



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:46 AM UTC

PDB ID : 2A40 / pdb_00002a40
Title : Ternary complex of the WH2 domain of WAVE with Actin-DNAse I
Authors : Chereau, D.; Kerff, F.; Dominguez, R.
Deposited on : 2005-06-27
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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

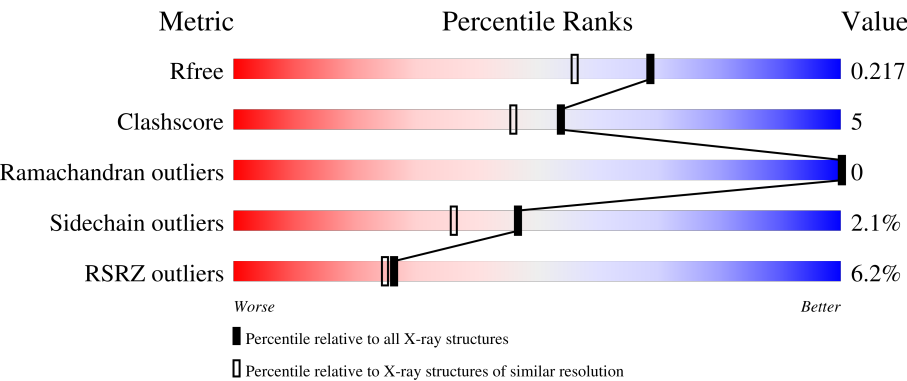
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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.



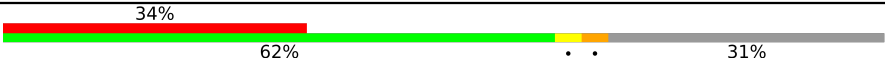
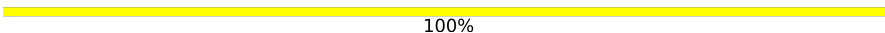
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	375	3% 86% 10% ••
1	D	375	10% 84% 12% •
2	B	260	5% 93% 7%
2	E	260	2% 90% 10%
3	C	32	12% 56% 9% • 31%

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Mol	Chain	Length	Quality of chain
3	F	32	
4	G	2	
4	H	2	

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 11357 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	15	0
			2899	1843	481	552	23			
1	D	362	Total	C	N	O	S	0	12	0
			2878	1829	477	549	23			

- Molecule 2 is a protein called Deoxyribonuclease-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	260	Total	C	N	O	S	0	5	0
			2071	1312	345	406	8			
2	E	260	Total	C	N	O	S	0	12	0
			2109	1340	351	410	8			

- Molecule 3 is a protein called Wiskott-Aldrich syndrome protein family member 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	22	Total	C	N	O	0	1	0
			181	109	36	36			
3	F	22	Total	C	N	O	0	1	0
			181	109	36	36			

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



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

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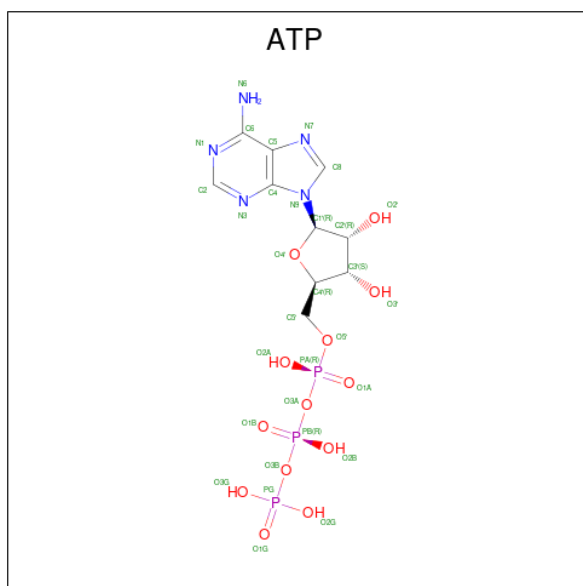
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	B	1	Total	Ca	0	0
			1	1		
5	D	1	Total	Ca	0	0
			1	1		
5	E	1	Total	Ca	0	0
			1	1		

- Molecule 6 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Mg	0	0
			1	1		
8	E	1	Total	Mg	0	0
			1	1		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	288	Total	O	0	0
			288	288		
9	B	167	Total	O	0	0
			167	167		
9	C	7	Total	O	0	0
			7	7		
9	D	253	Total	O	0	0
			253	253		
9	E	183	Total	O	0	0
			183	183		

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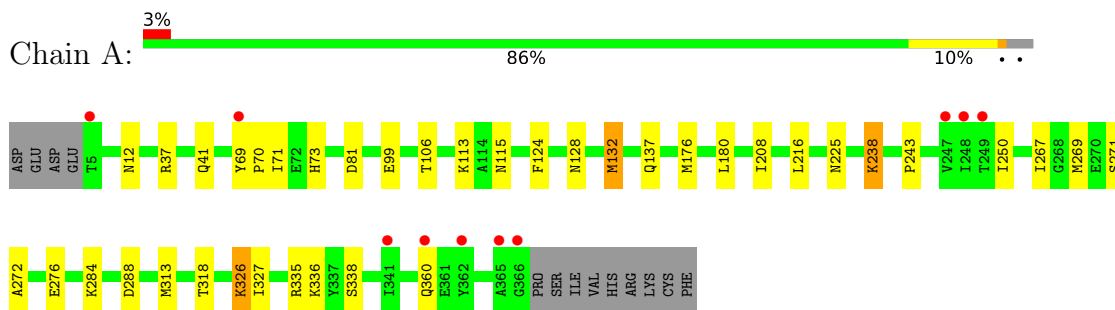
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	F	4	Total	O	0	0
			4	4		

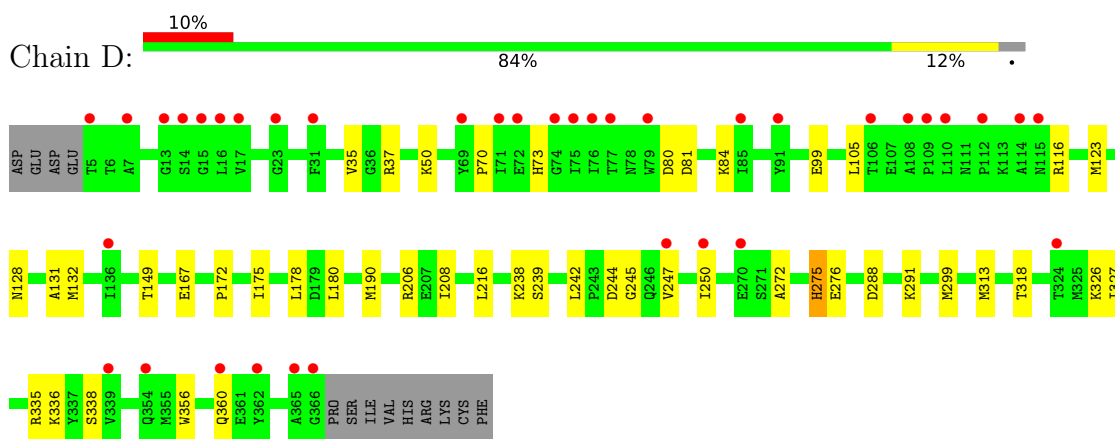
3 Residue-property plots [i](#)

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.

