



Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 02:17 pm BST

PDB ID : 6C8T
Title : The structure of MppP soaked with the substrate L-Arg
Authors : Han, L.; Silvaggi, N.R.
Deposited on : 2018-01-25
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

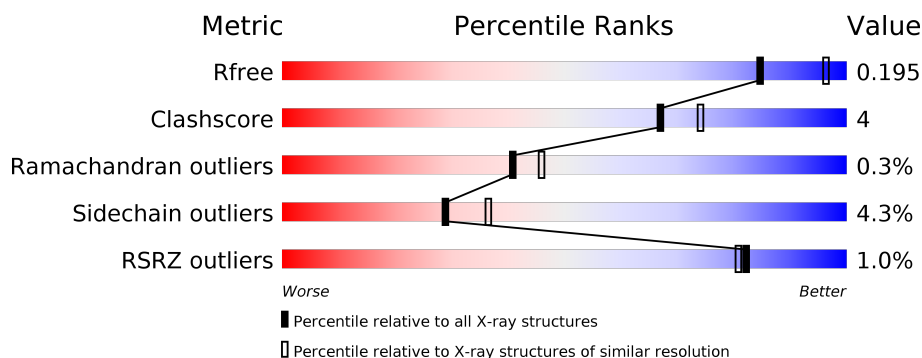
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 on 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	376	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 89%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 89% 7% </div> </div>
1	B	376	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 12%, green 85%, grey 1%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 85% 12% </div> </div>
1	C	376	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 11%, green 86%, grey 1%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 86% 11% </div> </div>
2	D	376	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 7%, green 86%, grey 6%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 86% 7% </div> </div>

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.

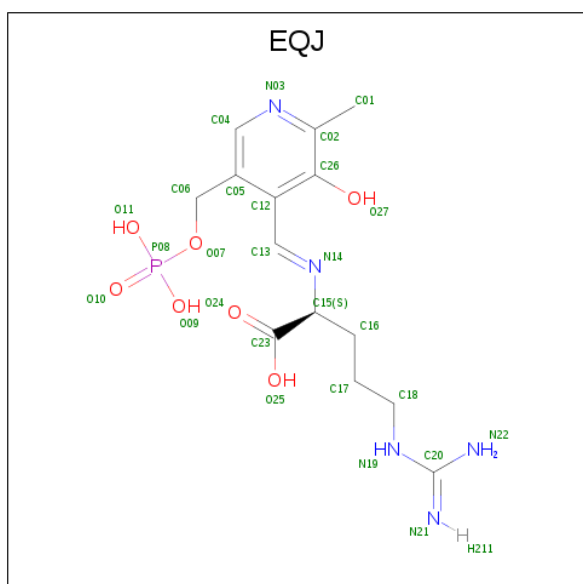
- Molecule 1 is a protein called PLP-Dependent L-Arginine Hydroxylase MppP.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	368	Total 5665	C 1800	H 2806	N 506	O 546	S 7	6	0	0
1	B	368	Total 5706	C 1811	H 2828	N 509	O 551	S 7	6	5	0
1	C	368	Total 5677	C 1803	H 2812	N 507	O 548	S 7	6	2	0

- Molecule 2 is a protein called PLP-Dependent L-Arginine Hydroxylase MppP.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
2	D	354	Total	C	H	N	O	P	S	0	5	0
			5490	1743	2715	491	533	1	7			

- Molecule 3 is (E)-N 2 -({3-hydroxy-2-methyl-5-[(phosphonoxy)methyl]pyridin-4-yl}methylidene)-L-arginine (three-letter code: EQJ) (formula: C₁₄H₂₂N₅O₇P) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	0	0
			45	14	18	5	7	1		
3	B	1	Total	C	H	N	O	P	0	0
			45	14	18	5	7	1		
3	C	1	Total	C	H	N	O	P	0	0
			45	14	18	5	7	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	Cl	0	0
			1	1		

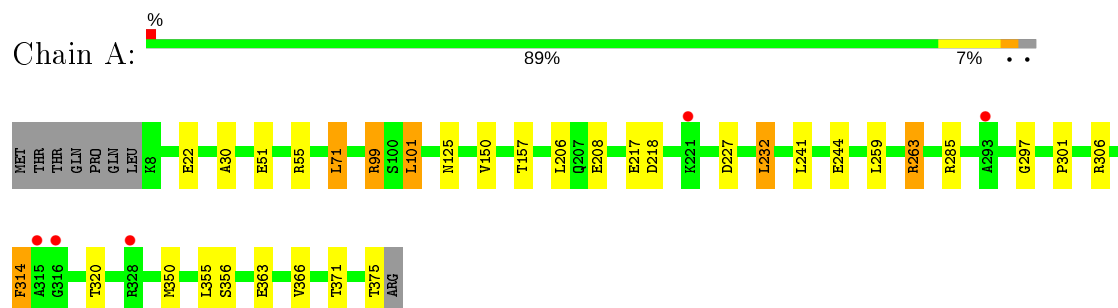
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	197	Total	O	0	0
			197	197		
5	B	187	Total	O	0	0
			187	187		
5	C	169	Total	O	0	0
			169	169		
5	D	175	Total	O	0	0
			175	175		

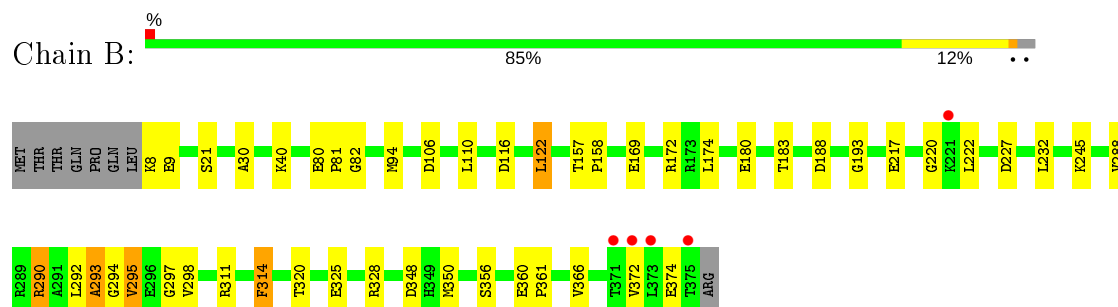
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

