



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 15, 2022 – 07:18 pm BST

PDB ID : 7ZZO  
Title : HDAC2 in complex with an inhibitor  
Authors : Cleasby, A.; Tisi, D.  
Deposited on : 2022-05-25  
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](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 : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.30  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.30

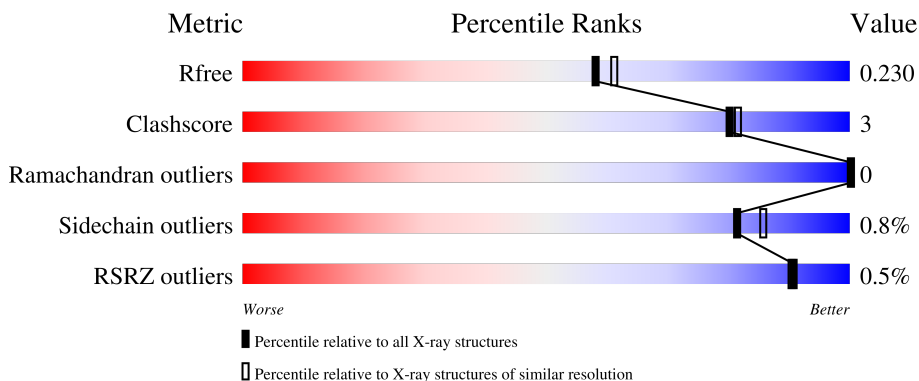
# 1 Overall quality at a glance i

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)
RSRZ outliers	127900	7900 (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  $\geq 3$ , 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	498	 68% 5% 26%
1	B	498	 68% 5% 27%
1	C	498	 % 68% 6% 26%

## 2 Entry composition i

There are 9 unique types of molecules in this entry. The entry contains 9936 atoms, of which 103 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 Histone deacetylase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	368	2984	1907	504	548	25	0	11	0
1	B	366	2974	1901	501	546	26	0	12	0
1	C	367	2974	1901	503	545	25	0	8	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	493	GLY	-	expression tag	UNP Q92769
A	494	SER	-	expression tag	UNP Q92769
A	495	SER	-	expression tag	UNP Q92769
A	496	GLY	-	expression tag	UNP Q92769
A	497	HIS	-	expression tag	UNP Q92769
A	498	HIS	-	expression tag	UNP Q92769
A	499	HIS	-	expression tag	UNP Q92769
A	500	HIS	-	expression tag	UNP Q92769
A	501	HIS	-	expression tag	UNP Q92769
A	502	HIS	-	expression tag	UNP Q92769
B	493	GLY	-	expression tag	UNP Q92769
B	494	SER	-	expression tag	UNP Q92769
B	495	SER	-	expression tag	UNP Q92769
B	496	GLY	-	expression tag	UNP Q92769
B	497	HIS	-	expression tag	UNP Q92769
B	498	HIS	-	expression tag	UNP Q92769
B	499	HIS	-	expression tag	UNP Q92769
B	500	HIS	-	expression tag	UNP Q92769
B	501	HIS	-	expression tag	UNP Q92769
B	502	HIS	-	expression tag	UNP Q92769
C	493	GLY	-	expression tag	UNP Q92769
C	494	SER	-	expression tag	UNP Q92769
C	495	SER	-	expression tag	UNP Q92769

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Chain	Residue	Modelled	Actual	Comment	Reference
C	496	GLY	-	expression tag	UNP Q92769
C	497	HIS	-	expression tag	UNP Q92769
C	498	HIS	-	expression tag	UNP Q92769
C	499	HIS	-	expression tag	UNP Q92769
C	500	HIS	-	expression tag	UNP Q92769
C	501	HIS	-	expression tag	UNP Q92769
C	502	HIS	-	expression tag	UNP Q92769

- Molecule 2 is ZINC ION (three-letter code: 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
2	C	1	Total Zn 1 1	0	0

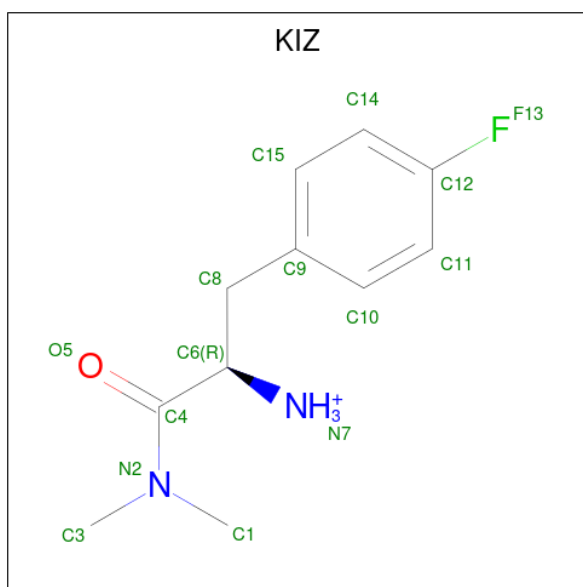
- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

