

wwPDB X-ray Structure Validation Summary Report (i)

Oct 9, 2023 – 08:11 PM EDT

PDB ID : 6XKD

Title: Structure of ligand-bound mouse cGAMP hydrolase ENPP1

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Deposited on : 2020-06-26

Resolution : 3.20 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 : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.35.1buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

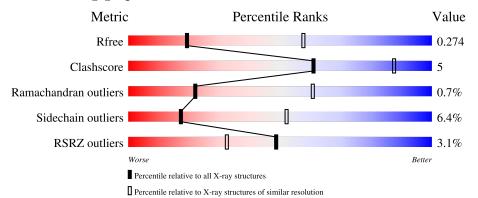
Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.20 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	A	823	68%	13%	17%
1	В	823	69%	12%	17%
2	С	4	100%		
2	D	4	100%		



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 10875 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 1.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace
1	A	679	Total 5374	C 3466	N 882	O 997	S 29	0	0	0
1	В	681	Total 5308	C 3436	N 870	O 976	S 26	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	83	TRP	-	expression tag	UNP G3X9S2
A	84	THR	-	expression tag	UNP G3X9S2
A	85	ASN	-	expression tag	UNP G3X9S2
A	86	THR	-	expression tag	UNP G3X9S2
A	87	SER	-	expression tag	UNP G3X9S2
A	88	GLY	-	expression tag	UNP G3X9S2
A	89	SER	-	expression tag	UNP G3X9S2
A	90	CYS	-	expression tag	UNP G3X9S2
A	91	ARG	-	expression tag	UNP G3X9S2
В	83	TRP	-	expression tag	UNP G3X9S2
В	84	THR	-	expression tag	UNP G3X9S2
В	85	ASN	-	expression tag	UNP G3X9S2
В	86	THR	-	expression tag	UNP G3X9S2
В	87	SER	-	expression tag	UNP G3X9S2
В	88	GLY	-	expression tag	UNP G3X9S2
В	89	SER	-	expression tag	UNP G3X9S2
В	90	CYS	-	expression tag	UNP G3X9S2
В	91	ARG	_	expression tag	UNP G3X9S2

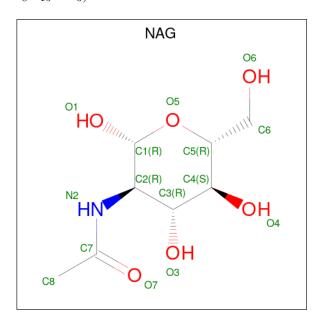
• Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranos e-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.





Mol	Chain	Residues	A	ton	ıs	ZeroOcc	AltConf	Trace
2	С	4	Total 50			0	0	0
2	D	4	Total 50	C 28		0	0	0

• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	Δ	1	Total	С	N	О	0	0	
3	Λ	1	14	8	1	5			
9	۸	1	Total	С	N	О	0	0	
3	A	1	14	8	1	5	0	U	

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

N	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	4	A	2	Total Zn 2 2	0	0
	4	В	2	Total Zn 2 2	0	0

• Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

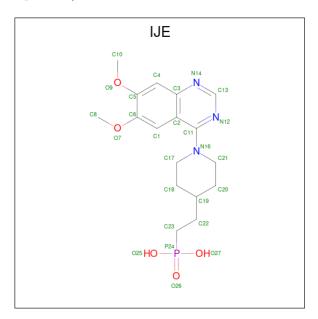


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Ca 1 1	0	0
5	В	1	Total Ca 1 1	0	0

• Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Cl 1 1	0	0

• Molecule 7 is $\{2-[1-(6,7-dimethoxyquinazolin-4-yl)piperidin-4-yl]ethyl\}$ phosphonic acid (three-letter code: IJE) (formula: $C_{17}H_{24}N_3O_5P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ato	oms		ZeroOcc	AltConf
7	A	1	Total 26		N 3	P 1	0	0

• Molecule 8 is water.

