



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 7, 2024 – 02:33 pm GMT

PDB ID : 6F90  
Title : Structure of the family GH92 alpha-mannosidase BT3130 from *Bacteroides thetaiotaomicron* in complex with Mannoimidazole (ManI)  
Authors : Thompson, A.J.; Spears, R.J.; Zhu, Y.; Suits, M.D.L.; Williams, S.J.; Gilbert, H.J.; Davies, G.J.  
Deposited on : 2017-12-13  
Resolution : 2.40 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

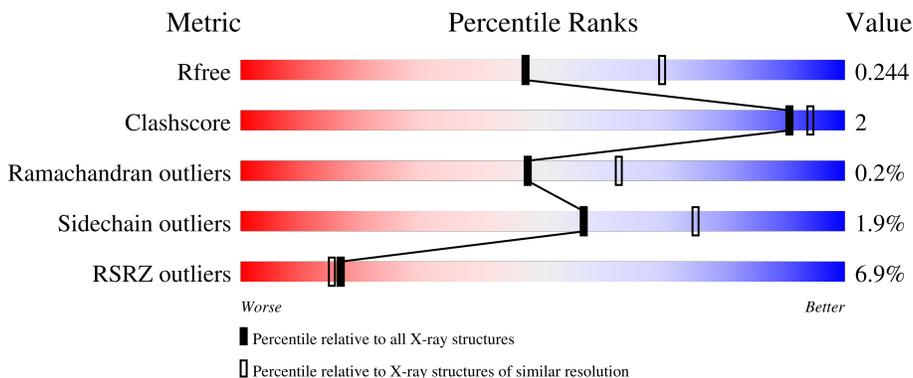
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	727	 94%
1	B	727	 2% 92% 5%
1	C	727	 18% 91% 5%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17665 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 Alpha-1,2-mannosidase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	714	5651	3590	956	1078	27	0	1	0
1	B	708	5523	3523	926	1047	27	0	0	0
1	C	692	5260	3330	895	1011	24	0	3	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	MET	-	initiating methionine	UNP A0A174L250
A	18	GLY	-	expression tag	UNP A0A174L250
A	736	LEU	-	expression tag	UNP A0A174L250
A	737	GLU	-	expression tag	UNP A0A174L250
A	738	HIS	-	expression tag	UNP A0A174L250
A	739	HIS	-	expression tag	UNP A0A174L250
A	740	HIS	-	expression tag	UNP A0A174L250
A	741	HIS	-	expression tag	UNP A0A174L250
A	742	HIS	-	expression tag	UNP A0A174L250
A	743	HIS	-	expression tag	UNP A0A174L250
B	17	MET	-	initiating methionine	UNP A0A174L250
B	18	GLY	-	expression tag	UNP A0A174L250
B	736	LEU	-	expression tag	UNP A0A174L250
B	737	GLU	-	expression tag	UNP A0A174L250
B	738	HIS	-	expression tag	UNP A0A174L250
B	739	HIS	-	expression tag	UNP A0A174L250
B	740	HIS	-	expression tag	UNP A0A174L250
B	741	HIS	-	expression tag	UNP A0A174L250
B	742	HIS	-	expression tag	UNP A0A174L250
B	743	HIS	-	expression tag	UNP A0A174L250
C	17	MET	-	initiating methionine	UNP A0A174L250
C	18	GLY	-	expression tag	UNP A0A174L250
C	736	LEU	-	expression tag	UNP A0A174L250

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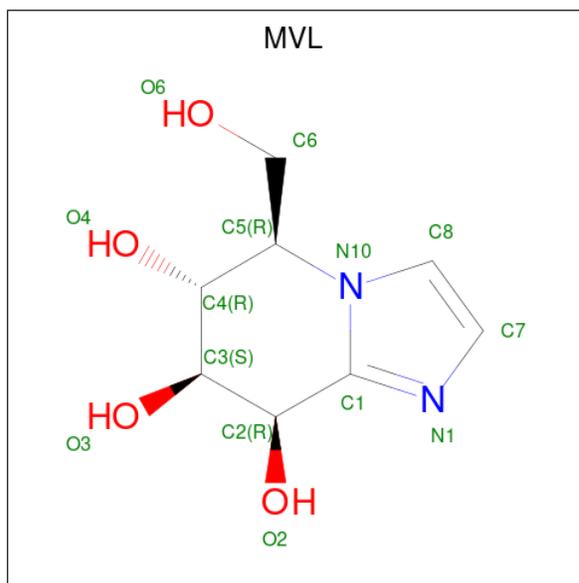
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Chain	Residue	Modelled	Actual	Comment	Reference
C	737	GLU	-	expression tag	UNP A0A174L250
C	738	HIS	-	expression tag	UNP A0A174L250
C	739	HIS	-	expression tag	UNP A0A174L250
C	740	HIS	-	expression tag	UNP A0A174L250
C	741	HIS	-	expression tag	UNP A0A174L250
C	742	HIS	-	expression tag	UNP A0A174L250
C	743	HIS	-	expression tag	UNP A0A174L250

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

- Molecule 3 is (5R,6R,7S,8R)-5-(HYDROXYMETHYL)-5,6,7,8-TETRAHYDROIMIDAZO[1,2-A]PYRIDINE-6,7,8-TRIOL (three-letter code: MVL) (formula: C<sub>8</sub>H<sub>12</sub>N<sub>2</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 14 8 2 4	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	8	2	4		
3	C	1	Total	C	N	O	0	0
			14	8	2	4		

- Molecule 4 is water.