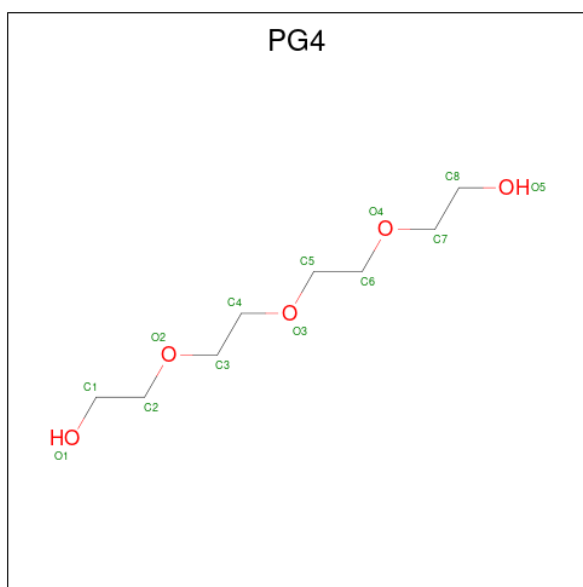
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0

- Molecule 5 is [(2 {R})-1-(dimethylamino)-3-(4-fluorophenyl)-1-oxidanylidene-propan-2-yl]azanium (three-letter code: KIZ) (formula: C<sub>11</sub>H<sub>16</sub>FN<sub>2</sub>O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	H	N			O
5	A	1	Total	C	F	H	N	O	0	0
			31	11	1	16	2	1		
5	B	1	Total	C	F	H	N	O	0	0
			31	11	1	16	2	1		
5	C	1	Total	C	F	H	N	O	0	0
			31	11	1	16	2	1		

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



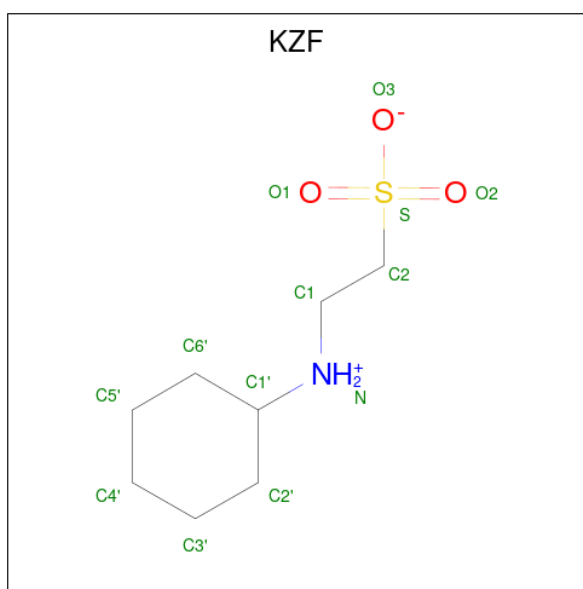
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	H			O
6	B	1	Total	C	H	O	1	0
			31	8	18	5		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	H	O	1	0
			17	4	10	3		
7	C	1	Total	C	H	O	1	0
			17	4	10	3		

- Molecule 8 is 2-(cyclohexylazanumyl)ethanesulfonate (three-letter code: KZF) (formula:  $C_8H_{17}NO_3S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			S
8	B	1	30	8	17	1	3	1	0	0

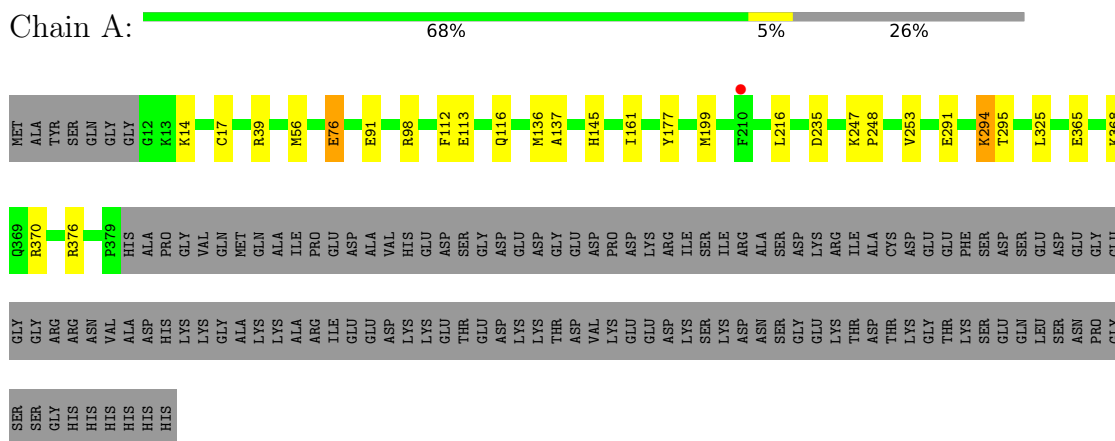
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	289	Total 289	O 289	0	0
9	B	313	Total 313	O 313	0	0
9	C	205	Total 205	O 205	0	0

