



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 07:59 PM GMT

PDB ID : 3R4L
Title : Human very long half life Plasminogen Activator Inhibitor type-1
Authors : Yang, J.; Zheng, H.; Han, Q.; Skrzypczak-Jankun, E.; Jankun, J.
Deposited on : 2011-03-17
Resolution : 2.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

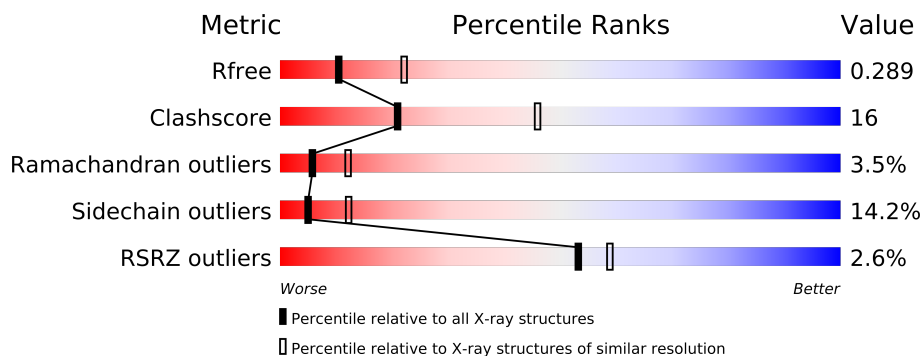
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance


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}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	379	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3086 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Plasminogen activator inhibitor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	0	0
			2995	1918	511	548	18			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	197	CYS	GLN	ENGINEERED MUTATION	UNP P05121
A	355	CYS	GLY	ENGINEERED MUTATION	UNP P05121

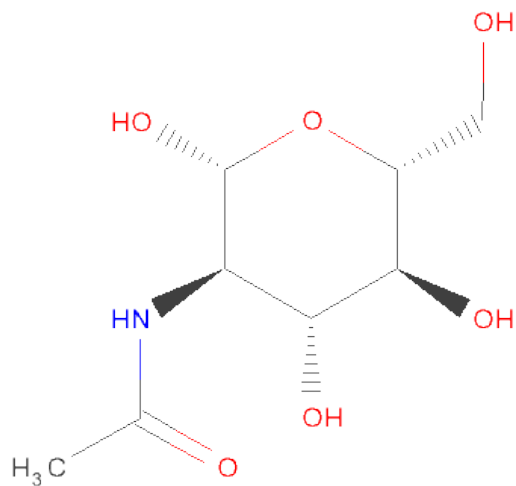
- Molecule 2 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	5	Total	C	N	O	0	0
			60	34	2	24		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	197	CYS	GLN	ENGINEERED MUTATION	UNP P05121
A	355	CYS	GLY	ENGINEERED MUTATION	UNP P05121

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

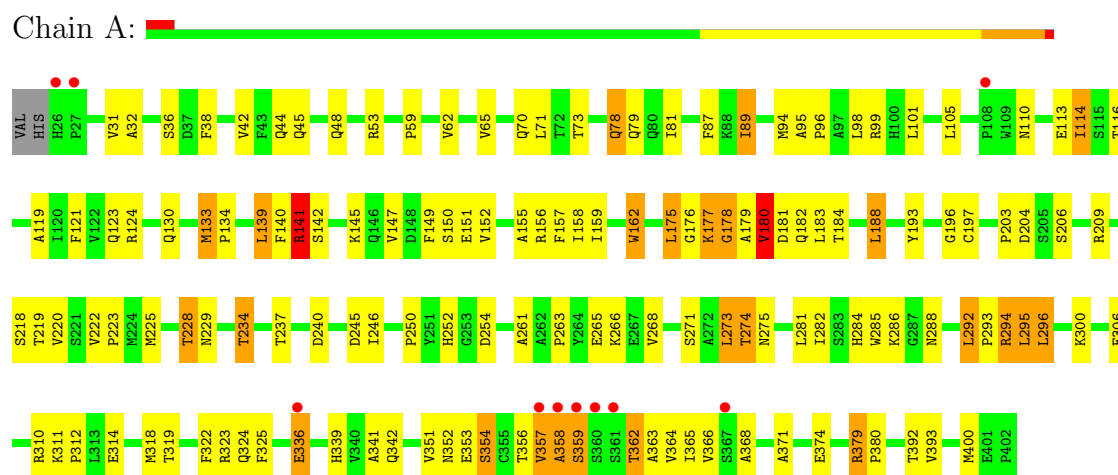
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	17	Total	O	0	0
			17	17		