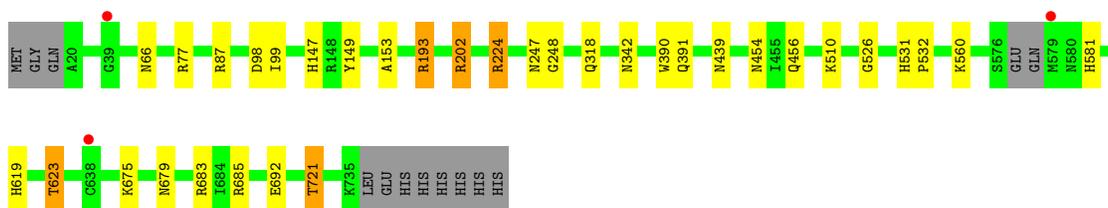
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	679	Total	O	0	0
			679	679		
4	B	323	Total	O	0	1
			324	324		
4	C	183	Total	O	0	0
			183	183		

### 3 Residue-property plots [i](#)

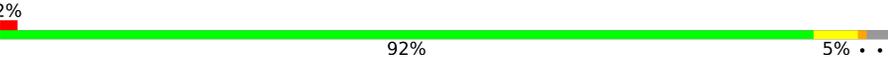
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

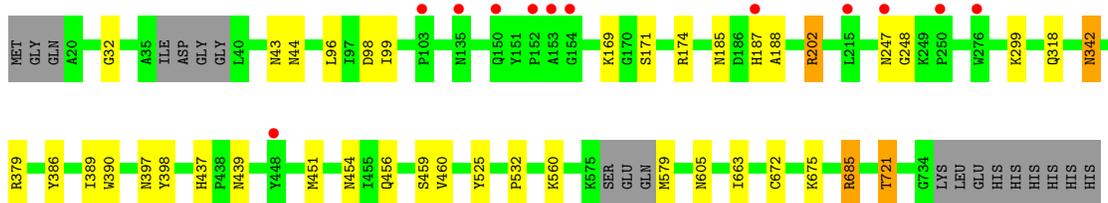
- Molecule 1: Alpha-1,2-mannosidase, putative

Chain A:  94%

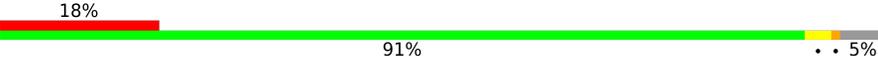


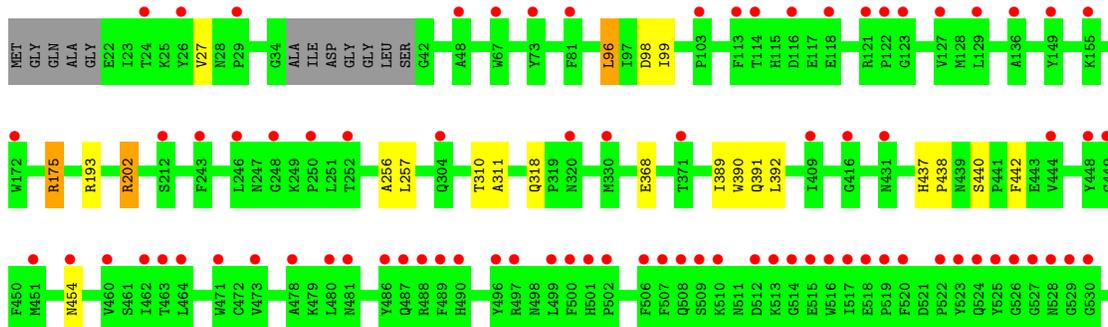
- Molecule 1: Alpha-1,2-mannosidase, putative

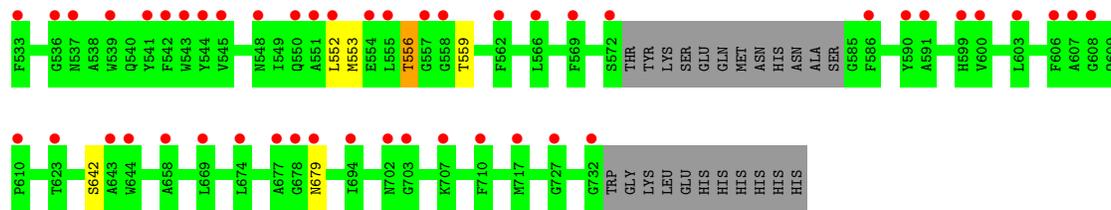
Chain B:  92% 5%



- Molecule 1: Alpha-1,2-mannosidase, putative

Chain C:  91% 18% 5%





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	273.67Å 273.67Å 189.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.38 – 2.40 49.38 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.38-2.40) 99.4 (49.38-2.40)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.11 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0131	Depositor
R, $R_{free}$	0.207 , 0.242 0.210 , 0.244	Depositor DCC
$R_{free}$ test set	7949 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.8	Xtrriage
Anisotropy	0.044	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 47.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	17665	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.09% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MVL, 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	0.47	0/5819	0.70	8/7913 (0.1%)
1	B	0.43	0/5687	0.62	4/7749 (0.1%)
1	C	0.47	0/5420	0.61	2/7398 (0.0%)
All	All	0.46	0/16926	0.65	14/23060 (0.1%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	202	ARG	NE-CZ-NH2	-10.12	115.24	120.30
1	A	202	ARG	NE-CZ-NH1	8.27	124.43	120.30
1	A	224	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	B	202	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	C	202	ARG	NE-CZ-NH1	6.27	123.44	120.30
1	A	224	ARG	NE-CZ-NH2	-5.73	117.43	120.30
1	A	193	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	C	202	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	B	685	ARG	NE-CZ-NH1	5.35	122.98	120.30
1	A	193	ARG	NE-CZ-NH2	-5.23	117.69	120.30
1	A	77	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	A	87	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	B	379	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	B	202	ARG	NE-CZ-NH2	-5.03	117.78	120.30

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	5651	0	5238	16	0
1	B	5523	0	5060	20	0
1	C	5260	0	4637	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	14	0	10	0	0
3	B	14	0	10	0	0
3	C	14	0	10	0	0
4	A	679	0	0	6	1
4	B	324	0	0	5	0
4	C	183	0	0	1	0
All	All	17665	0	14965	54	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 2.

