



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:29 AM UTC

PDB ID : 3F7I / pdb_00003f7i
Title : Structure of an ML-IAP/XIAP chimera bound to a peptidomimetic
Authors : Franklin, M.C.; Fairbrother, W.J.; Cohen, F.
Deposited on : 2008-11-09
Resolution : 1.90 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

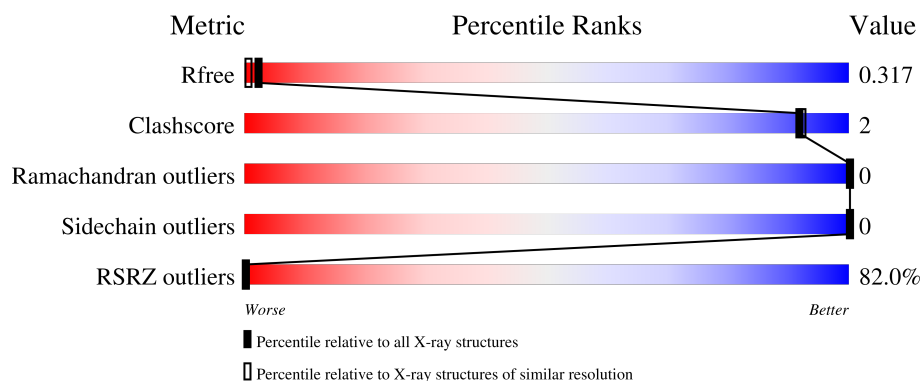
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	133	63% 68%32%
1	B	133	50% 66%.30%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 1772 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 Baculoviral IAP repeat-containing protein 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	90	Total	C	N	O	S	0	0	0
			727	473	124	126	4			
1	B	93	Total	C	N	O	S	0	0	0
			752	489	129	130	4			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	MET	-	expression tag	UNP Q6R308
A	41	GLY	-	expression tag	UNP Q6R308
A	42	SER	-	expression tag	UNP Q6R308
A	43	SER	-	expression tag	UNP Q6R308
A	44	HIS	-	expression tag	UNP Q6R308
A	45	HIS	-	expression tag	UNP Q6R308
A	46	HIS	-	expression tag	UNP Q6R308
A	47	HIS	-	expression tag	UNP Q6R308
A	48	HIS	-	expression tag	UNP Q6R308
A	49	HIS	-	expression tag	UNP Q6R308
A	50	SER	-	expression tag	UNP Q6R308
A	51	SER	-	expression tag	UNP Q6R308
A	52	GLY	-	expression tag	UNP Q6R308
A	53	GLU	-	expression tag	UNP Q6R308
A	54	VAL	-	expression tag	UNP Q6R308
A	55	PRO	-	expression tag	UNP Q6R308
A	56	ARG	-	expression tag	UNP Q6R308
A	57	GLY	-	expression tag	UNP Q6R308
A	58	SER	-	expression tag	UNP Q6R308
A	59	HIS	-	expression tag	UNP Q6R308
A	60	MET	-	expression tag	UNP Q6R308
A	61	LEU	-	expression tag	UNP Q6R308
A	62	GLU	-	expression tag	UNP Q6R308
A	150	GLY	SER	engineered mutation	UNP Q6R308
A	160	GLN	ARG	engineered mutation	UNP Q6R308

