



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 04:58 am BST

PDB ID : 2WTV
Title : Aurora-A Inhibitor Structure
Authors : Kosmopoulou, M.; Bayliss, R.
Deposited on : 2009-09-22
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

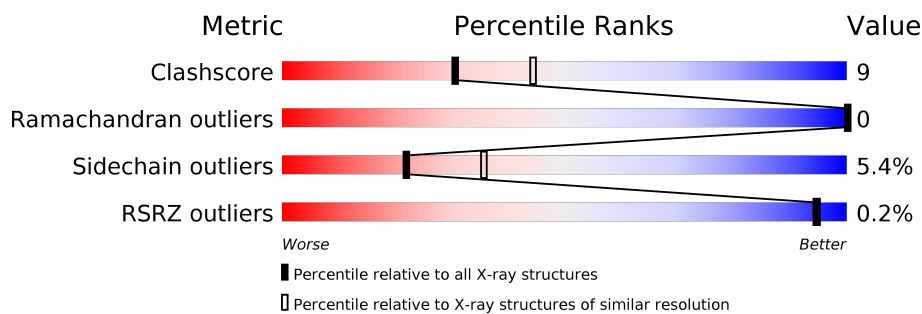
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 on 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	285	
1	B	285	
1	C	285	
1	D	285	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	TPO	A	287	X	-	-	-
1	TPO	B	287	X	-	-	-
1	TPO	C	287	X	-	-	-
1	TPO	D	287	X	-	-	-
3	EDO	B	1399	-	-	X	-
4	ACT	C	1393	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9657 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.

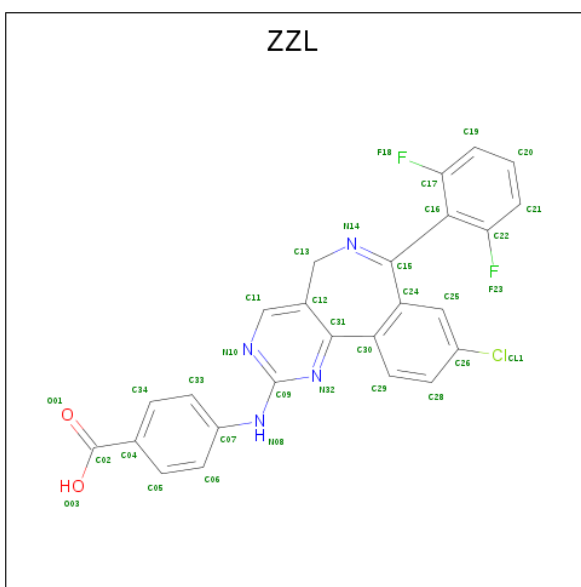
- Molecule 1 is a protein called SERINE/THREONINE-PROTEIN KINASE 6 AURORA/IPL1-RELATED KINASE 1, BREAST TUMOR-AMPLIFIED KINASE, AURORA-A, AURORA-RELATED KINASE 1, HARK1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	P	S	0	1	0
			2190	1400	385	396	2	7			
1	B	264	Total	C	N	O	P	S	0	0	0
			2158	1383	375	391	2	7			
1	C	264	Total	C	N	O	P	S	0	1	0
			2170	1390	376	395	2	7			
1	D	265	Total	C	N	O	P	S	0	0	0
			2172	1390	378	395	2	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	215	ARG	LEU	engineered mutation	UNP O14965
A	217	GLU	THR	engineered mutation	UNP O14965
A	220	LYS	ARG	engineered mutation	UNP O14965
B	215	ARG	LEU	engineered mutation	UNP O14965
B	217	GLU	THR	engineered mutation	UNP O14965
B	220	LYS	ARG	engineered mutation	UNP O14965
C	215	ARG	LEU	engineered mutation	UNP O14965
C	217	GLU	THR	engineered mutation	UNP O14965
C	220	LYS	ARG	engineered mutation	UNP O14965
D	215	ARG	LEU	engineered mutation	UNP O14965
D	217	GLU	THR	engineered mutation	UNP O14965
D	220	LYS	ARG	engineered mutation	UNP O14965

- Molecule 2 is 4-{[9-CHLORO-7-(2,6-DIFLUOROPHENYL)-5H-PYRIMIDO[5,4-D][2]BENZAZEPIN-2-YL]AMINO}BENZOIC ACID (three-letter code: ZZL) (formula: C₂₅H₁₅ClF₂N₄O₂).



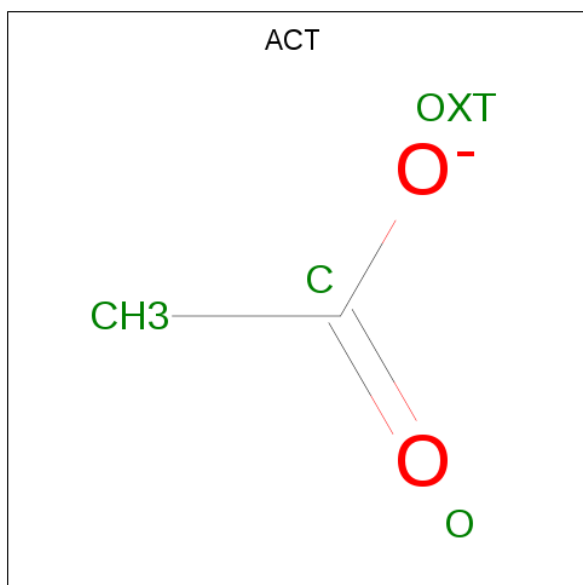
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 34	C 25	Cl 1	F 2	N 4	O 2	0	0
2	B	1	Total 34	C 25	Cl 1	F 2	N 4	O 2	0	0
2	C	1	Total 34	C 25	Cl 1	F 2	N 4	O 2	0	0
2	D	1	Total 34	C 25	Cl 1	F 2	N 4	O 2	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



