



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:20 AM UTC

PDB ID : 6OHS / pdb_00006ohs
Title : Structure of compound 3 (ML299) bound human Phospholipase D2 catalytic domain
Authors : Metrick, C.M.; Chodaparambil, J.V.
Deposited on : 2019-04-06
Resolution : 3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

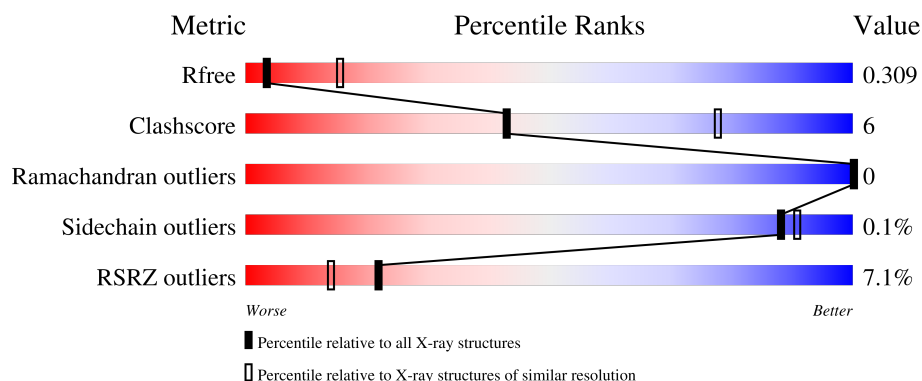
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 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	640	8% 78% 13% 9%
1	B	640	4% 79% 12% 9%
1	C	640	7% 77% 15% 9%
1	D	640	6% 73% 18% 9%

2 Entry composition [i](#)

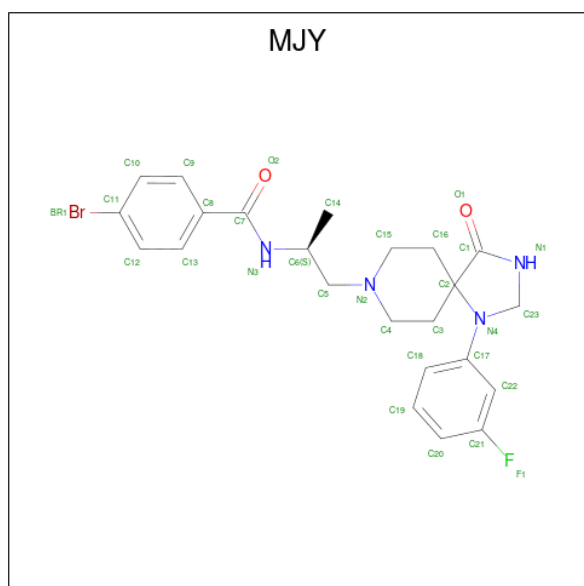
There are 2 unique types of molecules in this entry. The entry contains 18932 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Phospholipase D2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	584	Total	C	N	O	S	0	0	0
			4702	3015	825	846	16			
1	B	584	Total	C	N	O	S	0	0	0
			4702	3015	825	846	16			
1	C	584	Total	C	N	O	S	0	0	0
			4702	3015	825	846	16			
1	D	584	Total	C	N	O	S	0	0	0
			4702	3015	825	846	16			

- Molecule 2 is 4-bromo-N-{(2S)-1-[1-(3-fluorophenyl)-4-oxo-1,3,8-triazaspiro[4.5]decan-8-yl]propan-2-yl}benzamide (CCD ID: MJY) (formula: C₂₃H₂₆BrFN₄O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	Br	C	F	N	O	0	0
			31	1	23	1	4	2		

