



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2021 – 10:35 AM EST

PDB ID : 6XFP
Title : Crystal Structure of BRAF kinase domain bound to Belvarafenib
Authors : Yin, J.; Sudhamsu, J.
Deposited on : 2020-06-16
Resolution : 2.00 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 : 2.17.1
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) : 2.17.1

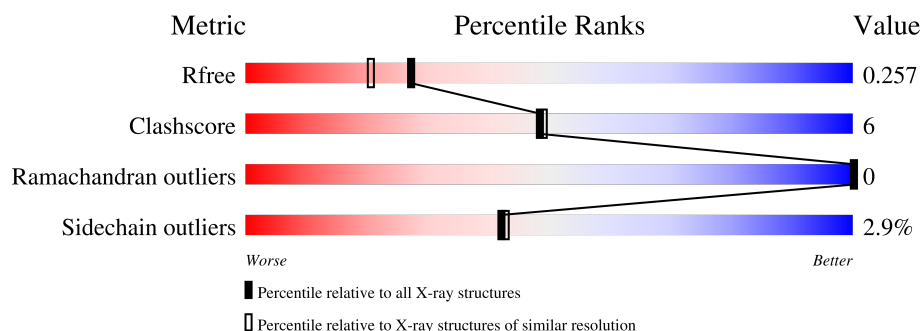
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	288	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2333 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.

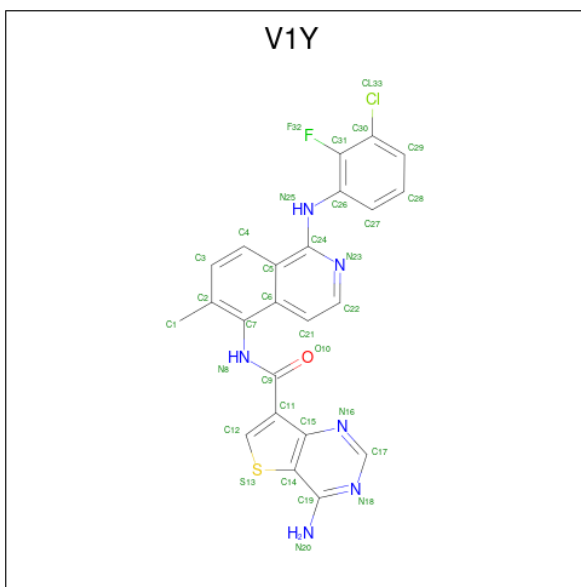
- Molecule 1 is a protein called Serine/threonine-protein kinase B-raf.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	272	2208	1398	395	402	13	0	5	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	436	MET	-	expression tag	UNP H7C560
A	437	HIS	-	expression tag	UNP H7C560
A	438	HIS	-	expression tag	UNP H7C560
A	439	HIS	-	expression tag	UNP H7C560
A	440	HIS	-	expression tag	UNP H7C560
A	441	HIS	-	expression tag	UNP H7C560
A	443	SER	ARG	conflict	UNP H7C560
A	539	LYS	HIS	conflict	UNP H7C560
A	543	ALA	ILE	conflict	UNP H7C560
A	544	SER	ILE	conflict	UNP H7C560
A	551	LYS	ILE	conflict	UNP H7C560
A	562	ARG	GLN	conflict	UNP H7C560
A	588	ASN	LEU	conflict	UNP H7C560
A	630	SER	LYS	conflict	UNP H7C560
A	667	GLU	PHE	conflict	UNP H7C560
A	673	SER	TYR	conflict	UNP H7C560
A	688	ARG	ALA	conflict	UNP H7C560
A	706	SER	LEU	conflict	UNP H7C560
A	709	ARG	GLN	conflict	UNP H7C560
A	713	GLU	SER	conflict	UNP H7C560
A	716	GLU	LEU	conflict	UNP H7C560
A	720	GLU	SER	conflict	UNP H7C560
A	722	SER	-	expression tag	UNP H7C560
A	723	GLY	-	expression tag	UNP H7C560

- Molecule 2 is 4-amino-N-{1-[(3-chloro-2-fluorophenyl)amino]-6-methylisoquinolin-5-yl}thien o[3,2-d]pyrimidine-7-carboxamide (three-letter code: V1Y) (formula: C₂₃H₁₆ClFN₆OS).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	F	N	O	S	
			33	23	1	1	6	1	1	

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	Cl		
			6	6	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	86	Total	O		
			86	86	0	0

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. 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. 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.

