



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:03 PM UTC

PDB ID : 8AV9 / pdb_00008av9
Title : INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN
FABCOMPLEX IN COMPLEX WITH COMPOUND 1
Authors : Hargreaves, D.
Deposited on : 2022-08-26
Resolution : 1.99 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

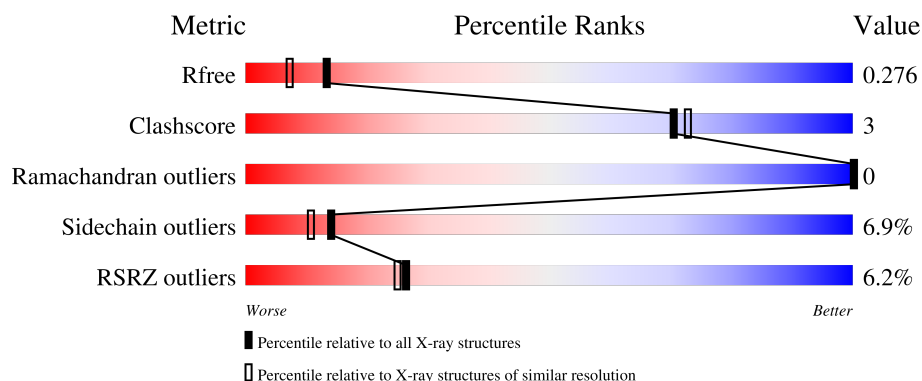
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 $\leq 5\%$. 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	162	8% 81% 15% ..
2	H	230	8% 77% 11% • 10%
3	L	236	2% 81% 9% • 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4766 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 Induced myeloid leukemia cell differentiation protein Mcl-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	0	0
			1249	783	229	234	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	GLY	-	expression tag	UNP Q07820
A	167	PRO	-	expression tag	UNP Q07820
A	168	LEU	-	expression tag	UNP Q07820
A	169	GLY	-	expression tag	UNP Q07820
A	170	SER	-	expression tag	UNP Q07820
A	171	GLU	-	expression tag	UNP Q07820
A	172	ASP	-	expression tag	UNP Q07820
A	173	ASP	-	expression tag	UNP Q07820
A	193	SER	ALA	conflict	UNP Q07820
A	196	SER	THR	conflict	UNP Q07820
A	199	LEU	MET	conflict	UNP Q07820
A	201	GLU	ARG	conflict	UNP Q07820
A	202	ALA	SER	conflict	UNP Q07820
A	205	ALA	THR	conflict	UNP Q07820
A	206	GLY	SER	conflict	UNP Q07820
A	208	ARG	LYS	conflict	UNP Q07820

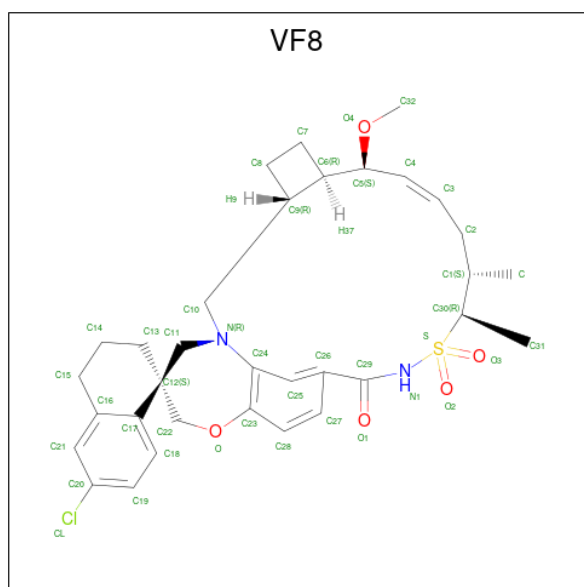
- Molecule 2 is a protein called Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	207	Total	C	N	O	S	0	0	0
			1547	983	256	301	7			

- Molecule 3 is a protein called Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	0	0
			1594	988	269	331	6			

- Molecule 4 is (3R,6R,7S,8E,11S,12R,22S)-6'-chloro-7-methoxy-11,12-dimethyl-13,13-dioxo-spiro[20-oxa-13-gamma6-thia-1,14-diazatetracyclo[14.7.2.03,6.019,24]pentacosa-8,16(25),17,19(24)-tetraene-22,1'-tetralin]-15-one (CCD ID: VF8) (formula: C₃₃H₄₁ClN₂O₅S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	O	S	0	0
			42	33	1	2	5	1		