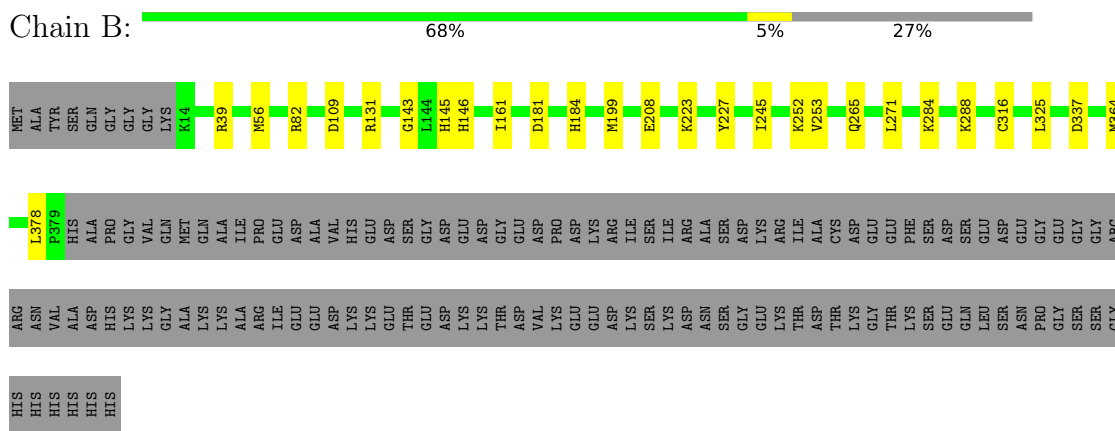
### 3 Residue-property plots [i](#)

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.

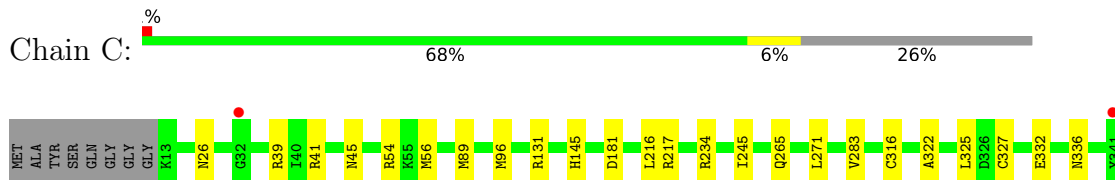
- Molecule 1: Histone deacetylase 2



- Molecule 1: Histone deacetylase 2



- Molecule 1: Histone deacetylase 2





M364	GLU	ASN
E365	GLY	PRO
	GLY	GLY
K368	GLY	SER
Q369	ARG	GLY
R370	ARG	HIS
	ASN	HIS
P379	VAL	HIS
	ALA	HIS
	PRO	HIS
	GLY	
	VAL	
	GLN	
	MET	
	GLN	
	ALA	
	ALA	
	ILE	
	PRO	
	GLU	
	ASP	
	ALA	
	VAL	
	HIS	
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	GLY	
	ASP	
	GLY	
	GLY	
	GLY	
	PRO	
	ASP	
	LYS	
	ARG	
	ILE	
	SER	
	ILE	
	SER	
	ARG	
	ALA	
	SER	
	ASP	
	LYS	
	ARG	
	ALA	
	CYS	
	ASP	
	GLU	
	GLU	
	PHE	
	SER	
	ASP	
	SER	
	GLU	
	GLN	
	SER	
	ASP	

GLU	GLY
GLY	GLY
GLY	GLY
ARG	GLY
ARG	ASN
ASN	VAL
VAL	ALA
ASP	HIS
HIS	LYS
LYS	LYS
GLY	ALA
ALA	LYS
LYS	LYS
LYS	ALA
ARG	ILE
ILE	GLU
GLU	GLY
ASP	ASP
HIS	LYS
LYS	LYS
GLU	THR
THR	THR
GLY	GLY
ASP	ASP
GLY	LYS
LYS	LYS
THR	THR
THR	THR
ASP	ASP
LYS	LYS
LYS	LYS
ILE	ILE
ILE	ILE
ASP	ASP
ASN	ASN
SER	SER
GLY	GLY
LYS	LYS
LYS	LYS
THR	THR
THR	THR
ASP	ASP
THR	THR
LYS	LYS
GLY	GLY
THR	THR
LYS	LYS
SER	SER
GLU	GLU
GLN	GLN
SER	SER

ASN
PRO
GLY
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.08Å 97.44Å 139.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.80 – 2.00 79.80 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.3 (79.80-2.00) 94.3 (79.80-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.85 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0232	Depositor
R, $R_{free}$	0.172 , 0.225 0.182 , 0.230	Depositor DCC
$R_{free}$ test set	3946 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.3	Xtriage
Anisotropy	0.457	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9936	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: PG4, NA, KIZ, PEG, KZF, ZN, CA

