



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:21 PM UTC

PDB ID : 4OXS / pdb_00004oxs
Title : Structure of NavMS in complex with channel blocking compound
Authors : Naylor, C.E.; Bagneris, C.; Wallace, B.A.
Deposited on : 2014-02-06
Resolution : 2.80 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

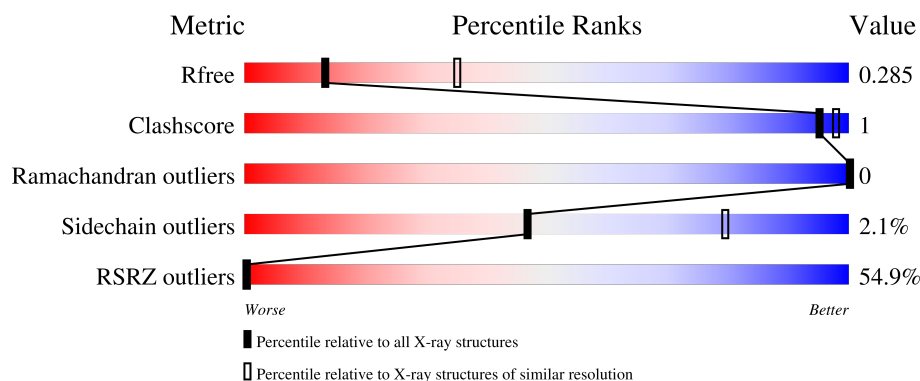
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 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	149	32% 56% 5% 38%
1	B	149	32% 57% • 38%
1	C	149	35% 56% 5% 39%
1	D	149	36% 54% 7% 39%

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
3	NA	A	303	-	-	-	X
4	BR	C	305[A]	-	-	-	X
4	BR	C	305[B]	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3055 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.

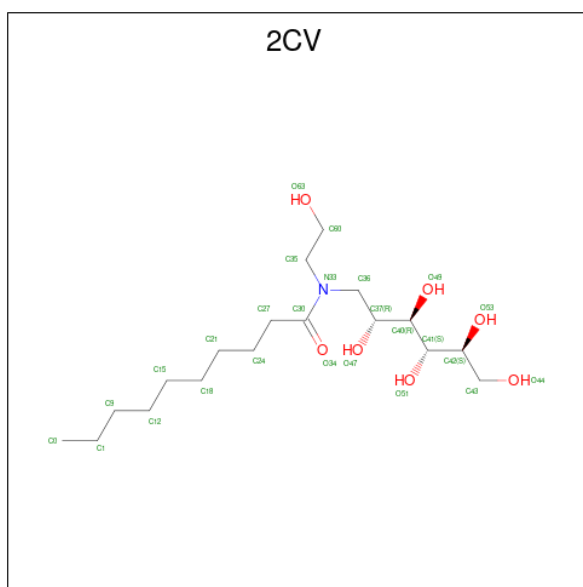
- Molecule 1 is a protein called Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	92	Total	C	N	O	S	0	0	0
			710	479	106	119	6			
1	B	92	Total	C	N	O	S	0	0	0
			706	476	106	119	5			
1	C	91	Total	C	N	O	S	0	1	0
			701	471	105	119	6			
1	D	91	Total	C	N	O	S	0	0	0
			692	464	105	118	5			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	126	GLY	-	expression tag	UNP A0L5S6
A	127	SER	-	expression tag	UNP A0L5S6
A	128	HIS	-	expression tag	UNP A0L5S6
A	129	MET	-	expression tag	UNP A0L5S6
B	126	GLY	-	expression tag	UNP A0L5S6
B	127	SER	-	expression tag	UNP A0L5S6
B	128	HIS	-	expression tag	UNP A0L5S6
B	129	MET	-	expression tag	UNP A0L5S6
C	126	GLY	-	expression tag	UNP A0L5S6
C	127	SER	-	expression tag	UNP A0L5S6
C	128	HIS	-	expression tag	UNP A0L5S6
C	129	MET	-	expression tag	UNP A0L5S6
D	126	GLY	-	expression tag	UNP A0L5S6
D	127	SER	-	expression tag	UNP A0L5S6
D	128	HIS	-	expression tag	UNP A0L5S6
D	129	MET	-	expression tag	UNP A0L5S6

- Molecule 2 is HEGA-10 (CCD ID: 2CV) (formula: $C_{18}H_{37}NO_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			17	13	1	3		
2	A	1	Total	C	N	O	0	0
			17	13	1	3		
2	C	1	Total	C	N	O	0	0
			17	13	1	3		
2	C	1	Total	C	N	O	0	0
			17	13	1	3		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 4 is BROMIDE ION (CCD ID: BR) (formula: Br).