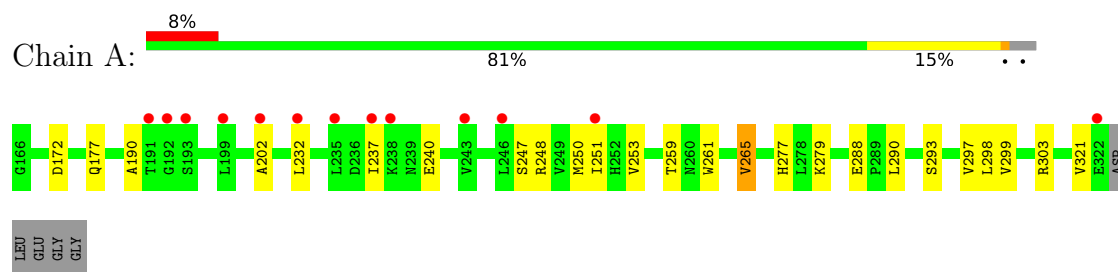
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	75	Total O 75 75	0	0
5	H	114	Total O 114 114	0	0
5	L	145	Total O 145 145	0	0

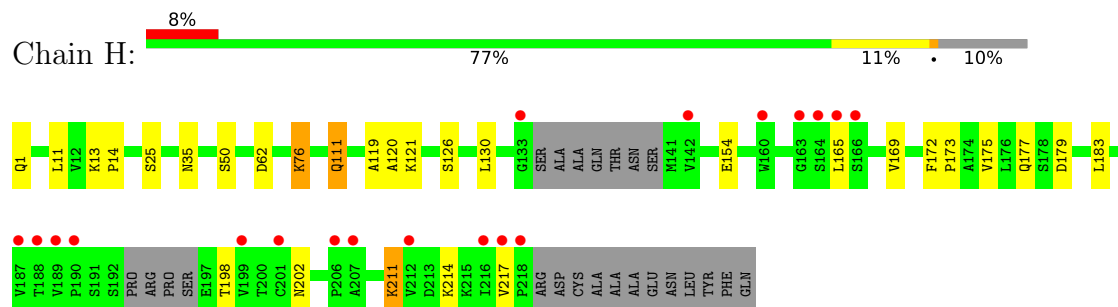
3 Residue-property plots [i](#)

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 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.

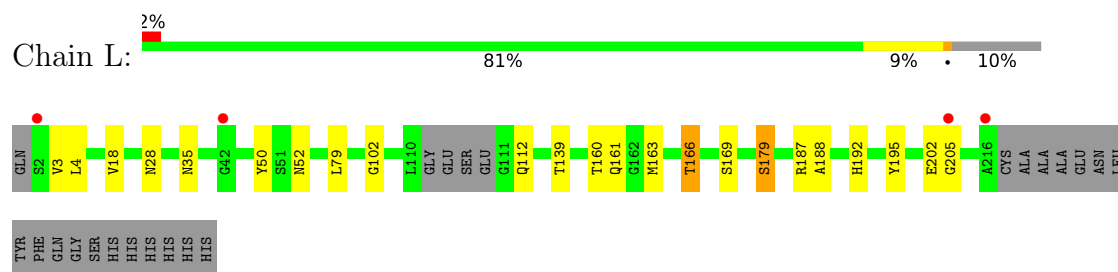
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1



- Molecule 2: Fab Heavy Chain



- Molecule 3: Fab Light Chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	149.28Å 41.95Å 106.07Å 90.00° 112.72° 90.00°	Depositor
Resolution (Å)	70.58 – 1.99 70.58 – 1.99	Depositor EDS
% Data completeness (in resolution range)	98.3 (70.58-1.99) 98.3 (70.58-1.99)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 1.98Å)	Xtriage
Refinement program	BUSTER 2.11.8 (24-FEB-2021)	Depositor
R, R_{free}	0.223 , 0.272 0.223 , 0.276	Depositor DCC
R_{free} test set	2087 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	26.9	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4766	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 6.65% 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: VF8

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	0.71	0/1270	1.15	1/1709 (0.1%)
2	H	0.78	0/1584	0.97	1/2160 (0.0%)
3	L	0.78	1/1631 (0.1%)	0.99	1/2226 (0.0%)
All	All	0.76	1/4485 (0.0%)	1.03	3/6095 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	28	ASN	CA-C	7.45	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	ASP	CA-CB-CG	5.85	118.45	112.60
2	H	177	GLN	N-CA-C	-5.53	98.34	108.02
3	L	52	ASN	CA-CB-CG	5.45	118.05	112.60

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	1249	0	1248	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	1547	0	1529	10	0
3	L	1594	0	1524	9	0
4	A	42	0	0	1	0
5	A	75	0	0	0	0
5	H	114	0	0	0	0
5	L	145	0	0	0	1
All	All	4766	0	4301	29	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 3.