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	0.53	0/3075	0.71	1/4150 (0.0%)
1	B	0.53	0/3068	0.73	2/4142 (0.0%)
1	C	0.47	0/3062	0.65	0/4133
All	All	0.51	0/9205	0.70	3/12425 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	2
1	C	0	3
All	All	0	8

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	337	ASP	CB-CG-OD1	5.55	123.30	118.30
1	B	109	ASP	CB-CG-OD1	5.45	123.21	118.30
1	A	235	ASP	CB-CG-OD1	5.10	122.89	118.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	376[A]	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	376[B]	ARG	Sidechain
1	A	39	ARG	Sidechain
1	B	39	ARG	Sidechain
1	B	82	ARG	Sidechain
1	C	234	ARG	Sidechain
1	C	39	ARG	Sidechain
1	C	54	ARG	Sidechain

## 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	2984	0	2878	16	0
1	B	2974	0	2867	14	0
1	C	2974	0	2873	19	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	15	16	0	0	0
5	B	15	16	0	0	0
5	C	15	16	0	0	0
6	B	13	18	18	1	0
7	B	7	10	10	0	0
7	C	7	10	10	0	0
8	B	13	17	0	0	0
9	A	289	0	0	1	0
9	B	313	0	0	2	0
9	C	205	0	0	1	0
All	All	9833	103	8656	47	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 (47) 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:56:MET:HB3	1:A:325:LEU:HD21	1.81	0.62
1:C:131:ARG:NH2	9:C:701:HOH:O	2.33	0.60
1:A:76:GLU:OE1	1:A:98:ARG:NH2	2.35	0.59
1:A:14:LYS:HB2	1:A:136:MET:HE3	1.87	0.56
1:C:26:ASN:OD1	1:C:41:ARG:NH2	2.32	0.56
1:B:146:HIS:HE1	1:B:184:HIS:O	1.90	0.54
1:B:143:GLY:HA2	1:B:161:ILE:HD11	1.91	0.53
1:C:216:LEU:HD21	1:C:370:ARG:HD2	1.91	0.52
1:C:365:GLU:O	1:C:369:GLN:HG2	2.11	0.51
1:C:216:LEU:HD21	1:C:370:ARG:CD	2.41	0.50
1:A:370:ARG:NH1	9:A:709:HOH:O	2.45	0.50
1:B:223:LYS:HE2	9:B:742:HOH:O	2.10	0.50
1:A:113:GLU:OE1	1:B:131:ARG:NH2	2.45	0.49
1:C:56:MET:HB3	1:C:325:LEU:HD21	1.95	0.48
1:C:131:ARG:HH21	1:C:131:ARG:CG	2.25	0.48
1:C:365:GLU:OE1	1:C:368:LYS:NZ	2.45	0.48
1:B:199:MET:SD	1:B:253:VAL:HG13	2.54	0.48
1:B:199:MET:CE	1:B:378:LEU:HD11	2.44	0.48
1:B:56:MET:HB3	1:B:325:LEU:HD21	1.95	0.47
1:A:216:LEU:HD23	1:A:216:LEU:H	1.80	0.46
1:C:245:ILE:HG21	1:C:364:MET:HE3	1.96	0.46
1:C:322:ALA:HB1	1:C:327:CYS:O	2.16	0.46
1:A:91:GLU:OE2	1:C:217:ARG:NH2	2.50	0.45
1:A:161:ILE:HG21	1:A:177:TYR:CE1	2.52	0.45
1:B:284:LYS:HE3	6:B:604:PG4:H72	1.98	0.45
1:A:291:GLU:O	1:A:295:THR:HG23	2.17	0.45
1:B:245:ILE:HG12	1:B:364:MET:CE	2.47	0.45
1:A:136:MET:HE1	1:A:294:LYS:HE3	1.99	0.45
1:C:181:ASP:HB2	1:C:265:GLN:OE1	2.17	0.45
1:B:181:ASP:HB2	1:B:265:GLN:OE1	2.18	0.44
1:A:14:LYS:HB2	1:A:136:MET:CE	2.47	0.44
1:C:332:GLU:CD	1:C:332:GLU:N	2.71	0.44
1:B:227:TYR:CZ	1:B:378:LEU:HD22	2.52	0.43
1:C:89:MET:HE2	1:C:96:MET:HE1	2.00	0.43
1:C:131:ARG:HH21	1:C:131:ARG:HG3	1.84	0.43
1:C:271:LEU:HD11	1:C:316:CYS:HB2	2.00	0.43
1:A:199:MET:SD	1:A:253:VAL:HG13	2.58	0.43
1:A:112:PHE:O	1:A:116:GLN:HG3	2.19	0.42
1:B:199:MET:HE3	1:B:378:LEU:HD11	2.01	0.42
1:C:283:VAL:HG13	1:C:316:CYS:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:ASN:OD1	1:C:336:ASN:HB2	2.20	0.42
1:A:365[A]:GLU:OE1	1:A:368:LYS:NZ	2.46	0.42
1:B:271:LEU:HD11	1:B:316:CYS:HB2	2.00	0.42
1:A:17:CYS:O	1:A:137:ALA:HA	2.19	0.42
1:A:247:LYS:HB3	1:A:248:PRO:HD3	2.02	0.41
1:B:252:LYS:NZ	9:B:725:HOH:O	2.53	0.41
1:C:369:GLN:HA	1:C:369:GLN:OE1	2.21	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	370/498 (74%)	364 (98%)	6 (2%)	0	100	100
1	B	369/498 (74%)	363 (98%)	6 (2%)	0	100	100
1	C	368/498 (74%)	360 (98%)	8 (2%)	0	100	100
All	All	1107/1494 (74%)	1087 (98%)	20 (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	321/425 (76%)	318 (99%)	3 (1%)	78	83
1	B	321/425 (76%)	318 (99%)	3 (1%)	78	83
1	C	320/425 (75%)	318 (99%)	2 (1%)	86	90
All	All	962/1275 (76%)	954 (99%)	8 (1%)	81	86

