



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:06 AM UTC

PDB ID : 9F9K / pdb_00009f9k
Title : Crystal structure of MUS81-EME1 bound by compound 15.
Authors : Collie, G.W.
Deposited on : 2024-05-07
Resolution : 2.73 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

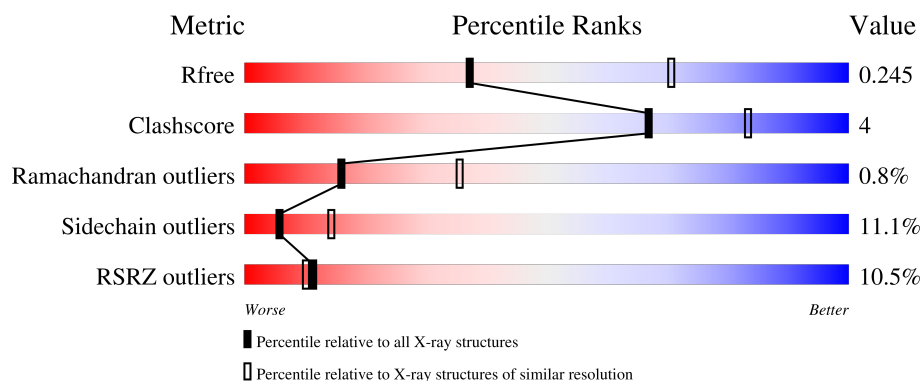
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

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	308	4% 50% 7% • 42%
1	C	308	5% 48% 9% • 42%
2	B	326	6% 36% 6% • 58%
2	D	326	6% 32% 9% • 57%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4919 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 Crossover junction endonuclease MUS81.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	180	Total	C	N	O	S	0	0	0
			1412	895	252	261	4			
1	C	179	Total	C	N	O	S	0	0	0
			1408	894	254	256	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	244	GLY	-	expression tag	UNP Q96NY9
A	245	SER	-	expression tag	UNP Q96NY9
C	244	GLY	-	expression tag	UNP Q96NY9
C	245	SER	-	expression tag	UNP Q96NY9

- Molecule 2 is a protein called Crossover junction endonuclease EME1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	138	Total	C	N	O	S	0	0	0
			1036	659	173	196	8			
2	D	139	Total	C	N	O	S	0	0	0
			1015	648	165	194	8			

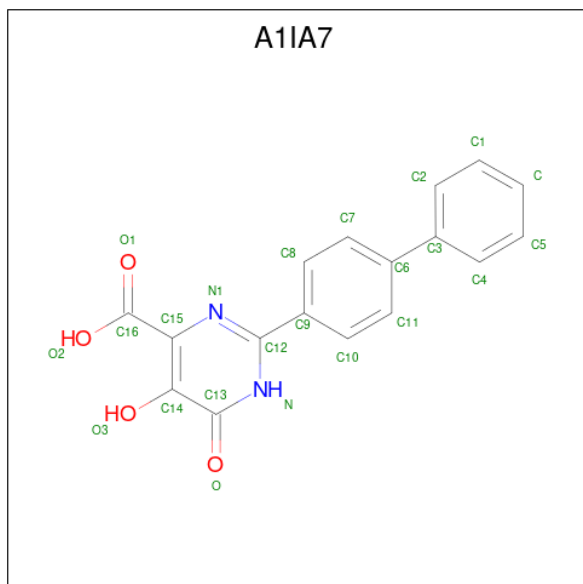
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	245	GLY	-	expression tag	UNP Q96AY2
D	245	GLY	-	expression tag	UNP Q96AY2

