



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:38 AM UTC

PDB ID : 9EGU / pdb\_00009egu  
Title : Crystal structure of Danio rerio histone deacetylase 6 catalytic domain 2 complexed with TO-599  
Authors : Erdogan, F.; Seo, H.-S.; Dhe-Paganon, S.  
Deposited on : 2024-11-21  
Resolution : 1.27 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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (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

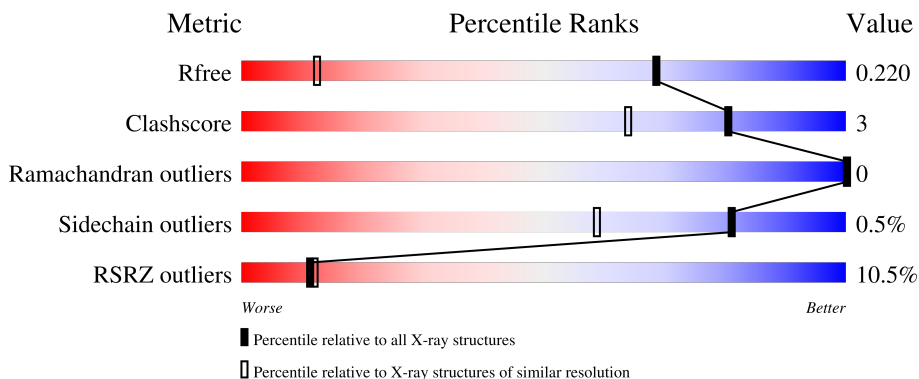
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.27 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	2836 (1.30-1.26)
Clashscore	190562	2911 (1.30-1.26)
Ramachandran outliers	187476	2841 (1.30-1.26)
Sidechain outliers	187428	2840 (1.30-1.26)
RSRZ outliers	180081	2832 (1.30-1.26)

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	357	 11% 95% 5%
1	B	357	 10% 93% 6%

## 2 Entry composition i

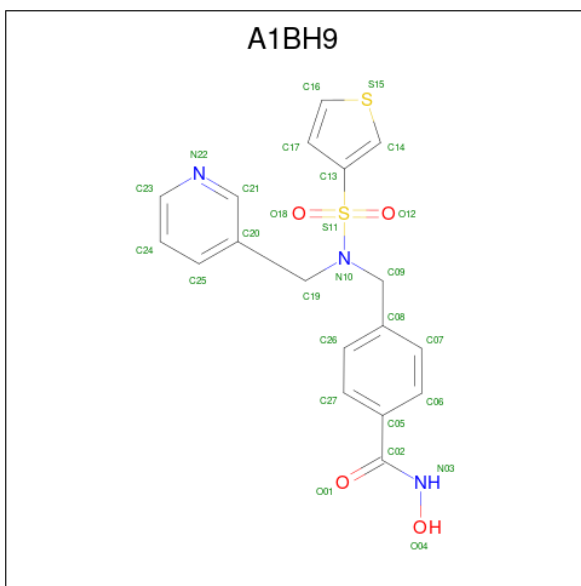
There are 5 unique types of molecules in this entry. The entry contains 6332 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Hdac6 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	357	Total 2856	C 1792	N 516	O 529	S 19	0	9	0
1	B	357	Total 2854	C 1791	N 517	O 527	S 19	0	9	0

- Molecule 2 is N-hydroxy-4-({[(pyridin-3-yl)methyl](thiophene-3-sulfonyl)amino}methyl)benzamide (CCD ID: A1BH9) (formula: C<sub>18</sub>H<sub>17</sub>N<sub>3</sub>O<sub>4</sub>S<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	Total 27	C 18	N 3	O 4	S 2	0	0
2	B	1	Total 27	C 18	N 3	O 4	S 2	0	0

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	K 1	0	0
4	B	1	Total 1	K 1	0	0