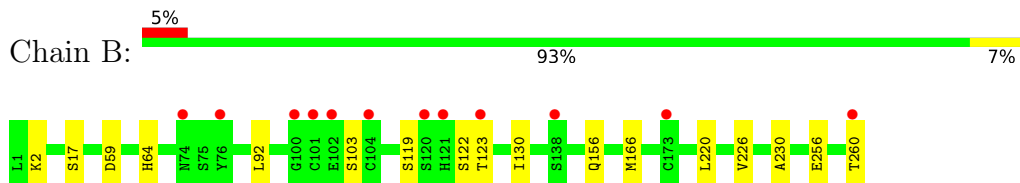
- Molecule 1: Actin, alpha skeletal muscle



- Molecule 1: Actin, alpha skeletal muscle

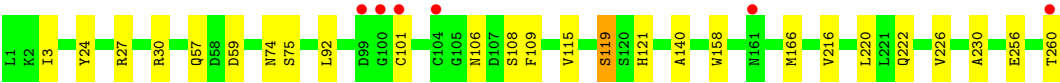


- Molecule 2: Deoxyribonuclease-1

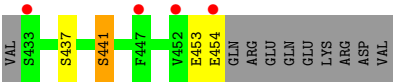


- Molecule 2: Deoxyribonuclease-1

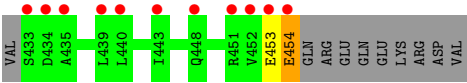




● Molecule 3: Wiskott-Aldrich syndrome protein family member 2



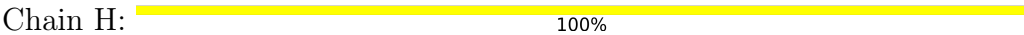
● Molecule 3: Wiskott-Aldrich syndrome protein family member 2



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	118.72Å 41.60Å 153.05Å 90.00° 108.79° 90.00°	Depositor
Resolution (Å)	47.51 – 1.80 47.51 – 1.80	Depositor EDS
% Data completeness (in resolution range)	80.6 (47.51-1.80) 80.6 (47.51-1.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.48 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.166 , 0.215 0.167 , 0.217	Depositor DCC
R_{free} test set	5386 reflections (4.06%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtriage
Anisotropy	0.327	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11357	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 84.91 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4638e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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.

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: GOL, HIC, NAG, MG, ATP, CA

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	0.76	0/2988	0.90	0/4043
1	D	0.70	0/2961	0.85	0/4007
2	B	0.82	3/2132 (0.1%)	0.89	1/2902 (0.0%)
2	E	0.73	0/2192	0.90	1/2981 (0.0%)
3	C	0.60	0/184	0.68	0/244
3	F	0.48	0/184	0.67	0/244
All	All	0.74	3/10641 (0.0%)	0.88	2/14421 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	122	SER	C-O	8.48	1.35	1.24
2	B	122	SER	C-N	7.11	1.44	1.33
2	B	123	THR	C-O	6.64	1.32	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	122	SER	O-C-N	5.57	130.09	122.46
2	E	140	ALA	N-CA-C	5.07	116.81	111.28

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	2899	0	2912	34	0
1	D	2878	0	2886	38	0
2	B	2071	0	2014	10	0
2	E	2109	0	2074	18	0
3	C	181	0	182	2	0
3	F	181	0	182	1	0
4	G	28	0	25	0	0
4	H	28	0	25	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
6	A	31	0	12	0	0
6	D	31	0	12	0	0
7	A	6	0	8	0	0
7	B	6	0	8	0	0
8	B	1	0	0	0	0
8	E	1	0	0	0	0
9	A	288	0	0	9	0
9	B	167	0	0	2	1
9	C	7	0	0	0	0
9	D	253	0	0	5	0
9	E	183	0	0	4	0
9	F	4	0	0	0	0
All	All	11357	0	10340	102	1