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

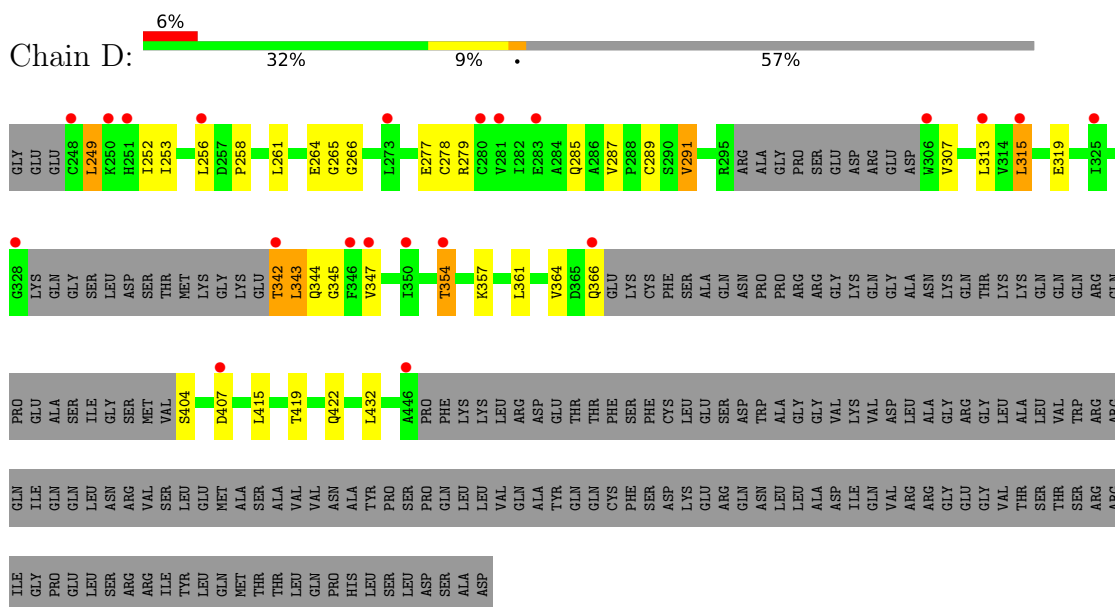
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		

- Molecule 4 is 5-oxidanyl-6-oxidanylidene-2-(4-phenylphenyl)-1H-pyrimidine-4-carboxylic acid (CCD ID: A1IA7) (formula: $C_{17}H_{12}N_2O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			23	17	2	4		
4	A	1	Total	C	N	O	0	0
			23	17	2	4		

- Molecule 2: Crossover junction endonuclease EME1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.26Å 79.07Å 84.84Å 90.00° 91.37° 90.00°	Depositor
Resolution (Å)	71.24 – 2.73 71.24 – 2.73	Depositor EDS
% Data completeness (in resolution range)	72.6 (71.24-2.73) 72.6 (71.24-2.73)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 2.73Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.233 , 0.254 0.233 , 0.245	Depositor DCC
R_{free} test set	935 reflections (3.70%)	wwPDB-VP
Wilson B-factor (Å ²)	69.4	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4919	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.42% 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: A1IA7, MG

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	0.63	0/1436	1.09	5/1946 (0.3%)
1	C	0.65	0/1433	1.09	0/1942
2	B	0.70	1/1047 (0.1%)	0.99	0/1424
2	D	0.66	0/1025	1.05	0/1398
All	All	0.66	1/4941 (0.0%)	1.06	5/6710 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	355	ALA	CA-C	9.54	1.61	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	369	GLU	CA-C-N	5.69	131.95	121.70
1	A	369	GLU	C-N-CA	5.69	131.95	121.70
1	A	328	LEU	N-CA-C	5.48	122.48	110.80
1	A	348	ARG	CA-C-N	5.38	127.75	120.38
1	A	348	ARG	C-N-CA	5.38	127.75	120.38

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	1412	0	1400	8	0
1	C	1408	0	1408	11	0
2	B	1036	0	1040	6	0
2	D	1015	0	1003	11	0
3	A	2	0	0	0	0
4	A	46	0	0	0	0
All	All	4919	0	4851	36	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 4.

