



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2017 – 01:35 PM EDT

PDB ID : 5M0D
Title : Structure-based evolution of a hybrid steroid series of Autotaxin inhibitors
Authors : Keune, W.-J.; Heidebrecht, T.; Perrakis, A.
Deposited on : unknown
Resolution : 2.40 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

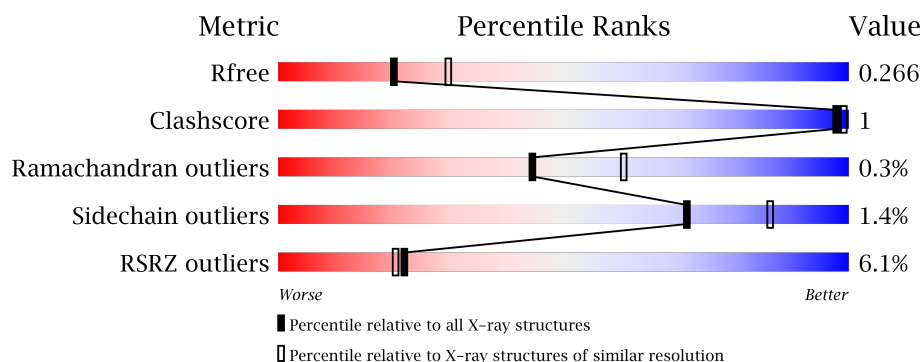
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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	827	<div> <div style="width: 6%; background-color: red;"></div> <div style="width: 90%; background-color: green;"></div> <div style="width: 6%; background-color: yellow;"></div> <div style="width: 0%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></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
10	SCN	A	925	-	-	-	X
11	GOL	A	927	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	GOL	A	929	-	-	-	X
4	MAN	A	908	-	-	-	X

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 6451 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 Ectonucleotide pyrophosphatase/phosphodiesterase family member 2, Ectonucleotide pyrophosphatase/phosphodiesterase family member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	775	Total	C	N	O	S	0	0	0
			6251	3963	1077	1163	48			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	410	ALA	ASN	engineered mutation	UNP Q64610
A	581	PHE	LEU	engineered mutation	UNP Q64610
A	806	ALA	ASN	engineered mutation	UNP Q64610

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



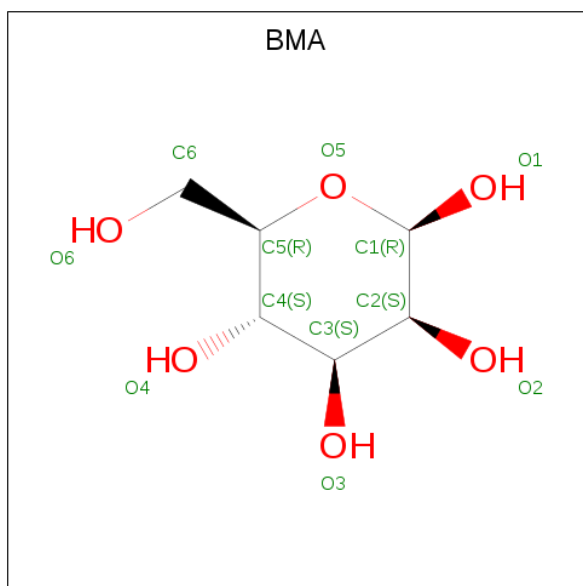
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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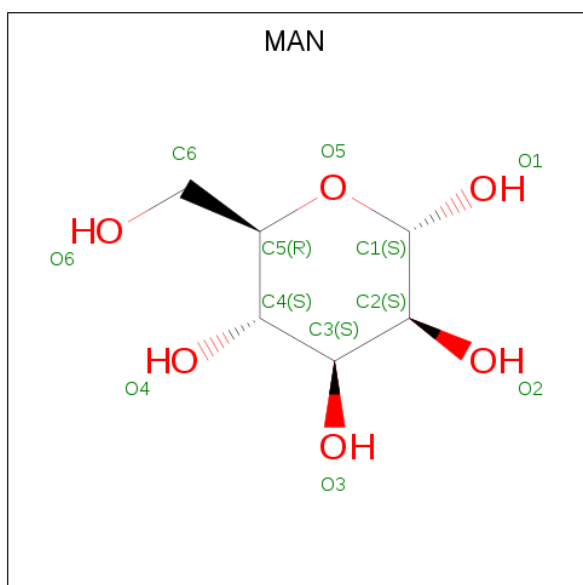
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