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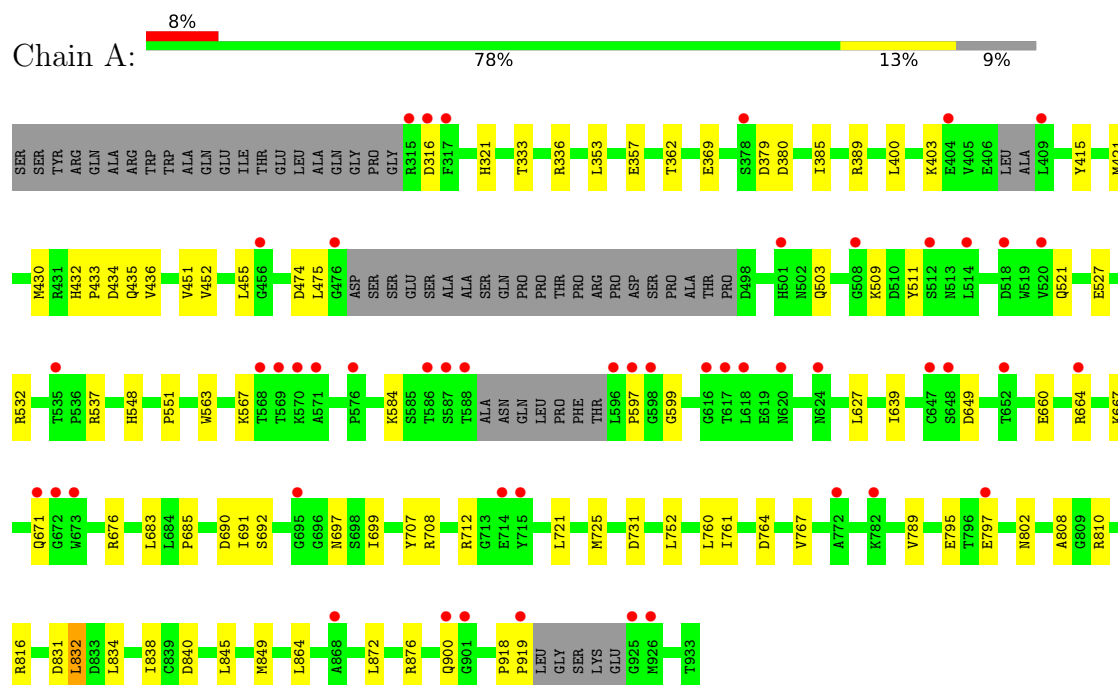
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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	Br	C	F	N	O	0	0
			31	1	23	1	4	2		
2	C	1	Total	Br	C	F	N	O	0	0
			31	1	23	1	4	2		
2	D	1	Total	Br	C	F	N	O	0	0
			31	1	23	1	4	2		

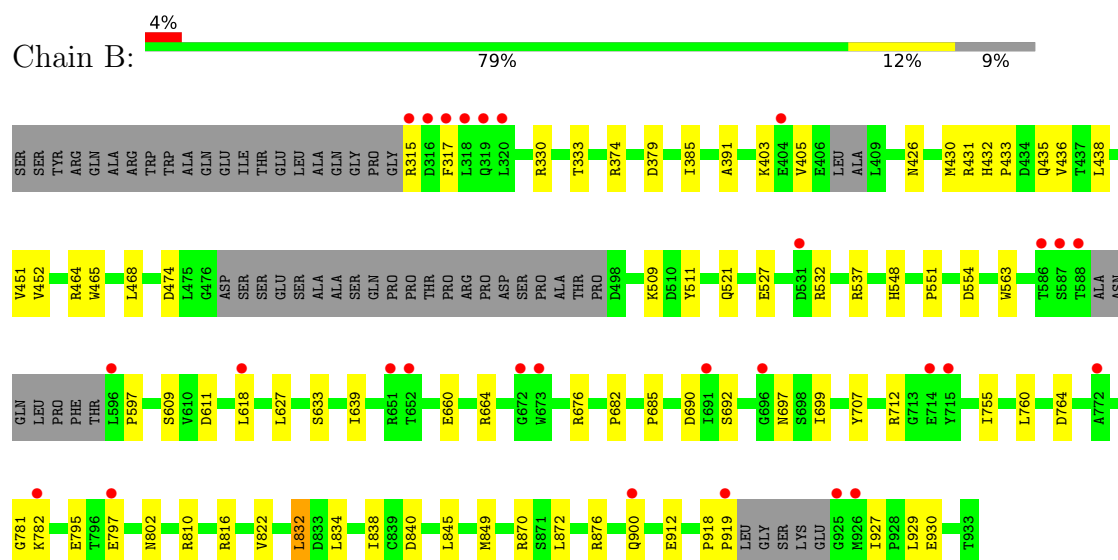
3 Residue-property plots [i](#)

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: Phospholipase D2



• Molecule 1: Phospholipase D2



[illegible]

Chain D:

SER	L420	Y511	C647	T796
SER	S512	E797	E659	F798
TYR	L223	N513	E660	S799
ARG	L266	L514		
GLN		T515		
ALA		T516		N802
ARG	V429			Y806
TRP	M430	Q521	K667	Q807
TRP	R431			A808
ALA	H432	E527	Q671	G809
GLN	P433	N528		R810
GLU	E434	F529	Y875	
ILE	Q435		R876	R816
THR	T437	R532	L880	P830
GLU	L438		L681	D831
LEU		T536		L832
ALA		P538		D833
GLN		R537		L834
GLY		M538		
PRO	V451	R541		F887
GLY	V452			E888
		H548		G889
	L455		D690	C899
			I891	D840
		P551	S892	
				C863
		M563		L864
		K567		P865
	ASP	A571	Y707	S871
	SER			L872
	SER		C711	R873
	GLU	R712		T874
	SER	T588		L875
	ALA		L718	R876
	ALA	ASN	H719	
	SER	GLN	R720	V881
	GLN	LEU	L721	
	PRO	PRO		R893
	PRO	PHE	M725	
	THR	THR		
		L596	D731	H905
		P597		L917
	ARG		E743	P918
	PRO	Q598		P919
	ASP	G599		
	ASP	Q600		LEU
	PRO		G746	GLY
	ALA	V604		SER
	E393		I755	LYS
				GLU
	S398		L760	
	L399			G925
		D498	D764	N926
		L499		I927
	K403	S500	L627	P928
	E404	H501		L929
	V405	N502	S633	E930
			Q634	P931
				V932
	LEU	F505	I639	
	ALA		E640	
				T933
	L409	K509	S646	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.06Å 132.32Å 114.61Å 90.00° 100.01° 90.00°	Depositor
Resolution (Å)	48.17 – 3.20 48.17 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.17-3.20) 99.5 (48.17-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.278 , 0.319 0.272 , 0.309	Depositor DCC
R_{free} test set	2147 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	56.9	Xtriage
Anisotropy	0.503	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	18932	wwPDB-VP
Average B, all atoms (Å ²)	65.0	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 52.44 % 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 4.8634e-05. 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

