



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 11:25 am BST

PDB ID : 5OTO
Title : The crystal structure of CK2alpha in complex with compound 30
Authors : Brear, P.; De Fusco, C.; Iegre, J.; Yoshida, M.; Mitchell, S.; Rossmann, M.; Carro, L.; Sore, H.; Hyvonen, M.; Spring, D.
Deposited on : 2017-08-22
Resolution : 1.51 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 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

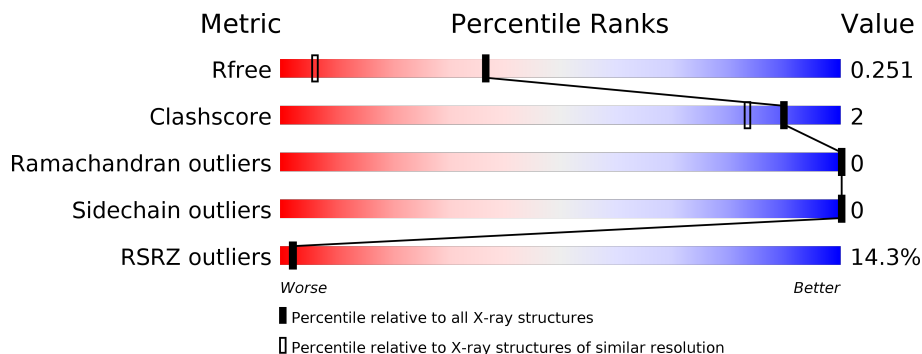
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.51 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	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (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 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	352	
1	B	352	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6094 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 Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	324	2763	1770	485	497	11	0	3	0
1	A	327	2802	1793	491	507	11	0	6	0

There are 50 discrepancies between the modelled and reference sequences:

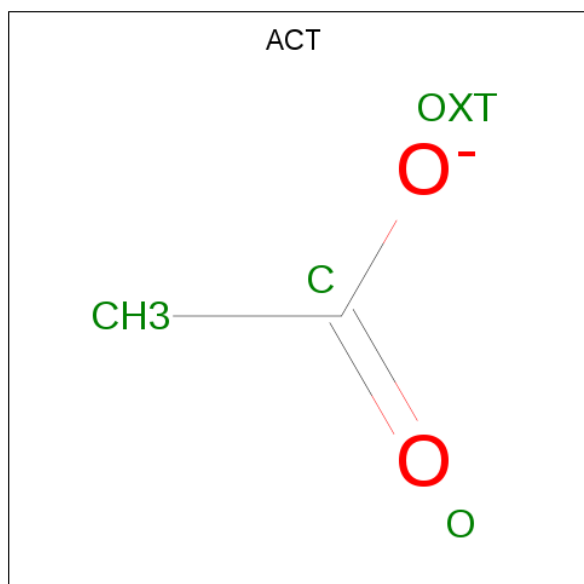
Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	GLY	-	expression tag	UNP P68400
B	-21	SER	-	expression tag	UNP P68400
B	-20	MET	-	expression tag	UNP P68400
B	-19	ASP	-	expression tag	UNP P68400
B	-18	ILE	-	expression tag	UNP P68400
B	-17	GLU	-	expression tag	UNP P68400
B	-16	PHE	-	expression tag	UNP P68400
B	-15	ASP	-	expression tag	UNP P68400
B	-14	ASP	-	expression tag	UNP P68400
B	-13	ASP	-	expression tag	UNP P68400
B	-12	ALA	-	expression tag	UNP P68400
B	-11	ASP	-	expression tag	UNP P68400
B	-10	ASP	-	expression tag	UNP P68400
B	-9	ASP	-	expression tag	UNP P68400
B	-8	GLY	-	expression tag	UNP P68400
B	-7	SER	-	expression tag	UNP P68400
B	-6	GLY	-	expression tag	UNP P68400
B	-5	SER	-	expression tag	UNP P68400
B	-4	GLY	-	expression tag	UNP P68400
B	-3	SER	-	expression tag	UNP P68400
B	-2	GLY	-	expression tag	UNP P68400
B	-1	SER	-	expression tag	UNP P68400
B	0	GLY	-	expression tag	UNP P68400
B	1	SER	-	expression tag	UNP P68400
B	21	SER	ARG	engineered mutation	UNP P68400

Continued on next page...

Continued from previous page...