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

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



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

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	9	Total I 9 9	0	0

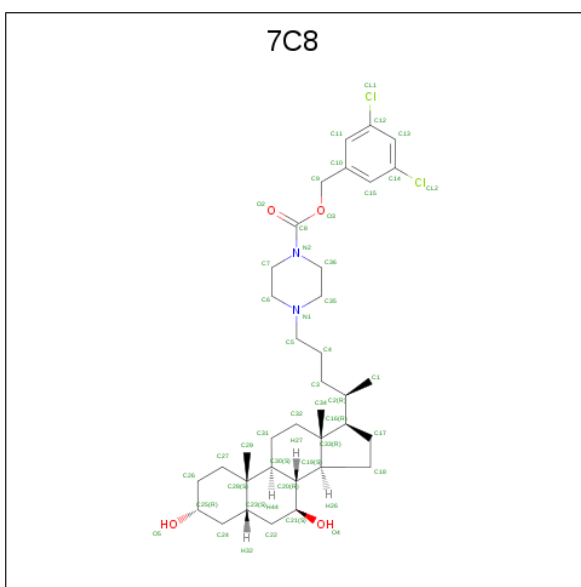
- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	2	Total Zn 2 2	0	0

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Ca 1 1	0	0

- Molecule 8 is [3,5-bis(chloranyl)phenyl]methyl 4-[(4 {R})-4-[(3 {R},5 {S},7 {S},8 {R},9 {S},10 {S},13 {R},14 {S},17 {R})-10,13-dimethyl-3,7-bis(oxidanyl)-2,3,4,5,6,7,8,9,11,12,14,15,16,17-tetradecahydro-1 {H}-cyclopenta[a]phenanthren-17-yl]pentyl]piperazine-1-carboxylate (three-letter code: 7C8) (formula: C₃₆H₅₄Cl₂N₂O₄).

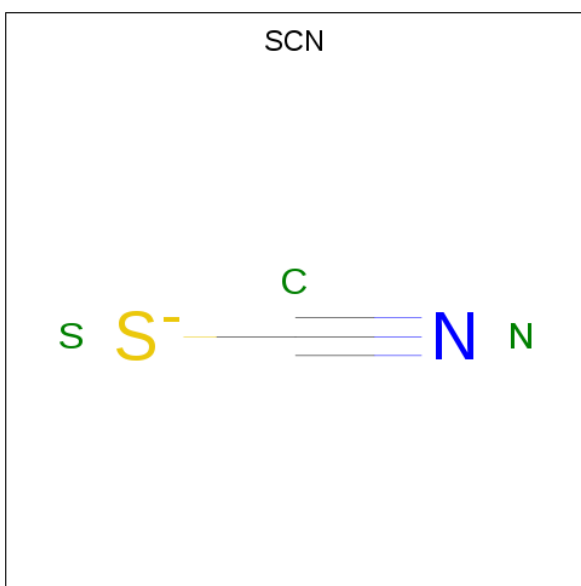


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total 44	C 36	Cl 2	N 2	O 4	0	0

- Molecule 9 is SODIUM ION (three-letter code: NA) (formula: Na).

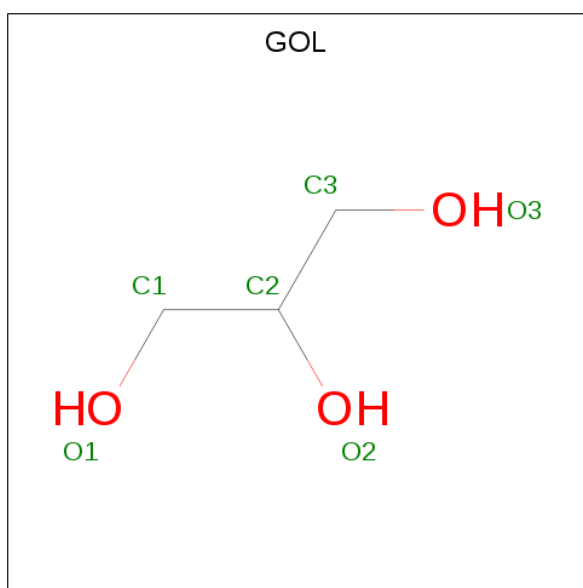
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total Na 1 1	0	0

