

Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 09:51 PM JST

PDB ID	:	6AEK
Title	:	Crystal structure of ENPP1 in complex with pApG
Authors	:	Kato, K.; Nishimasu, H.; Hirano, S.; Hirano, H.; Ishitani, R.; Nureki, O.
Deposited on		
Resolution	:	1.80 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 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:

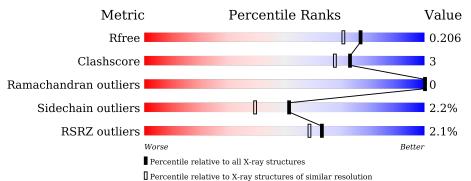
Xtriage (Phenix) EDS buster-report Percentile statistics	: : :	20191225.v01 (using entries in the PDB archive December 25th 2019)
-	:	
CCP4 Ideal geometry (proteins)		7.0.044 (Gargrove) Engh & Huber (2001)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		

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 1.80 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	738	2%	90%	9%	·			
2	В	3	33%	67%		_			



6AEK

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 6299 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 1, isoform CRA_d.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	726	Total 5817	C 3741	N 968	O 1080	S 28	0	2	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	168	GLY	-	See sequence details	UNP G3X9S2
А	169	PRO	-	See sequence details	UNP G3X9S2
А	238	ALA	THR	engineered mutation	UNP G3X9S2

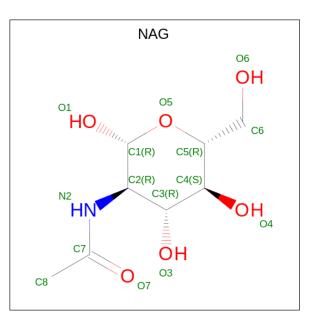
• Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxybeta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	В	3	Total 39	C 22	N 2	0 15	0	0	0

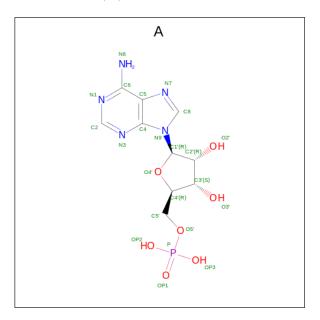
• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





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

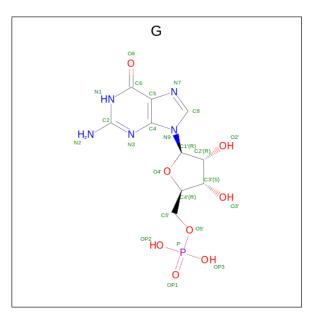
• Molecule 4 is ADENOSINE-5'-MONOPHOSPHATE (three-letter code: A) (formula: $C_{10}H_{14}N_5O_7P$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	۸	1	Total	С	Ν	Ο	Р	0	0
4	А		23	10	5	7	1	0	0

• Molecule 5 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: G) (formula: $C_{10}H_{14}N_5O_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
Б.	٨	1	Total	С	Ν	0	Р	0	0
0	A	1	23	10	5	7	1	0	0

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

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

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

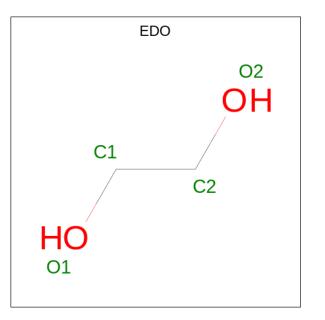
Μ	ol	Chain	Residues	Ator	ns	ZeroOcc	AltConf
7	,	А	1	Total 1	Ca 1	0	0

• Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	6	Total Cl 6 6	0	0



• Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
9	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
9	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
9	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
9	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
9	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 10 is water.

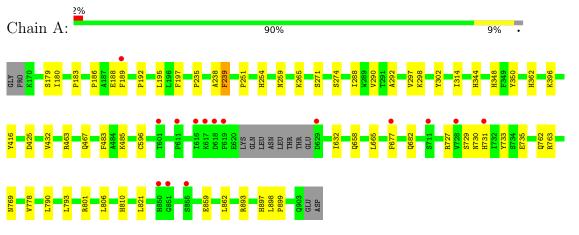
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	322	Total O 322 322	0	0



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 1, isoform CRA_d



• Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose

Chain B:	33%	67%
-		



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	54.49Å 94.07Å 74.68Å	Depositor
a, b, c, α , β , γ	90.00° 96.86° 90.00°	Depositor
Resolution (Å)	47.00 - 1.80	Depositor
Resolution (A)	47.04 - 1.80	EDS
% Data completeness	99.9 (47.00-1.80)	Depositor
(in resolution range)	$100.0 \ (47.04 - 1.80)$	EDS
R _{merge}	0.05	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.97 (at 1.79 \text{\AA})$	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
D D.	0.183 , 0.208	Depositor
R, R_{free}	0.181 , 0.206	DCC
R_{free} test set	3433 reflections $(4.96%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	27.4	Xtriage
Anisotropy	0.807	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34,47.1	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6299	wwPDB-VP
Average B, all atoms $(Å^2)$	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.63% of the height of the origin peak. No significant pseudotranslation is detected.

