

# wwPDB X-ray Structure Validation Summary Report (i)

#### Dec 19, 2022 – 03:16 pm GMT

PDB ID	:	7P4J
Title	:	Crystal structure of Autotaxin and tetrahydrocannabinol
Authors	:	Eymery, M.C.; McCarthy, A.A.; Hausmann, J.
Deposited on		
Resolution	:	1.79 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

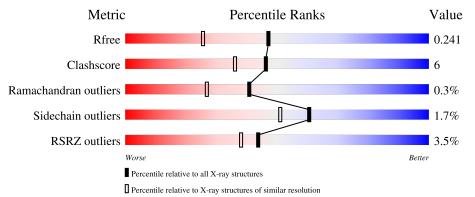
MolProbity		4 02b-467
·		
Mogul	:	1.8.4, CSD as $541$ be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.31.3
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.79 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	5950(1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	А	827	3% 	15%	• 7%				
2	В	2	100%						



# 2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 6792 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.

Mol	Chain	Residues		Α	toms			ZeroOcc	AltConf	Trace
1	А	770	Total 6222	C 3950	N 1073	0 1150	S 49	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	410	ALA	ASN	engineered mutation	UNP Q64610
А	581	PHE	LEU	engineered mutation	UNP Q64610
А	591	THR	ARG	engineered mutation	UNP Q64610
А	806	ALA	ASN	engineered mutation	UNP Q64610

• Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.



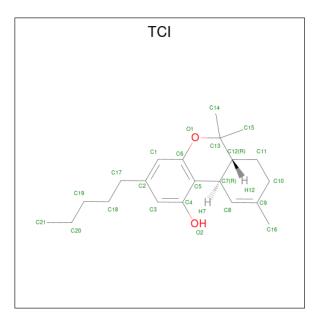
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
2	В	2	Total         C         N           28         16         2	N O 2 10	0	0	0

• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atom	s	ZeroOcc	AltConf
3	А	2	Total 2	Zn 2	0	0

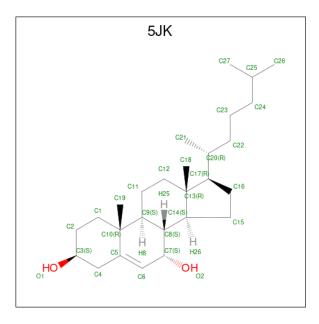
• Molecule 4 is (6aR,10aR)-6,6,9-trimethyl-3-pentyl-6a,7,8,10a-tetrahydro-6H-benzo[c]chro men-1-ol (three-letter code: TCI) (formula: C<sub>21</sub>H<sub>30</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	А	1	Total 23	C 21	O2	0	0

• Molecule 5 is 7alpha-hydroxycholesterol (three-letter code: 5JK) (formula:  $C_{27}H_{46}O_2$ ).



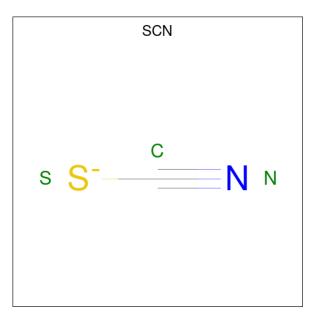
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
5	А	1	Total 29	C 27	O 2	0	0

• Molecule 6 is IODIDE ION (three-letter code: IOD) (formula: I).