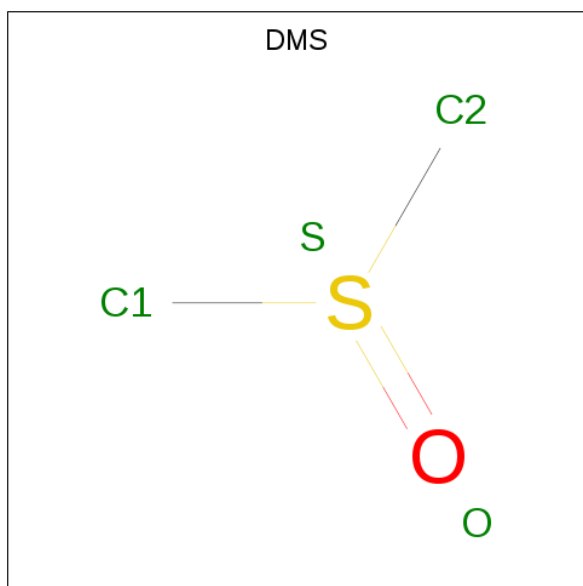
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0

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

- Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	S	0	0
			4	2	1	1		
5	B	1	Total	C	O	S	0	0
			4	2	1	1		

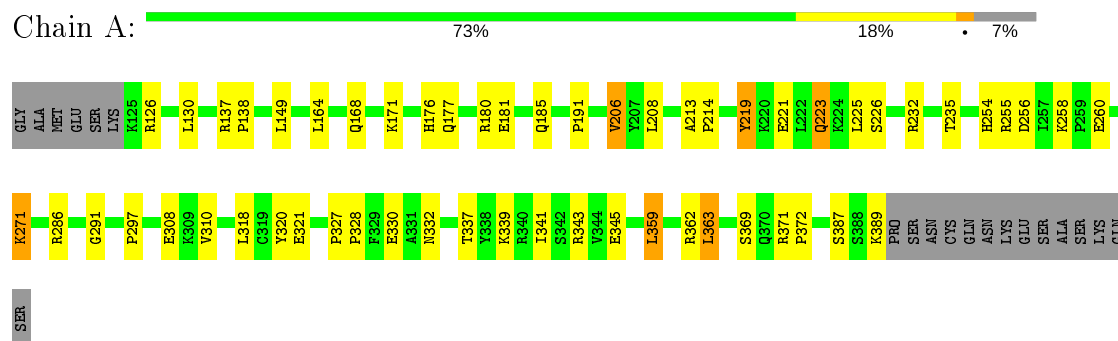
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	165	Total 165	O 165	0	0
6	B	197	Total 197	O 197	0	0
6	C	197	Total 197	O 197	0	0
6	D	184	Total 184	O 184	0	0

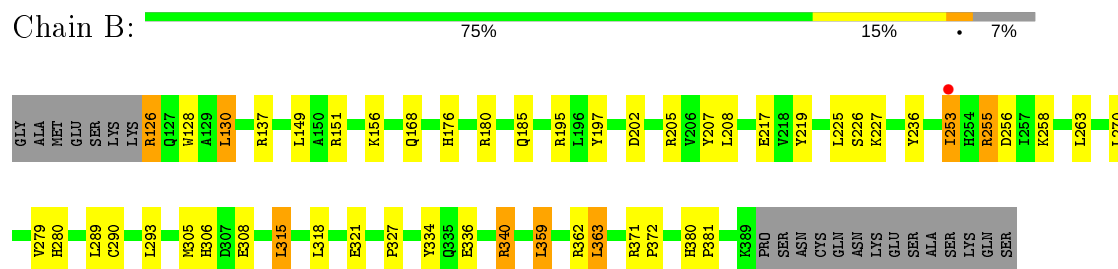
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

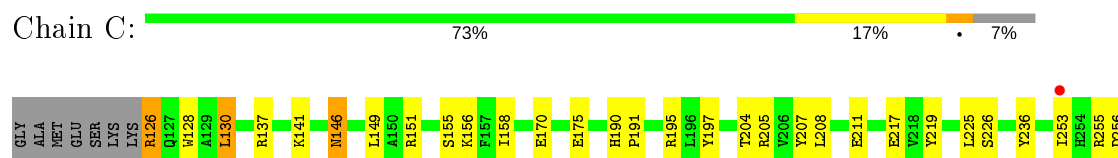
- Molecule 1: SERINE/THREONINE-PROTEIN KINASE 6 AURORA/IPL1-RELATED KINASE 1, BREAST TUMOR-AMPLIFIED KINASE, AURORA-A, AURORA-RELATED KINASE 1, HARK1

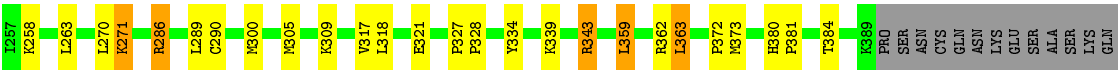


- Molecule 1: SERINE/THREONINE-PROTEIN KINASE 6 AURORA/IPL1-RELATED KINASE 1, BREAST TUMOR-AMPLIFIED KINASE, AURORA-A, AURORA-RELATED KINASE 1, HARK1



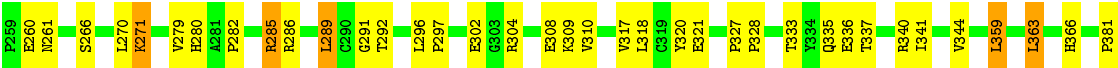
- Molecule 1: SERINE/THREONINE-PROTEIN KINASE 6 AURORA/IPL1-RELATED KINASE 1, BREAST TUMOR-AMPLIFIED KINASE, AURORA-A, AURORA-RELATED KINASE 1, HARK1





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- Molecule 1: SERINE/THREONINE-PROTEIN KINASE 6 AURORA/IPL1-RELATED KINASE 1, BREAST TUMOR-AMPLIFIED KINASE, AURORA-A, AURORA-RELATED KINASE 1, HARK1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	118.71Å 118.71Å 135.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.78 – 2.40 56.68 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.7 (19.78-2.40) 99.5 (56.68-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.40Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.164 , 0.211 0.164 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.626	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 35.1	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 0.479 for h,-h-k,-l 0.018 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9657	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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: DMS, TPO, CME, EDO, ZZL, ACT

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	0.33	0/2211	0.50	0/2984
1	B	0.42	1/2178 (0.0%)	0.50	1/2941 (0.0%)
1	C	0.43	1/2190 (0.0%)	0.51	1/2956 (0.0%)
1	D	0.33	0/2192	0.51	0/2960
All	All	0.38	2/8771 (0.0%)	0.51	2/11841 (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	1	0
1	B	1	0
1	C	1	0
1	D	1	0
All	All	4	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	126	ARG	NE-CZ	13.07	1.50	1.33
1	B	126	ARG	NE-CZ	12.99	1.50	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	126	ARG	CD-NE-CZ	-9.38	110.46	123.60
1	C	126	ARG	CD-NE-CZ	-7.96	112.45	123.60

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	287	TPO	CB
1	B	287	TPO	CB
1	C	287	TPO	CB
1	D	287	TPO	CB

There are no planarity outliers.