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 (102) 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:12[B]:ASN:ND2	9:A:1461:HOH:O	1.62	1.30
2:E:121[B]:HIS:HD2	9:E:1433:HOH:O	1.19	1.21
1:D:299:MET:CE	1:D:313[B]:MET:HG3	1.80	1.11
1:D:37:ARG:NH2	1:D:84:LYS:HE3	1.67	1.08
1:D:216:LEU:HD22	1:D:238:LYS:HE3	1.43	1.01
1:D:299:MET:HE1	1:D:313[B]:MET:HG3	1.50	0.91
1:D:299:MET:HE3	1:D:313[B]:MET:HG3	1.55	0.88
2:E:92[A]:LEU:HD11	2:E:119:SER:HB3	1.57	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:190:MET:HE1	1:D:206:ARG:NH2	1.96	0.81
2:E:121[B]:HIS:ND1	9:E:1434:HOH:O	2.15	0.80
1:D:37:ARG:HH22	1:D:84:LYS:HE3	1.47	0.77
2:B:103:SER:OG	9:B:1502:HOH:O	1.96	0.76
2:B:226:VAL:CG2	2:B:260:THR:HG23	2.17	0.73
1:A:360:GLN:NE2	1:A:360:GLN:H	1.87	0.73
1:D:244:ASP:OD1	1:D:245:GLY:N	2.22	0.72
1:A:115[A]:ASN:ND2	9:A:1640:HOH:O	2.23	0.72
1:A:176:MET:HE1	1:A:284[B]:LYS:CE	2.22	0.70
2:B:17[B]:SER:OG	9:B:1523:HOH:O	2.11	0.67
1:D:291:LYS:HE3	9:D:1622:HOH:O	1.94	0.67
1:D:216:LEU:HD22	1:D:238:LYS:CE	2.21	0.67
1:D:216:LEU:CD2	1:D:238:LYS:HE3	2.25	0.65
1:D:190:MET:HE1	1:D:206:ARG:HH22	1.63	0.60
1:A:176:MET:HE1	1:A:284[B]:LYS:HE3	1.84	0.59
2:E:92[A]:LEU:HD11	2:E:119:SER:CB	2.31	0.59
1:D:313[B]:MET:HE2	9:D:1612:HOH:O	2.03	0.57
1:A:176:MET:HE2	1:A:284[B]:LYS:HD2	1.86	0.57
1:D:275:HIS:CD2	1:D:275:HIS:H	2.23	0.56
1:A:12[B]:ASN:CG	9:A:1461:HOH:O	2.26	0.55
1:D:326:LYS:NZ	9:D:1622:HOH:O	2.39	0.55
1:A:176:MET:HE1	1:A:284[B]:LYS:NZ	2.22	0.55
1:A:326:LYS:NZ	9:A:1571:HOH:O	2.39	0.54
1:D:116[B]:ARG:CZ	9:D:1499:HOH:O	2.55	0.54
1:A:360:GLN:H	1:A:360:GLN:HE21	1.56	0.53
2:B:226:VAL:HG22	2:B:260:THR:HG23	1.90	0.53
1:D:37:ARG:HH21	1:D:84:LYS:HE3	1.66	0.53
1:D:35:VAL:HG11	1:D:84:LYS:HD2	1.91	0.52
1:A:216:LEU:HD22	1:A:238[A]:LYS:HE3	1.91	0.52
1:A:106:THR:HB	1:A:137:GLN:HG3	1.91	0.52
3:C:453:GLU:HA	3:C:453:GLU:OE2	2.10	0.52
1:D:272:ALA:HB1	1:D:276:GLU:HB2	1.92	0.51
1:D:299:MET:HE1	1:D:313[B]:MET:CG	2.32	0.51
1:D:99:GLU:H	1:D:99:GLU:CD	2.19	0.51
1:A:115[B]:ASN:ND2	9:A:1440:HOH:O	2.43	0.51
1:A:176:MET:CE	1:A:284[B]:LYS:HD2	2.41	0.50
1:A:70:PRO:HG3	1:A:81:ASP:HB3	1.94	0.50
1:D:80:ASP:O	1:D:84:LYS:HE2	2.12	0.49
2:E:260:THR:HG22	9:E:1344:HOH:O	2.12	0.49
1:D:37:ARG:NH2	1:D:84:LYS:CE	2.58	0.49
1:A:272:ALA:HB1	1:A:276[B]:GLU:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:172:PRO:HA	1:D:175:ILE:HD12	1.95	0.48
2:E:121[B]:HIS:CD2	9:E:1433:HOH:O	2.11	0.48
1:A:12[A]:ASN:HB3	1:A:71:ILE:CD1	2.43	0.48
1:A:37:ARG:NH2	1:A:81:ASP:OD1	2.36	0.48
3:C:437:SER:O	3:C:441[A]:SER:OG	2.30	0.48
2:E:24:TYR:HE1	2:E:27[B]:ARG:HH21	1.59	0.48
1:A:41:GLN:HB2	2:B:64:HIS:CD2	2.49	0.48
1:D:318:THR:HA	1:D:327:ILE:HD13	1.96	0.47
2:E:226:VAL:CG2	2:E:260:THR:HG23	2.45	0.47
1:D:326:LYS:HB3	1:D:326:LYS:HE3	1.69	0.47
2:B:130:ILE:HG21	2:B:166:MET:HE2	1.96	0.47
1:D:149:THR:OG1	1:D:167:GLU:OE2	2.30	0.47
1:A:132:MET:HE2	1:A:132:MET:HB2	1.81	0.47
1:A:180[B]:LEU:HD13	1:A:267:ILE:HD11	1.97	0.46
1:D:275:HIS:H	1:D:275:HIS:HD2	1.63	0.46
1:A:69:TYR:HE1	9:A:1564:HOH:O	1.97	0.46
2:E:106:ASN:HA	2:E:109:PHE:O	2.15	0.46
1:A:360:GLN:NE2	1:A:360:GLN:N	2.60	0.46
1:D:335:ARG:HA	1:D:338:SER:OG	2.17	0.45
1:D:105:LEU:HD11	1:D:123:MET:HG3	1.98	0.45
2:E:3:ILE:HG22	2:E:166:MET:HE1	1.99	0.45
2:E:24:TYR:HE1	2:E:27[B]:ARG:NH2	2.14	0.45
1:D:336:LYS:HG2	9:D:1545:HOH:O	2.16	0.44
2:E:230:ALA:HA	2:E:256:GLU:O	2.17	0.44
1:A:318:THR:HA	1:A:327:ILE:CD1	2.47	0.44
1:D:208:ILE:HD13	1:D:242:LEU:HD22	1.99	0.44
1:A:115[A]:ASN:CG	9:A:1640:HOH:O	2.58	0.44
1:A:336:LYS:HE2	9:A:1632:HOH:O	2.18	0.44
3:F:454:GLU:H	3:F:454:GLU:HG3	1.56	0.44
1:D:70:PRO:HG3	1:D:81:ASP:HB3	2.00	0.43
1:A:113:LYS:HB3	1:A:113:LYS:HE3	1.91	0.43
1:A:124:PHE:O	1:A:128[A]:ASN:HA	2.19	0.43
1:A:124:PHE:O	1:A:128[B]:ASN:HA	2.19	0.43
2:B:220:LEU:HD12	2:B:220:LEU:HA	1.92	0.42
2:E:74:ASN:CG	2:E:75:SER:H	2.27	0.42
2:E:59:ASP:OD1	2:E:59:ASP:C	2.62	0.42
1:D:178:LEU:HG	1:D:180[B]:LEU:HB3	2.02	0.42
1:A:335:ARG:HA	1:A:338:SER:OG	2.20	0.42
2:E:115:VAL:HG12	2:E:158:TRP:CZ3	2.55	0.42
1:D:132:MET:HE2	1:D:132:MET:HB2	1.83	0.41
1:D:131:ALA:HB1	1:D:356:TRP:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:92:LEU:HD11	2:B:119:SER:HB2	2.02	0.41
2:B:230:ALA:HA	2:B:256:GLU:O	2.19	0.41
1:A:269[A]:MET:HG2	1:A:271:SER:HB3	2.02	0.41
1:A:313:MET:HE2	1:A:313:MET:HB2	1.91	0.41
2:E:30[B]:ARG:HH22	2:E:57:GLN:HE21	1.69	0.41
2:E:216:VAL:HG23	2:E:222:GLN:HG2	2.03	0.41
1:A:208:ILE:HD11	1:A:243:PRO:HG2	2.03	0.40
2:B:59:ASP:OD1	2:B:59:ASP:C	2.63	0.40
1:A:336:LYS:HG2	9:A:1441:HOH:O	2.21	0.40
1:D:275:HIS:CD2	1:D:275:HIS:N	2.89	0.40
1:D:239:SER:HB3	1:D:247:VAL:CG1	2.52	0.40

All (1) 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)
9:B:1464:HOH:O	9:B:1550:HOH:O[2_556]	2.18	0.02

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	374/375 (100%)	369 (99%)	5 (1%)	0	100	100
1	D	371/375 (99%)	365 (98%)	6 (2%)	0	100	100
2	B	263/260 (101%)	255 (97%)	8 (3%)	0	100	100
2	E	270/260 (104%)	266 (98%)	4 (2%)	0	100	100
3	C	21/32 (66%)	21 (100%)	0	0	100	100
3	F	21/32 (66%)	21 (100%)	0	0	100	100
All	All	1320/1334 (99%)	1297 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	319/317 (101%)	311 (98%)	8 (2%)	42	30
1	D	316/317 (100%)	310 (98%)	6 (2%)	50	41
2	B	234/229 (102%)	232 (99%)	2 (1%)	70	67
2	E	241/229 (105%)	236 (98%)	5 (2%)	47	36
3	C	20/29 (69%)	17 (85%)	3 (15%)	3	0
3	F	20/29 (69%)	18 (90%)	2 (10%)	7	2
All	All	1150/1150 (100%)	1124 (98%)	26 (2%)	47	33

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	GLU
1	A	132	MET
1	A	225	ASN
1	A	238[A]	LYS
1	A	238[B]	LYS
1	A	250	ILE
1	A	288	ASP
1	A	326	LYS
2	B	2	LYS
2	B	156	GLN
3	C	441[A]	SER
3	C	441[B]	SER
3	C	454	GLU
1	D	50	LYS
1	D	128	ASN
1	D	250	ILE
1	D	275	HIS
1	D	288	ASP
1	D	360	GLN

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Mol	Chain	Res	Type
2	E	101	CYS
2	E	108[A]	SER
2	E	108[B]	SER
2	E	119	SER
2	E	220	LEU
3	F	453	GLU
3	F	454	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	ASN
1	A	162	ASN
1	A	225	ASN
1	A	280	ASN
1	A	360	GLN
2	B	61	ASN
2	B	156	GLN
2	B	236	GLN
2	B	243	ASN
1	D	49	GLN
1	D	92	ASN
1	D	275	HIS
1	D	280	ASN
2	E	57	GLN
2	E	74	ASN
2	E	106	ASN
2	E	161	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	HIC	D	73	1	10,11,12	0.93	0	9,14,16	4.79	3 (33%)
1	HIC	A	73	1	10,11,12	0.98	0	9,14,16	3.96	2 (22%)

