



Full wwPDB X-ray Structure Validation Report i

Nov 15, 2023 – 06:18 pm GMT

PDB ID : 8C7R
Title : Crystal structure of rat autotaxin and compound MEY-003
Authors : Eymery, M.C.; McCarthy, A.A.
Deposited on : 2023-01-17
Resolution : 2.53 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:

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

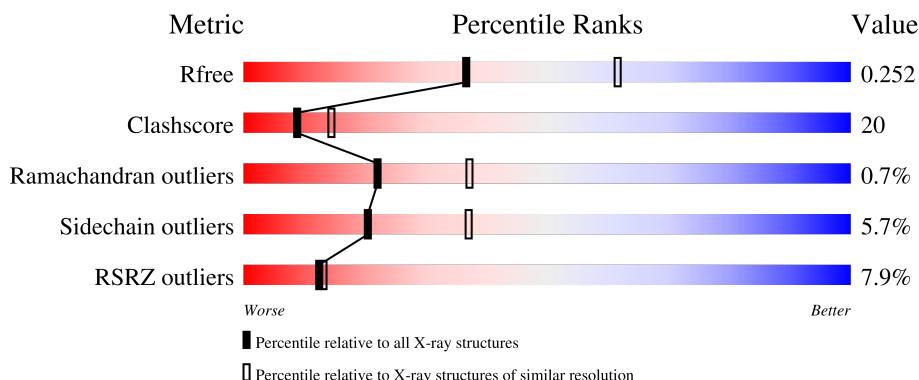
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

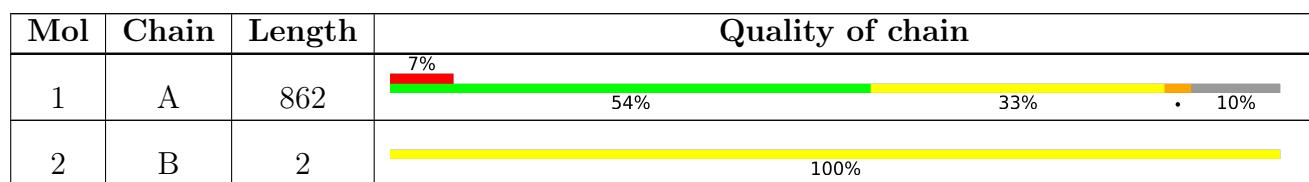
The reported resolution of this entry is 2.53 Å.

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	5743 (2.54-2.50)
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630 (2.54-2.50)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 6494 atoms, of which 46 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	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	775	6262	3971	1078	1164	49	0	0	0

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	ALA	ASN	engineered mutation	UNP Q64610
A	410	ALA	ASN	engineered mutation	UNP Q64610
A	?	-	GLU	deletion	UNP Q64610
A	?	-	ALA	deletion	UNP Q64610
A	?	-	GLU	deletion	UNP Q64610
A	?	-	THR	deletion	UNP Q64610
A	?	-	GLY	deletion	UNP Q64610
A	?	-	LYS	deletion	UNP Q64610
A	?	-	PHE	deletion	UNP Q64610
A	?	-	ARG	deletion	UNP Q64610
A	?	-	GLY	deletion	UNP Q64610
A	?	-	SER	deletion	UNP Q64610
A	?	-	LYS	deletion	UNP Q64610
A	?	-	HIS	deletion	UNP Q64610
A	?	-	GLU	deletion	UNP Q64610
A	?	-	ASN	deletion	UNP Q64610
A	?	-	LYS	deletion	UNP Q64610
A	?	-	LYS	deletion	UNP Q64610
A	?	-	ASN	deletion	UNP Q64610
A	?	-	LEU	deletion	UNP Q64610
A	?	-	ASN	deletion	UNP Q64610
A	?	-	GLY	deletion	UNP Q64610
A	?	-	SER	deletion	UNP Q64610
A	?	-	VAL	deletion	UNP Q64610
A	?	-	GLU	deletion	UNP Q64610
A	?	-	PRO	deletion	UNP Q64610

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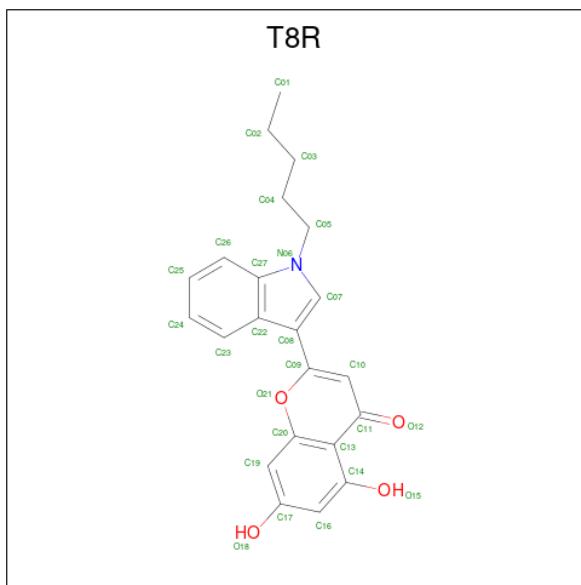
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	deletion	UNP Q64610

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



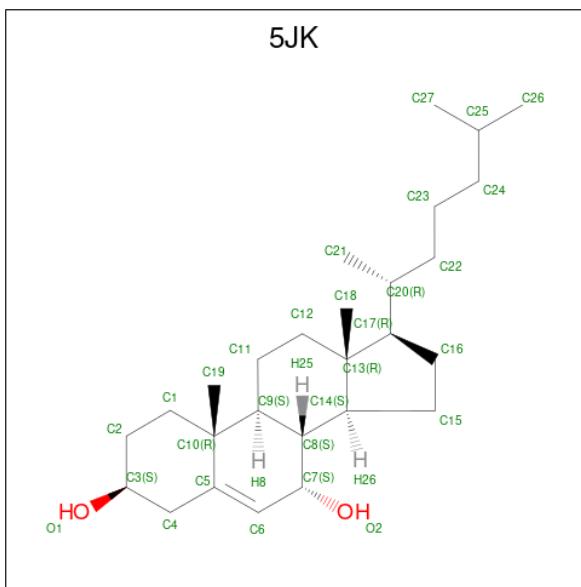
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	B	2	Total C N O 28 16 2 10	0	0	0

- Molecule 3 is 5,7-bis(oxidanyl)-2-(1-pentylindol-3-yl)chromen-4-one (three-letter code: T8R) (formula: C₂₂H₂₁NO₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 27 22 1 4	0	0

- Molecule 4 is 7alpha-hydroxycholesterol (three-letter code: 5JK) (formula: C₂₇H₄₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			75	27	46	2		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total I		0	0
			4	4		