5.1 Standard geometry

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

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	0.14	0/4823	0.45	0/6553
1	B	0.15	0/4823	0.45	0/6553
1	C	0.14	0/4823	0.45	0/6553
1	D	0.13	0/4823	0.45	0/6553
All	All	0.14	0/19292	0.45	0/26212

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	4702	0	4634	57	0
1	B	4702	0	4634	51	0
1	C	4702	0	4634	64	1
1	D	4702	0	4634	72	1
2	A	31	0	0	0	0
2	B	31	0	0	1	0
2	C	31	0	0	1	0
2	D	31	0	0	1	0
All	All	18932	0	18536	231	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 6.

The worst 5 of 231 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:503:GLN:HG2	1:C:831:ASP:HB3	1.65	0.79
1:C:712:ARG:NH2	1:C:910:PHE:O	2.18	0.77
1:D:797:GLU:HG2	1:D:810:ARG:HG2	1.67	0.77
1:B:509:LYS:NZ	1:B:521:GLN:O	2.17	0.76
1:A:797:GLU:HG2	1:A:810:ARG:HG2	1.68	0.73

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)
1:C:855:ASN:ND2	1:D:671:GLN:O[1_554]	2.02	0.18

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	574/640 (90%)	551 (96%)	23 (4%)	0	100	100
1	B	574/640 (90%)	553 (96%)	21 (4%)	0	100	100
1	C	574/640 (90%)	553 (96%)	21 (4%)	0	100	100
1	D	574/640 (90%)	552 (96%)	22 (4%)	0	100	100
All	All	2296/2560 (90%)	2209 (96%)	87 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	504/554 (91%)	503 (100%)	1 (0%)	87	89
1	B	504/554 (91%)	503 (100%)	1 (0%)	87	89
1	C	504/554 (91%)	504 (100%)	0	100	100
1	D	504/554 (91%)	504 (100%)	0	100	100
All	All	2016/2216 (91%)	2014 (100%)	2 (0%)	88	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	832	LEU
1	B	832	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	642	GLN
1	D	818	HIS
1	D	635	HIS
1	B	818	HIS
1	C	635	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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MJY	D	1001	-	34,34,34	0.86	1 (2%)	48,49,49	1.01	3 (6%)
2	MJY	A	1001	-	34,34,34	0.68	1 (2%)	48,49,49	1.40	6 (12%)
2	MJY	C	1001	-	34,34,34	0.77	1 (2%)	48,49,49	1.51	7 (14%)
2	MJY	B	1001	-	34,34,34	0.90	1 (2%)	48,49,49	0.95	3 (6%)

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	MJY	D	1001	-	-	2/16/45/45	0/4/4/4
2	MJY	A	1001	-	-	4/16/45/45	0/4/4/4
2	MJY	C	1001	-	-	5/16/45/45	0/4/4/4
2	MJY	B	1001	-	-	2/16/45/45	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	MJY	C23-N1	4.67	1.48	1.44
2	D	1001	MJY	C23-N1	4.45	1.48	1.44
2	C	1001	MJY	C23-N1	4.10	1.47	1.44
2	A	1001	MJY	C23-N1	3.39	1.47	1.44

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1001	MJY	C16-C2-N4	7.35	118.09	112.87
2	A	1001	MJY	C16-C2-N4	4.45	116.03	112.87
2	A	1001	MJY	C3-C2-N4	3.78	115.56	112.87
2	A	1001	MJY	C4-C3-C2	3.66	116.16	113.05
2	D	1001	MJY	C23-N4-C17	3.49	122.00	117.94

