



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:35 AM UTC

PDB ID : 8RGF / pdb_00008rgf
Title : Arginase 2 in complex with inhibitor
Authors : Petersen, J.
Deposited on : 2023-12-13
Resolution : 1.86 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

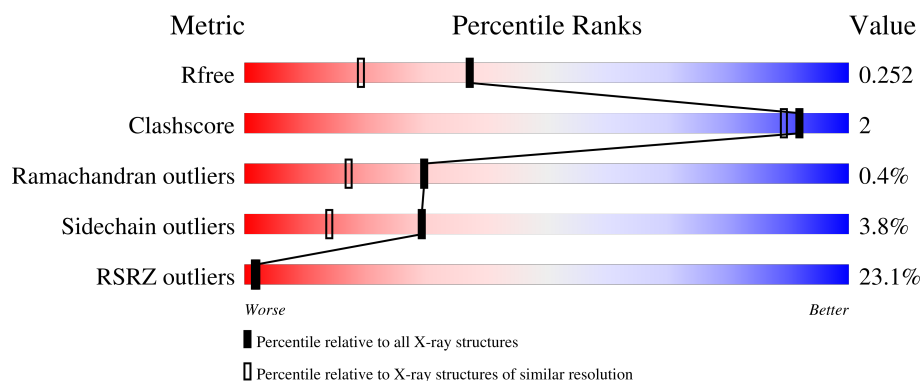
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	335	6% 87% 7% • 5%
1	B	335	55% 89% 7% • •
1	C	335	5% 85% 9% • 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7644 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 Arginase-2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2430	1536	422	463	9			
1	B	324	Total	C	N	O	S	0	0	0
			2477	1567	428	473	9			
1	C	318	Total	C	N	O	S	0	0	0
			2430	1536	422	463	9			

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	HIS	-	expression tag	UNP P78540
A	8	HIS	-	expression tag	UNP P78540
A	9	HIS	-	expression tag	UNP P78540
A	10	HIS	-	expression tag	UNP P78540
A	11	HIS	-	expression tag	UNP P78540
A	12	HIS	-	expression tag	UNP P78540
A	13	GLY	-	expression tag	UNP P78540
A	14	GLY	-	expression tag	UNP P78540
A	15	GLY	-	expression tag	UNP P78540
A	16	GLU	-	expression tag	UNP P78540
A	17	ASN	-	expression tag	UNP P78540
A	18	LEU	-	expression tag	UNP P78540
A	19	TYR	-	expression tag	UNP P78540
A	20	PHE	-	expression tag	UNP P78540
A	21	GLN	-	expression tag	UNP P78540
B	7	HIS	-	expression tag	UNP P78540
B	8	HIS	-	expression tag	UNP P78540
B	9	HIS	-	expression tag	UNP P78540
B	10	HIS	-	expression tag	UNP P78540
B	11	HIS	-	expression tag	UNP P78540
B	12	HIS	-	expression tag	UNP P78540
B	13	GLY	-	expression tag	UNP P78540
B	14	GLY	-	expression tag	UNP P78540

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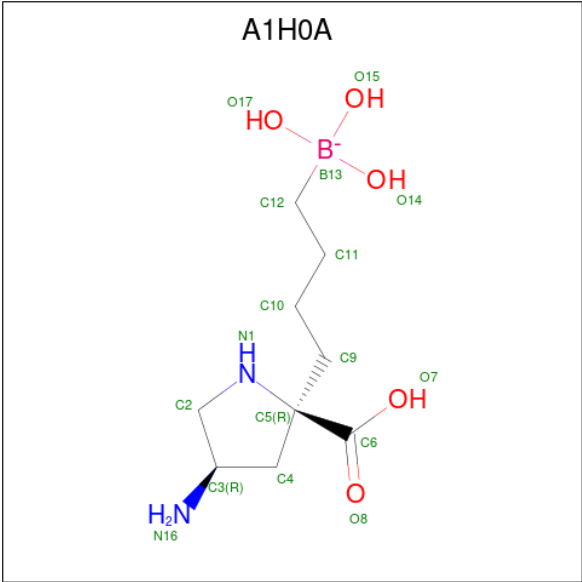
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Chain	Residue	Modelled	Actual	Comment	Reference
B	15	GLY	-	expression tag	UNP P78540
B	16	GLU	-	expression tag	UNP P78540
B	17	ASN	-	expression tag	UNP P78540
B	18	LEU	-	expression tag	UNP P78540
B	19	TYR	-	expression tag	UNP P78540
B	20	PHE	-	expression tag	UNP P78540
B	21	GLN	-	expression tag	UNP P78540
C	7	HIS	-	expression tag	UNP P78540
C	8	HIS	-	expression tag	UNP P78540
C	9	HIS	-	expression tag	UNP P78540
C	10	HIS	-	expression tag	UNP P78540
C	11	HIS	-	expression tag	UNP P78540
C	12	HIS	-	expression tag	UNP P78540
C	13	GLY	-	expression tag	UNP P78540
C	14	GLY	-	expression tag	UNP P78540
C	15	GLY	-	expression tag	UNP P78540
C	16	GLU	-	expression tag	UNP P78540
C	17	ASN	-	expression tag	UNP P78540
C	18	LEU	-	expression tag	UNP P78540
C	19	TYR	-	expression tag	UNP P78540
C	20	PHE	-	expression tag	UNP P78540
C	21	GLN	-	expression tag	UNP P78540

