Full wwPDB X-ray Structure Validation Report (i)

Jan 14, 2024 – 06:38 am GMT

PDB ID	:	6S1Z
Title	:	Crystal structure of Anopheles gambiae AnoACE2 in complex with fosinoprilat
Authors	:	Cozier, G.E.; Acharya, K.R.; Cashman, J.S.
Deposited on	:	2019-06-19
Resolution	:	2.50 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 (i)) were used in the production of this report:

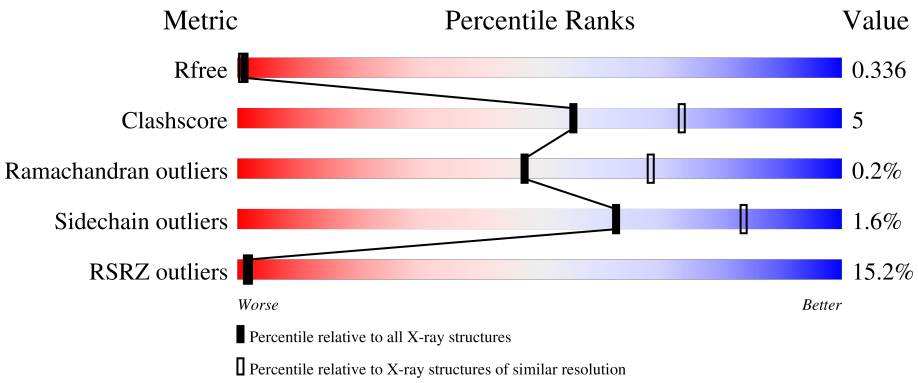
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	621	14% / 81% / 13% / 6%
2	B	3	100%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9558 atoms, of which 4687 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.

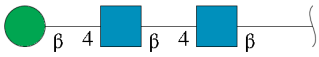
- Molecule 1 is a protein called Angiotensin-converting enzyme.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	585	9397	3067	4621	802	888	19	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

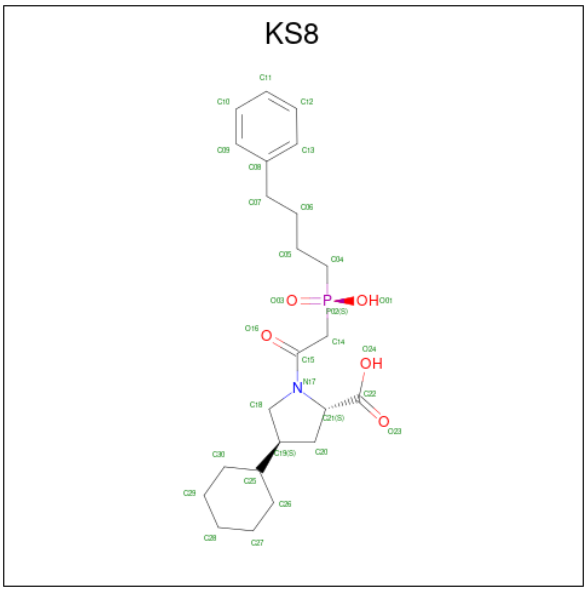
Chain	Residue	Modelled	Actual	Comment	Reference
A	639	LYS	-	expression tag	UNP A0NFU8
A	640	HIS	-	expression tag	UNP A0NFU8
A	641	HIS	-	expression tag	UNP A0NFU8
A	642	HIS	-	expression tag	UNP A0NFU8
A	643	HIS	-	expression tag	UNP A0NFU8
A	644	HIS	-	expression tag	UNP A0NFU8
A	645	HIS	-	expression tag	UNP A0NFU8
A	646	HIS	-	expression tag	UNP A0NFU8
A	647	HIS	-	expression tag	UNP A0NFU8

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	B	3	73	22	34	2	15	0	0	0

- Molecule 3 is fosinoprilat (three-letter code: KS8) (formula: $C_{23}H_{34}NO_5P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	P		
3	A	1	62	23	32	1	5	1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	1	1	1	0	0

- Molecule 5 is water.