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.



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: ZN, MAN, NAG, CA, EDO, CL

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			lengths	Bond angles	
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.36	0/5996	0.53	0/8170

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 (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 asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	5817	0	5578	36	0
2	В	39	0	34	1	0
3	А	42	0	39	0	0
4	А	23	0	11	2	0
5	А	23	0	12	1	0
6	А	2	0	0	0	0
7	А	1	0	0	0	0
8	А	6	0	0	1	0
9	А	24	0	36	4	0
10	А	322	0	0	4	0
All	All	6299	0	5710	38	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 3.



A. 1	A.L. D	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
8:A:1012:CL:CL	9:A:1021:EDO:O1	2.41	0.75
1:A:898:LEU:HD12	1:A:899:PRO:HD2	1.73	0.71
9:A:1022:EDO:H21	2:B:2:NAG:H3	1.74	0.70
1:A:658:GLN:OE1	1:A:727:ARG:NH2	2.30	0.64
1:A:769:ASN:OD1	10:A:1101:HOH:O	2.15	0.64
1:A:180:ILE:HG12	1:A:396:LYS:HD3	1.84	0.59
1:A:432:VAL:HA	9:A:1021:EDO:H21	1.85	0.57
1:A:658:GLN:HB3	1:A:727:ARG:NH2	2.20	0.55
1:A:188:GLU:OE1	1:A:188:GLU:N	2.32	0.54
1:A:733:TYR:CZ	1:A:735:GLU:HB2	2.44	0.53
1:A:763:ARG:NH1	1:A:859:GLU:OE2	2.41	0.53
1:A:348:HIS:ND1	10:A:1105:HOH:O	2.34	0.52
1:A:251:PRO:HA	1:A:254:HIS:CE1	2.46	0.51
1:A:432:VAL:HG13	9:A:1021:EDO:H22	1.92	0.50
1:A:362:HIS:HB3	5:A:1008:G:O6	2.12	0.50
1:A:195:LEU:HD23	1:A:350:TYR:HB2	1.94	0.49
1:A:893:ARG:HD2	10:A:1316:HOH:O	2.14	0.47
1:A:235:PRO:HD3	1:A:483:PHE:CE1	2.50	0.46
1:A:186:PRO:HG2	1:A:189:PHE:CD1	2.50	0.46
1:A:769:ASN:ND2	1:A:821:LEU:O	2.47	0.46
1:A:793:LEU:HD22	1:A:806:LEU:HD21	1.98	0.46
1:A:292:ALA:HB1	1:A:297:VAL:HB	1.98	0.45
1:A:778:VAL:HB	1:A:810:HIS:HB2	1.99	0.44
1:A:298:LYS:HE3	1:A:344:HIS:O	2.17	0.43
1:A:195:LEU:HD23	1:A:350:TYR:CB	2.48	0.43
1:A:463:ARG:N	1:A:467:GLN:OE1	2.48	0.43
1:A:897:HIS:ND1	10:A:1107:HOH:O	2.36	0.43
1:A:485:LYS:HD2	1:A:485:LYS:HA	1.65	0.43
1:A:183:PRO:HB3	1:A:192:PRO:HG3	2.01	0.43
1:A:677:PHE:HZ	1:A:762:GLN:HG2	1.82	0.43
1:A:238:ALA:HB2	4:A:1007:A:P	2.59	0.42
1:A:596:CYS:SG	1:A:665:LEU:HD21	2.60	0.42
1:A:632:ILE:HD13	1:A:632:ILE:HA	1.87	0.42
1:A:239:PHE:HB2	1:A:259:ASN:OD1	2.21	0.41
1:A:729:SER:HB3	1:A:731:HIS:CE1	2.55	0.41
1:A:238:ALA:HB2	4:A:1007:A:OP2	2.20	0.41
1:A:290:VAL:HG13	1:A:314:ILE:HD12	2.02	0.41
1:A:265:LYS:HE2	1:A:265:LYS:HB2	1.82	0.40

All (38) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	А	724/738~(98%)	701 (97%)	23~(3%)	0	100 100

There are no Ramachandran outliers to report.