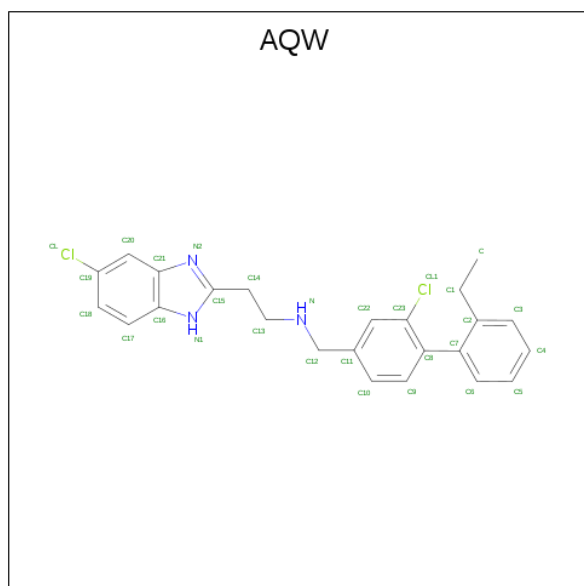
Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	GLY	-	expression tag	UNP P68400
A	-21	SER	-	expression tag	UNP P68400
A	-20	MET	-	expression tag	UNP P68400
A	-19	ASP	-	expression tag	UNP P68400
A	-18	ILE	-	expression tag	UNP P68400
A	-17	GLU	-	expression tag	UNP P68400
A	-16	PHE	-	expression tag	UNP P68400
A	-15	ASP	-	expression tag	UNP P68400
A	-14	ASP	-	expression tag	UNP P68400
A	-13	ASP	-	expression tag	UNP P68400
A	-12	ALA	-	expression tag	UNP P68400
A	-11	ASP	-	expression tag	UNP P68400
A	-10	ASP	-	expression tag	UNP P68400
A	-9	ASP	-	expression tag	UNP P68400
A	-8	GLY	-	expression tag	UNP P68400
A	-7	SER	-	expression tag	UNP P68400
A	-6	GLY	-	expression tag	UNP P68400
A	-5	SER	-	expression tag	UNP P68400
A	-4	GLY	-	expression tag	UNP P68400
A	-3	SER	-	expression tag	UNP P68400
A	-2	GLY	-	expression tag	UNP P68400
A	-1	SER	-	expression tag	UNP P68400
A	0	GLY	-	expression tag	UNP P68400
A	1	SER	-	expression tag	UNP P68400
A	21	SER	ARG	engineered mutation	UNP P68400

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



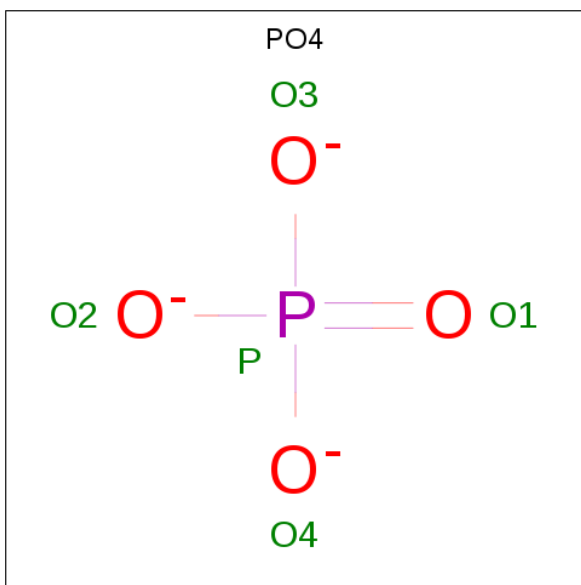
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is 2-(5-chloranyl-1 {H}-benzimidazol-2-yl)- {N}-[[3-chloranyl-4-(2-ethylphenyl)phenyl]methyl]ethanamine (three-letter code: AQW) (formula: C₂₄H₂₃Cl₂N₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	Cl	N	0	0
			29	24	2	3		
3	A	1	Total	C	Cl	N	0	1
			58	48	4	6		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	111	Total O 111 111	0	0
5	A	293	Total O 293 293	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	65.48Å 69.54Å 337.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	168.60 – 1.51 168.60 – 1.51	Depositor EDS
% Data completeness (in resolution range)	93.9 (168.60-1.51) 93.9 (168.60-1.51)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 1.51Å)	Xtrriage
Refinement program	BUSTER 2.10.1	Depositor
R, R_{free}	0.239 , 0.253 0.250 , 0.251	Depositor DCC
R_{free} test set	5760 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	20.3	Xtrriage
Anisotropy	0.479	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6094	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.85% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, AQW, 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	0.60	0/2877	0.60	0/3893
1	B	0.52	0/2838	0.62	0/3839
All	All	0.57	0/5715	0.61	0/7732

There are no bond length outliers.

There are no bond angle outliers.

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	2802	0	2735	13	0
1	B	2763	0	2702	7	0
2	A	20	0	15	1	0
2	B	8	0	6	0	0
3	A	58	0	0	3	0
3	B	29	0	0	1	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
5	A	293	0	0	3	0
5	B	111	0	0	0	0
All	All	6094	0	5458	20	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 2.