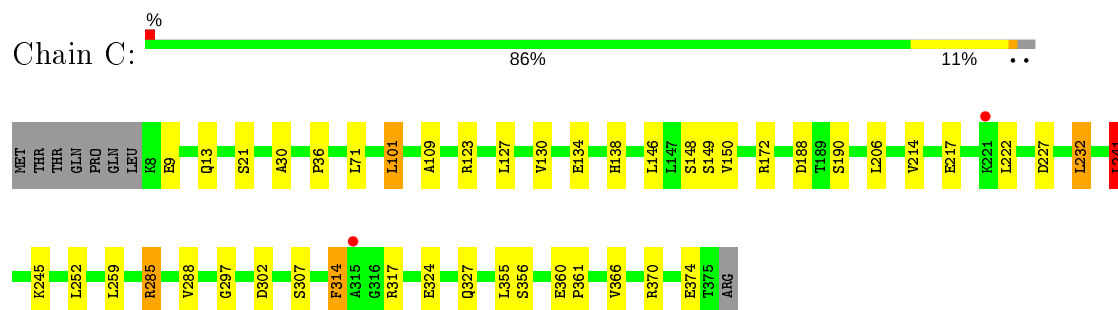
• Molecule 1: PLP-Dependent L-Arginine Hydroxylase MppP



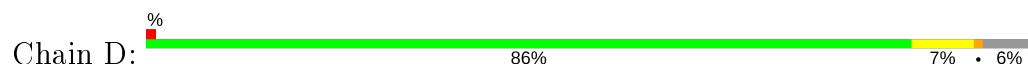
• Molecule 1: PLP-Dependent L-Arginine Hydroxylase MppP

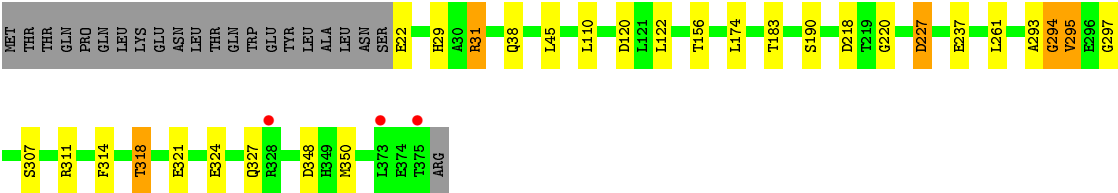


• Molecule 1: PLP-Dependent L-Arginine Hydroxylase MppP



• Molecule 2: PLP-Dependent L-Arginine Hydroxylase MppP





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.79Å 108.42Å 196.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.05 – 2.20 49.05 – 2.20	Depositor EDS
% Data completeness (in resolution range)	91.6 (49.05-2.20) 91.6 (49.05-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.78 (at 2.20Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.146 , 0.195 0.146 , 0.195	Depositor DCC
R_{free} test set	1999 reflections (2.33%)	wwPDB-VP
Wilson B-factor (Å ²)	23.2	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 57.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	23402	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.19% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EQJ, LLP, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.48	0/2920	0.71	8/3976 (0.2%)
1	B	0.47	0/2957	0.65	1/4026 (0.0%)
1	C	0.51	1/2932 (0.0%)	0.69	4/3992 (0.1%)
2	D	0.49	0/2826	0.65	0/3847
All	All	0.49	1/11635 (0.0%)	0.68	13/15841 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	134	GLU	CB-CG	-5.29	1.42	1.52

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	263	ARG	NE-CZ-NH2	-8.96	115.82	120.30
1	A	263	ARG	NE-CZ-NH1	8.70	124.65	120.30
1	C	285	ARG	NE-CZ-NH2	-7.95	116.32	120.30
1	A	55	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	A	285	ARG	NE-CZ-NH2	-6.73	116.94	120.30
1	C	127	LEU	CA-CB-CG	-5.98	101.55	115.30
1	A	55	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	285	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	C	285	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	C	241	LEU	CA-CB-CG	5.23	127.33	115.30
1	A	101	LEU	CA-CB-CG	5.16	127.17	115.30
1	B	116	ASP	CB-CG-OD1	5.16	122.94	118.30
1	A	71	LEU	CA-CB-CG	5.02	126.85	115.30

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	2859	2806	2806	13	0
1	B	2878	2828	2812	34	0
1	C	2865	2812	2806	25	0
2	D	2775	2715	2702	16	0
3	A	27	18	0	0	0
3	B	27	18	0	1	0
3	C	27	18	0	1	0
4	D	1	0	0	0	0
5	A	197	0	0	2	0
5	B	187	0	0	12	1
5	C	169	0	0	10	1
5	D	175	0	0	6	2
All	All	12187	11215	11126	87	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 4.