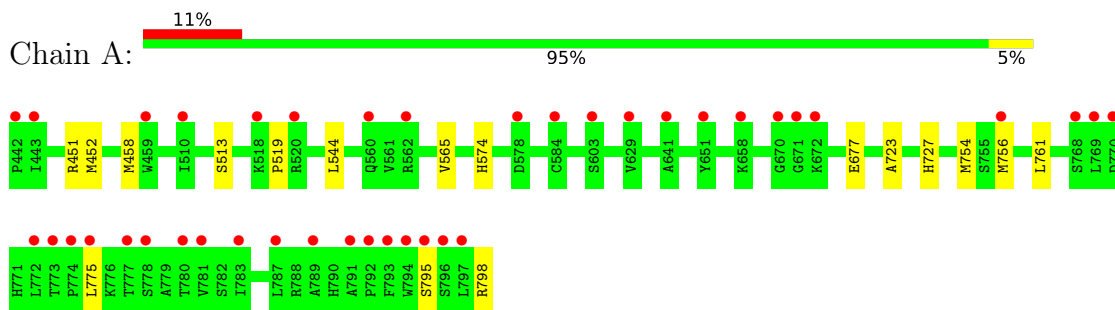
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	258	Total 258	O 258	0	0
5	B	306	Total 306	O 306	0	0

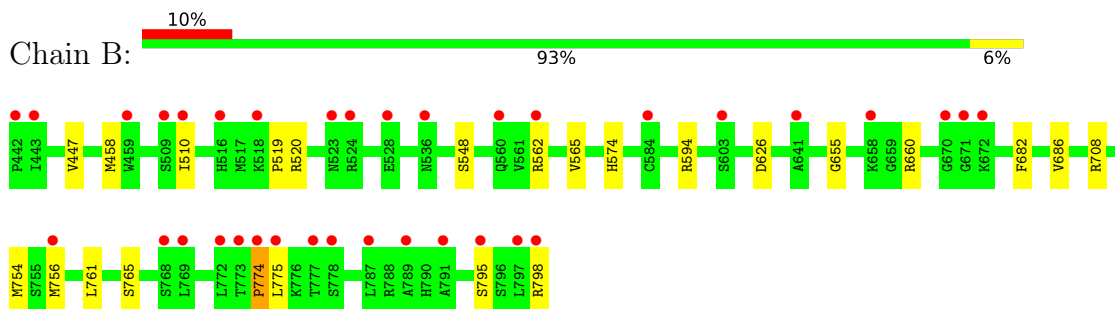
### 3 Residue-property plots [i](#)

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: Hdac6 protein



- Molecule 1: Hdac6 protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.79Å 91.19Å 96.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.04 – 1.27 59.04 – 1.27	Depositor EDS
% Data completeness (in resolution range)	93.5 (59.04-1.27) 93.5 (59.04-1.27)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.15 (at 1.27Å)	Xtrriage
Refinement program	PHENIX 1.20_4459	Depositor
R, $R_{free}$	0.208 , 0.221 0.206 , 0.220	Depositor DCC
$R_{free}$ test set	8160 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.8	Xtrriage
Anisotropy	0.342	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 29.4	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	0.97	EDS
Total number of atoms	6332	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.49 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.4205e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: A1BH9, ZN, K

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	0.28	0/2930	0.50	0/3971
1	B	0.27	0/2927	0.53	1/3966 (0.0%)
All	All	0.27	0/5857	0.51	1/7937 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	774	PRO	N-CA-CB	-10.31	94.38	103.35