All (36) 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:402:THR:HG21	1:A:408:SER:HB3	1.56	0.85
2:B:366:GLN:HE21	2:B:366:GLN:H	1.20	0.85
1:A:405:ILE:H	1:A:405:ILE:HD12	1.55	0.71
2:B:347:VAL:HG21	2:B:415:LEU:HD11	1.77	0.66
2:D:249:LEU:HD12	2:D:278:CYS:HB3	1.78	0.65
2:D:261:LEU:HA	2:D:266:GLY:HA3	1.82	0.61
1:C:262:LEU:HD13	1:C:267:TYR:HB3	1.82	0.61
2:D:342:THR:HG22	2:D:345:GLY:H	1.69	0.57
2:D:347:VAL:HG21	2:D:415:LEU:HD11	1.86	0.55
2:B:291:VAL:HG13	2:B:313:LEU:HB3	1.88	0.55
1:A:317:PRO:HG2	1:A:320:PRO:HA	1.89	0.54
1:C:308:PHE:HB2	1:C:332:VAL:HB	1.92	0.51
1:C:369:GLU:HG2	1:C:402:THR:HG22	1.92	0.50
2:D:291:VAL:HG13	2:D:313:LEU:HB3	1.94	0.49
2:B:260:LEU:HB2	2:B:289:CYS:HA	1.95	0.47
2:D:354:THR:HG23	2:D:357:LYS:H	1.79	0.47
1:C:345:ILE:HD11	1:C:379:LEU:HD13	1.97	0.47
1:C:317:PRO:HG3	1:C:323:PRO:HB3	1.96	0.47
1:C:416:THR:O	1:C:420:GLN:HG3	2.15	0.47
2:D:343:LEU:HD22	2:D:415:LEU:HD13	1.97	0.46
2:B:261:LEU:HD11	2:B:282:ILE:HD12	1.97	0.46
1:A:367:LEU:HD21	1:A:408:SER:HB2	1.97	0.46
1:C:379:LEU:HG	1:C:380:PRO:HD2	1.97	0.45
1:A:369:GLU:HG3	1:A:402:THR:HG22	2.00	0.44
1:A:329:ASP:HA	1:A:361:LEU:HG	2.00	0.44
2:D:315:LEU:HD21	2:D:364:VAL:HG23	2.00	0.43
2:D:253:ILE:HG12	2:D:279:ARG:HB3	2.01	0.42
1:C:306:GLY:HA3	1:C:331:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:258:PRO:HA	2:D:261:LEU:HD12	2.01	0.42
2:D:404:SER:HB3	2:D:407:ASP:HB2	2.02	0.42
1:A:277:GLU:O	1:A:278:THR:OG1	2.30	0.41
1:C:422:LEU:HD13	1:C:449:PRO:HB3	2.02	0.41
2:B:422:GLN:HE21	2:B:422:GLN:HB2	1.56	0.41
1:A:448:ASN:HA	1:A:449:PRO:HA	1.97	0.41
1:C:319:ASP:HA	1:C:320:PRO:HD2	1.94	0.40
1:C:366:TYR:HD1	1:C:397:PHE:HD2	1.68	0.40

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	172/308 (56%)	168 (98%)	3 (2%)	1 (1%)	21	42
1	C	171/308 (56%)	163 (95%)	7 (4%)	1 (1%)	21	42
2	B	130/326 (40%)	127 (98%)	3 (2%)	0	100	100
2	D	131/326 (40%)	126 (96%)	2 (2%)	3 (2%)	5	12
All	All	604/1268 (48%)	584 (97%)	15 (2%)	5 (1%)	16	35

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	433	TRP
1	A	432	PRO
2	D	264	GLU
2	D	277	GLU
2	D	265	GLY

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	153/260 (59%)	141 (92%)	12 (8%)	11	28
1	C	153/260 (59%)	140 (92%)	13 (8%)	10	24
2	B	110/275 (40%)	96 (87%)	14 (13%)	4	10
2	D	105/275 (38%)	86 (82%)	19 (18%)	2	4
All	All	521/1070 (49%)	463 (89%)	58 (11%)	6	14

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	268	ARG
1	A	286	GLU
1	A	288	LEU
1	A	300	VAL
1	A	363	ARG
1	A	378	SER
1	A	379	LEU
1	A	384	LEU
1	A	402	THR
1	A	405	ILE
1	A	422	LEU
1	A	429	ARG
2	B	249	LEU
2	B	264	GLU
2	B	273	LEU
2	B	285	GLN
2	B	287	VAL
2	B	291	VAL
2	B	319	GLU
2	B	323	SER
2	B	344	GLN
2	B	354	THR
2	B	366	GLN
2	B	405	ARG

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Mol	Chain	Res	Type
2	B	412	LEU
2	B	422	GLN
1	C	270	LEU
1	C	328	LEU
1	C	358	ARG
1	C	364	ARG
1	C	379	LEU
1	C	381	GLU
1	C	384	LEU
1	C	400	LYS
1	C	402	THR
1	C	408	SER
1	C	415	LEU
1	C	422	LEU
1	C	428	LEU
2	D	249	LEU
2	D	252	ILE
2	D	256	LEU
2	D	285	GLN
2	D	287	VAL
2	D	289	CYS
2	D	291	VAL
2	D	307	VAL
2	D	315	LEU
2	D	319	GLU
2	D	342	THR
2	D	343	LEU
2	D	344	GLN
2	D	354	THR
2	D	361	LEU
2	D	366	GLN
2	D	419	THR
2	D	422	GLN
2	D	432	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	330	HIS
1	A	420	GLN
1	A	426	HIS
1	A	448	ASN