All (87) 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:370:ARG:NH1	1:C:374:GLU:OE2	1.99	0.95
2:D:220:GLY:O	5:D:501:HOH:O	1.90	0.88
1:C:138:HIS:NE2	5:C:503:HOH:O	2.06	0.88
1:B:180:GLU:OE1	5:B:501:HOH:O	1.92	0.86
1:B:220:GLY:O	5:B:502:HOH:O	1.94	0.84
1:B:180:GLU:OE1	5:B:503:HOH:O	1.97	0.81
1:B:8:LYS:N	5:B:508:HOH:O	2.12	0.81
1:C:302:ASP:OD1	5:C:501:HOH:O	2.00	0.80
1:C:227:ASP:OD2	5:C:502:HOH:O	2.02	0.77
2:D:237:GLU:OE2	5:D:502:HOH:O	2.06	0.72
1:B:169:GLU:OE1	5:B:504:HOH:O	2.08	0.71
1:B:180:GLU:OE1	5:B:506:HOH:O	2.10	0.69
1:B:80:GLU:OE1	5:B:505:HOH:O	2.10	0.69
1:B:106:ASP:OD2	5:B:507:HOH:O	2.11	0.67
2:D:120:ASP:OD2	5:D:503:HOH:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:ARG:NH1	5:B:511:HOH:O	2.29	0.64
2:D:311:ARG:HD2	2:D:350:MET:HE2	1.80	0.63
1:C:360:GLU:HG2	1:C:361:PRO:HD3	1.82	0.61
1:B:40:LYS:NZ	5:B:512:HOH:O	2.32	0.61
1:C:148:SER:OG	5:C:504:HOH:O	2.16	0.60
1:A:301:PRO:HG2	1:A:350:MET:CE	2.34	0.58
1:B:311:ARG:HB3	1:B:350:MET:CE	2.34	0.58
1:A:301:PRO:HG2	1:A:350:MET:HE1	1.86	0.57
1:B:325:GLU:OE1	1:B:328:ARG:NH2	2.37	0.57
1:A:244:GLU:OE2	5:A:501:HOH:O	2.18	0.56
1:B:311:ARG:HD2	1:B:350:MET:HE2	1.88	0.56
1:C:285:ARG:NH2	1:C:307:SER:O	2.39	0.55
1:A:371:THR:O	1:A:375:THR:HG22	2.06	0.55
1:A:218:ASP:O	5:A:502:HOH:O	2.18	0.54
2:D:227:ASP:CG	5:D:507:HOH:O	2.48	0.52
1:B:30:ALA:HA	1:B:356:SER:HB3	1.91	0.51
2:D:311:ARG:HD2	2:D:350:MET:CE	2.41	0.51
1:B:360:GLU:HB2	1:B:361:PRO:HD3	1.93	0.50
1:A:208:GLU:OE1	2:D:324:GLU:OE1	2.29	0.50
1:B:294:GLY:O	1:B:295:VAL:C	2.50	0.50
1:B:311:ARG:HD2	1:B:350:MET:CE	2.40	0.50
1:B:245:LYS:HE2	5:B:548:HOH:O	2.12	0.50
1:C:252:LEU:CD2	5:C:645:HOH:O	2.59	0.50
1:A:30:ALA:HA	1:A:356:SER:HB3	1.94	0.49
1:C:109:ALA:HA	1:C:130:VAL:HG22	1.93	0.49
1:B:320:THR:HG23	5:B:631:HOH:O	2.12	0.49
1:C:36:PRO:HD2	5:C:590:HOH:O	2.12	0.49
1:C:217:GLU:HB2	1:C:232:LEU:HB2	1.94	0.49
1:C:9:GLU:HB2	1:C:13:GLN:OE1	2.13	0.48
1:C:101:LEU:HD13	1:C:241:LEU:HD21	1.94	0.48
1:C:297:GLY:O	1:C:314:PHE:HA	2.14	0.48
1:A:99:ARG:HG2	1:A:125:ASN:OD1	2.14	0.48
1:C:123:ARG:HD3	5:C:553:HOH:O	2.14	0.47
1:B:169:GLU:H	1:B:169:GLU:CD	2.17	0.47
1:C:190:SER:HB2	5:C:556:HOH:O	2.15	0.47
2:D:297:GLY:O	2:D:314:PHE:HA	2.15	0.47
2:D:318:THR:HG22	2:D:321:GLU:H	1.80	0.46
1:B:94:MET:CE	1:B:122:LEU:HD13	2.46	0.46
1:A:217:GLU:HB2	1:A:232:LEU:HB2	1.96	0.46
1:C:360:GLU:HG2	1:C:361:PRO:CD	2.46	0.45
1:B:188:ASP:OD2	3:B:401:EQJ:N03	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:81:PRO:HA	1:B:82:GLY:HA2	1.83	0.45
2:D:294:GLY:O	2:D:295:VAL:O	2.35	0.45
1:B:295:VAL:HG23	1:B:298:VAL:HB	1.99	0.45
1:C:252:LEU:HD23	5:C:645:HOH:O	2.16	0.45
1:A:363:GLU:HA	1:A:366:VAL:HG12	2.00	0.44
1:B:94:MET:HE3	1:B:122:LEU:HD13	2.00	0.44
1:C:30:ALA:HA	1:C:356:SER:HB3	2.00	0.44
2:D:45:LEU:HD21	2:D:261:LEU:HD13	2.00	0.43
1:A:157:THR:HG23	1:A:157:THR:O	2.19	0.43
1:B:193:GLY:HA3	1:B:222:LEU:HD11	2.00	0.43
1:C:288:VAL:HG22	1:C:366:VAL:HG21	2.00	0.43
2:D:190:SER:HA	2:D:218:ASP:HB3	2.01	0.43
2:D:29:HIS:HB2	2:D:31:ARG:NH1	2.33	0.43
1:B:372:VAL:C	1:B:374:GLU:H	2.23	0.42
1:C:245:LYS:NZ	5:C:509:HOH:O	2.35	0.42
1:C:324:GLU:O	1:C:327:GLN:HG3	2.19	0.42
2:D:311:ARG:HB3	2:D:350:MET:CE	2.49	0.42
1:B:80:GLU:CD	1:B:80:GLU:H	2.23	0.42
1:A:51:GLU:OE2	1:A:263:ARG:NH2	2.41	0.42
1:B:360:GLU:CD	1:B:360:GLU:H	2.22	0.42
1:C:130:VAL:HG21	1:C:146:LEU:HD11	2.01	0.41
1:C:188:ASP:OD2	3:C:401:EQJ:N03	2.52	0.41
1:B:217:GLU:HB2	1:B:232:LEU:HB2	2.03	0.41
1:C:130:VAL:HG23	1:C:130:VAL:O	2.19	0.41
1:B:157:THR:HA	1:B:158:PRO:C	2.40	0.41
1:B:297:GLY:O	1:B:314:PHE:HA	2.21	0.41
2:D:237:GLU:CD	5:D:502:HOH:O	2.56	0.41
1:B:288:VAL:HG22	1:B:366:VAL:HG11	2.02	0.41
2:D:38:GLN:NE2	5:D:508:HOH:O	2.37	0.40
1:B:290:ARG:O	1:B:293:ALA:HB2	2.21	0.40
1:A:297:GLY:O	1:A:314:PHE:HA	2.22	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)
5:B:681:HOH:O	5:D:664:HOH:O[1_455]	1.98	0.22
5:C:506:HOH:O	5:D:625:HOH:O[4_497]	2.15	0.05