All (20) 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:237:ASP:OD2	5:A:501:HOH:O	1.91	0.87
1:B:120:ASP:OD2	1:B:123:GLN:HG3	2.03	0.58
1:A:225:MET:CE	3:A:406[B]:AQW:CL1	2.90	0.57
1:A:225:MET:HE3	3:A:406[B]:AQW:CL1	2.45	0.53
1:B:120:ASP:HB3	1:B:123:GLN:OE1	2.08	0.53
1:A:225:MET:HE1	3:A:406[B]:AQW:CL1	2.50	0.48
1:A:279:LYS:HB3	1:A:283:ARG:HD3	1.95	0.48
1:A:163:MET:CE	1:A:174:ILE:HG21	2.45	0.46
1:B:258:ILE:HA	1:B:263:ILE:HD12	1.98	0.46
1:A:116:VAL:HB	1:A:163:MET:HE3	1.96	0.45
1:B:73:VAL:HG23	1:B:74:LYS:HD2	1.99	0.44
1:A:133:ILE:HD12	1:A:292:LEU:HD22	1.99	0.43
1:A:103:ASP:OD2	1:A:105:VAL:HG23	2.19	0.43
1:A:40:GLN:HB3	1:A:57:ILE:HG22	2.00	0.43
1:A:213:LEU:CD1	5:A:506:HOH:O	2.67	0.42
1:A:213:LEU:HD11	5:A:506:HOH:O	2.20	0.41
1:A:286:HIS:HE1	2:A:403:ACT:OXT	2.02	0.41
1:B:162:VAL:HG11	3:B:403:AQW:CL1	2.57	0.41
1:B:303:LYS:HB3	1:B:313:LEU:HG	2.03	0.41
1:B:120:ASP:HB3	1:B:123:GLN:CD	2.42	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	331/352 (94%)	325 (98%)	6 (2%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	325/352 (92%)	318 (98%)	7 (2%)	0	100	100
All	All	656/704 (93%)	643 (98%)	13 (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	307/319 (96%)	307 (100%)	0	100	100
1	B	302/319 (95%)	302 (100%)	0	100	100
All	All	609/638 (96%)	609 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	186	GLN
1	B	270	ASN
1	A	168	HIS
1	A	236	HIS
1	A	262	ASN
1	A	270	ASN
1	A	286	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

12 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
3	AQW	B	403	-	30,32,32	0.56	0	37,44,44	0.51	0
2	ACT	A	401	-	1,3,3	6.26	1 (100%)	0,3,3	0.00	-
3	AQW	A	406[B]	-	30,32,32	0.57	0	37,44,44	0.54	0
2	ACT	A	405	-	1,3,3	3.39	1 (100%)	0,3,3	0.00	-
3	AQW	A	406[A]	-	30,32,32	0.57	0	37,44,44	0.52	0
4	PO4	B	404	-	4,4,4	2.49	1 (25%)	6,6,6	0.55	0
2	ACT	B	402	-	1,3,3	5.22	1 (100%)	0,3,3	0.00	-
2	ACT	A	404	-	1,3,3	4.50	1 (100%)	0,3,3	0.00	-
4	PO4	A	407	-	4,4,4	2.55	1 (25%)	6,6,6	0.56	0
2	ACT	B	401	-	1,3,3	4.33	1 (100%)	0,3,3	0.00	-
2	ACT	A	403	-	1,3,3	4.97	1 (100%)	0,3,3	0.00	-
2	ACT	A	402	-	1,3,3	5.00	1 (100%)	0,3,3	0.00	-

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	AQW	A	406[B]	-	-	1/13/13/13	0/4/4/4
3	AQW	B	403	-	-	1/13/13/13	0/4/4/4
3	AQW	A	406[A]	-	-	2/13/13/13	0/4/4/4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	ACT	CH3-C	6.26	1.56	1.48
2	B	402	ACT	CH3-C	5.22	1.55	1.48
2	A	402	ACT	CH3-C	5.00	1.55	1.48
2	A	403	ACT	CH3-C	4.97	1.55	1.48
2	A	404	ACT	CH3-C	4.50	1.54	1.48
2	B	401	ACT	CH3-C	4.33	1.54	1.48
4	B	404	PO4	P-O1	4.17	1.60	1.50
4	A	407	PO4	P-O1	4.11	1.60	1.50
2	A	405	ACT	CH3-C	3.39	1.53	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