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

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

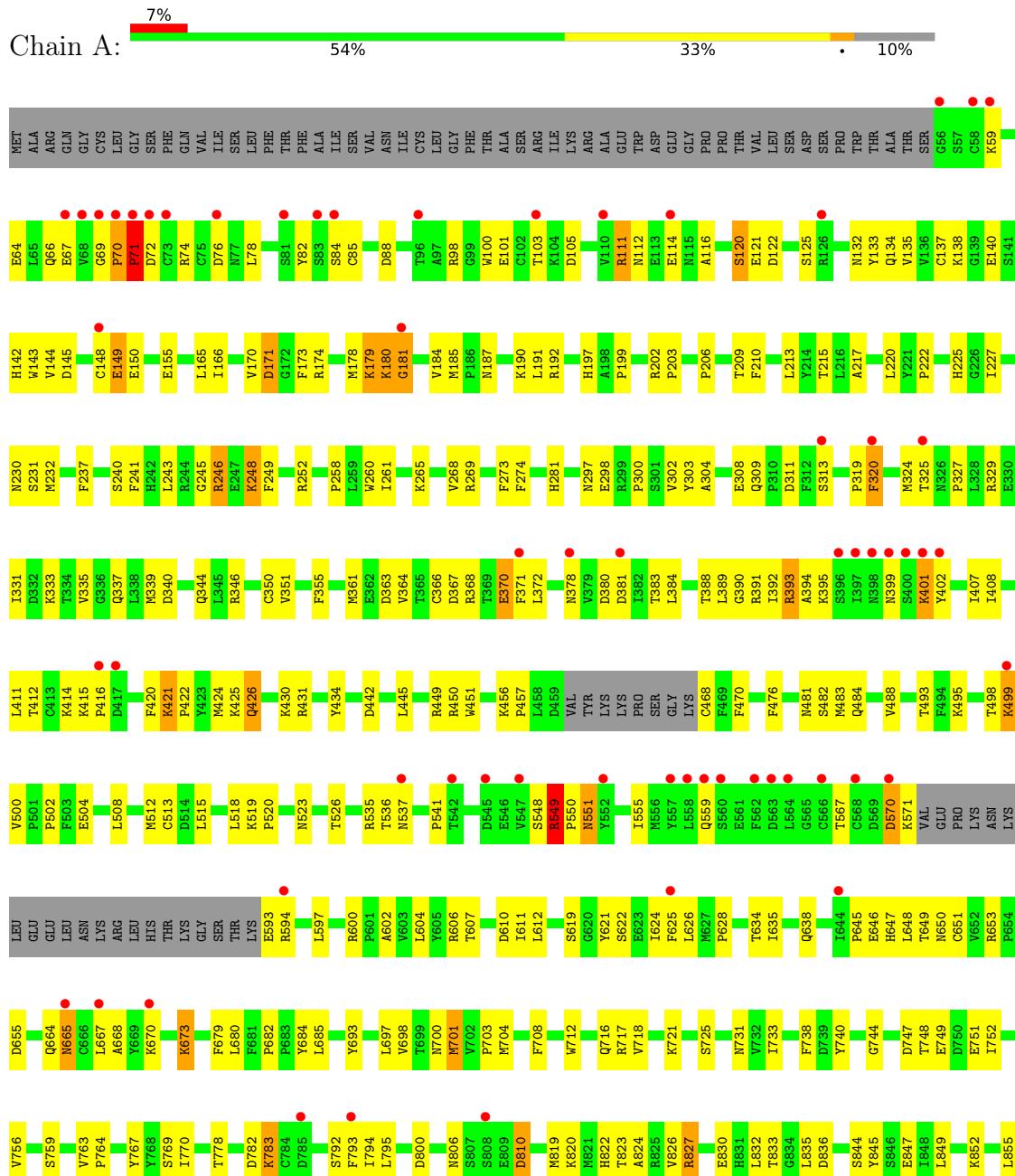
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	94	Total O		0	0
			94	94		

3 Residue-property plots

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 2



H856	T857	Y858	E859
SER	GLU		
ILE			

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

Chain B:  100%

MAG1
MAG2

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.53 Å 61.84 Å 63.85 Å 104.01° 98.43° 93.27°	Depositor
Resolution (Å)	43.64 – 2.53 43.64 – 2.53	Depositor EDS
% Data completeness (in resolution range)	98.2 (43.64-2.53) 98.2 (43.64-2.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ ¹	2.13 (at 2.54 Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R , R_{free}	0.205 , 0.254 0.202 , 0.252	Depositor DCC
R_{free} test set	2004 reflections (7.81%)	wwPDB-VP
Wilson B-factor (Å ²)	36.7	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.2	EDS
L-test for twinning ²	$< L > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6494	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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: CA, T8R, NAG, ZN, 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.39	2/6440 (0.0%)	0.59	3/8736 (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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	548	SER	C-N	-6.30	1.19	1.34
1	A	549	ARG	CZ-NH2	6.02	1.40	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	499	LYS	CA-CB-CG	-7.62	96.64	113.40
1	A	71	PRO	CA-N-CD	-5.76	103.44	111.50
1	A	88	ASP	CB-CG-OD1	5.07	122.86	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	549	ARG	Sidechain

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	6262	0	6003	250	2
2	B	28	0	25	2	0
3	A	27	0	0	1	0
4	A	29	46	0	1	0
5	A	2	0	0	0	0
6	A	4	0	0	0	0
7	A	2	0	0	0	0
8	A	94	0	0	7	0
All	All	6448	46	6028	252	2

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 20.