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Chain	Residue	Modelled	Actual	Comment	Reference
A	161	GLU	ASP	engineered mutation	UNP Q6R308
A	162	TYR	PHE	engineered mutation	UNP Q6R308
A	163	ILE	VAL	engineered mutation	UNP Q6R308
A	164	ASN	HIS	engineered mutation	UNP Q6R308
A	165	ASN	SER	engineered mutation	UNP Q6R308
A	166	ILE	VAL	engineered mutation	UNP Q6R308
A	167	HIS	GLN	engineered mutation	UNP Q6R308
A	168	LEU	GLU	engineered mutation	UNP Q6R308
A	172	LEU	GLN	engineered mutation	UNP Q6R308
B	40	MET	-	expression tag	UNP Q6R308
B	41	GLY	-	expression tag	UNP Q6R308
B	42	SER	-	expression tag	UNP Q6R308
B	43	SER	-	expression tag	UNP Q6R308
B	44	HIS	-	expression tag	UNP Q6R308
B	45	HIS	-	expression tag	UNP Q6R308
B	46	HIS	-	expression tag	UNP Q6R308
B	47	HIS	-	expression tag	UNP Q6R308
B	48	HIS	-	expression tag	UNP Q6R308
B	49	HIS	-	expression tag	UNP Q6R308
B	50	SER	-	expression tag	UNP Q6R308
B	51	SER	-	expression tag	UNP Q6R308
B	52	GLY	-	expression tag	UNP Q6R308
B	53	GLU	-	expression tag	UNP Q6R308
B	54	VAL	-	expression tag	UNP Q6R308
B	55	PRO	-	expression tag	UNP Q6R308
B	56	ARG	-	expression tag	UNP Q6R308
B	57	GLY	-	expression tag	UNP Q6R308
B	58	SER	-	expression tag	UNP Q6R308
B	59	HIS	-	expression tag	UNP Q6R308
B	60	MET	-	expression tag	UNP Q6R308
B	61	LEU	-	expression tag	UNP Q6R308
B	62	GLU	-	expression tag	UNP Q6R308
B	150	GLY	SER	engineered mutation	UNP Q6R308
B	160	GLN	ARG	engineered mutation	UNP Q6R308
B	161	GLU	ASP	engineered mutation	UNP Q6R308
B	162	TYR	PHE	engineered mutation	UNP Q6R308
B	163	ILE	VAL	engineered mutation	UNP Q6R308
B	164	ASN	HIS	engineered mutation	UNP Q6R308
B	165	ASN	SER	engineered mutation	UNP Q6R308
B	166	ILE	VAL	engineered mutation	UNP Q6R308
B	167	HIS	GLN	engineered mutation	UNP Q6R308
B	168	LEU	GLU	engineered mutation	UNP Q6R308

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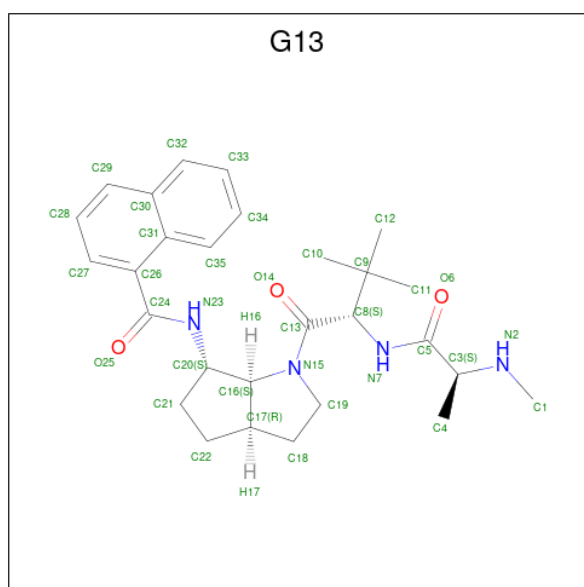
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Chain	Residue	Modelled	Actual	Comment	Reference
B	172	LEU	GLN	engineered mutation	UNP Q6R308

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is N-[(3aR,6S,6aS)-1-(N-methyl-L-alanyl-3-methyl-L-valyl)octahydrocyclopenta[b]pyrrol-6-yl]naphthalene-1-carboxamide (CCD ID: G13) (formula: C₂₈H₃₈N₄O₃).