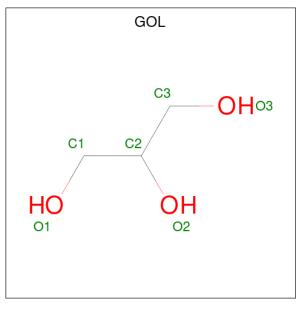
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	19	Total I 19 19	0	0

• Molecule 7 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	1	$\begin{array}{cccc} \text{Total} & \text{C} & \text{N} & \text{S} \\ 3 & 1 & 1 & 1 \end{array}$	0	0
7	А	1	Total         C         N         S           3         1         1         1	0	0

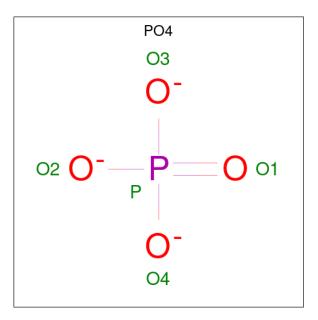
• Molecule 8 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0

• Molecule 9 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
0	Λ	1	Total	0	Р	0	0
9	Л	1	5	4	1	0	0

• Molecule 10 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	2	Total Ca 2 2	0	0



• Molecule 11 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	А	1	Total Na 1 1	0	0

• Molecule 12 is water.

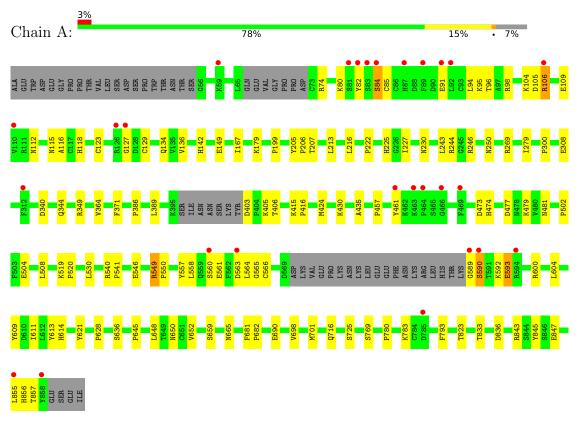
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	А	407	Total         O           407         407	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

 $\bullet$  Molecule 1: Ectonucleotide pyrophosphatase/phosphodiesterase family member 2



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

100%

NAG1 NAG2



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	53.70Å 60.98Å 63.60Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$103.15^{\circ}$ $97.39^{\circ}$ $94.23^{\circ}$	Depositor
Resolution (Å)	61.24 - 1.79	Depositor
Resolution (A)	61.24 - 1.79	EDS
% Data completeness	65.9 (61.24-1.79)	Depositor
(in resolution range)	65.9(61.24-1.79)	EDS
R <sub>merge</sub>	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.24 (at 1.80 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.17_3644	Depositor
D D.	0.183 , $0.241$	Depositor
$R, R_{free}$	0.183 , $0.241$	DCC
$R_{free}$ test set	2005 reflections $(4.19%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	20.1	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.40,67.0	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.51, < L^2>=0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6792	wwPDB-VP
Average B, all atoms $(Å^2)$	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.44% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: ZN, SCN, PO4, NAG, NA, GOL, CA, TCI, IOD, 5JK

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).

Mal	Chain	Bond lengths		Bond angles	
Mol Chair	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.42	0/6398	0.60	2/8674~(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	А	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	А	540	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	А	540	ARG	NE-CZ-NH1	5.83	123.21	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	590	SER	Peptide
1	А	593	GLU	Peptide
1	А	82	TYR	Peptide

#### 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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	6222	0	5984	78	1
2	В	28	0	25	0	0
3	А	2	0	0	0	0
4	А	23	0	29	3	0
5	А	29	0	0	0	0
6	А	19	0	0	2	0
7	А	6	0	0	0	0
8	А	48	0	64	7	0
9	А	5	0	0	0	0
10	А	2	0	0	0	0
11	А	1	0	0	0	0
12	А	407	0	0	5	1
All	All	6792	0	6102	79	2

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.

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 6.

