



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 08:02 am BST

PDB ID : 4WBO
Title : Bovine G Protein Coupled Receptor Kinase 1 in Complex with Amlexanox
Authors : Homan, K.T.; Tesmer, J.J.G.
Deposited on : 2014-09-03
Resolution : 2.81 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

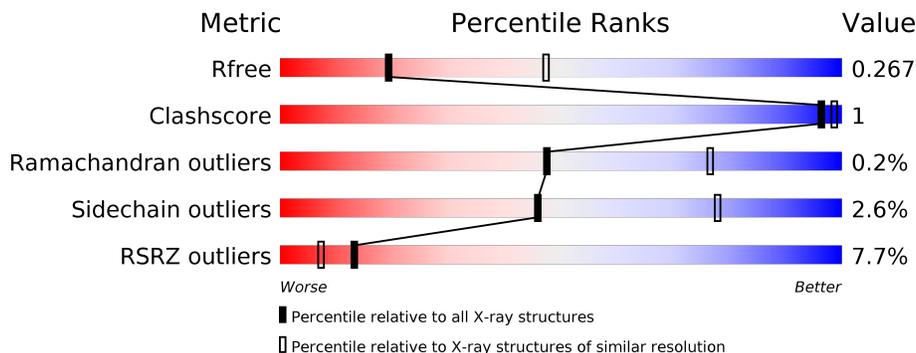
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 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	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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	541	<p>6% 87% 8%</p>
1	B	541	<p>5% 88% 9%</p>
1	C	541	<p>8% 86% 11%</p>
1	D	541	<p>9% 88% 9%</p>

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 15932 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 Rhodopsin kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	497	3988	2559	689	721	19	0	0	0
1	B	495	3976	2550	687	720	19	0	0	0
1	C	481	3865	2481	664	701	19	0	0	0
1	D	491	3957	2541	681	716	19	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

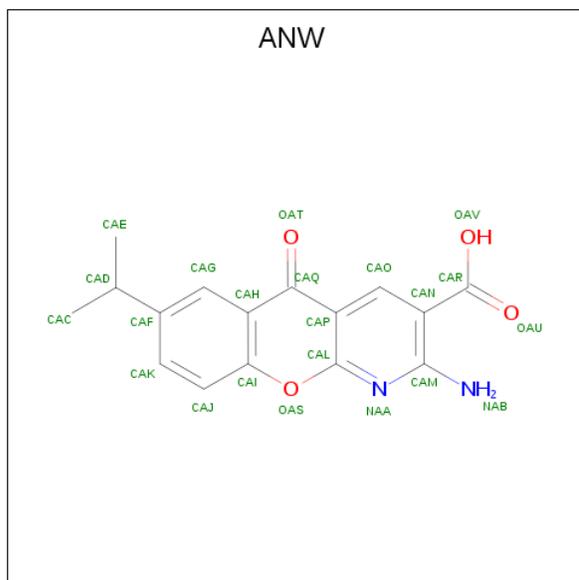
Chain	Residue	Modelled	Actual	Comment	Reference
A	536	HIS	-	expression tag	UNP P28327
A	537	HIS	-	expression tag	UNP P28327
A	538	HIS	-	expression tag	UNP P28327
A	539	HIS	-	expression tag	UNP P28327
A	540	HIS	-	expression tag	UNP P28327
A	541	HIS	-	expression tag	UNP P28327
B	536	HIS	-	expression tag	UNP P28327
B	537	HIS	-	expression tag	UNP P28327
B	538	HIS	-	expression tag	UNP P28327
B	539	HIS	-	expression tag	UNP P28327
B	540	HIS	-	expression tag	UNP P28327
B	541	HIS	-	expression tag	UNP P28327
C	536	HIS	-	expression tag	UNP P28327
C	537	HIS	-	expression tag	UNP P28327
C	538	HIS	-	expression tag	UNP P28327
C	539	HIS	-	expression tag	UNP P28327
C	540	HIS	-	expression tag	UNP P28327
C	541	HIS	-	expression tag	UNP P28327
D	536	HIS	-	expression tag	UNP P28327
D	537	HIS	-	expression tag	UNP P28327
D	538	HIS	-	expression tag	UNP P28327

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Chain	Residue	Modelled	Actual	Comment	Reference
D	539	HIS	-	expression tag	UNP P28327
D	540	HIS	-	expression tag	UNP P28327
D	541	HIS	-	expression tag	UNP P28327

- Molecule 2 is 2-amino-7-(1-methylethyl)-5-oxo-5H-chromeno[2,3-b]pyridine-3-carboxylic acid (three-letter code: ANW) (formula: C₁₆H₁₄N₂O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	22	16	2	4	0	0
2	B	1	22	16	2	4	0	0
2	C	1	22	16	2	4	0	0
2	D	1	22	16	2	4	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total Cl 1 1	0	0