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 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: Plasminogen activator inhibitor 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	72.01Å 72.01Å 194.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.00 – 2.70 33.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	81.8 (33.00-2.70) 81.8 (33.00-2.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.12 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.6.0093	Depositor
R, R_{free}	0.209 , 0.282 0.213 , 0.289	Depositor DCC
R_{free} test set	709 reflections (5.44%)	DCC
Wilson B-factor (Å ²)	60.1	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 31.8	EDS
Estimated twinning fraction	0.042 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 13747 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3086	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, NDG, 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	0.70	0/3068	0.84	1/4160 (0.0%)

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	124	ARG	O-C-N	-5.53	113.86	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	336	GLU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the

Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2995	0	2983	94	0
2	A	60	0	52	1	0
3	A	14	0	13	2	0
4	A	17	0	0	1	0
All	All	3086	0	3048	95	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 16.

All (95) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:123:GLN:HE22	1:A:149:PHE:H	1.03	0.94
1:A:155:ALA:O	1:A:158:ILE:HG22	1.68	0.93
1:A:123:GLN:NE2	1:A:149:PHE:H	1.72	0.87
1:A:123:GLN:HE22	1:A:149:PHE:N	1.79	0.78
1:A:133:MET:HB2	1:A:134:PRO:CD	2.18	0.74
1:A:156:ARG:CZ	1:A:177:LYS:HA	2.17	0.74
1:A:31:VAL:HG12	1:A:94:MET:HE1	1.70	0.73
1:A:197:CYS:HB2	1:A:252:HIS:HD2	1.53	0.73
1:A:70:GLN:NE2	1:A:89:ILE:H	1.87	0.73
1:A:292:LEU:HD23	1:A:293:PRO:HD2	1.73	0.70
1:A:265:GLU:HB2	1:A:268:VAL:HG23	1.73	0.69
1:A:156:ARG:HB3	1:A:175:LEU:HD12	1.76	0.67
1:A:300:LYS:HG3	1:A:352:ASN:HB3	1.79	0.65
2:A:406:BMA:H62	2:A:407:BMA:O2	1.95	0.65
1:A:70:GLN:HE22	1:A:89:ILE:H	1.41	0.65
1:A:179:ALA:O	1:A:180:VAL:HB	1.99	0.63
1:A:322:PHE:O	1:A:339:HIS:HD2	1.81	0.62
1:A:284:HIS:O	1:A:288:ASN:HB2	1.98	0.62
1:A:324:GLN:HG3	1:A:325:PHE:CD2	2.35	0.62
1:A:38:PHE:O	1:A:42:VAL:HG23	1.98	0.61
1:A:250:PRO:HG3	3:A:408:NAG:H81	1.82	0.61
1:A:31:VAL:HG12	1:A:94:MET:CE	2.30	0.61
1:A:362:THR:HG22	1:A:363:ALA:HA	1.83	0.61
1:A:203:PRO:HB2	1:A:206:SER:OG	2.01	0.61
1:A:188:LEU:N	1:A:188:LEU:HD23	2.16	0.60
1:A:133:MET:CE	1:A:133:MET:HA	2.32	0.58
1:A:133:MET:HE3	1:A:133:MET:HA	1.86	0.57
1:A:250:PRO:HG3	3:A:408:NAG:C8	2.35	0.57
1:A:263:PRO:HD3	1:A:273:LEU:HD13	1.87	0.57
1:A:101:LEU:O	1:A:105:LEU:HG	2.05	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:310:ARG:O	1:A:314:GLU:HG3	2.05	0.56
1:A:263:PRO:HG2	1:A:379:ARG:NH2	2.20	0.56
1:A:113:GLU:HG2	1:A:196:GLY:HA2	1.86	0.55
1:A:265:GLU:HB2	1:A:268:VAL:CG2	2.35	0.55
1:A:133:MET:HB2	1:A:134:PRO:HD3	1.89	0.55