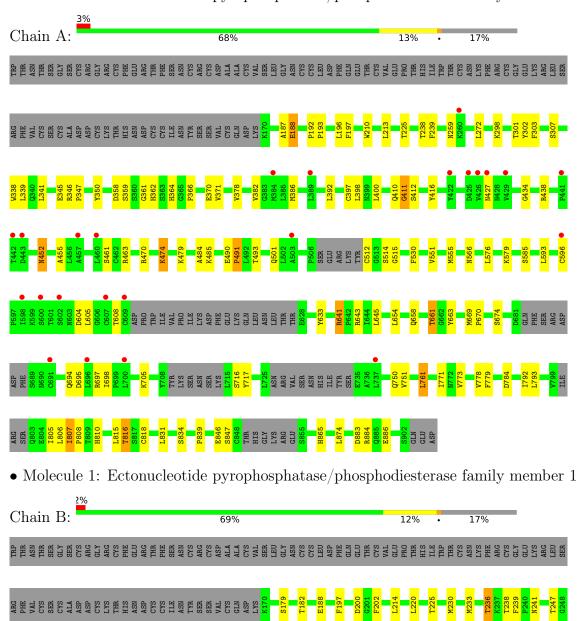
\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
8	A	18	Total O 18 18	0	0
8	В	14	Total O 14 14	0	0



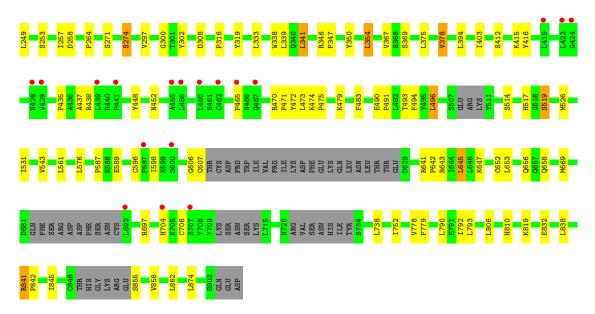
3 Residue-property plots (i)

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.

• Molecule 1: Ectonucleotide pyrophosphatase/phosphodiesterase family member 1







 \bullet Molecule 2: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C: 100%

NAG1 NAG2 BMA3 MAN4

 $\bullet \ \, Molecule \ 2: \ alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyrano$

Chain D: 100%

NAG1 NAG2 BMA3 MAN4



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants	102.35Å 102.35Å 172.89Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.64 - 3.20	Depositor
Resolution (A)	51.18 - 3.20	EDS
% Data completeness	91.7 (30.64-3.20)	Depositor
(in resolution range)	91.8 (51.18-3.20)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$< I/\sigma(I) > 1$	$1.90 \; (at \; 3.19 \text{Å})$	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.201 , 0.273	Depositor
it, it free	0.202 , 0.274	DCC
R_{free} test set	1522 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	64.3	Xtriage
Anisotropy	0.353	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 56.8	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
	0.015 for -h,-k,l	
Estimated twinning fraction	0.043 for h,-h-k,-l	Xtriage
	0.026 for -k,-h,-l	
F_o, F_c correlation	0.92	EDS
Total number of atoms	10875	wwPDB-VP
Average B, all atoms (\mathring{A}^2)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.84% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities 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: BMA, CL, NAG, MAN, CA, ZN, IJE

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.47	0/5530	0.67	0/7539	
1	В	0.46	0/5465	0.67	1/7465~(0.0%)	
All	All	0.46	0/10995	0.67	1/15004 (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	$Observed(^o)$	$Ideal(^{o})$
1	В	855	SER	N-CA-CB	6.13	119.70	110.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	411	GLY	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 atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within



the	asvmmetric	unit.	whereas S	Svmm-	Clashes	lists s	vmmetr	v-related	clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5374	0	5119	52	0
1	В	5308	0	5006	43	0
2	С	50	0	43	0	0
2	D	50	0	43	0	0
3	A	28	0	26	0	0
4	A	2	0	0	0	0
4	В	2	0	0	0	0
5	A	1	0	0	0	0
5	В	1	0	0	0	0
6	A	1	0	0	0	0
7	A	26	0	0	3	0
8	A	18	0	0	0	0
8	В	14	0	0	0	0
All	All	10875	0	10237	95	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 5.