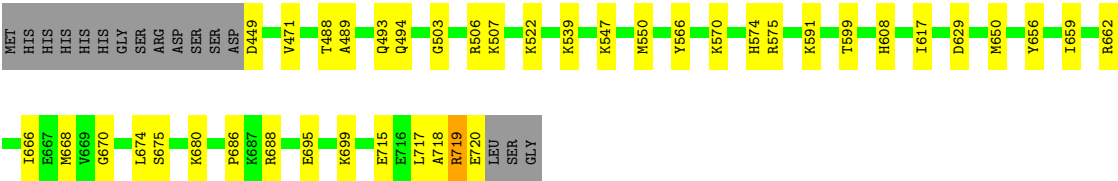
- Molecule 1: Serine/threonine-protein kinase B-raf

Chain A:

80%

14%

6%



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	48.79Å 119.56Å 103.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.78 – 2.00 59.78 – 1.53	Depositor EDS
% Data completeness (in resolution range)	95.6 (59.78-2.00) 56.4 (59.78-1.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.07 (at 1.53Å)	Xtriage
Refinement program	PHENIX 1.12-2829_final	Depositor
R, R_{free}	0.204 , 0.257 0.204 , 0.257	Depositor DCC
R_{free} test set	2000 reflections (6.15%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 53.8	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	0.93	EDS
Total number of atoms	2333	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.67% 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: CL, V1Y

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	0.40	0/2269	0.57	0/3056

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	2208	0	2233	27	0
2	A	33	0	0	0	0
3	A	6	0	0	1	0
4	A	86	0	0	7	0
All	All	2333	0	2233	27	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 6.

All (27) 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:591:LYS:NZ	4:A:906:HOH:O	2.31	0.62
1:A:550:MET:SD	1:A:650:MET:HE1	2.43	0.59
1:A:493[B]:GLN:HG3	1:A:494:GLN:N	2.18	0.58
1:A:656:TYR:HB3	1:A:659:ILE:HD13	1.88	0.56
1:A:566:TYR:OH	1:A:570:LYS:HE2	2.07	0.55
1:A:566:TYR:CZ	1:A:570:LYS:HE2	2.43	0.54
1:A:719:ARG:HA	1:A:719:ARG:HE	1.71	0.53
1:A:670:GLY:O	4:A:902:HOH:O	2.18	0.53
1:A:686:PRO:HG2	1:A:717:LEU:HD11	1.91	0.52
1:A:471:VAL:HG23	1:A:599:THR:HG21	1.91	0.51
1:A:695[A]:GLU:OE1	4:A:903:HOH:O	2.20	0.49
1:A:668:MET:HB3	1:A:674:LEU:HB2	1.95	0.49
1:A:719:ARG:HA	1:A:719:ARG:NE	2.29	0.47
1:A:718:ALA:O	1:A:720:GLU:HG3	2.14	0.47
1:A:715:GLU:O	1:A:719:ARG:HG2	2.14	0.47
1:A:715:GLU:OE2	3:A:806:CL:CL	2.70	0.47
1:A:506:ARG:NH2	4:A:915:HOH:O	2.50	0.45
1:A:488:THR:HG23	1:A:489:ALA:H	1.82	0.45
1:A:574:HIS:O	1:A:575[A]:ARG:HB2	2.17	0.45
1:A:449:ASP:HA	4:A:915:HOH:O	2.17	0.44
1:A:608:HIS:ND1	4:A:909:HOH:O	2.35	0.44
1:A:522:LYS:HB2	1:A:522:LYS:HE3	1.60	0.43
1:A:617:ILE:HD11	1:A:666:ILE:HD13	2.00	0.42
1:A:662:ARG:HD3	1:A:662:ARG:HA	1.89	0.42
1:A:503:GLY:O	1:A:507:LYS:HG3	2.20	0.42
1:A:539:LYS:HD2	4:A:953:HOH:O	2.20	0.41
1:A:719:ARG:HE	1:A:719:ARG:CA	2.33	0.41