1:A:295:LEU:HD13	1:A:374:GLU:HG3	1.88	0.55
1:A:292:LEU:HD22	1:A:294:ARG:HH11	1.73	0.54
1:A:188:LEU:H	1:A:188:LEU:HD23	1.74	0.53
1:A:123:GLN:HE21	1:A:149:PHE:HD2	1.58	0.52
1:A:62:VAL:HA	1:A:65:VAL:HG12	1.92	0.52
1:A:184:THR:HG23	1:A:341:ALA:CB	2.41	0.51
1:A:133:MET:CB	1:A:134:PRO:CD	2.88	0.50
1:A:357:VAL:C	1:A:359:SER:H	2.15	0.50
1:A:36:SER:OG	1:A:392:THR:HA	2.12	0.50
1:A:324:GLN:HA	1:A:324:GLN:OE1	2.12	0.50
1:A:282:ILE:O	1:A:285:TRP:HB2	2.12	0.49
1:A:356:THR:O	1:A:358:ALA:N	2.45	0.49
1:A:145:LYS:HE3	1:A:162:TRP:CH2	2.48	0.49
1:A:114:ILE:HA	1:A:193:TYR:O	2.13	0.49
1:A:81:ILE:HG12	1:A:318:MET:HG2	1.95	0.49
1:A:245:ASP:O	1:A:261:ALA:HA	2.13	0.48
1:A:133:MET:HB2	1:A:134:PRO:HD2	1.95	0.48
1:A:300:LYS:NZ	1:A:353:GLU:OE1	2.43	0.47
1:A:42:VAL:O	1:A:45:GLN:HB2	2.14	0.47
1:A:157:PHE:C	1:A:157:PHE:CD1	2.87	0.47
1:A:176:GLY:O	1:A:178:GLY:N	2.48	0.47
1:A:322:PHE:O	1:A:339:HIS:CD2	2.66	0.47
1:A:95:ALA:HB3	1:A:96:PRO:HD3	1.97	0.47
1:A:324:GLN:O	1:A:325:PHE:HB2	2.16	0.46
1:A:158:ILE:CG2	1:A:159:ILE:N	2.79	0.46
1:A:274:THR:HG22	1:A:275:ASN:OD1	2.16	0.46
1:A:181:ASP:O	1:A:183:LEU:N	2.48	0.46
1:A:31:VAL:HG23	1:A:32:ALA:N	2.30	0.45
1:A:151:GLU:HA	1:A:151:GLU:OE2	2.16	0.45
1:A:222:VAL:HB	1:A:223:PRO:CD	2.47	0.45
1:A:354:SER:C	1:A:356:THR:H	2.20	0.44
1:A:158:ILE:HG23	1:A:159:ILE:N	2.31	0.44
1:A:252:HIS:C	1:A:254:ASP:H	2.19	0.44
1:A:265:GLU:O	1:A:266:LYS:C	2.54	0.44
1:A:162:TRP:C	1:A:162:TRP:CD1	2.91	0.44
1:A:357:VAL:O	1:A:359:SER:N	2.51	0.44
1:A:140:PHE:C	1:A:141:ARG:O	2.56	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:319:THR:HB	1:A:323:ARG:NH1	2.33	0.43
1:A:311:LYS:HB2	1:A:312:PRO:HD3	2.00	0.43
1:A:119:ALA:HB1	1:A:121:PHE:CE1	2.53	0.43
1:A:366:VAL:HG12	1:A:366:VAL:O	2.18	0.43
1:A:139:LEU:N	1:A:139:LEU:HD23	2.33	0.43
1:A:271:SER:HA	1:A:274:THR:HB	2.01	0.42
1:A:156:ARG:NH1	1:A:177:LYS:HA	2.35	0.42
1:A:44:GLN:O	1:A:45:GLN:C	2.58	0.42
1:A:379:ARG:HD3	1:A:380:PRO:O	2.20	0.41
1:A:114:ILE:HG12	1:A:114:ILE:O	2.19	0.41
1:A:175:LEU:HA	1:A:175:LEU:HD22	1.83	0.41
1:A:228:THR:HG22	1:A:295:LEU:HD23	2.01	0.41
1:A:225:MET:SD	1:A:353:GLU:HG3	2.60	0.41
1:A:295:LEU:HD22	1:A:296:LEU:N	2.35	0.41
1:A:310:ARG:NH2	4:A:516:HOH:O	2.52	0.41
1:A:176:GLY:C	1:A:178:GLY:N	2.74	0.41
1:A:204:ASP:N	1:A:362:THR:HG23	2.35	0.41
1:A:274:THR:HG22	1:A:275:ASN:N	2.35	0.41
1:A:234:THR:CG2	1:A:246:ILE:HD13	2.51	0.41
1:A:59:PRO:HG2	1:A:393:VAL:CG1	2.51	0.41
1:A:87:PHE:HB2	1:A:94:MET:HE2	2.03	0.40
1:A:73:THR:OG1	1:A:78:GLN:CG	2.68	0.40
1:A:65:VAL:HG22	1:A:188:LEU:HD12	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 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	375/379 (99%)	326 (87%)	36 (10%)	13 (4%)	6	12

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	VAL
1	A	336	GLU
1	A	357	VAL
1	A	358	ALA
1	A	152	VAL
1	A	178	GLY
1	A	368	ALA
1	A	141	ARG
1	A	142	SER
1	A	177	LYS
1	A	218	SER
1	A	371	ALA
1	A	182	GLN

5.3.2 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	332/334 (99%)	285 (86%)	47 (14%)	5 12