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
1	HIC	D	73	1	-	0/5/6/8	0/1/1/1
1	HIC	A	73	1	-	0/5/6/8	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	73	HIC	NE2-CE1-ND1	-12.34	107.94	112.66
1	A	73	HIC	NE2-CE1-ND1	-10.09	108.80	112.66
1	D	73	HIC	CD2-NE2-CE1	6.28	109.19	106.71
1	A	73	HIC	CD2-NE2-CE1	5.29	108.80	106.71
1	D	73	HIC	CB-CG-ND1	2.07	127.93	121.74

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

4 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	$\# Z > 2$
4	NAG	G	1	2,4	14,14,15	0.51	0	17,19,21	0.98	0
4	NAG	G	2	4	14,14,15	0.58	0	17,19,21	1.18	2 (11%)
4	NAG	H	1	2,4	14,14,15	0.66	0	17,19,21	1.00	1 (5%)
4	NAG	H	2	4	14,14,15	0.46	0	17,19,21	1.21	2 (11%)

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	NAG	G	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	1/6/23/26	0/1/1/1
4	NAG	H	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	2	NAG	C1-O5-C5	2.95	116.14	112.19
4	H	1	NAG	O5-C1-C2	-2.94	106.75	111.29
4	G	2	NAG	C4-C3-C2	-2.61	107.20	111.02
4	H	2	NAG	C1-O5-C5	2.28	115.24	112.19
4	H	2	NAG	C2-N2-C7	-2.01	120.21	122.90

There are no chirality outliers.

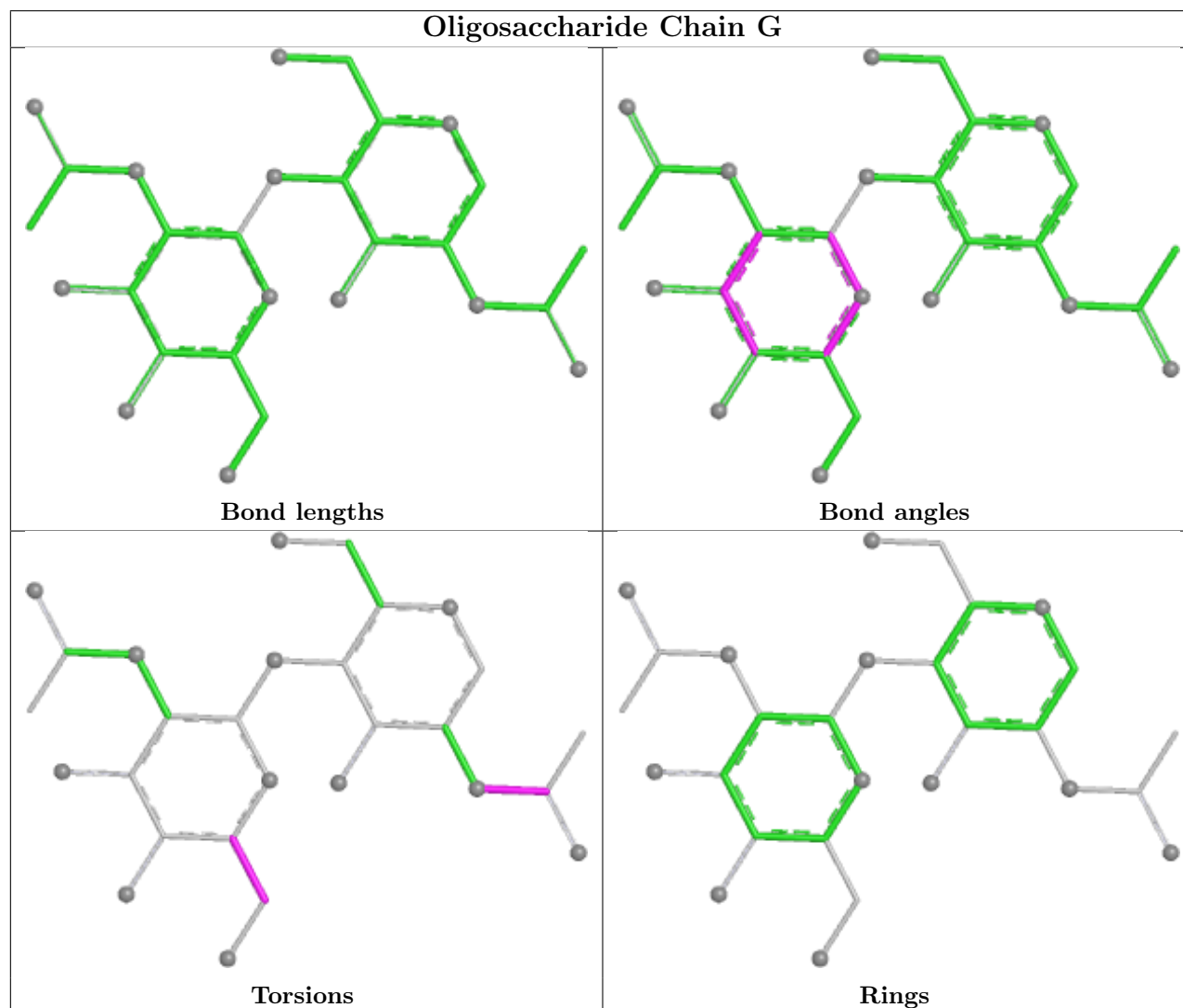
All (5) torsion outliers are listed below:

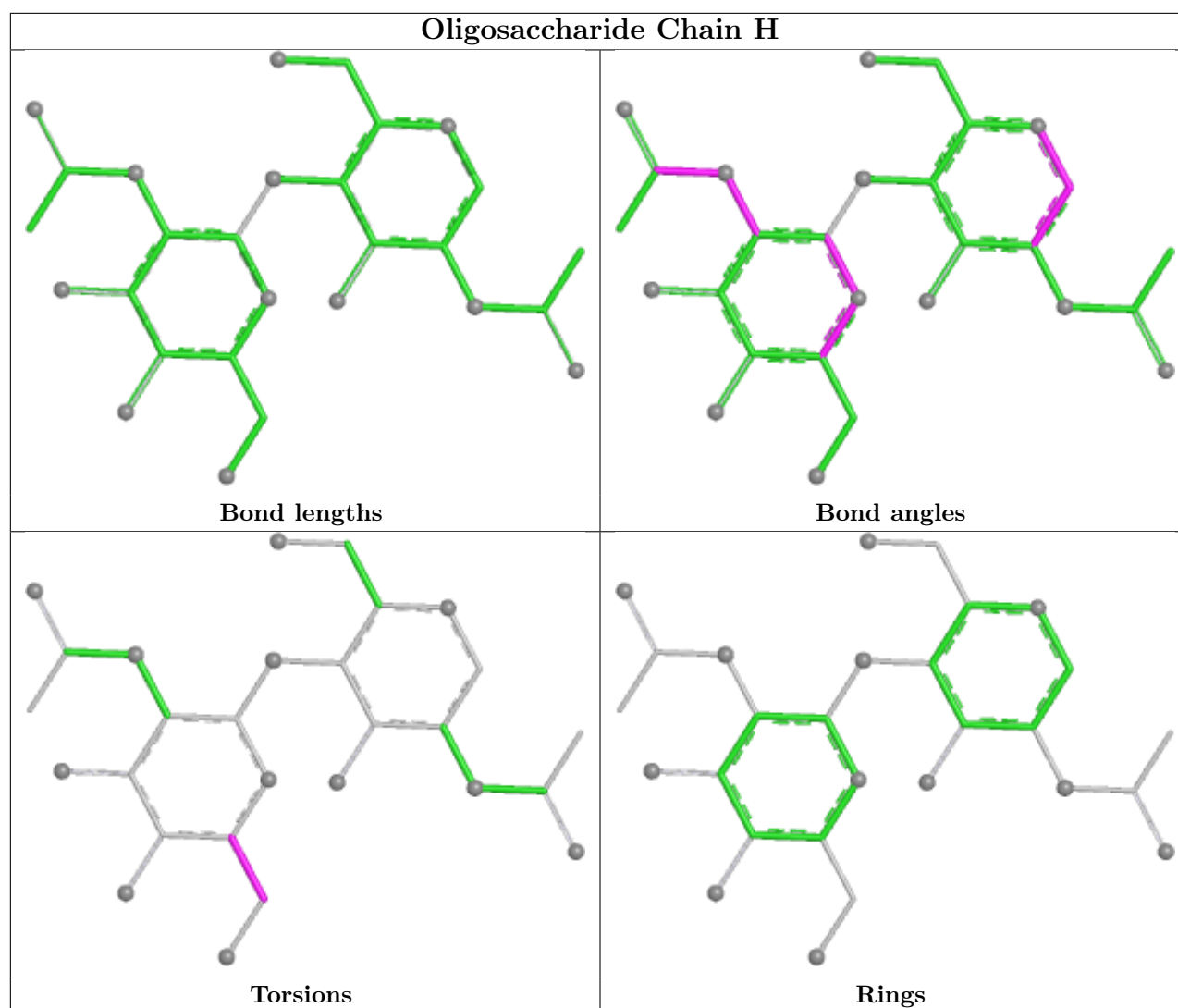
Mol	Chain	Res	Type	Atoms
4	H	2	NAG	O5-C5-C6-O6
4	H	2	NAG	C4-C5-C6-O6
4	G	1	NAG	C8-C7-N2-C2
4	G	1	NAG	O7-C7-N2-C2
4	G	2	NAG	C4-C5-C6-O6