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	275/288 (96%)	263 (96%)	12 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	244/253 (96%)	237 (97%)	7 (3%)	42	43

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	547	LYS
1	A	629	ASP
1	A	675	SER
1	A	680	LYS
1	A	688	ARG
1	A	699	LYS
1	A	719	ARG

Sometimes 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 ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 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
2	V1Y	A	801	-	33,37,37	0.86	0	46,54,54	2.25	14 (30%)

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	V1Y	A	801	-	-	1/10/12/12	0/5/5/5

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	V1Y	C17-N16-C15	7.94	120.99	114.81
2	A	801	V1Y	C14-C15-N16	-5.88	118.03	124.96
2	A	801	V1Y	N16-C17-N18	-3.90	122.58	128.68
2	A	801	V1Y	C29-C30-C31	3.63	121.29	119.29
2	A	801	V1Y	C22-N23-C24	3.32	123.47	116.79
2	A	801	V1Y	C2-C7-N8	3.21	125.31	119.33
2	A	801	V1Y	C6-C7-N8	-2.83	115.38	119.13
2	A	801	V1Y	C11-C9-N8	2.61	118.68	114.79
2	A	801	V1Y	C7-C6-C5	2.56	120.71	117.66
2	A	801	V1Y	C26-C31-C30	-2.51	119.08	121.20
2	A	801	V1Y	C21-C22-N23	-2.49	121.36	123.81
2	A	801	V1Y	C26-N25-C24	-2.41	122.64	129.29
2	A	801	V1Y	C31-C30-CL33	-2.26	118.63	119.50
2	A	801	V1Y	C31-C26-N25	2.24	121.53	117.00

There are no chirality outliers.

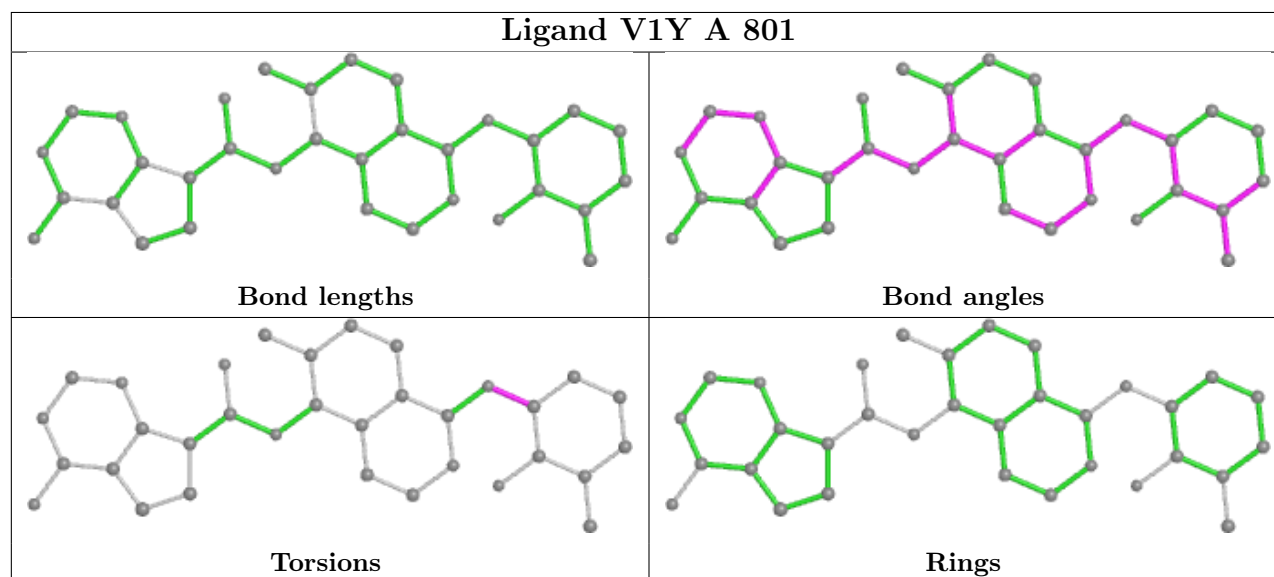
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	V1Y	C31-C26-N25-C24