All (54) 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:175[B]:ARG:HH11	1:C:175[B]:ARG:HG3	0.97	1.07
1:C:175[B]:ARG:HG3	1:C:175[B]:ARG:NH1	1.77	0.86
1:B:386:TYR:HH	1:B:398:TYR:HH	1.25	0.84
1:C:553:MET:CE	1:C:559:THR:HG22	2.08	0.84
1:C:175[B]:ARG:HH11	1:C:175[B]:ARG:CG	1.88	0.83
1:B:672:CYS:SG	4:B:1169:HOH:O	2.41	0.77
1:C:553:MET:HE1	1:C:559:THR:HG22	1.68	0.75
1:C:552:LEU:O	1:C:556:THR:OG1	2.03	0.75
1:A:619:HIS:O	1:A:623:THR:HB	1.96	0.65
1:A:439:ASN:HD22	1:A:456:GLN:HE22	1.46	0.64
1:C:98:ASP:OD2	1:C:202:ARG:NH2	2.34	0.60
1:C:553:MET:HE2	1:C:559:THR:HG22	1.84	0.59
1:B:342:ASN:HD22	1:B:342:ASN:H	1.50	0.59
1:B:98:ASP:OD2	1:B:202:ARG:NH2	2.36	0.58
1:C:202:ARG:HD3	4:C:903:HOH:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:672:CYS:HB3	4:B:1169:HOH:O	2.09	0.51
1:B:32:GLY:HA3	1:B:44:ASN:HD22	1.74	0.51
1:A:98:ASP:OD2	1:A:202:ARG:NH2	2.39	0.51
1:A:692:GLU:CB	4:A:1400:HOH:O	2.60	0.50
4:A:1110:HOH:O	1:B:721:THR:HG21	2.12	0.49
1:C:437:HIS:HB2	1:C:438:PRO:CD	2.43	0.48
1:A:202:ARG:HD3	4:A:1080:HOH:O	2.13	0.48
1:A:683:ARG:HG2	1:A:685:ARG:NH1	2.28	0.48
1:B:185:ASN:OD1	1:B:188:ALA:N	2.47	0.48
1:A:224:ARG:NH2	4:A:904:HOH:O	2.45	0.47
1:B:185:ASN:OD1	1:B:187:HIS:N	2.45	0.47
1:A:247:ASN:HA	1:A:248:GLY:HA2	1.58	0.47
1:B:439:ASN:HD22	1:B:456:GLN:HE22	1.63	0.47
1:B:672:CYS:CB	4:B:1169:HOH:O	2.63	0.47
1:A:510:LYS:NZ	4:A:907:HOH:O	2.48	0.45
1:C:440:SER:HB3	1:C:442:PHE:CZ	2.52	0.45
1:C:96:LEU:HD11	1:C:392:LEU:HD11	1.99	0.45
1:A:153:ALA:HA	1:A:247:ASN:CB	2.47	0.45
1:B:460:VAL:HG23	1:B:532:PRO:HB2	1.98	0.44
1:A:679:ASN:CB	4:A:1411:HOH:O	2.65	0.44
1:C:98:ASP:CG	1:C:202:ARG:HH22	2.20	0.44
1:B:43:ASN:HD22	1:B:43:ASN:HA	1.66	0.43
1:A:721:THR:HG21	4:B:952:HOH:O	2.18	0.43
1:B:389:ILE:HD11	1:B:437:HIS:CE1	2.54	0.42
1:A:526:GLY:HA3	1:A:531:HIS:CD2	2.55	0.42
1:B:171:SER:N	4:B:901:HOH:O	2.52	0.42
1:B:525:TYR:CD1	1:B:579:MET:HA	2.54	0.42
1:C:311:ALA:O	1:C:642:SER:HB3	2.19	0.42
1:C:96:LEU:CD1	1:C:392:LEU:HD11	2.49	0.42
1:A:147:HIS:HD2	1:A:149:TYR:OH	2.02	0.42
1:B:451:MET:O	1:B:459:SER:HB2	2.20	0.42
1:C:389:ILE:HD11	1:C:437:HIS:CE1	2.55	0.42
1:A:531:HIS:CG	1:A:532:PRO:HD2	2.56	0.41
1:C:27:VAL:HG13	1:C:310:THR:HA	2.02	0.41
1:B:169:LYS:HA	1:B:174:ARG:HB3	2.02	0.41
1:B:247:ASN:HA	1:B:248:GLY:HA2	1.80	0.41
1:C:256:ALA:O	1:C:257:LEU:HD12	2.20	0.41
1:A:98:ASP:CG	1:A:202:ARG:HH22	2.24	0.40
1:B:605:ASN:HD22	1:B:663:ILE:CG2	2.33	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)
4:A:1172:HOH:O	4:A:1172:HOH:O[10_664]	2.08	0.12

### 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	711/727 (98%)	686 (96%)	24 (3%)	1 (0%)	51 68
1	B	702/727 (97%)	663 (94%)	38 (5%)	1 (0%)	51 68
1	C	689/727 (95%)	653 (95%)	34 (5%)	2 (0%)	41 55
All	All	2102/2181 (96%)	2002 (95%)	96 (5%)	4 (0%)	47 62

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	96	LEU
1	A	99	ILE
1	B	99	ILE
1	C	99	ILE

#### 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	585/618 (95%)	573 (98%)	12 (2%)	53 72
1	B	560/618 (91%)	549 (98%)	11 (2%)	55 74
1	C	505/618 (82%)	495 (98%)	10 (2%)	55 74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1650/1854 (89%)	1617 (98%)	33 (2%)	57 74