All (29) 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)
3:L:202:GLU:C	3:L:205:GLY:HA3	2.15	0.71
2:H:14:PRO:HD2	2:H:119:ALA:HB2	1.77	0.66
3:L:166:THR:HG22	3:L:179:SER:H	1.63	0.64
2:H:13:LYS:HE3	2:H:119:ALA:HA	1.85	0.58
1:A:232:LEU:HD12	1:A:237:ILE:HD13	1.85	0.58
2:H:202:ASN:HB3	2:H:211:LYS:NZ	2.20	0.56
1:A:250:MET:HE3	1:A:297:VAL:HG21	1.89	0.54
2:H:111:GLN:NE2	2:H:111:GLN:H	2.07	0.53
2:H:120:ALA:HB2	2:H:179:ASP:HB3	1.91	0.52
3:L:192:HIS:HB2	3:L:195:TYR:OH	2.10	0.51
1:A:250:MET:HE1	1:A:293:SER:HB3	1.91	0.51
1:A:290:LEU:HD11	4:A:401:VF8:CL	2.48	0.50
2:H:13:LYS:HG2	2:H:119:ALA:HA	1.95	0.49
2:H:173:PRO:HG3	3:L:169:SER:HB2	1.94	0.49
1:A:237:ILE:CG2	1:A:277:HIS:CD2	2.98	0.47
1:A:299:VAL:O	1:A:303:ARG:HB2	2.15	0.46
1:A:247:SER:HA	1:A:250:MET:HE2	1.98	0.45
1:A:190:ALA:O	1:A:279:LYS:HD2	2.18	0.44
3:L:4:LEU:HB2	3:L:102:GLY:HA2	2.00	0.43
1:A:251:ILE:HG12	1:A:297:VAL:HG22	1.99	0.43
2:H:35:ASN:OD1	2:H:50:SER:HB3	2.20	0.42
3:L:18:VAL:HG21	3:L:79:LEU:HD11	2.01	0.42
3:L:35:ASN:HD22	3:L:50:TYR:HA	1.83	0.42
1:A:261:TRP:O	1:A:265:VAL:HG13	2.18	0.42
2:H:76:LYS:HE2	2:H:76:LYS:HB3	1.81	0.41
2:H:172:PHE:CZ	3:L:139:THR:HB	2.54	0.41
1:A:237:ILE:HG21	1:A:277:HIS:HD2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:GLN:HE21	1:A:202:ALA:HB2	1.86	0.41
3:L:188:ALA:O	3:L:192:HIS:HD2	2.04	0.41

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)
5:L:367:HOH:O	5:L:367:HOH:O[2_555]	2.16	0.04

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	155/162 (96%)	151 (97%)	4 (3%)	0	100	100
2	H	201/230 (87%)	196 (98%)	5 (2%)	0	100	100
3	L	209/236 (89%)	203 (97%)	6 (3%)	0	100	100
All	All	565/628 (90%)	550 (97%)	15 (3%)	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	134/137 (98%)	126 (94%)	8 (6%)	17	14
2	H	174/192 (91%)	156 (90%)	18 (10%)	7	4
3	L	182/200 (91%)	174 (96%)	8 (4%)	25	24
All	All	490/529 (93%)	456 (93%)	34 (7%)	14	11