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	2190	0	2171	33	0
1	B	2158	0	2133	45	0
1	C	2170	0	2142	42	0
1	D	2172	0	2147	43	0
2	A	34	0	15	0	0
2	B	34	0	15	1	0
2	C	34	0	15	0	0
2	D	34	0	15	0	0
3	A	4	0	6	1	0
3	B	24	0	36	7	0
3	C	12	0	18	2	0
3	D	4	0	6	0	0
4	A	8	0	6	0	0
4	B	12	0	9	0	0
4	C	8	0	6	3	0
4	D	8	0	6	1	0
5	A	4	0	6	0	0
5	B	4	0	6	0	0
6	A	165	0	0	3	0
6	B	197	0	0	6	0
6	C	197	0	0	5	0
6	D	184	0	0	5	0
All	All	9657	0	8758	163	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 9.

The worst 5 of 163 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:340:ARG:HG3	1:B:340:ARG:HH21	0.94	1.03
1:D:286:ARG:HD3	1:D:291:GLY:HA2	1.40	1.02
1:B:340:ARG:HG3	1:B:340:ARG:NH2	1.67	1.00
1:A:286:ARG:HD3	1:A:291:GLY:HA2	1.46	0.93
1:B:340:ARG:CG	1:B:340:ARG:HH21	1.82	0.90

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	261/285 (92%)	253 (97%)	8 (3%)	0	100	100
1	B	259/285 (91%)	254 (98%)	5 (2%)	0	100	100
1	C	260/285 (91%)	253 (97%)	7 (3%)	0	100	100
1	D	260/285 (91%)	254 (98%)	6 (2%)	0	100	100
All	All	1040/1140 (91%)	1014 (98%)	26 (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	229/248 (92%)	215 (94%)	14 (6%)	18	30
1	B	225/248 (91%)	215 (96%)	10 (4%)	28	45
1	C	226/248 (91%)	215 (95%)	11 (5%)	25	40
1	D	226/248 (91%)	212 (94%)	14 (6%)	18	29
All	All	906/992 (91%)	857 (95%)	49 (5%)	22	36

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	359	LEU
1	C	208	LEU
1	D	318	LEU
1	C	130	LEU
1	C	253	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	223	GLN
1	B	231	GLN
1	C	231	GLN
1	D	223	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

12 non-standard protein/DNA/RNA residues are modelled in this entry.

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
1	CME	B	290	1	8,9,10	0.83	0	5,9,11	0.90	0
1	CME	D	290	1	8,9,10	0.81	0	5,9,11	1.14	0
1	TPO	B	288	1	8,10,11	0.87	0	10,14,16	0.92	0
1	TPO	A	287	1	8,10,11	0.71	0	10,14,16	1.44	0
1	TPO	C	287	1	8,10,11	0.81	0	10,14,16	1.26	1 (10%)
1	TPO	B	287	1	8,10,11	0.82	0	10,14,16	1.31	1 (10%)
1	TPO	D	288	1	8,10,11	0.73	0	10,14,16	1.23	1 (10%)
1	TPO	C	288	1	8,10,11	0.92	0	10,14,16	0.81	0
1	TPO	D	287	1	8,10,11	0.67	0	10,14,16	1.40	0
1	TPO	A	288	1	8,10,11	0.77	0	10,14,16	1.21	0
1	CME	C	290	1	8,9,10	0.81	0	5,9,11	0.82	0
1	CME	A	290	1	8,9,10	0.82	0	5,9,11	1.27	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
1	CME	B	290	1	-	2/5/8/10	-
1	CME	D	290	1	-	2/5/8/10	-
1	TPO	B	288	1	-	1/9/11/13	-
1	TPO	A	287	1	1/1/3/4	4/9/11/13	-
1	TPO	C	287	1	1/1/3/4	4/9/11/13	-
1	TPO	B	287	1	1/1/3/4	6/9/11/13	-
1	TPO	D	288	1	-	3/9/11/13	-
1	TPO	C	288	1	-	1/9/11/13	-
1	TPO	D	287	1	1/1/3/4	4/9/11/13	-
1	TPO	A	288	1	-	1/9/11/13	-
1	CME	C	290	1	-	1/5/8/10	-
1	CME	A	290	1	-	1/5/8/10	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	288	TPO	O3P-P-O2P	2.49	117.14	107.64
1	B	287	TPO	CG2-CB-CA	-2.18	108.86	113.16
1	C	287	TPO	CB-CA-N	-2.04	101.02	114.41

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	287	TPO	CB
1	C	287	TPO	CB
1	B	287	TPO	CB
1	D	287	TPO	CB

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	288	TPO	N-CA-CB-OG1
1	A	287	TPO	N-CA-CB-OG1
1	A	287	TPO	C-CA-CB-CG2
1	A	287	TPO	O-C-CA-CB
1	C	287	TPO	N-CA-CB-CG2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	290	CME	1	0
1	C	290	CME	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

26 ligands are modelled in this entry.