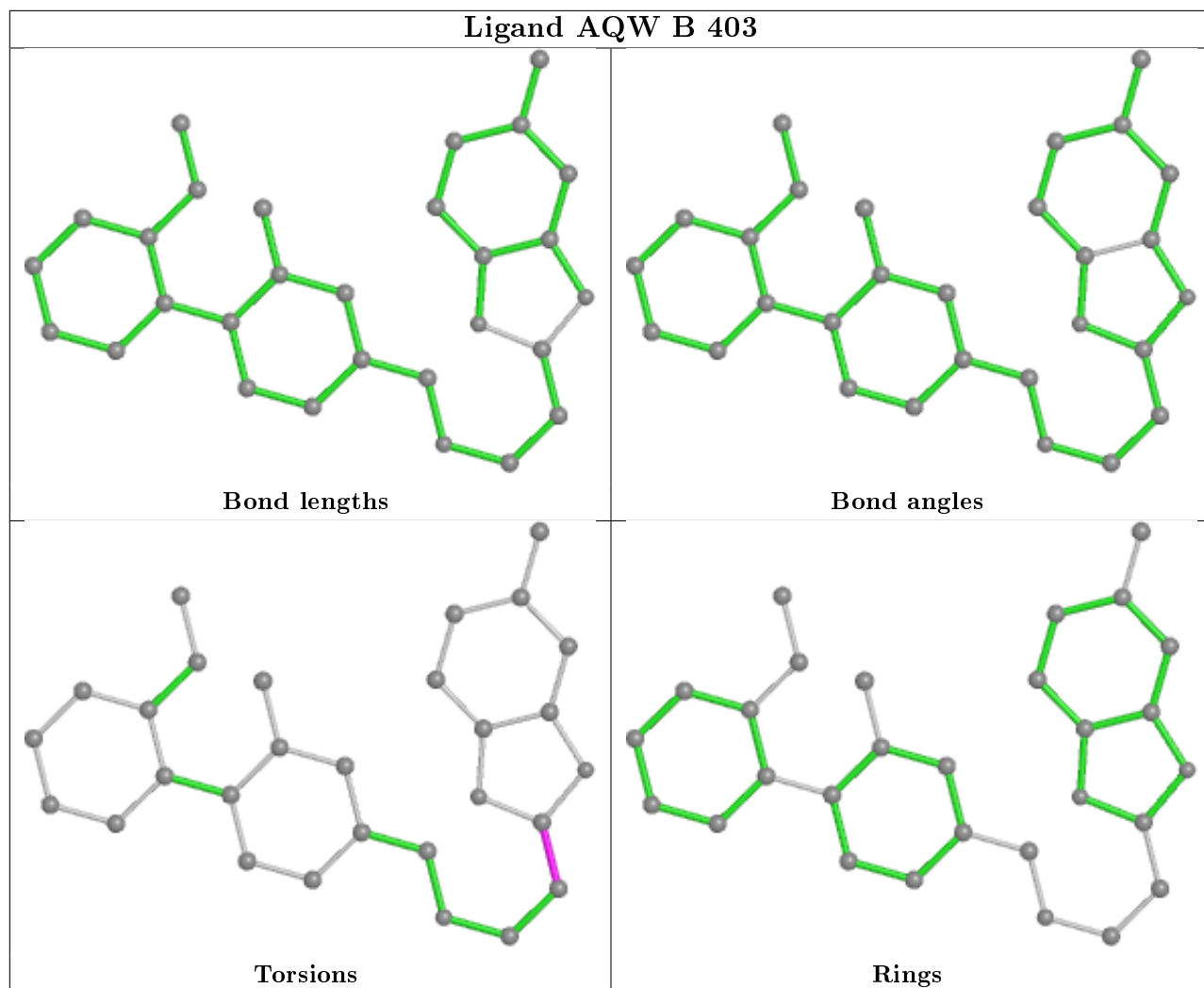
Mol	Chain	Res	Type	Atoms
3	B	403	AQW	C13-C14-C15-N2
3	A	406[B]	AQW	C13-C14-C15-N2
3	A	406[A]	AQW	C13-C14-C15-N2
3	A	406[A]	AQW	C14-C13-N-C12