All (252) 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:749:GLU:OE1	8:A:1001:HOH:O	1.61	1.19
1:A:424:MET:HB3	1:A:426:GLN:HE21	1.12	1.15
1:A:456:LYS:HD3	1:A:457:PRO:HD2	1.34	1.09
1:A:499:LYS:HG2	1:A:500:VAL:N	1.72	1.00
1:A:499:LYS:HG2	1:A:500:VAL:H	1.27	1.00
1:A:645:PRO:HG2	1:A:648:LEU:HD12	1.49	0.94
1:A:76:ASP:OD2	1:A:78:LEU:N	2.02	0.93
1:A:199:PRO:HG2	1:A:502:PRO:HG3	1.50	0.90
1:A:698:VAL:HG23	1:A:701:MET:HE1	1.54	0.88
1:A:456:LYS:HD3	1:A:457:PRO:CD	2.04	0.88
1:A:166:ILE:HD12	1:A:351:VAL:HG11	1.55	0.87
1:A:673:LYS:H	1:A:673:LYS:HD3	1.41	0.86
1:A:78:LEU:HD11	1:A:274:PHE:HB2	1.59	0.84
1:A:424:MET:HB3	1:A:426:GLN:NE2	1.92	0.84
1:A:593:GLU:OE1	8:A:1002:HOH:O	1.97	0.82
1:A:363:ASP:OD2	1:A:368:ARG:NH2	2.13	0.81
1:A:456:LYS:CD	1:A:457:PRO:HD2	2.11	0.79
1:A:415:LYS:HG3	1:A:416:PRO:HD2	1.64	0.79
1:A:717:ARG:HG2	1:A:718:VAL:HG23	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:THR:OG1	1:A:105:ASP:OD1	2.02	0.75
1:A:112:ASN:HD21	1:A:114:GLU:HG2	1.51	0.74
2:B:2:NAG:O7	2:B:2:NAG:O3	2.07	0.72
1:A:222:PRO:HA	1:A:225:HIS:CE1	2.25	0.72
1:A:390:GLY:HA3	1:A:445:LEU:HB2	1.72	0.70
1:A:645:PRO:CG	1:A:648:LEU:HD12	2.21	0.70
1:A:243:LEU:HD23	1:A:243:LEU:O	1.92	0.70
1:A:782:ASP:OD1	1:A:783:LYS:HG2	1.92	0.70
1:A:202:ARG:HH11	1:A:504:GLU:HG2	1.57	0.70
1:A:415:LYS:HG3	1:A:416:PRO:CD	2.21	0.69
1:A:515:LEU:HA	1:A:537:ASN:HD22	1.56	0.69
1:A:395:LYS:O	1:A:399:ASN:HB2	1.93	0.69
1:A:179:LYS:O	1:A:181:GLY:N	2.25	0.68
1:A:673:LYS:H	1:A:673:LYS:CD	2.07	0.68
1:A:181:GLY:CA	1:A:184:VAL:HG22	2.23	0.68
1:A:704:MET:HE1	1:A:708:PHE:HE2	1.59	0.67
1:A:646:GLU:HA	1:A:649:THR:HG23	1.77	0.67
1:A:66:GLN:HA	1:A:66:GLN:OE1	1.94	0.66
1:A:698:VAL:HG23	1:A:701:MET:CE	2.24	0.66
1:A:449:ARG:HG3	1:A:450:ARG:HG3	1.77	0.66
1:A:638:GLN:O	1:A:638:GLN:HG3	1.94	0.66
1:A:394:ALA:HB1	1:A:399:ASN:ND2	2.12	0.65
1:A:112:ASN:ND2	1:A:114:GLU:HG2	2.11	0.64
1:A:258:PRO:HG2	1:A:261:ILE:HG12	1.79	0.64
1:A:329:ARG:HG2	1:A:329:ARG:HH11	1.62	0.64
1:A:468:CYS:N	8:A:1006:HOH:O	2.30	0.64
1:A:149:GLU:OE2	1:A:149:GLU:HA	1.97	0.63
1:A:184:VAL:HB	1:A:329:ARG:HG2	1.80	0.63
1:A:64:GLU:HG3	1:A:66:GLN:H	1.62	0.63
1:A:721:LYS:HE3	1:A:725:SER:OG	1.98	0.62
1:A:526:THR:OG1	1:A:827:ARG:HD3	1.99	0.62
1:A:150:GLU:OE2	1:A:535:ARG:NH2	2.33	0.62
1:A:206:PRO:HB3	1:A:389:LEU:HD22	1.82	0.62
1:A:795:LEU:HD21	1:A:819:MET:HA	1.82	0.62
1:A:536:THR:HG22	1:A:537:ASN:H	1.63	0.62
1:A:820:LYS:HD3	1:A:858:TYR:CD1	2.35	0.61
1:A:845:TYR:O	1:A:849:LEU:HG	2.01	0.61
1:A:425:LYS:HD3	1:A:442:ASP:HA	1.82	0.61
1:A:549:ARG:HG3	1:A:550:PRO:HD2	1.82	0.61
1:A:665:ASN:OD1	1:A:667:LEU:HB2	2.01	0.61
1:A:231:SER:O	1:A:391:ARG:NH2	2.29	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:733:ILE:O	1:A:769:SER:HA	2.00	0.60
1:A:822:HIS:ND1	8:A:1007:HOH:O	2.31	0.60
1:A:604:LEU:HD11	1:A:836:ASP:HB2	1.83	0.60
1:A:74:ARG:HD3	1:A:84:SER:HB3	1.81	0.60
1:A:665:ASN:OD1	1:A:668:ALA:N	2.33	0.60
1:A:856:HIS:HD2	1:A:858:TYR:CZ	2.20	0.60
1:A:593:GLU:HG2	1:A:594:ARG:N	2.17	0.59
1:A:622:SER:HG	1:A:625:PHE:HD1	1.50	0.59
1:A:273:PHE:HA	1:A:304:ALA:HB3	1.84	0.59
1:A:823:THR:HG23	1:A:855:LEU:HD11	1.85	0.59
1:A:769:SER:HB3	1:A:793:PHE:CZ	2.38	0.59
1:A:495:LYS:HD3	1:A:498:THR:HG21	1.85	0.58
1:A:499:LYS:CG	1:A:500:VAL:H	2.10	0.58
1:A:181:GLY:HA2	1:A:184:VAL:HG22	1.84	0.58
1:A:199:PRO:HD3	1:A:499:LYS:HE2	1.84	0.58
1:A:197:HIS:O	1:A:499:LYS:HG3	2.04	0.58
1:A:370:GLU:HG2	1:A:420:PHE:HE1	1.68	0.58
1:A:744:GLY:HA2	1:A:832:LEU:HD21	1.86	0.58
1:A:324:MET:C	1:A:327:PRO:HD2	2.24	0.58
1:A:679:PHE:HB3	1:A:700:ASN:ND2	2.19	0.58
1:A:324:MET:O	1:A:327:PRO:HD2	2.04	0.58
1:A:281:HIS:NE2	1:A:308:GLU:OE1	2.37	0.57
1:A:593:GLU:OE2	1:A:593:GLU:N	2.37	0.57
1:A:135:VAL:HA	1:A:140:GLU:O	2.04	0.57
1:A:499:LYS:CG	1:A:500:VAL:N	2.58	0.57
1:A:685:LEU:HD22	1:A:685:LEU:N	2.20	0.57
1:A:845:TYR:CZ	1:A:849:LEU:HD21	2.38	0.57
1:A:833:THR:HB	1:A:835:LEU:HG	1.88	0.56
1:A:148:CYS:SG	1:A:190:LYS:HE3	2.45	0.56
1:A:508:LEU:O	1:A:512:MET:HG3	2.05	0.56
1:A:793:PHE:CD1	1:A:795:LEU:HG	2.40	0.56
1:A:682:PRO:HB3	1:A:716:GLN:HB3	1.88	0.56
1:A:431:ARG:HD3	1:A:823:THR:O	2.07	0.55
1:A:733:ILE:HD11	8:A:1027:HOH:O	2.07	0.55
1:A:220:LEU:CD2	1:A:523:ASN:HA	2.36	0.55
1:A:199:PRO:CD	1:A:499:LYS:HE2	2.36	0.55
1:A:142:HIS:ND1	1:A:340:ASP:OD2	2.38	0.55
1:A:370:GLU:HG2	1:A:420:PHE:CE1	2.41	0.55
1:A:749:GLU:HA	1:A:752:ILE:HD12	1.88	0.55
1:A:202:ARG:NH1	1:A:504:GLU:HG2	2.21	0.54
1:A:513:CYS:HB2	1:A:520:PRO:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:LEU:HD12	1:A:391:ARG:O	2.08	0.54
1:A:142:HIS:HB2	1:A:145:ASP:OD2	2.09	0.53
1:A:67:GLU:O	1:A:67:GLU:HG2	2.08	0.53
1:A:493:THR:HB	1:A:515:LEU:CD2	2.39	0.53
1:A:111:ARG:HD3	1:A:122:ASP:OD2	2.09	0.53
1:A:246:ARG:HA	1:A:249:PHE:HD2	1.73	0.53
1:A:559:GLN:CD	1:A:559:GLN:H	2.10	0.53
1:A:717:ARG:CG	1:A:718:VAL:HG23	2.39	0.52
1:A:199:PRO:HD3	1:A:499:LYS:CE	2.40	0.52
1:A:220:LEU:HD21	1:A:523:ASN:HA	1.92	0.51
1:A:100:TRP:CZ3	1:A:116:ALA:HB1	2.46	0.51
1:A:698:VAL:HA	1:A:701:MET:CE	2.40	0.51
1:A:399:ASN:ND2	1:A:402:TYR:HB3	2.25	0.51
1:A:820:LYS:HD3	1:A:858:TYR:CG	2.45	0.51
1:A:333:LYS:O	1:A:337:GLN:HG3	2.10	0.51
1:A:325:THR:O	1:A:329:ARG:HG3	2.10	0.51
1:A:550:PRO:HG3	1:A:600:ARG:NH1	2.26	0.51
1:A:355:PHE:HB3	1:A:488:VAL:HB	1.93	0.50
1:A:378:ASN:HD22	1:A:401:LYS:HD3	1.76	0.50
1:A:134:GLN:HB3	1:A:140:GLU:HG3	1.94	0.50
1:A:748:THR:HG23	1:A:751:GLU:H	1.75	0.50
1:A:199:PRO:N	1:A:499:LYS:HE2	2.26	0.50
1:A:309:GLN:HB2	1:A:331:ILE:HD11	1.93	0.50
1:A:426:GLN:H	1:A:426:GLN:CD	2.15	0.50