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	GLU
1	A	145	HIS
1	A	294	LYS
1	B	145	HIS
1	B	208[A]	GLU
1	B	288[A]	LYS
1	C	145	HIS
1	C	379	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 9 are monoatomic - leaving 7 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
5	KIZ	A	604	2	15,15,15	0.28	0	20,20,20	0.49	0
5	KIZ	C	605	2	15,15,15	0.27	0	20,20,20	0.49	0
5	KIZ	B	606	2	15,15,15	0.28	0	20,20,20	0.51	0
6	PG4	B	604	-	12,12,12	0.47	0	11,11,11	0.51	0
7	PEG	B	605	-	6,6,6	0.42	0	5,5,5	0.32	0
8	KZF	B	607	-	13,13,13	0.55	0	16,17,17	0.56	0
7	PEG	C	604	-	6,6,6	0.38	0	5,5,5	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
5	KIZ	A	604	2	-	0/12/12/12	0/1/1/1
5	KIZ	C	605	2	-	0/12/12/12	0/1/1/1
5	KIZ	B	606	2	-	0/12/12/12	0/1/1/1
6	PG4	B	604	-	-	3/10/10/10	-
7	PEG	B	605	-	-	3/4/4/4	-
8	KZF	B	607	-	-	2/7/15/15	0/1/1/1
7	PEG	C	604	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	607	KZF	C2'-C1'-N-C1
7	B	605	PEG	O2-C3-C4-O4
6	B	604	PG4	O3-C5-C6-O4
7	B	605	PEG	O1-C1-C2-O2
6	B	604	PG4	O4-C7-C8-O5
8	B	607	KZF	C2-C1-N-C1'
7	B	605	PEG	C1-C2-O2-C3
7	C	604	PEG	O1-C1-C2-O2
6	B	604	PG4	C6-C5-O3-C4