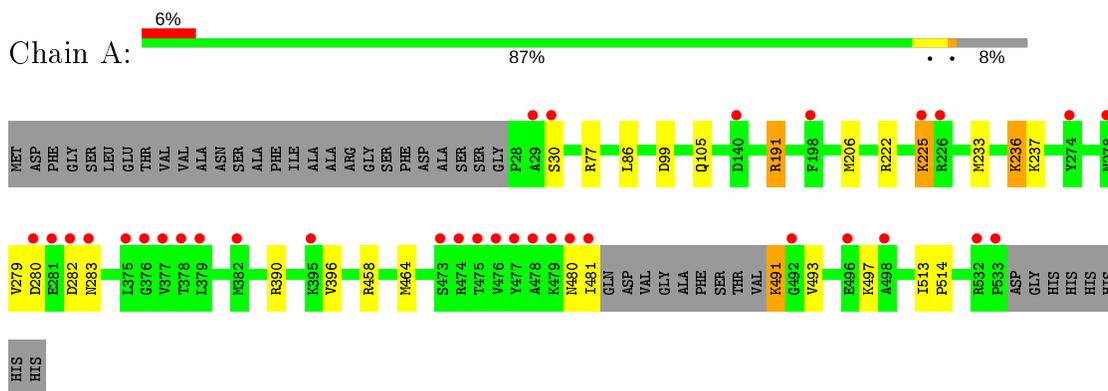
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	19	Total O 19 19	0	0
4	B	14	Total O 14 14	0	0
4	C	12	Total O 12 12	0	0
4	D	9	Total O 9 9	0	0

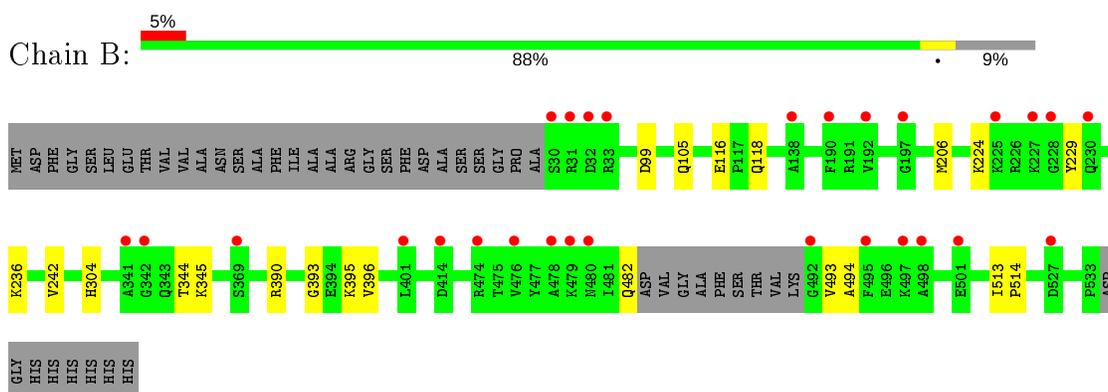
3 Residue-property plots [i](#)

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.

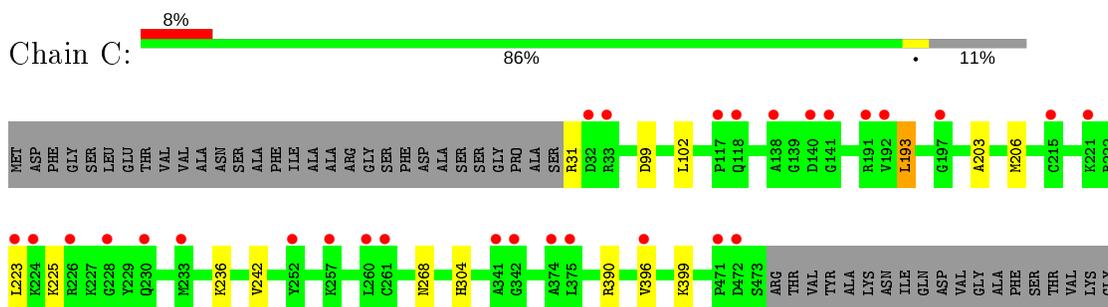
- Molecule 1: Rhodopsin kinase



- Molecule 1: Rhodopsin kinase



- Molecule 1: Rhodopsin kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	118.11Å 119.17Å 174.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.89 – 2.81 24.89 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.4 (24.89-2.81) 99.6 (24.89-2.81)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.80Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.241 , 0.267 0.241 , 0.267	Depositor DCC
R_{free} test set	3023 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	75.1	Xtrriage
Anisotropy	0.023	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.013 for k,h,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15932	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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: ANW, CL

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	0.32	0/4083	0.51	1/5507 (0.0%)
1	B	0.31	0/4070	0.51	0/5490
1	C	0.31	0/3957	0.52	3/5337 (0.1%)
1	D	0.30	0/4049	0.49	0/5460
All	All	0.31	0/16159	0.51	4/21794 (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	B	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	495	PHE	CB-CG-CD2	-6.07	116.55	120.80
1	C	495	PHE	CB-CG-CD1	5.98	124.99	120.80
1	C	31	ARG	NE-CZ-NH1	5.11	122.86	120.30
1	A	458	ARG	N-CA-CB	-5.07	101.48	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	393	GLY	Peptide