1:A:378:ASN:OD1	1:A:381:ASP:HB2	2.11	0.50
1:A:232:MET:HB2	1:A:241:PHE:HB3	1.94	0.50
1:A:541:PRO:HB2	1:A:845:TYR:CD2	2.47	0.49
1:A:703:PRO:HG2	1:A:764:PRO:CD	2.43	0.49
1:A:225:HIS:CE1	1:A:227:ILE:HB	2.47	0.49
2:B:2:NAG:HO3	2:B:2:NAG:C7	2.21	0.49
1:A:222:PRO:HA	1:A:225:HIS:NE2	2.27	0.49
1:A:536:THR:HG22	1:A:537:ASN:N	2.27	0.49
1:A:570:ASP:OD2	1:A:653:ARG:HD2	2.13	0.49
1:A:69:GLY:O	1:A:70:PRO:C	2.50	0.49
1:A:648:LEU:HD21	1:A:693:TYR:CE1	2.48	0.49
1:A:698:VAL:HA	1:A:701:MET:HE2	1.94	0.49
1:A:133:TYR:O	1:A:137:CYS:HB2	2.13	0.49
1:A:78:LEU:O	1:A:82:TYR:HD1	1.95	0.48
1:A:300:PRO:HG2	1:A:303:TYR:CE1	2.48	0.48
1:A:456:LYS:HD3	1:A:457:PRO:N	2.27	0.48
1:A:513:CYS:CB	1:A:520:PRO:HG3	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:ASN:HD21	1:A:668:ALA:HB2	1.78	0.48
1:A:217:ALA:HA	3:A:901:T8R:C02	2.44	0.48
1:A:770:ILE:HD13	1:A:826:VAL:HG22	1.95	0.48
1:A:237:PHE:CE2	1:A:252:ARG:HD2	2.49	0.48
1:A:830:GLU:OE2	1:A:852:LYS:HE2	2.14	0.48
1:A:481:ASN:HA	1:A:484:GLN:HG2	1.96	0.48
1:A:536:THR:CG2	1:A:537:ASN:H	2.25	0.48
1:A:703:PRO:HG2	1:A:764:PRO:HD3	1.96	0.48
1:A:227:ILE:HA	1:A:232:MET:HE2	1.96	0.47
1:A:180:LYS:HD3	1:A:180:LYS:C	2.34	0.47
1:A:493:THR:HB	1:A:515:LEU:HD23	1.96	0.47
1:A:171:ASP:O	1:A:311:ASP:N	2.47	0.47
1:A:756:VAL:HB	1:A:759:SER:OG	2.15	0.47
1:A:260:TRP:NE1	4:A:902:5JK:O2	2.48	0.47
1:A:513:CYS:HB3	1:A:518:LEU:O	2.15	0.47
1:A:626:LEU:O	1:A:664:GLN:NE2	2.40	0.47
1:A:792:SER:HB2	1:A:824:ALA:O	2.15	0.47
1:A:281:HIS:CE1	1:A:308:GLU:OE1	2.68	0.46
1:A:402:TYR:CD2	1:A:407:ILE:HD11	2.50	0.46
1:A:174:ARG:NH1	1:A:482:SER:HB2	2.31	0.46
1:A:268:VAL:HG21	1:A:518:LEU:HD21	1.96	0.46
1:A:388:THR:HG22	1:A:476:PHE:CZ	2.50	0.46
1:A:597:LEU:HD12	1:A:731:ASN:HB2	1.96	0.46
1:A:364:VAL:HG22	1:A:450:ARG:HA	1.96	0.46
1:A:133:TYR:OH	1:A:138:LYS:HE3	2.16	0.46
1:A:155:GLU:O	1:A:350:CYS:HB2	2.15	0.46
1:A:421:LYS:HG3	1:A:422:PRO:HD2	1.97	0.46
1:A:415:LYS:HG3	1:A:416:PRO:N	2.28	0.46
1:A:628:PRO:HG2	1:A:680:LEU:HD12	1.98	0.46
1:A:144:VAL:HB	1:A:187:ASN:OD1	2.16	0.45
1:A:180:LYS:CG	1:A:180:LYS:O	2.65	0.45
1:A:298:GLU:O	1:A:300:PRO:HD3	2.15	0.45
1:A:703:PRO:O	1:A:767:TYR:OH	2.24	0.45
1:A:393:ARG:HG2	1:A:394:ALA:N	2.31	0.45
1:A:740:TYR:OH	1:A:763:VAL:O	2.29	0.45
1:A:371:PHE:CE2	1:A:457:PRO:HA	2.51	0.45
1:A:716:GLN:NE2	8:A:1015:HOH:O	2.50	0.45
1:A:368:ARG:HB3	1:A:451:TRP:CD2	2.51	0.45
1:A:738:PHE:CZ	1:A:764:PRO:HG3	2.52	0.45
1:A:134:GLN:HG3	1:A:344:GLN:HG3	1.99	0.45
1:A:184:VAL:HG23	1:A:185:MET:CG	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:ILE:CD1	1:A:351:VAL:HG11	2.37	0.45
1:A:602:ALA:HB3	1:A:836:ASP:HB3	1.98	0.45
1:A:684:TYR:C	1:A:685:LEU:HD22	2.36	0.44
1:A:738:PHE:O	1:A:747:ASP:HB2	2.17	0.44
1:A:612:LEU:HB2	1:A:619:SER:OG	2.17	0.44
1:A:383:THR:OG1	1:A:395:LYS:NZ	2.49	0.44
1:A:329:ARG:HH11	1:A:329:ARG:CG	2.30	0.44
1:A:606:ARG:HA	1:A:606:ARG:HD2	1.58	0.44
1:A:625:PHE:CD1	1:A:625:PHE:N	2.85	0.44
1:A:844:SER:OG	1:A:847:GLU:HG3	2.18	0.44
1:A:71:PRO:HD2	1:A:72:ASP:H	1.82	0.44
1:A:806:ASN:OD1	1:A:806:ASN:N	2.42	0.44
1:A:181:GLY:HA3	1:A:184:VAL:HG22	1.96	0.44
1:A:621:TYR:HA	1:A:628:PRO:HA	2.00	0.44
1:A:793:PHE:CD1	1:A:793:PHE:C	2.91	0.43
1:A:206:PRO:HD3	1:A:434:TYR:CE1	2.53	0.43
1:A:665:ASN:ND2	1:A:668:ALA:HB2	2.34	0.43
1:A:679:PHE:HA	1:A:700:ASN:O	2.18	0.43
1:A:704:MET:HE1	1:A:708:PHE:CE2	2.46	0.43
1:A:133:TYR:HB3	1:A:344:GLN:OE1	2.18	0.43
1:A:171:ASP:HB3	1:A:311:ASP:HB2	2.00	0.43
1:A:335:VAL:O	1:A:339:MET:HG2	2.19	0.43
1:A:300:PRO:HG2	1:A:303:TYR:HE1	1.83	0.43
1:A:638:GLN:O	1:A:638:GLN:CG	2.63	0.43
1:A:372:LEU:HD22	1:A:411:LEU:HD21	2.00	0.43
1:A:481:ASN:OD1	1:A:481:ASN:N	2.52	0.43
1:A:647:HIS:CD2	1:A:648:LEU:HG	2.53	0.43
1:A:248:LYS:HE2	1:A:249:PHE:CE2	2.54	0.42
1:A:165:LEU:O	1:A:302:VAL:HA	2.19	0.42
1:A:634:THR:O	1:A:635:ILE:HD13	2.19	0.42
1:A:67:GLU:O	1:A:67:GLU:CG	2.67	0.42
1:A:149:GLU:OE2	1:A:149:GLU:CA	2.66	0.42
1:A:173:PHE:CZ	1:A:178:MET:HE1	2.54	0.42
1:A:704:MET:HE1	1:A:712:TRP:CG	2.55	0.42
1:A:412:THR:O	1:A:414:LYS:HG2	2.20	0.42
1:A:210:PHE:HB2	1:A:230:ASN:OD1	2.19	0.42
1:A:319:PRO:HG2	1:A:320:PHE:CE2	2.55	0.42
1:A:607:THR:OG1	1:A:624:ILE:HG13	2.19	0.42
1:A:120:SER:HG	1:A:122:ASP:CG	2.18	0.42
1:A:366:CYS:HA	8:A:1038:HOH:O	2.18	0.42
1:A:184:VAL:HA	1:A:329:ARG:NH1	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:LEU:HD13	1:A:392:ILE:HG12	2.01	0.41
1:A:570:ASP:HA	1:A:693:TYR:HE1	1.84	0.41
1:A:655:ASP:HB2	1:A:697:LEU:HD22	2.03	0.41
1:A:794:ILE:HD13	1:A:832:LEU:HD12	2.01	0.41
1:A:209:THR:HG22	1:A:213:LEU:HD12	2.01	0.41
1:A:857:THR:O	1:A:858:TYR:HB2	2.20	0.41
1:A:143:TRP:HH2	1:A:191:LEU:HG	1.86	0.41
1:A:74:ARG:O	1:A:85:CYS:HA	2.20	0.41
1:A:782:ASP:CG	1:A:783:LYS:HE3	2.41	0.41
1:A:112:ASN:OD1	1:A:114:GLU:HG2	2.19	0.41
1:A:364:VAL:HG12	1:A:470:PHE:HE2	1.86	0.41
1:A:142:HIS:HD1	1:A:340:ASP:CG	2.23	0.41
1:A:430:LYS:HD2	1:A:430:LYS:HA	1.83	0.41
1:A:101:GLU:HB3	1:A:132:ASN:ND2	2.36	0.40
1:A:220:LEU:HD23	1:A:523:ASN:HA	2.03	0.40
1:A:378:ASN:O	1:A:380:ASP:N	2.54	0.40
1:A:701:MET:HE3	1:A:701:MET:HB3	1.76	0.40
1:A:215:THR:OG1	1:A:222:PRO:HD3	2.21	0.40
1:A:550:PRO:HB3	1:A:611:ILE:HD13	2.03	0.40
1:A:684:TYR:HB2	1:A:685:LEU:HD22	2.02	0.40
1:A:810:ASP:OD2	1:A:810:ASP:N	2.53	0.40
1:A:203:PRO:HG3	1:A:483:MET:O	2.20	0.40
1:A:245:GLY:O	1:A:248:LYS:NZ	2.38	0.40
1:A:685:LEU:N	1:A:685:LEU:CD2	2.83	0.40
1:A:311:ASP:OD1	1:A:361:MET:CE	2.70	0.40
1:A:515:LEU:HA	1:A:537:ASN:ND2	2.30	0.40
1:A:551:ASN:O	1:A:610:ASP:HA	2.21	0.40
1:A:650:ASN:HD22	1:A:650:ASN:HA	1.61	0.40

