



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:09 PM UTC

PDB ID : 7ZZP / pdb_00007zzp
Title : Structure of HDAC2 complexed with an inhibitory ligand
Authors : Cleasby, A.; Tisi, D.
Deposited on : 2022-05-25
Resolution : 1.52 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

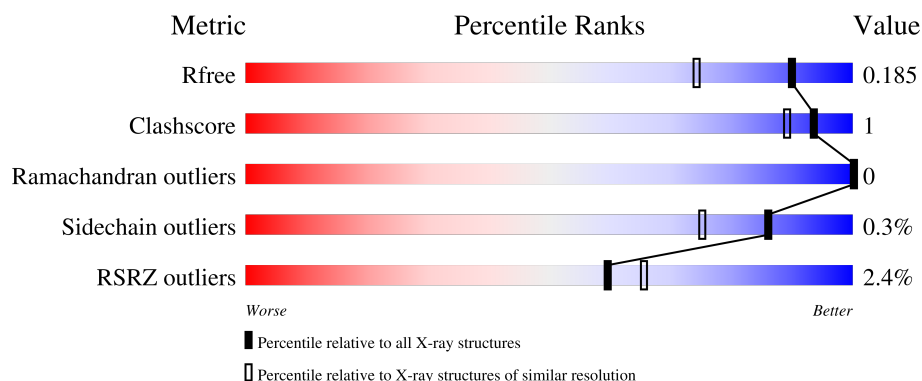
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.52 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	5890 (1.54-1.50)
Clashscore	190562	6116 (1.54-1.50)
Ramachandran outliers	187476	6002 (1.54-1.50)
Sidechain outliers	187428	5999 (1.54-1.50)
RSRZ outliers	180081	5891 (1.54-1.50)

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	498	71% 26%
1	B	498	69% 26%
1	C	498	72% 26%

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 10272 atoms, of which 238 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
1	A	369	Total	C	N	O	S	0	7	0
			3019	1930	509	555	25			
1	B	367	Total	C	N	O	S	0	6	0
			3000	1916	505	553	26			
1	C	367	Total	C	N	O	S	0	2	0
			2974	1899	502	548	25			

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 (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
2	C	1	Total Zn 1 1	0	0

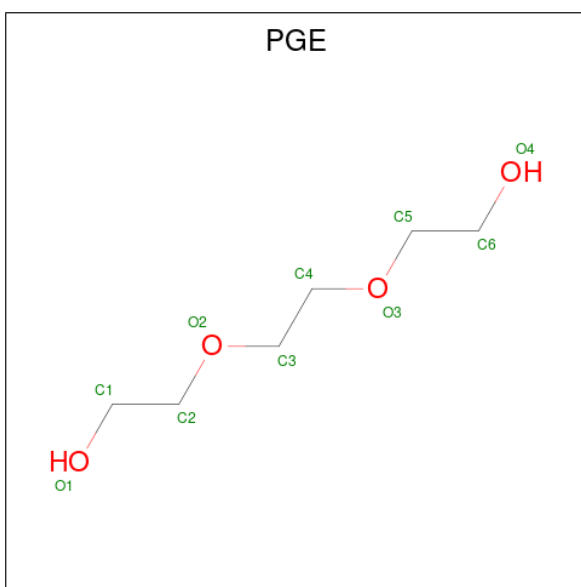
- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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 (CCD ID: NA) (formula: Na).

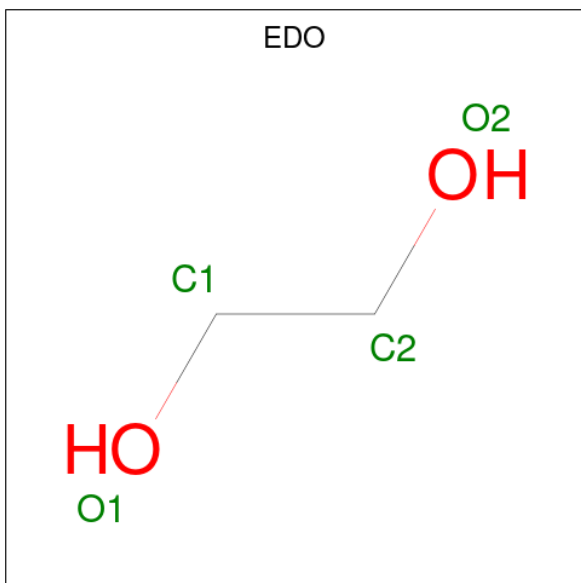
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0

- Molecule 5 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



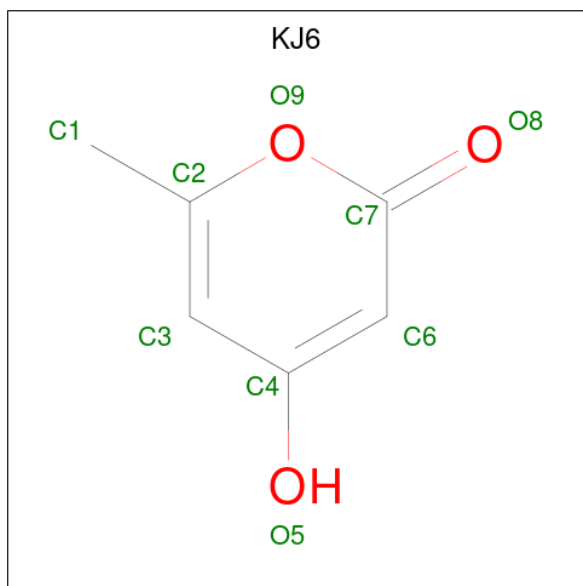
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	1	0
			24	6	14	4		
5	B	1	Total	C	H	O	1	0
			24	6	14	4		
5	B	1	Total	C	H	O	1	0
			24	6	14	4		
5	B	1	Total	C	H	O	1	0
			24	6	14	4		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	1	0
			10	2	6	2		
6	A	1	Total	C	H	O	1	0
			10	2	6	2		
6	A	1	Total	C	H	O	1	0
			10	2	6	2		
6	A	1	Total	C	H	O	1	0
			10	2	6	2		
6	A	1	Total	C	H	O	1	0
			10	2	6	2		
6	B	1	Total	C	H	O	1	0
			10	2	6	2		
6	C	1	Total	C	H	O	1	0
			10	2	6	2		
6	C	1	Total	C	H	O	1	0
			10	2	6	2		

- Molecule 7 is 6-methyl-4-oxidanyl-pyran-2-one (CCD ID: KJ6) (formula: C₆H₆O₃) (labeled as "Ligand of Interest" by depositor).