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	240	GLU
1	A	248	ARG
1	A	253	VAL
1	A	259	THR
1	A	265	VAL
1	A	288	GLU
1	A	298	LEU
1	A	321	VAL
2	H	1	GLN
2	H	11	LEU
2	H	25	SER
2	H	62	ASP
2	H	76	LYS
2	H	111	GLN
2	H	121	LYS
2	H	126	SER
2	H	130	LEU
2	H	154	GLU
2	H	165	LEU
2	H	169	VAL
2	H	175	VAL
2	H	183	LEU
2	H	198	THR
2	H	211	LYS
2	H	214	LYS
2	H	217	VAL
3	L	3	VAL
3	L	112	GLN
3	L	160	THR
3	L	161	GLN
3	L	163	MET
3	L	166	THR
3	L	179	SER
3	L	187	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	177	GLN
1	A	189	GLN
1	A	221	GLN
1	A	224	HIS
1	A	239	ASN
2	H	1	GLN
2	H	82	GLN
2	H	111	GLN
3	L	54	GLN
3	L	161	GLN
3	L	192	HIS
3	L	201	HIS
3	L	206	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](#)

1 ligand 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
4	VF8	A	401	-	40,47,47	0.50	1 (2%)	50,71,71	0.75	1 (2%)

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
4	VF8	A	401	-	-	6/29/72/72	0/4/6/6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	VF8	C11-N	2.41	1.48	1.45

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	401	VF8	C1-C2-C3	-3.45	108.71	114.11

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	401	VF8	C6-C5-O4-C32
4	A	401	VF8	C25-C26-C29-N1
4	A	401	VF8	C27-C26-C29-N1
4	A	401	VF8	C4-C5-O4-C32
4	A	401	VF8	C25-C26-C29-O1
4	A	401	VF8	C27-C26-C29-O1

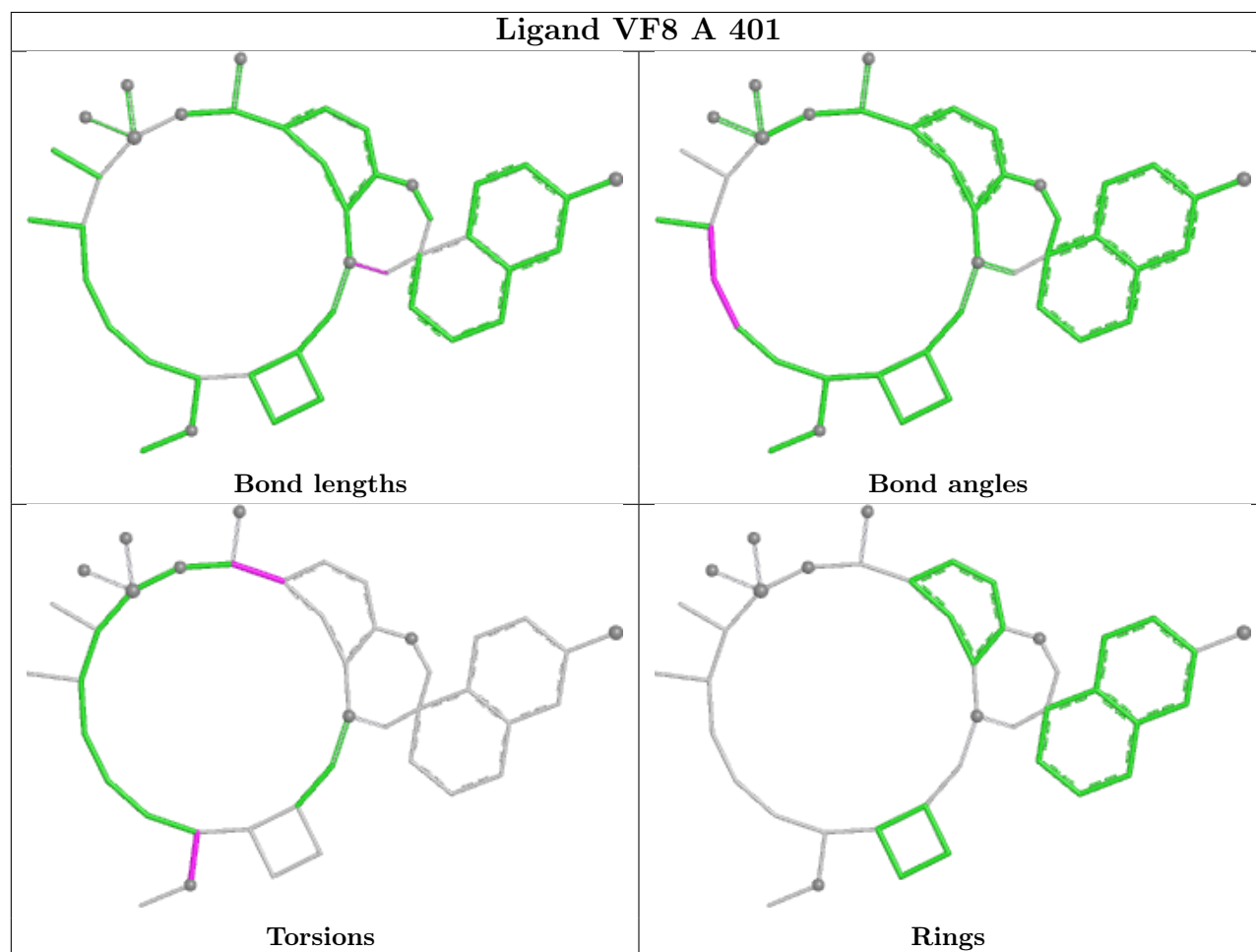
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	VF8	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L	202:GLU	C	205:GLY	N	3.75