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	366/376 (97%)	360 (98%)	6 (2%)	0	100	100
1	B	371/376 (99%)	359 (97%)	10 (3%)	2 (0%)	29	31
1	C	368/376 (98%)	360 (98%)	8 (2%)	0	100	100
2	D	356/376 (95%)	347 (98%)	6 (2%)	3 (1%)	19	19
All	All	1461/1504 (97%)	1426 (98%)	30 (2%)	5 (0%)	41	46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	293	ALA
1	B	295	VAL
2	D	293	ALA
2	D	294	GLY
2	D	295	VAL

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	307/315 (98%)	293 (95%)	14 (5%)	27	34
1	B	312/315 (99%)	301 (96%)	11 (4%)	36	46
1	C	309/315 (98%)	294 (95%)	15 (5%)	25	31
2	D	298/314 (95%)	286 (96%)	12 (4%)	31	40
All	All	1226/1259 (97%)	1174 (96%)	52 (4%)	29	38

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLU
1	A	71	LEU
1	A	99	ARG
1	A	101	LEU
1	A	150	VAL
1	A	206	LEU
1	A	227	ASP
1	A	232	LEU
1	A	241	LEU
1	A	259	LEU
1	A	306	ARG
1	A	314	PHE
1	A	320	THR
1	A	355	LEU
1	B	9	GLU
1	B	21	SER
1	B	110	LEU
1	B	122	LEU
1	B	174	LEU
1	B	183	THR
1	B	227	ASP
1	B	290	ARG
1	B	292	LEU
1	B	314	PHE
1	B	348	ASP
1	C	21	SER
1	C	71	LEU
1	C	101	LEU
1	C	149	SER
1	C	150	VAL
1	C	172	ARG
1	C	206	LEU
1	C	214	VAL
1	C	222	LEU
1	C	232	LEU
1	C	241	LEU
1	C	259	LEU
1	C	314	PHE
1	C	317	ARG
1	C	355	LEU
2	D	22	GLU
2	D	31	ARG

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Mol	Chain	Res	Type
2	D	110	LEU
2	D	122	LEU
2	D	156	THR
2	D	174	LEU
2	D	183	THR
2	D	227	ASP
2	D	307	SER
2	D	318	THR
2	D	327	GLN
2	D	348	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	LLP	D	221	2	23,24,25	1.27	2 (8%)	25,32,34	1.65	5 (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
2	LLP	D	221	2	-	4/16/17/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	221	LLP	O-C	3.89	1.35	1.19
2	D	221	LLP	C3-C2	3.16	1.44	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	221	LLP	OP2-P-OP4	-4.43	94.95	106.73
2	D	221	LLP	OP4-C5'-C5	3.22	115.49	109.35
2	D	221	LLP	OP4-P-OP1	3.02	114.96	106.47
2	D	221	LLP	OP2-P-OP1	2.69	121.23	110.68
2	D	221	LLP	C2'-C2-C3	-2.45	117.87	120.89

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	221	LLP	C4-C5-C5'-OP4
2	D	221	LLP	C6-C5-C5'-OP4
2	D	221	LLP	CG-CD-CE-NZ
2	D	221	LLP	C4-C4'-NZ-CE

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	EQJ	C	401	-	24,27,27	2.35	7 (29%)	28,37,37	1.72	5 (17%)
3	EQJ	A	401	-	24,27,27	2.14	5 (20%)	28,37,37	1.87	4 (14%)
3	EQJ	B	401	-	24,27,27	2.23	6 (25%)	28,37,37	1.11	3 (10%)

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	EQJ	C	401	-	-	3/18/22/22	0/1/1/1
3	EQJ	A	401	-	-	3/18/22/22	0/1/1/1
3	EQJ	B	401	-	-	4/18/22/22	0/1/1/1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	401	EQJ	C20-N19	8.10	1.49	1.33
3	B	401	EQJ	C20-N19	8.03	1.49	1.33
3	A	401	EQJ	C20-N19	7.32	1.47	1.33
3	B	401	EQJ	C12-C13	4.03	1.54	1.46
3	C	401	EQJ	C12-C13	3.74	1.53	1.46
3	A	401	EQJ	C12-C13	3.74	1.53	1.46
3	B	401	EQJ	C13-N14	3.07	1.32	1.27
3	A	401	EQJ	C16-C15	3.01	1.57	1.53
3	C	401	EQJ	C20-N21	2.99	1.44	1.32
3	C	401	EQJ	C13-N14	2.92	1.32	1.27
3	A	401	EQJ	C20-N21	2.92	1.43	1.32
3	C	401	EQJ	C16-C15	2.79	1.56	1.53
3	A	401	EQJ	C13-N14	2.74	1.32	1.27
3	B	401	EQJ	C20-N21	2.58	1.42	1.32
3	C	401	EQJ	C06-C05	2.53	1.57	1.50
3	B	401	EQJ	C06-C05	2.36	1.57	1.50
3	C	401	EQJ	C26-C02	-2.31	1.38	1.40
3	B	401	EQJ	C26-C02	-2.26	1.38	1.40

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	EQJ	C15-N14-C13	7.38	127.40	117.40
3	C	401	EQJ	C15-N14-C13	6.62	126.38	117.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	EQJ	O07-P08-O10	2.91	114.64	106.47
3	C	401	EQJ	C17-C16-C15	2.66	119.41	114.78
3	B	401	EQJ	C05-C04-N03	-2.48	119.68	123.82
3	C	401	EQJ	C05-C04-N03	-2.41	119.80	123.82
3	A	401	EQJ	C05-C04-N03	-2.40	119.82	123.82
3	A	401	EQJ	C17-C16-C15	2.35	118.87	114.78
3	C	401	EQJ	C04-N03-C02	2.15	123.16	119.17
3	B	401	EQJ	C01-C02-C26	-2.11	118.28	120.89
3	C	401	EQJ	O07-P08-O10	2.06	112.25	106.47
3	B	401	EQJ	C12-C26-C02	-2.03	118.93	120.19