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	ASN
1	A	193	ARG
1	A	318	GLN
1	A	342	ASN
1	A	390	TRP
1	A	391	GLN
1	A	454	ASN
1	A	560	LYS
1	A	581	HIS
1	A	623	THR
1	A	675	LYS
1	A	721	THR
1	B	96	LEU
1	B	299	LYS
1	B	318	GLN
1	B	342	ASN
1	B	390	TRP
1	B	397	ASN
1	B	454	ASN
1	B	560	LYS
1	B	675	LYS
1	B	685	ARG
1	B	721	THR
1	C	175[A]	ARG
1	C	175[B]	ARG
1	C	193	ARG
1	C	318	GLN
1	C	368	GLU
1	C	390	TRP
1	C	391	GLN
1	C	454	ASN
1	C	556	THR
1	C	679	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	44	ASN
1	A	66	ASN
1	A	147	HIS
1	A	226	HIS
1	A	267	GLN
1	A	292	GLN
1	A	318	GLN
1	A	342	ASN
1	A	391	GLN
1	A	439	ASN
1	A	454	ASN
1	A	498	ASN
1	A	508	GLN
1	A	531	HIS
1	A	697	GLN
1	B	43	ASN
1	B	44	ASN
1	B	147	HIS
1	B	292	GLN
1	B	318	GLN
1	B	320	ASN
1	B	342	ASN
1	B	397	ASN
1	B	403	ASN
1	B	437	HIS
1	B	439	ASN
1	B	454	ASN
1	B	466	GLN
1	B	487	GLN
1	B	498	ASN
1	B	508	GLN
1	B	531	HIS
1	B	589	GLN
1	B	635	ASN
1	B	697	GLN
1	B	713	HIS
1	C	267	GLN
1	C	292	GLN
1	C	437	HIS
1	C	439	ASN
1	C	454	ASN
1	C	508	GLN

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Mol	Chain	Res	Type
1	C	697	GLN
1	C	713	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are 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	MVL	C	802	2	13,15,15	0.81	0	11,22,22	1.88	2 (18%)
3	MVL	B	802	2	13,15,15	0.87	1 (7%)	11,22,22	1.84	2 (18%)
3	MVL	A	802	2	13,15,15	0.73	0	11,22,22	1.83	2 (18%)

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	MVL	C	802	2	-	0/2/22/22	0/1/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MVL	B	802	2	-	0/2/22/22	0/1/2/2
3	MVL	A	802	2	-	0/2/22/22	0/1/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	802	MVL	C1-C2	-2.04	1.48	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	802	MVL	C4-C3-C2	4.90	117.68	110.24
3	C	802	MVL	C4-C3-C2	4.73	117.43	110.24
3	A	802	MVL	C4-C3-C2	4.73	117.42	110.24
3	C	802	MVL	C3-C4-C5	2.98	116.41	111.37
3	A	802	MVL	C3-C4-C5	2.69	115.91	111.37
3	B	802	MVL	C3-C4-C5	2.37	115.37	111.37

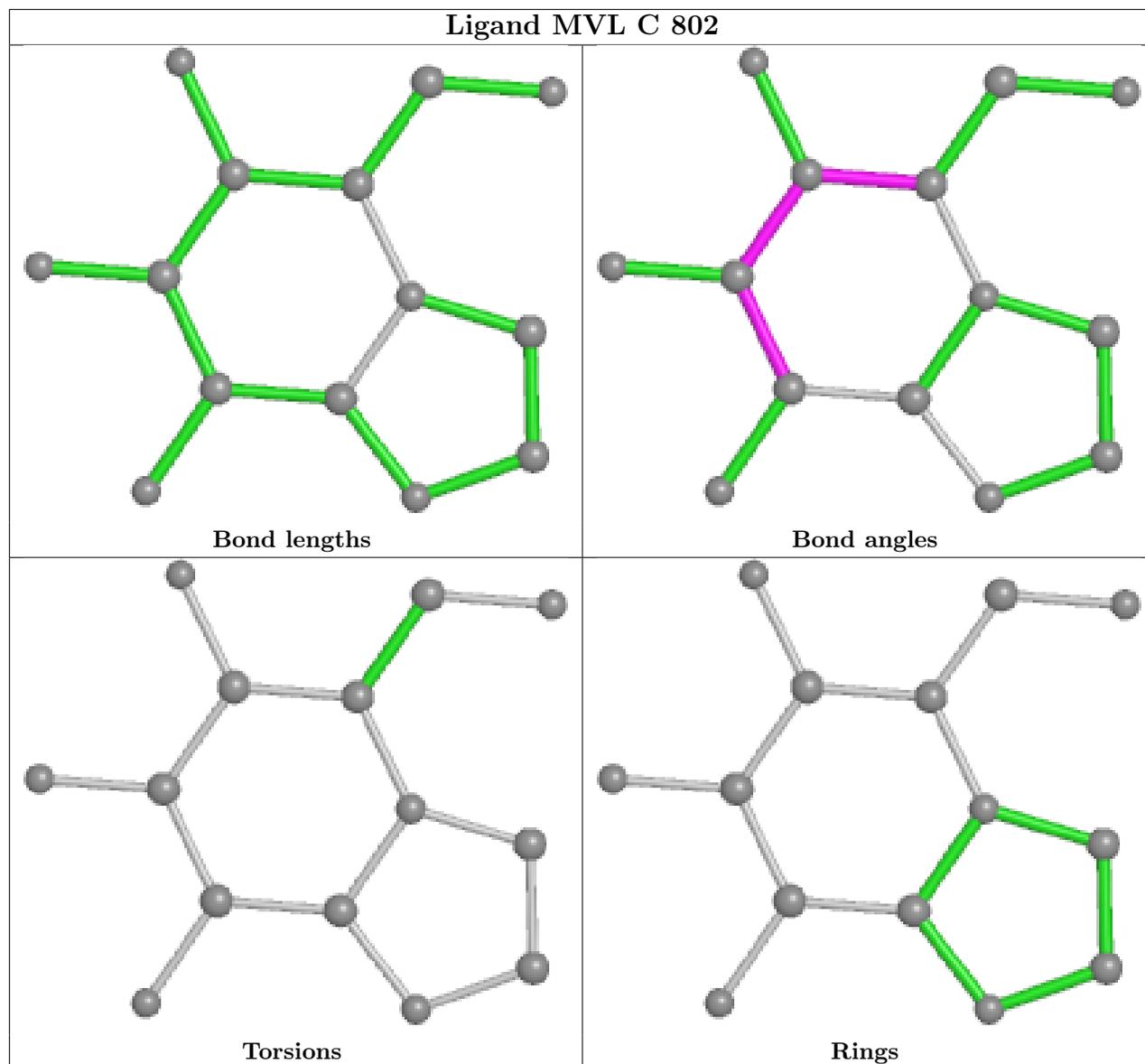
There are no chirality outliers.