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

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

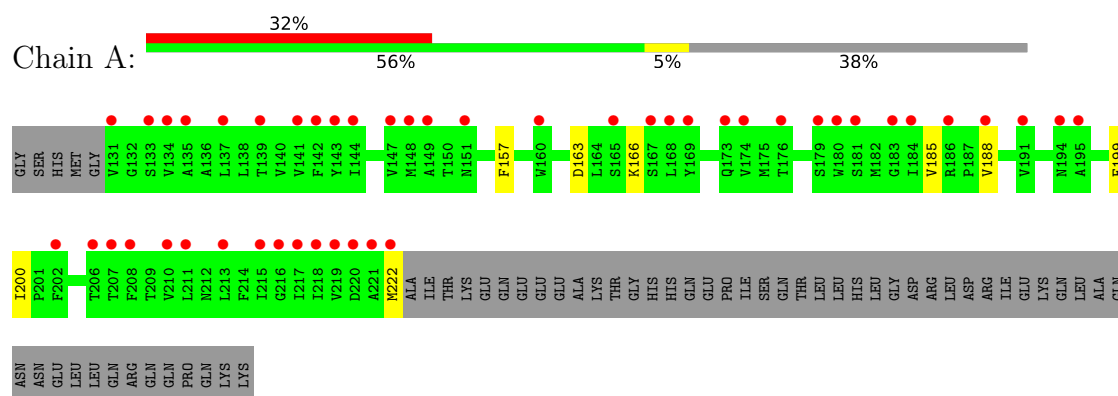
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	42	Total 42	O 42	0	0
5	B	34	Total 34	O 34	0	0
5	C	46	Total 46	O 46	0	0
5	D	46	Total 46	O 46	0	0

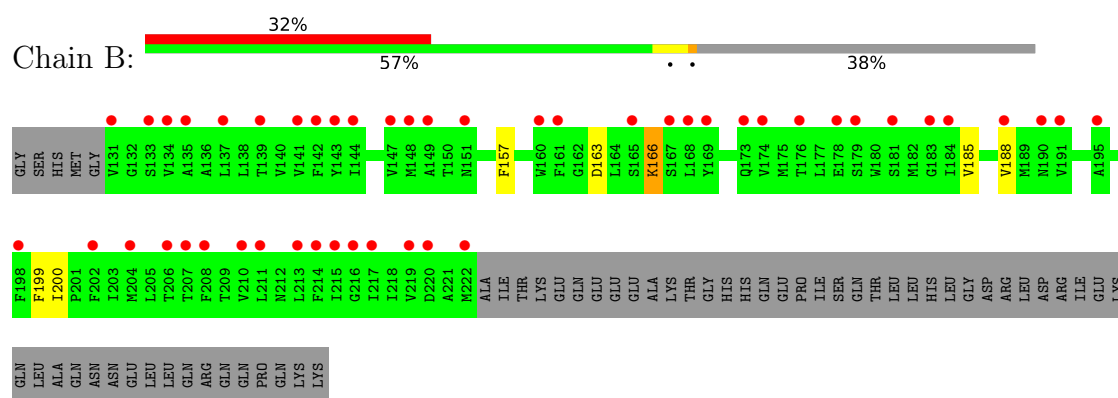
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