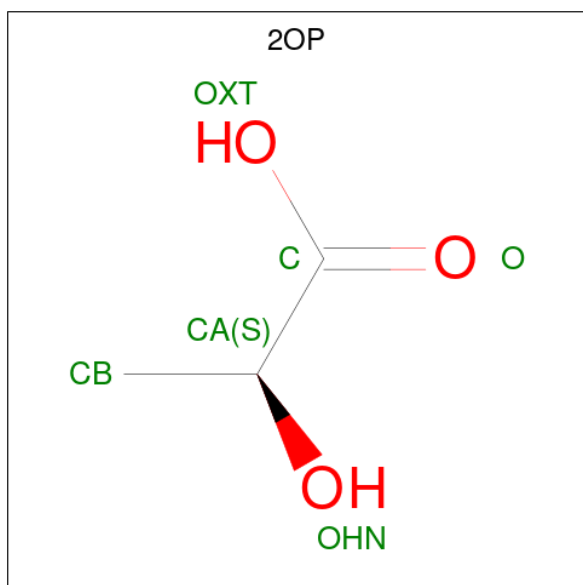
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	1	0
			15	6	6	3		
7	B	1	Total	C	H	O	1	0
			15	6	6	3		

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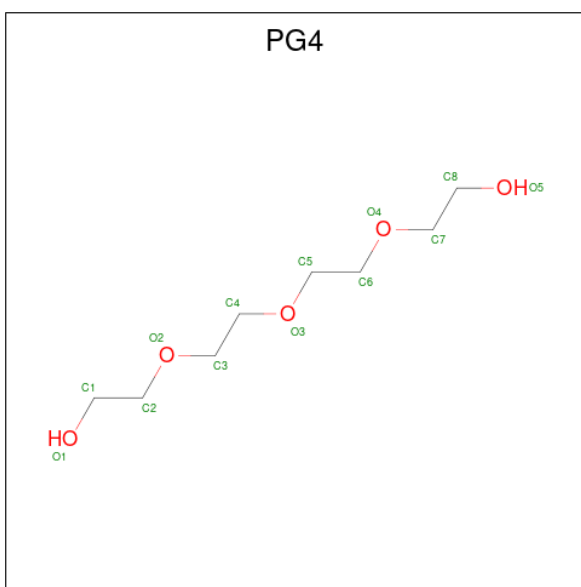
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	H	O	1	0
			15	6	6	3		
7	C	1	Total	C	H	O	1	0
			15	6	6	3		

- Molecule 8 is (2S)-2-HYDROXYPROPANOIC ACID (CCD ID: 2OP) (formula: C₃H₆O₃).



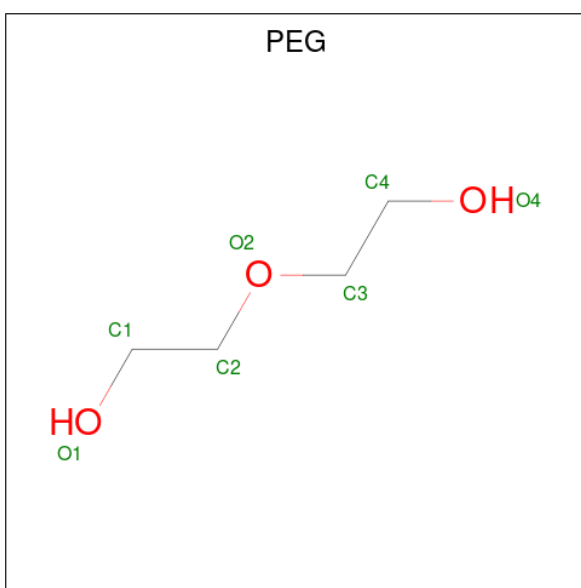
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	H	O	1	0
			11	3	5	3		
8	B	1	Total	C	H	O	1	0
			11	3	5	3		
8	C	1	Total	C	H	O	1	0
			11	3	5	3		

- Molecule 9 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



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

- Molecule 10 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



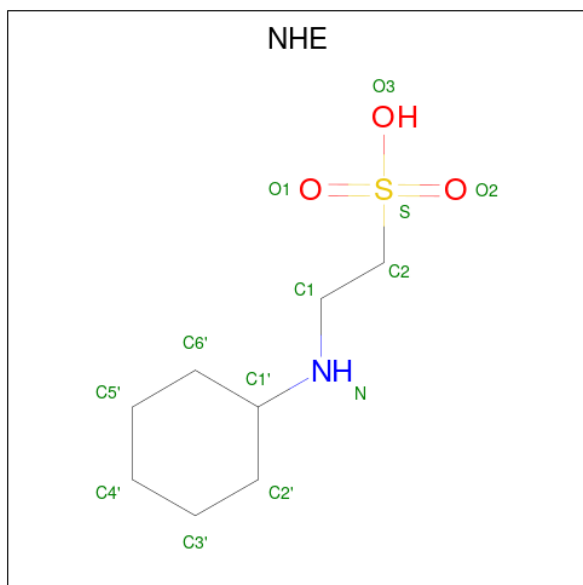
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	1	Total	C	H	O	1	0
			17	4	10	3		
10	B	1	Total	C	H	O	1	0
			17	4	10	3		

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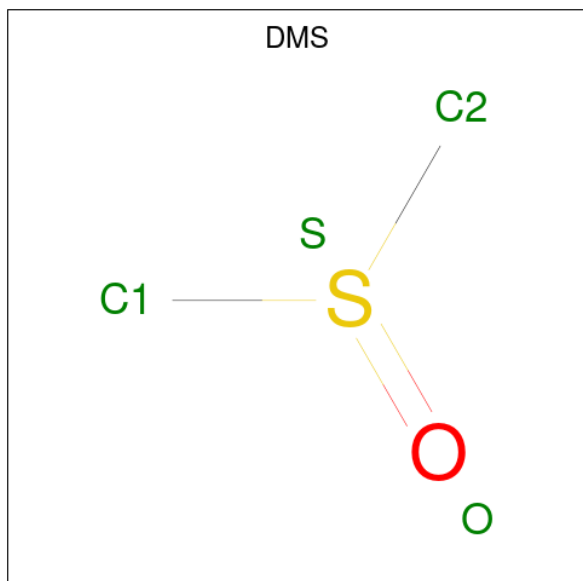
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	C	1	Total	C	H	O	1	0
			17	4	10	3		

- Molecule 11 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (CCD ID: NHE) (formula: $C_8H_{17}NO_3S$).