The worst 5 of 95 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:A:778:VAL:HB	1:A:810:HIS:HB2	1.73	0.71
1:A:238:THR:OG1	7:A:1011:IJE:O26	2.12	0.67
1:A:438:ARG:HG2	1:A:493:THR:HG22	1.77	0.66
1:A:238:THR:OG1	7:A:1011:IJE:P24	2.55	0.65
1:A:193:PRO:HG2	1:A:398:LEU:HD12	1.79	0.63

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	P	erce	entiles
1	A	663/823 (81%)	602 (91%)	58 (9%)	3 (0%)		29	67
1	В	667/823 (81%)	616 (92%)	45 (7%)	6 (1%)		17	56
All	All	1330/1646 (81%)	1218 (92%)	103 (8%)	9 (1%)		22	61

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	188	GLU
1	A	303	PHE
1	В	465	PRO
1	В	606	GLY
1	В	179	SER

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	Rotameric Outliers	
1	A	593/755 (78%)	555 (94%)	38 (6%)	17 52
1	В	570/755 (76%)	533 (94%)	37 (6%)	17 51
All	All	1163/1510 (77%)	1088 (94%)	75 (6%)	17 52

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	496	LEU
1	В	832	GLU
1	В	519	SER
1	В	658	GLN
1	A	658	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	452	ASN

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Mol	Chain	Res	Type
1	В	482	HIS
1	В	810	HIS
1	В	583	ASN
1	A	885	GLN

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)

8 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).

Mol	Type	Chain	Res	Link	Вс	ond leng	ths	В	ond ang	les
WIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	С	1	1,2	14,14,15	0.59	0	17,19,21	1.43	3 (17%)
2	NAG	С	2	2	14,14,15	0.40	0	17,19,21	1.32	1 (5%)
2	BMA	С	3	2	11,11,12	0.57	0	15,15,17	1.40	1 (6%)
2	MAN	С	4	2	11,11,12	0.76	0	15,15,17	1.52	3 (20%)
2	NAG	D	1	1,2	14,14,15	0.45	0	17,19,21	1.60	4 (23%)
2	NAG	D	2	2	14,14,15	0.56	0	17,19,21	1.39	2 (11%)
2	BMA	D	3	2	11,11,12	0.93	1 (9%)	15,15,17	1.11	1 (6%)
2	MAN	D	4	2	11,11,12	0.76	0	15,15,17	1.48	2 (13%)

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	С	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	С	2	2	-	0/6/23/26	0/1/1/1
2	BMA	С	3	2	-	0/2/19/22	0/1/1/1
2	MAN	С	4	2	-	2/2/19/22	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	D	3	BMA	C2-C3	2.09	1.55	1.52

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
2	D	2	NAG	C1-O5-C5	4.56	118.37	112.19
2	С	2	NAG	C1-O5-C5	4.53	118.33	112.19
2	D	1	NAG	C1-O5-C5	3.99	117.59	112.19
2	D	4	MAN	C1-C2-C3	3.93	114.49	109.67
2	С	3	BMA	C3-C4-C5	3.62	116.70	110.24

There are no chirality outliers.

All (5) torsion outliers are listed below:

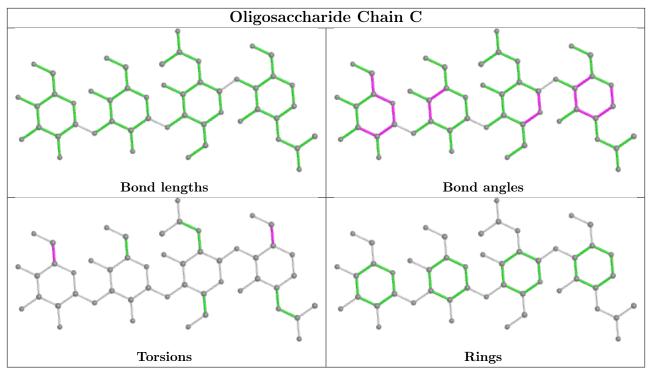
Mol	Chain	Res	Type	Atoms
2	С	4	MAN	O5-C5-C6-O6
2	С	4	MAN	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	С	1	NAG	O5-C5-C6-O6

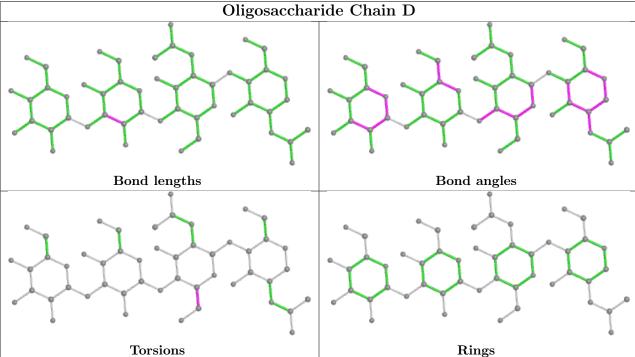
There are no ring outliers.