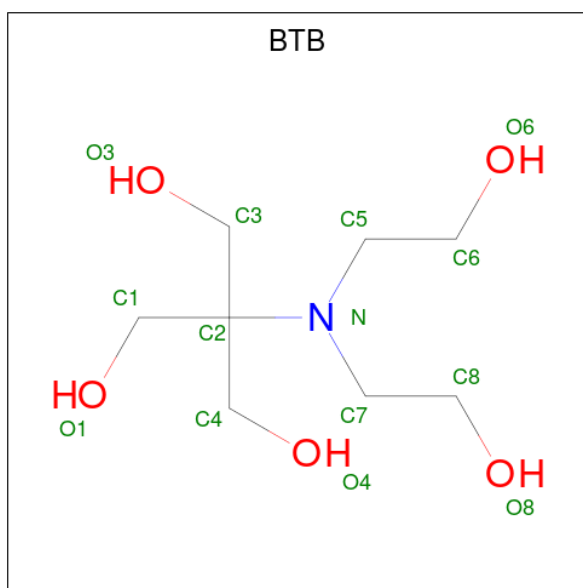
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 35 28 4 3	0	0
3	B	1	Total C N O 35 28 4 3	0	0

- Molecule 4 is LITHIUM ION (CCD ID: LI) (formula: Li).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Li 1 1	0	0

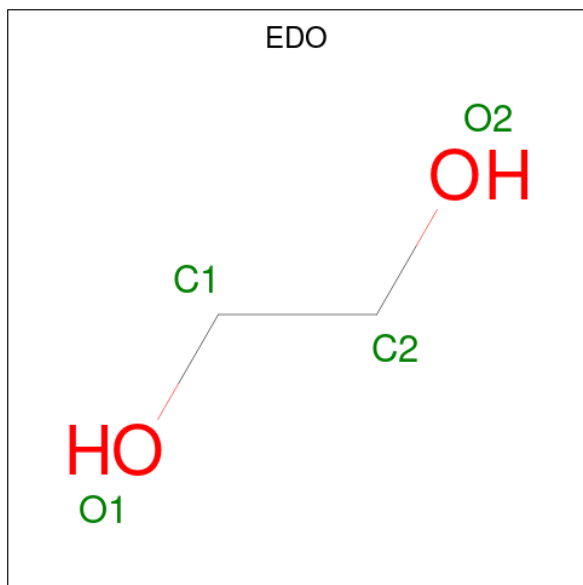
- Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN

E-1,3-DIOL (CCD ID: BTB) (formula: $C_8H_{19}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	94	Total 94	O 94	0	0
7	B	104	Total 104	O 104	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	87.16Å 87.16Å 73.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.80 – 1.90 19.80 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.80-1.90) 99.8 (19.80-1.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.53 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.155 , 0.181 0.297 , 0.317	Depositor DCC
R_{free} test set	1359 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	14.9	Xtriage
Anisotropy	0.577	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 31.4	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	0.85	EDS
Total number of atoms	1772	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% 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: EDO, G13, ZN, BTB, LI

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	0.43	0/756	0.65	0/1026
1	B	0.44	0/782	0.64	0/1062
All	All	0.44	0/1538	0.65	0/2088

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 [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	727	0	670	0	0
1	B	752	0	695	5	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	35	0	38	0	0
3	B	35	0	38	0	0
4	B	1	0	0	0	0
5	B	14	0	19	0	0
6	B	8	0	11	0	0
7	A	94	0	0	0	0
7	B	104	0	0	1	1
All	All	1772	0	1471	5	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 (5) 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:B:88:GLU:HG2	7:B:293:HOH:O	1.87	0.74
1:B:146:LYS:HE2	1:B:170:HIS:HE2	1.82	0.45
1:B:146:LYS:HE2	1:B:170:HIS:NE2	2.33	0.44
1:B:146:LYS:HE2	1:B:170:HIS:CD2	2.53	0.43
1:B:145:ALA:HA	1:B:154:LEU:HD21	2.03	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)
7:B:197:HOH:O	7:B:278:HOH:O[7_556]	2.12	0.08