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	157/162 (96%)	0.71	13 (8%) 17 16	19, 40, 83, 92	0
2	H	207/230 (90%)	0.43	19 (9%) 14 13	16, 32, 65, 82	0
3	L	213/236 (90%)	0.13	4 (1%) 66 66	14, 31, 46, 55	0
All	All	577/628 (91%)	0.40	36 (6%) 26 25	14, 33, 65, 92	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	205	GLY	6.6
3	L	216	ALA	4.7
1	A	235	LEU	4.4
2	H	165	LEU	3.6
1	A	243	VAL	3.6
1	A	237	ILE	3.4
2	H	216	ILE	3.2
2	H	188	THR	3.1
1	A	246	LEU	2.9
2	H	189	VAL	2.8
2	H	217	VAL	2.8
2	H	201	CYS	2.8
2	H	212	VAL	2.8
2	H	207	ALA	2.6
3	L	2	SER	2.6
2	H	164	SER	2.6
2	H	206	PRO	2.6
2	H	199	VAL	2.6
2	H	163	GLY	2.4
2	H	187	VAL	2.4
2	H	166	SER	2.4
3	L	42	GLY	2.3
1	A	202	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
2	H	190	PRO	2.3
2	H	133	GLY	2.2
1	A	199	LEU	2.2
1	A	192	GLY	2.2
1	A	232	LEU	2.2
2	H	218	PRO	2.1
1	A	193	SER	2.1
2	H	160	TRP	2.1
1	A	191	THR	2.1
1	A	238	LYS	2.0
1	A	322	GLU	2.0
1	A	251	ILE	2.0
2	H	142	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

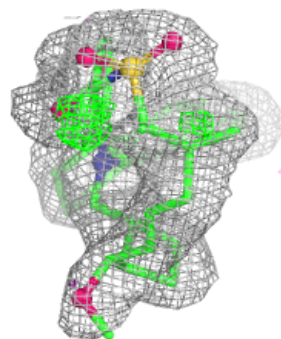
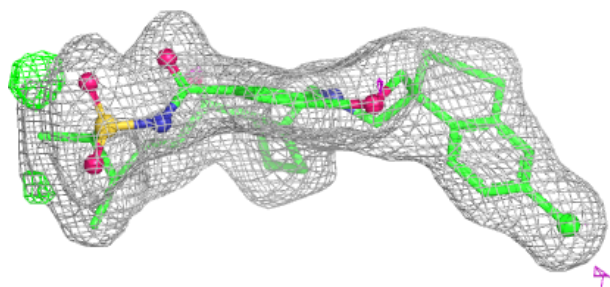
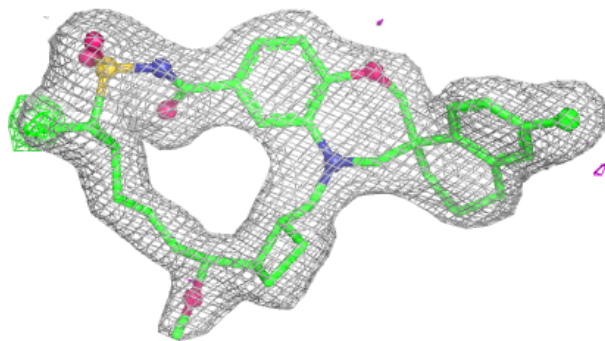
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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
4	VF8	A	401	42/42	0.90	0.11	42,43,45,46	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 VF8 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.