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mn 2 2	0	0
2	B	2	Total Mn 2 2	0	0
2	C	2	Total Mn 2 2	0	0

- Molecule 3 is 4-[(2 {R},4 {R})-4-azanyl-2-carboxy-pyrrolidin-2-yl]butyl-tris(oxidanyl) boranuide (CCD ID: A1H0A) (formula: C₉H₂₀BN₂O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	B	C	N	O	0	0
			17	1	9	2	5		
3	C	1	Total	B	C	N	O	0	0
			17	1	9	2	5		

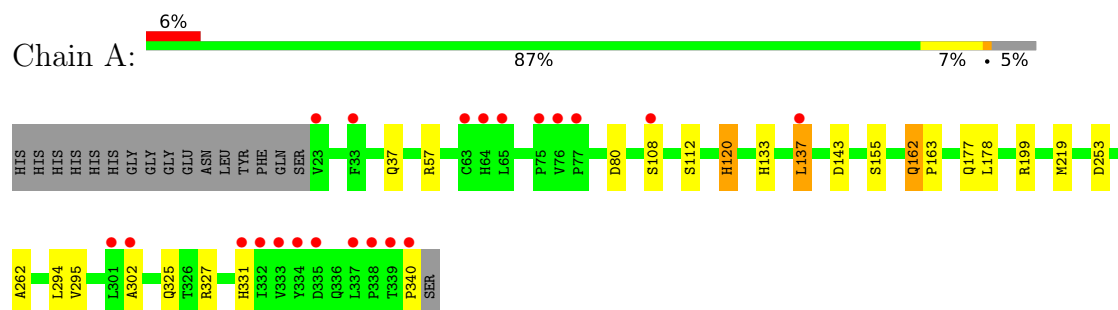
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total	O	0	0
			101	101		
4	B	52	Total	O	0	0
			52	52		
4	C	114	Total	O	0	0
			114	114		

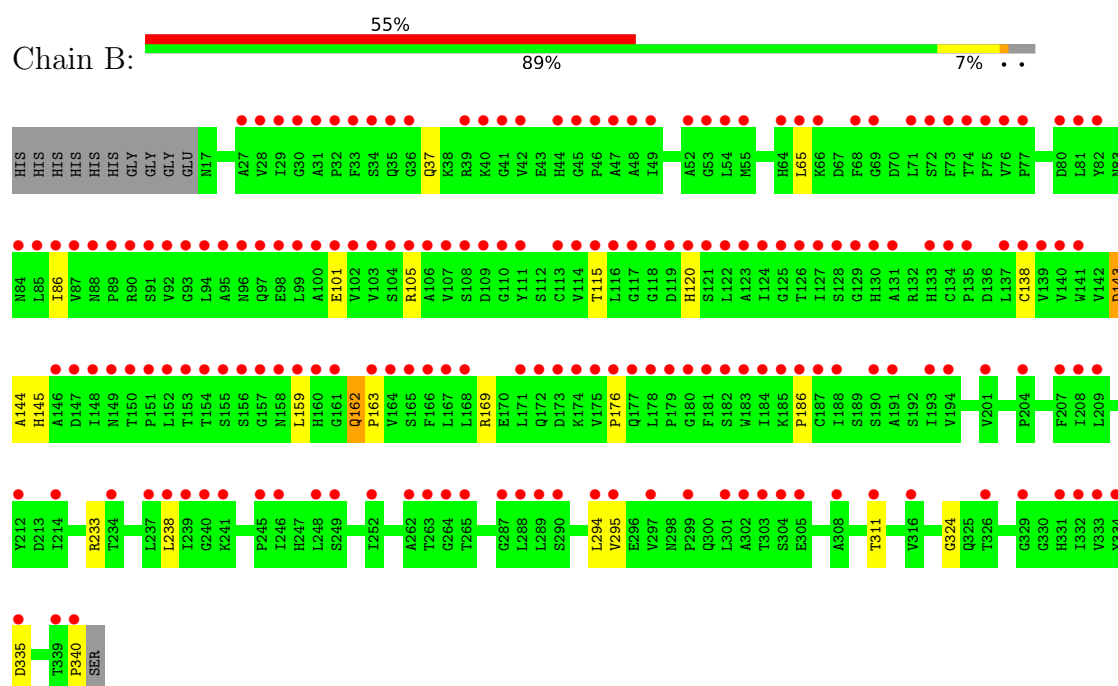
3 Residue-property plots [i](#)

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.