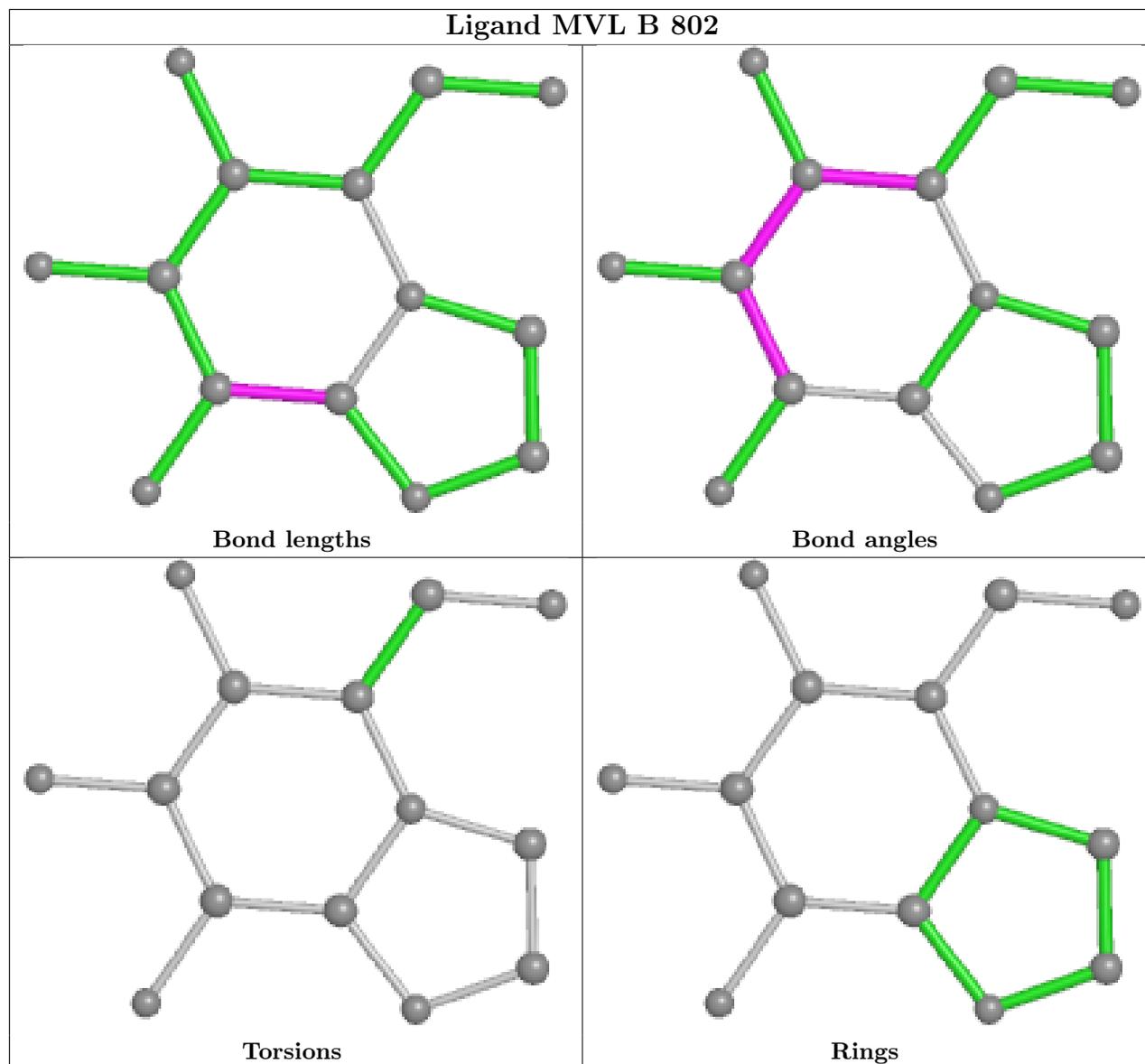
There are no torsion outliers.