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	3988	0	3961	10	0
1	B	3976	0	3943	6	0
1	C	3865	0	3825	8	0
1	D	3957	0	3930	6	0
2	A	22	0	13	1	0
2	B	22	0	13	0	0
2	C	22	0	13	2	0
2	D	22	0	13	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	19	0	0	0	0
4	B	14	0	0	0	0
4	C	12	0	0	0	0
4	D	9	0	0	0	0
All	All	15932	0	15711	30	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 (30) 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:D:478:ALA:HB2	2:D:601:ANW:HACA	1.75	0.67
1:A:191:ARG:HA	1:C:102:LEU:HD11	1.84	0.59
1:A:233:MET:HE2	1:A:237:LYS:HG3	1.86	0.58
1:D:198:PHE:O	1:D:199:GLY:O	2.23	0.57
1:A:481:ILE:HG23	1:A:481:ILE:O	2.05	0.56
1:B:344:THR:HG23	1:B:345:LYS:HG3	1.88	0.56
1:A:77:ARG:HG3	1:A:86:LEU:HD21	1.88	0.53
1:B:224:LYS:HA	1:B:229:TYR:HE1	1.74	0.53
1:A:233:MET:CE	1:A:237:LYS:HG3	2.39	0.52
1:D:242:VAL:HG13	1:D:304:HIS:CD2	2.45	0.52
1:C:242:VAL:HG13	1:C:304:HIS:CD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:242:VAL:HG13	1:B:304:HIS:CD2	2.45	0.51
1:B:116:GLU:OE1	1:B:118:GLN:N	2.43	0.50
1:C:495:PHE:N	1:C:495:PHE:CD1	2.80	0.50
1:D:478:ALA:CB	2:D:601:ANW:HAEB	2.42	0.49
1:A:191:ARG:HA	1:C:102:LEU:CD1	2.44	0.48
1:C:193:LEU:HD11	1:C:203:ALA:HB2	1.96	0.48
1:A:513:ILE:HB	1:A:514:PRO:HD3	1.97	0.46
1:D:513:ILE:HB	1:D:514:PRO:HD3	1.99	0.44
2:C:601:ANW:NAB	2:C:601:ANW:OAU	2.51	0.43
1:D:478:ALA:HB2	2:D:601:ANW:HAEB	2.00	0.43
1:C:513:ILE:HB	1:C:514:PRO:HD3	2.00	0.43
2:A:601:ANW:NAB	2:A:601:ANW:OAU	2.51	0.43
1:B:224:LYS:NZ	1:B:494:ALA:O	2.52	0.42
1:C:268:ASN:HA	2:C:601:ANW:HAJ	2.00	0.42
1:B:513:ILE:HB	1:B:514:PRO:HD3	2.02	0.42
1:A:225:LYS:HB2	1:A:225:LYS:HE3	1.89	0.41
1:A:233:MET:HE3	1:A:236:LYS:HE3	2.02	0.41
1:C:223:LEU:O	1:C:225:LYS:O	2.38	0.40
1:A:491:LYS:HD3	1:A:491:LYS:N	2.37	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	493/541 (91%)	475 (96%)	16 (3%)	2 (0%)	34	64
1	B	491/541 (91%)	476 (97%)	15 (3%)	0	100	100
1	C	477/541 (88%)	461 (97%)	16 (3%)	0	100	100
1	D	485/541 (90%)	471 (97%)	13 (3%)	1 (0%)	47	76
All	All	1946/2164 (90%)	1883 (97%)	60 (3%)	3 (0%)	47	76

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	199	GLY
1	A	280	ASP
1	A	30	SER

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	414/447 (93%)	397 (96%)	17 (4%)	30	63
1	B	413/447 (92%)	404 (98%)	9 (2%)	52	81
1	C	401/447 (90%)	393 (98%)	8 (2%)	55	83
1	D	413/447 (92%)	405 (98%)	8 (2%)	57	84
All	All	1641/1788 (92%)	1599 (97%)	42 (3%)	46	78

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	ASP
1	A	105	GLN
1	A	191	ARG
1	A	206	MET
1	A	222	ARG
1	A	225	LYS
1	A	236	LYS
1	A	279	VAL
1	A	282	ASP
1	A	283	ASN
1	A	390	ARG
1	A	396	VAL
1	A	464	MET
1	A	480	ASN
1	A	491	LYS
1	A	493	VAL
1	A	497	LYS