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

- Molecule 12 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	C	1	Total	C	H	O	S	0	0
			10	2	6	1	1		

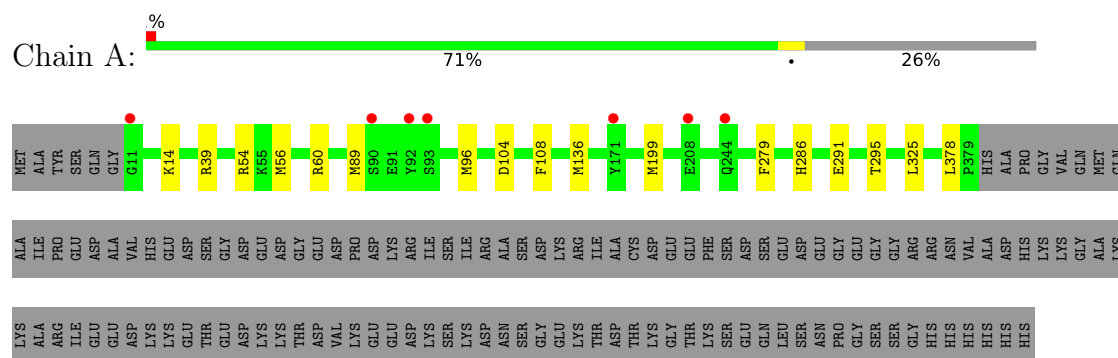
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	302	Total	O	0	0
			302	302		
13	B	343	Total	O	0	0
			343	343		
13	C	193	Total	O	0	0
			193	193		

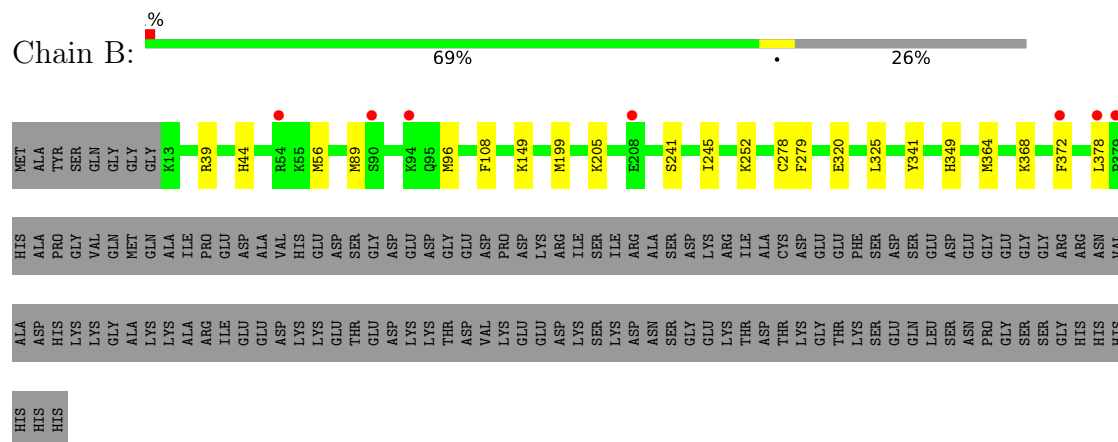
3 Residue-property plots [i](#)

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.

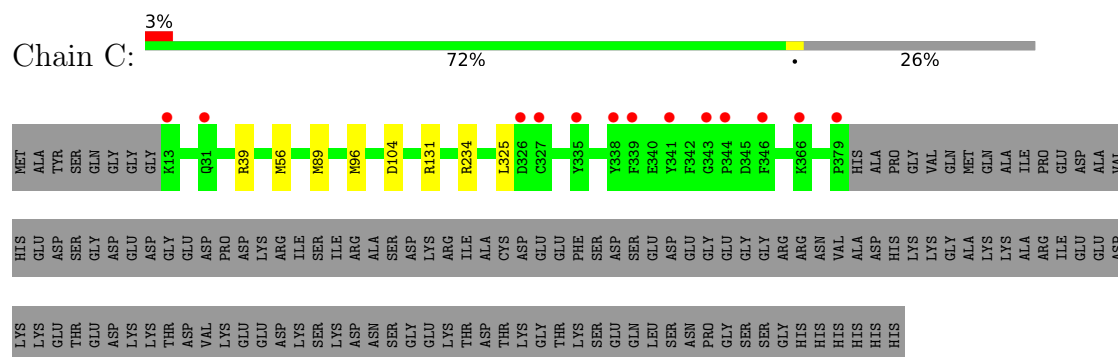
• Molecule 1: Histone deacetylase 2



• Molecule 1: Histone deacetylase 2



• Molecule 1: Histone deacetylase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.25Å 98.85Å 140.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.90 – 1.52 80.89 – 1.52	Depositor EDS
% Data completeness (in resolution range)	100.0 (80.90-1.52) 100.0 (80.89-1.52)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 1.52Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.153 , 0.174 0.168 , 0.185	Depositor DCC
R_{free} test set	9932 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10272	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, PG4, NHE, DMS, PGE, 2OP, KJ6, CA, PEG, ZN, NA

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	0.89	0/3105	0.89	3/4190 (0.1%)
1	B	0.92	0/3080	0.88	4/4158 (0.1%)
1	C	0.81	0/3051	0.82	0/4118
All	All	0.88	0/9236	0.86	7/12466 (0.1%)

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	1
1	C	0	2
All	All	0	6

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	108	PHE	CA-CB-CG	5.69	119.49	113.80
1	A	286	HIS	CA-CB-CG	5.60	119.40	113.80
1	B	320	GLU	CB-CG-CD	5.33	121.67	112.60
1	B	279	PHE	CA-CB-CG	5.25	119.05	113.80
1	A	108	PHE	CA-CB-CG	5.21	119.01	113.80
1	A	279	PHE	CA-CB-CG	5.08	118.88	113.80
1	B	349	HIS	CA-CB-CG	-5.02	108.78	113.80

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	39	ARG	Sidechain
1	A	54	ARG	Sidechain
1	A	60	ARG	Sidechain
1	B	39	ARG	Sidechain
1	C	234	ARG	Sidechain
1	C	39	ARG	Sidechain

5.2 Too-close contacts ⓘ

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	3019	0	2935	9	0
1	B	3000	0	2906	12	0
1	C	2974	0	2880	4	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	10	14	14	0	0
5	B	30	42	42	1	0
6	A	24	36	36	0	0
6	B	4	6	6	0	0
6	C	8	12	12	0	0
7	A	9	6	0	1	0
7	B	18	12	0	0	0
7	C	9	6	0	0	0
8	A	6	5	5	0	0
8	B	6	5	5	0	0
8	C	6	5	5	0	0
9	B	26	36	36	0	0
10	B	14	20	20	0	0
10	C	7	10	10	0	0
11	B	13	17	16	0	0
12	C	4	6	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	A	302	0	0	0	0
13	B	343	0	0	2	0
13	C	193	0	0	0	0
All	All	10034	238	8934	25	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 1.