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Mol	Chain	Res	Type
2	B	366	GLN
2	B	422	GLN
1	C	304	HIS
2	D	285	GLN
2	D	366	GLN
2	D	422	GLN

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
4	A1IA7	A	603	3	23,25,25	0.45	0	28,35,35	0.44	0
4	A1IA7	A	604	-	23,25,25	0.39	0	28,35,35	0.40	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
4	A1IA7	A	603	3	-	1/12/12/12	0/3/3/3
4	A1IA7	A	604	-	-	1/12/12/12	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

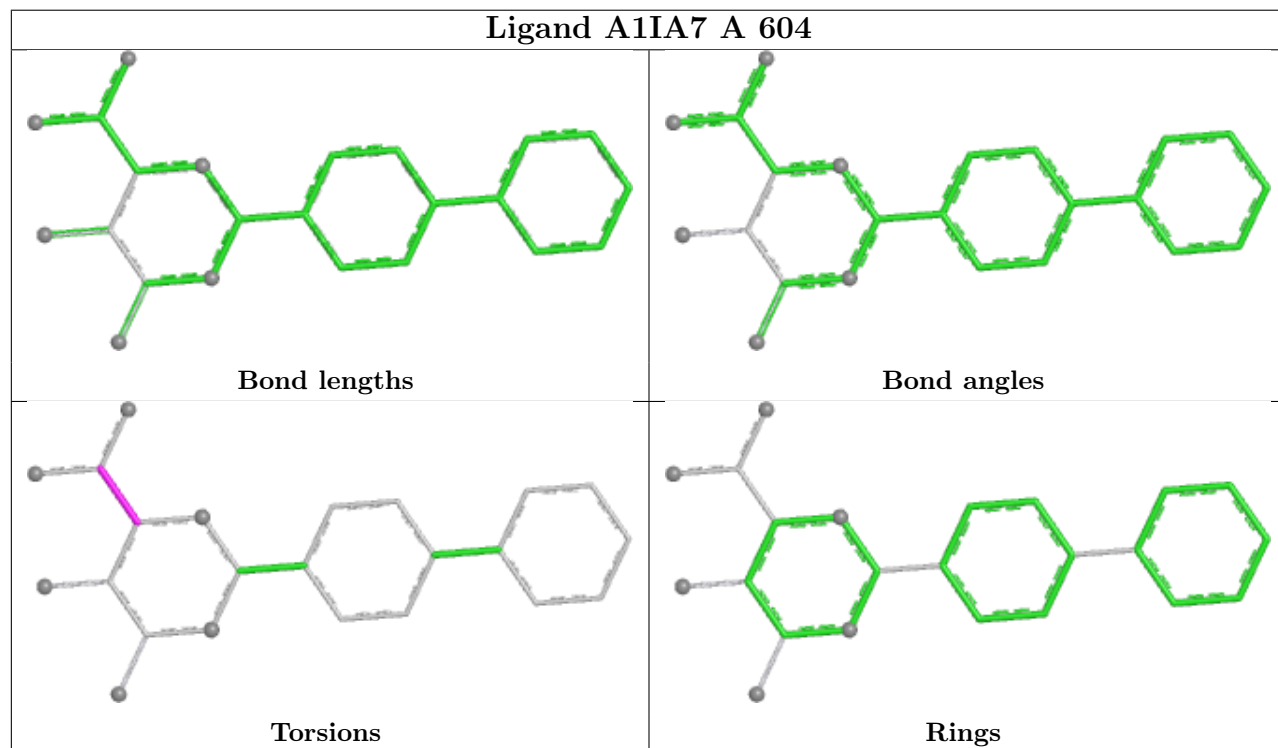
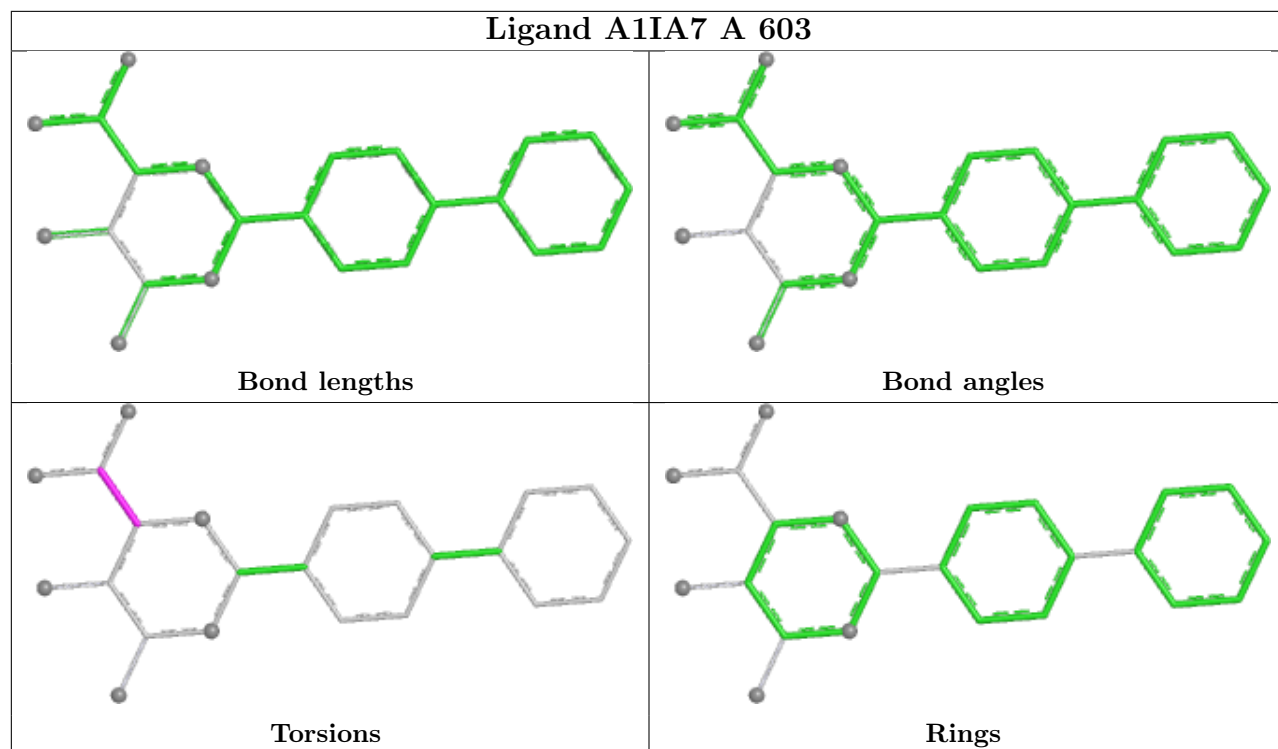
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	604	A1IA7	C14-C15-C16-O1
4	A	603	A1IA7	N1-C15-C16-O1