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:246:ARG:NH1	1:A:555:ILE:O[1_656]	2.15	0.05
1:A:265:LYS:NZ	1:A:778:THR:OG1[1_655]	2.17	0.03

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	769/862 (89%)	722 (94%)	42 (6%)	5 (1%)	22 37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	71	PRO
1	A	180	LYS
1	A	570	ASP
1	A	70	PRO
1	A	181	GLY

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	702/778 (90%)	662 (94%)	40 (6%)	20 37

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	LYS
1	A	98	ARG
1	A	111	ARG
1	A	120	SER
1	A	121	GLU
1	A	125	SER

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Mol	Chain	Res	Type
1	A	149	GLU
1	A	170	VAL
1	A	171	ASP
1	A	179	LYS
1	A	192	ARG
1	A	240	SER
1	A	246	ARG
1	A	248	LYS
1	A	269	ARG
1	A	297	ASN
1	A	313	SER
1	A	320	PHE
1	A	346	ARG
1	A	367	ASP
1	A	370	GLU
1	A	393	ARG
1	A	401	LYS
1	A	408	ILE
1	A	421	LYS
1	A	426	GLN
1	A	519	LYS
1	A	551	ASN
1	A	567	THR
1	A	571	LYS
1	A	651	CYS
1	A	665	ASN
1	A	670	LYS
1	A	673	LYS
1	A	701	MET
1	A	783	LYS
1	A	800	ASP
1	A	810	ASP
1	A	827	ARG
1	A	857	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	378	ASN
1	A	399	ASN
1	A	426	GLN
1	A	537	ASN

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Mol	Chain	Res	Type
1	A	650	ASN
1	A	716	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 [\(i\)](#)

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	B	1	2,1	14,14,15	0.46	0	17,19,21	0.64	1 (5%)
2	NAG	B	2	2	14,14,15	0.28	0	17,19,21	0.53	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	2,1	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	C1-O5-C5	2.21	115.19	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

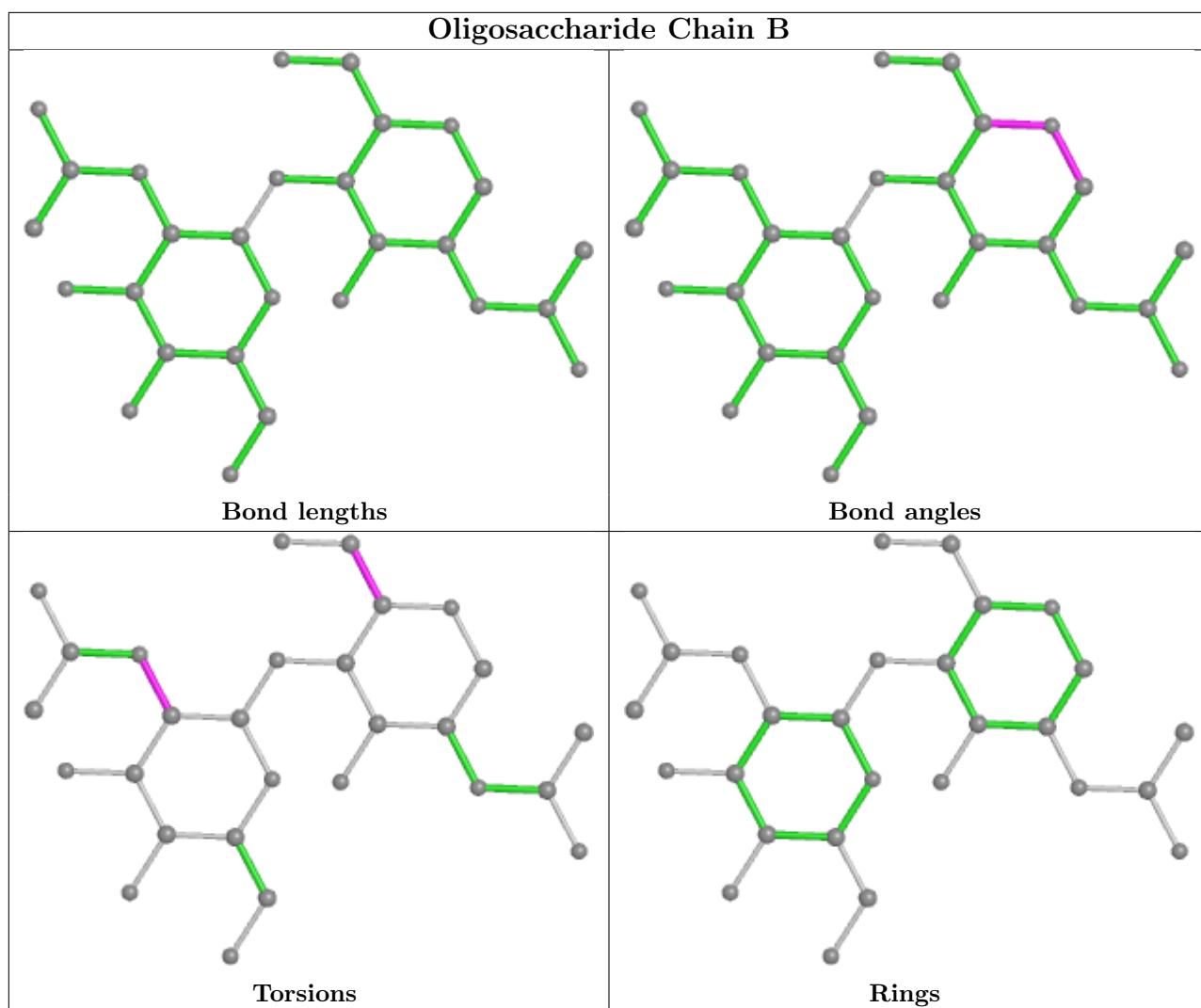
Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6
2	B	2	NAG	C1-C2-N2-C7
2	B	2	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 2 short contacts:

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



5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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
4	5JK	A	902	-	32,32,32	4.11	15 (46%)	47,50,50	2.92	15 (31%)
3	T8R	A	901	-	28,30,30	3.07	15 (53%)	36,43,43	2.55	9 (25%)

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	5JK	A	902	-	-	0/10/71/71	0/4/4/4
3	T8R	A	901	-	-	3/5/9/9	0/4/4/4