All (25) 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:89:MET:HE3	1:A:96:MET:HE1	1.51	0.91
1:C:89:MET:HE3	1:C:96:MET:HE1	1.78	0.64
1:B:241:SER:HB3	1:B:364[B]:MET:SD	2.44	0.58
1:A:89:MET:HE3	1:A:96:MET:CE	2.33	0.56
1:B:44:HIS:NE2	5:B:606:PGE:H22	2.21	0.56
1:A:14:LYS:HB2	1:A:136:MET:CE	2.37	0.55
1:A:89:MET:CE	1:A:96:MET:HE1	2.29	0.55
1:B:56:MET:HB3	1:B:325:LEU:HD21	1.87	0.54
1:A:291[A]:GLU:O	1:A:295:THR:HG23	2.07	0.54
1:C:89:MET:HE3	1:C:96:MET:CE	2.38	0.54
1:B:89:MET:HE3	1:B:96:MET:HE1	1.89	0.53
1:C:89:MET:CE	1:C:96:MET:HE1	2.39	0.51
1:A:291[B]:GLU:O	1:A:295:THR:HG23	2.12	0.50
1:A:104:ASP:OD2	7:A:611:KJ6:O5	2.31	0.49
1:A:199:MET:HE1	1:A:378:LEU:HD11	1.95	0.48
1:B:89:MET:CE	1:B:96:MET:HE1	2.44	0.47
1:B:149:LYS:HE3	13:B:846:HOH:O	2.14	0.47
1:B:205:LYS:HD2	1:B:278:CYS:SG	2.57	0.45
1:B:252:LYS:NZ	13:B:709:HOH:O	2.52	0.43
1:B:199:MET:HE1	1:B:378:LEU:HD11	2.00	0.42
1:A:56:MET:HB3	1:A:325:LEU:HD21	2.01	0.41
1:B:245:ILE:HG22	1:B:368:LYS:HE2	2.02	0.41
1:C:56:MET:HB3	1:C:325:LEU:HD21	2.03	0.41
1:B:252:LYS:HE3	1:B:372:PHE:CE2	2.56	0.41
1:B:364[B]:MET:HE2	1:B:364[B]:MET:HB3	1.97	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	374/498 (75%)	370 (99%)	4 (1%)	0	100	100
1	B	371/498 (74%)	366 (99%)	5 (1%)	0	100	100
1	C	367/498 (74%)	363 (99%)	4 (1%)	0	100	100
All	All	1112/1494 (74%)	1099 (99%)	13 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	324/425 (76%)	324 (100%)	0	100	100
1	B	323/425 (76%)	322 (100%)	1 (0%)	86	75
1	C	319/425 (75%)	317 (99%)	2 (1%)	78	61
All	All	966/1275 (76%)	963 (100%)	3 (0%)	86	75

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	341	TYR
1	C	104	ASP
1	C	131	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such

sidechains are listed below:

Mol	Chain	Res	Type
1	C	369	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 36 ligands modelled in this entry, 9 are monoatomic - leaving 27 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	$\# Z > 2$
6	EDO	A	605	-	3,3,3	0.39	0	2,2,2	0.32	0
6	EDO	A	608	-	3,3,3	0.44	0	2,2,2	0.32	0
9	PG4	B	607	-	12,12,12	0.47	0	11,11,11	0.51	0
10	PEG	B	610	-	6,6,6	0.52	0	5,5,5	0.31	0
6	EDO	C	606	-	3,3,3	0.43	0	2,2,2	0.24	0
5	PGE	B	606	-	9,9,9	0.45	0	8,8,8	0.45	0
7	KJ6	B	612	-	8,9,9	0.76	0	10,12,12	0.73	0
6	EDO	B	611	-	3,3,3	0.40	0	2,2,2	0.37	0
7	KJ6	A	611	-	8,9,9	0.70	0	10,12,12	0.72	0
11	NHE	B	614	-	13,13,13	0.55	0	16,17,17	0.44	0
6	EDO	A	609	-	3,3,3	0.45	0	2,2,2	0.36	0
9	PG4	B	608	-	12,12,12	0.48	0	11,11,11	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	KJ6	C	608	-	8,9,9	0.73	0	10,12,12	0.73	0
8	2OP	B	613	2	4,5,5	1.07	0	2,6,6	0.13	0
6	EDO	A	606	-	3,3,3	0.43	0	2,2,2	0.31	0
6	EDO	A	607	-	3,3,3	0.42	0	2,2,2	0.36	0
5	PGE	B	605	-	9,9,9	0.47	0	8,8,8	0.18	0
12	DMS	C	607	-	3,3,3	0.25	0	3,3,3	0.09	0
6	EDO	C	605	-	3,3,3	0.40	0	2,2,2	0.25	0
10	PEG	B	609	-	6,6,6	0.44	0	5,5,5	0.26	0
10	PEG	C	604	-	6,6,6	0.41	0	5,5,5	0.32	0
5	PGE	A	604	-	9,9,9	0.46	0	8,8,8	0.53	0
8	2OP	C	609	2	4,5,5	1.00	0	2,6,6	0.47	0
7	KJ6	B	615	-	8,9,9	0.71	0	10,12,12	0.76	0
8	2OP	A	612	2	4,5,5	0.92	0	2,6,6	0.22	0
5	PGE	B	604	-	9,9,9	0.44	0	8,8,8	0.36	0
6	EDO	A	610	-	3,3,3	0.38	0	2,2,2	0.44	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
6	EDO	A	605	-	-	1/1/1/1	-
6	EDO	A	608	-	-	0/1/1/1	-
9	PG4	B	607	-	-	6/10/10/10	-
10	PEG	B	610	-	-	0/4/4/4	-
6	EDO	C	606	-	-	0/1/1/1	-
5	PGE	B	606	-	-	2/7/7/7	-
7	KJ6	B	612	-	-	-	0/1/1/1
6	EDO	B	611	-	-	0/1/1/1	-
7	KJ6	A	611	-	-	-	0/1/1/1
11	NHE	B	614	-	-	0/7/15/15	0/1/1/1
6	EDO	A	609	-	-	0/1/1/1	-
9	PG4	B	608	-	-	4/10/10/10	-
7	KJ6	C	608	-	-	-	0/1/1/1
8	2OP	B	613	2	-	0/4/4/4	-
6	EDO	A	606	-	-	0/1/1/1	-
6	EDO	A	607	-	-	1/1/1/1	-
5	PGE	B	605	-	-	0/7/7/7	-
6	EDO	C	605	-	-	0/1/1/1	-
10	PEG	B	609	-	-	0/4/4/4	-
10	PEG	C	604	-	-	1/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PGE	A	604	-	-	1/7/7/7	-
8	2OP	C	609	2	-	1/4/4/4	-
7	KJ6	B	615	-	-	-	0/1/1/1
8	2OP	A	612	2	-	2/4/4/4	-
5	PGE	B	604	-	-	0/7/7/7	-
6	EDO	A	610	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	607	PG4	O3-C5-C6-O4
9	B	607	PG4	O4-C7-C8-O5
5	B	606	PGE	O3-C5-C6-O4
9	B	608	PG4	O1-C1-C2-O2
9	B	608	PG4	O3-C5-C6-O4
9	B	607	PG4	O2-C3-C4-O3
9	B	608	PG4	O2-C3-C4-O3
9	B	607	PG4	C5-C6-O4-C7
5	A	604	PGE	C4-C3-O2-C2
9	B	607	PG4	C6-C5-O3-C4
5	B	606	PGE	C6-C5-O3-C4
9	B	608	PG4	C5-C6-O4-C7
8	A	612	2OP	OXT-C-CA-CB
10	C	604	PEG	O2-C3-C4-O4
9	B	607	PG4	C8-C7-O4-C6
6	A	605	EDO	O1-C1-C2-O2
6	A	607	EDO	O1-C1-C2-O2
8	C	609	2OP	OXT-C-CA-CB
6	A	610	EDO	O1-C1-C2-O2
8	A	612	2OP	O-C-CA-CB