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	401	EQJ	C16-C15-N14-C13
3	C	401	EQJ	C06-O07-P08-O10
3	C	401	EQJ	C06-O07-P08-O11
3	A	401	EQJ	C16-C15-N14-C13
3	B	401	EQJ	C06-O07-P08-O09
3	B	401	EQJ	C23-C15-N14-C13
3	B	401	EQJ	C16-C17-C18-N19
3	A	401	EQJ	C06-O07-P08-O10
3	B	401	EQJ	C06-O07-P08-O11
3	A	401	EQJ	C06-O07-P08-O09

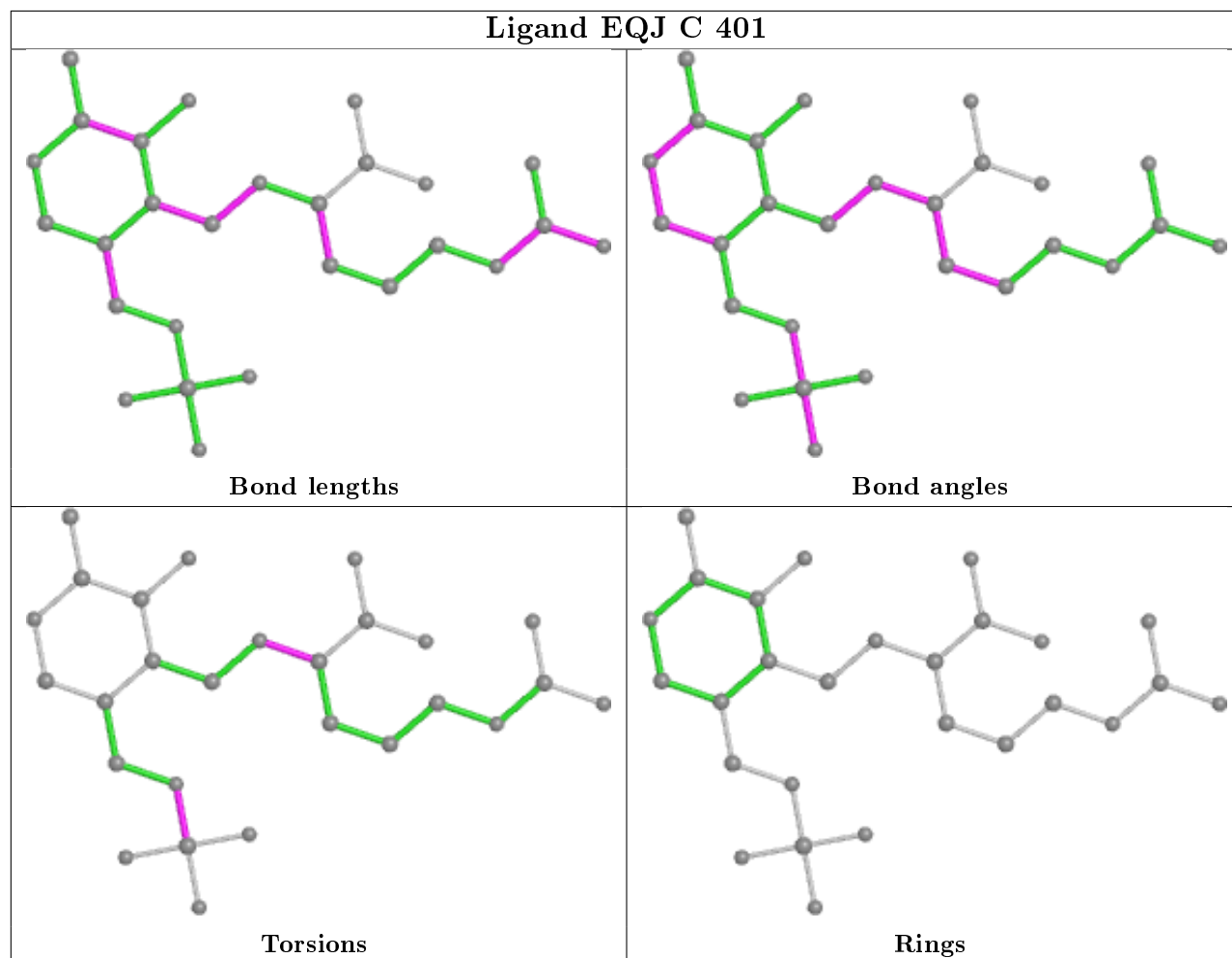
There are no ring outliers.

2 monomers are involved in 2 short contacts:

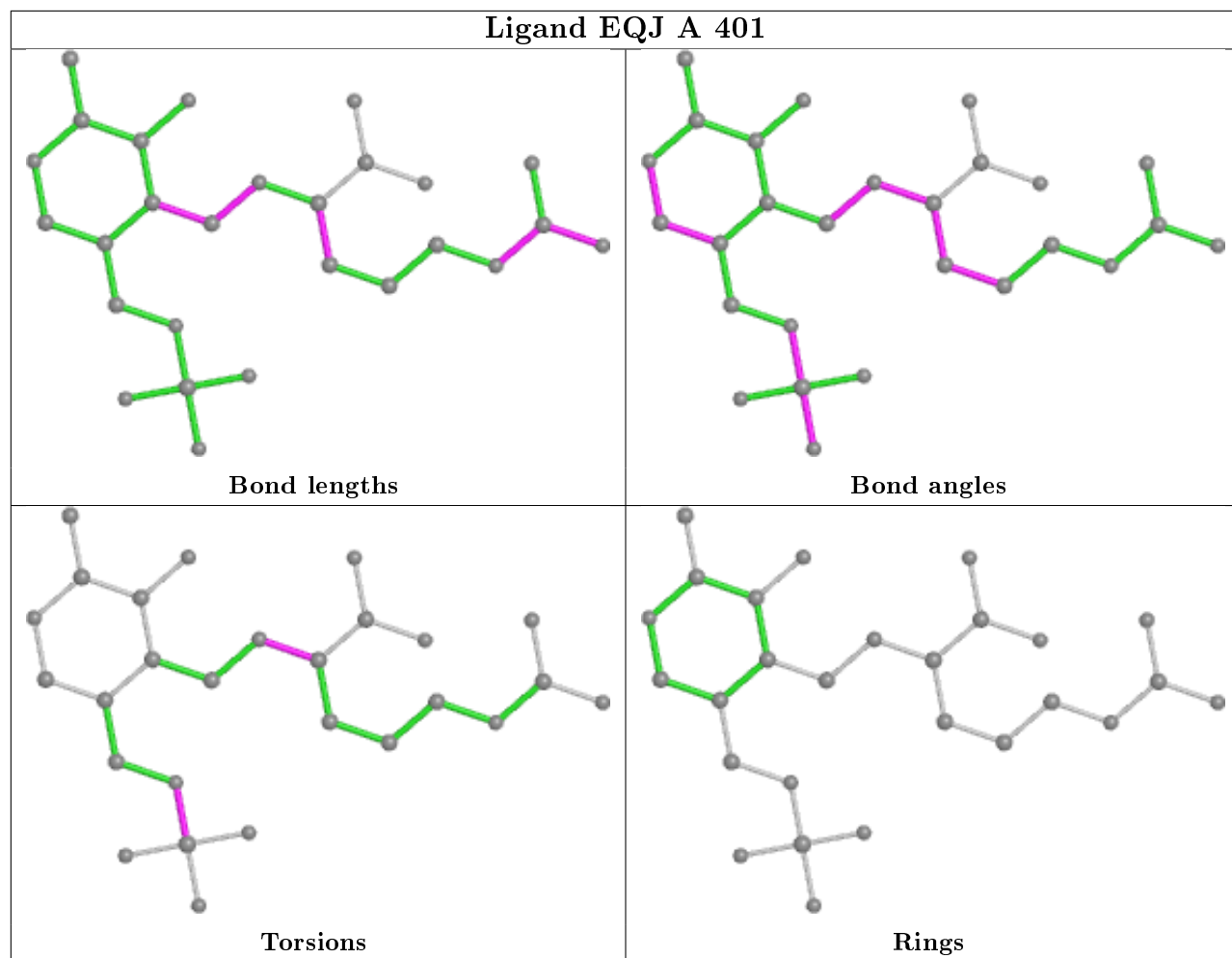
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	EQJ	1	0
3	B	401	EQJ	1	0

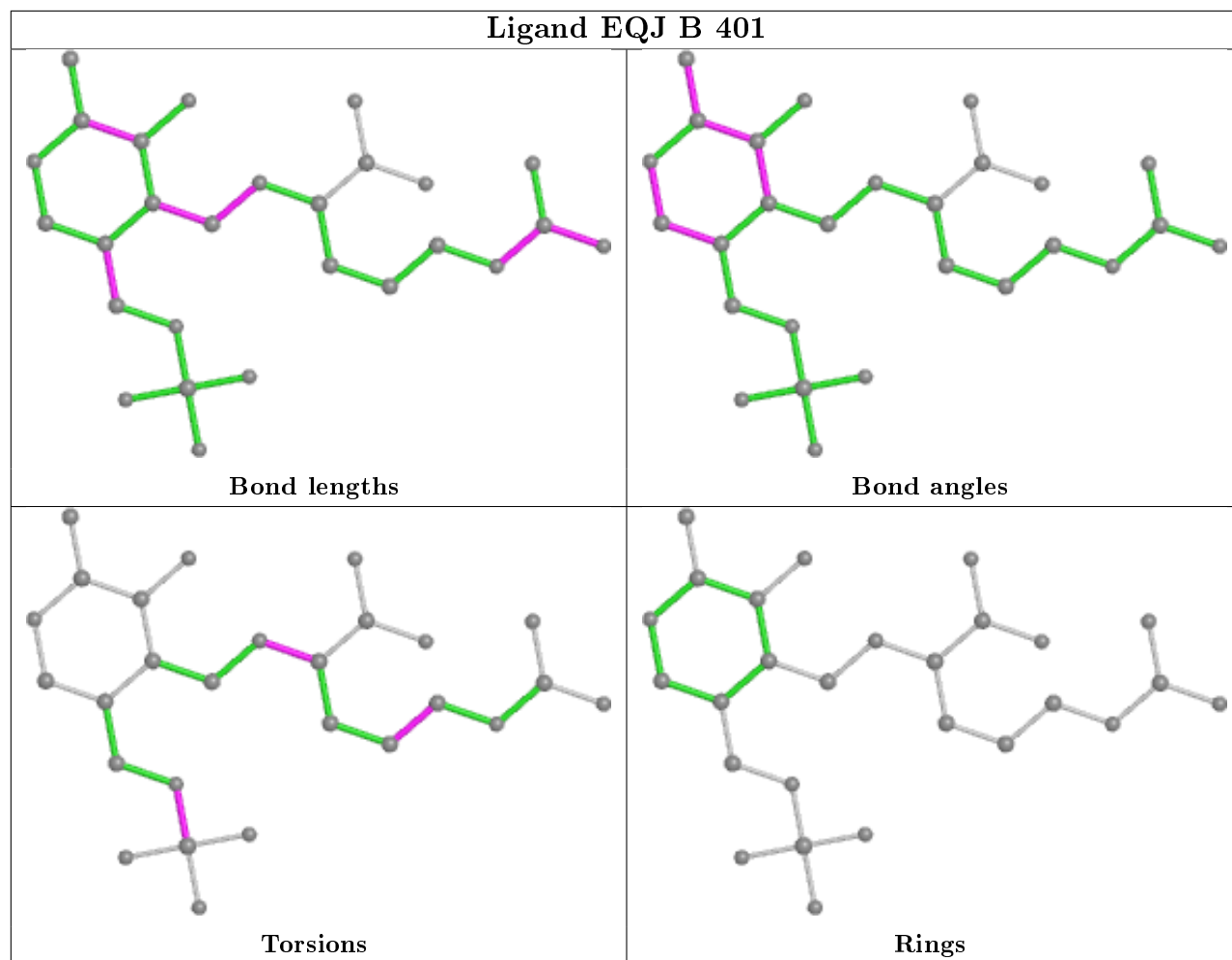
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