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	902	5JK	C6-C5	14.69	1.59	1.33
3	A	901	T8R	C08-C22	10.18	1.51	1.42
4	A	902	5JK	C8-C7	8.91	1.63	1.53
4	A	902	5JK	C16-C15	6.34	1.71	1.54
4	A	902	5JK	C20-C17	-6.04	1.43	1.54
4	A	902	5JK	C15-C14	5.77	1.66	1.54
3	A	901	T8R	C19-C20	5.34	1.48	1.38
4	A	902	5JK	C13-C17	4.70	1.63	1.55
4	A	902	5JK	C12-C13	-4.60	1.45	1.54
4	A	902	5JK	C12-C11	4.28	1.62	1.53
3	A	901	T8R	O21-C09	4.13	1.42	1.36
4	A	902	5JK	O2-C7	-3.70	1.36	1.43
3	A	901	T8R	C27-N06	3.66	1.43	1.39
3	A	901	T8R	C07-N06	3.40	1.43	1.38
4	A	902	5JK	C10-C9	3.22	1.61	1.56
3	A	901	T8R	C19-C17	3.08	1.43	1.39
3	A	901	T8R	C16-C17	3.00	1.43	1.39
3	A	901	T8R	C10-C11	2.96	1.51	1.44
3	A	901	T8R	C16-C14	2.71	1.42	1.38
3	A	901	T8R	O21-C20	2.71	1.42	1.38
3	A	901	T8R	C07-C08	2.70	1.42	1.38
4	A	902	5JK	C8-C14	-2.56	1.48	1.53
3	A	901	T8R	O15-C14	2.53	1.41	1.36
4	A	902	5JK	C10-C5	-2.35	1.48	1.52
3	A	901	T8R	C26-C27	2.34	1.45	1.41
4	A	902	5JK	C22-C20	2.30	1.60	1.54
4	A	902	5JK	C4-C3	2.27	1.56	1.52
4	A	902	5JK	C8-C9	2.21	1.58	1.53
3	A	901	T8R	C05-N06	2.07	1.54	1.49
3	A	901	T8R	C25-C24	2.02	1.43	1.38

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	902	5JK	C7-C6-C5	-14.72	115.84	125.42
3	A	901	T8R	O21-C09-C08	8.31	120.55	110.57
3	A	901	T8R	O21-C09-C10	-6.26	115.56	121.68
3	A	901	T8R	O21-C20-C19	5.66	124.28	115.79
3	A	901	T8R	C20-O21-C09	5.08	125.66	119.53
4	A	902	5JK	C4-C5-C10	-4.38	110.60	116.42
4	A	902	5JK	C19-C10-C9	-4.30	106.55	111.68
4	A	902	5JK	C13-C14-C8	3.97	119.33	113.98
3	A	901	T8R	C14-C13-C20	3.60	121.01	117.35
4	A	902	5JK	C1-C10-C9	-3.53	103.80	108.73
4	A	902	5JK	C10-C9-C8	-3.34	109.01	113.27
4	A	902	5JK	C1-C10-C5	3.29	114.77	108.75
3	A	901	T8R	C20-C13-C11	-3.26	116.35	119.59
4	A	902	5JK	C9-C10-C5	3.14	114.58	109.65
4	A	902	5JK	C17-C13-C14	2.98	103.61	100.07
4	A	902	5JK	C13-C17-C20	-2.73	115.21	119.49
4	A	902	5JK	C22-C20-C17	-2.69	104.72	110.28
3	A	901	T8R	O21-C20-C13	-2.69	118.47	121.18
4	A	902	5JK	C10-C5-C6	-2.66	118.84	122.81
3	A	901	T8R	C19-C20-C13	-2.62	117.26	121.86
4	A	902	5JK	C2-C3-C4	2.46	113.68	110.31
4	A	902	5JK	C18-C13-C12	-2.36	106.87	110.59
3	A	901	T8R	C07-C08-C09	-2.34	123.43	127.83
4	A	902	5JK	C4-C5-C6	2.12	122.44	120.77

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	901	T8R	C04-C05-N06-C07
3	A	901	T8R	C04-C05-N06-C27
3	A	901	T8R	C02-C03-C04-C05

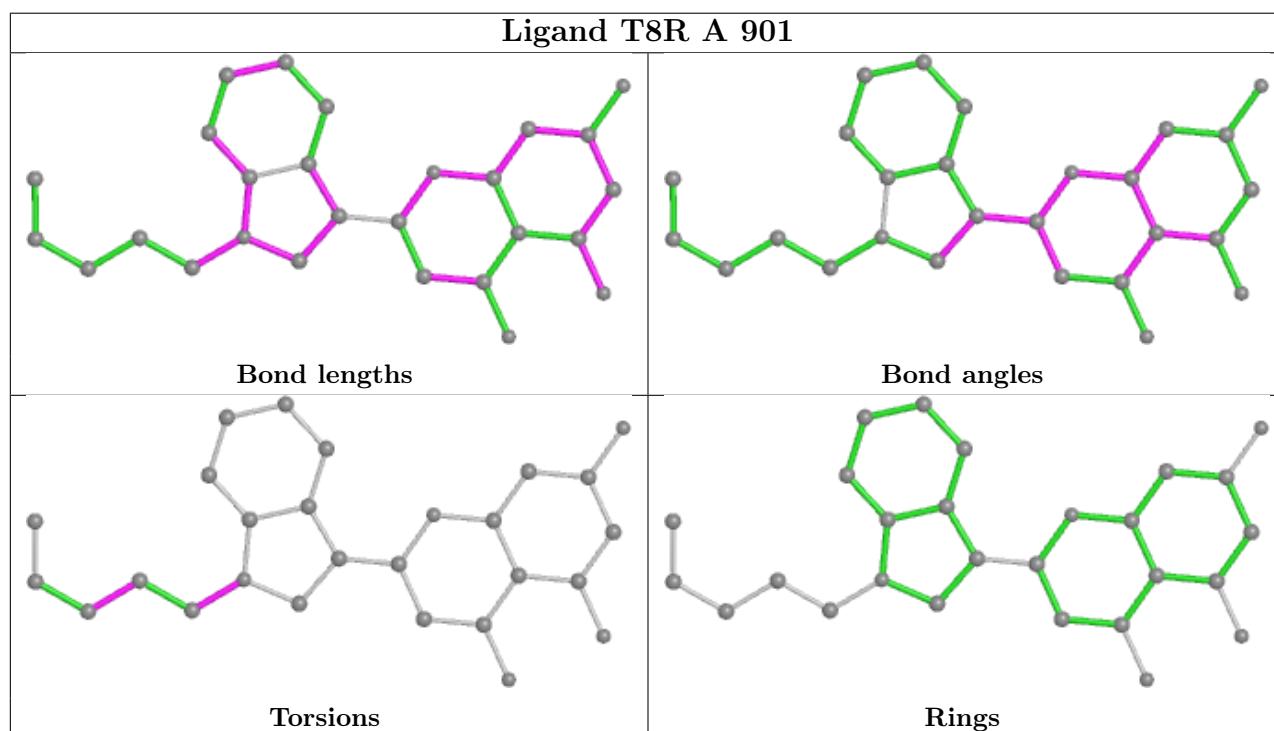
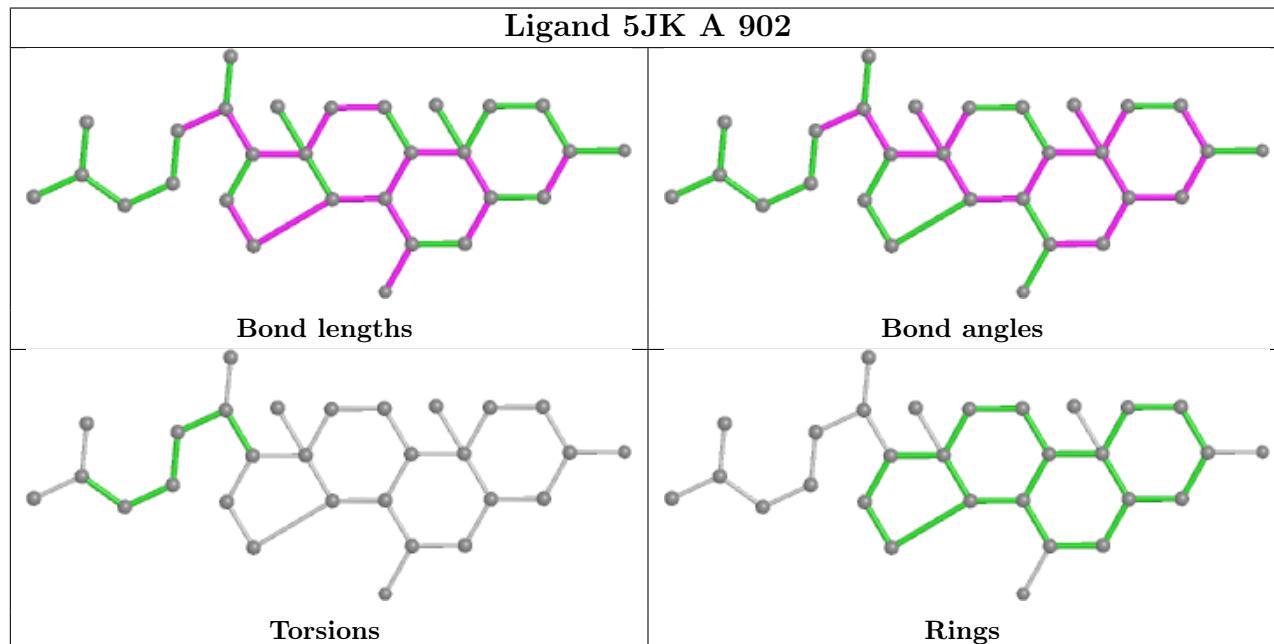
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	902	5JK	1	0
3	A	901	T8R	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 than 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 [\(i\)](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	548:SER	C	549:ARG	N	1.19