The worst 5 of 79 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:592:LYS:HD3	1:A:613:TYR:HB3	1.49	0.94
1:A:134:GLN:OE1	1:A:344:GLN:NE2	2.04	0.89
1:A:558:LEU:N	1:A:561:GLU:OE1	2.17	0.73
1:A:564:LEU:HB2	6:A:926:IOD:I	2.60	0.72
1:A:519:LYS:NZ	12:A:1002:HOH:O	2.23	0.71

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:GLU:OE2	1:A:549:ARG:NH2[1_656]	1.87	0.33
12:A:1270:HOH:O	12:A:1321:HOH:O[1_666]	2.14	0.06



## 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 Allowe		Outliers	Percentiles	
1	А	763/827~(92%)	733~(96%)	28~(4%)	2~(0%)	41 27	

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	84	SER
1	А	386	PRO

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	696/749~(93%)	684~(98%)	12 (2%)	60 51	

5 of 12 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	А	479	LYS
1	А	549	ARG
1	А	856	HIS
1	А	560	SER
1	А	244	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:



Mol	Chain	Res	Type
1	А	326	ASN
1	А	474	HIS

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

#### 5.5 Carbohydrates (i)

2 monosaccharides 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).

Mal	Mol Type Chain I	Dec	Link	Bo	Bond lengths			Bond angles		
IVIOI	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
2	NAG	В	1	2,1	14,14,15	0.29	0	$17,\!19,\!21$	0.63	0
2	NAG	В	2	2	14,14,15	0.43	0	17,19,21	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	В	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	В	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

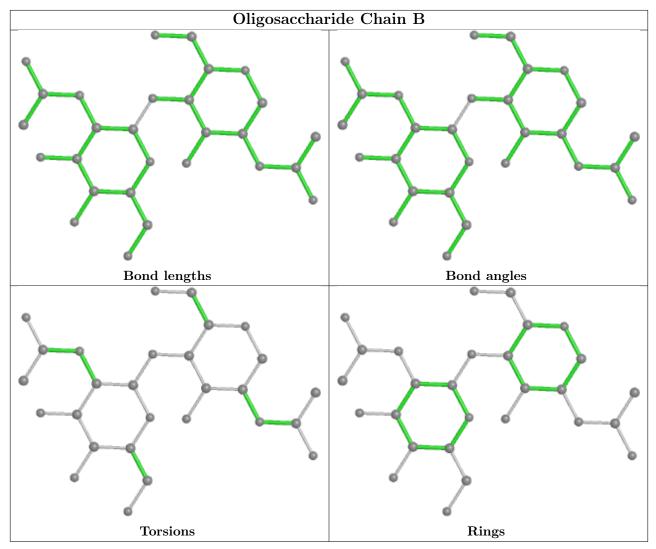
There are no torsion outliers.



There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



#### 5.6 Ligand geometry (i)

Of 37 ligands modelled in this entry, 24 are monoatomic - leaving 13 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	Turne	Chain	Res	Link	B	ond leng	gths	B	ond ang	gles
10101	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	TCI	А	903	-	$25,\!25,\!25$	0.29	0	32,37,37	0.67	1 (3%)
8	GOL	А	910	-	$5,\!5,\!5$	0.87	0	$5,\!5,\!5$	0.93	0
8	GOL	А	916	-	$5,\!5,\!5$	0.94	0	$5,\!5,\!5$	0.73	0
7	SCN	А	917	-	1,2,2	1.37	0	0,1,1	-	-
8	GOL	А	914	-	$5,\!5,\!5$	0.75	0	$5,\!5,\!5$	0.97	0
8	GOL	А	912	-	$5,\!5,\!5$	1.34	1 (20%)	$5,\!5,\!5$	1.01	0
8	GOL	А	913	-	$5,\!5,\!5$	0.57	0	$5,\!5,\!5$	0.99	0
8	GOL	А	918	-	$5,\!5,\!5$	0.98	0	$5,\!5,\!5$	1.19	0
7	SCN	А	909	-	1,2,2	0.72	0	0,1,1	-	-
5	5JK	А	904	-	32,32,32	<mark>3.91</mark>	12 (37%)	47,50,50	3.28	13 (27%)
8	GOL	А	919	-	$5,\!5,\!5$	0.60	0	$5,\!5,\!5$	1.04	0
8	GOL	А	911	-	$5,\!5,\!5$	1.08	0	$5,\!5,\!5$	0.67	0
9	PO4	А	915	3	4,4,4	0.69	0	6,6,6	0.71	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	TCI	А	903	-	-	3/5/33/33	0/3/3/3
8	GOL	А	910	-	-	3/4/4/4	-
8	GOL	А	916	-	-	1/4/4/4	-
8	GOL	А	914	-	-	2/4/4/4	-
8	GOL	А	912	-	-	2/4/4/4	-
8	GOL	А	913	-	-	3/4/4/4	-
8	GOL	А	918	-	-	2/4/4/4	-
5	5JK	А	904	-	-	0/10/71/71	0/4/4/4
8	GOL	А	919	-	-	0/4/4/4	-
8	GOL	А	911	-	-	0/4/4/4	-