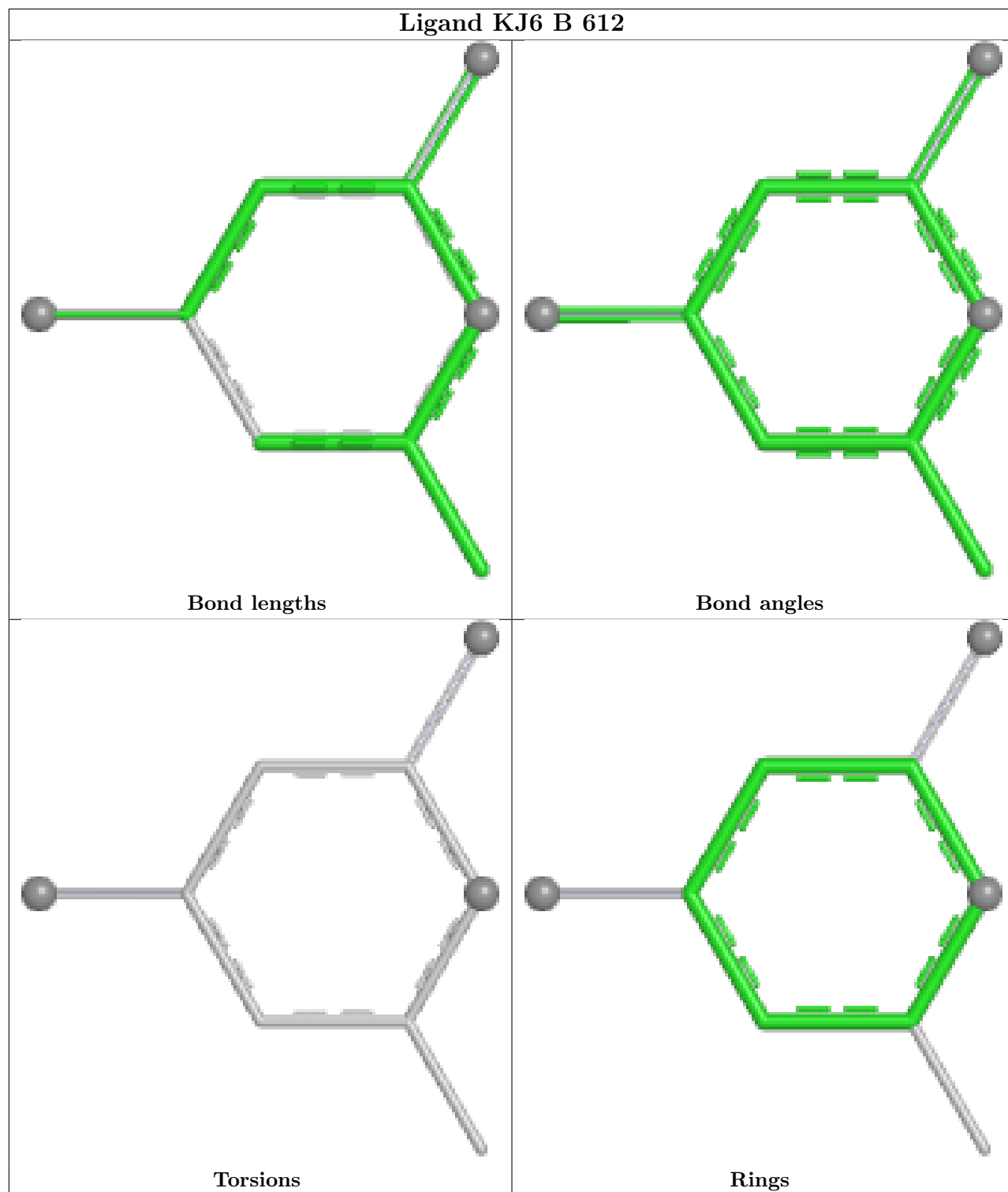
There are no ring outliers.

2 monomers are involved in 2 short contacts:

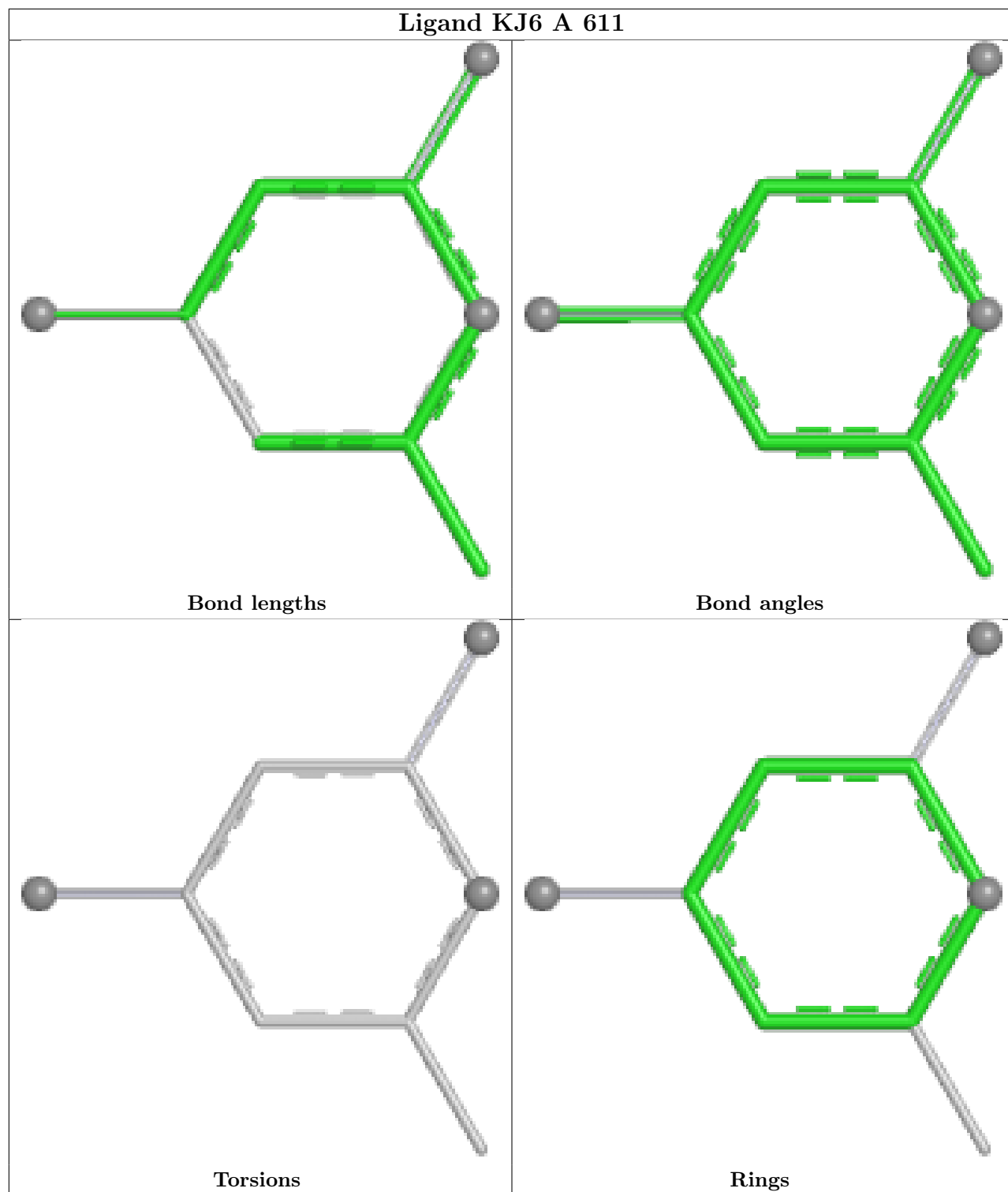
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	606	PGE	1	0
7	A	611	KJ6	1	0

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.