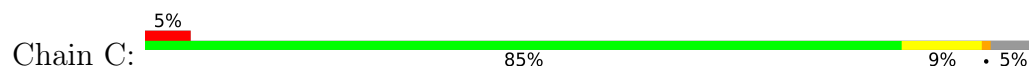
- Molecule 1: Arginase-2, mitochondrial

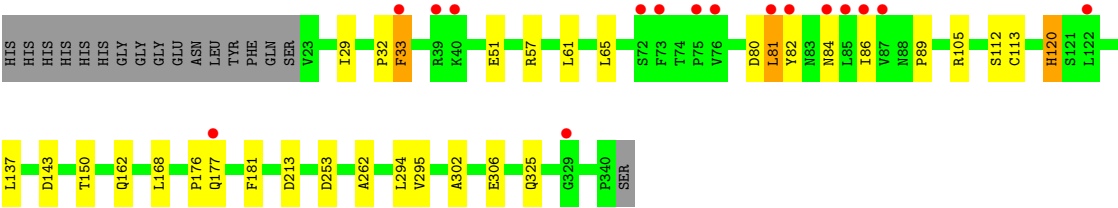


- Molecule 1: Arginase-2, mitochondrial



- Molecule 1: Arginase-2, mitochondrial





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	46.94Å 135.16Å 145.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	98.92 – 1.86 98.92 – 1.86	Depositor EDS
% Data completeness (in resolution range)	99.7 (98.92-1.86) 99.7 (98.92-1.86)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 1.86Å)	Xtriage
Refinement program	BUSTER 2.11.7 PACIOREK	Depositor
R, R_{free}	0.239 , 0.260 0.228 , 0.252	Depositor DCC
R_{free} test set	3781 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.754	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7644	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% of the height of the origin peak. No significant pseudotranslation is detected.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, A1H0A

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	0.85	0/2484	1.19	4/3382 (0.1%)
1	B	0.86	0/2531	1.30	7/3444 (0.2%)
1	C	0.88	0/2484	1.23	7/3382 (0.2%)
All	All	0.87	0/7499	1.24	18/10208 (0.2%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	143	ASP	CA-CB-CG	8.12	120.72	112.60
1	C	33	PHE	CA-CB-CG	7.18	120.98	113.80
1	A	143	ASP	CA-CB-CG	7.11	119.71	112.60
1	C	32	PRO	CA-C-N	6.56	131.49	122.77
1	C	32	PRO	C-N-CA	6.56	131.49	122.77
1	A	253	ASP	CA-CB-CG	6.45	119.05	112.60
1	C	112	SER	N-CA-C	-6.00	100.07	109.25
1	B	324	GLY	N-CA-C	5.97	120.77	113.79
1	B	295	VAL	CA-C-N	5.95	131.31	122.74
1	B	295	VAL	C-N-CA	5.95	131.31	122.74
1	A	112	SER	N-CA-C	-5.75	100.46	109.25
1	C	253	ASP	CA-CB-CG	5.59	118.19	112.60
1	A	155	SER	N-CA-C	-5.58	106.15	113.12
1	C	150	THR	N-CA-C	-5.32	103.93	110.31
1	C	143	ASP	CA-CB-CG	5.25	117.85	112.60
1	B	233	ARG	CA-C-N	5.21	127.27	120.28
1	B	233	ARG	C-N-CA	5.21	127.27	120.28
1	B	144	ALA	N-CA-C	-5.08	106.34	112.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	2430	0	2410	9	0
1	B	2477	0	2451	8	0
1	C	2430	0	2410	9	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	17	0	0	0	0
3	C	17	0	0	0	0
4	A	101	0	0	0	0
4	B	52	0	0	0	0
4	C	114	0	0	0	0
All	All	7644	0	7271	24	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 2.