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	А	904	5JK	C6-C5	13.67	1.57	1.33
5	А	904	5JK	C8-C7	8.02	1.62	1.53
5	А	904	5JK	C16-C15	6.36	1.71	1.54
5	А	904	5JK	C20-C17	-6.16	1.43	1.54
5	А	904	5JK	C13-C17	5.56	1.65	1.55



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
5	А	904	5JK	C7-C6-C5	-18.40	113.45	125.42
5	А	904	5JK	C16-C17-C20	-4.15	105.72	112.15
5	А	904	5JK	C22-C20-C17	-4.13	101.75	110.28
5	А	904	5JK	C17-C13-C14	3.97	104.78	100.07
5	А	904	5JK	C12-C13-C17	3.73	122.15	116.57

The worst 5 of 14 bond angle outliers are listed below:

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	А	910	GOL	C1-C2-C3-O3
8	А	912	GOL	O1-C1-C2-C3
8	А	913	GOL	O1-C1-C2-C3
8	А	914	GOL	C1-C2-C3-O3
8	А	913	GOL	O1-C1-C2-O2

There are no ring outliers.

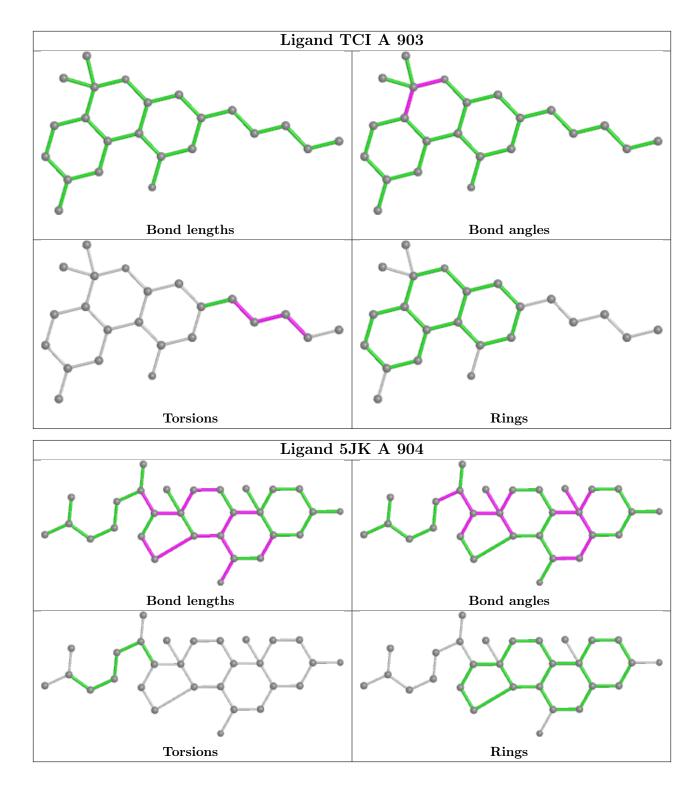
7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	903	TCI	3	0
8	А	916	GOL	1	0
8	А	914	GOL	1	0
8	А	912	GOL	2	0
8	А	913	GOL	1	0
8	А	918	GOL	1	0
8	А	919	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







### 5.7 Other polymers (i)

There are no such residues in this entry.



## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 6 Fit of model and data (i)

## 6.1 Protein, DNA and RNA chains (i)

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,  $95^{th}$  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	< <b>RSRZ</b> >	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	770/827~(93%)	0.01	27 (3%) 44 38	10, 22, 43, 57	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	461	TYR	5.8
1	А	469	PHE	5.3
1	А	83	SER	4.9
1	А	464	PRO	4.3
1	А	590	SER	3.9

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

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

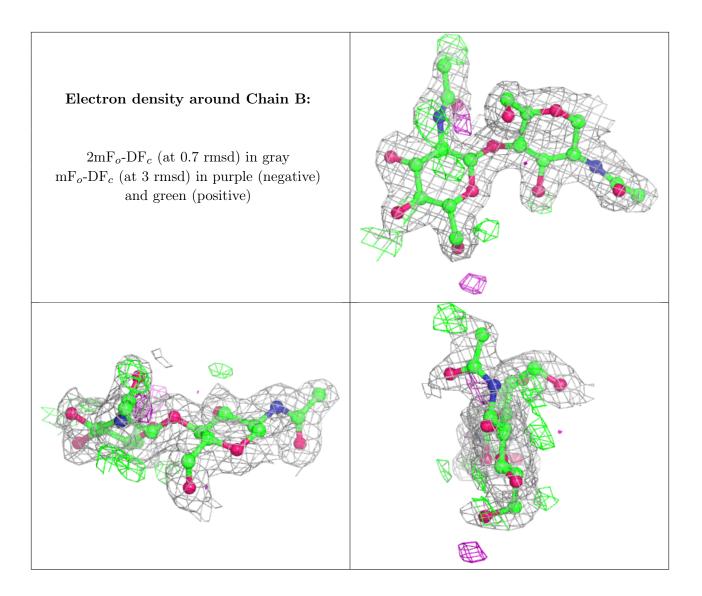
#### 6.3 Carbohydrates (i)

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. The B-factors column lists the minimum, median,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	NAG	В	2	14/15	0.82	0.13	30,32,42,46	0
2	NAG	В	1	14/15	0.97	0.07	13,18,21,23	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





#### 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,  $95^{th}$  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
8	GOL	А	910	6/6	0.56	0.34	$50,\!53,\!59,\!59$	0
9	PO4	А	915	5/5	0.69	0.18	23,30,43,57	0
8	GOL	А	914	6/6	0.84	0.20	32,34,45,49	0
7	SCN	А	917	3/3	0.87	0.20	13,13,28,69	0
8	GOL	А	911	6/6	0.87	0.25	27,30,34,36	0
8	GOL	А	918	6/6	0.89	0.36	23,28,29,30	0
4	TCI	А	903	23/23	0.90	0.16	17,29,37,40	0
6	IOD	А	925	1/1	0.90	0.09	118,118,118,118	0