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.





5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 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	$\# Z > 2$
6	ATP	D	1380	5	32,33,33	1.55	6 (18%)	48,52,52	1.81	10 (20%)
7	GOL	A	1383	-	5,5,5	0.37	0	5,5,5	0.93	0
7	GOL	B	1384	-	5,5,5	0.46	0	5,5,5	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	ATP	A	1379	5	32,33,33	1.82	8 (25%)	48,52,52	1.67	12 (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
6	ATP	D	1380	5	-	1/22/38/38	0/3/3/3
7	GOL	A	1383	-	-	2/4/4/4	-
7	GOL	B	1384	-	-	4/4/4/4	-
6	ATP	A	1379	5	-	1/22/38/38	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1379	ATP	C5-C4	4.34	1.46	1.39
6	A	1379	ATP	PA-O3A	4.09	1.63	1.59
6	A	1379	ATP	PB-O3B	3.96	1.63	1.59
6	D	1380	ATP	C5-C4	3.91	1.46	1.39
6	D	1380	ATP	PB-O3B	3.45	1.63	1.59
6	A	1379	ATP	C5-N7	-3.16	1.33	1.39
6	D	1380	ATP	PA-O3A	2.99	1.62	1.59
6	D	1380	ATP	C8-N7	2.97	1.37	1.31
6	A	1379	ATP	C4-N9	-2.88	1.31	1.37
6	A	1379	ATP	C8-N7	2.59	1.36	1.31
6	D	1380	ATP	C5-N7	-2.43	1.34	1.39
6	A	1379	ATP	PB-O3A	2.33	1.62	1.59
6	D	1380	ATP	C5-C6	2.04	1.46	1.41
6	A	1379	ATP	C5-C6	2.03	1.46	1.41

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1379	ATP	C5-C4-N3	-5.04	119.78	126.72
6	D	1380	ATP	C5-C4-N3	-4.92	119.94	126.72
6	D	1380	ATP	N3-C4-N9	4.22	134.34	127.17
6	A	1379	ATP	N3-C4-N9	3.96	133.90	127.17
6	D	1380	ATP	N3-C2-N1	-3.70	122.98	128.58
6	D	1380	ATP	C4-N9-C8	3.58	109.50	105.74
6	D	1380	ATP	C2-N3-C4	3.45	120.25	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1379	ATP	C2-N3-C4	2.95	119.04	111.83
6	D	1380	ATP	N9-C8-N7	-2.94	109.77	113.94
6	A	1379	ATP	O3G-PG-O2G	2.82	118.38	107.80
6	A	1379	ATP	N3-C2-N1	-2.82	124.32	128.58
6	A	1379	ATP	C4-N9-C8	2.81	108.69	105.74
6	D	1380	ATP	O3G-PG-O2G	2.78	118.24	107.80
6	A	1379	ATP	C4-C5-N7	-2.68	107.52	110.58
6	D	1380	ATP	C4-C5-N7	-2.52	107.70	110.58
6	D	1380	ATP	C5-N7-C8	2.47	107.34	103.45
6	A	1379	ATP	N9-C8-N7	-2.27	110.71	113.94
6	A	1379	ATP	O4'-C1'-C2'	-2.16	102.00	106.62
6	A	1379	ATP	C5-N7-C8	2.11	106.77	103.45
6	A	1379	ATP	N6-C6-N1	2.05	122.95	118.38
6	D	1380	ATP	C2-N1-C6	2.05	122.10	118.73
6	A	1379	ATP	O4'-C4'-C5'	-2.02	102.88	109.33

There are no chirality outliers.

All (8) torsion outliers are listed below:

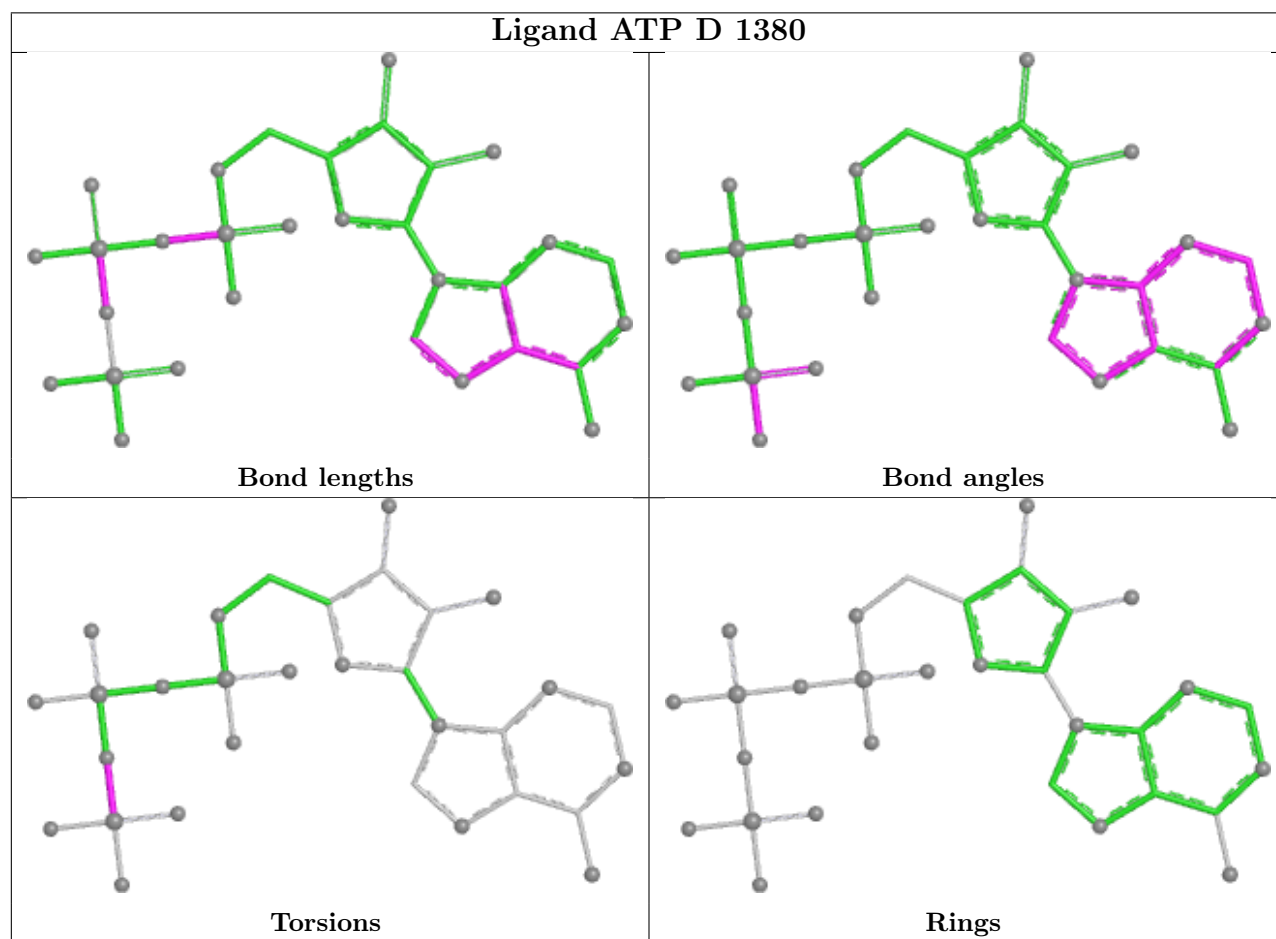
Mol	Chain	Res	Type	Atoms
7	A	1383	GOL	C1-C2-C3-O3
7	B	1384	GOL	O1-C1-C2-C3
7	B	1384	GOL	C1-C2-C3-O3
7	B	1384	GOL	O2-C2-C3-O3
7	A	1383	GOL	O2-C2-C3-O3
6	A	1379	ATP	PB-O3B-PG-O1G
7	B	1384	GOL	O1-C1-C2-O2
6	D	1380	ATP	PB-O3B-PG-O1G

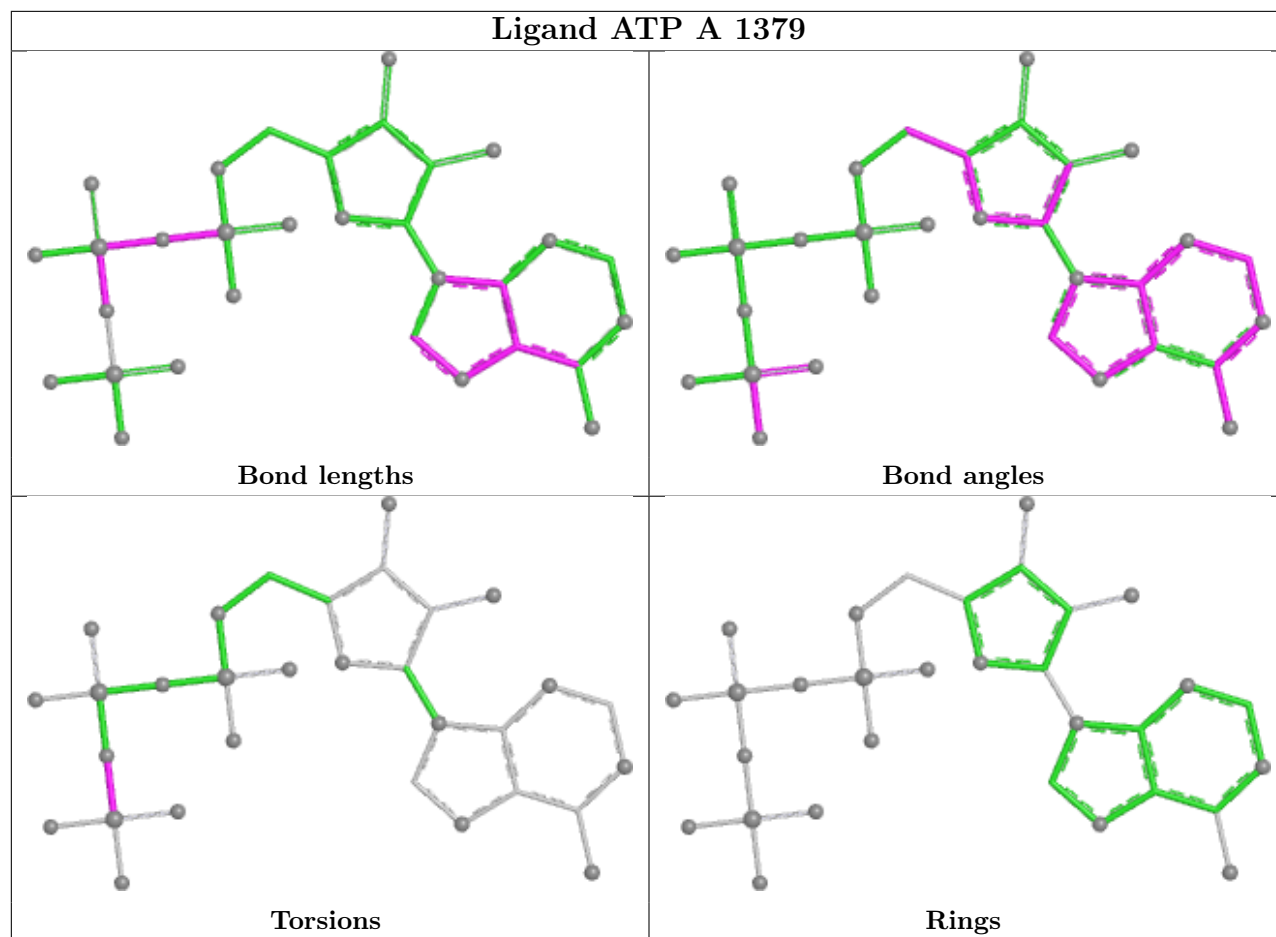
There are no ring outliers.