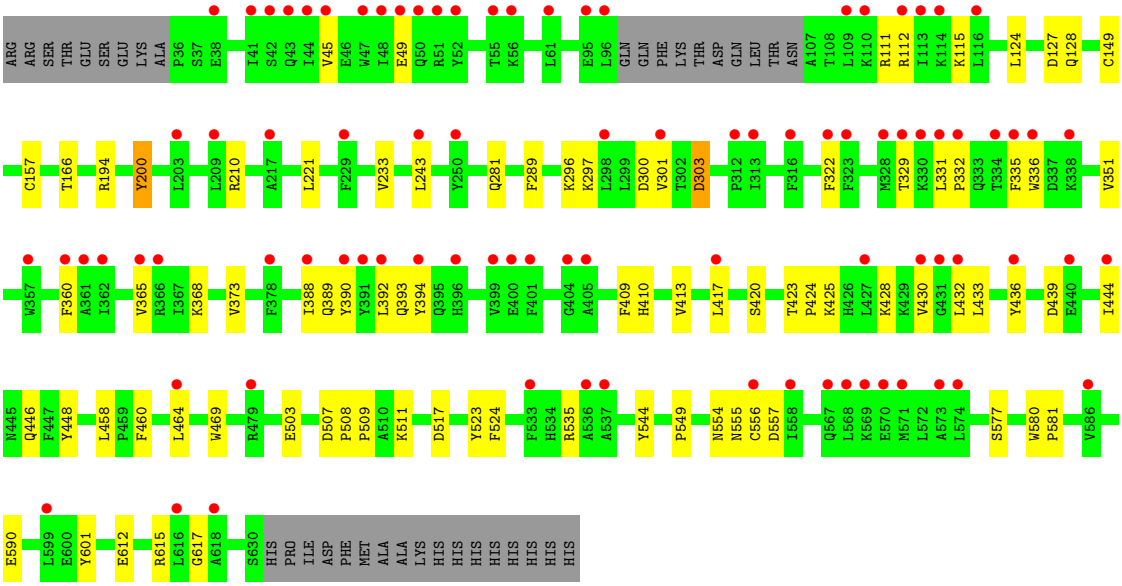
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	25	25	25	0	0

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.

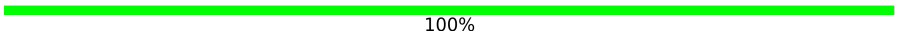
• Molecule 1: Angiotensin-converting enzyme

Chain A:



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

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α, β, γ	166.72Å 166.72Å 117.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	72.19 – 2.50 91.12 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (72.19-2.50) 100.0 (91.12-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.17 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.294 , 0.337 0.294 , 0.336	Depositor DCC
R_{free} test set	1695 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	54.3	Xtriage
Anisotropy	0.327	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 65.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.36$, $< L^2 > = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	9558	wwPDB-VP
Average B, all atoms (Å^2)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical 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.

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: NAG, ZN, KS8, BMA

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	0.25	0/4905	0.39	0/6648

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	A	4776	4621	4622	48	0
2	B	39	34	34	0	0
3	A	30	32	0	1	0
4	A	1	0	0	0	0
5	A	25	0	0	4	0
All	All	4871	4687	4656	48	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.