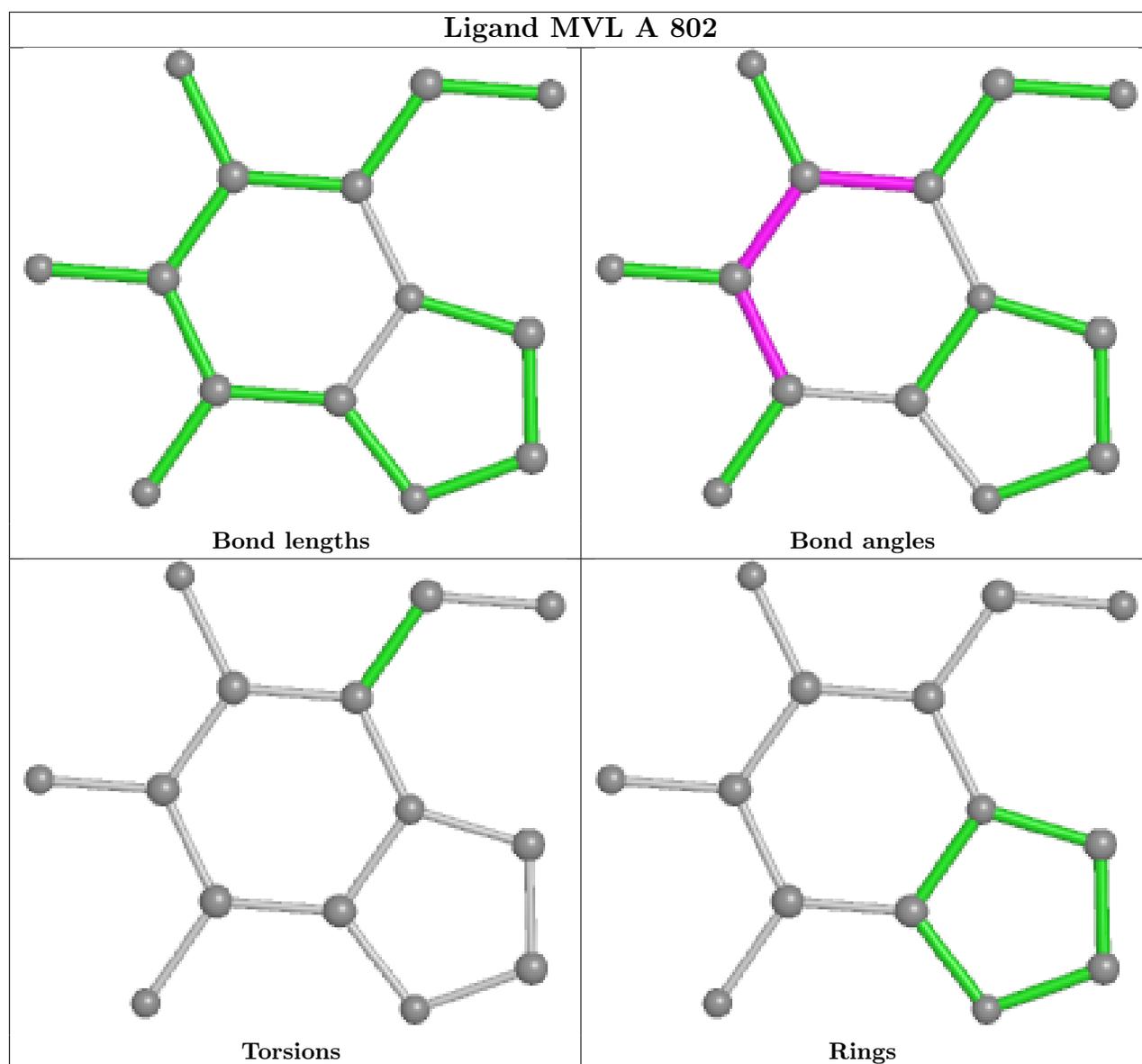
There are no ring outliers.

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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	714/727 (98%)	-0.38	3 (0%) 92   91	27, 37, 58, 116	0
1	B	708/727 (97%)	-0.10	12 (1%) 70   68	31, 60, 93, 131	0
1	C	692/727 (95%)	1.01	130 (18%) 1   1	56, 97, 126, 159	0
All	All	2114/2181 (96%)	0.17	145 (6%) 16   15	27, 61, 115, 159	0

All (145) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	527	GLY	8.2
1	C	464	LEU	5.8
1	B	153	ALA	5.8
1	C	529	GLY	5.2
1	C	516	TRP	5.1
1	C	29	PRO	5.1
1	B	154	GLY	5.1
1	C	552	LEU	5.1
1	C	539	TRP	4.8
1	C	520	PHE	4.7
1	C	113	PHE	4.6
1	C	460	VAL	4.5
1	C	530	GLY	4.5
1	C	500	PHE	4.5
1	C	513	LYS	4.3
1	C	122	PRO	4.2
1	C	528	ASN	4.2
1	C	558	GLY	4.2
1	C	502	PRO	4.0
1	C	149	TYR	3.8
1	B	135	ASN	3.7
1	C	496	TYR	3.7
1	B	276	TRP	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	448	TYR	3.7
1	C	544	TYR	3.7
1	C	550	GLN	3.7
1	B	187	HIS	3.7
1	A	39	GLY	3.6
1	C	703	GLY	3.6
1	C	543	TRP	3.6
1	C	501	HIS	3.6
1	C	67	TRP	3.6
1	C	542	PHE	3.6
1	C	514	GLY	3.6
1	C	555	LEU	3.5
1	C	536	GLY	3.5
1	C	123	GLY	3.5
1	C	497	ARG	3.4
1	C	172[A]	TRP	3.4
1	C	246	LEU	3.4
1	C	677	ALA	3.3
1	C	510	LYS	3.3
1	C	512	ASP	3.3
1	C	24	THR	3.2
1	C	73	TYR	3.2
1	C	658	ALA	3.2
1	C	623	THR	3.2
1	C	569	PHE	3.2
1	C	606	PHE	3.2
1	C	471	TRP	3.1
1	C	541	TYR	3.1
1	C	416	GLY	3.1
1	C	608	GLY	3.1
1	C	523	TYR	3.1
1	C	486	TYR	3.1
1	C	517	ILE	3.1
1	C	515	GLU	3.1
1	B	215	LEU	3.1
1	C	431	ASN	3.0
1	C	533	PHE	3.0
1	C	129	LEU	3.0
1	C	81	PHE	3.0
1	A	579	MET	2.9
1	C	444	VAL	2.9
1	C	116	ASP	2.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	519	PRO	2.9
1	C	522	PRO	2.9
1	C	702	ASN	2.9
1	C	525	TYR	2.9
1	C	304	GLN	2.9
1	C	557	GLY	2.8
1	B	150	GLN	2.8
1	C	330	MET	2.8
1	C	478	ALA	2.8
1	C	674	LEU	2.8
1	C	473	VAL	2.8
1	C	732	GLY	2.7
1	C	136	ALA	2.7
1	C	643	ALA	2.7
1	C	566	LEU	2.7
1	C	526	GLY	2.7
1	C	600	VAL	2.7
1	B	247	ASN	2.7
1	C	489	PHE	2.7
1	C	114	THR	2.7
1	C	591	ALA	2.6
1	C	371	THR	2.6
1	C	669	LEU	2.6
1	C	509	SER	2.6
1	C	487	GLN	2.6
1	C	508	GLN	2.6
1	A	638	CYS	2.6
1	C	155	LYS	2.6
1	C	463	THR	2.5
1	C	409	ILE	2.5
1	C	678	GLY	2.5
1	C	727	GLY	2.5
1	C	48	ALA	2.5
1	C	644	TRP	2.5
1	C	121	ARG	2.5
1	C	717	MET	2.4
1	B	152	PRO	2.4
1	C	26	TYR	2.4
1	C	524	GLN	2.4
1	C	545	VAL	2.4
1	C	248	GLY	2.4
1	C	507	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	599	HIS	2.4
1	B	448	TYR	2.4
1	C	250	PRO	2.4
1	C	607	ALA	2.4
1	C	127	VAL	2.4
1	C	462	ILE	2.4
1	C	490	HIS	2.3
1	C	243	PHE	2.3
1	C	551	ALA	2.3
1	C	449	GLY	2.3
1	C	103	PRO	2.3
1	C	506	PHE	2.3
1	C	562	PHE	2.3
1	C	572	SER	2.3
1	C	451	MET	2.3
1	C	454	ASN	2.2
1	C	481	ASN	2.2
1	C	518	GLU	2.2
1	B	103	PRO	2.2
1	C	212	SER	2.2
1	C	694	ILE	2.2
1	C	586	PHE	2.2
1	C	590	TYR	2.1
1	C	320	ASN	2.1
1	C	679	ASN	2.1
1	C	603	LEU	2.1
1	C	488	ARG	2.1
1	C	610	PRO	2.1
1	C	118	GLU	2.1
1	C	707	LYS	2.1
1	C	252	THR	2.1
1	C	499	LEU	2.1
1	B	250	PRO	2.0
1	C	480	LEU	2.0
1	C	710	PHE	2.0
1	C	537	ASN	2.0
1	C	548	ASN	2.0
1	C	554	GLU	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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