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	775/862 (89%)	0.57	61 (7%) 12 13	23, 39, 71, 280	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	399	ASN	10.8
1	A	71	PRO	9.3
1	A	72	ASP	9.1
1	A	398	ASN	7.2
1	A	397	ILE	6.7
1	A	70	PRO	6.7
1	A	68	VAL	5.5
1	A	400	SER	5.3
1	A	557	TYR	4.6
1	A	570	ASP	4.6
1	A	59	LYS	4.5
1	A	558	LEU	4.5
1	A	560	SER	4.5
1	A	67	GLU	4.2
1	A	562	PHE	4.0
1	A	416	PRO	3.9
1	A	396	SER	3.8
1	A	537	ASN	3.8
1	A	84	SER	3.7
1	A	73	CYS	3.6
1	A	181	GLY	3.4
1	A	69	GLY	3.3
1	A	378	ASN	3.2
1	A	381	ASP	3.2
1	A	103	THR	3.2
1	A	563	ASP	3.1
1	A	594	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	81	SER	3.0
1	A	110	VAL	2.9
1	A	56	GLY	2.8
1	A	667	LEU	2.8
1	A	401	LYS	2.8
1	A	568	CYS	2.7
1	A	552	TYR	2.7
1	A	58	CYS	2.5
1	A	566	CYS	2.5
1	A	83	SER	2.5
1	A	808	SER	2.5
1	A	402	TYR	2.5
1	A	417	ASP	2.5
1	A	670	LYS	2.5
1	A	76	ASP	2.5
1	A	313	SER	2.4
1	A	499	LYS	2.4
1	A	559	GLN	2.4
1	A	96	THR	2.3
1	A	114	GLU	2.3
1	A	126	ARG	2.3
1	A	547	VAL	2.2
1	A	148	CYS	2.2
1	A	325	THR	2.2
1	A	542	THR	2.2
1	A	320	PHE	2.1
1	A	793	PHE	2.1
1	A	785	ASP	2.1
1	A	545	ASP	2.1
1	A	625	PHE	2.1
1	A	644	ILE	2.0
1	A	564	LEU	2.0
1	A	665	ASN	2.0
1	A	371	PHE	2.0

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

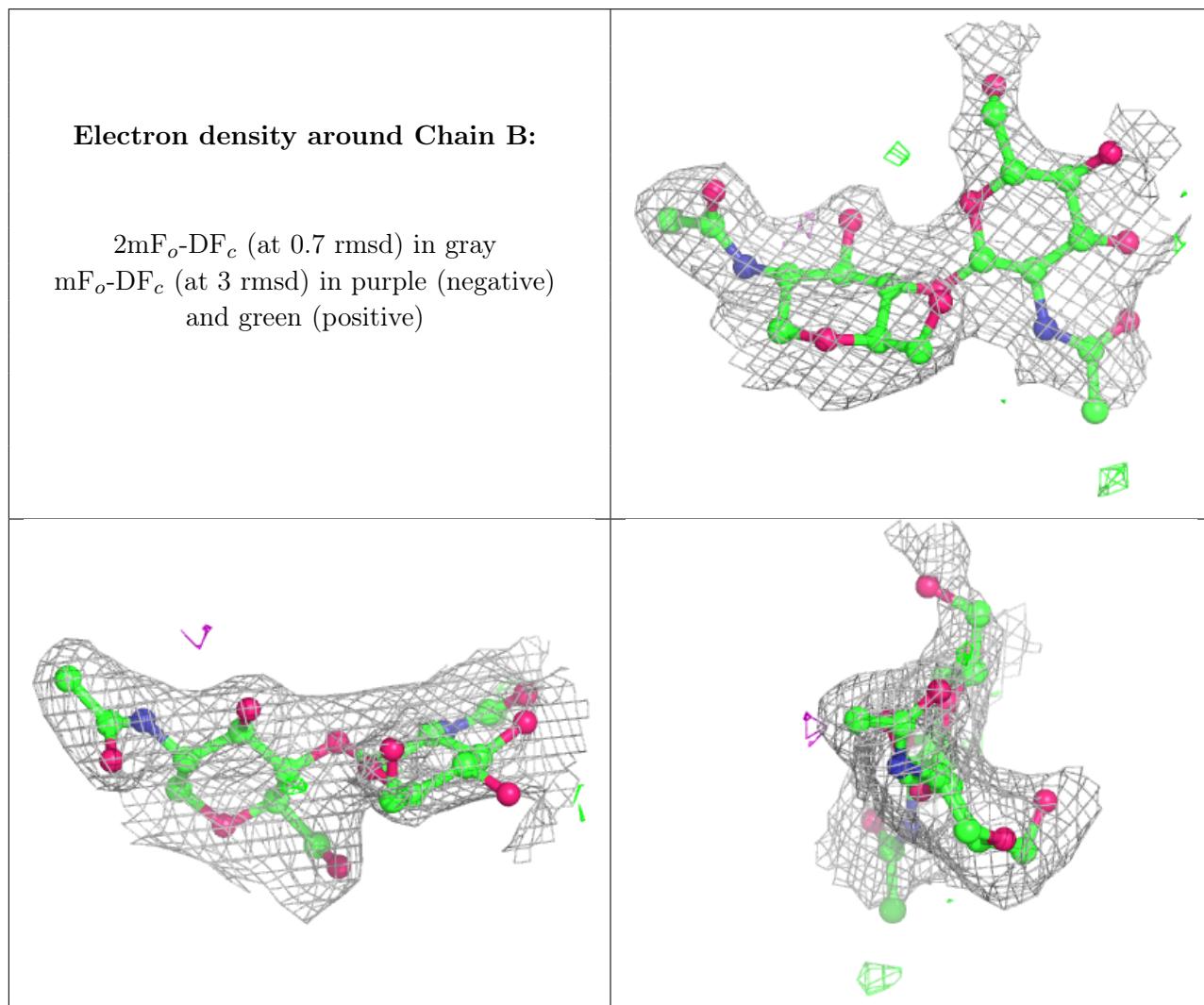
There are no non-standard protein/DNA/RNA residues in this entry.