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Mol	Chain	Res	Type
1	B	99	ASP
1	B	105	GLN
1	B	206	MET
1	B	236	LYS
1	B	390	ARG
1	B	395	LYS
1	B	396	VAL
1	B	482	GLN
1	B	493	VAL
1	C	99	ASP
1	C	193	LEU
1	C	206	MET
1	C	236	LYS
1	C	390	ARG
1	C	396	VAL
1	C	399	LYS
1	C	495	PHE
1	D	99	ASP
1	D	206	MET
1	D	236	LYS
1	D	390	ARG
1	D	396	VAL
1	D	474	ARG
1	D	480	ASN
1	D	504	GLN

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	480	ASN
1	B	304	HIS
1	C	304	HIS
1	D	480	ASN

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](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ANW	A	601	-	19,24,24	1.80	2 (10%)	17,36,36	1.60	4 (23%)
2	ANW	C	601	-	19,24,24	1.83	2 (10%)	17,36,36	1.67	4 (23%)
2	ANW	B	601	-	19,24,24	1.93	2 (10%)	17,36,36	1.24	2 (11%)
2	ANW	D	601	-	19,24,24	1.92	2 (10%)	17,36,36	1.31	3 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ANW	A	601	-	-	0/4/8/8	0/3/3/3
2	ANW	C	601	-	-	2/4/8/8	0/3/3/3
2	ANW	B	601	-	-	0/4/8/8	0/3/3/3
2	ANW	D	601	-	-	0/4/8/8	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	ANW	CAM-NAB	6.11	1.49	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	ANW	CAM-NAB	6.06	1.49	1.34
2	A	601	ANW	CAM-NAB	5.89	1.48	1.34
2	D	601	ANW	CAM-NAB	5.81	1.48	1.34
2	D	601	ANW	CAN-CAR	4.21	1.51	1.47
2	B	601	ANW	CAN-CAR	3.95	1.51	1.47
2	A	601	ANW	CAN-CAR	3.26	1.50	1.47
2	C	601	ANW	CAN-CAR	2.81	1.50	1.47

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	ANW	CAO-CAN-CAM	3.63	119.78	117.26
2	A	601	ANW	CAG-CAF-CAD	-3.37	117.18	121.67
2	A	601	ANW	CAO-CAN-CAM	3.31	119.55	117.26
2	C	601	ANW	CAG-CAH-CAI	3.16	119.95	116.39
2	C	601	ANW	CAG-CAF-CAD	-3.08	117.57	121.67
2	D	601	ANW	CAG-CAH-CAI	2.99	119.76	116.39
2	A	601	ANW	CAG-CAH-CAI	2.71	119.44	116.39
2	A	601	ANW	CAN-CAO-CAP	-2.55	118.93	122.85
2	B	601	ANW	CAG-CAH-CAI	2.48	119.19	116.39
2	B	601	ANW	CAO-CAN-CAM	2.47	118.97	117.26
2	C	601	ANW	CAN-CAO-CAP	-2.15	119.54	122.85
2	D	601	ANW	CAN-CAO-CAP	-2.15	119.55	122.85
2	D	601	ANW	CAO-CAN-CAM	2.14	118.74	117.26

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	601	ANW	CAC-CAD-CAF-CAK
2	C	601	ANW	CAC-CAD-CAF-CAG