- Molecule 10 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total C N S 3 1 1 1	0	0
10	A	1	Total C N S 3 1 1 1	0	0
10	A	1	Total C N S 3 1 1 1	0	0
10	A	1	Total C N S 3 1 1 1	0	0

- Molecule 11 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

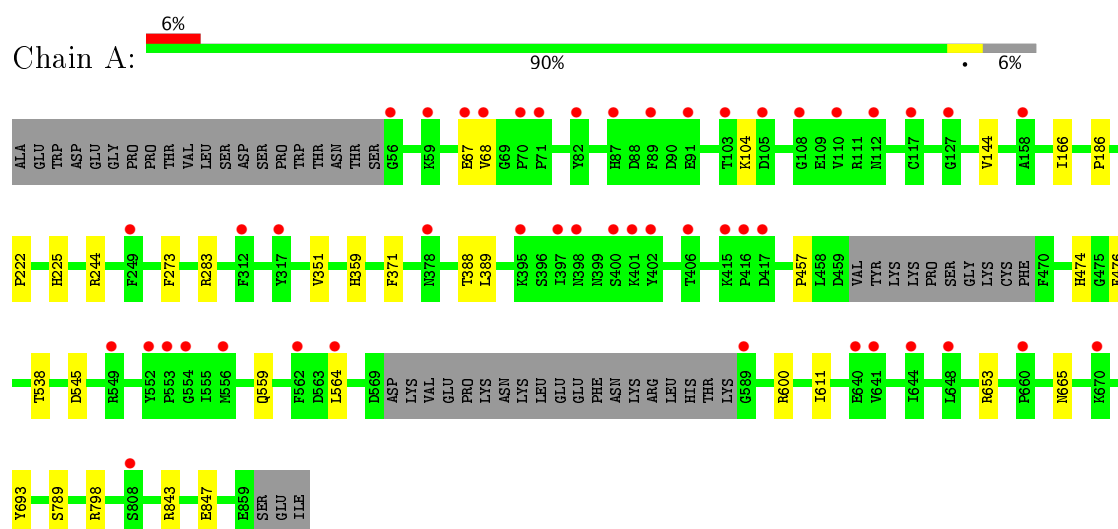
- Molecule 12 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	19	Total O 19 19	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: Ectonucleotide pyrophosphatase/phosphodiesterase family member 2, Ectonucleotide pyrophosphatase/phosphodiesterase family member 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.93Å 88.01Å 77.36Å 90.00° 103.10° 90.00°	Depositor
Resolution (Å)	75.34 – 2.40 45.97 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (75.34-2.40) 99.7 (45.97-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.225 , 0.270 0.225 , 0.266	Depositor DCC
R_{free} test set	1568 reflections (5.13%)	DCC
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	1.529	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 25.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6451	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, BMA, NAG, 7C8, CA, SCN, NA, IOD, 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	A	0.44	0/6428	0.67	0/8720

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	6251	0	6001	11	0
2	A	28	0	24	0	0
3	A	11	0	8	0	0
4	A	55	0	47	0	0
5	A	9	0	0	0	0
6	A	2	0	0	0	0
7	A	1	0	0	0	0
8	A	44	0	0	0	0
9	A	1	0	0	0	0
10	A	12	0	0	0	0
11	A	18	0	24	0	0
12	A	19	0	0	0	0
All	All	6451	0	6104	11	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 1.

All (11) 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:843:ARG:NH1	1:A:847:GLU:OE1	2.35	0.59
1:A:388:THR:HG22	1:A:476:PHE:CZ	2.46	0.51
1:A:144:VAL:HG21	1:A:186:PRO:HB2	1.96	0.48
1:A:166:ILE:HD12	1:A:351:VAL:HG11	1.96	0.47
1:A:222:PRO:HA	1:A:225:HIS:CE1	2.50	0.47
1:A:359:HIS:CE1	1:A:474:HIS:CE1	3.04	0.45
1:A:653:ARG:NH1	1:A:693:TYR:HB3	2.33	0.43
1:A:564:LEU:HB3	1:A:665:ASN:HA	2.01	0.43
1:A:388:THR:HG22	1:A:476:PHE:CE1	2.54	0.42
1:A:600:ARG:HD2	1:A:611:ILE:HD11	2.01	0.41
1:A:371:PHE:CE1	1:A:457:PRO:HA	2.56	0.41

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	769/827 (93%)	729 (95%)	38 (5%)	2 (0%)	44	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	ARG
1	A	68	VAL

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	700 / 749 (94%)	690 (99%)	10 (1%)	71 86

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	GLU
1	A	104	LYS
1	A	244	ARG
1	A	273	PHE
1	A	389	LEU
1	A	538	THR
1	A	545	ASP
1	A	559	GLN
1	A	789	SER
1	A	798	ARG

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 29 ligands modelled in this entry, 13 are monoatomic - leaving 16 for Mogul analysis.