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	2856	0	2772	14	0
1	B	2854	0	2776	16	0
2	A	27	0	0	1	0
2	B	27	0	0	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	258	0	0	3	0
5	B	306	0	0	5	0
All	All	6332	0	5548	29	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 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)
1:B:660[B]:ARG:NH1	5:B:901:HOH:O	2.02	0.80
1:A:451[A]:ARG:HD2	5:A:1024:HOH:O	1.89	0.72
1:B:708[B]:ARG:NE	5:B:902:HOH:O	2.21	0.72
1:B:795[B]:SER:HA	1:B:798:ARG:HD2	1.80	0.64
1:B:795[A]:SER:HA	1:B:798:ARG:HD2	1.80	0.64
1:A:677:GLU:HA	1:A:775:LEU:HD11	1.80	0.63
1:B:458:MET:HE1	1:B:519:PRO:HB3	1.82	0.61
1:A:795[A]:SER:HA	1:A:798:ARG:HD2	1.85	0.58
1:A:795[B]:SER:HA	1:A:798:ARG:HD2	1.85	0.58
1:B:520:ARG:NH1	5:B:908:HOH:O	2.42	0.53
1:A:458:MET:HE1	1:A:519:PRO:HB3	1.92	0.52
1:A:565[B]:VAL:HG23	1:A:761:LEU:HD12	1.91	0.52
1:A:727:HIS:HD2	5:A:1134:HOH:O	1.94	0.51
1:B:574:HIS:NE2	2:B:801:A1BH9:N03	2.59	0.51
1:B:565[B]:VAL:HG23	1:B:761:LEU:HD12	1.92	0.50
1:A:723:ALA:HB2	1:A:756[A]:MET:HG3	1.94	0.50
1:A:565[B]:VAL:HG13	1:A:754:MET:HE2	1.95	0.48
1:A:513:SER:HB2	1:B:765:SER:CB	2.43	0.48
1:B:594:ARG:NH2	1:B:626:ASP:OD2	2.46	0.47
1:A:574:HIS:NE2	2:A:801:A1BH9:N03	2.64	0.46
1:B:447:VAL:HG21	1:B:548:SER:HB3	1.98	0.45
1:B:655:GLY:O	1:B:660[B]:ARG:HD3	2.17	0.44
1:A:565[A]:VAL:CG2	1:A:754:MET:HE2	2.47	0.44
1:A:727:HIS:HE1	5:A:1127:HOH:O	2.00	0.43
1:A:452:MET:HG3	1:A:544:LEU:HD23	2.00	0.43
1:B:562:ARG:NH1	5:B:918:HOH:O	2.52	0.43
1:B:510:ILE:HG21	5:B:949:HOH:O	2.19	0.41
1:B:565[B]:VAL:HG13	1:B:754:MET:HE2	2.01	0.41
1:B:682:PHE:HA	1:B:686:VAL:HB	2.02	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	364/357 (102%)	356 (98%)	8 (2%)	0	100	100
1	B	364/357 (102%)	353 (97%)	11 (3%)	0	100	100
All	All	728/714 (102%)	709 (97%)	19 (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	309/301 (103%)	309 (100%)	0	100	100
1	B	308/301 (102%)	304 (99%)	4 (1%)	61	25
All	All	617/602 (102%)	613 (99%)	4 (1%)	81	53

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	756[A]	MET
1	B	756[B]	MET
1	B	774	PRO
1	B	775	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	523	ASN
1	A	727	HIS
1	B	560	GLN
1	B	645	ASN
1	B	727	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](#)

Of 6 ligands modelled in this entry, 4 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
2	A1BH9	A	801	3	27,29,29	2.80	5 (18%)	35,40,40	2.72	8 (22%)
2	A1BH9	B	801	3	27,29,29	2.92	7 (25%)	35,40,40	2.47	4 (11%)

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	A1BH9	A	801	3	-	4/24/26/26	0/3/3/3
2	A1BH9	B	801	3	-	4/24/26/26	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	A1BH9	C17-C13	9.53	1.53	1.42
2	B	801	A1BH9	C02-N03	9.39	1.44	1.32
2	B	801	A1BH9	C17-C13	8.89	1.52	1.42
2	A	801	A1BH9	C02-N03	8.47	1.43	1.32
2	B	801	A1BH9	O18-S11	4.09	1.47	1.43
2	B	801	A1BH9	O12-S11	3.59	1.46	1.43
2	A	801	A1BH9	O01-C02	-3.29	1.15	1.23
2	A	801	A1BH9	C14-S15	-3.24	1.60	1.70
2	B	801	A1BH9	C14-C13	3.16	1.43	1.35
2	A	801	A1BH9	C14-C13	2.44	1.41	1.35
2	B	801	A1BH9	C14-S15	-2.38	1.63	1.70
2	B	801	A1BH9	O01-C02	-2.32	1.17	1.23