All (24) 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:C:57:ARG:HD2	1:C:325:GLN:HE22	1.48	0.79
1:A:57:ARG:HH21	1:A:325:GLN:HE22	1.40	0.70
1:B:101:GLU:HB3	1:B:105:ARG:HH22	1.68	0.57
1:B:138:CYS:HB2	1:B:238:LEU:HD22	1.90	0.54
1:B:143:ASP:HB3	1:B:145:HIS:O	2.10	0.52
1:B:340:PRO:HB3	1:C:176:PRO:HB3	1.94	0.50
1:A:57:ARG:NH2	1:A:325:GLN:HE22	2.07	0.50
1:A:262:ALA:HB2	1:A:302:ALA:HB2	1.94	0.50
1:B:169:ARG:HG2	1:B:186:PRO:HB2	1.94	0.49
1:C:120:HIS:CG	1:C:295:VAL:HG21	2.49	0.48
1:C:137:LEU:HD12	1:C:137:LEU:C	2.40	0.47
1:A:108:SER:HB3	1:A:133:HIS:CE1	2.50	0.46
1:A:137:LEU:C	1:A:137:LEU:HD12	2.40	0.46
1:A:340:PRO:HB3	1:B:176:PRO:HB3	1.97	0.46
1:C:81:LEU:H	1:C:81:LEU:HD23	1.81	0.46
1:C:262:ALA:HB2	1:C:302:ALA:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ARG:HD3	1:A:219:MET:HG3	1.97	0.45
1:A:120:HIS:CG	1:A:295:VAL:HG21	2.52	0.45
1:A:162:GLN:N	1:A:163:PRO:HD2	2.33	0.44
1:B:101:GLU:HB3	1:B:105:ARG:NH2	2.31	0.43
1:C:29:ILE:HD12	1:C:113:CYS:SG	2.59	0.43
1:C:82:TYR:HB3	1:C:86:ILE:HB	2.02	0.40
1:C:89:PRO:O	1:C:181:PHE:HE1	2.04	0.40
1:B:162:GLN:N	1:B:163:PRO:HD2	2.36	0.40

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	316/335 (94%)	308 (98%)	7 (2%)	1 (0%)	36	25
1	B	321/335 (96%)	308 (96%)	11 (3%)	2 (1%)	21	10
1	C	316/335 (94%)	310 (98%)	5 (2%)	1 (0%)	36	25
All	All	953/1005 (95%)	926 (97%)	23 (2%)	4 (0%)	30	17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	86	ILE
1	A	162	GLN
1	B	162	GLN
1	C	162	GLN

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	268/282 (95%)	259 (97%)	9 (3%)	32	17
1	B	273/282 (97%)	265 (97%)	8 (3%)	37	22
1	C	268/282 (95%)	254 (95%)	14 (5%)	21	7
All	All	809/846 (96%)	778 (96%)	31 (4%)	29	14

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	80	ASP
1	A	120	HIS
1	A	137	LEU
1	A	177	GLN
1	A	178	LEU
1	A	294	LEU
1	A	327	ARG
1	A	331	HIS
1	B	37	GLN
1	B	65	LEU
1	B	115	THR
1	B	120	HIS
1	B	159	LEU
1	B	294	LEU
1	B	311	THR
1	B	335	ASP
1	C	33	PHE
1	C	51	GLU
1	C	61	LEU
1	C	65	LEU
1	C	80	ASP
1	C	81	LEU
1	C	84	ASN
1	C	105	ARG
1	C	120	HIS

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Mol	Chain	Res	Type
1	C	168	LEU
1	C	177	GLN
1	C	213	ASP
1	C	294	LEU
1	C	306	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	HIS
1	A	88	ASN
1	A	149	ASN
1	A	284	HIS
1	A	325	GLN
1	B	83	ASN
1	B	211	ASN
1	B	284	HIS
1	B	325	GLN
1	B	331	HIS
1	C	228	GLN
1	C	284	HIS

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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 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$
3	A1H0A	A	403	2	15,17,17	2.39	4 (26%)	15,25,25	1.37	3 (20%)
3	A1H0A	C	403	2	15,17,17	2.62	5 (33%)	15,25,25	1.33	3 (20%)

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	A1H0A	A	403	2	-	4/12/26/26	0/1/1/1
3	A1H0A	C	403	2	-	3/12/26/26	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	A1H0A	B13-O15	-5.45	1.36	1.47
3	A	403	A1H0A	B13-O14	-5.14	1.37	1.47
3	C	403	A1H0A	B13-O15	-5.08	1.37	1.47
3	C	403	A1H0A	B13-O14	-5.07	1.37	1.47
3	C	403	A1H0A	B13-O17	-4.96	1.37	1.47
3	A	403	A1H0A	B13-O17	-4.48	1.38	1.47
3	C	403	A1H0A	O8-C6	3.89	1.34	1.22
3	C	403	A1H0A	O7-C6	-2.54	1.21	1.30
3	A	403	A1H0A	C4-C3	2.10	1.56	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	403	A1H0A	O7-C6-C5	2.80	120.63	113.59
3	C	403	A1H0A	O7-C6-C5	2.73	120.44	113.59
3	A	403	A1H0A	C10-C9-C5	2.40	119.43	115.21
3	C	403	A1H0A	C4-C3-C2	2.29	105.94	102.19
3	C	403	A1H0A	C9-C10-C11	-2.10	106.92	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	403	A1H0A	C9-C10-C11	-2.07	107.03	113.19

There are no chirality outliers.