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 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](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	361/375 (96%)	0.39	10 (2%)	55 55	13, 26, 40, 61	15 (4%)
1	D	361/375 (96%)	0.76	37 (10%)	12 10	13, 30, 43, 61	12 (3%)
2	B	260/260 (100%)	0.70	12 (4%)	37 36	16, 28, 41, 55	5 (1%)
2	E	260/260 (100%)	0.31	6 (2%)	61 61	16, 27, 37, 50	12 (4%)
3	C	22/32 (68%)	1.12	4 (18%)	3 3	22, 40, 55, 59	1 (4%)
3	F	22/32 (68%)	2.01	11 (50%)	0 0	23, 43, 53, 61	1 (4%)
All	All	1286/1334 (96%)	0.58	80 (6%)	26 25	13, 28, 43, 61	46 (3%)

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	71	ILE	4.6
1	D	74	GLY	4.2
1	D	75	ILE	4.2
1	D	114	ALA	4.0
1	D	360	GLN	4.0
2	B	101	CYS	3.9
2	E	100	GLY	3.9
1	D	77	THR	3.9
1	D	76	ILE	3.8
2	B	100	GLY	3.6
1	D	5	THR	3.6
2	E	260	THR	3.6
1	D	79	TRP	3.5
1	D	110	LEU	3.5
3	F	448	GLN	3.5
1	A	366	GLY	3.5
1	D	14	SER	3.5
1	D	365	ALA	3.4
2	B	121	HIS	3.3

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Mol	Chain	Res	Type	RSRZ
2	B	123	THR	3.2
1	D	69	TYR	3.2
3	F	452	VAL	3.2
1	D	108	ALA	3.1
1	D	366	GLY	3.1
1	D	324	THR	3.1
1	A	365	ALA	3.1
3	F	435	ALA	3.0
3	C	433	SER	2.9
1	D	112	PRO	2.8
3	F	453	GLU	2.8
3	F	454	GLU	2.8
1	A	248	ILE	2.8
2	B	260	THR	2.8
1	A	360	GLN	2.8
1	D	13	GLY	2.8
3	F	440	LEU	2.8
3	C	447	PHE	2.7
1	A	5	THR	2.7
1	D	7	ALA	2.6
1	D	15	GLY	2.6
2	B	76	TYR	2.6
3	F	443	ILE	2.6
1	D	85	ILE	2.5
1	D	339	VAL	2.5
1	D	16	LEU	2.5
2	E	161	ASN	2.5
1	D	136	ILE	2.5
3	F	433	SER	2.5
1	D	115	ASN	2.4
1	A	69	TYR	2.4
1	D	109	PRO	2.4
1	D	17	VAL	2.4
2	E	99	ASP	2.4
1	A	341	ILE	2.4
3	C	452	VAL	2.3
2	E	101	CYS	2.3
1	D	91	TYR	2.3
1	D	23	GLY	2.3
1	A	247	VAL	2.3
2	B	74[A]	ASN	2.3
3	F	451	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	362	TYR	2.2
1	D	72	GLU	2.2
2	B	173	CYS	2.2
2	E	104	CYS	2.2
3	F	434	ASP	2.2
1	D	270	GLU	2.1
2	B	102	GLU	2.1
2	B	104	CYS	2.1
1	D	31	PHE	2.1
1	D	362	TYR	2.1
1	A	249	THR	2.1
1	D	106	THR	2.1
3	F	439	LEU	2.1
2	B	138	SER	2.0
1	D	247	VAL	2.0
3	C	454	GLU	2.0
2	B	120	SER	2.0
1	D	250	ILE	2.0
1	D	354	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	HIC	D	73	11/12	0.85	0.20	26,34,38,39	0
1	HIC	A	73	11/12	0.92	0.10	23,30,34,35	0

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.

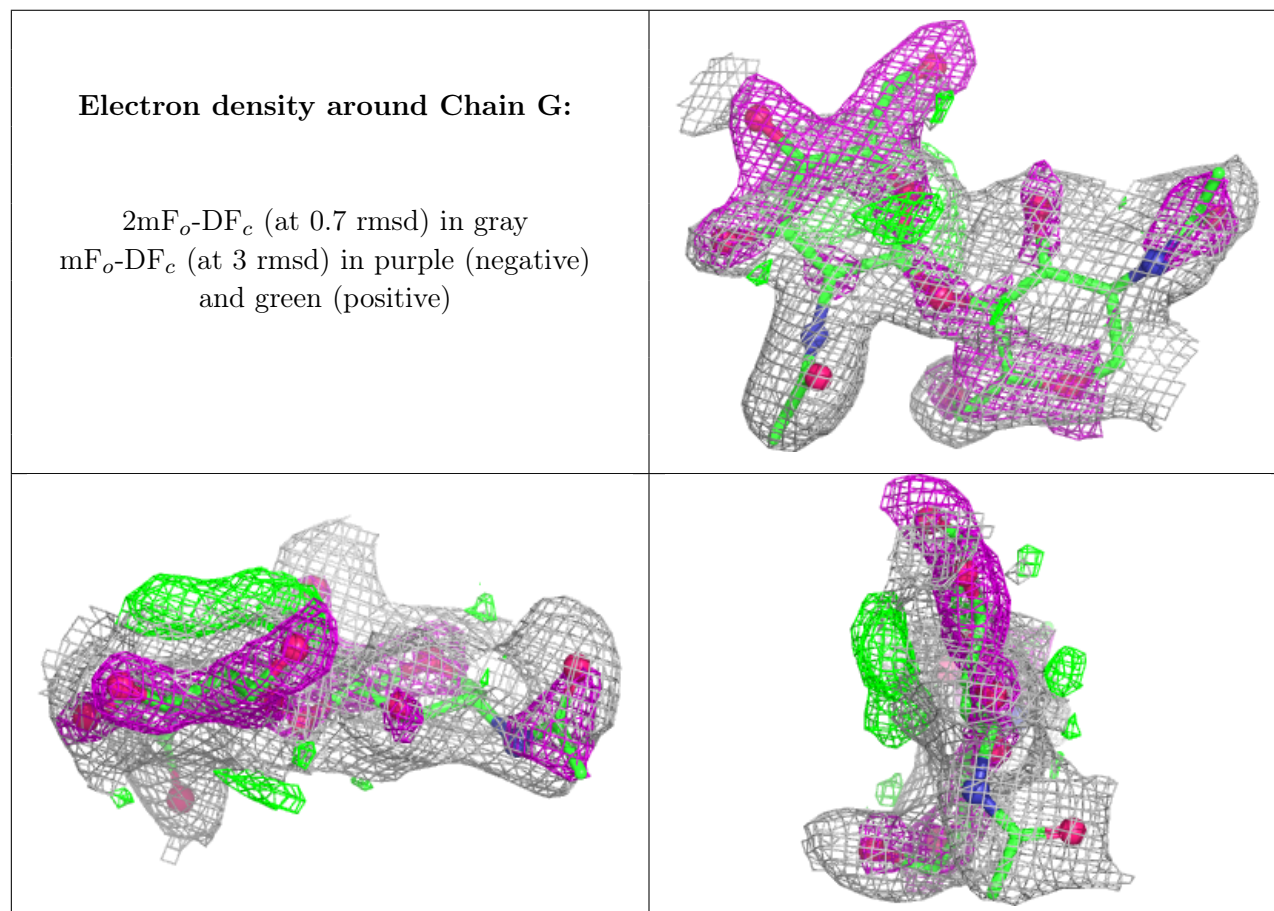
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	G	2	14/15	0.63	0.17	40,43,45,45	0
4	NAG	H	2	14/15	0.75	0.15	42,44,46,47	0