All (48) 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:49:GLU:OE2	1:A:112:ARG:NH2	2.18	0.76
1:A:329:THR:HG21	1:A:392:LEU:HD13	1.67	0.76
1:A:351:VAL:O	1:A:368:LYS:NZ	2.19	0.75
1:A:373:VAL:O	5:A:801:HOH:O	2.05	0.74
1:A:360:PHE:O	5:A:802:HOH:O	2.07	0.71
1:A:617:GLY:O	5:A:803:HOH:O	2.10	0.68
1:A:535:ARG:NH2	1:A:590:GLU:OE2	2.29	0.66
1:A:289:PHE:O	5:A:804:HOH:O	2.15	0.63
1:A:389:GLN:OE1	1:A:393:GLN:NE2	2.30	0.62
1:A:523:TYR:OH	3:A:704:KS8:O16	2.20	0.59
1:A:194:ARG:NH2	1:A:503:GLU:O	2.36	0.57
1:A:331:LEU:HD21	1:A:335:PHE:CD1	2.41	0.56
1:A:127:ASP:OD1	1:A:128:GLN:N	2.40	0.54
1:A:507:ASP:N	1:A:508:PRO:CD	2.71	0.53
1:A:425:LYS:HD2	1:A:557:ASP:HB3	1.91	0.53
1:A:331:LEU:HD23	1:A:332:PRO:O	2.09	0.53
1:A:424:PRO:O	1:A:428:LYS:N	2.37	0.52
1:A:296:LYS:NZ	1:A:439:ASP:OD2	2.37	0.52
1:A:301:VAL:HG12	1:A:301:VAL:O	2.10	0.51
1:A:124:LEU:HD23	1:A:210:ARG:HD2	1.92	0.50
1:A:444:ILE:O	1:A:448:TYR:N	2.40	0.50
1:A:303:ASP:OD1	1:A:303:ASP:N	2.47	0.48
1:A:221:LEU:HD21	1:A:469:TRP:CH2	2.49	0.48
1:A:111:ARG:NH1	1:A:577:SER:O	2.48	0.47
1:A:233:VAL:HG13	1:A:524:PHE:CE2	2.49	0.47
1:A:446:GLN:NE2	1:A:555:ASN:OD1	2.47	0.47
1:A:45:VAL:O	1:A:49:GLU:N	2.47	0.46
1:A:200:TYR:OH	1:A:517:ASP:OD1	2.22	0.46
1:A:580:TRP:N	1:A:581:PRO:CD	2.79	0.46
1:A:297:LYS:HG2	1:A:436:TYR:HD1	1.80	0.46
1:A:243:LEU:HD12	1:A:243:LEU:N	2.32	0.44
1:A:329:THR:CG2	1:A:392:LEU:HD13	2.42	0.44
1:A:535:ARG:HG3	1:A:544:TYR:CE2	2.52	0.44
1:A:331:LEU:HD22	1:A:336:TRP:CE2	2.52	0.44
1:A:365:VAL:HB	1:A:388:ILE:HG23	2.00	0.44
1:A:300:ASP:OD1	1:A:301:VAL:N	2.51	0.44
1:A:554:ASN:ND2	1:A:601:TYR:O	2.47	0.43
1:A:281:GLN:OE1	1:A:511:LYS:NZ	2.42	0.43
1:A:420:SER:O	1:A:423:THR:OG1	2.24	0.43
1:A:430:VAL:O	1:A:432:LEU:N	2.47	0.43
1:A:322:PHE:CE1	1:A:417:LEU:HD22	2.54	0.42
1:A:460:PHE:CE1	1:A:464:LEU:HD11	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:ARG:O	1:A:115:LYS:N	2.45	0.42
1:A:612:GLU:OE2	1:A:615:ARG:NH2	2.53	0.42
1:A:424:PRO:HB3	1:A:433:LEU:HD21	2.01	0.41
1:A:409:PHE:O	1:A:413:VAL:HG23	2.20	0.41
1:A:149:CYS:HA	1:A:157:CYS:HA	2.03	0.41
1:A:508:PRO:N	1:A:509:PRO:CD	2.84	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	581/621 (94%)	538 (93%)	42 (7%)	1 (0%)	47 68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	549	PRO

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	A	505/538 (94%)	497 (98%)	8 (2%)	62 84

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	THR
1	A	200	TYR
1	A	303	ASP
1	A	390	TYR
1	A	394	TYR
1	A	410	HIS
1	A	458	LEU
1	A	556	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	446	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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	B	1	1,2	14,14,15	0.46	0	17,19,21	0.60	0
2	NAG	B	2	2	14,14,15	0.28	0	17,19,21	0.39	0
2	BMA	B	3	2	11,11,12	0.65	0	15,15,17	0.80	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	B	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