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 10 ligands modelled in this entry, 7 are monoatomic - leaving 3 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	Во	ond leng	ths	Е	ond ang	gles
WIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	1005	1	14,14,15	0.65	0	17,19,21	1.61	3 (17%)
7	IJE	A	1011	4	28,28,28	1.74	7 (25%)	39,40,40	2.50	13 (33%)
3	NAG	A	1006	1	14,14,15	0.72	0	17,19,21	0.99	1 (5%)

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	1005	1	-	0/6/23/26	0/1/1/1
7	IJE	A	1011	4	-	8/14/24/24	0/3/3/3
3	NAG	A	1006	1	-	0/6/23/26	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
7	A	1011	IJE	C6-C5	4.14	1.49	1.40
7	A	1011	IJE	P24-C23	3.69	1.82	1.78
7	A	1011	IJE	C2-C3	3.56	1.48	1.42
7	A	1011	IJE	P24-O26	2.97	1.56	1.50
7	A	1011	IJE	C4-C3	-2.89	1.37	1.41

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
7	A	1011	IJE	O9-C5-C4	-7.94	114.97	125.24
7	A	1011	IJE	O9-C5-C6	6.13	123.95	115.41
7	A	1011	IJE	O7-C6-C1	-4.73	119.13	125.24
3	A	1005	NAG	C4-C3-C2	4.19	117.17	111.02
7	A	1011	IJE	C10-O9-C5	-3.99	111.50	117.53

There are no chirality outliers.

5 of 8 torsion outliers are listed below:



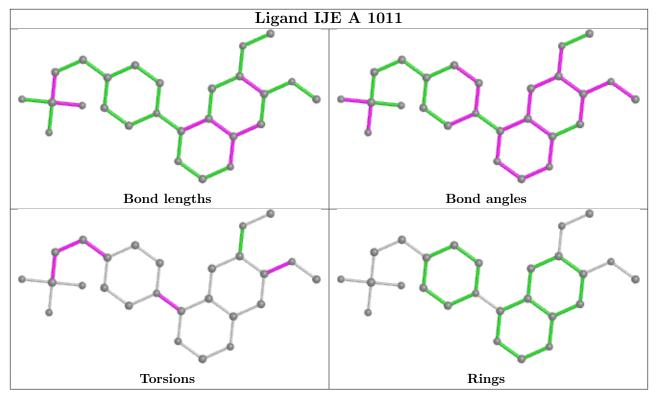
Mol	Chain	Res	Type	Atoms
7	A	1011	IJE	C22-C23-P24-O25
7	A	1011	IJE	C22-C23-P24-O26
7	A	1011	IJE	C19-C22-C23-P24
7	A	1011	IJE	C2-C11-N16-C21
7	A	1011	IJE	N12-C11-N16-C21

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1011	IJE	3	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	<RSRZ $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	679/823 (82%)	0.12	24 (3%) 44 28	36, 64, 100, 132	0
1	В	681/823 (82%)	0.01	18 (2%) 56 40	36, 64, 96, 123	0
All	All	1360/1646 (82%)	0.06	42 (3%) 49 32	36, 64, 98, 132	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	600	SER	3.9
1	A	609	CYS	3.8
1	A	602	SER	3.7
1	В	467	GLN	3.5
1	A	442	THR	3.5

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	$\operatorname{B-factors}({\c A}^2)$	Q < 0.9
2	BMA	D	3	11/12	0.73	0.23	103,109,117,117	0
2	MAN	D	4	11/12	0.73	0.30	110,118,120,129	0
2	MAN	С	4	11/12	0.89	0.15	94,95,97,97	0
2	NAG	D	2	14/15	0.90	0.18	65,77,87,96	0
2	BMA	С	3	11/12	0.91	0.15	85,91,95,95	0