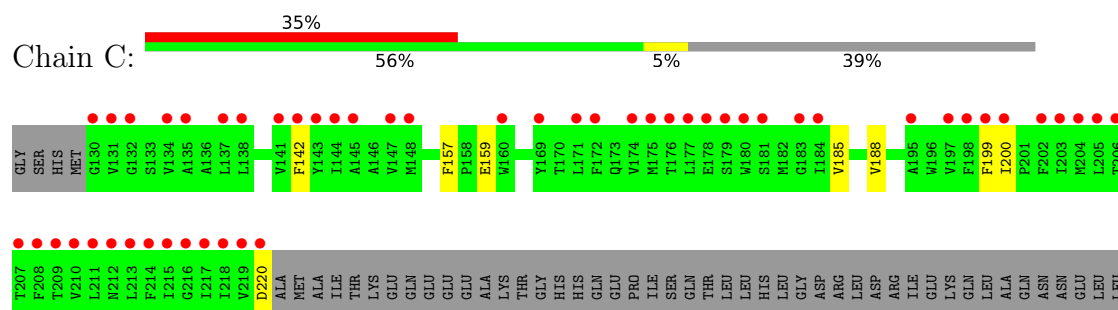
• Molecule 1: Ion transport protein



• Molecule 1: Ion transport protein

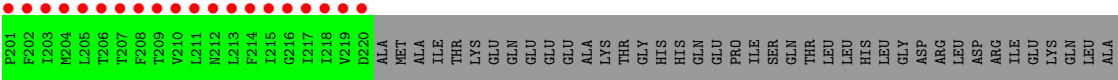
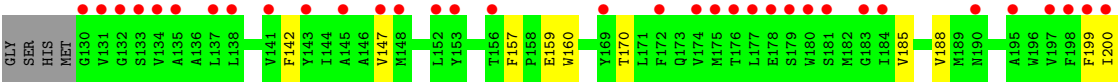


• Molecule 1: Ion transport protein



GLN
ARG
GLN
GLN
PRO
GLN
LYS
LYS

● Molecule 1: Ion transport protein



GLN
ASN
ASN
GLU
LEU
LEU
GLN
ARG
GLN
GLN
PRO
GLN
LYS
LYS

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	79.89Å 329.02Å 79.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.43 – 2.80 33.43 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (33.43-2.80) 99.8 (33.43-2.80)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.55 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.266 , 0.285 0.267 , 0.285	Depositor DCC
R_{free} test set	1363 reflections (3.05%)	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	1.426	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 74.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	3055	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 48.74 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.2347e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 2CV, NA, BR

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	0.90	0/732	1.51	4/1003 (0.4%)
1	B	0.88	0/728	1.51	6/999 (0.6%)
1	C	0.88	1/724 (0.1%)	1.47	3/992 (0.3%)
1	D	0.88	0/713	1.50	4/978 (0.4%)
All	All	0.89	1/2897 (0.0%)	1.50	17/3972 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	200	ILE	CA-CB	5.41	1.57	1.54

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	200	ILE	N-CA-CB	7.19	116.06	110.45
1	D	200	ILE	N-CA-CB	6.99	115.90	110.45
1	C	199	PHE	N-CA-C	6.91	118.47	111.07
1	D	199	PHE	N-CA-C	6.87	118.42	111.07
1	A	200	ILE	N-CA-CB	6.77	115.73	110.45
1	A	199	PHE	N-CA-C	6.72	118.27	111.07
1	A	163	ASP	CA-CB-CG	6.70	119.30	112.60
1	B	200	ILE	N-CA-CB	6.59	115.59	110.45
1	B	199	PHE	N-CA-C	6.56	118.09	111.07
1	A	185	VAL	N-CA-C	6.30	116.46	110.42
1	B	185	VAL	N-CA-C	6.19	116.36	110.42
1	B	166	LYS	CA-C-N	6.12	128.39	120.44
1	B	166	LYS	C-N-CA	6.12	128.39	120.44
1	B	163	ASP	CA-CB-CG	5.83	118.43	112.60
1	C	185	VAL	N-CA-C	5.78	115.97	110.42
1	D	185	VAL	N-CA-C	5.73	115.92	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	147	VAL	N-CA-C	-5.07	105.90	110.82

There are no chirality outliers.