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	DMS	B	1391	-	3,3,3	0.78	0	3,3,3	1.58	1 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	1398	-	3,3,3	0.46	0	2,2,2	0.80	0
2	ZZL	A	1390	-	34,38,38	1.83	5 (14%)	44,55,55	2.43	13 (29%)
4	ACT	C	1393	-	1,3,3	3.64	1 (100%)	0,3,3	0.00	-
3	EDO	A	1391	-	3,3,3	0.49	0	2,2,2	0.71	0
3	EDO	C	1395	-	3,3,3	0.48	0	2,2,2	0.76	0
4	ACT	B	1393	-	1,3,3	3.82	1 (100%)	0,3,3	0.00	-
4	ACT	A	1392	-	1,3,3	3.68	1 (100%)	0,3,3	0.00	-
5	DMS	A	1394	-	3,3,3	0.78	0	3,3,3	1.52	1 (33%)
2	ZZL	D	1390	-	34,38,38	1.91	7 (20%)	44,55,55	2.32	12 (27%)
4	ACT	C	1394	-	1,3,3	3.75	1 (100%)	0,3,3	0.00	-
3	EDO	B	1395	-	3,3,3	0.47	0	2,2,2	0.69	0
4	ACT	B	1392	-	1,3,3	3.86	1 (100%)	0,3,3	0.00	-
3	EDO	C	1390	-	3,3,3	0.50	0	2,2,2	0.78	0
3	EDO	D	1391	-	3,3,3	0.48	0	2,2,2	0.76	0
4	ACT	D	1393	-	1,3,3	4.00	1 (100%)	0,3,3	0.00	-
4	ACT	B	1400	-	1,3,3	3.66	1 (100%)	0,3,3	0.00	-
3	EDO	B	1397	-	3,3,3	0.48	0	2,2,2	1.01	0
3	EDO	C	1391	-	3,3,3	0.49	0	2,2,2	0.75	0
4	ACT	D	1392	-	1,3,3	3.42	1 (100%)	0,3,3	0.00	-
2	ZZL	C	1392	-	34,38,38	1.96	7 (20%)	44,55,55	2.45	12 (27%)
3	EDO	B	1396	-	3,3,3	0.49	0	2,2,2	0.67	0
2	ZZL	B	1390	-	34,38,38	1.87	7 (20%)	44,55,55	2.44	11 (25%)
3	EDO	B	1399	-	3,3,3	0.51	0	2,2,2	0.67	0
4	ACT	A	1393	-	1,3,3	4.07	1 (100%)	0,3,3	0.00	-
3	EDO	B	1394	-	3,3,3	0.48	0	2,2,2	0.73	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	1391	-	-	0/1/1/1	-
3	EDO	B	1398	-	-	1/1/1/1	-
3	EDO	C	1390	-	-	1/1/1/1	-
3	EDO	C	1395	-	-	0/1/1/1	-
3	EDO	D	1391	-	-	1/1/1/1	-
3	EDO	B	1396	-	-	1/1/1/1	-
2	ZZL	D	1390	-	-	2/8/25/25	0/4/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ZZL	B	1390	-	-	2/8/25/25	0/4/5/5
2	ZZL	A	1390	-	-	2/8/25/25	0/4/5/5
3	EDO	B	1397	-	-	1/1/1/1	-
3	EDO	B	1399	-	-	1/1/1/1	-
2	ZZL	C	1392	-	-	2/8/25/25	0/4/5/5
3	EDO	B	1394	-	-	1/1/1/1	-
3	EDO	A	1391	-	-	0/1/1/1	-
3	EDO	B	1395	-	-	1/1/1/1	-

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1390	ZZL	C30-C31	-6.03	1.41	1.49
2	A	1390	ZZL	C30-C31	-5.78	1.42	1.49
2	C	1392	ZZL	C30-C31	-5.78	1.42	1.49
2	B	1390	ZZL	C30-C31	-5.32	1.42	1.49
2	C	1392	ZZL	C04-C02	5.22	1.52	1.47

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1390	ZZL	C13-N14-C15	9.98	128.80	117.48
2	C	1392	ZZL	C13-N14-C15	9.87	128.68	117.48
2	A	1390	ZZL	C13-N14-C15	9.07	127.77	117.48
2	D	1390	ZZL	C13-N14-C15	8.04	126.60	117.48
2	A	1390	ZZL	C24-C15-C16	-7.06	109.91	118.10

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

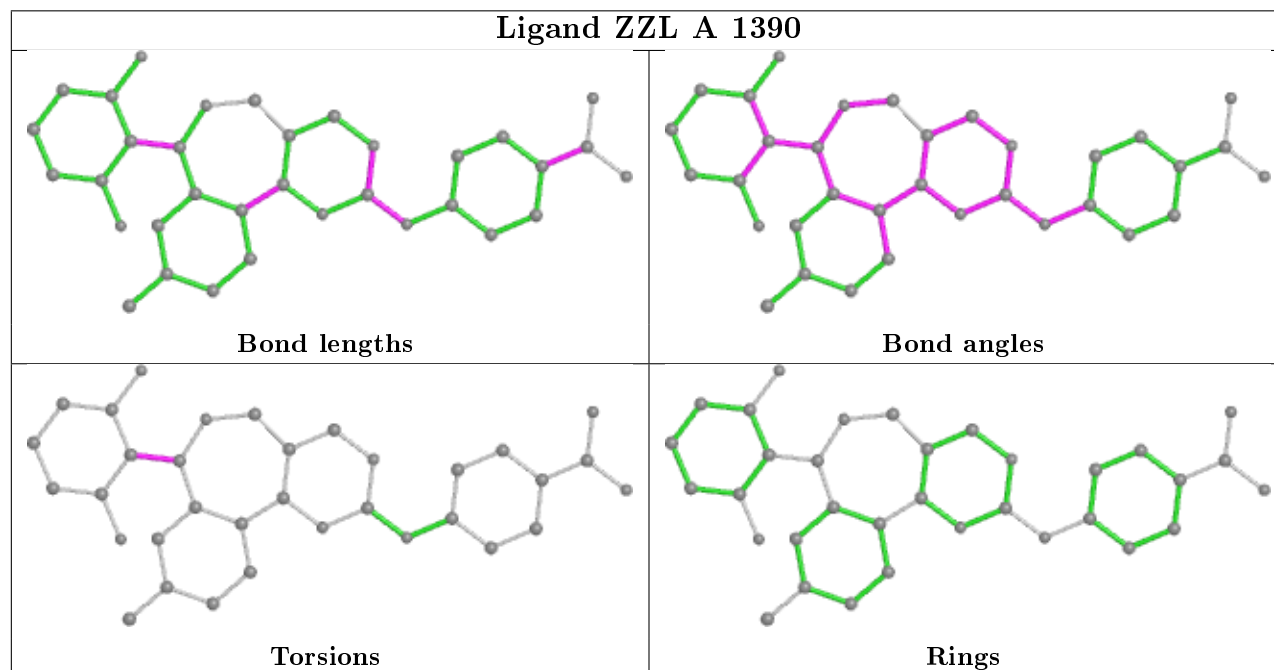
Mol	Chain	Res	Type	Atoms
3	B	1398	EDO	O1-C1-C2-O2
3	D	1391	EDO	O1-C1-C2-O2
3	C	1390	EDO	O1-C1-C2-O2
3	B	1399	EDO	O1-C1-C2-O2
3	B	1394	EDO	O1-C1-C2-O2