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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

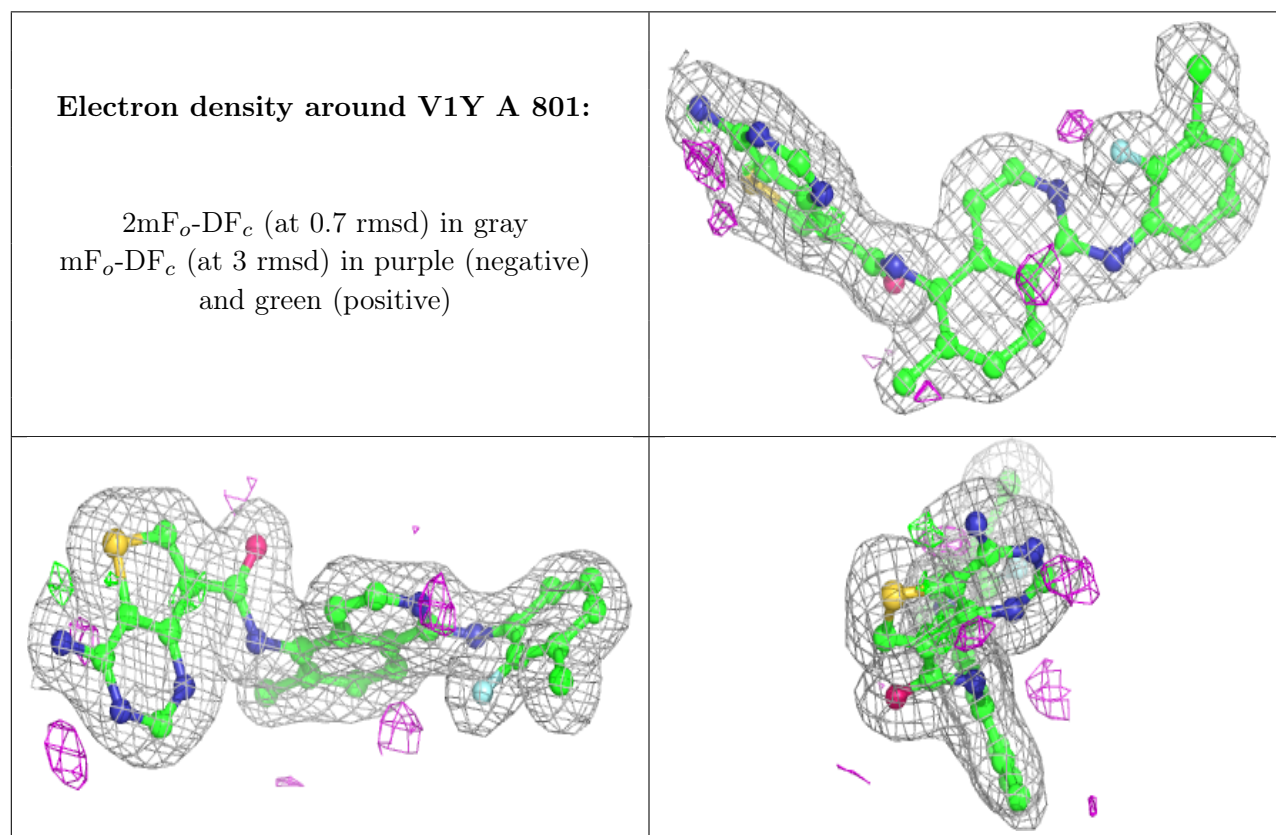
6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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.



6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.