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	710	0	699	2	0
1	B	706	0	690	2	0
1	C	701	0	701	1	0
1	D	692	0	672	2	0
2	A	34	0	43	2	0
2	C	34	0	44	0	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
4	A	2	0	0	0	0
4	C	2	0	0	0	0
5	A	42	0	0	0	0
5	B	34	0	0	0	0
5	C	46	0	0	0	0
5	D	46	0	0	0	0
All	All	3055	0	2849	7	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 (7) 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:157:PHE:CZ	1:D:188:VAL:HA	2.46	0.51
1:A:157:PHE:CZ	1:A:188:VAL:HA	2.46	0.50
1:C:157:PHE:CZ	1:C:188:VAL:HA	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:PHE:CZ	1:B:188:VAL:HA	2.46	0.50
1:A:166:LYS:HA	2:A:301:2CV:H601	1.97	0.47
2:A:302:2CV:H602	1:B:166:LYS:HA	2.01	0.43
1:D:160:TRP:HB3	1:D:170:THR:HG21	2.01	0.41

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	90/149 (60%)	87 (97%)	3 (3%)	0	100	100
1	B	90/149 (60%)	87 (97%)	3 (3%)	0	100	100
1	C	90/149 (60%)	86 (96%)	4 (4%)	0	100	100
1	D	89/149 (60%)	85 (96%)	4 (4%)	0	100	100
All	All	359/596 (60%)	345 (96%)	14 (4%)	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	74/129 (57%)	73 (99%)	1 (1%)	59	85
1	B	73/129 (57%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	75/129 (58%)	72 (96%)	3 (4%)	28	63
1	D	71/129 (55%)	69 (97%)	2 (3%)	38	73
All	All	293/516 (57%)	287 (98%)	6 (2%)	47	80

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	222	MET
1	C	142	PHE
1	C	159	GLU
1	C	220	ASP
1	D	142	PHE
1	D	159	GLU

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 10 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	2CV	C	301	-	16,16,25	0.24	0	17,17,30	0.32	0
2	2CV	A	302	-	16,16,25	0.30	0	17,18,30	0.59	1 (5%)
2	2CV	C	302	-	16,16,25	0.24	0	17,17,30	0.31	0
2	2CV	A	301	-	16,16,25	0.26	0	17,17,30	0.32	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
2	2CV	C	301	-	-	1/18/18/34	-
2	2CV	A	302	-	-	0/18/18/34	-
2	2CV	C	302	-	-	1/18/18/34	-
2	2CV	A	301	-	-	1/18/18/34	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	302	2CV	C35-N33-C36	2.10	118.51	116.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	301	2CV	N33-C36-C37-O47
2	C	302	2CV	N33-C36-C37-O47
2	A	301	2CV	N33-C36-C37-O47

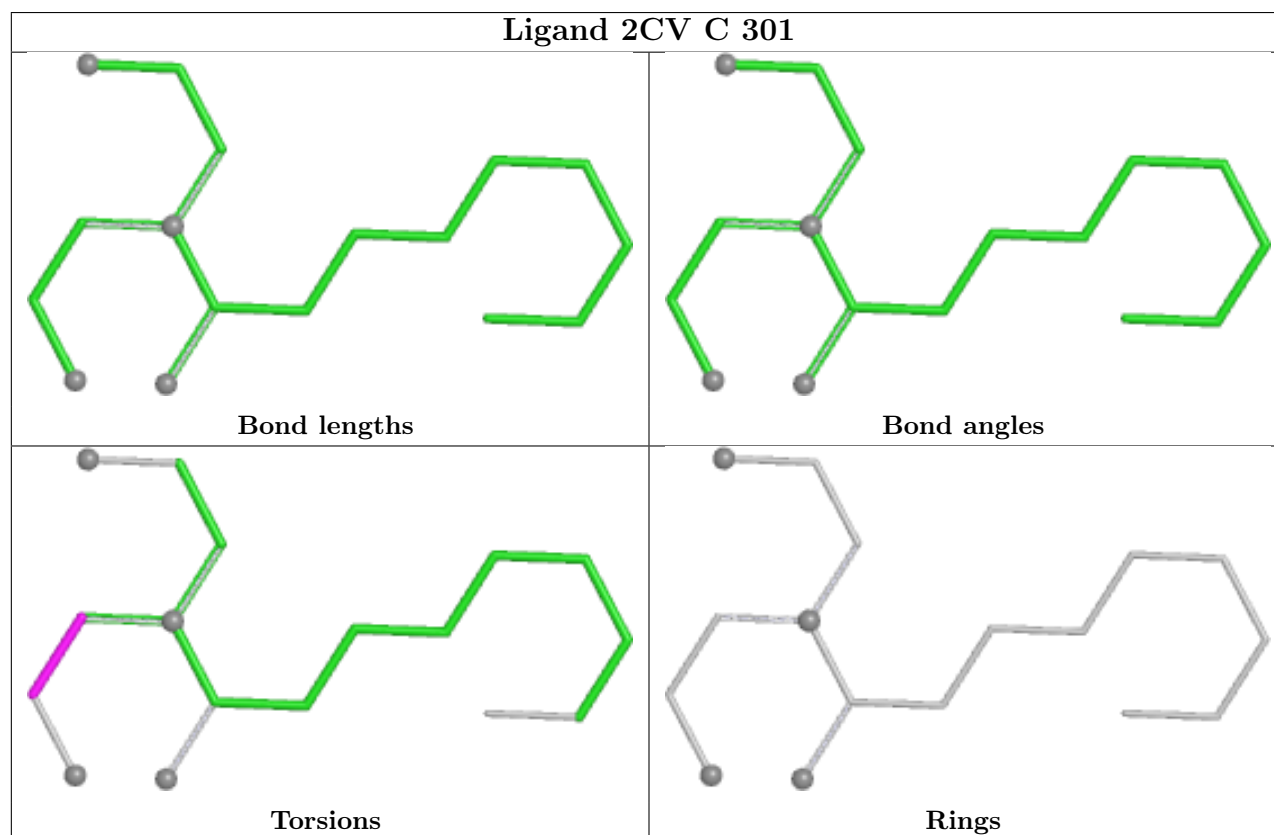
There are no ring outliers.