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	A1BH9	O18-S11-O12	-13.23	100.70	119.69
2	B	801	A1BH9	O18-S11-O12	-12.13	102.29	119.69
2	A	801	A1BH9	O01-C02-N03	-4.41	114.78	122.90
2	B	801	A1BH9	O12-S11-C13	3.64	114.47	107.88
2	A	801	A1BH9	O12-S11-N10	3.27	112.96	107.26
2	A	801	A1BH9	C16-S15-C14	3.07	104.95	94.52
2	A	801	A1BH9	C05-C02-N03	3.03	120.93	116.26
2	B	801	A1BH9	O01-C02-N03	-2.91	117.55	122.90
2	B	801	A1BH9	C23-N22-C21	2.86	121.86	116.85
2	A	801	A1BH9	C23-N22-C21	2.53	121.29	116.85
2	A	801	A1BH9	O04-N03-C02	2.10	125.00	119.73
2	A	801	A1BH9	C19-N10-C09	2.07	120.51	116.27

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	A1BH9	C17-C13-S11-O12
2	B	801	A1BH9	C20-C19-N10-C09
2	A	801	A1BH9	C09-N10-S11-O18

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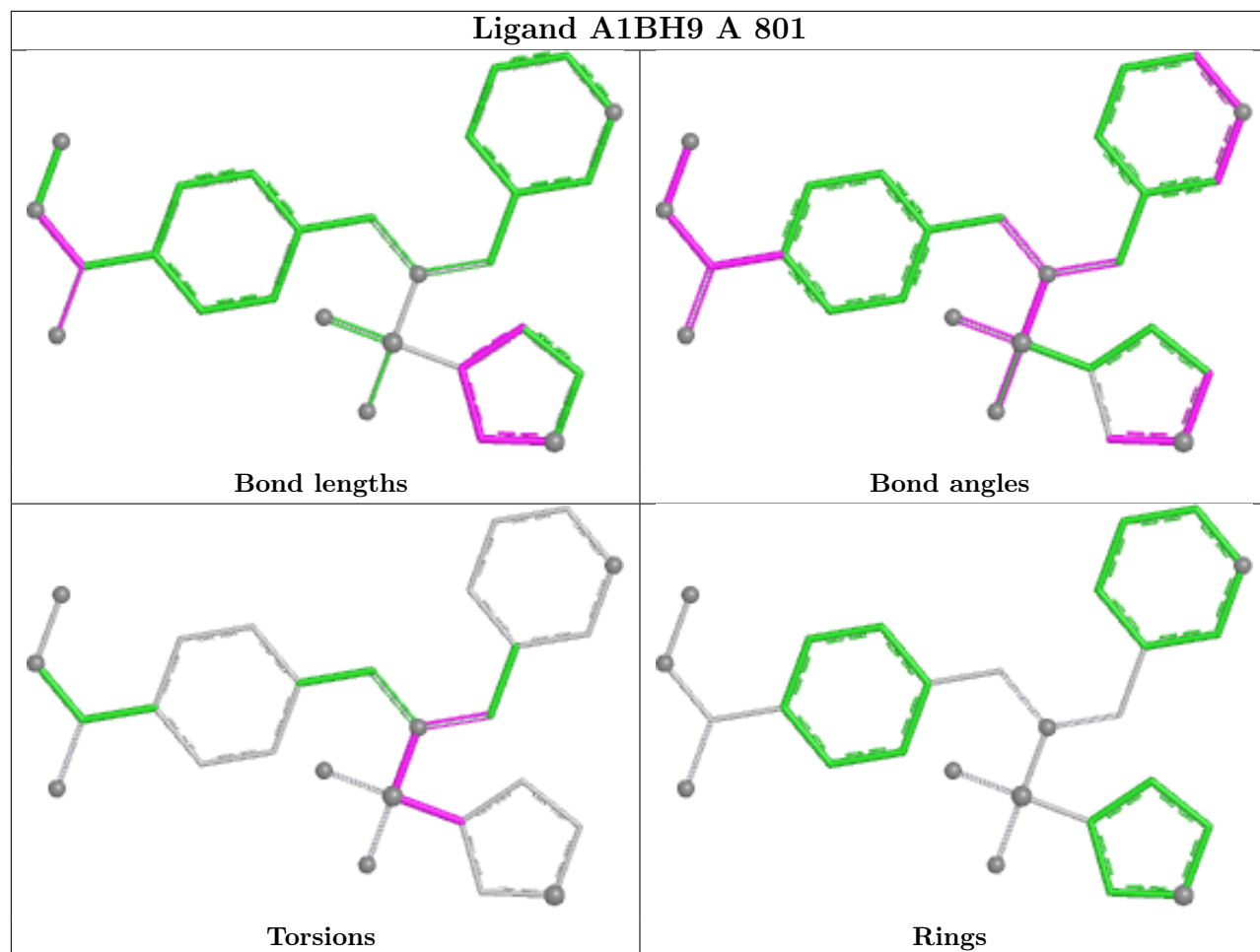
Mol	Chain	Res	Type	Atoms
2	A	801	A1BH9	C20-C19-N10-C09
2	B	801	A1BH9	C09-N10-S11-O18
2	B	801	A1BH9	C19-N10-S11-O18
2	A	801	A1BH9	C20-C19-N10-S11
2	B	801	A1BH9	C20-C19-N10-S11