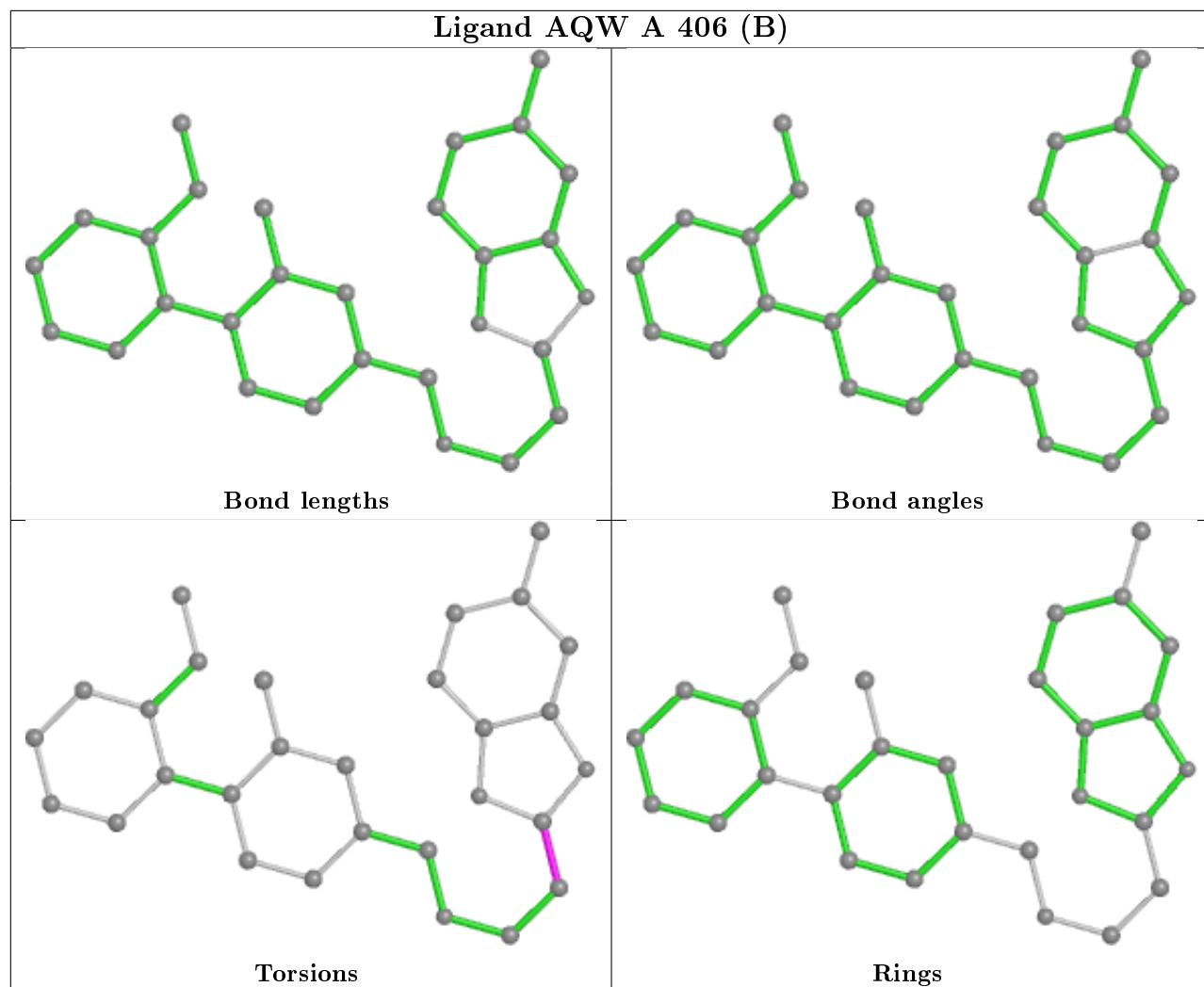
There are no ring outliers.

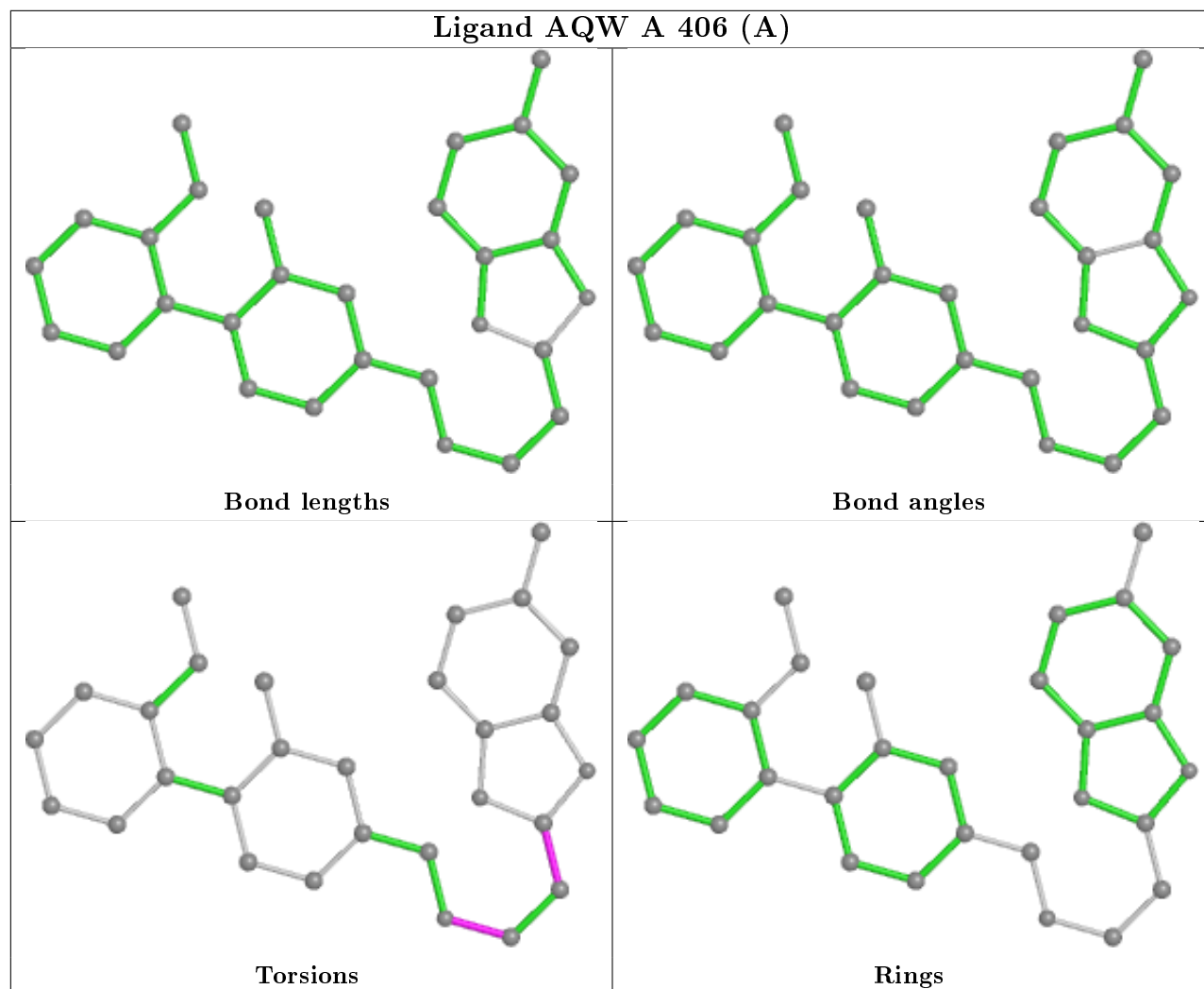
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	403	AQW	1	0
3	A	406[B]	AQW	3	0
2	A	403	ACT	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