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	NAG	B	2	14/15	0.82	0.25	59,69,73,78	0
2	NAG	B	1	14/15	0.92	0.16	29,39,44,51	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.

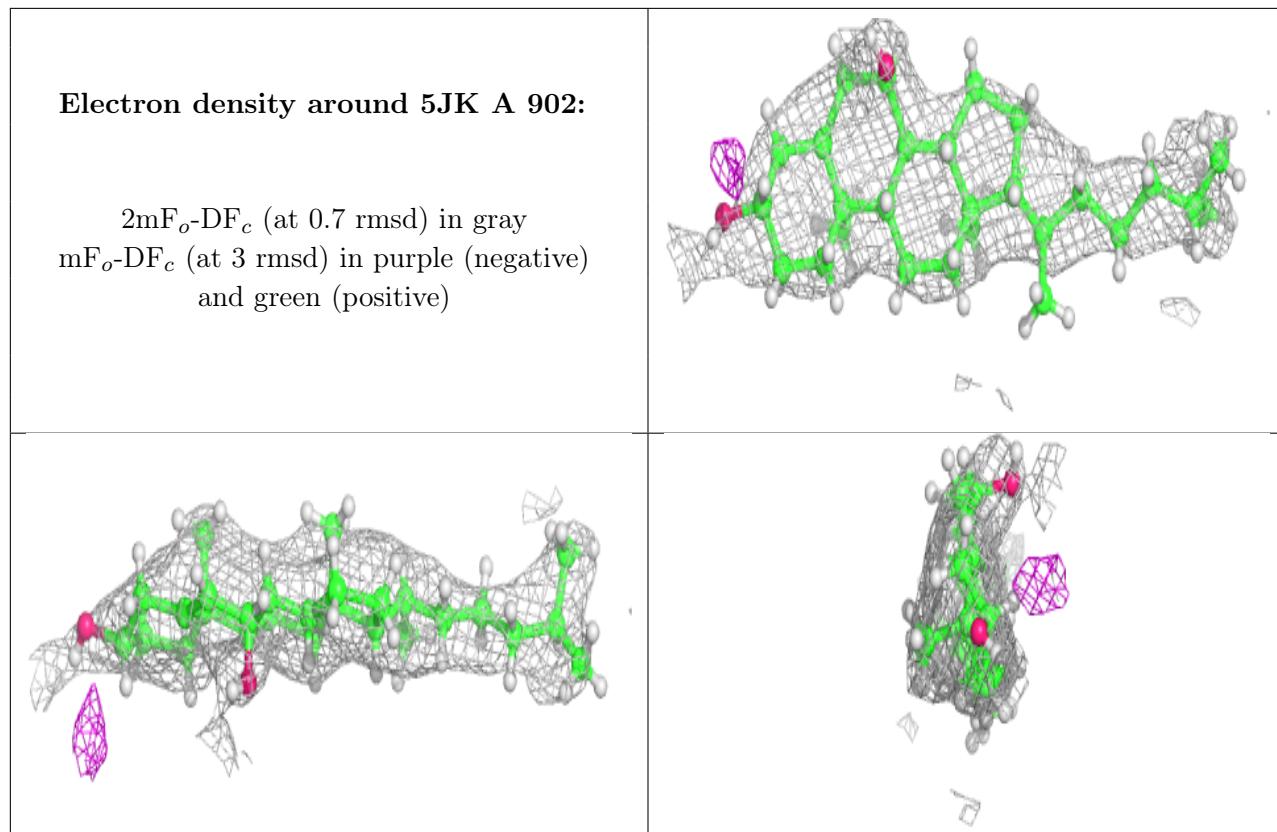


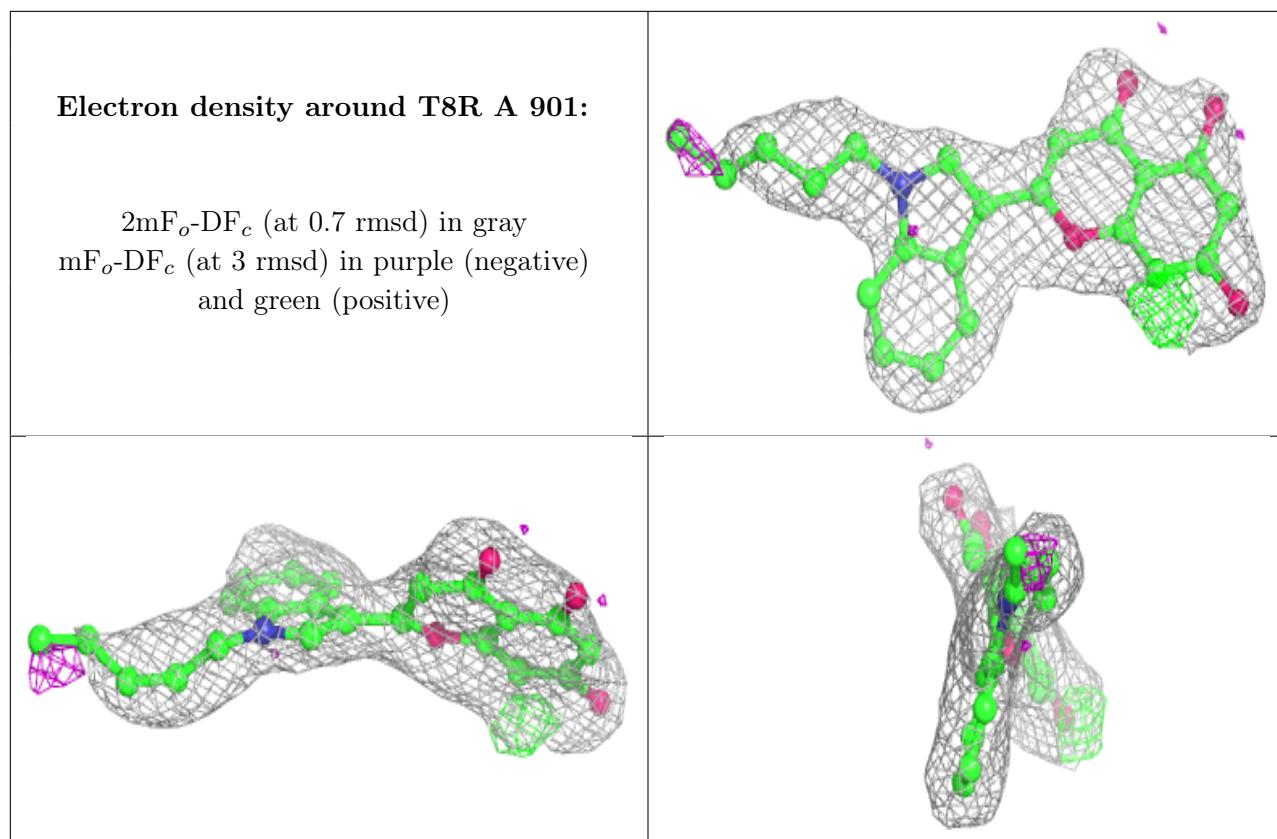
6.4 Ligands [\(i\)](#)

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, 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
5	ZN	A	904	1/1	0.84	0.06	90,90,90,90	0
4	5JK	A	902	29/29	0.86	0.23	30,42,61,68	75
3	T8R	A	901	27/27	0.86	0.25	42,44,48,53	0
7	CA	A	909	1/1	0.94	0.15	60,60,60,60	0
7	CA	A	910	1/1	0.94	0.06	40,40,40,40	0
5	ZN	A	903	1/1	0.95	0.14	46,46,46,46	0
6	IOD	A	905	1/1	0.98	0.08	50,50,50,50	0
6	IOD	A	908	1/1	0.99	0.09	71,71,71,71	0
6	IOD	A	906	1/1	0.99	0.09	78,78,78,78	0
6	IOD	A	907	1/1	0.99	0.07	72,72,72,72	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.