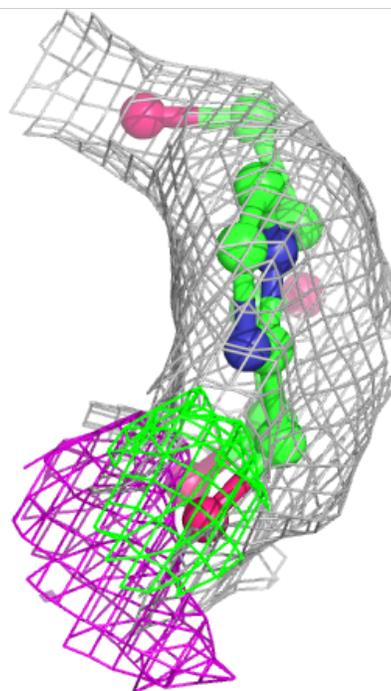
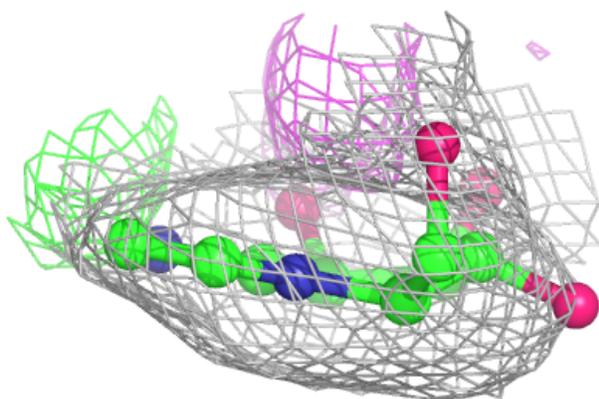
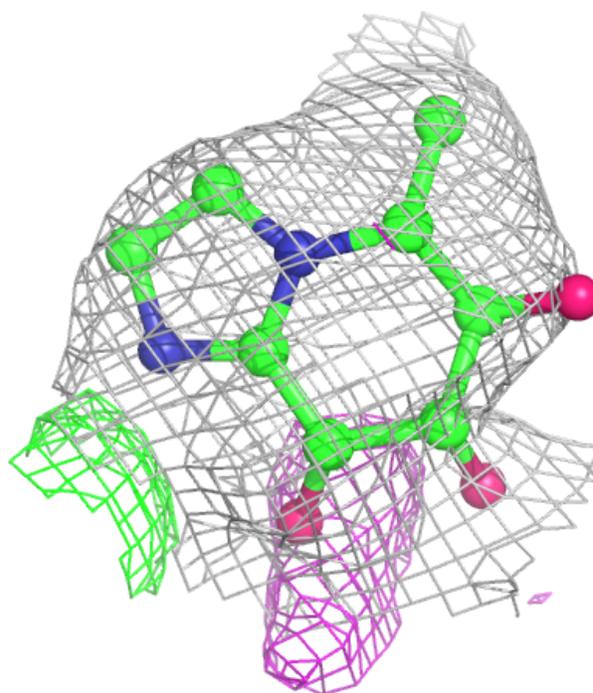
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
3	MVL	C	802	14/14	0.77	0.19	90,97,101,103	0
2	CA	C	801	1/1	0.87	0.18	100,100,100,100	0
3	MVL	B	802	14/14	0.93	0.14	54,68,70,70	0
3	MVL	A	802	14/14	0.96	0.16	30,33,34,35	0
2	CA	B	801	1/1	0.98	0.07	55,55,55,55	0
2	CA	A	801	1/1	0.99	0.09	33,33,33,33	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.