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	327/352 (92%)	0.31	12 (3%) 41 46	13, 23, 52, 80	0
1	B	324/352 (92%)	1.37	81 (25%) 0 0	22, 45, 80, 107	0
All	All	651/704 (92%)	0.84	93 (14%) 2 2	13, 33, 73, 107	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	121	PHE	14.7
1	B	50	TYR	12.4
1	B	126	GLN	12.1
1	A	50	TYR	10.0
1	B	288	GLU	7.6
1	B	124	LEU	6.8
1	B	125	TYR	5.7
1	B	307	TYR	5.6
1	B	49	LYS	5.4
1	B	263	ILE	5.2
1	B	123	GLN	5.1
1	B	255	TYR	4.8
1	B	47	ARG	4.8
1	B	283	ARG	4.7
1	A	121	PHE	4.7
1	A	49	LYS	4.7
1	B	254	LEU	4.6
1	A	126	GLN	4.6
1	B	72	PRO	4.6
1	B	273	LEU	4.5
1	B	233	PHE	4.4
1	A	125	TYR	4.4
1	A	2	SER	4.3
1	B	280	ARG	4.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	272	ILE	4.1
1	B	73	VAL	4.0
1	B	46	GLY	4.0
1	B	5	VAL	4.0
1	B	216	TRP	3.9
1	B	325	TYR	3.8
1	A	123	GLN	3.7
1	B	257	TYR	3.6
1	B	259	ASP	3.5
1	A	124	LEU	3.5
1	B	271	ASP	3.4
1	B	258	ILE	3.3
1	B	48	GLY	3.3
1	B	117	ASN	3.2
1	B	122	LYS	3.2
1	B	128	LEU	3.2
1	B	269	PHE	3.2
1	B	245	ILE	3.2
1	B	127	THR	3.1
1	B	249	LEU	3.1
1	B	33	TRP	3.1
1	A	117	ASN	3.0
1	B	116	VAL	3.0
1	B	281	TRP	2.9
1	B	298	LEU	2.9
1	B	300	PHE	2.9
1	B	292	LEU	2.9
1	B	57	ILE	2.9
1	B	301	LEU	2.8
1	B	227	PHE	2.7
1	A	122	LYS	2.7
1	B	305	LEU	2.7
1	B	243	VAL	2.7
1	B	118	ASN	2.6
1	B	51	SER	2.6
1	B	167	GLU	2.6
1	B	232	PHE	2.5
1	B	264	GLU	2.5
1	B	284	PHE	2.5
1	B	324	PHE	2.5
1	B	291	HIS	2.5
1	B	42	VAL	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	320	GLU	2.4
1	B	261	TYR	2.4
1	B	6	PRO	2.4
1	B	242	LEU	2.4
1	B	54	PHE	2.4
1	B	270	ASN	2.3
1	B	251	THR	2.3
1	A	33	TRP	2.3
1	A	116	VAL	2.3
1	B	239	TYR	2.2
1	B	45	LEU	2.2
1	B	206	TYR	2.2
1	B	70	LEU	2.2
1	B	267	PRO	2.2
1	B	71	LYS	2.2
1	B	43	ARG	2.1
1	B	265	LEU	2.1
1	B	323	TYR	2.1
1	B	290	GLN	2.1
1	B	53	VAL	2.1
1	B	296	GLU	2.1
1	B	66	VAL	2.1
1	B	295	PRO	2.1
1	B	276	HIS	2.1
1	B	170	LYS	2.1
1	B	322	PRO	2.0
1	B	222	LEU	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 carbohydrates in this entry.