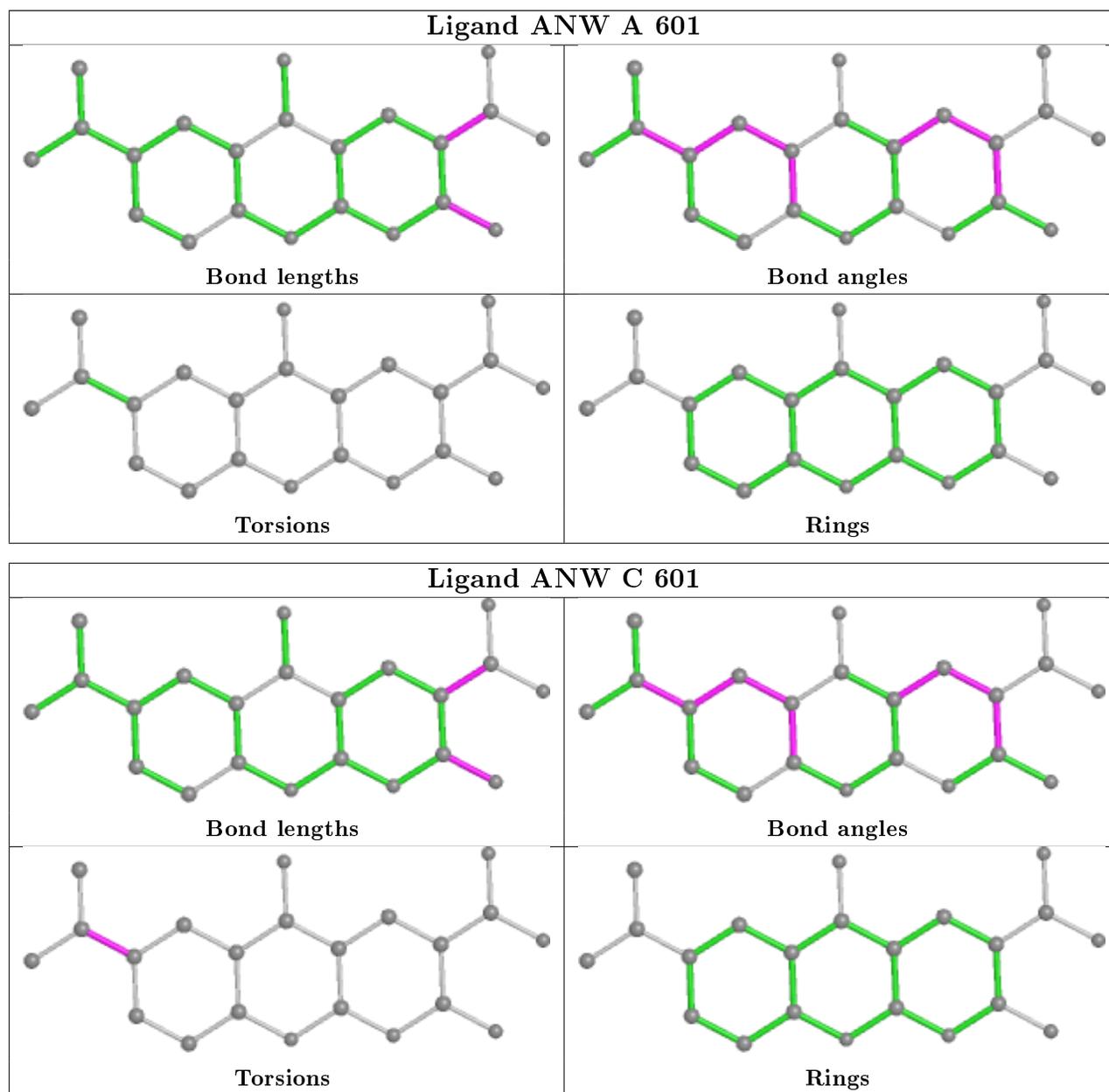
There are no ring outliers.

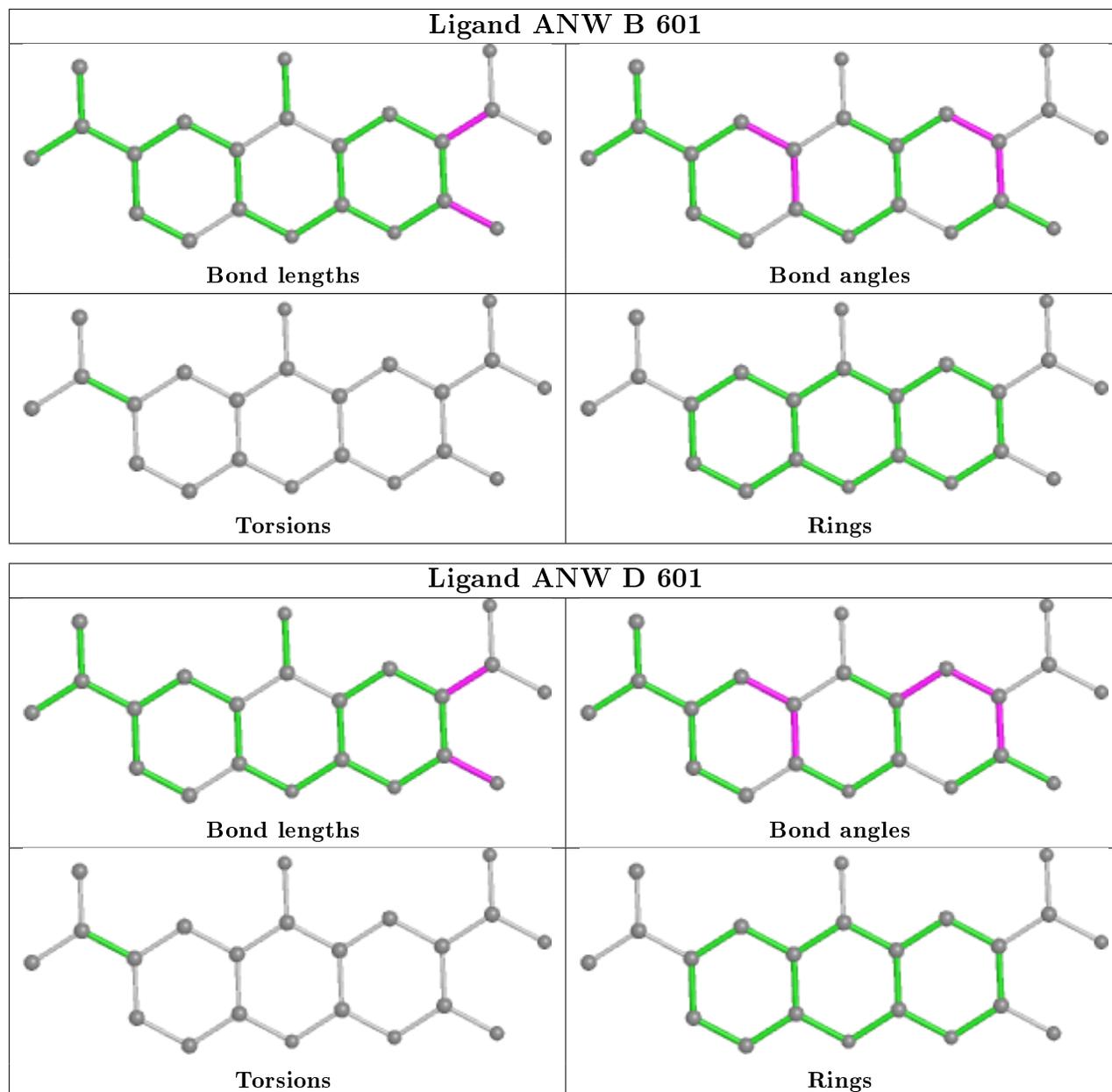
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	ANW	1	0
2	C	601	ANW	2	0
2	D	601	ANW	3	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	497/541 (91%)	0.20	33 (6%) 18 11	46, 80, 140, 174	0
1	B	495/541 (91%)	0.25	28 (5%) 23 15	46, 84, 161, 232	0
1	C	481/541 (88%)	0.43	42 (8%) 10 5	54, 89, 156, 232	0
1	D	491/541 (90%)	0.46	48 (9%) 7 4	43, 97, 157, 190	0
All	All	1964/2164 (90%)	0.33	151 (7%) 13 7	43, 88, 154, 232	0