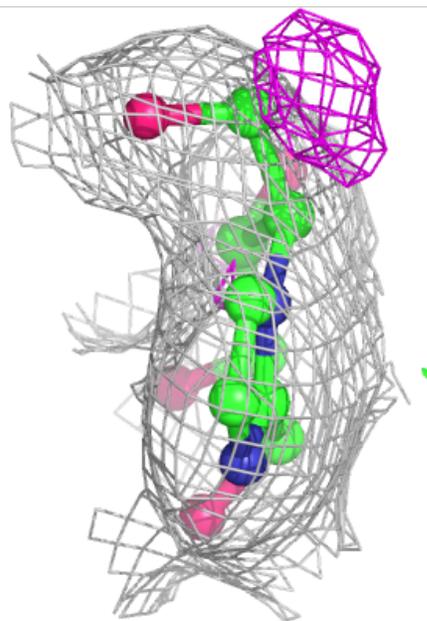
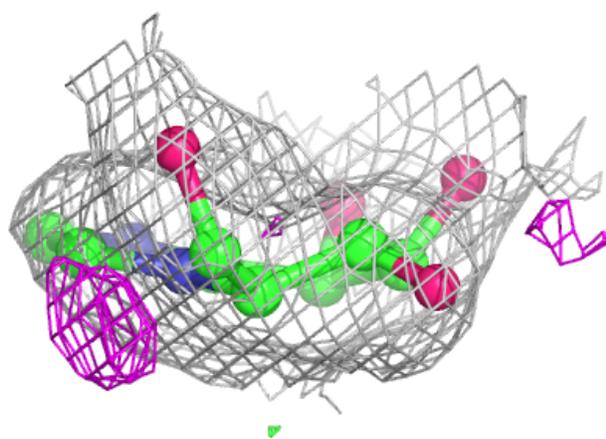
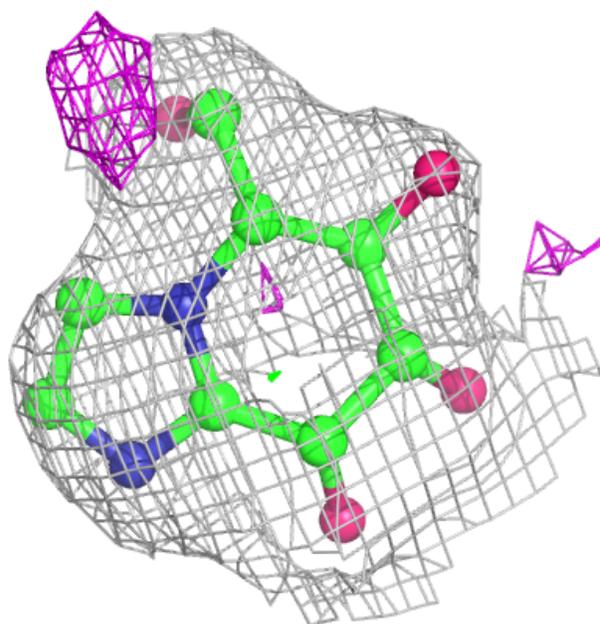
**Electron density around MVL C 802:**

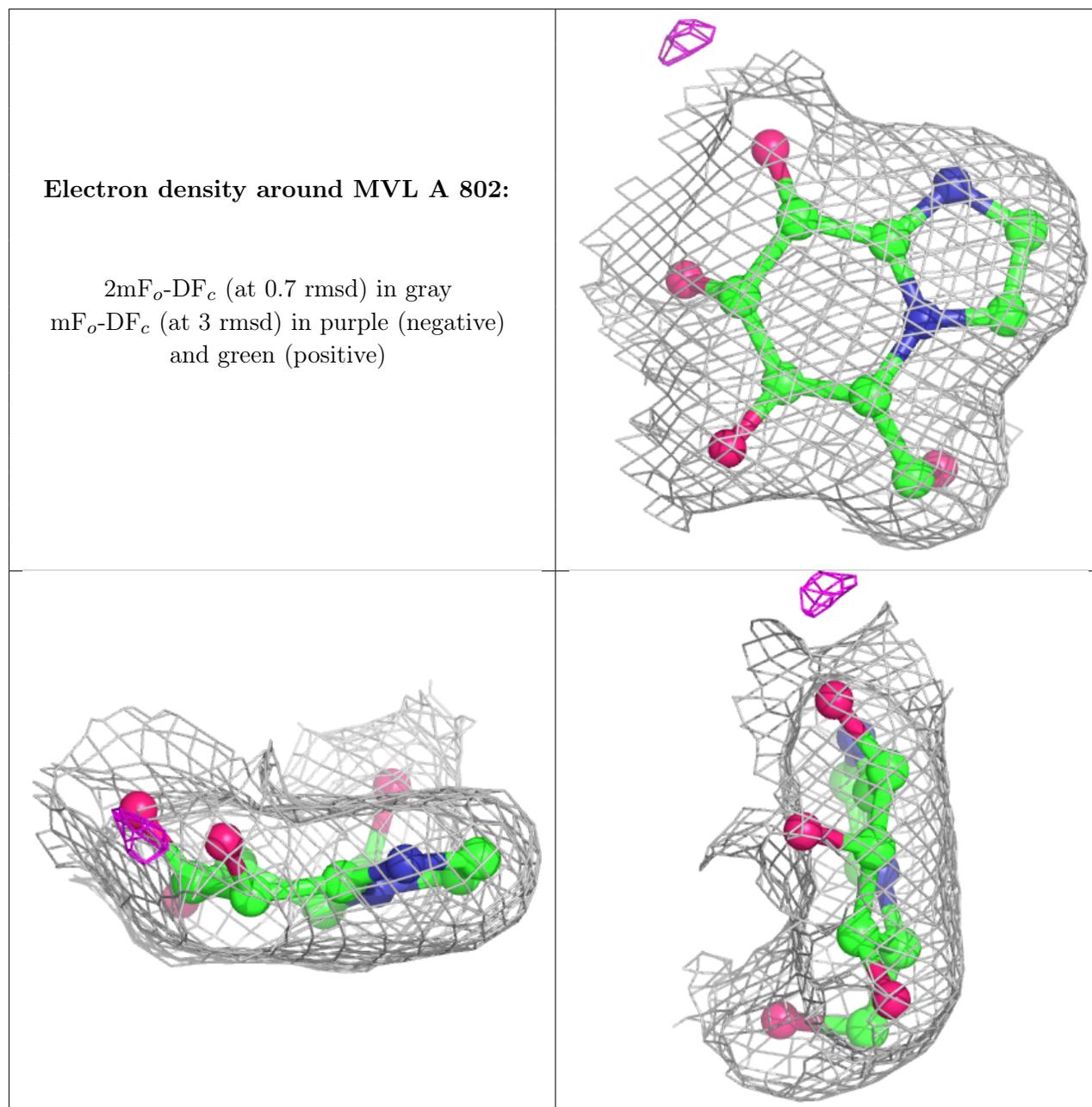
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around MVL B 802:**

$2mF_o-DF_c$  (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.