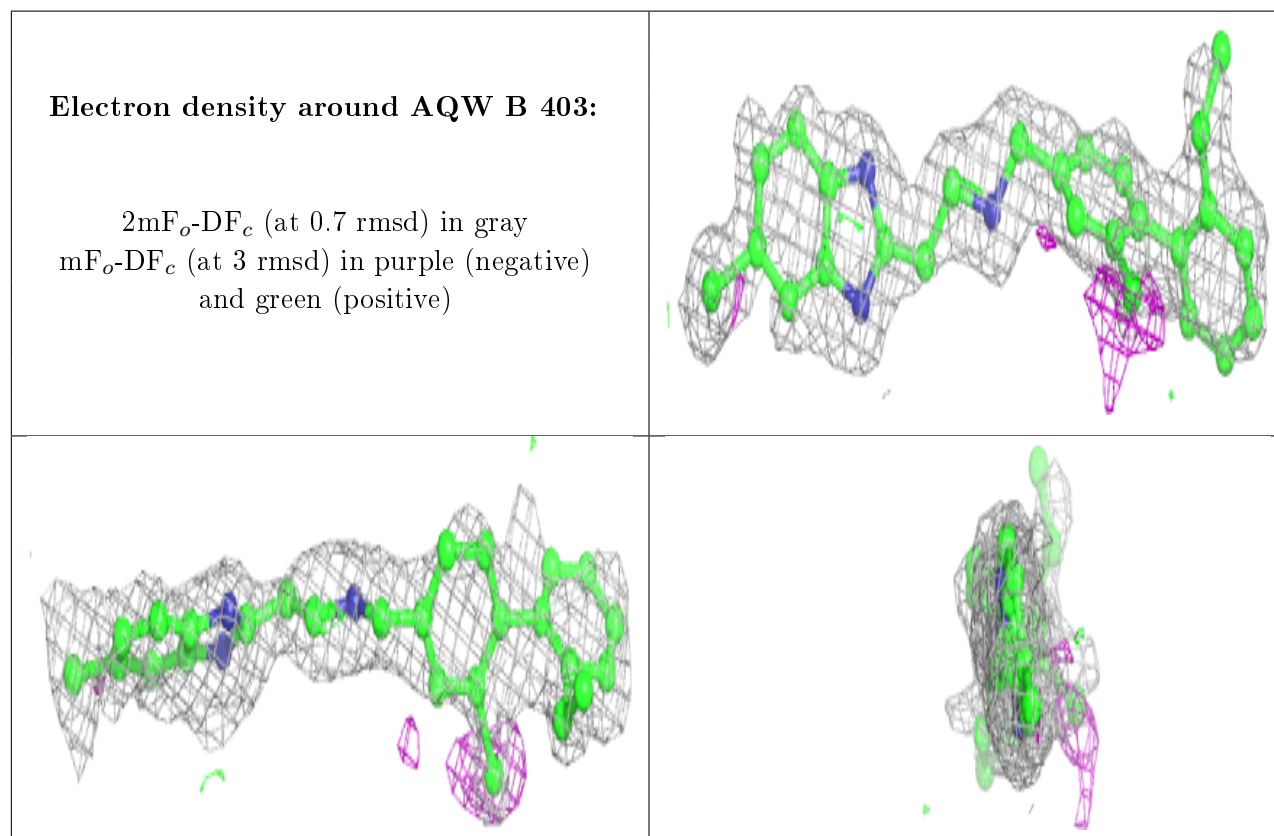
6.4 Ligands [i](#)

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.