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	901	1,2	14,14,15	0.39	0	15,19,21	1.86	2 (13%)
2	NAG	A	902	3,2	14,14,15	0.88	1 (7%)	15,19,21	0.98	2 (13%)
3	BMA	A	903	2,4	11,11,12	0.31	0	13,15,17	0.93	0
4	MAN	A	904	3	11,11,12	0.51	0	13,15,17	1.14	1 (7%)
4	MAN	A	905	3,4	11,11,12	0.42	0	13,15,17	0.65	0
4	MAN	A	906	4	11,11,12	0.48	0	13,15,17	1.17	1 (7%)
4	MAN	A	907	4	11,11,12	0.32	0	13,15,17	1.01	1 (7%)
4	MAN	A	908	4	11,11,12	0.41	0	13,15,17	1.16	1 (7%)
8	7C8	A	921	-	49,49,49	1.30	3 (6%)	74,74,74	1.71	9 (12%)
10	SCN	A	923	-	1,2,2	0.29	0	0,1,1	0.00	-
10	SCN	A	924	-	1,2,2	0.24	0	0,1,1	0.00	-
10	SCN	A	925	-	1,2,2	0.18	0	0,1,1	0.00	-
10	SCN	A	926	-	1,2,2	0.25	0	0,1,1	0.00	-
11	GOL	A	927	-	5,5,5	0.34	0	5,5,5	0.42	0
11	GOL	A	928	-	5,5,5	0.26	0	5,5,5	0.22	0
11	GOL	A	929	-	5,5,5	0.36	0	5,5,5	0.47	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	901	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	902	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	903	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	904	3	-	0/2/19/22	0/1/1/1
4	MAN	A	905	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	906	4	-	0/2/19/22	0/1/1/1
4	MAN	A	907	4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MAN	A	908	4	-	0/2/19/22	0/1/1/1
8	7C8	A	921	-	-	0/19/90/90	0/6/6/6
10	SCN	A	923	-	-	0/0/0/0	0/0/0/0
10	SCN	A	924	-	-	0/0/0/0	0/0/0/0
10	SCN	A	925	-	-	0/0/0/0	0/0/0/0
10	SCN	A	926	-	-	0/0/0/0	0/0/0/0
11	GOL	A	927	-	-	0/4/4/4	0/0/0/0
11	GOL	A	928	-	-	0/4/4/4	0/0/0/0
11	GOL	A	929	-	-	0/4/4/4	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	902	NAG	O5-C1	-2.89	1.39	1.43
8	A	921	7C8	C12-CL1	2.21	1.79	1.74
8	A	921	7C8	C14-CL2	2.51	1.80	1.74
8	A	921	7C8	O3-C8	7.27	1.48	1.34

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	NAG	O5-C1-C2	-5.01	104.50	111.47
8	A	921	7C8	O3-C8-O2	-3.92	118.02	124.83
2	A	901	NAG	O4-C4-C3	-3.36	103.06	110.36
8	A	921	7C8	C30-C20-C21	-2.67	108.79	111.92
2	A	902	NAG	O5-C1-C2	-2.37	108.17	111.47
8	A	921	7C8	C13-C14-CL2	-2.25	116.33	119.14
8	A	921	7C8	C29-C28-C27	-2.17	104.67	108.24
2	A	902	NAG	O4-C4-C5	-2.01	104.23	109.28
8	A	921	7C8	C16-C33-C19	2.05	102.52	100.07
8	A	921	7C8	C7-N2-C36	2.41	117.16	112.61
4	A	904	MAN	C1-C2-C3	2.42	112.72	109.65
4	A	907	MAN	C1-O5-C5	2.83	116.07	112.17
4	A	906	MAN	C1-O5-C5	2.94	116.21	112.17
4	A	908	MAN	C1-O5-C5	3.03	116.35	112.17
8	A	921	7C8	C9-O3-C8	3.15	124.65	115.65
8	A	921	7C8	C15-C14-CL2	3.56	123.60	119.14
8	A	921	7C8	O3-C8-N2	9.66	120.00	111.66