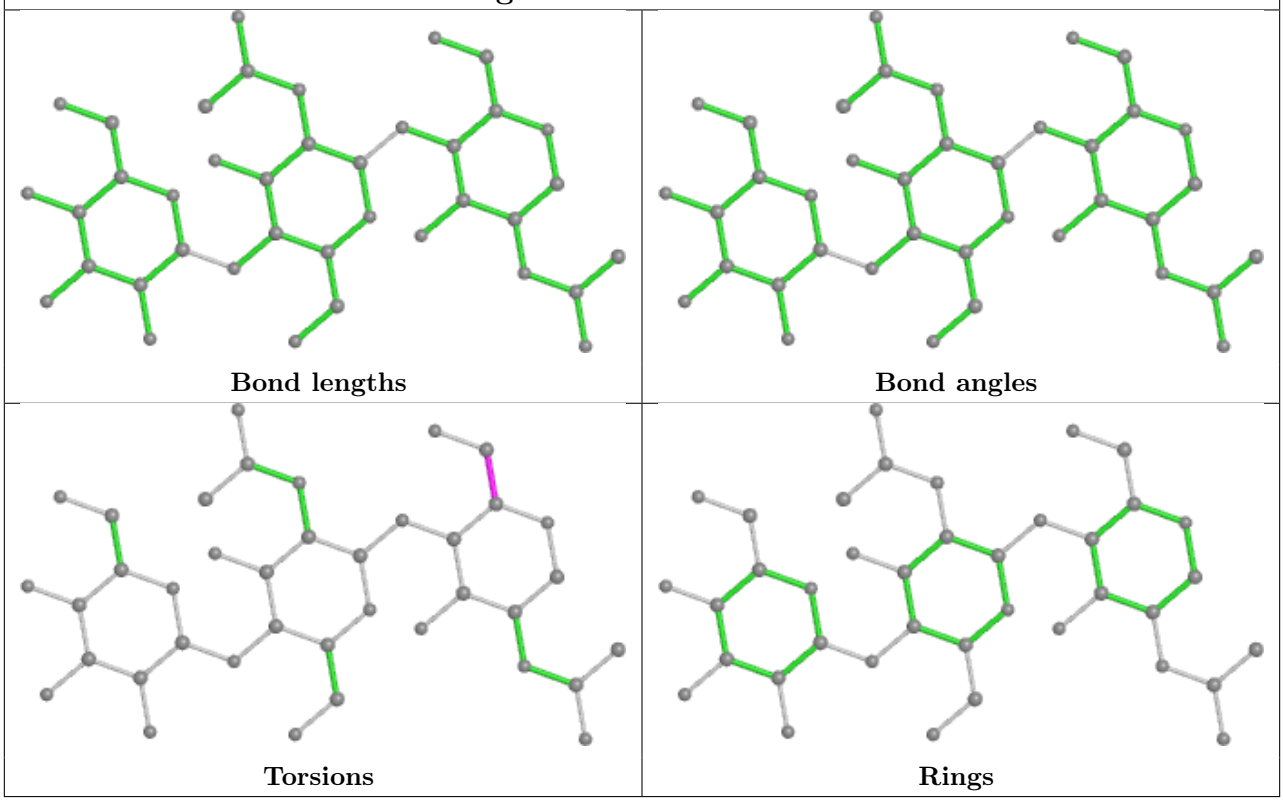
Mol	Chain	Res	Type	Atoms
2	B	1	NAG	O5-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6

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.

Oligosaccharide Chain B



5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\#\|Z\| > 2$
3	KS8	A	704	4	29,32,32	2.95	9 (31%)	35,44,44	1.11	1 (2%)

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	KS8	A	704	4	-	5/25/45/45	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	704	KS8	C20-C21	-7.97	1.38	1.53
3	A	704	KS8	C18-N17	-7.88	1.34	1.47
3	A	704	KS8	C21-N17	5.37	1.57	1.47
3	A	704	KS8	C15-N17	5.18	1.51	1.35
3	A	704	KS8	C14-C15	4.56	1.57	1.51
3	A	704	KS8	C18-C19	3.08	1.57	1.52
3	A	704	KS8	O24-C22	-2.99	1.20	1.30
3	A	704	KS8	C07-C08	2.95	1.60	1.51
3	A	704	KS8	C05-C04	2.20	1.59	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	704	KS8	C18-N17-C21	-3.37	106.83	111.70