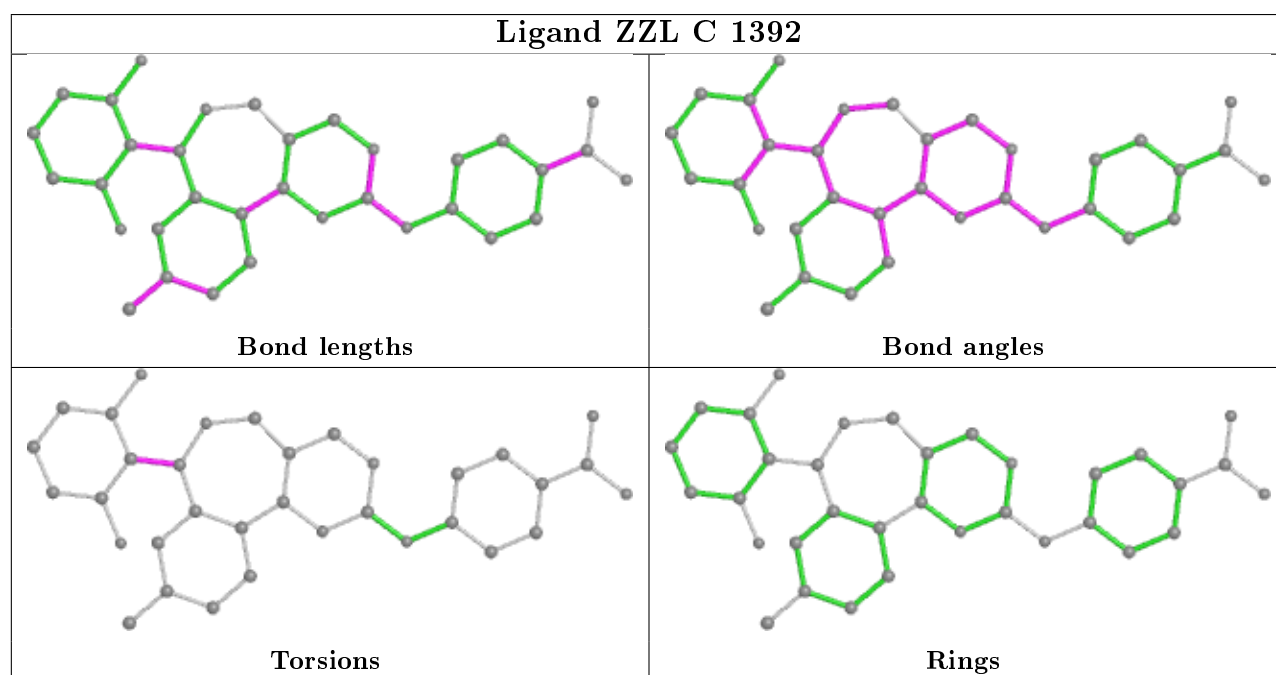
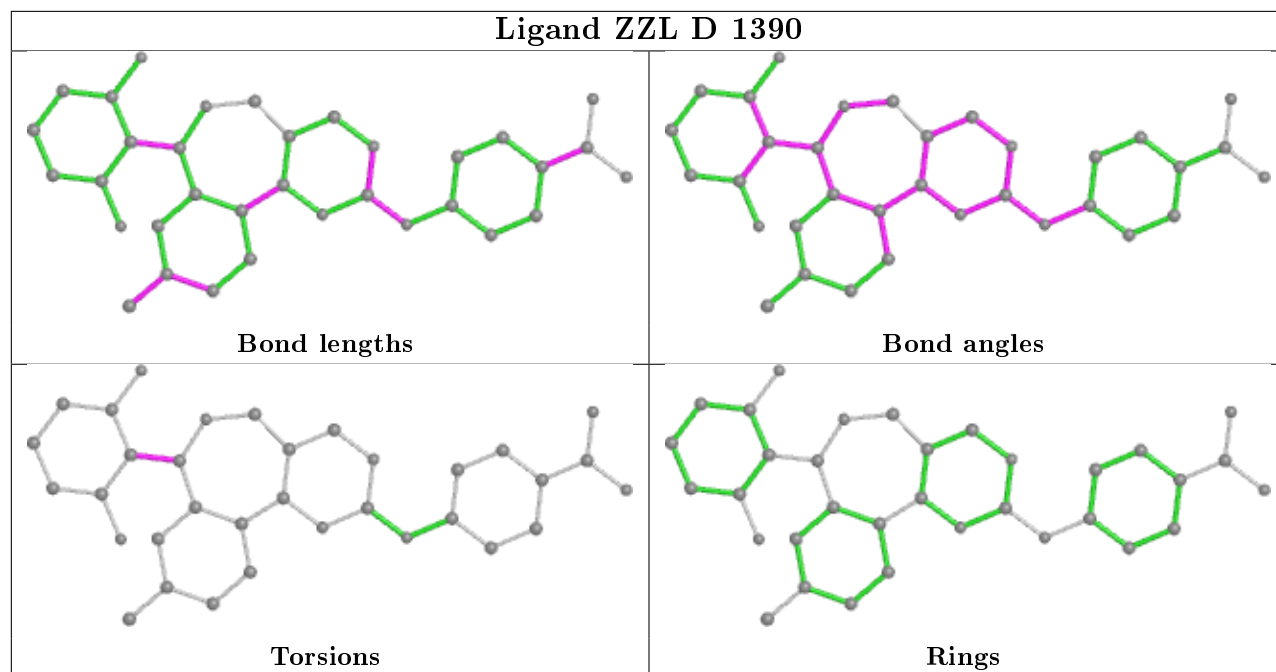
There are no ring outliers.