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

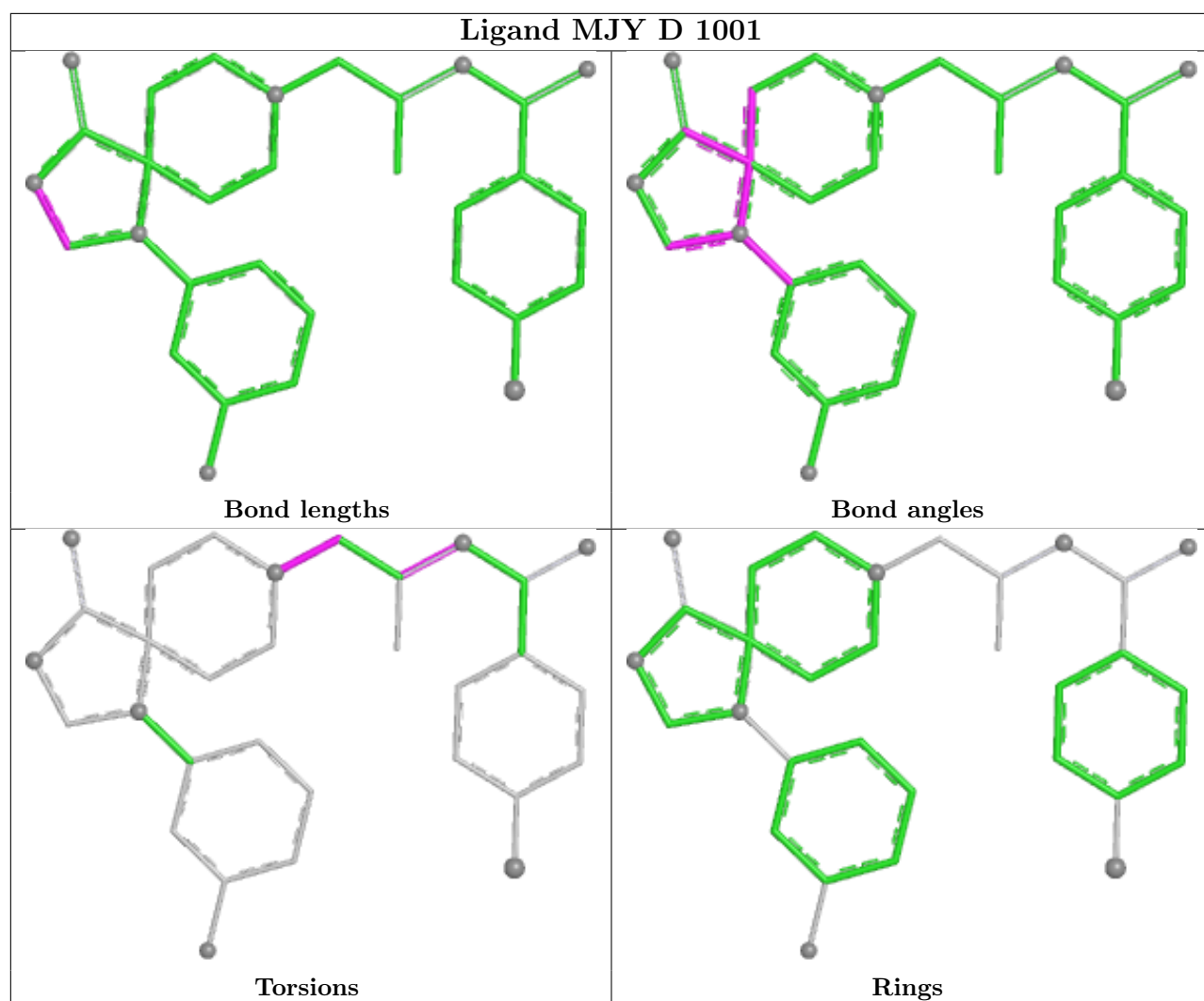
Mol	Chain	Res	Type	Atoms
2	A	1001	MJY	N2-C5-C6-C14
2	A	1001	MJY	N2-C5-C6-N3
2	A	1001	MJY	C8-C7-N3-C6
2	B	1001	MJY	C6-C5-N2-C15
2	C	1001	MJY	N2-C5-C6-N3