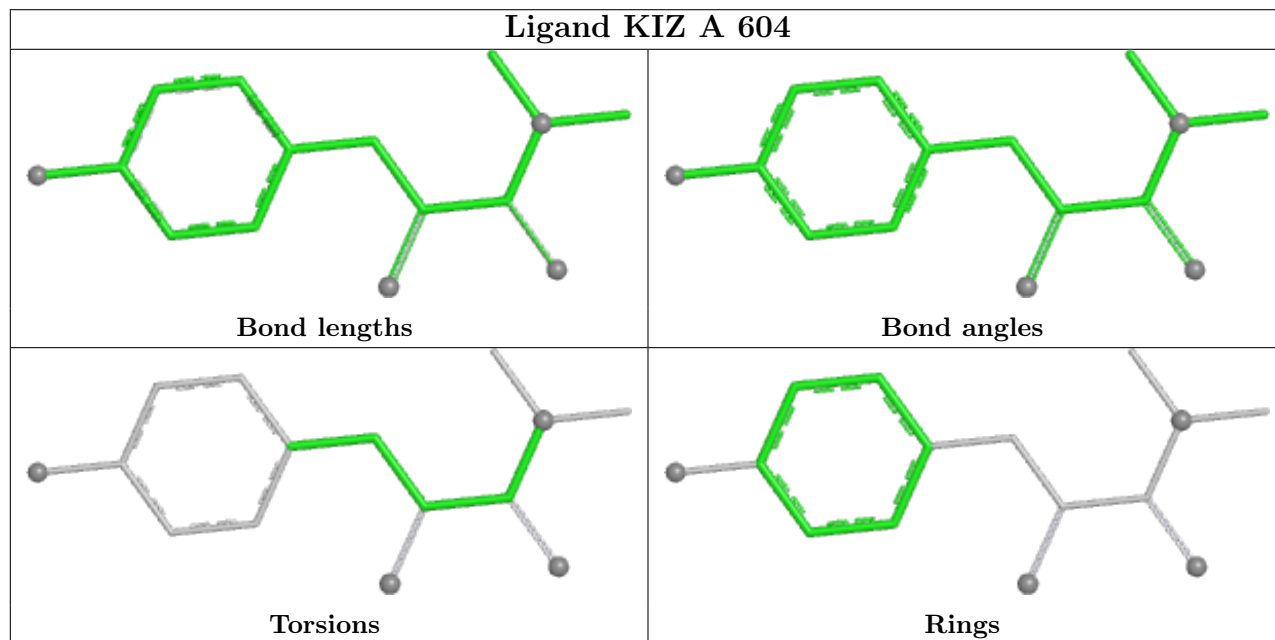


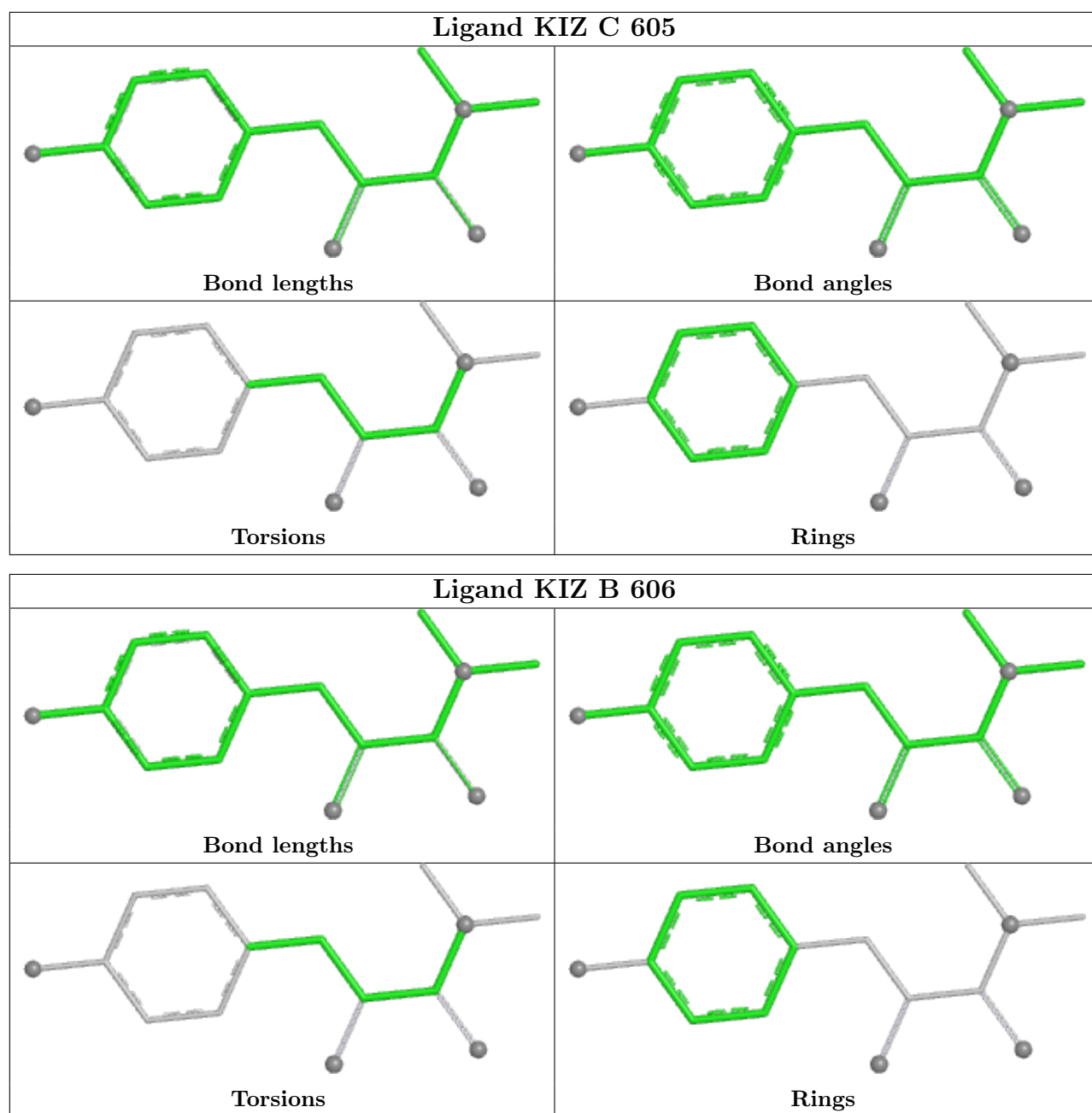
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	604	PG4	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	368/498 (73%)	-0.34	1 (0%) 94 93	11, 20, 36, 58	3 (0%)
1	B	366/498 (73%)	-0.38	0 100 100	10, 18, 36, 54	3 (0%)
1	C	367/498 (73%)	-0.03	4 (1%) 80 79	16, 30, 50, 73	2 (0%)
All	All	1101/1494 (73%)	-0.25	5 (0%) 91 90	10, 22, 46, 73	8 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	32	GLY	3.4
1	A	210	PHE	2.9
1	C	341	TYR	2.7
1	C	370	ARG	2.6
1	C	379	PRO	2.2