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 ⓘ

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	180/308 (58%)	0.74	11 (6%)	27 24	46, 65, 84, 91	0
1	C	179/308 (58%)	0.80	16 (8%)	15 13	47, 71, 91, 104	0
2	B	138/326 (42%)	1.02	19 (13%)	6 6	56, 75, 88, 98	0
2	D	139/326 (42%)	0.98	21 (15%)	5 5	54, 73, 89, 94	0
All	All	636/1268 (50%)	0.87	67 (10%)	11 10	46, 70, 89, 104	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	446	ALA	5.1
1	A	433	TRP	3.7
1	A	434	GLY	3.5
2	D	342	THR	3.4
1	A	285	PRO	3.4
1	C	435	THR	3.3
1	C	433	TRP	3.3
1	C	436	PRO	3.1
2	D	328	GLY	3.0
1	A	395	ASP	3.0
1	C	299	THR	3.0
1	A	275	ILE	2.9
2	D	273	LEU	2.9
1	C	366	TYR	2.9
1	C	285	PRO	2.9
2	B	276	MET	2.9
2	D	280	CYS	2.9
2	D	251	HIS	2.8
2	D	248	CYS	2.8
2	B	410	GLU	2.7
1	C	338	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	297	THR	2.7
2	D	366	GLN	2.6
2	D	325	ILE	2.6
1	A	278	THR	2.5
2	D	350	ILE	2.5
2	D	256	LEU	2.5
2	D	346	PHE	2.5
2	D	347	VAL	2.5
2	D	446	ALA	2.5
2	D	283	GLU	2.5
2	B	325	ILE	2.4
2	B	251	HIS	2.4
1	A	276	GLY	2.4
2	D	313	LEU	2.4
2	B	250	LYS	2.4
1	A	259	PRO	2.3
2	B	280	CYS	2.3
2	B	279	ARG	2.3
2	D	281	VAL	2.3
2	B	283	GLU	2.3
2	D	306	TRP	2.3
1	C	291	LEU	2.3
2	B	445	GLU	2.2
1	C	346	ASP	2.2
2	B	366	GLN	2.2
1	C	271	LEU	2.2
2	D	354	THR	2.2
1	C	447	PRO	2.2
2	B	407	ASP	2.2
2	D	407	ASP	2.2
1	A	328	LEU	2.2
2	B	315	LEU	2.2
2	B	281	VAL	2.2
2	D	250	LYS	2.1
2	B	316	LEU	2.1
2	B	287	VAL	2.1
2	B	352	ALA	2.1
1	A	277	GLU	2.1
2	D	315	LEU	2.1
1	C	300	VAL	2.1
1	C	377	LEU	2.0
2	B	343	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	276	GLY	2.0
1	C	405	ILE	2.0
1	C	294	LEU	2.0
2	B	356	GLY	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](#)