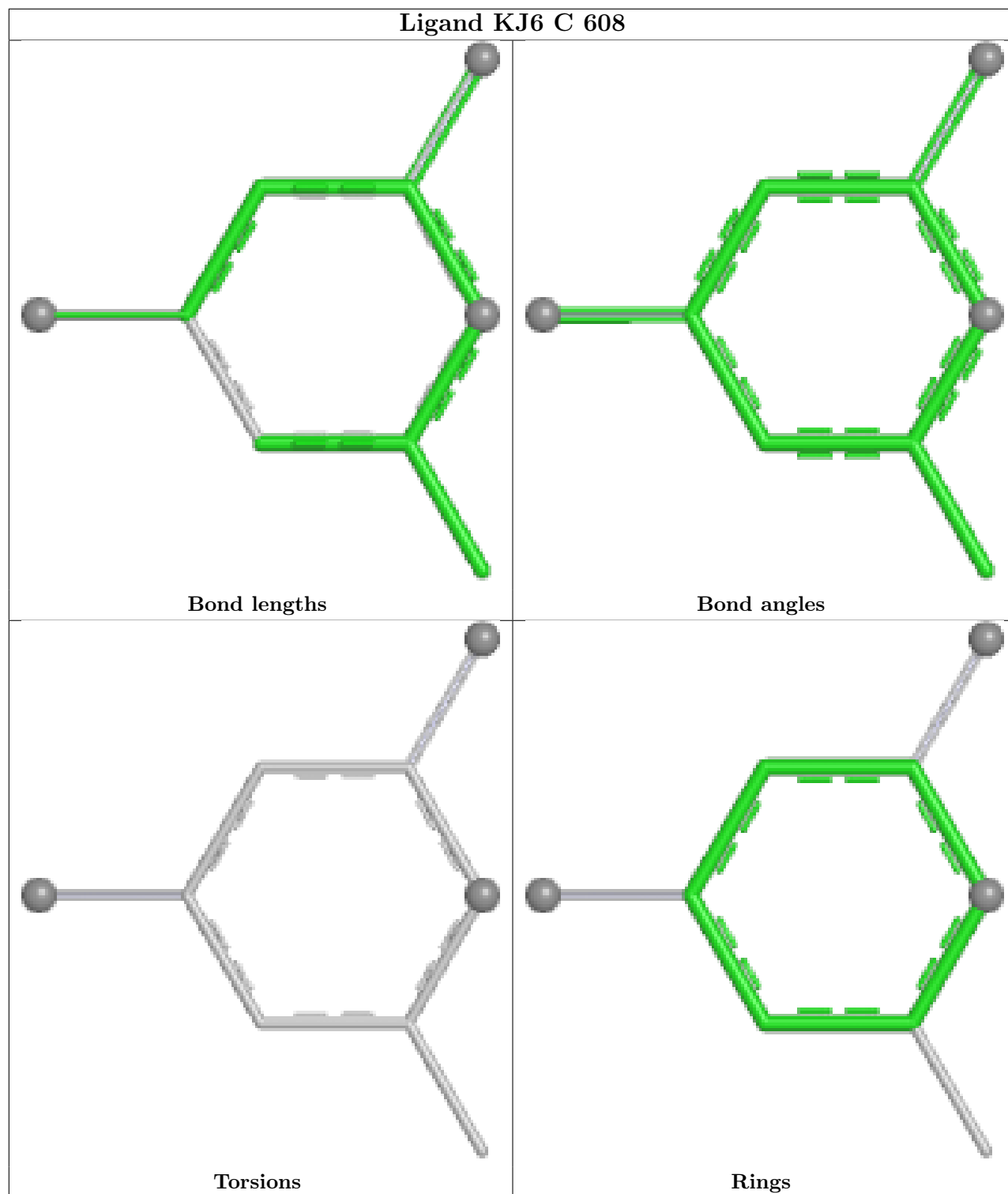
Ligand KJ6 B 612

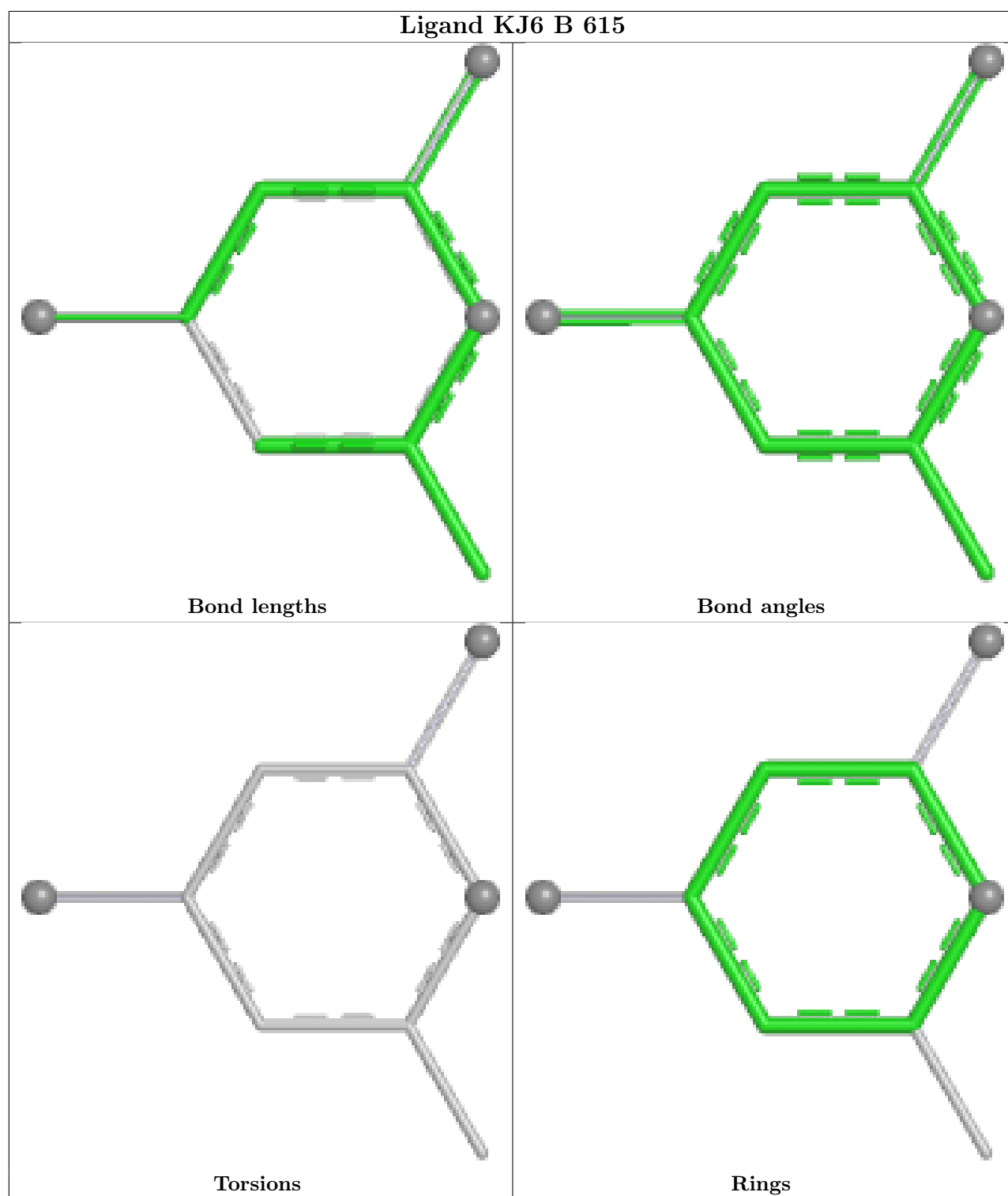


Ligand KJ6 A 611



Ligand KJ6 C 608





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	369/498 (74%)	-0.10	7 (1%) 66 72	6, 17, 33, 54	7 (1%)
1	B	367/498 (73%)	-0.20	7 (1%) 66 72	5, 15, 31, 46	6 (1%)
1	C	367/498 (73%)	0.41	13 (3%) 47 54	8, 25, 45, 68	2 (0%)
All	All	1103/1494 (73%)	0.04	27 (2%) 59 65	5, 18, 39, 68	15 (1%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	11	GLY	3.9
1	C	341	TYR	3.1
1	C	335	TYR	3.1
1	C	344	PRO	3.0
1	A	92	TYR	2.9
1	C	327	CYS	2.8
1	B	208	GLU	2.7
1	C	379	PRO	2.7
1	B	94	LYS	2.6
1	C	366	LYS	2.5
1	B	378	LEU	2.5
1	C	13	LYS	2.5
1	B	54	ARG	2.4
1	C	346	PHE	2.4
1	B	379	PRO	2.3
1	A	90	SER	2.3
1	B	90	SER	2.3
1	C	343	GLY	2.3
1	A	93	SER	2.3
1	A	171	TYR	2.2
1	C	326	ASP	2.2
1	B	372	PHE	2.2
1	C	338	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	208	GLU	2.1
1	C	339	PHE	2.1
1	C	31	GLN	2.1
1	A	244	GLN	2.1

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
6	EDO	A	609	4/4	0.71	0.20	29,49,51,52	1
9	PG4	B	608	13/13	0.72	0.16	29,42,49,50	1
5	PGE	A	604	10/10	0.76	0.16	29,44,49,55	1
7	KJ6	C	608	9/9	0.77	0.20	27,37,46,49	15
6	EDO	A	608	4/4	0.80	0.15	29,41,42,43	1
5	PGE	B	606	10/10	0.81	0.14	29,39,46,48	1
6	EDO	C	606	4/4	0.84	0.13	29,43,45,46	1
6	EDO	A	605	4/4	0.84	0.16	29,43,47,49	1
6	EDO	A	610	4/4	0.84	0.15	29,47,48,51	1