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	Outliers	Percentiles
1	А	647/675~(96%)	633~(98%)	14 (2%)	52 39

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	179	SER
1	А	197	PHE
1	А	239	PHE
1	А	271	SER
1	А	274	SER
1	А	288	ILE
1	А	302	TYR
1	А	416	TYR
1	А	425	ASP
1	А	682	GLN
1	А	730	ASN
1	А	790	LEU
1	А	801	ARG

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type
1	А	862	LEU

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such side chains are listed below:

Mol	Chain	Res	Type
1	А	466	ASN
1	А	583	ASN
1	А	731	HIS
1	А	820	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)

3 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	Trune	Chain	Chain Res	Link	Bo	ond leng	\mathbf{ths}	В	Bond angles		
	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
2	NAG	В	1	2,1	14,14,15	0.24	0	17,19,21	0.67	0	
2	NAG	В	2	2	14,14,15	0.53	0	17,19,21	0.74	0	
2	MAN	В	3	2	11,11,12	1.29	2 (18%)	$15,\!15,\!17$	1.15	1 (6%)	

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
2	MAN	В	3	2	-	0/2/19/22	1/1/1/1

All (2) bond length outliers are listed below:

M	bl	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2		В	3	MAN	C1-C2	2.86	1.58	1.52
2		В	3	MAN	O5-C5	2.30	1.48	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	3	MAN	C1-O5-C5	2.80	115.98	112.19

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

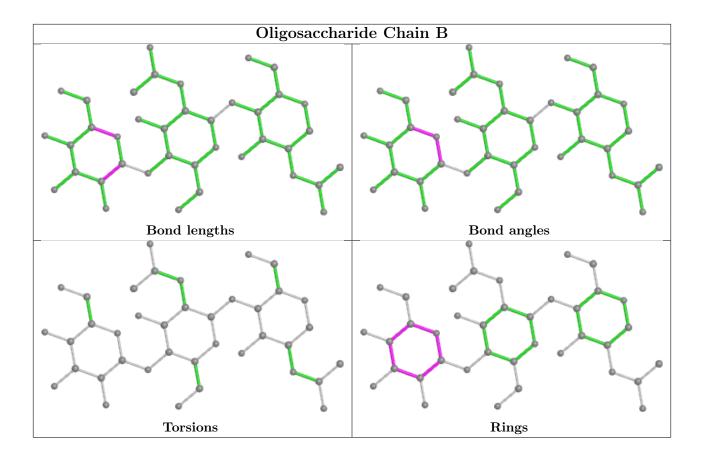
Mol	Chain	Res	Type	Atoms
2	В	3	MAN	C1-C2-C3-C4-C5-O5

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	2	NAG	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 oligosaccharide.





5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 9 are monoatomic - leaving 11 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	Bo	ond leng	ths	В	ond ang	les
NIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	G	А	1008	-	18,25,26	1.04	2 (11%)	19,37,40	0.71	1 (5%)
9	EDO	А	1022	-	3,3,3	0.50	0	2,2,2	0.07	0
9	EDO	А	1023	-	3,3,3	0.43	0	2,2,2	0.40	0
3	NAG	А	1001	1	$14,\!14,\!15$	0.26	0	17,19,21	0.61	0
9	EDO	А	1018	-	3, 3, 3	0.45	0	$2,\!2,\!2$	0.41	0
3	NAG	А	1002	1	14,14,15	0.32	0	$17,\!19,\!21$	1.16	1 (5%)
9	EDO	А	1019	-	3,3,3	0.46	0	2,2,2	0.38	0
3	NAG	А	1003	1	14,14,15	0.56	0	17,19,21	0.92	1 (5%)
9	EDO	А	1021	-	3,3,3	0.35	0	2,2,2	0.37	0



Mol	Type	Chain	Res	Link	Bo	Bond lengths			ond ang	les
IVIOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	EDO	А	1020	-	3,3,3	0.46	0	$2,\!2,\!2$	0.24	0
4	А	А	1007	6	22,25,25	0.80	0	$25,\!38,\!38$	0.95	1 (4%)