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	88/133 (66%)	87 (99%)	1 (1%)	0	100	100
1	B	91/133 (68%)	89 (98%)	2 (2%)	0	100	100
All	All	179/266 (67%)	176 (98%)	3 (2%)	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	73/109 (67%)	73 (100%)	0	100	100
1	B	76/109 (70%)	76 (100%)	0	100	100
All	All	149/218 (68%)	149 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	132	GLN
1	B	160	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 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	G13	B	1	-	38,38,38	0.87	0	50,56,56	1.07	4 (8%)
3	G13	A	1	-	38,38,38	0.82	0	50,56,56	1.20	6 (12%)
6	EDO	B	175	-	3,3,3	0.39	0	2,2,2	0.42	0
5	BTB	B	173	-	13,13,13	0.29	0	7,16,16	0.38	0
6	EDO	B	174	4	3,3,3	0.50	0	2,2,2	0.29	0

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	G13	B	1	-	-	0/32/54/54	0/4/4/4
3	G13	A	1	-	-	1/32/54/54	0/4/4/4
6	EDO	B	175	-	-	1/1/1/1	-
5	BTB	B	173	-	-	4/21/21/21	-
6	EDO	B	174	4	-	1/1/1/1	-

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	G13	C22-C17-C16	2.94	107.58	103.71
3	A	1	G13	C21-C22-C17	2.65	107.85	103.50
3	B	1	G13	C16-C20-N23	-2.49	109.28	113.24
3	B	1	G13	C18-C17-C16	2.46	106.95	103.71
3	A	1	G13	C22-C21-C20	2.38	107.76	103.91
3	B	1	G13	C18-C19-N15	2.26	105.70	103.22
3	A	1	G13	C16-C20-N23	-2.18	109.78	113.24
3	A	1	G13	C18-C17-C16	2.14	106.53	103.71
3	A	1	G13	C21-C20-C16	2.01	107.26	103.95
3	B	1	G13	C22-C17-C16	2.00	106.35	103.71

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	173	BTB	O1-C1-C2-C4
6	B	175	EDO	O1-C1-C2-O2
6	B	174	EDO	O1-C1-C2-O2