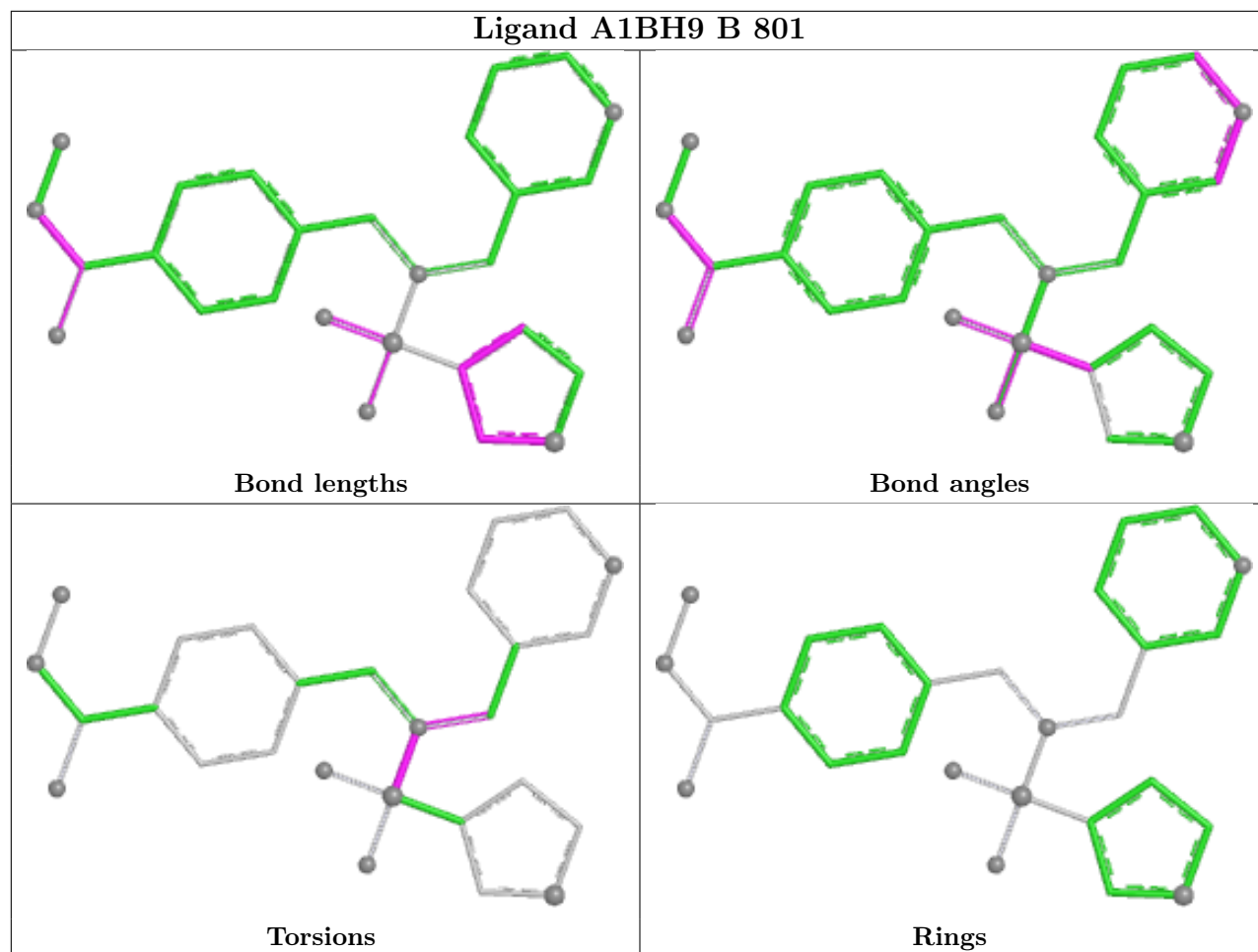
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	A1BH9	1	0
2	B	801	A1BH9	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](#)