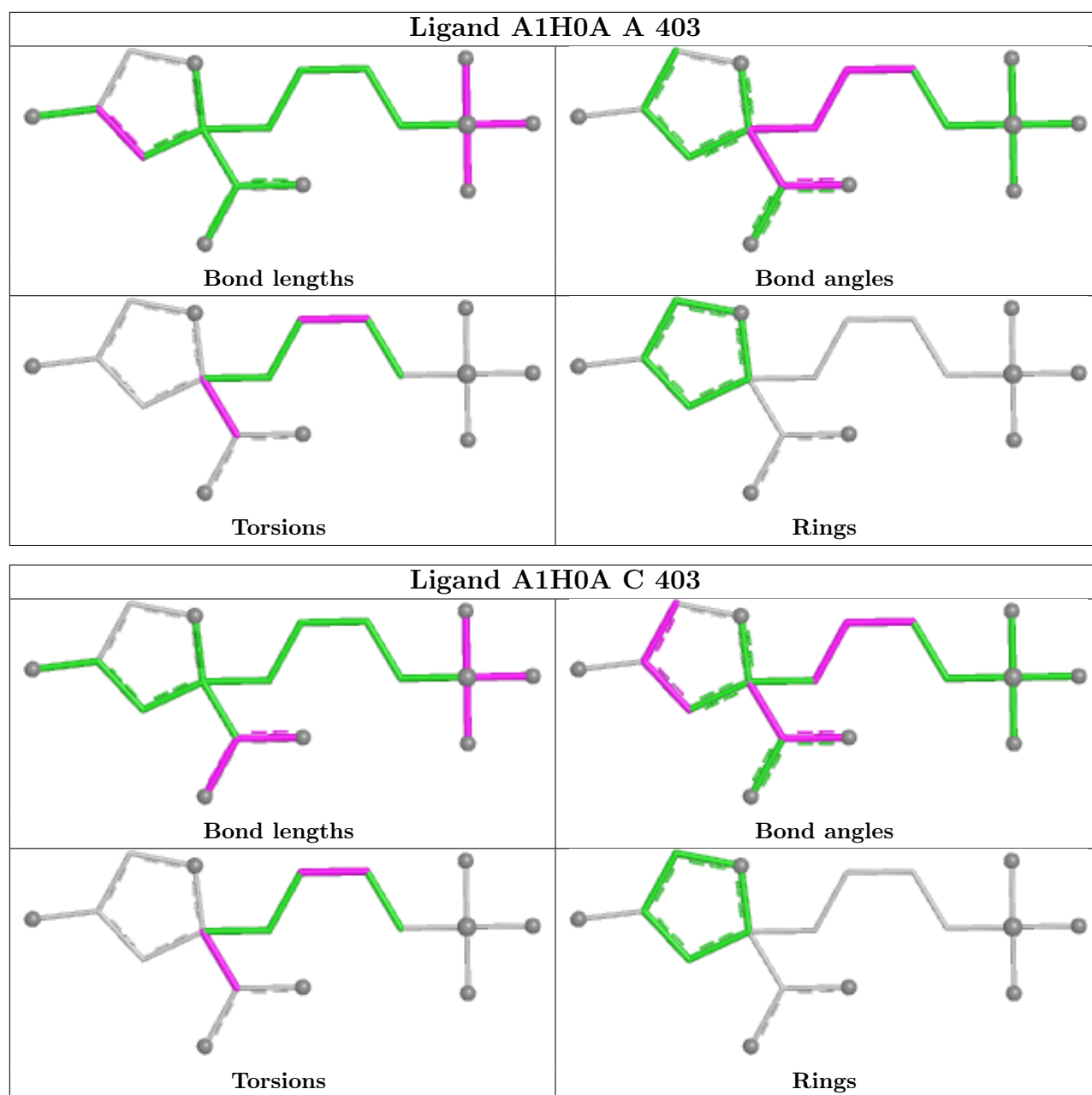
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	403	A1H0A	C9-C10-C11-C12
3	A	403	A1H0A	C4-C5-C6-O7
3	C	403	A1H0A	C4-C5-C6-O7
3	C	403	A1H0A	C4-C5-C6-O8
3	A	403	A1H0A	C9-C10-C11-C12
3	A	403	A1H0A	C4-C5-C6-O8
3	A	403	A1H0A	N1-C5-C6-O8