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	704	KS8	C05-C04-P02-O03
3	A	704	KS8	C04-C05-C06-C07
3	A	704	KS8	C15-C14-P02-O01
3	A	704	KS8	C05-C04-P02-C14
3	A	704	KS8	C05-C04-P02-O01

There are no ring outliers.

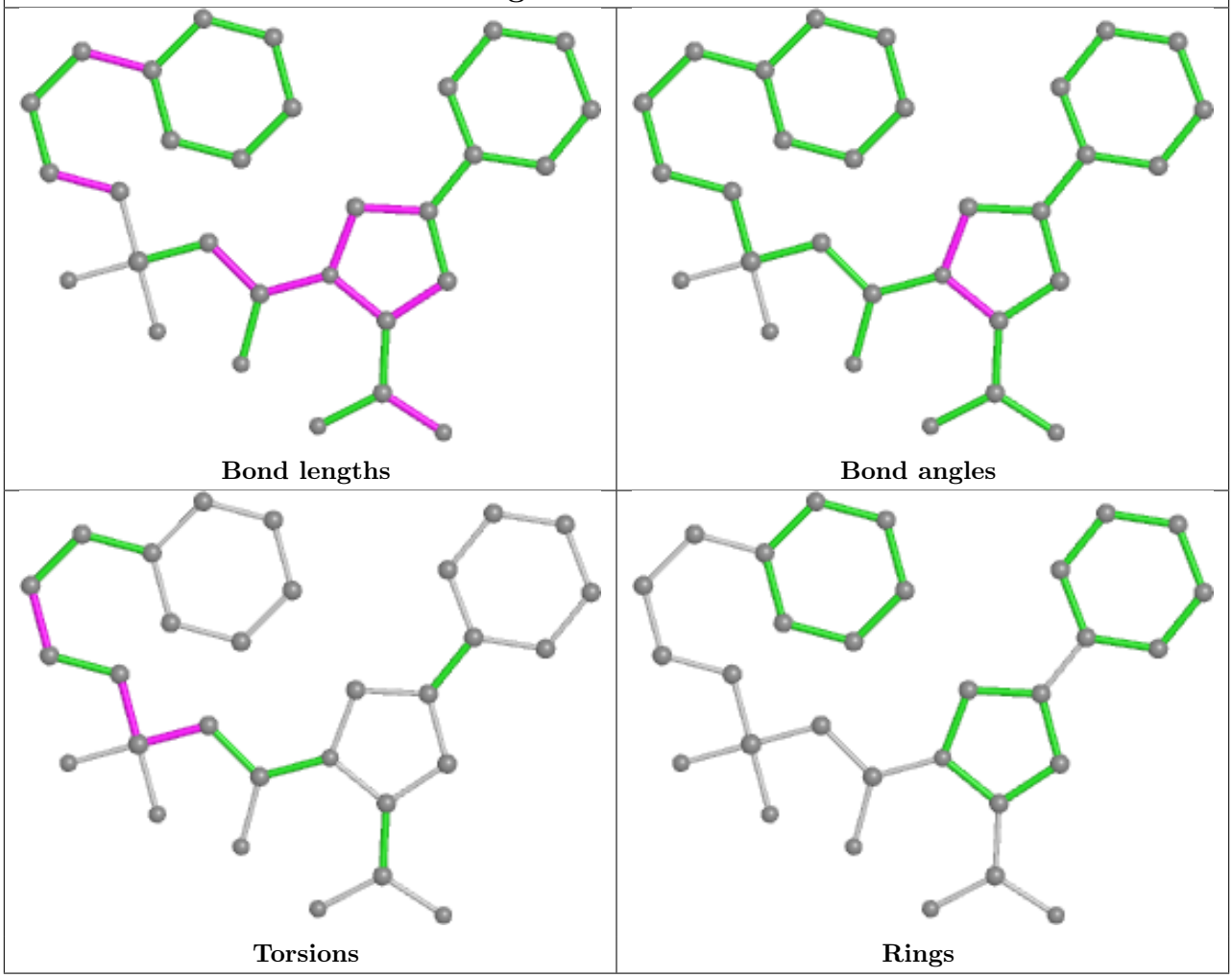
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	704	KS8	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.