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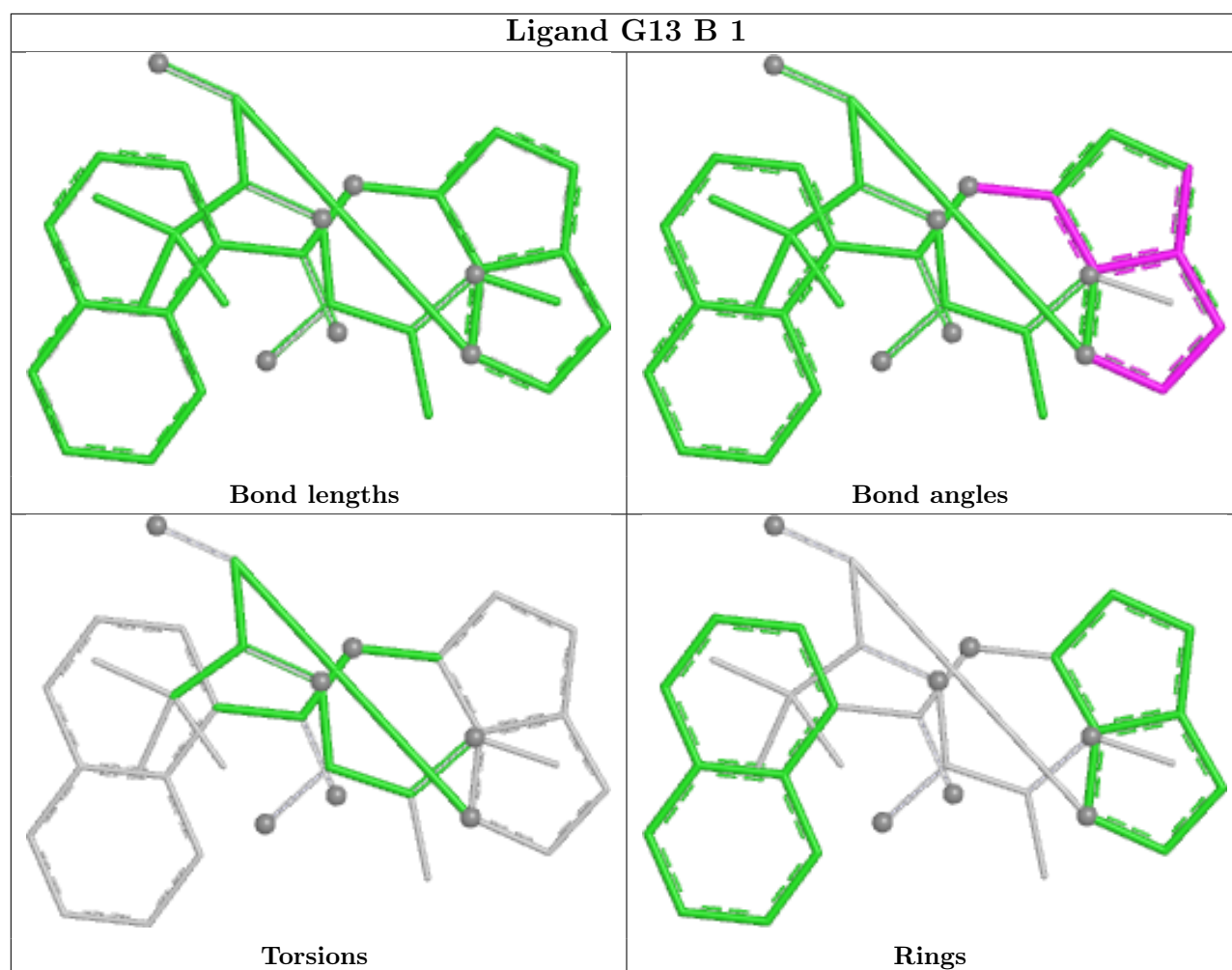
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