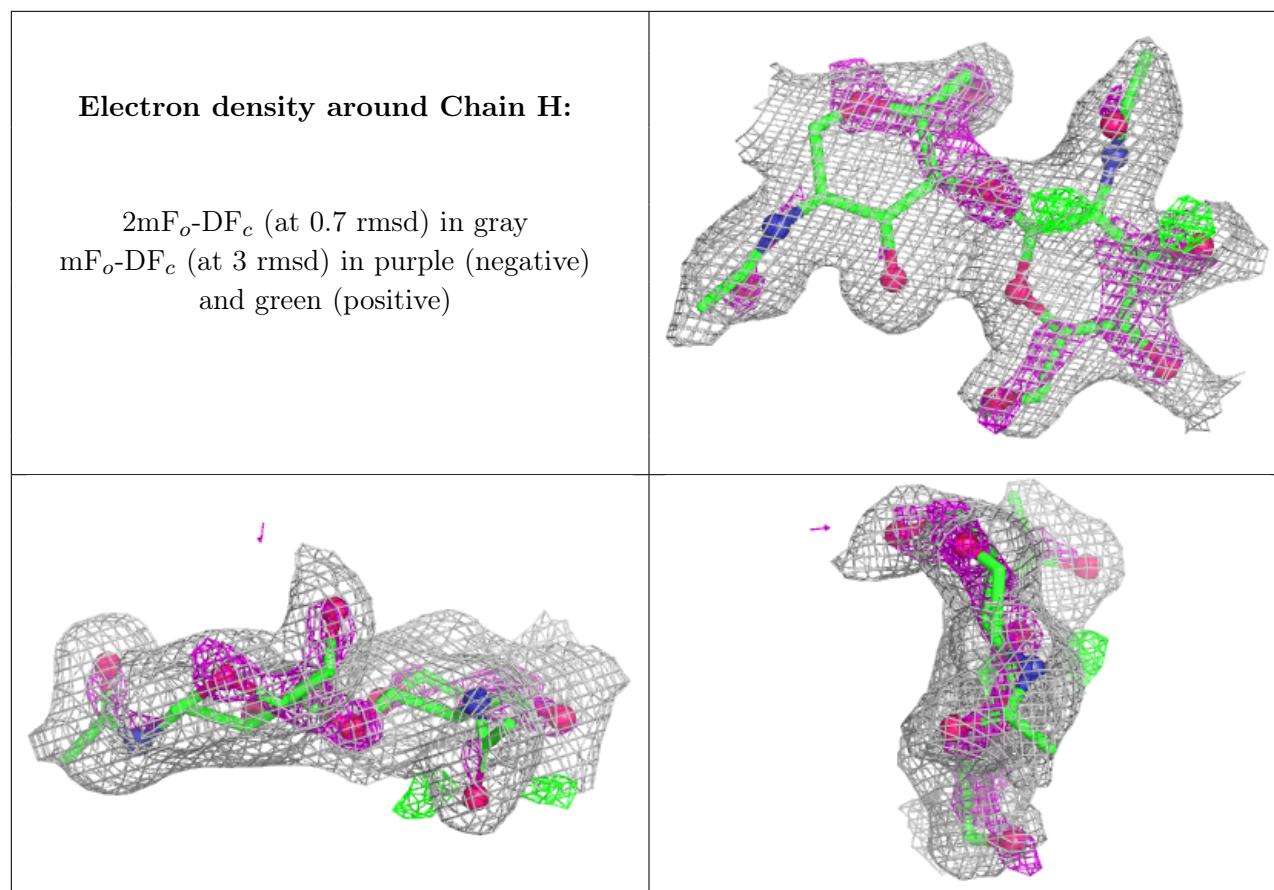
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	G	1	14/15	0.83	0.14	34,35,42,43	0
4	NAG	H	1	14/15	0.89	0.12	33,37,43,44	0

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 ⓘ

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.

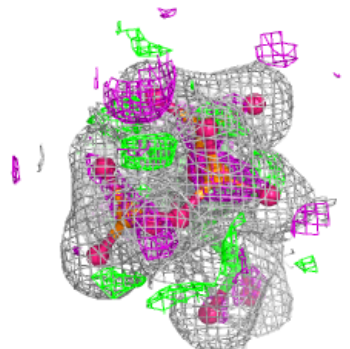
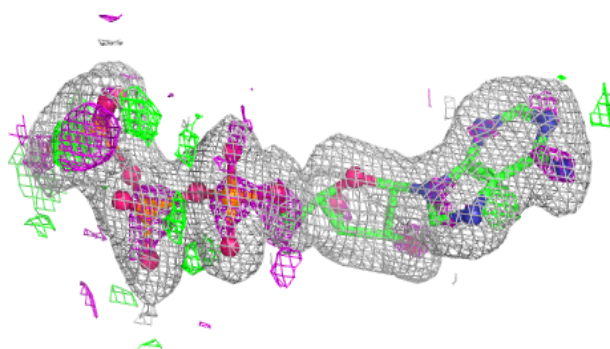
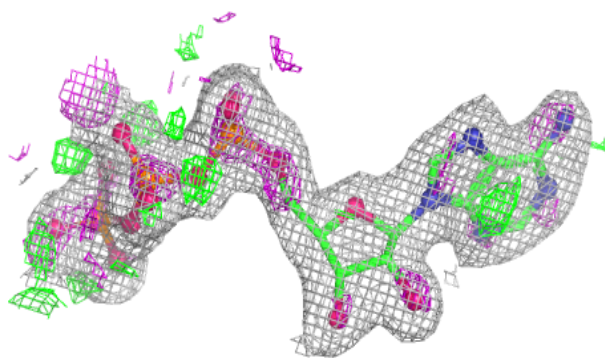
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	GOL	A	1383	6/6	0.73	0.20	52,58,59,60	0
7	GOL	B	1384	6/6	0.84	0.15	29,32,35,37	0
6	ATP	D	1380	31/31	0.97	0.08	21,24,26,27	0
5	CA	E	1272	1/1	0.97	0.14	23,23,23,23	0
6	ATP	A	1379	31/31	0.97	0.08	18,21,25,25	0
8	MG	E	1275	1/1	0.97	0.13	27,27,27,27	0
8	MG	B	1274	1/1	0.98	0.17	32,32,32,32	0
5	CA	B	1273	1/1	0.99	0.13	24,24,24,24	0
5	CA	D	1382	1/1	0.99	0.12	23,23,23,23	0
5	CA	A	1381	1/1	0.99	0.12	20,20,20,20	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.

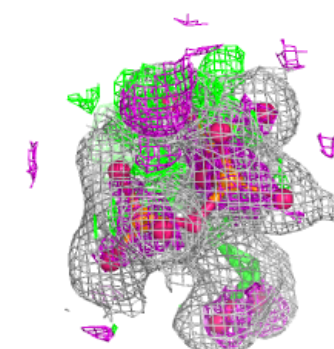
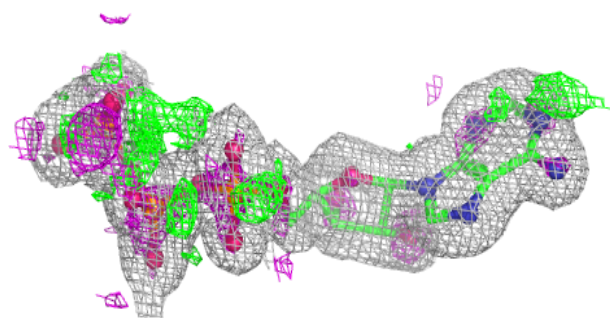
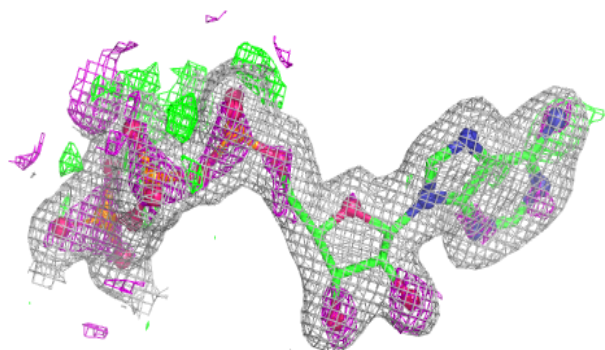
Electron density around ATP D 1380:

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



Electron density around ATP A 1379:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.