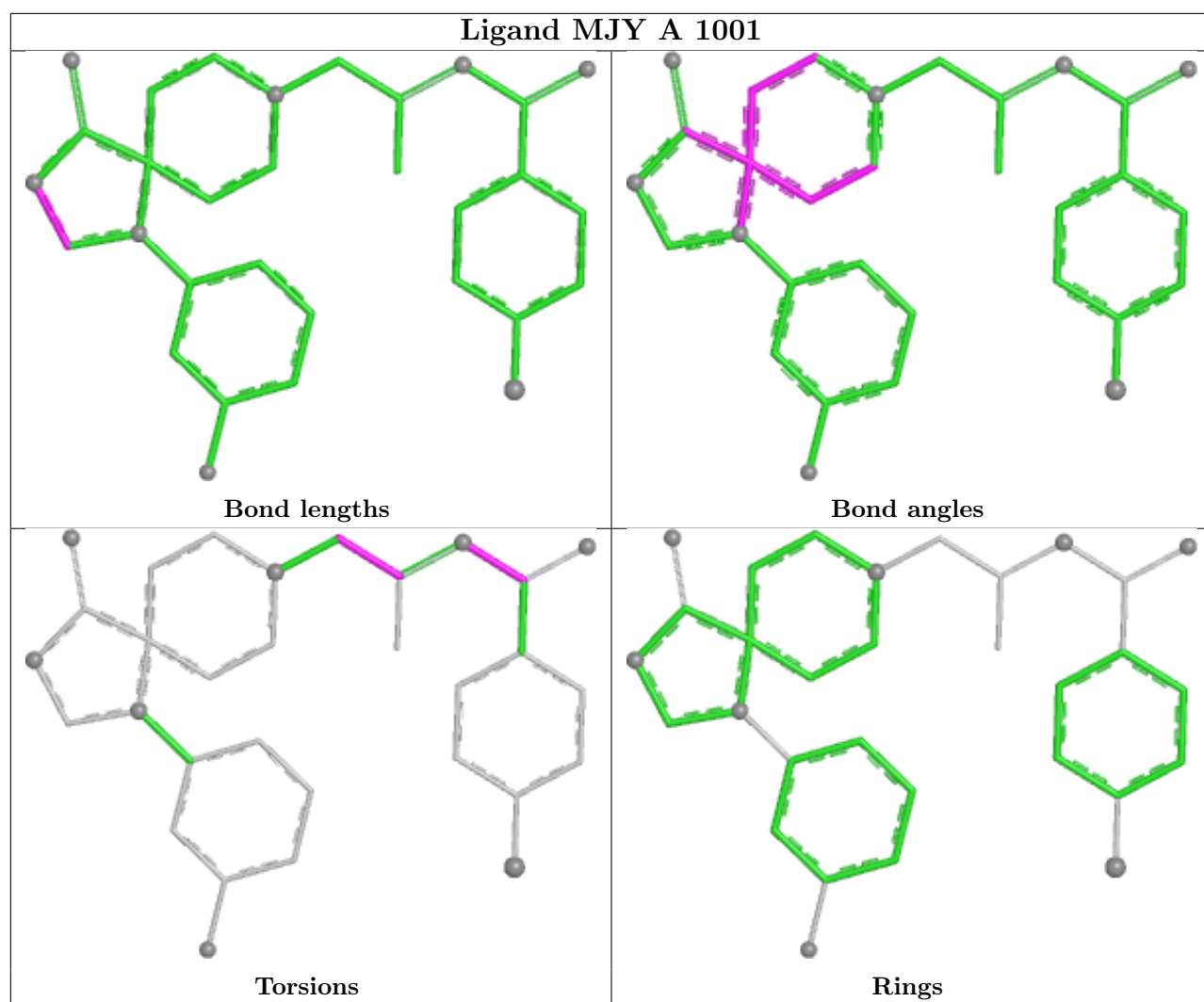
There are no ring outliers.