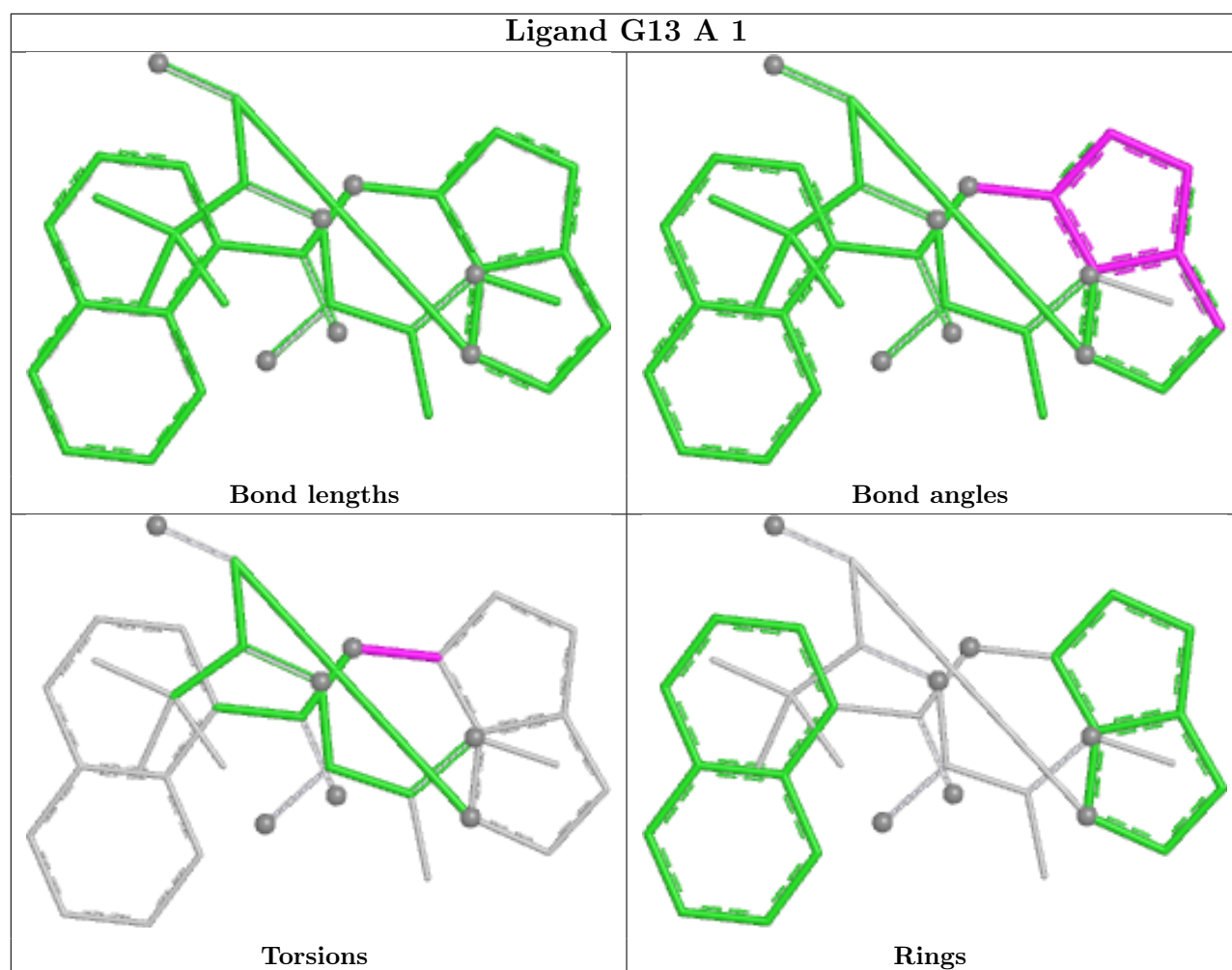
Mol	Chain	Res	Type	Atoms
5	B	173	BTB	C3-C2-N-C7
5	B	173	BTB	C4-C2-N-C7
3	A	1	G13	C16-C20-N23-C24
5	B	173	BTB	O1-C1-C2-N