Ligand KS8 A 704



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, 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	585/621 (94%)	0.99	89 (15%) 2 1	26, 86, 133, 169	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	113	ILE	13.5
1	A	573	ALA	11.4
1	A	109	LEU	9.3
1	A	116	LEU	9.2
1	A	47	TRP	9.1
1	A	335	PHE	9.0
1	A	45	VAL	7.9
1	A	52	TYR	7.0
1	A	328	MET	7.0
1	A	360	PHE	6.9
1	A	399	VAL	6.9
1	A	323	PHE	6.7
1	A	43	GLN	6.5
1	A	48	ILE	6.1
1	A	229	PHE	6.0
1	A	568	LEU	5.9
1	A	362	ILE	5.2
1	A	38	GLU	5.0
1	A	336	TRP	4.9
1	A	537	ALA	4.8
1	A	332	PRO	4.7
1	A	41	ILE	4.7
1	A	112	ARG	4.5
1	A	44	ILE	4.4
1	A	330	LYS	4.4
1	A	114	LYS	4.0
1	A	338	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	444	ILE	3.8
1	A	365	VAL	3.8
1	A	110	LYS	3.7
1	A	331	LEU	3.7
1	A	417	LEU	3.7
1	A	95	GLU	3.6
1	A	394	TYR	3.5
1	A	401	PHE	3.5
1	A	316	PHE	3.5
1	A	616	LEU	3.4
1	A	366	ARG	3.4
1	A	313	ILE	3.3
1	A	49	GLU	3.3
1	A	357	TRP	3.3
1	A	50	GLN	3.3
1	A	567	GLN	3.1
1	A	388	ILE	3.0
1	A	209	LEU	3.0
1	A	243	LEU	3.0
1	A	436	TYR	2.9
1	A	571	MET	2.9
1	A	329	THR	2.9
1	A	361	ALA	2.9
1	A	56	LYS	2.9
1	A	405	ALA	2.8
1	A	431	GLY	2.8
1	A	301	VAL	2.8
1	A	574	LEU	2.7
1	A	396	HIS	2.7
1	A	427	LEU	2.7
1	A	51	ARG	2.7
1	A	569	LYS	2.6
1	A	536	ALA	2.6
1	A	391	TYR	2.6
1	A	390	TYR	2.5
1	A	217	ALA	2.5
1	A	378	PHE	2.5
1	A	334	THR	2.5
1	A	618	ALA	2.4
1	A	322	PHE	2.4
1	A	599	LEU	2.4
1	A	298	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	400	GLU	2.3
1	A	430	VAL	2.3
1	A	432	LEU	2.3
1	A	464	LEU	2.3
1	A	203	LEU	2.3
1	A	570	GLU	2.3
1	A	404	GLY	2.2
1	A	533	PHE	2.2
1	A	392	LEU	2.2
1	A	42	SER	2.2
1	A	440	GLU	2.2
1	A	55	THR	2.2
1	A	558	ILE	2.2
1	A	61	LEU	2.2
1	A	586	VAL	2.1
1	A	479	ARG	2.1
1	A	556	CYS	2.1
1	A	96	LEU	2.1
1	A	312	PRO	2.0
1	A	250	TYR	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)