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	357/357 (100%)	0.77	40 (11%) 10 11	6, 18, 34, 54	11 (3%)
1	B	357/357 (100%)	0.74	35 (9%) 13 14	7, 17, 34, 54	11 (3%)
All	All	714/714 (100%)	0.75	75 (10%) 11 12	6, 18, 34, 54	22 (3%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	670	GLY	5.7
1	B	510	ILE	5.7
1	B	459	TRP	5.3
1	A	777	THR	5.1
1	A	459	TRP	4.9
1	A	775	LEU	4.7
1	B	769	LEU	4.7
1	B	671	GLY	4.6
1	A	442	PRO	4.4
1	A	769	LEU	4.2
1	A	510	ILE	4.1
1	A	770	ASP	4.0
1	B	442	PRO	3.9
1	B	775	LEU	3.9
1	B	658	LYS	3.8
1	B	584	CYS	3.8
1	B	773	THR	3.7
1	A	797	LEU	3.7
1	A	774	PRO	3.4
1	B	443	ILE	3.4
1	A	773	THR	3.4
1	A	778	SER	3.4
1	B	774	PRO	3.3
1	B	516	HIS	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	772	LEU	3.2
1	A	658	LYS	3.2
1	A	791	ALA	3.2
1	A	671	GLY	3.2
1	B	777	THR	3.1
1	B	603	SER	3.1
1	B	778	SER	3.0
1	B	518	LYS	2.9
1	A	443	ILE	2.9
1	A	603	SER	2.9
1	A	772	LEU	2.8
1	B	797	LEU	2.8
1	A	789	ALA	2.7
1	B	528	GLU	2.7
1	A	670	GLY	2.6
1	A	780	THR	2.6
1	B	524	ARG	2.6
1	A	584	CYS	2.6
1	B	562	ARG	2.5
1	A	795[A]	SER	2.5
1	A	783	ILE	2.5
1	B	791	ALA	2.5
1	B	795[A]	SER	2.4
1	A	641	ALA	2.4
1	B	768	SER	2.4
1	A	562	ARG	2.4
1	A	672	LYS	2.4
1	A	794	TRP	2.4
1	A	781	VAL	2.3
1	A	792	PRO	2.3
1	A	796	SER	2.3
1	B	523	ASN	2.2
1	B	641	ALA	2.2
1	A	578	ASP	2.2
1	A	793	PHE	2.2
1	A	520	ARG	2.2
1	A	756[A]	MET	2.1
1	B	672	LYS	2.1
1	B	798	ARG	2.1
1	A	768	SER	2.1
1	A	560	GLN	2.1
1	B	536	ASN	2.1