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 ⓘ

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	90/133 (67%)	3.15	84 (93%) 0 0	20, 26, 33, 43	0
1	B	93/133 (69%)	2.63	66 (70%) 0 0	20, 25, 33, 52	0
All	All	183/266 (68%)	2.89	150 (81%) 0 0	20, 26, 33, 52	0

All (150) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	170	HIS	7.1
1	A	166	ILE	6.4
1	B	130	GLY	6.1
1	B	169	THR	5.9
1	A	147	TRP	5.3
1	A	134	TRP	5.1
1	A	167	HIS	5.0
1	A	130	GLY	4.9
1	A	163	ILE	4.9
1	A	148	PHE	4.7
1	B	148	PHE	4.7
1	A	131	LEU	4.6
1	A	81	PHE	4.6
1	B	136	ARG	4.4
1	A	119	GLN	4.4
1	A	109	ALA	4.3
1	A	114	PHE	4.2
1	A	125	PHE	4.2
1	A	104	PRO	4.2
1	A	100	THR	4.1
1	A	132	GLN	4.1
1	A	107	LEU	4.1
1	A	165	ASN	4.1
1	A	78	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	153	PHE	4.0
1	B	78	GLY	4.0
1	A	89	LEU	4.0
1	B	155	LEU	4.0
1	A	139	ASP	3.9
1	B	135	LYS	3.9
1	B	125	PHE	3.9
1	B	126	PHE	3.9
1	A	95	TYR	3.8
1	A	135	LYS	3.8
1	B	134	TRP	3.8
1	A	103	VAL	3.8
1	A	80	ALA	3.7
1	A	156	ARG	3.7
1	B	145	ALA	3.7
1	B	129	GLY	3.7
1	A	122	VAL	3.6
1	B	124	CYS	3.6
1	A	94	PHE	3.6
1	B	161	GLU	3.5
1	B	166	ILE	3.5
1	A	92	ALA	3.5
1	A	128	TYR	3.5
1	A	124	CYS	3.5
1	B	127	CYS	3.5
1	B	80	ALA	3.4
1	A	129	GLY	3.4
1	A	113	PHE	3.4
1	A	146	LYS	3.4
1	B	88	GLU	3.4
1	A	97	TRP	3.3
1	A	161	GLU	3.3
1	A	142	THR	3.3
1	A	98	PRO	3.3
1	A	93	SER	3.3
1	B	128	TYR	3.2
1	B	101	ALA	3.2
1	B	107	LEU	3.2
1	B	151	CYS	3.2
1	B	147	TRP	3.2
1	B	162	TYR	3.2
1	A	164	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	91	LEU	3.2
1	A	136	ARG	3.2
1	B	109	ALA	3.1
1	A	112	GLY	3.1
1	B	154	LEU	3.1
1	A	133	SER	3.1
1	B	141	TRP	3.1
1	A	116	THR	3.0
1	A	160	GLN	3.0
1	B	168	LEU	3.0
1	A	144	HIS	3.0
1	A	79	PRO	3.0
1	B	106	GLU	3.0
1	A	153	PHE	2.9
1	A	99	LEU	2.9
1	B	152	GLN	2.9
1	A	149	PRO	2.9
1	B	81	PHE	2.9
1	B	123	ARG	2.9
1	A	96	ASP	2.9
1	A	126	PHE	2.8
1	A	85	GLY	2.8
1	A	91	LEU	2.8
1	B	122	VAL	2.8
1	B	97	TRP	2.7
1	A	117	GLY	2.7
1	B	83	GLY	2.7
1	A	82	PRO	2.7
1	A	138	ASP	2.7
1	B	163	ILE	2.7
1	A	162	TYR	2.6
1	B	146	LYS	2.6
1	B	102	GLU	2.6
1	B	158	LYS	2.6
1	A	155	LEU	2.6
1	A	83	GLY	2.6
1	B	142	THR	2.6
1	A	88	GLU	2.6
1	A	150	GLY	2.6
1	A	101	ALA	2.6
1	B	79	PRO	2.5
1	A	154	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	139	ASP	2.5
1	B	150	GLY	2.5
1	B	157	SER	2.5
1	A	145	ALA	2.4
1	A	120	ASP	2.4
1	B	140	PRO	2.4
1	A	123	ARG	2.4
1	A	115	HIS	2.4
1	B	132	GLN	2.4
1	A	84	MET	2.4
1	B	110	ALA	2.4
1	B	108	LEU	2.3
1	A	121	LYS	2.3
1	B	113	PHE	2.3
1	B	114	PHE	2.3
1	A	111	ALA	2.3
1	A	152	GLN	2.3
1	A	141	TRP	2.3
1	A	118	HIS	2.3
1	B	156	ARG	2.2
1	B	82	PRO	2.2
1	B	133	SER	2.2
1	B	118	HIS	2.2
1	B	144	HIS	2.2
1	A	87	GLU	2.2
1	A	159	GLY	2.2
1	B	159	GLY	2.2
1	A	108	LEU	2.2
1	A	137	GLY	2.2
1	B	92	ALA	2.2
1	B	165	ASN	2.2
1	B	112	GLY	2.2
1	B	131	LEU	2.2
1	A	127	CYS	2.1
1	A	90	ARG	2.1
1	B	149	PRO	2.1
1	A	143	GLU	2.1
1	A	110	ALA	2.1
1	A	86	SER	2.1
1	B	117	GLY	2.1
1	A	140	PRO	2.1
1	B	121	LYS	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](#)