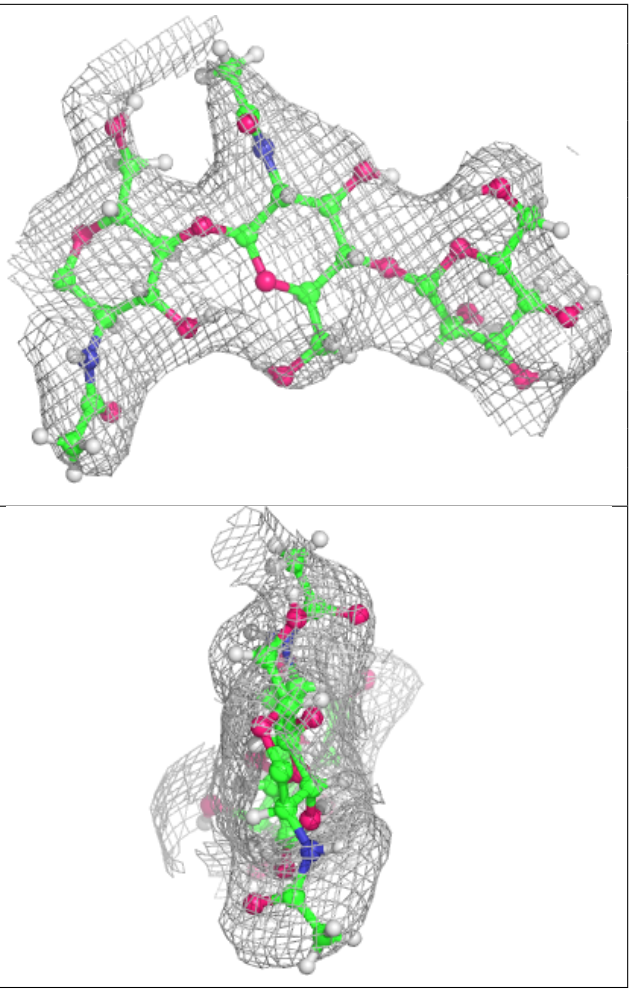
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	BMA	B	3	11/12	0.78	0.17	74,113,133,137	0
2	NAG	B	1	14/15	0.86	0.17	71,93,116,133	0
2	NAG	B	2	14/15	0.87	0.15	83,103,129,135	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.

Electron density around Chain B:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.4 Ligands (i)

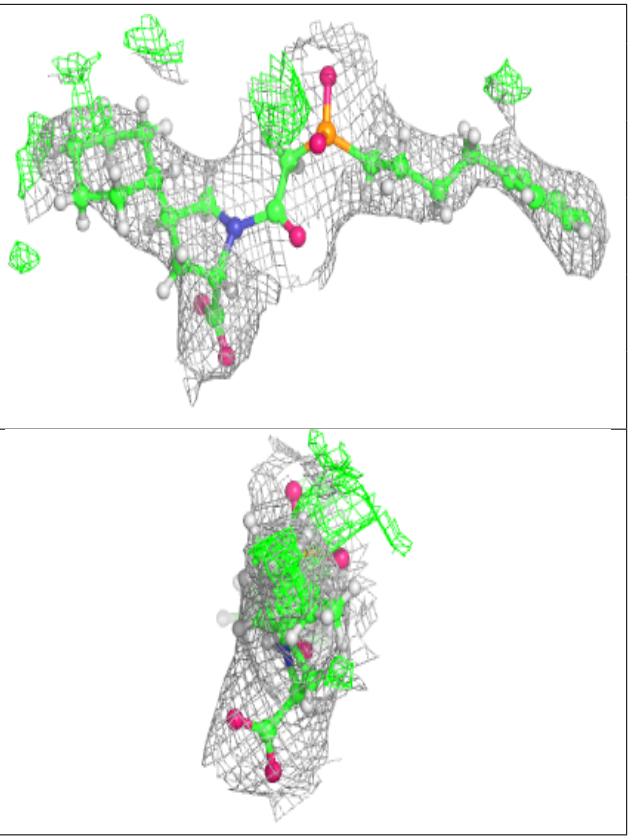
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	KS8	A	704	30/30	0.92	0.20	63,94,116,118	0
4	ZN	A	705	1/1	0.95	0.22	87,87,87,87	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.

Electron density around KS8 A 704:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.