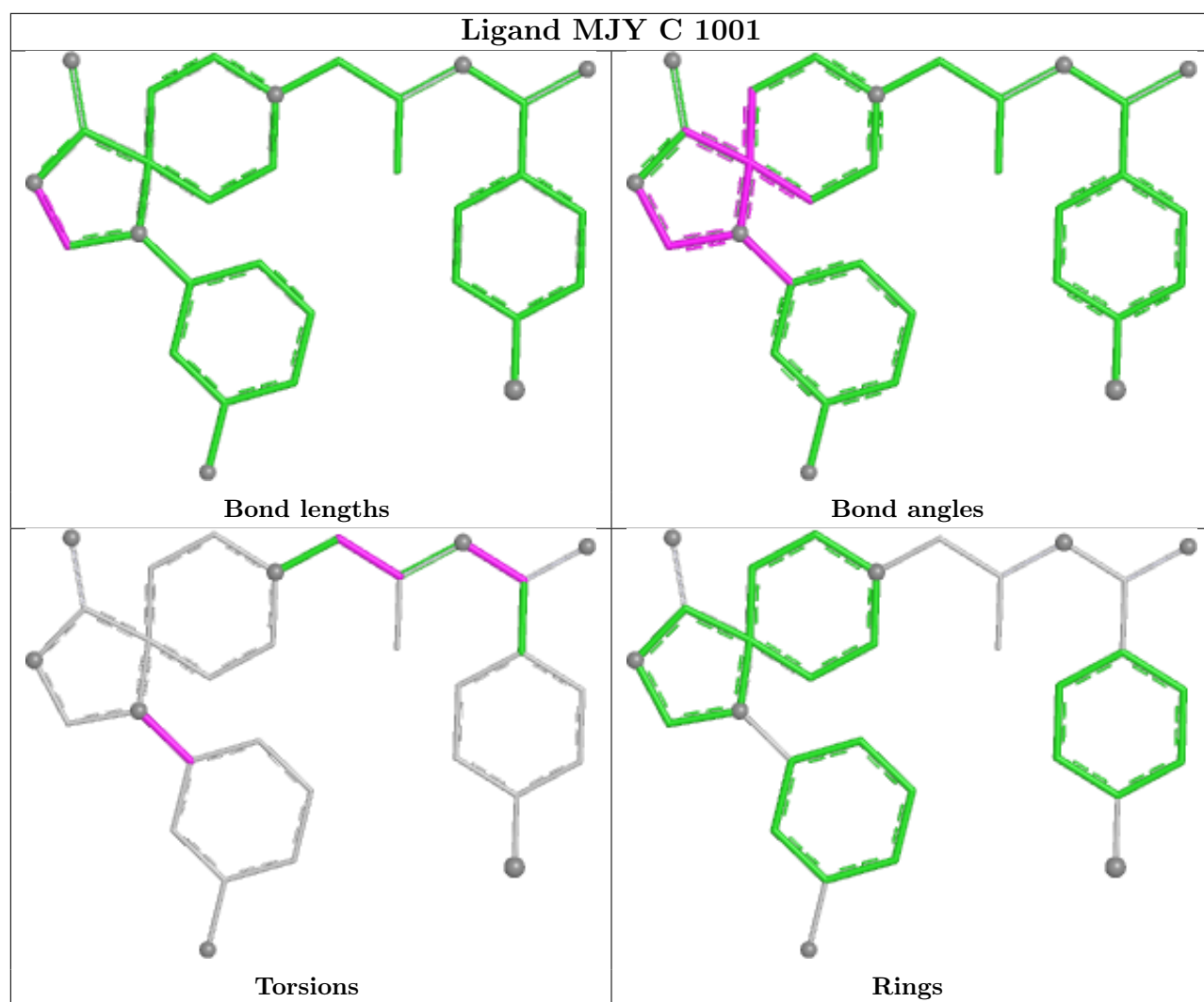
3 monomers are involved in 3 short contacts:

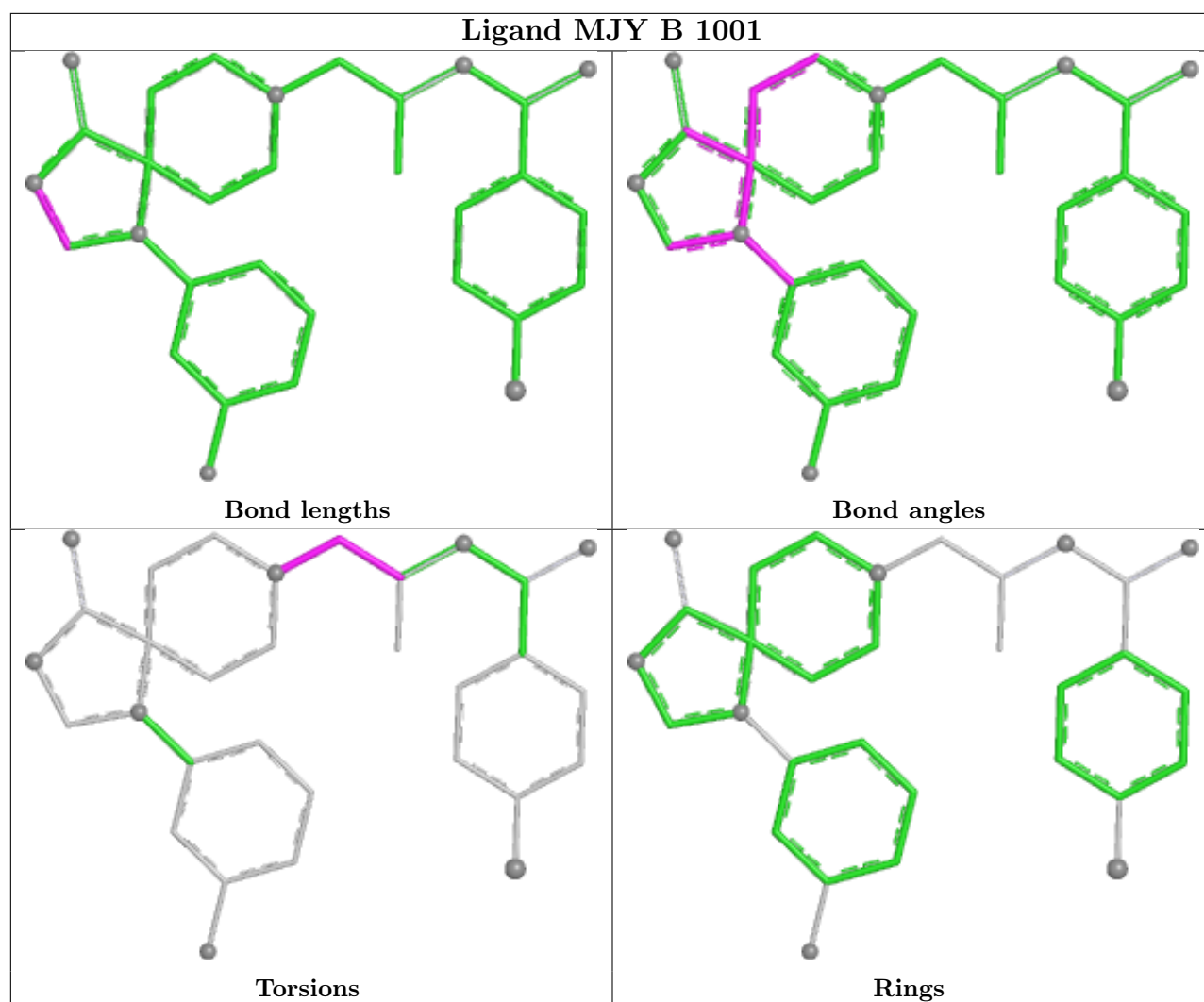
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1001	MJY	1	0
2	C	1001	MJY	1	0
2	B	1001	MJY	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	584/640 (91%)	0.69	50 (8%)	16	11	28, 54, 105, 178	0
1	B	584/640 (91%)	0.37	28 (4%)	35	22	15, 43, 93, 172	0
1	C	584/640 (91%)	0.83	47 (8%)	18	12	37, 77, 123, 197	0
1	D	584/640 (91%)	0.66	40 (6%)	23	15	34, 69, 115, 180	0
All	All	2336/2560 (91%)	0.64	165 (7%)	22	14	15, 62, 114, 197	0