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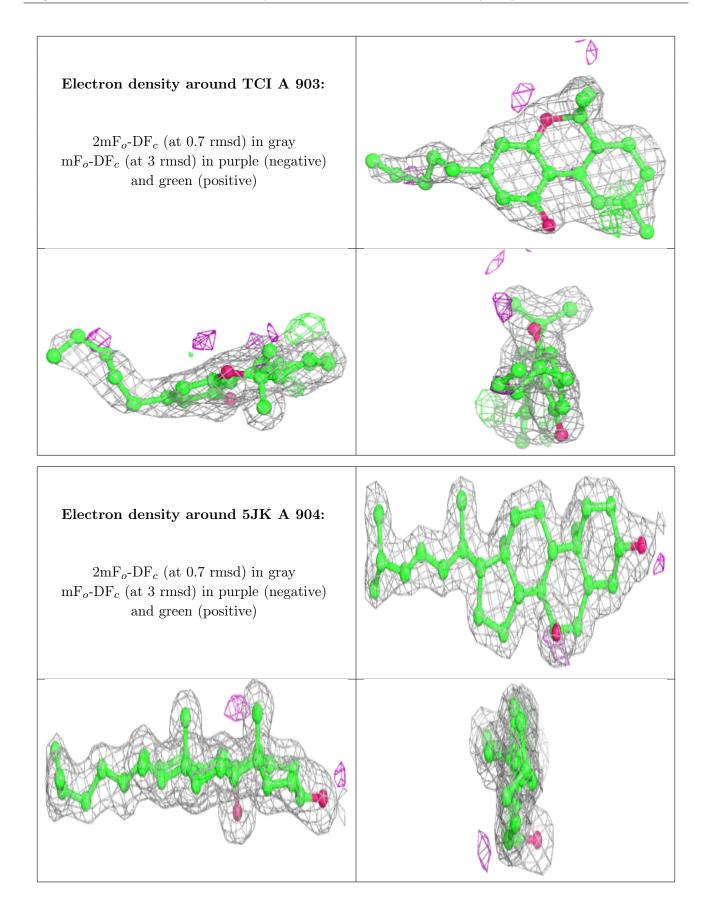


Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	IOD	А	927	1/1	0.90	0.14	117,117,117,117	0
8	GOL	А	919	6/6	0.91	0.10	29,34,41,42	0
7	SCN	А	909	3/3	0.93	0.08	34,34,36,46	0
6	IOD	А	931	1/1	0.93	0.04	64,64,64,64	1
8	GOL	А	916	6/6	0.94	0.13	16,23,25,30	0
8	GOL	А	912	6/6	0.94	0.14	17,24,26,29	0
8	GOL	А	913	6/6	0.95	0.09	21,24,26,28	0
5	5JK	А	904	29/29	0.95	0.09	11,18,23,30	0
6	IOD	А	920	1/1	0.96	0.07	89,89,89,89	0
6	IOD	А	934	1/1	0.97	0.06	54,54,54,54	1
6	IOD	А	908	1/1	0.97	0.06	108,108,108,108	0
6	IOD	А	922	1/1	0.98	0.07	33,33,33,33	1
6	IOD	А	926	1/1	0.98	0.03	$50,\!50,\!50,\!50$	0
6	IOD	А	932	1/1	0.98	0.08	37,37,37,37	1
10	CA	А	936	1/1	0.98	0.04	49,49,49,49	0
11	NA	А	937	1/1	0.98	0.16	$14,\!14,\!14,\!14$	0
6	IOD	А	921	1/1	0.99	0.08	38, 38, 38, 38	1
3	ZN	А	902	1/1	0.99	0.06	16, 16, 16, 16	1
6	IOD	А	928	1/1	0.99	0.06	$31,\!31,\!31,\!31$	1
6	IOD	А	929	1/1	0.99	0.06	41,41,41,41	1
6	IOD	А	923	1/1	0.99	0.09	33,33,33,33	1
6	IOD	А	905	1/1	0.99	0.12	21,21,21,21	1
6	IOD	А	933	1/1	0.99	0.02	73,73,73,73	1
6	IOD	А	924	1/1	1.00	0.13	$17,\!17,\!17,\!17$	1
6	IOD	А	907	1/1	1.00	0.10	$25,\!25,\!25,\!25$	1
6	IOD	А	930	1/1	1.00	0.12	18,18,18,18	1
10	CA	А	935	1/1	1.00	0.10	$15,\!15,\!15,\!15$	0
3	ZN	А	901	1/1	1.00	0.09	16, 16, 16, 16	1
6	IOD	А	906	1/1	1.00	0.12	16, 16, 16, 16	1

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The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.







## 6.5 Other polymers (i)

There are no such residues in this entry.

