A	507	4	-	0/6/23/26	0/1/1/1
5	FUC	A	508	2	-	0/0/17/20	0/1/1/1
6	EDO	A	509	-	-	0/1/1/1	0/0/0/0
2	NAG	B	501	1,2,5	-	0/6/23/26	0/1/1/1
2	NAG	B	502	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	503	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	504	3,2	-	0/2/19/22	0/1/1/1
2	NAG	B	505	4	-	0/6/23/26	0/1/1/1
4	MAN	B	506	3,2	-	0/2/19/22	0/1/1/1
2	NAG	B	507	4	-	0/6/23/26	0/1/1/1
5	FUC	B	508	2	-	0/0/17/20	0/1/1/1
6	EDO	B	509	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	504	MAN	O2-C2-C3	-3.45	103.40	110.17
5	B	508	FUC	C1-C2-C3	-3.33	105.43	109.65
4	A	506	MAN	C2-C3-C4	-3.27	105.17	110.88
4	A	504	MAN	C2-C3-C4	-3.24	105.22	110.88
4	A	504	MAN	O2-C2-C3	-3.17	103.96	110.17
4	A	506	MAN	O2-C2-C3	-3.15	103.99	110.17
4	B	504	MAN	O5-C1-C2	-3.04	106.02	110.79
2	A	507	NAG	C2-N2-C7	-3.01	118.55	122.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	505	NAG	C4-C3-C2	-2.85	106.84	111.02
5	B	508	FUC	C6-C5-C4	-2.64	108.36	113.07
2	A	505	NAG	O5-C1-C2	-2.54	107.94	111.47
4	A	504	MAN	O5-C1-C2	-2.41	107.02	110.79
4	B	504	MAN	O3-C3-C2	-2.34	105.76	110.02
5	B	508	FUC	O5-C1-C2	-2.33	107.14	110.79
2	A	501	NAG	C6-C5-C4	-2.30	107.63	113.00
4	A	504	MAN	C6-C5-C4	-2.19	107.88	113.00
4	A	504	MAN	C3-C4-C5	2.04	113.81	110.22
5	A	508	FUC	C1-C2-C3	2.15	112.37	109.65
5	A	508	FUC	C3-C4-C5	2.65	113.85	109.68
3	B	503	BMA	C1-C2-C3	3.00	113.46	109.65
2	B	507	NAG	C1-O5-C5	3.16	116.52	112.17
4	A	504	MAN	C1-O5-C5	3.25	116.65	112.17
4	B	504	MAN	C1-C2-C3	3.30	113.83	109.65
5	B	508	FUC	O5-C5-C4	3.57	115.51	109.62
5	B	508	FUC	C3-C4-C5	4.24	116.35	109.68
2	B	501	NAG	C1-O5-C5	4.33	118.14	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

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

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 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	208/208 (100%)	0.41	9 (4%) 36 39	14, 37, 72, 97	0
1	B	208/208 (100%)	0.54	13 (6%) 21 24	16, 39, 66, 82	0
All	All	416/416 (100%)	0.48	22 (5%) 27 31	14, 38, 69, 97	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	296	TYR	4.1
1	B	330	ALA	3.1
1	A	368	LEU	3.0
1	B	282	VAL	2.6
1	B	368	LEU	2.6
1	B	381	TRP	2.6
1	A	359	THR	2.6
1	B	427	VAL	2.5
1	A	407	TYR	2.5
1	B	332	ILE	2.5
1	B	389	ASN	2.5
1	A	351	LEU	2.3
1	B	366	THR	2.3
1	B	355	ARG	2.3
1	A	369	VAL	2.3
1	B	351	LEU	2.3
1	B	407	TYR	2.2
1	B	254	SER	2.1
1	B	348	VAL	2.1
1	A	272	GLU	2.0
1	A	444	SER	2.0
1	A	355	ARG	2.0

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

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

5.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.4 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
2	NAG	B	507	14/15	0.86	0.21	2.86	36,49,66,69	0
6	EDO	A	509	4/4	0.75	0.22	2.39	44,53,55,57	0
2	NAG	B	502	14/15	0.93	0.18	2.04	35,45,54,55	0
2	NAG	A	507	14/15	0.87	0.15	1.17	34,55,78,79	0
2	NAG	A	501	14/15	0.87	0.17	0.64	48,60,72,74	0
6	EDO	B	509	4/4	0.92	0.15	0.32	20,42,49,51	0
2	NAG	B	501	14/15	0.88	0.13	-0.26	35,44,54,57	0
2	NAG	A	502	14/15	0.91	0.13	-0.61	47,58,63,66	0
4	MAN	B	504	11/12	0.87	0.27	-	48,62,66,76	0
2	NAG	B	505	14/15	0.61	0.41	-	90,98,100,101	0
4	MAN	A	504	11/12	0.83	0.31	-	76,87,93,94	0
3	BMA	B	503	11/12	0.92	0.18	-	33,41,47,47	0
2	NAG	A	505	14/15	0.76	0.36	-	85,94,98,99	0
4	MAN	B	506	11/12	0.91	0.25	-	35,39,52,54	0
5	FUC	B	508	10/11	0.55	0.34	-	71,81,87,91	0
5	FUC	A	508	10/11	0.76	0.34	-	82,89,98,104	0
4	MAN	A	506	11/12	0.84	0.19	-	49,58,67,68	0
3	BMA	A	503	11/12	0.91	0.10	-	49,57,65,68	0

5.5 Other polymers [i](#)

There are no such residues in this entry.