The worst 5 of 165 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	925	GLY	6.6
1	C	926	MET	5.3
1	C	925	GLY	4.7
1	A	597	PRO	4.6
1	A	315	ARG	4.6

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 [i](#)

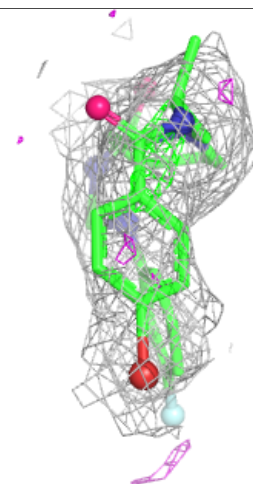
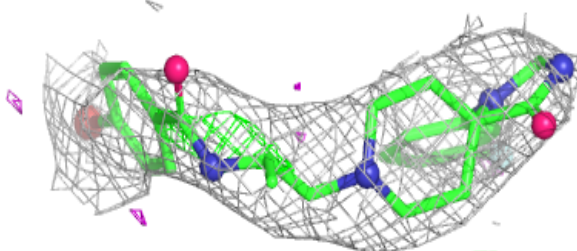
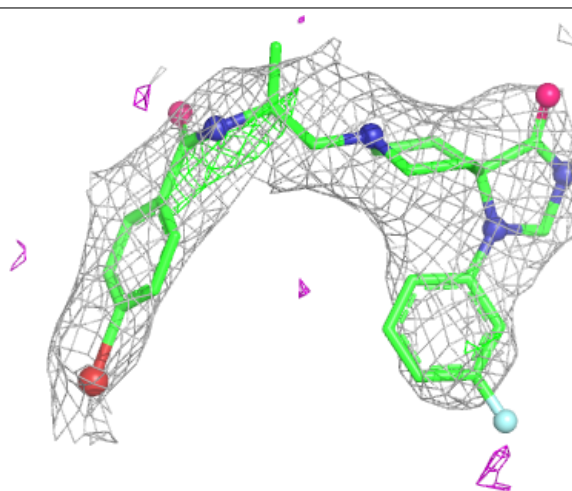
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MJY	C	1001	31/31	0.81	0.27	85,93,236,291	0
2	MJY	D	1001	31/31	0.81	0.29	71,77,244,300	0
2	MJY	A	1001	31/31	0.82	0.28	59,79,195,242	0
2	MJY	B	1001	31/31	0.88	0.31	64,99,213,269	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.