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	318/335 (94%)	0.53	21 (6%) 24 26	25, 37, 75, 123	0
1	B	324/335 (96%)	2.43	185 (57%) 0 0	30, 66, 124, 150	0
1	C	318/335 (94%)	0.51	16 (5%) 34 37	24, 36, 71, 101	0
All	All	960/1005 (95%)	1.16	222 (23%) 2 2	24, 43, 110, 150	0

All (222) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	99	LEU	7.4
1	B	92	VAL	7.2
1	B	94	LEU	6.4
1	B	33	PHE	6.4
1	C	33	PHE	6.3
1	B	29	ILE	6.2
1	B	31	ALA	6.1
1	B	159	LEU	6.0
1	B	71	LEU	5.7
1	A	337	LEU	5.7
1	B	106	ALA	5.7
1	B	107	VAL	5.7
1	B	86	ILE	5.5
1	B	81	LEU	5.4
1	B	76	VAL	5.3
1	B	176	PRO	5.2
1	B	122	LEU	5.1
1	B	42	VAL	5.1
1	B	111	TYR	5.1
1	B	103	VAL	5.0
1	B	184	ILE	5.0
1	B	181	PHE	4.9
1	B	93	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
1	B	85	LEU	4.9
1	B	183	TRP	4.8
1	B	100	ALA	4.8
1	B	124	ILE	4.8
1	B	193	ILE	4.8
1	B	171	LEU	4.7
1	A	338	PRO	4.6
1	B	102	VAL	4.6
1	B	129	GLY	4.6
1	B	95	ALA	4.5
1	B	134	CYS	4.5
1	B	178	LEU	4.5
1	B	238	LEU	4.5
1	B	168	LEU	4.5
1	B	113	CYS	4.4
1	B	46	PRO	4.4
1	B	137	LEU	4.4
1	B	47	ALA	4.4
1	A	334	TYR	4.4
1	B	308	ALA	4.3
1	B	28	VAL	4.2
1	B	289	LEU	4.2
1	B	98	GLU	4.2
1	B	153	THR	4.2
1	B	166	PHE	4.1
1	B	32	PRO	4.1
1	B	118	GLY	4.1
1	B	174	LYS	4.1
1	B	188	ILE	4.1
1	B	175	VAL	4.0
1	B	127	ILE	4.0
1	B	82	TYR	4.0
1	B	117	GLY	4.0
1	B	164	VAL	4.0
1	B	89	PRO	4.0
1	B	121	SER	4.0
1	B	152	LEU	3.9
1	A	339	THR	3.9
1	B	108	SER	3.9
1	B	179	PRO	3.9
1	B	138	CYS	3.9
1	B	297	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	68	PHE	3.9
1	B	116	LEU	3.8
1	B	130	HIS	3.8
1	B	302	ALA	3.8
1	B	87	VAL	3.8
1	B	207	PHE	3.8
1	B	45	GLY	3.8
1	B	77	PRO	3.8
1	B	295	VAL	3.7
1	B	208	ILE	3.7
1	C	81	LEU	3.6
1	B	287	GLY	3.6
1	B	126	THR	3.6
1	B	123	ALA	3.6
1	B	105	ARG	3.6
1	A	332	ILE	3.6
1	B	163	PRO	3.6
1	B	96	ASN	3.5
1	B	167	LEU	3.6
1	B	294	LEU	3.6
1	B	41	GLY	3.5
1	B	74	THR	3.5
1	B	115	THR	3.5
1	B	150	THR	3.5
1	B	30	GLY	3.5
1	B	157	GLY	3.5
1	B	151	PRO	3.5
1	A	340	PRO	3.4
1	B	84	ASN	3.4
1	B	329	GLY	3.4
1	B	75	PRO	3.4
1	B	209	LEU	3.4
1	A	23	VAL	3.4
1	B	131	ALA	3.4
1	B	165	SER	3.4
1	B	262	ALA	3.3
1	B	180	GLY	3.3
1	A	77	PRO	3.3
1	B	135	PRO	3.3
1	B	73	PHE	3.2
1	B	104	SER	3.2
1	C	86	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	194	VAL	3.1
1	B	119	ASP	3.1
1	B	49	ILE	3.1
1	B	239	ILE	3.1
1	B	65	LEU	3.1
1	B	139	VAL	3.1
1	B	154	THR	3.1
1	B	340	PRO	3.1
1	B	160	HIS	3.1
1	B	301	LEU	3.0
1	B	44	HIS	3.0
1	B	214	ILE	3.0
1	B	120	HIS	3.0
1	B	72	SER	3.0
1	B	146	ALA	2.9
1	B	148	ILE	2.9
1	B	114	VAL	2.9
1	B	125	GLY	2.9
1	B	88	ASN	2.9
1	B	204	PRO	2.9
1	B	91	SER	2.9
1	B	52	ALA	2.8
1	B	128	SER	2.8
1	B	191	ALA	2.8
1	B	290	SER	2.8
1	C	73	PHE	2.8
1	B	187	CYS	2.8
1	A	65	LEU	2.8
1	B	237	LEU	2.8
1	B	248	LEU	2.8
1	B	245	PRO	2.8
1	B	97	GLN	2.8
1	B	101	GLU	2.7
1	B	331	HIS	2.7
1	B	36	GLY	2.7
1	B	212	TYR	2.6
1	C	82	TYR	2.6
1	B	265	THR	2.6
1	B	303	THR	2.6
1	B	149	ASN	2.6
1	B	55	MET	2.6
1	B	54	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	39	ARG	2.6
1	A	335	ASP	2.6
1	B	264	GLY	2.6
1	B	156	SER	2.6
1	B	288	LEU	2.6
1	B	186	PRO	2.5
1	B	334	TYR	2.5
1	B	155	SER	2.5
1	B	133	HIS	2.5
1	B	27	ALA	2.5
1	A	333	VAL	2.5
1	B	240	GLY	2.5
1	A	76	VAL	2.5
1	B	201	VAL	2.5
1	C	75	PRO	2.5
1	B	172	GLN	2.4
1	B	305	GLU	2.4
1	B	34	SER	2.4
1	A	302	ALA	2.4
1	B	161	GLY	2.4
1	B	333	VAL	2.4
1	C	76	VAL	2.4
1	C	40	LYS	2.4
1	C	85	LEU	2.4
1	B	304	SER	2.4
1	B	173	ASP	2.3
1	B	263	THR	2.3
1	B	53	GLY	2.3
1	B	110	GLY	2.3
1	A	108	SER	2.3
1	B	316	VAL	2.3
1	B	141	TRP	2.3
1	B	158	ASN	2.3
1	B	332	ILE	2.3
1	B	299	PRO	2.3
1	B	66	LYS	2.3
1	B	185	LYS	2.3
1	B	190	SER	2.3
1	B	35	GLN	2.3
1	C	177	GLN	2.3
1	B	39	ARG	2.2
1	B	48	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	69	GLY	2.2
1	B	252	ILE	2.2
1	A	64	HIS	2.2
1	B	311	THR	2.2
1	A	63	CYS	2.2
1	C	122	LEU	2.2
1	A	33	PHE	2.2
1	B	246	ILE	2.2
1	A	331	HIS	2.2
1	C	84	ASN	2.2
1	A	301	LEU	2.2
1	A	75	PRO	2.2
1	B	40	LYS	2.2
1	B	177	GLN	2.1
1	B	80	ASP	2.1
1	B	147	ASP	2.1
1	B	335	ASP	2.1
1	B	182	SER	2.1
1	B	249	SER	2.1
1	B	64	HIS	2.1
1	B	326	THR	2.1
1	B	241	LYS	2.1
1	C	72	SER	2.1
1	B	339	THR	2.1
1	B	109	ASP	2.1
1	B	234	THR	2.0
1	C	329	GLY	2.0
1	B	140	VAL	2.0
1	C	87	VAL	2.0
1	A	137	LEU	2.0
1	B	90	ARG	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](#)