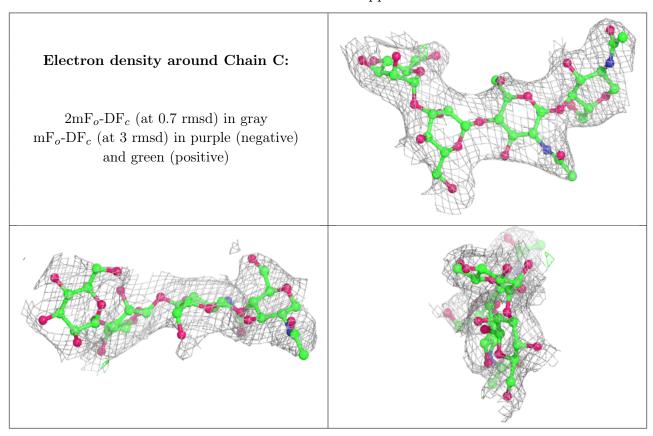
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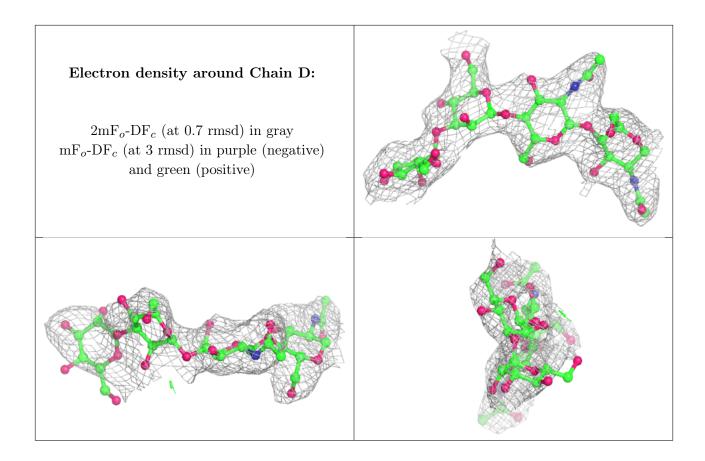
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	NAG	С	2	14/15	0.92	0.20	73,80,86,87	0
2	NAG	D	1	14/15	0.96	0.18	47,55,60,67	0
2	NAG	С	1	14/15	0.97	0.19	52,56,59,68	0

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.







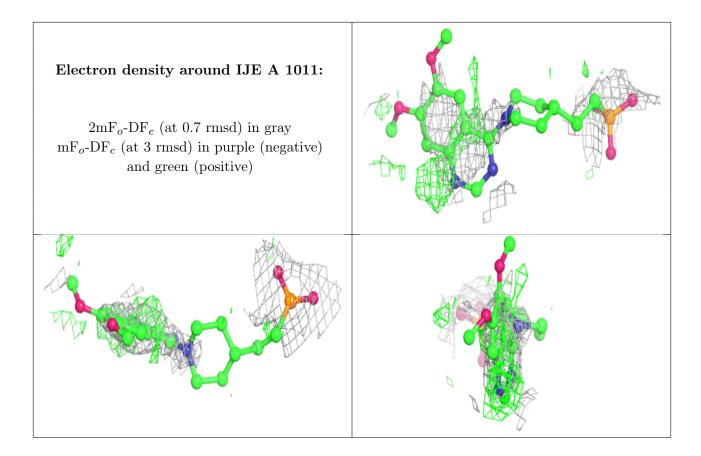
6.4 Ligands (i)

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	$\operatorname{B-factors}({ ext{\AA}}^2)$	Q<0.9
3	NAG	A	1006	14/15	0.77	0.34	85,97,106,112	0
3	NAG	A	1005	14/15	0.81	0.31	89,103,114,117	0
6	CL	A	1010	1/1	0.93	0.15	43,43,43,43	0
5	CA	В	1003	1/1	0.96	0.14	64,64,64,64	0
5	CA	A	1009	1/1	0.97	0.12	70,70,70,70	0
7	IJE	A	1011	26/26	0.97	0.27	59,66,68,70	26
4	ZN	В	1002	1/1	0.98	0.19	61,61,61,61	0
4	ZN	A	1008	1/1	0.99	0.16	54,54,54,54	0
4	ZN	A	1007	1/1	0.99	0.17	57,57,57,57	0
4	ZN	В	1001	1/1	1.00	0.17	45,45,45,45	0

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.