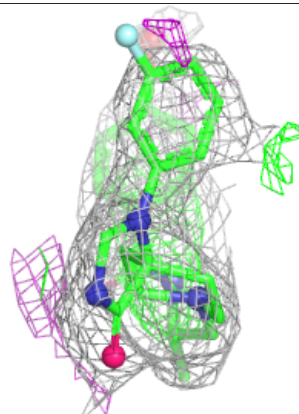
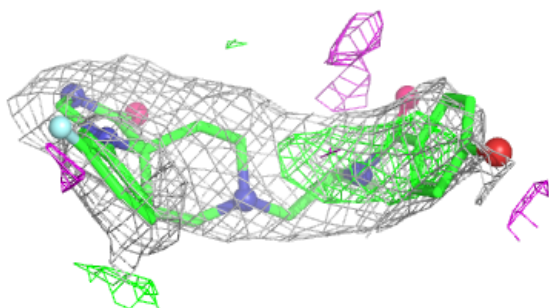
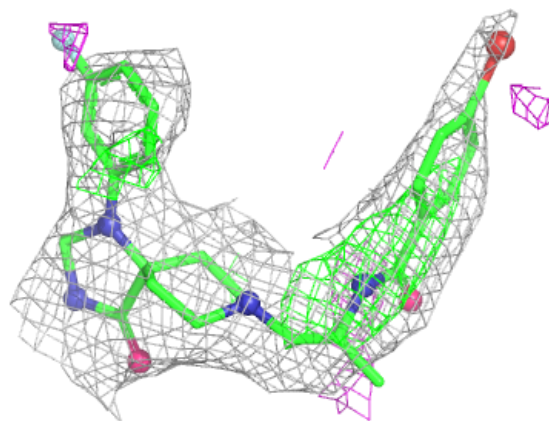
Electron density around MJY C 1001:

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



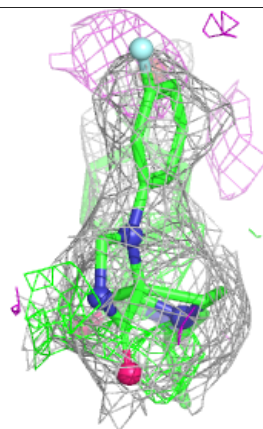
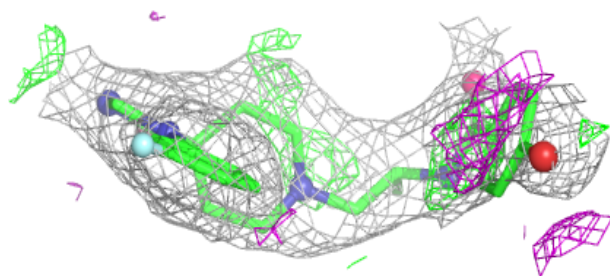
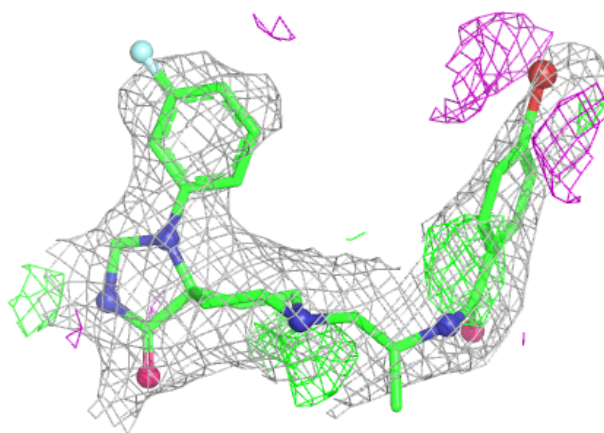
Electron density around MJY D 1001:

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



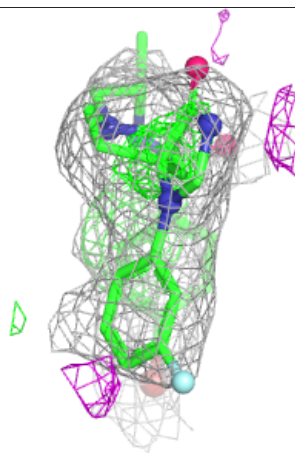
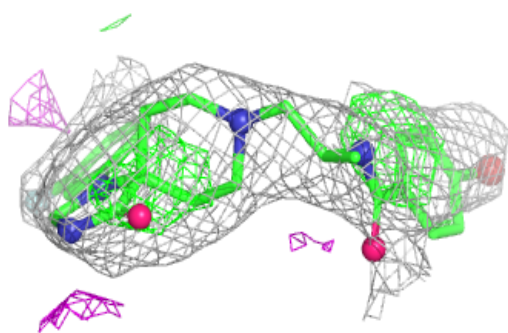
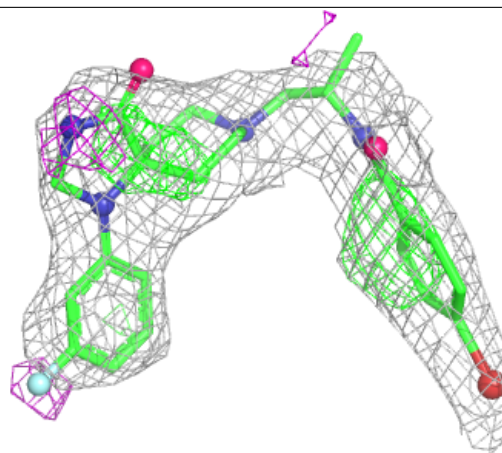
Electron density around MJY A 1001:

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



Electron density around MJY B 1001:

$2mF_o-DF_c$ (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.