All (151) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	197	GLY	7.7
1	D	478	ALA	7.5
1	D	279	VAL	5.8
1	C	471	PRO	5.4
1	C	496	GLU	5.2
1	D	477	TYR	5.2
1	C	499	ASP	5.1
1	C	191	ARG	5.1
1	C	472	ASP	5.0
1	A	282	ASP	4.8
1	D	474	ARG	4.6
1	C	504	GLN	4.6
1	D	281	GLU	4.5
1	B	498	ALA	4.4
1	D	473	SER	4.4
1	A	475	THR	4.2
1	A	473	SER	4.2
1	D	480	ASN	4.1
1	D	440	ASP	4.1
1	B	474	ARG	4.1
1	D	283	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	33	ARG	4.0
1	D	372	TYR	3.9
1	C	527	ASP	3.9
1	D	479	LYS	3.8
1	A	476	VAL	3.8
1	D	414	ASP	3.7
1	D	376	GLY	3.7
1	D	392	ARG	3.7
1	A	532	ARG	3.7
1	A	140	ASP	3.7
1	D	282	ASP	3.7
1	C	497	LYS	3.7
1	A	198	PHE	3.6
1	B	480	ASN	3.6
1	C	140	ASP	3.6
1	B	230	GLN	3.6
1	C	226	ARG	3.5
1	D	476	VAL	3.5
1	B	138	ALA	3.3
1	A	30	SER	3.3
1	D	416	PHE	3.3
1	D	384	ALA	3.2
1	A	375	LEU	3.2
1	A	283	ASN	3.2
1	A	29	ALA	3.2
1	B	497	LYS	3.2
1	D	274	TYR	3.2
1	B	225	LYS	3.2
1	A	479	LYS	3.1
1	A	474	ARG	3.1
1	D	482	GLN	3.1
1	C	503	PHE	3.0
1	D	197	GLY	3.0
1	D	530	VAL	3.0
1	B	227	LYS	3.0
1	A	480	ASN	3.0
1	D	280	ASP	3.0
1	A	478	ALA	3.0
1	C	501	GLU	3.0
1	C	342	GLY	2.9
1	C	192	VAL	2.9
1	C	498	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	141	GLY	2.8
1	D	278	ASN	2.8
1	B	495	PHE	2.8
1	B	30	SER	2.7
1	C	233	MET	2.7
1	D	135	ARG	2.7
1	A	477	TYR	2.7
1	D	403	GLN	2.7
1	B	479	LYS	2.7
1	C	224	LYS	2.7
1	D	374	ALA	2.7
1	A	395	LYS	2.7
1	D	369	SER	2.6
1	C	33	ARG	2.6
1	D	377	VAL	2.6
1	D	30	SER	2.6
1	D	198	PHE	2.6
1	B	492	GLY	2.6
1	D	407	GLU	2.6
1	A	481	ILE	2.6
1	D	430	LYS	2.6
1	D	100	ASP	2.6
1	D	373	PHE	2.6
1	C	197	GLY	2.5
1	A	379	LEU	2.5
1	A	281	GLU	2.5
1	C	502	PHE	2.5
1	C	500	THR	2.5
1	D	104	PRO	2.5
1	A	378	THR	2.4
1	D	33	ARG	2.4
1	C	230	GLN	2.4
1	C	531	TRP	2.4
1	D	454	ASP	2.4
1	A	278	ASN	2.4
1	B	341	ALA	2.4
1	B	369	SER	2.4
1	C	117	PRO	2.4
1	A	382	MET	2.3
1	C	341	ALA	2.3
1	D	295	THR	2.3
1	C	375	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	192	VAL	2.3
1	C	252	TYR	2.3
1	A	533	PRO	2.3
1	C	261	CYS	2.3
1	A	498	ALA	2.3
1	C	223	LEU	2.3
1	D	375	LEU	2.3
1	A	496	GLU	2.3
1	A	274	TYR	2.3
1	C	228	GLY	2.3
1	D	285	GLY	2.3
1	B	32	ASP	2.2
1	C	506	PHE	2.2
1	B	527	ASP	2.2
1	B	342	GLY	2.2
1	D	475	THR	2.2
1	B	501	GLU	2.2
1	A	376	GLY	2.2
1	B	414	ASP	2.2
1	C	260	LEU	2.2
1	B	190	PHE	2.1
1	D	531	TRP	2.1
1	B	31	ARG	2.1
1	C	215	CYS	2.1
1	D	443	CYS	2.1
1	C	495	PHE	2.1
1	C	221	LYS	2.1
1	A	377	VAL	2.1
1	C	396	VAL	2.1
1	A	492	GLY	2.1
1	B	478	ALA	2.1
1	C	257	LYS	2.1
1	D	341	ALA	2.1
1	D	413	PRO	2.1
1	A	280	ASP	2.1
1	D	289	PRO	2.1
1	B	476	VAL	2.0
1	C	118	GLN	2.0
1	D	408	GLN	2.0
1	A	225	LYS	2.0
1	C	32	ASP	2.0
1	B	228	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	401	LEU	2.0
1	C	138	ALA	2.0
1	C	374	ALA	2.0
1	A	226	ARG	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](#)