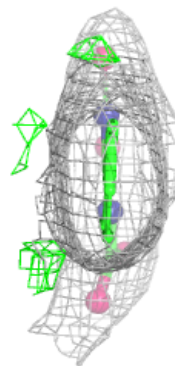
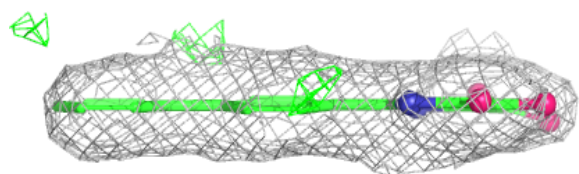
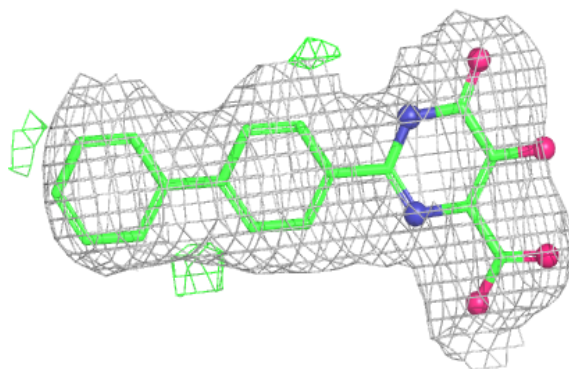
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	A1IA7	A	604	23/23	0.84	0.13	72,72,74,74	0
4	A1IA7	A	603	23/23	0.88	0.11	53,55,58,58	0
3	MG	A	601	1/1	0.96	0.15	49,49,49,49	0
3	MG	A	602	1/1	0.97	0.13	48,48,48,48	0

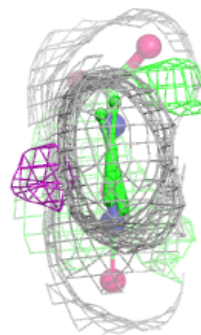
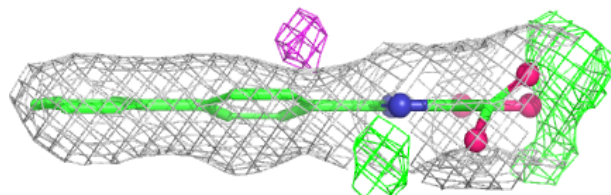
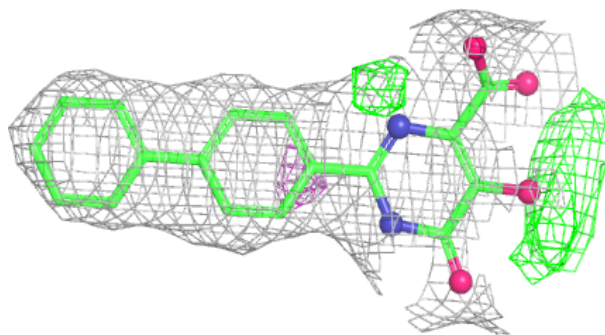
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1IA7 A 604:

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

**Electron density around A1IA7 A 603:**

$2mF_o-DF_c$ (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.