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
1	A	787	LEU	2.1
1	A	651	TYR	2.1
1	A	518	LYS	2.1
1	B	509	SER	2.0
1	B	787	LEU	2.0
1	B	789	ALA	2.0
1	B	560	GLN	2.0
1	A	629	VAL	2.0
1	B	756[A]	MET	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](#)

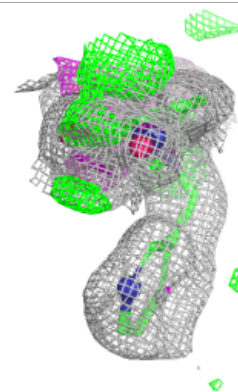
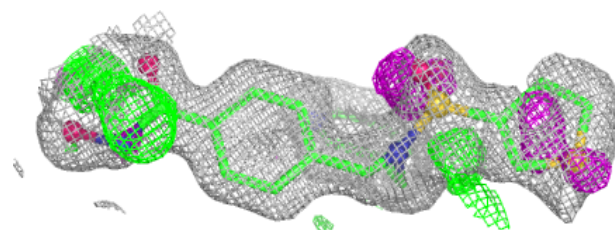
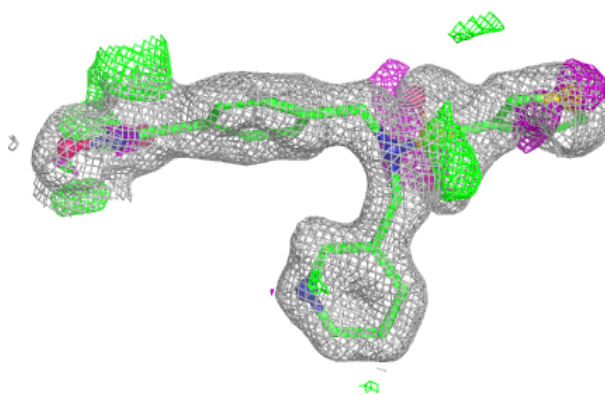
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	A1BH9	A	801	27/27	0.86	0.12	20,25,34,39	0
2	A1BH9	B	801	27/27	0.88	0.12	17,22,45,49	0
3	ZN	A	802	1/1	0.99	0.04	18,18,18,18	0
3	ZN	B	802	1/1	0.99	0.04	17,17,17,17	0
4	K	A	803	1/1	0.99	0.04	20,20,20,20	0
4	K	B	803	1/1	0.99	0.03	18,18,18,18	0

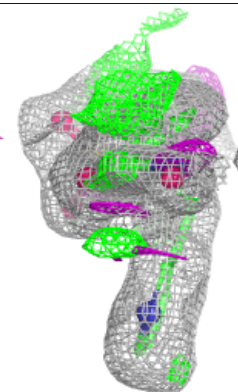
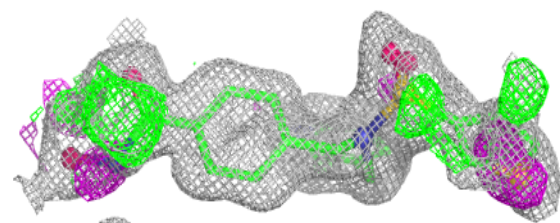
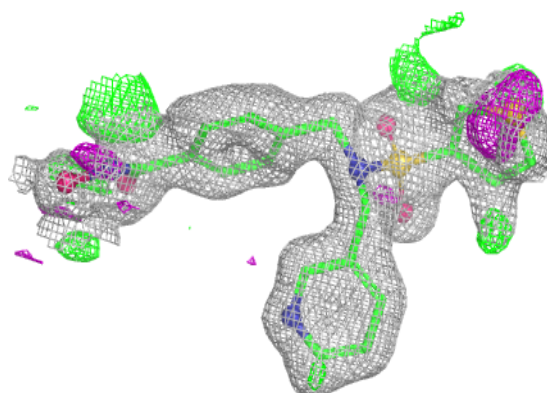
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around A1BH9 A 801:**

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

**Electron density around A1BH9 B 801:**

$2mF_o-DF_c$  (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.