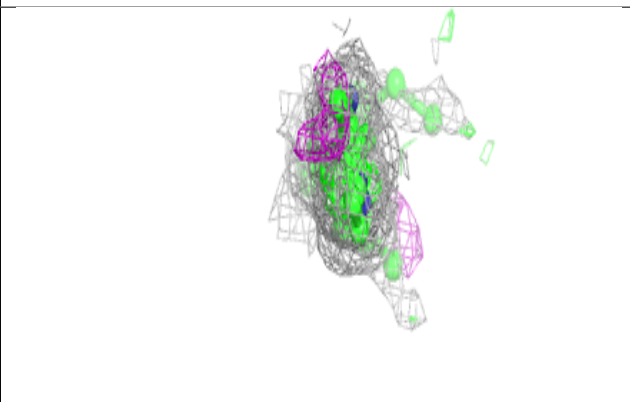
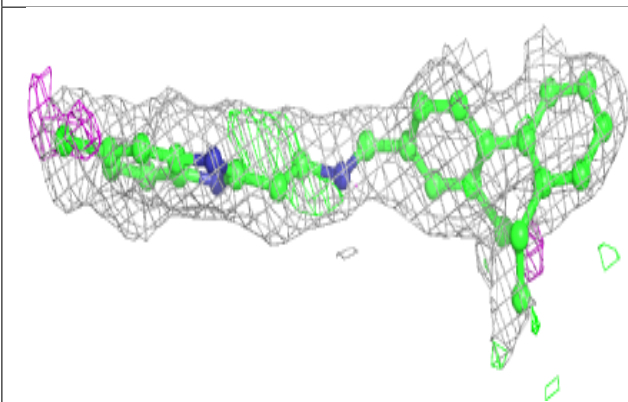
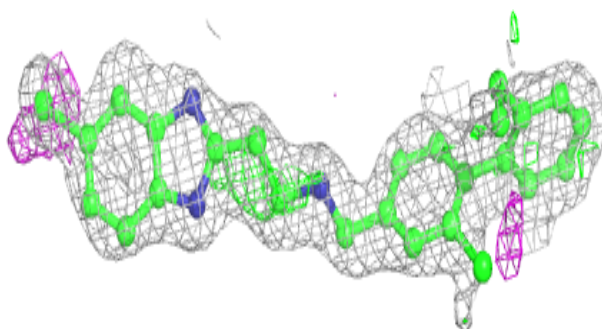
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ACT	A	405	4/4	0.54	0.19	39,39,41,45	0
3	AQW	B	403	29/29	0.63	0.23	56,65,69,74	0
3	AQW	A	406[B]	29/29	0.79	0.17	55,58,71,74	29
3	AQW	A	406[A]	29/29	0.79	0.17	16,21,31,37	29
2	ACT	A	403	4/4	0.81	0.12	38,42,43,44	0
4	PO4	A	407	5/5	0.91	0.11	36,37,39,40	0
4	PO4	B	404	5/5	0.93	0.12	46,46,47,48	0
2	ACT	B	401	4/4	0.94	0.13	43,43,44,45	0
2	ACT	A	404	4/4	0.94	0.15	32,33,37,37	0
2	ACT	B	402	4/4	0.94	0.10	31,33,36,37	0
2	ACT	A	402	4/4	0.95	0.09	27,31,32,32	0
2	ACT	A	401	4/4	0.97	0.07	21,22,23,25	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.

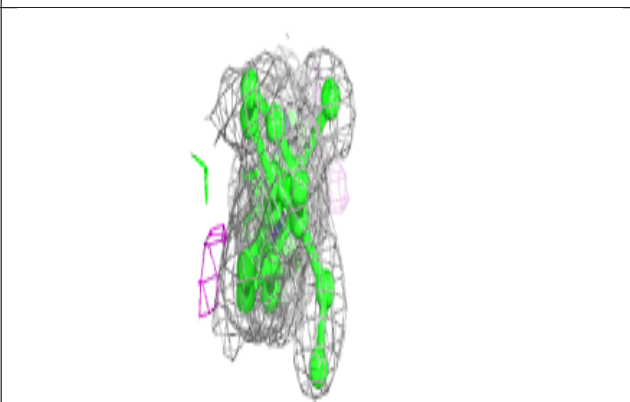
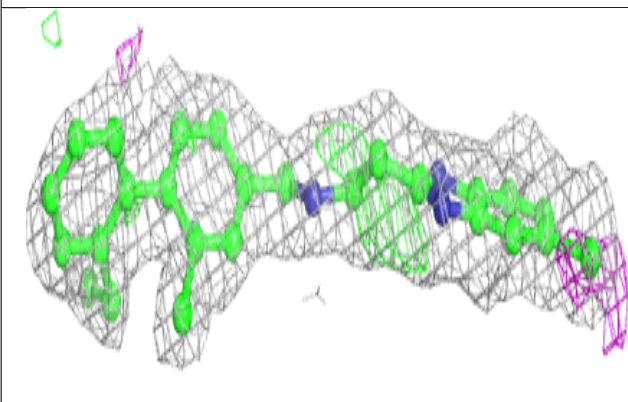
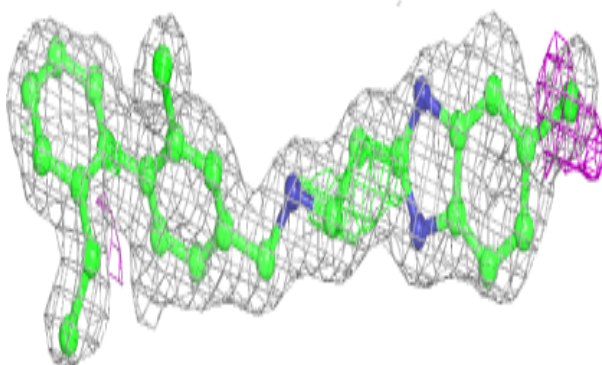


Electron density around AQW A 406 (B):

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

**Electron density around AQW A 406 (A):**

$2mF_o-DF_c$ (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.