### 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](#)

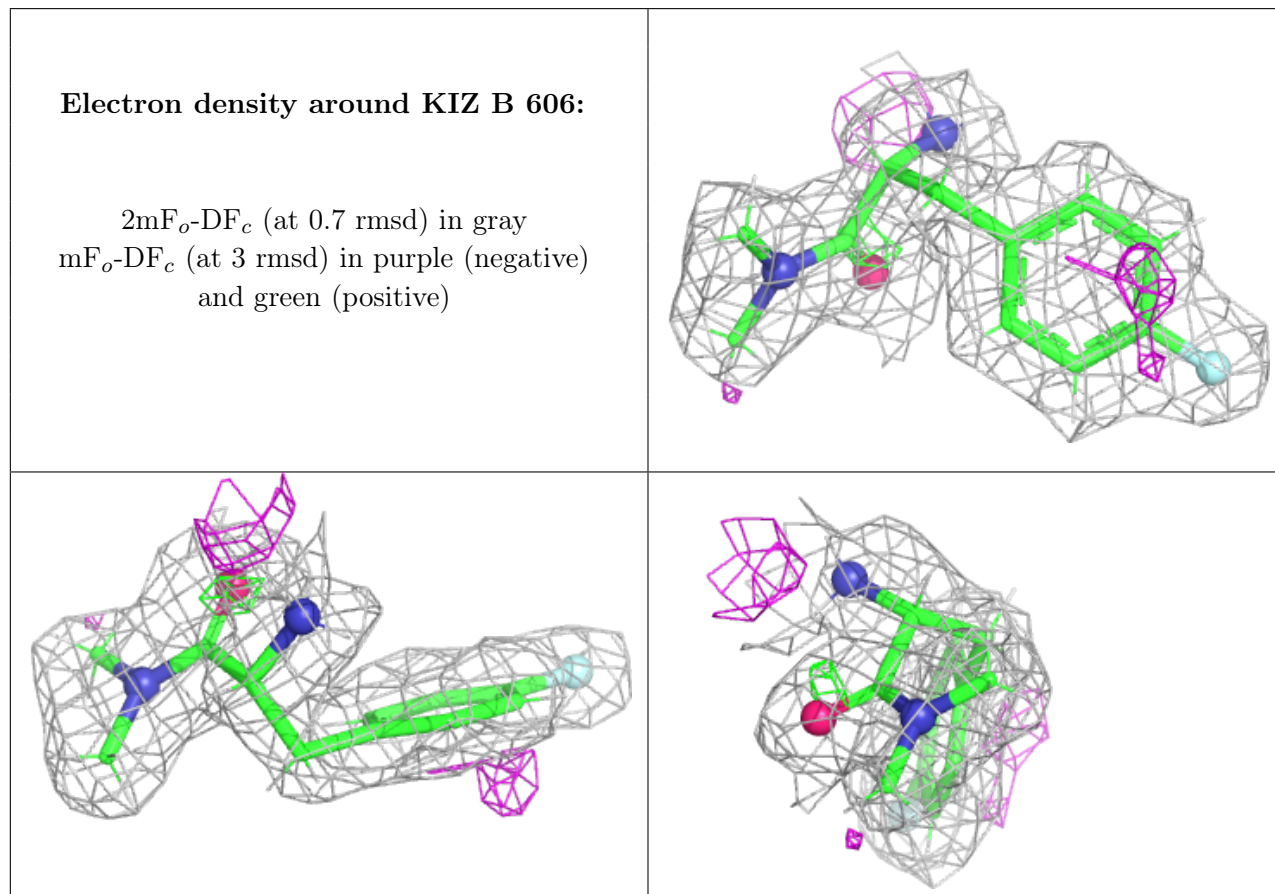
There are no monosaccharides in this entry.