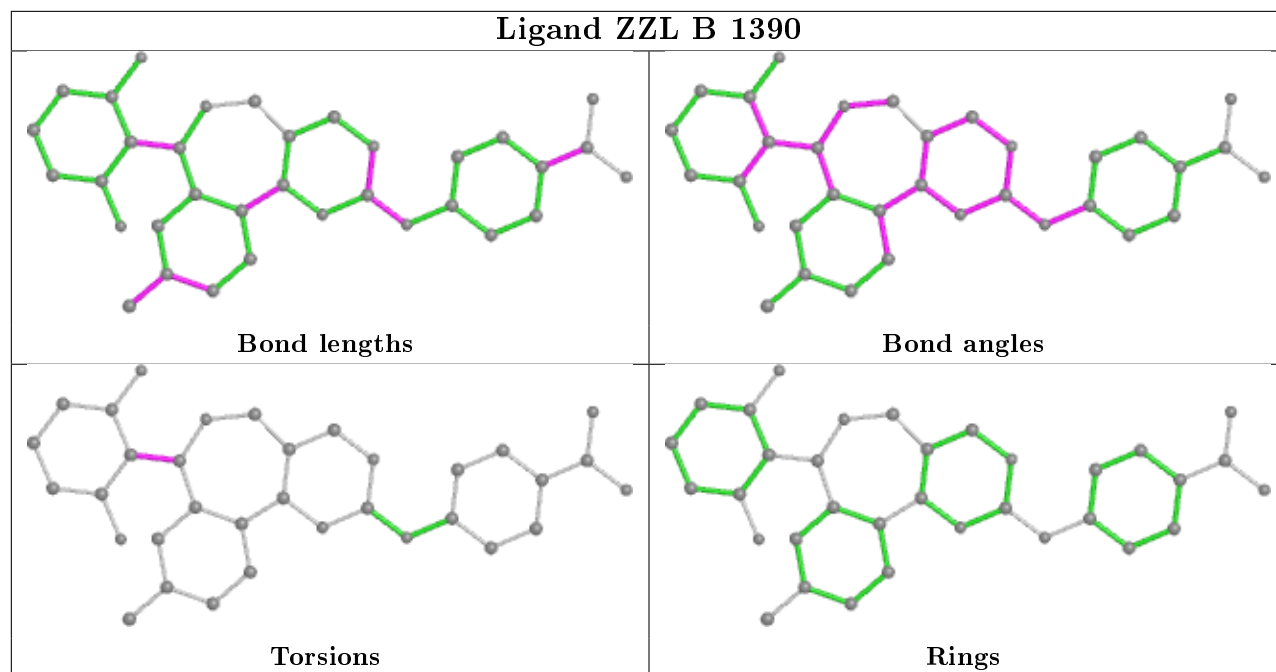
9 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1398	EDO	1	0
4	C	1393	ACT	3	0
3	A	1391	EDO	1	0
3	C	1390	EDO	2	0
3	B	1397	EDO	1	0
4	D	1392	ACT	1	0
2	B	1390	ZZL	1	0
3	B	1399	EDO	5	0
3	B	1394	EDO	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, 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	262/285 (91%)	-0.56	0 100 100	15, 27, 51, 69	0
1	B	261/285 (91%)	-0.55	1 (0%) 92 91	16, 27, 49, 71	0
1	C	261/285 (91%)	-0.58	1 (0%) 92 91	16, 27, 50, 72	0
1	D	262/285 (91%)	-0.54	0 100 100	13, 28, 50, 68	0
All	All	1046/1140 (91%)	-0.56	2 (0%) 95 94	13, 27, 51, 72	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	253	ILE	2.3
1	C	253	ILE	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CME	A	290	10/11	0.95	0.09	27,42,65,67	0
1	TPO	A	287	11/12	0.96	0.14	34,47,68,71	0
1	TPO	C	287	11/12	0.96	0.13	21,32,60,61	0
1	CME	D	290	10/11	0.96	0.11	31,40,69,70	0
1	TPO	D	287	11/12	0.97	0.11	37,48,67,69	0
1	TPO	D	288	11/12	0.98	0.12	32,39,48,52	0
1	CME	B	290	10/11	0.98	0.09	15,25,30,37	0
1	TPO	A	288	11/12	0.98	0.13	29,37,48,53	0
1	CME	C	290	10/11	0.98	0.10	18,25,30,34	0
1	TPO	B	287	11/12	0.98	0.13	20,25,61,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	TPO	B	288	11/12	0.99	0.11	14,22,23,24	0
1	TPO	C	288	11/12	0.99	0.13	16,20,27,28	0