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
5	G	А	1008	-	-	0/3/25/26	0/3/3/3
9	EDO	А	1022	-	-	0/1/1/1	-
9	EDO	А	1023	-	-	0/1/1/1	-
3	NAG	А	1001	1	-	2/6/23/26	0/1/1/1
9	EDO	А	1018	-	-	0/1/1/1	-
3	NAG	А	1002	1	-	2/6/23/26	0/1/1/1
9	EDO	А	1019	-	-	0/1/1/1	-
3	NAG	А	1003	1	-	2/6/23/26	0/1/1/1
9	EDO	А	1021	-	-	0/1/1/1	-
9	EDO	А	1020	-	_	0/1/1/1	-
4	А	А	1007	6	-	0/6/26/26	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	А	1008	G	C5-C6	-2.55	1.42	1.47
5	А	1008	G	C8-N7	-2.45	1.30	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	А	1002	NAG	C1-O5-C5	3.87	117.44	112.19
3	А	1003	NAG	C1-O5-C5	3.27	116.63	112.19
4	А	1007	А	C5-C6-N6	2.33	123.89	120.35
5	А	1008	G	O6-C6-C5	2.02	128.32	124.37

There are no chirality outliers.

All (6) torsion outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	Atoms
3	А	1002	NAG	O5-C5-C6-O6

Continued on next page...



Mol	Chain	Res	Type	Atoms
3	А	1002	NAG	C4-C5-C6-O6
3	А	1001	NAG	C4-C5-C6-O6
3	А	1001	NAG	O5-C5-C6-O6
3	А	1003	NAG	C4-C5-C6-O6
3	А	1003	NAG	O5-C5-C6-O6

Continued from previous page...

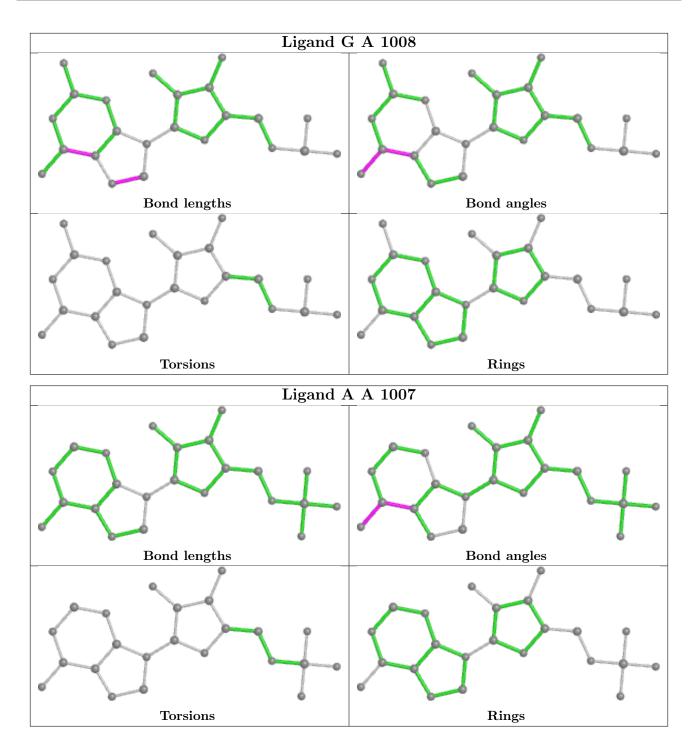
There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	А	1008	G	1	0
9	А	1022	EDO	1	0
9	А	1021	EDO	3	0
4	А	1007	А	2	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 $>$	#RSRZ>2		$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9	
1	А	726/738~(98%)	0.01	15 (2%)	63	59	21, 39, 69, 93	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	677	PHE	4.3
1	А	601	THR	3.7
1	А	616	ILE	3.6
1	А	851	GLY	3.5
1	А	617	LYS	3.4
1	А	850	HIS	3.1
1	А	611	PRO	3.0
1	А	619	PHE	2.6
1	А	728	VAL	2.5
1	А	189	PHE	2.4
1	А	618	ASP	2.3
1	А	629	ASP	2.2
1	А	731	HIS	2.1
1	А	711	SER	2.1
1	А	855	SER	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.

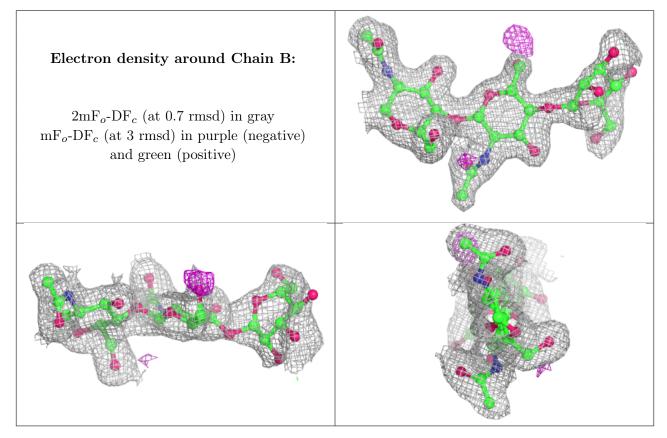
6.3 Carbohydrates (i)