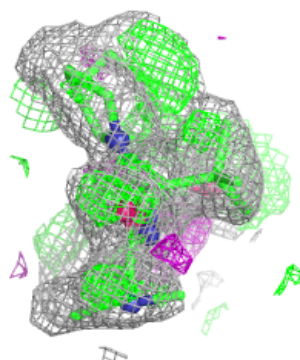
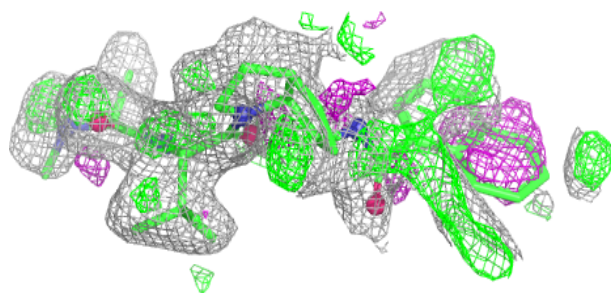
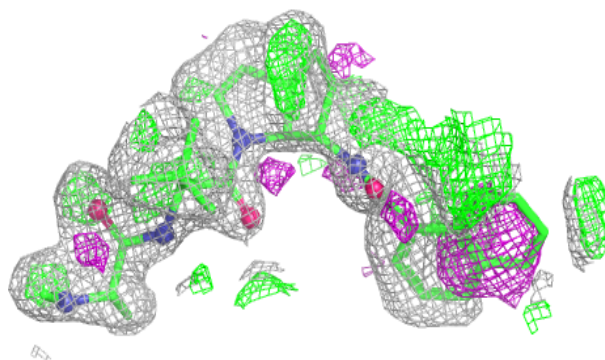
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	G13	A	1	35/35	0.52	0.30	24,25,26,27	0
5	BTB	B	173	14/14	0.56	0.22	39,40,44,46	0
3	G13	B	1	35/35	0.57	0.24	22,26,26,27	0
4	LI	B	1002	1/1	0.66	0.24	24,24,24,24	0
6	EDO	B	174	4/4	0.76	0.22	22,23,23,24	0
6	EDO	B	175	4/4	0.78	0.21	27,30,33,35	0
2	ZN	A	1001	1/1	0.83	0.13	26,26,26,26	0
2	ZN	B	1001	1/1	0.89	0.10	26,26,26,26	0

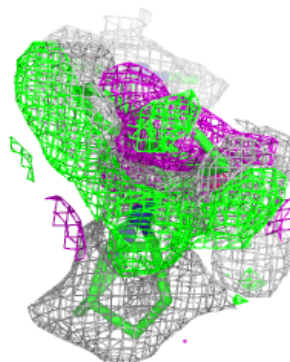
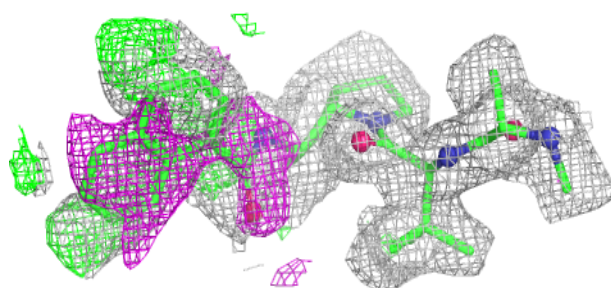
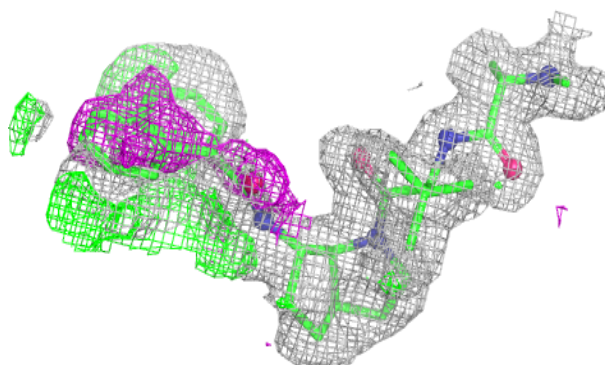
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around G13 A 1:

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

**Electron density around G13 B 1:**

$2mF_o-DF_c$ (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.