6.3 Carbohydrates [i](#)

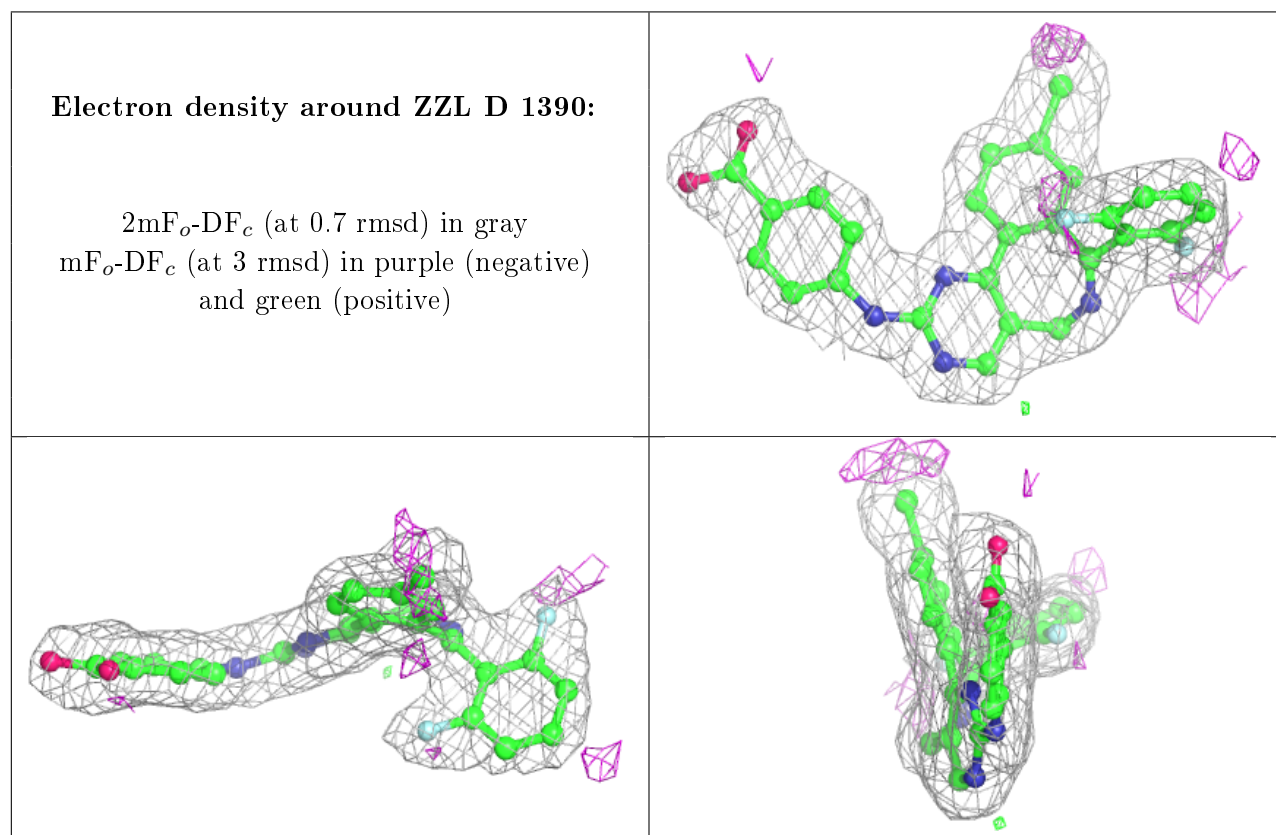
There are no carbohydrates in this entry.

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.

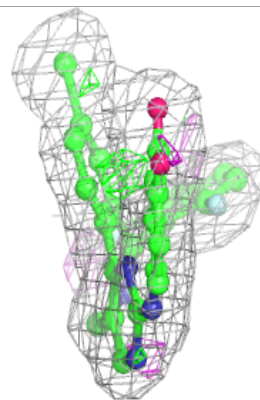
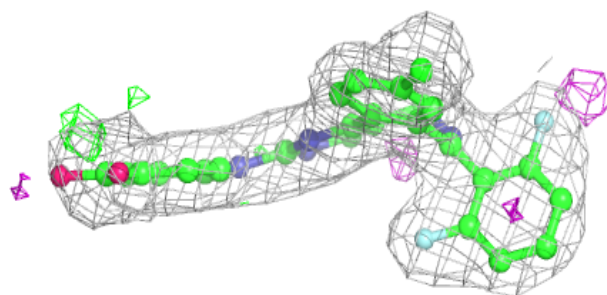
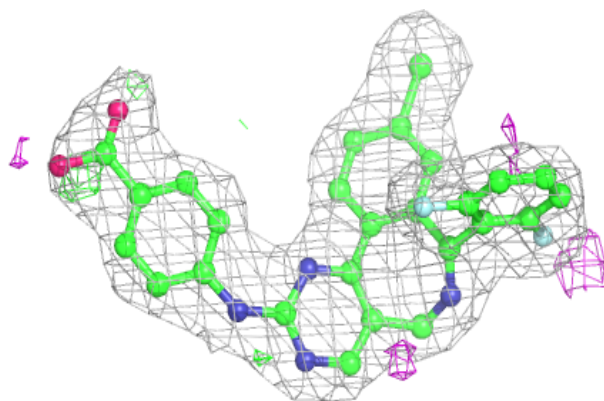
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	DMS	B	1391	4/4	0.80	0.14	18,24,35,74	0
4	ACT	B	1393	4/4	0.89	0.24	34,65,72,77	0
3	EDO	B	1397	4/4	0.91	0.17	46,49,50,58	0
3	EDO	B	1398	4/4	0.93	0.15	39,49,50,53	0
5	DMS	A	1394	4/4	0.93	0.12	16,28,32,67	0
4	ACT	B	1392	4/4	0.93	0.12	31,34,48,59	0
3	EDO	C	1395	4/4	0.93	0.12	38,41,50,74	0
4	ACT	B	1400	4/4	0.94	0.15	44,50,51,53	0
4	ACT	C	1394	4/4	0.94	0.18	40,46,61,70	0
3	EDO	B	1399	4/4	0.95	0.15	31,40,44,51	0
4	ACT	A	1392	4/4	0.96	0.09	43,52,56,59	0
4	ACT	C	1393	4/4	0.96	0.10	42,45,48,52	0
3	EDO	B	1396	4/4	0.96	0.15	39,44,47,61	0
3	EDO	C	1390	4/4	0.96	0.17	36,43,46,53	0
3	EDO	B	1394	4/4	0.96	0.13	41,54,55,58	0
4	ACT	D	1392	4/4	0.97	0.20	46,52,59,68	0
4	ACT	D	1393	4/4	0.97	0.10	38,42,44,45	0
3	EDO	B	1395	4/4	0.97	0.14	34,46,54,66	0
4	ACT	A	1393	4/4	0.97	0.09	34,37,43,52	0
3	EDO	D	1391	4/4	0.97	0.15	50,51,59,61	0
2	ZZL	D	1390	34/34	0.98	0.13	10,18,29,45	0
2	ZZL	B	1390	34/34	0.98	0.11	15,22,46,67	0
3	EDO	C	1391	4/4	0.98	0.35	30,32,36,38	0
3	EDO	A	1391	4/4	0.98	0.14	31,38,48,56	0
2	ZZL	C	1392	34/34	0.98	0.10	14,21,41,66	0
2	ZZL	A	1390	34/34	0.99	0.12	11,18,31,38	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.