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	MAN	В	3	11/12	0.69	0.23	70,74,76,77	0
2	NAG	В	2	14/15	0.89	0.12	36,44,54,64	0
2	NAG	В	1	14/15	0.97	0.09	21,26,28,31	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
3	NAG	А	1002	14/15	0.74	0.25	45,56,58,62	0
3	NAG	А	1001	14/15	0.80	0.17	50,60,63,65	0
5	G	А	1008	23/24	0.86	0.25	46,76,82,82	0
9	EDO	А	1020	4/4	0.86	0.24	44,44,48,49	0
9	EDO	А	1022	4/4	0.87	0.18	49,49,50,51	0
9	EDO	А	1023	4/4	0.88	0.15	54,55,55,56	0

Continued on next page...

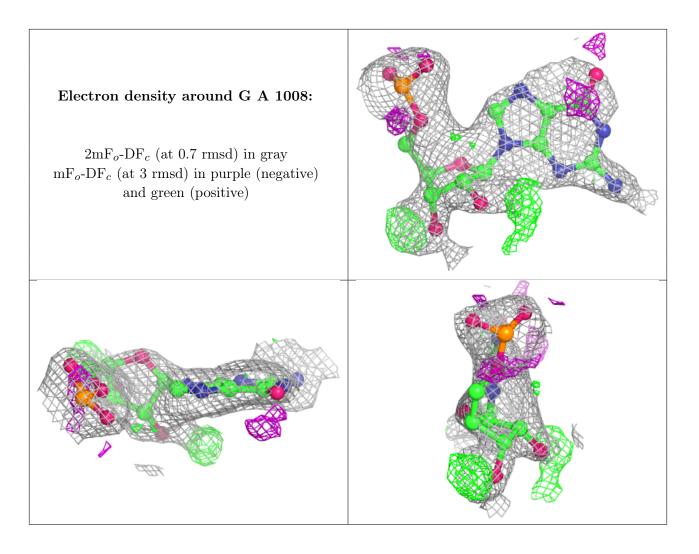


Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	А	1003	14/15	0.89	0.13	28,31,40,48	0
4	А	А	1007	23/23	0.92	0.11	28,32,40,42	0
8	CL	А	1017	1/1	0.94	0.10	41,41,41,41	0
9	EDO	А	1018	4/4	0.94	0.14	29,32,33,38	0
9	EDO	А	1019	4/4	0.94	0.10	36,40,40,43	0
8	CL	А	1013	1/1	0.95	0.08	$51,\!51,\!51,\!51$	0
9	EDO	А	1021	4/4	0.96	0.16	37,39,43,47	0
8	CL	А	1016	1/1	0.97	0.15	36,36,36,36	0
6	ZN	А	1010	1/1	0.97	0.08	38,38,38,38	0
6	ZN	А	1009	1/1	0.98	0.06	32,32,32,32	0
8	CL	А	1014	1/1	0.98	0.15	36,36,36,36	0
8	CL	А	1015	1/1	0.99	0.22	31,31,31,31	0
7	CA	А	1011	1/1	0.99	0.10	31,31,31,31	0
8	CL	А	1012	1/1	0.99	0.10	38,38,38,38	0

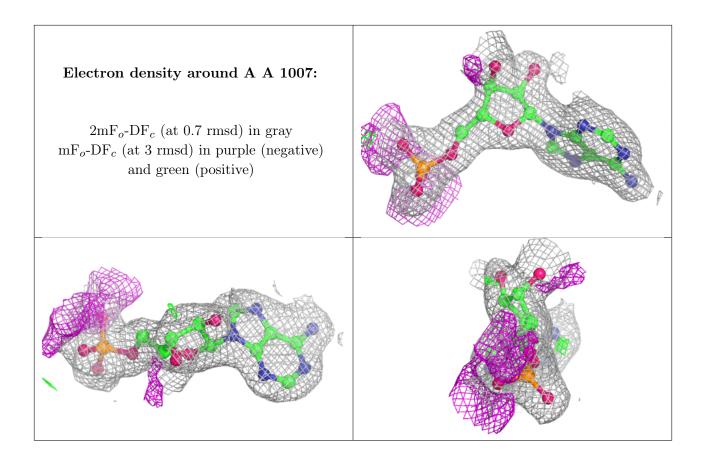
Continued from previous page...

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.