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	53	ARG
1	A	71	LEU
1	A	78	GLN
1	A	79	GLN
1	A	89	ILE
1	A	98	LEU
1	A	99	ARG
1	A	110	ASN
1	A	114	ILE
1	A	116	THR
1	A	130	GLN
1	A	133	MET
1	A	139	LEU
1	A	141	ARG

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Mol	Chain	Res	Type
1	A	147	VAL
1	A	150	SER
1	A	162	TRP
1	A	175	LEU
1	A	180	VAL
1	A	188	LEU
1	A	209	ARG
1	A	219	THR
1	A	220	VAL
1	A	228	THR
1	A	229	ASN
1	A	234	THR
1	A	237	THR
1	A	240	ASP
1	A	273	LEU
1	A	274	THR
1	A	281	LEU
1	A	286	LYS
1	A	292	LEU
1	A	294	ARG
1	A	295	LEU
1	A	296	LEU
1	A	306	GLU
1	A	342	GLN
1	A	351	VAL
1	A	354	SER
1	A	359	SER
1	A	362	THR
1	A	364	VAL
1	A	365	ILE
1	A	379	ARG
1	A	400	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	82	GLN
1	A	123	GLN
1	A	130	GLN
1	A	135	HIS
1	A	146	GLN

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Mol	Chain	Res	Type
1	A	227	GLN
1	A	229	ASN
1	A	326	GLN
1	A	339	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

5 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	NDG	A	403	1,2	12,14,15	0.87	0	15,19,21	1.83	5 (33%)
2	FUC	A	404	2	9,10,11	0.77	0	10,14,16	1.29	1 (10%)
2	NAG	A	405	2	12,14,15	0.64	0	15,19,21	1.34	1 (6%)
2	BMA	A	406	2	10,11,12	0.71	0	11,15,17	1.62	3 (27%)
2	BMA	A	407	2	10,11,12	0.62	0	11,15,17	2.49	3 (27%)

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	NDG	A	403	1,2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FUC	A	404	2	-	0/0/17/20	0/1/1/1
2	NAG	A	405	2	-	0/6/23/26	0/1/1/1
2	BMA	A	406	2	-	0/2/19/22	0/1/1/1
2	BMA	A	407	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	407	BMA	O5-C5-C6	5.85	113.12	106.98
2	A	407	BMA	C3-C4-C5	-4.09	102.90	110.20
2	A	403	NDG	O-C5-C6	3.18	110.32	106.98
2	A	403	NDG	C2-N2-C7	-3.13	117.83	123.09
2	A	406	BMA	C4-C3-C2	2.83	114.30	110.50
2	A	406	BMA	C3-C4-C5	2.66	114.94	110.20
2	A	406	BMA	O5-C5-C6	2.56	109.67	106.98
2	A	403	NDG	C3-C2-N2	2.45	115.48	111.76
2	A	405	NAG	O5-C5-C4	2.41	113.71	110.65
2	A	407	BMA	O4-C4-C5	2.35	115.47	109.28
2	A	403	NDG	O3-C3-C2	-2.31	104.23	109.09
2	A	404	FUC	O3-C3-C2	2.20	113.96	109.94
2	A	403	NDG	C3-C4-C5	-2.12	106.41	110.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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
3	NAG	A	408	1	12,14,15	0.40	0	15,19,21	2.84	6 (40%)

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	408	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	408	NAG	O5-C5-C6	5.75	113.01	106.98
3	A	408	NAG	O5-C5-C4	5.37	117.46	110.65
3	A	408	NAG	C2-N2-C7	4.55	130.72	123.09
3	A	408	NAG	C8-C7-N2	3.85	123.63	116.11
3	A	408	NAG	O7-C7-C8	-3.37	115.47	122.04
3	A	408	NAG	C3-C4-C5	2.28	114.28	110.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	377/379 (99%)	-0.34	10 (2%)	52 57	38, 64, 111, 155	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	357	VAL	4.0
1	A	336	GLU	3.5
1	A	367	SER	3.1
1	A	360	SER	3.0
1	A	359	SER	2.9
1	A	26	HIS	2.9
1	A	27	PRO	2.6
1	A	361	SER	2.3
1	A	358	ALA	2.1
1	A	108	PRO	2.1

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

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

6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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.

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	A	405	14/15	0.16	2.43	65,81,90,90	0
2	BMA	A	406	11/12	0.27	1.59	94,111,125,126	0
2	FUC	A	404	10/11	0.11	0.42	49,57,65,67	0
2	NDG	A	403	14/15	0.09	-0.16	57,64,80,82	0
2	BMA	A	407	11/12	0.31	-	85,109,118,119	0

6.4 Ligands

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	A	408	14/15	0.15	-0.28	65,88,106,122	0

6.5 Other polymers

There are no such residues in this entry.