10	PEG	C	604	7/7	0.84	0.15	29,47,57,58	1
6	EDO	B	611	4/4	0.85	0.14	29,35,40,45	1
10	PEG	B	610	7/7	0.86	0.12	28,33,42,42	1
6	EDO	C	605	4/4	0.86	0.15	29,44,50,51	1
7	KJ6	A	611	9/9	0.87	0.14	23,25,38,39	15
10	PEG	B	609	7/7	0.87	0.11	29,40,47,49	1
6	EDO	A	606	4/4	0.87	0.14	29,48,49,50	1
9	PG4	B	607	13/13	0.87	0.14	26,34,39,42	1
12	DMS	C	607	4/4	0.87	0.14	44,47,51,55	0
6	EDO	A	607	4/4	0.88	0.12	29,46,48,55	1

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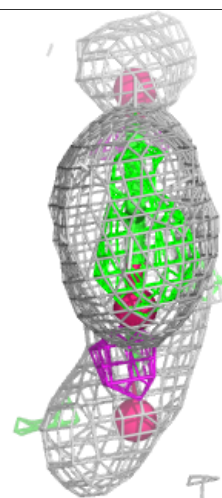
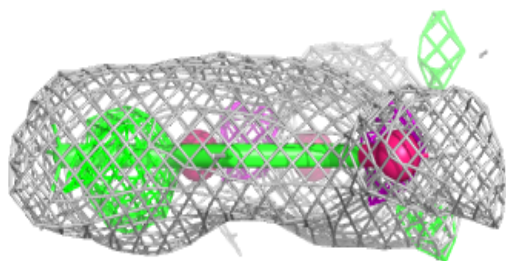
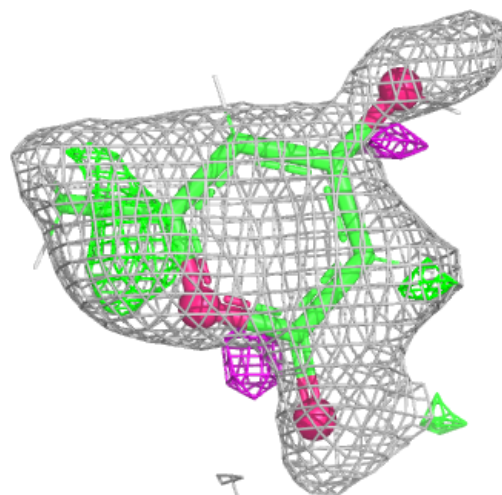
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	KJ6	B	612	9/9	0.90	0.11	16,18,23,26	15
5	PGE	B	605	10/10	0.91	0.10	25,28,36,47	1
5	PGE	B	604	10/10	0.94	0.09	24,26,39,46	1
8	2OP	C	609	6/6	0.95	0.10	14,17,24,26	11
8	2OP	A	612	6/6	0.96	0.10	12,16,22,28	11
8	2OP	B	613	6/6	0.96	0.09	10,13,20,27	11
7	KJ6	B	615	9/9	0.96	0.07	11,12,18,23	15
11	NHE	B	614	13/13	0.97	0.06	12,13,14,15	30
4	NA	A	603	1/1	0.98	0.04	18,18,18,18	0
4	NA	C	603	1/1	0.99	0.08	15,15,15,15	0
4	NA	B	603	1/1	0.99	0.02	16,16,16,16	0
2	ZN	A	601	1/1	1.00	0.01	11,11,11,11	0
2	ZN	B	601	1/1	1.00	0.01	9,9,9,9	0
2	ZN	C	601	1/1	1.00	0.02	16,16,16,16	0
3	CA	A	602	1/1	1.00	0.11	16,16,16,16	0
3	CA	B	602	1/1	1.00	0.11	16,16,16,16	0
3	CA	C	602	1/1	1.00	0.13	22,22,22,22	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.