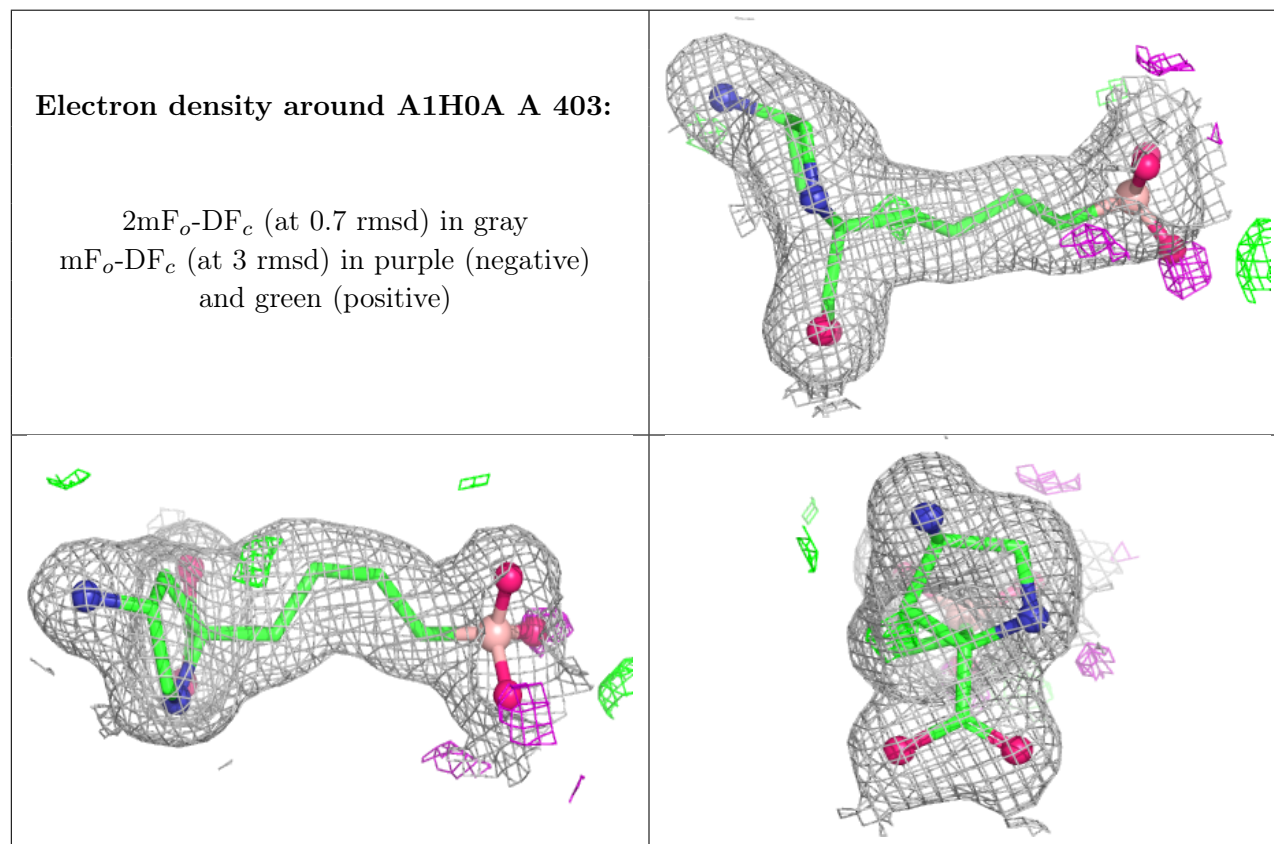
There are no oligosaccharides in this entry.