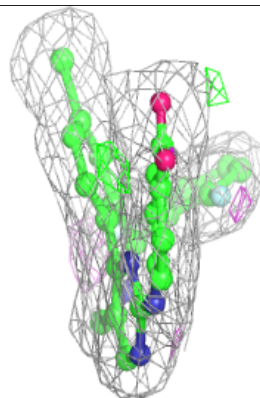
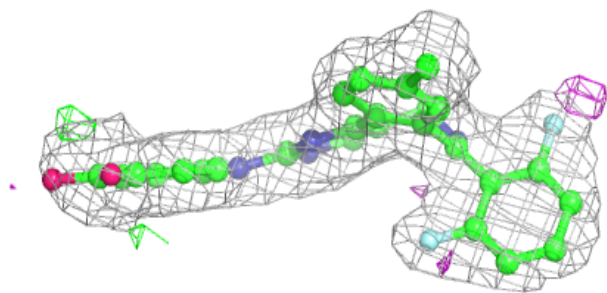
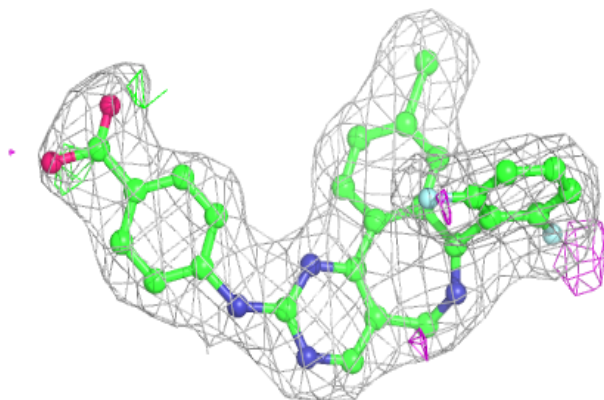


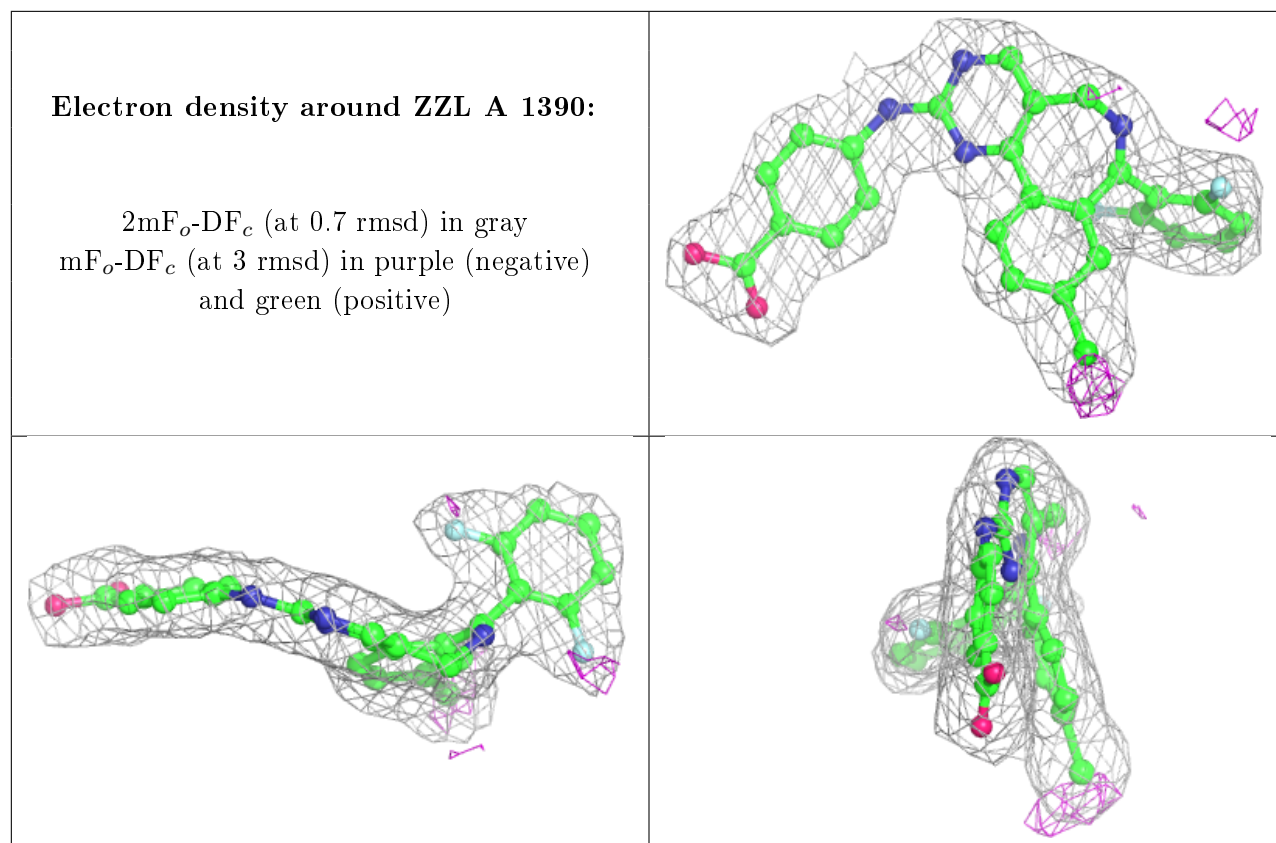
Electron density around ZZL B 1390:

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

**Electron density around ZZL C 1392:**

$2mF_o-DF_c$ (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.