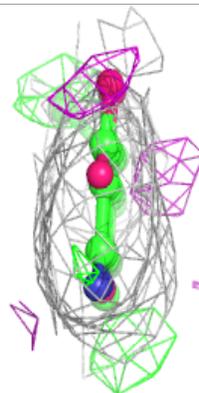
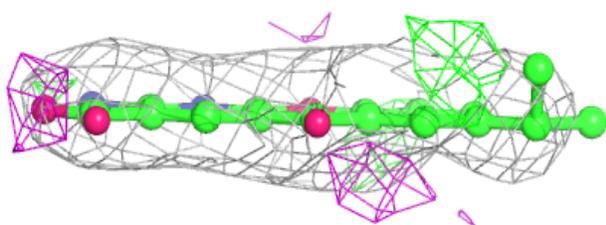
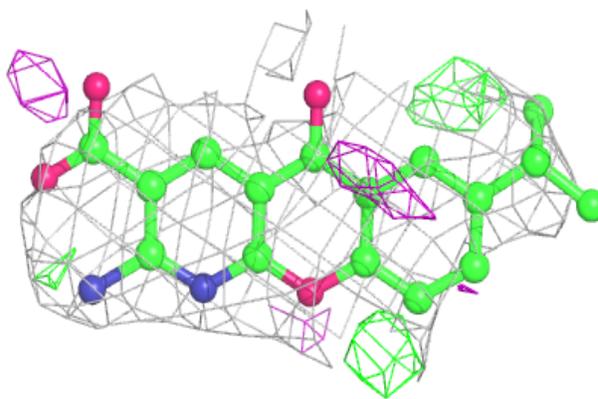
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	ANW	C	601	22/22	0.78	0.29	87,95,104,105	0
2	ANW	A	601	22/22	0.88	0.27	61,72,88,91	0
2	ANW	B	601	22/22	0.89	0.20	73,83,98,104	0
2	ANW	D	601	22/22	0.91	0.21	60,71,89,95	0
3	CL	D	602	1/1	0.96	0.22	64,64,64,64	0
3	CL	A	602	1/1	0.97	0.23	60,60,60,60	0
3	CL	B	602	1/1	0.98	0.09	63,63,63,63	0
3	CL	C	602	1/1	0.99	0.06	60,60,60,60	0