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	775/827 (93%)	0.49	47 (6%) 22 20	37, 59, 85, 102	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	554	GLY	5.6
1	A	110	VAL	5.0
1	A	397	ILE	4.7
1	A	68	VAL	3.9
1	A	562	PHE	3.7
1	A	640	GLU	3.6
1	A	417	ASP	3.5
1	A	103	THR	3.4
1	A	401	LYS	3.3
1	A	402	TYR	3.3
1	A	556	MET	3.3
1	A	641	VAL	3.2
1	A	108	GLY	3.0
1	A	398	ASN	3.0
1	A	59	LYS	3.0
1	A	70	PRO	2.9
1	A	82	TYR	2.9
1	A	589	GLY	2.8
1	A	549	ARG	2.7
1	A	87	HIS	2.7
1	A	112	ASN	2.7
1	A	89	PHE	2.6
1	A	553	PRO	2.5
1	A	312	PHE	2.5
1	A	670	LYS	2.4
1	A	105	ASP	2.4
1	A	127	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	56	GLY	2.4
1	A	660	PRO	2.4
1	A	71	PRO	2.4
1	A	378	ASN	2.4
1	A	564	LEU	2.3
1	A	91	GLU	2.3
1	A	415	LYS	2.3
1	A	808	SER	2.2
1	A	67	GLU	2.2
1	A	317	TYR	2.2
1	A	552	TYR	2.2
1	A	400	SER	2.2
1	A	416	PRO	2.2
1	A	158	ALA	2.1
1	A	406	THR	2.1
1	A	249	PHE	2.1
1	A	644	ILE	2.1
1	A	648	LEU	2.1
1	A	117	CYS	2.0
1	A	395	LYS	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](#)

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. 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
11	GOL	A	927	6/6	0.65	0.31	5.28	63,63,66,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
11	GOL	A	929	6/6	0.82	0.31	4.65	69,72,73,76	0
4	MAN	A	908	11/12	0.72	0.26	3.03	62,66,68,69	0
10	SCN	A	925	3/3	0.87	0.23	2.05	68,68,69,70	0
8	7C8	A	921	44/44	0.87	0.23	0.85	81,83,85,85	0
7	CA	A	920	1/1	0.97	0.18	0.64	45,45,45,45	0
11	GOL	A	928	6/6	0.52	0.27	0.57	79,84,85,85	0
2	NAG	A	901	14/15	0.96	0.20	0.40	40,41,43,44	0
5	IOD	A	909	1/1	1.00	0.16	-0.29	64,64,64,64	0
5	IOD	A	911	1/1	0.61	0.21	-0.45	154,154,154,154	1
6	ZN	A	918	1/1	0.99	0.14	-0.61	75,75,75,75	0
9	NA	A	922	1/1	0.93	0.10	-1.53	69,69,69,69	0
4	MAN	A	906	11/12	0.94	0.14	-1.60	62,63,66,67	0
6	ZN	A	919	1/1	0.95	0.10	-1.85	115,115,115,115	0
5	IOD	A	913	1/1	0.85	0.14	-2.26	140,140,140,140	1
5	IOD	A	910	1/1	0.99	0.09	-2.60	79,79,79,79	1
5	IOD	A	914	1/1	0.99	0.06	-2.76	103,103,103,103	1
5	IOD	A	912	1/1	0.99	0.06	-2.92	109,109,109,109	1
5	IOD	A	916	1/1	0.97	0.07	-3.82	92,92,92,92	1
2	NAG	A	902	14/15	0.97	0.16	-	46,47,49,52	0
5	IOD	A	917	1/1	0.99	0.11	-	81,81,81,81	1
4	MAN	A	905	11/12	0.87	0.18	-	60,62,64,65	0
5	IOD	A	915	1/1	0.99	0.05	-	84,84,84,84	1
10	SCN	A	923	3/3	0.82	0.25	-	69,69,70,70	0
10	SCN	A	924	3/3	0.79	0.14	-	65,65,66,69	0
10	SCN	A	926	3/3	0.36	0.30	-	99,99,100,102	0
4	MAN	A	904	11/12	0.83	0.19	-	60,62,64,65	0
3	BMA	A	903	11/12	0.92	0.17	-	55,58,61,61	0
4	MAN	A	907	11/12	0.93	0.14	-	60,61,63,64	0

6.5 Other polymers ⓘ

There are no such residues in this entry.