### 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.

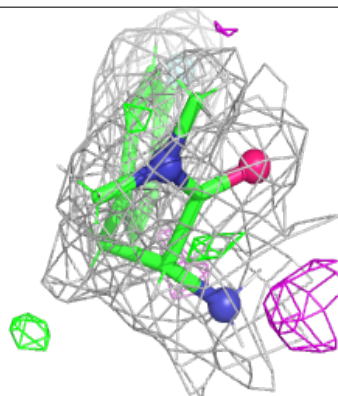
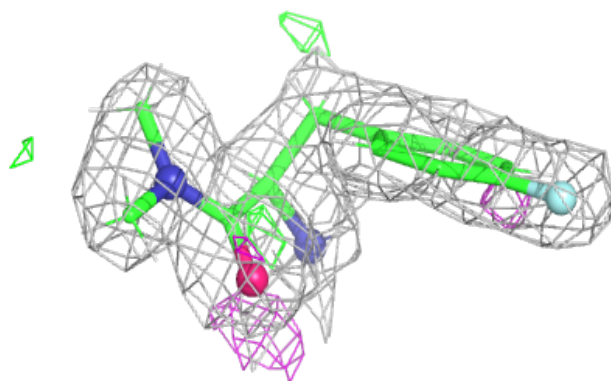
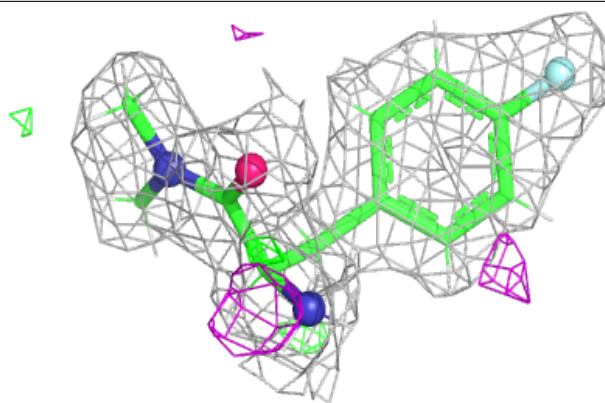
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	PG4	B	604	13/13	0.86	0.17	29,37,46,48	1
7	PEG	B	605	7/7	0.92	0.13	29,33,38,41	1
7	PEG	C	604	7/7	0.92	0.14	26,28,32,36	1
8	KZF	B	607	13/13	0.93	0.16	26,31,34,44	30
5	KIZ	B	606	15/15	0.95	0.16	10,16,19,22	31
5	KIZ	A	604	15/15	0.96	0.13	11,19,21,25	31
5	KIZ	C	605	15/15	0.96	0.13	14,16,22,24	31
4	NA	C	603	1/1	0.97	0.08	22,22,22,22	0
4	NA	B	603	1/1	0.99	0.06	17,17,17,17	0
3	CA	C	602	1/1	0.99	0.08	30,30,30,30	0
4	NA	A	603	1/1	0.99	0.05	21,21,21,21	0
2	ZN	B	601	1/1	1.00	0.05	12,12,12,12	0
2	ZN	C	601	1/1	1.00	0.04	19,19,19,19	0
3	CA	A	602	1/1	1.00	0.07	23,23,23,23	0
3	CA	B	602	1/1	1.00	0.05	22,22,22,22	0
2	ZN	A	601	1/1	1.00	0.05	13,13,13,13	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.

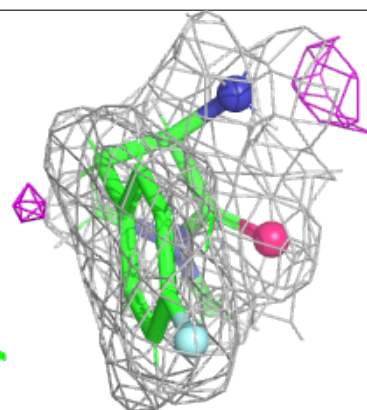
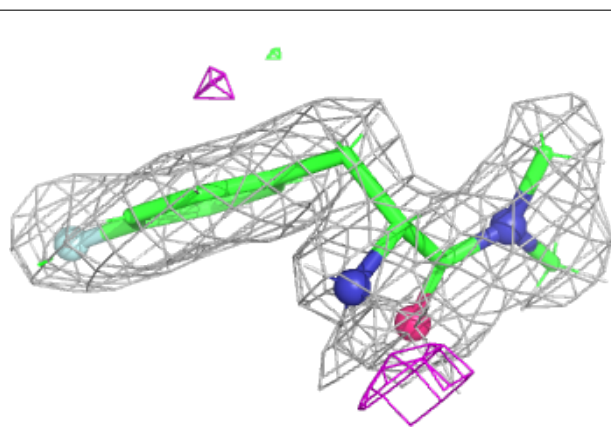
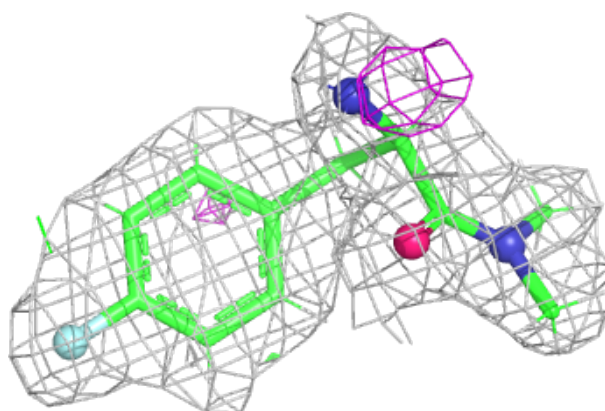


**Electron density around KIZ A 604:**

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

**Electron density around KIZ C 605:**

$2mF_o-DF_c$  (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.