Ligand EQJ A 401





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	368/376 (97%)	-0.48	5 (1%) 75 73	14, 28, 63, 110	1 (0%)
1	B	368/376 (97%)	-0.56	5 (1%) 75 73	14, 27, 68, 120	1 (0%)
1	C	368/376 (97%)	-0.55	2 (0%) 91 90	14, 28, 63, 98	1 (0%)
2	D	353/376 (93%)	-0.54	3 (0%) 86 85	14, 27, 71, 120	0
All	All	1457/1504 (96%)	-0.53	15 (1%) 82 81	14, 27, 68, 120	3 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	375	THR	5.7
1	A	315	ALA	4.8
1	C	221	LYS	4.2
2	D	375	THR	3.4
2	D	373	LEU	3.1
1	B	221	LYS	3.0
1	B	373	LEU	2.8
1	A	316	GLY	2.6
1	A	293	ALA	2.4
1	B	372	VAL	2.3
1	A	221	LYS	2.2
1	C	315	ALA	2.2
2	D	328	ARG	2.1
1	A	328	ARG	2.1
1	B	371	THR	2.1

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(\AA^2)	Q<0.9
2	LLP	D	221	24/25	0.99	0.10	12,24,32,36	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

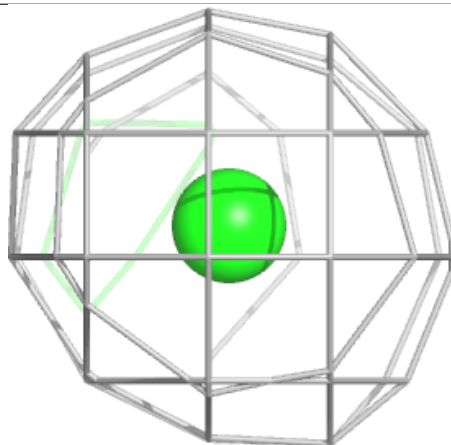
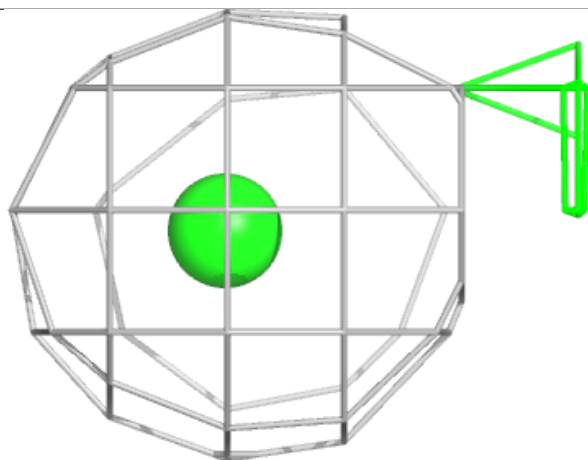
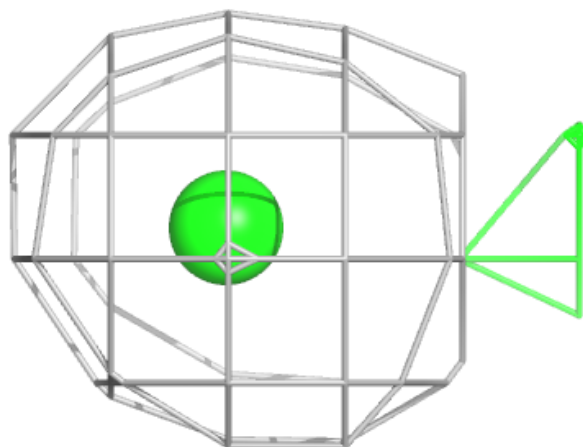
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CL	D	401	1/1	0.97	0.15	35,35,35,35	0
3	EQJ	B	401	27/27	0.97	0.13	14,29,43,50	0
3	EQJ	A	401	27/27	0.98	0.15	17,30,46,54	0
3	EQJ	C	401	27/27	0.98	0.14	17,29,49,59	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.

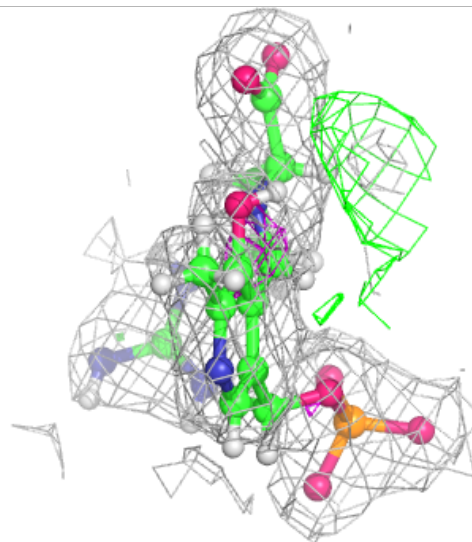
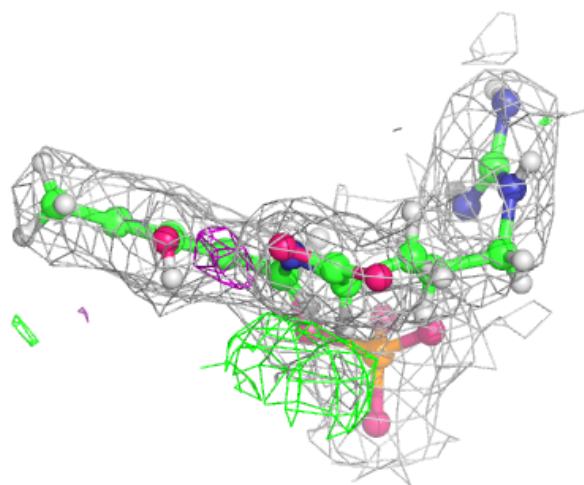
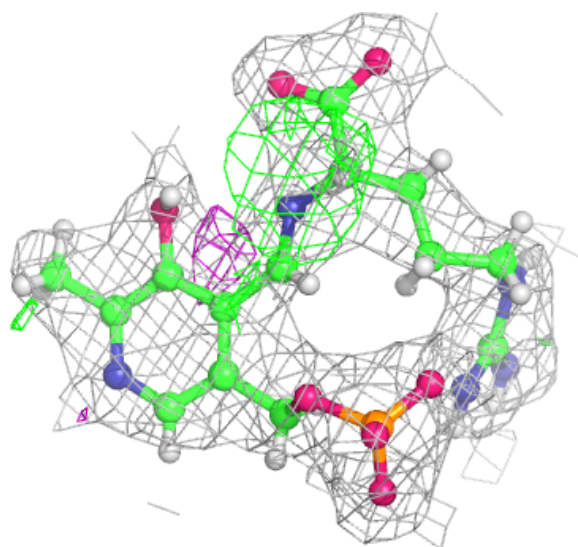
Electron density around CL D 401:

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



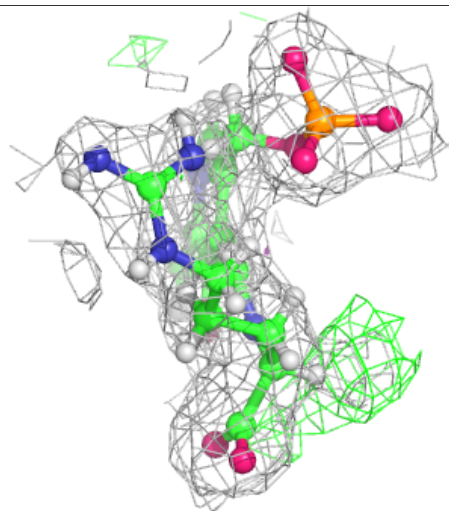
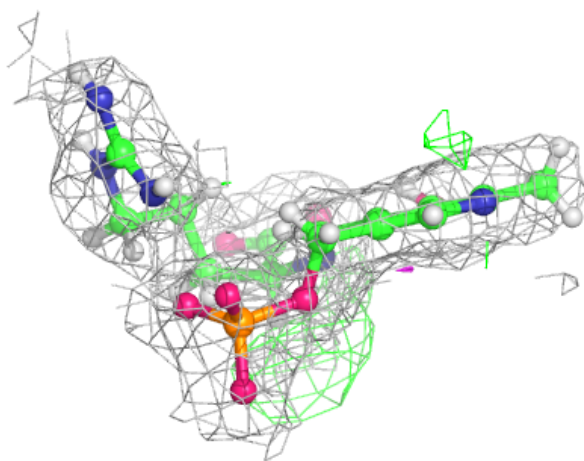
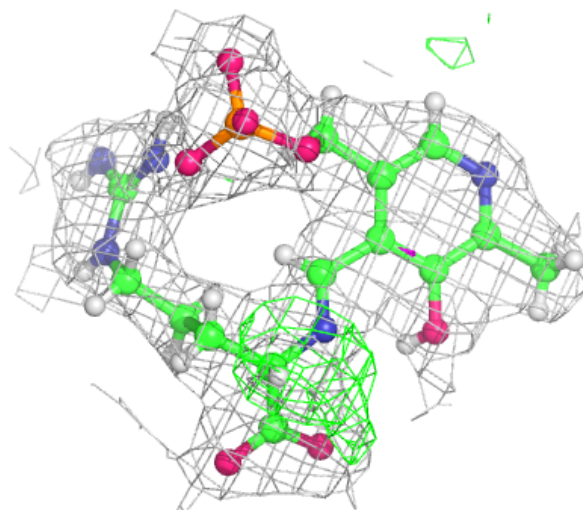
Electron density around EQJ B 401:

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



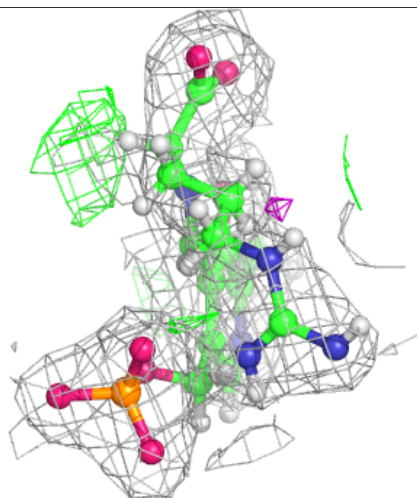
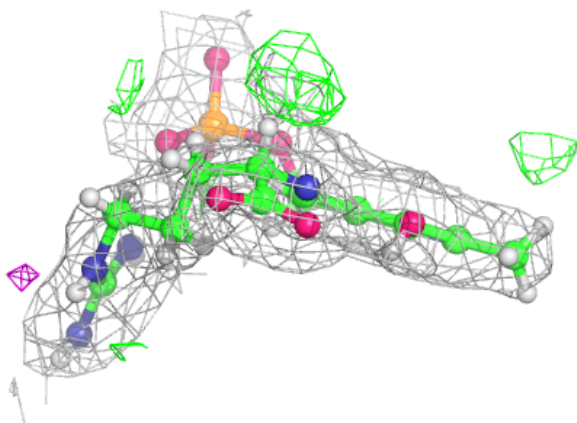
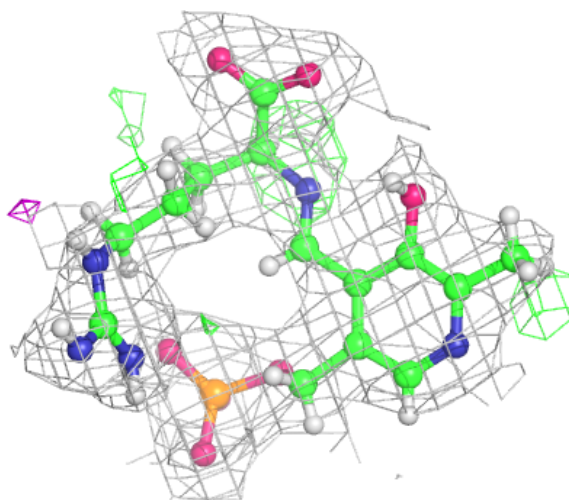
Electron density around EQJ A 401:

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



Electron density around EQJ C 401:

$2mF_o-DF_c$ (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.