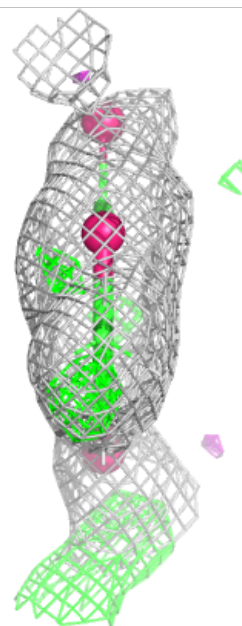
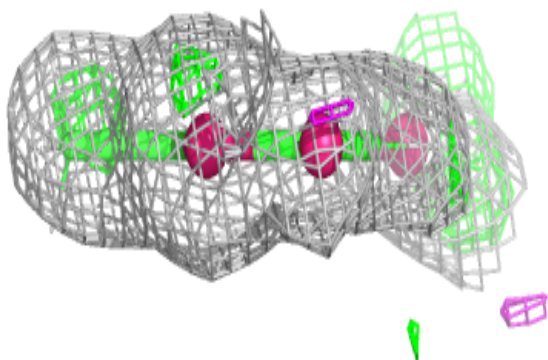
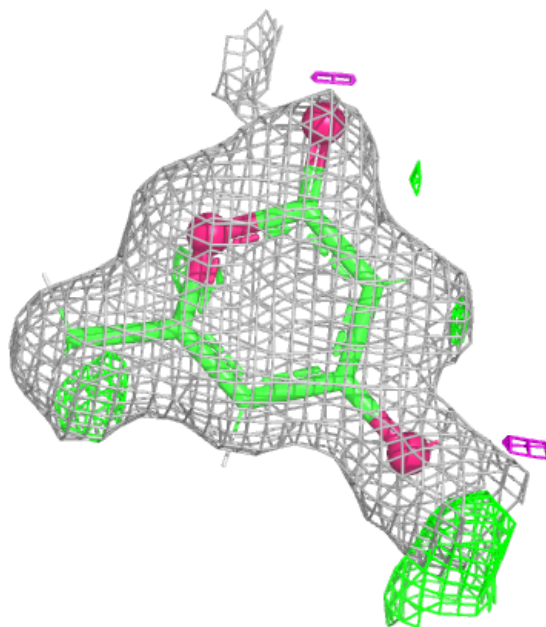
Electron density around KJ6 C 608:

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



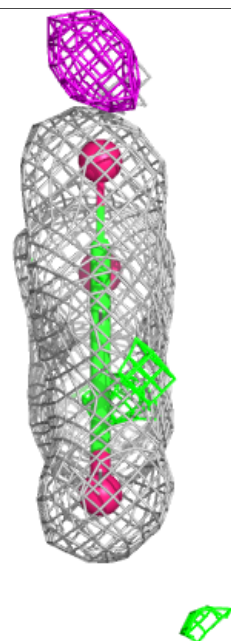
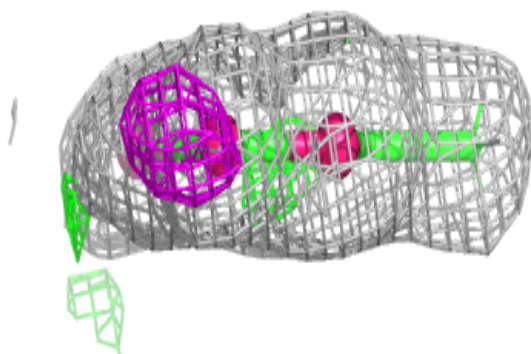
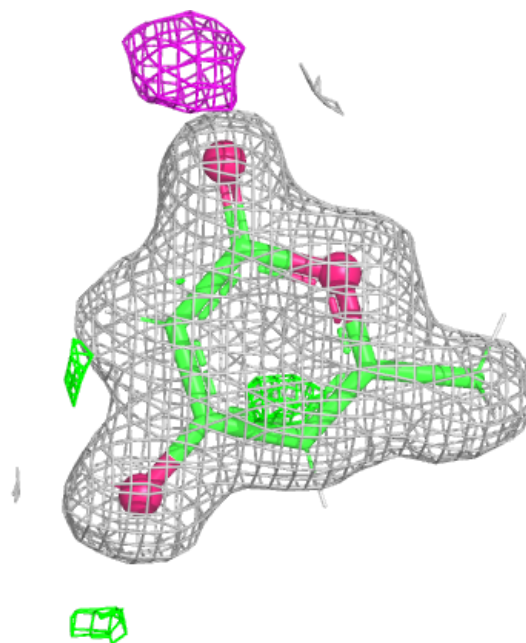
Electron density around KJ6 A 611:

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and green (positive)



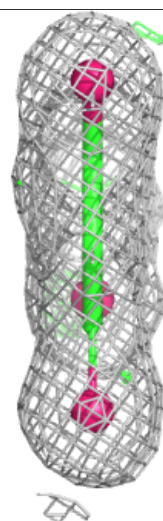
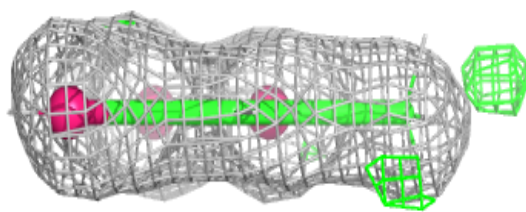
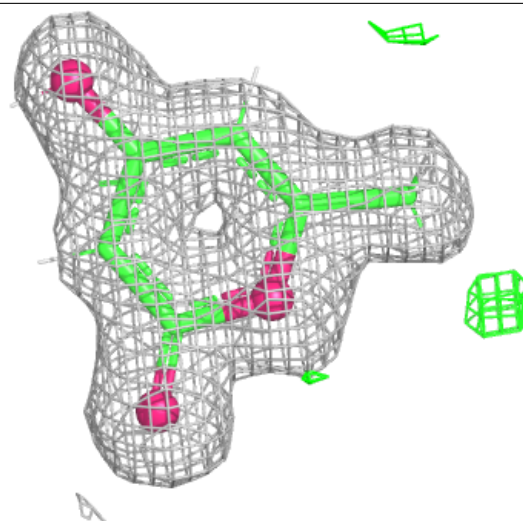
Electron density around KJ6 B 612:

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



Electron density around KJ6 B 615:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.