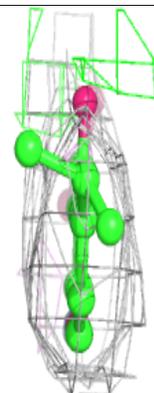
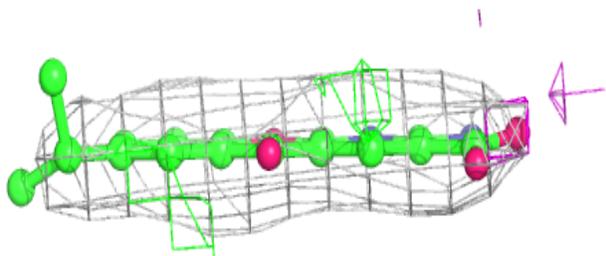
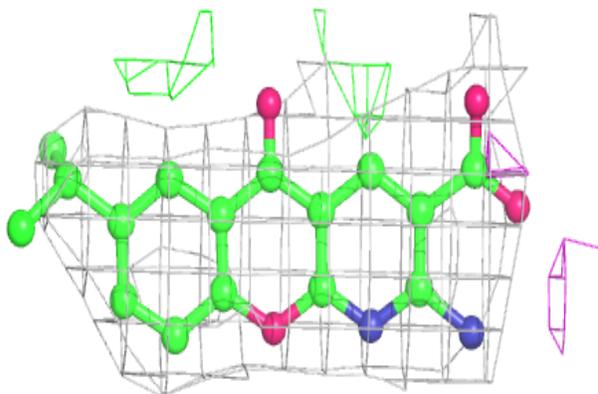
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

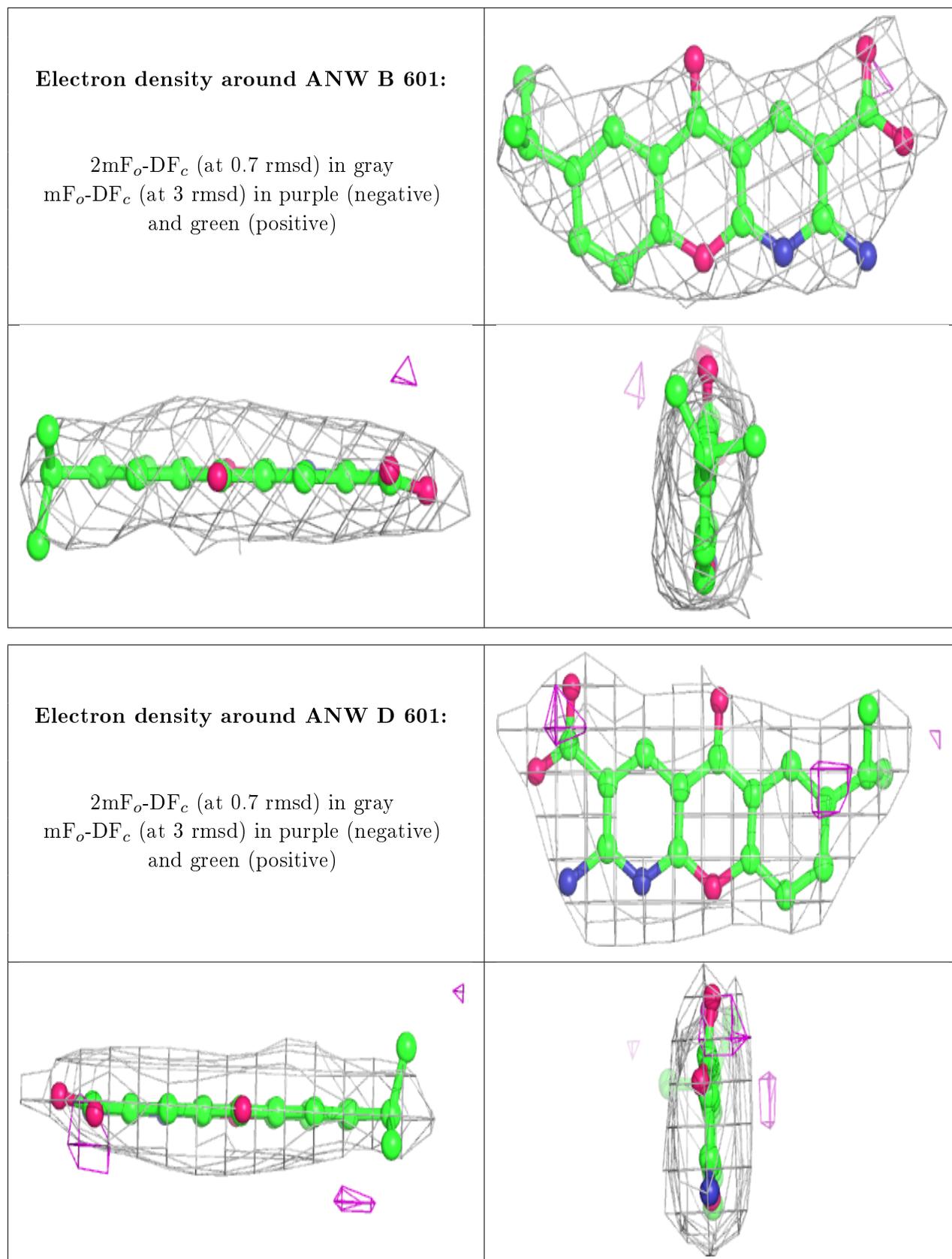
Electron density around ANW C 601:

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

**Electron density around ANW A 601:**

$2mF_o-DF_c$ (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.