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.

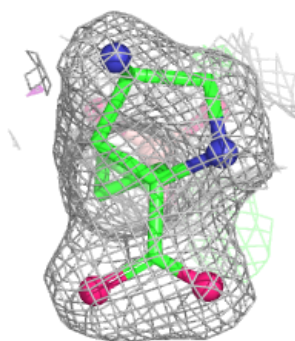
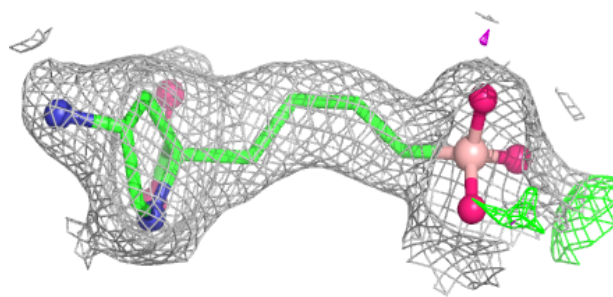
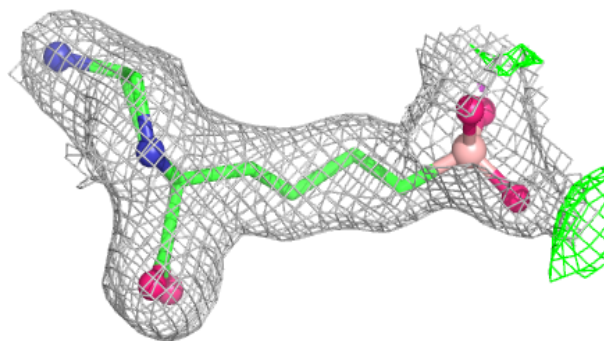
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MN	B	500	1/1	0.87	0.11	59,59,59,59	0
3	A1H0A	A	403	17/17	0.89	0.10	33,36,40,48	0
3	A1H0A	C	403	17/17	0.91	0.09	32,38,43,43	0
2	MN	B	501	1/1	0.93	0.07	48,48,48,48	0
2	MN	A	402	1/1	0.97	0.06	35,35,35,35	0
2	MN	C	402	1/1	0.98	0.03	31,31,31,31	0
2	MN	C	401	1/1	0.99	0.02	29,29,29,29	0
2	MN	A	401	1/1	0.99	0.04	31,31,31,31	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 A1H0A C 403:

$2mF_o-DF_c$ (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.