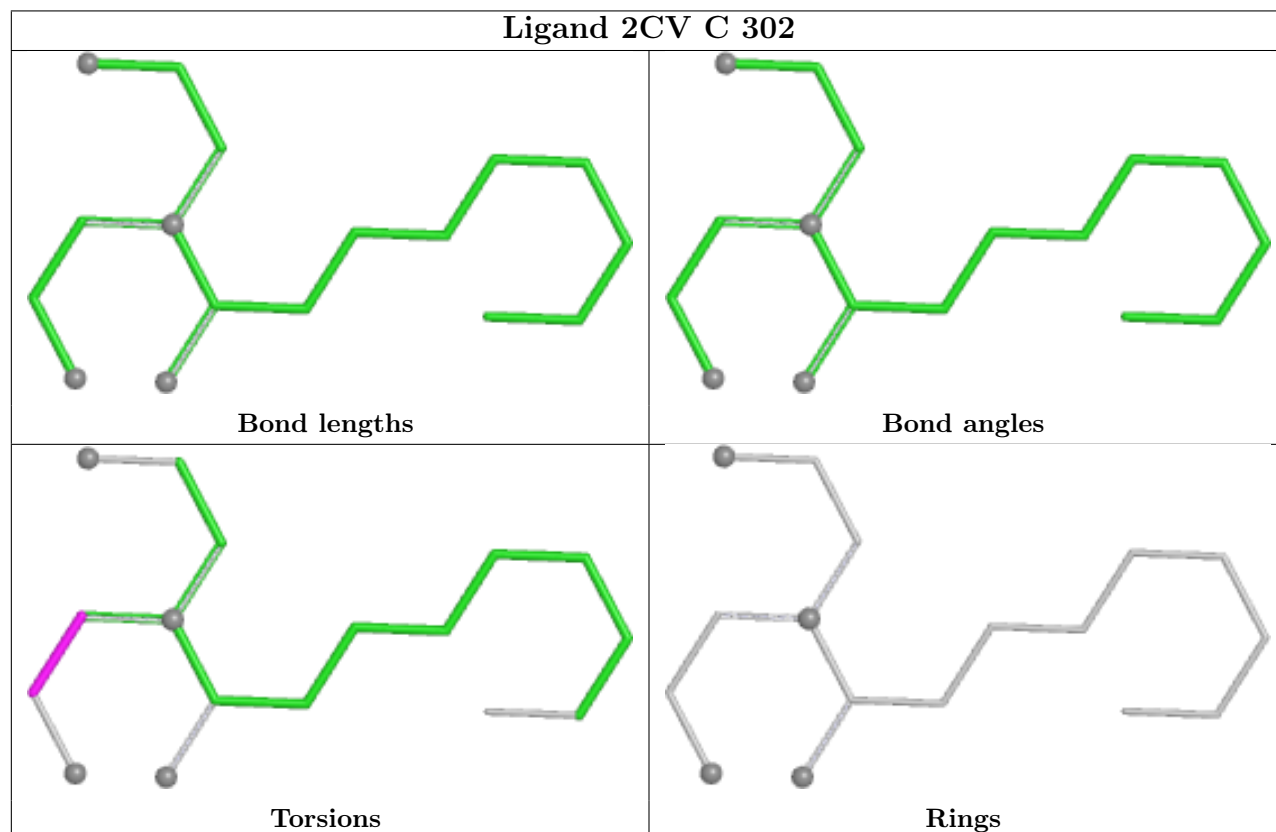
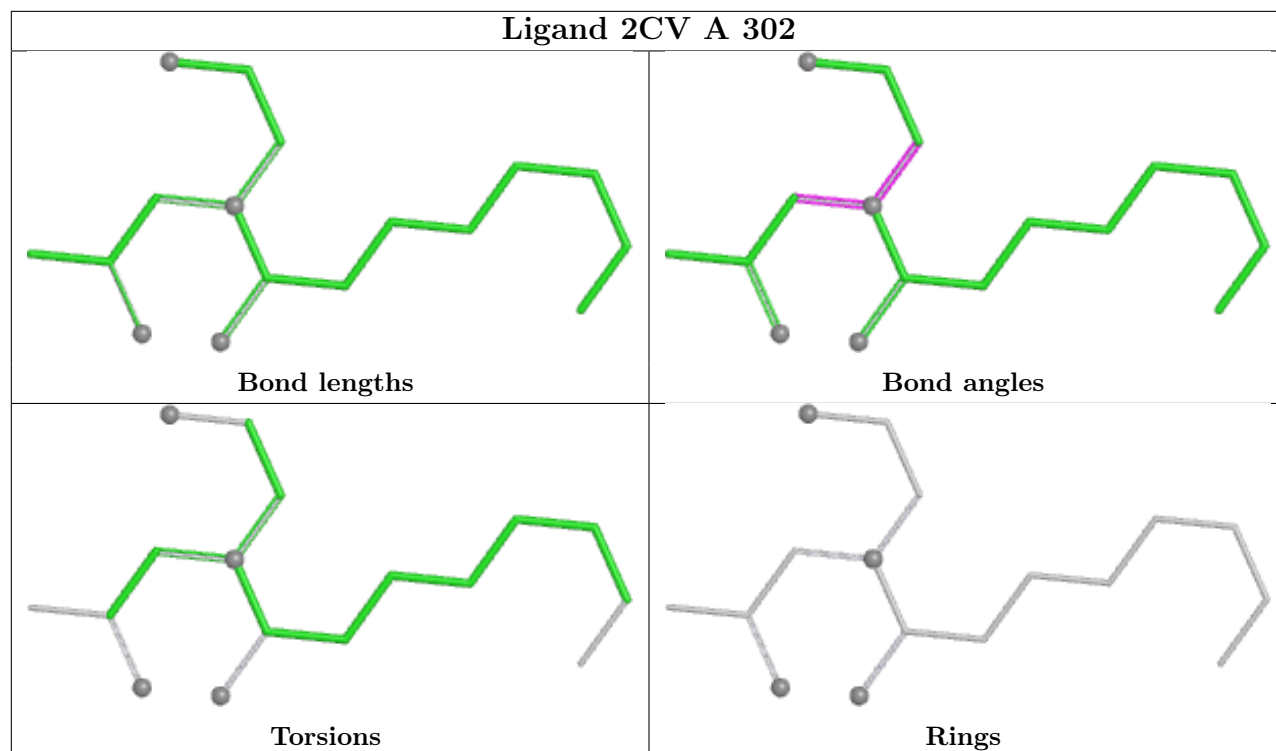
2 monomers are involved in 2 short contacts:

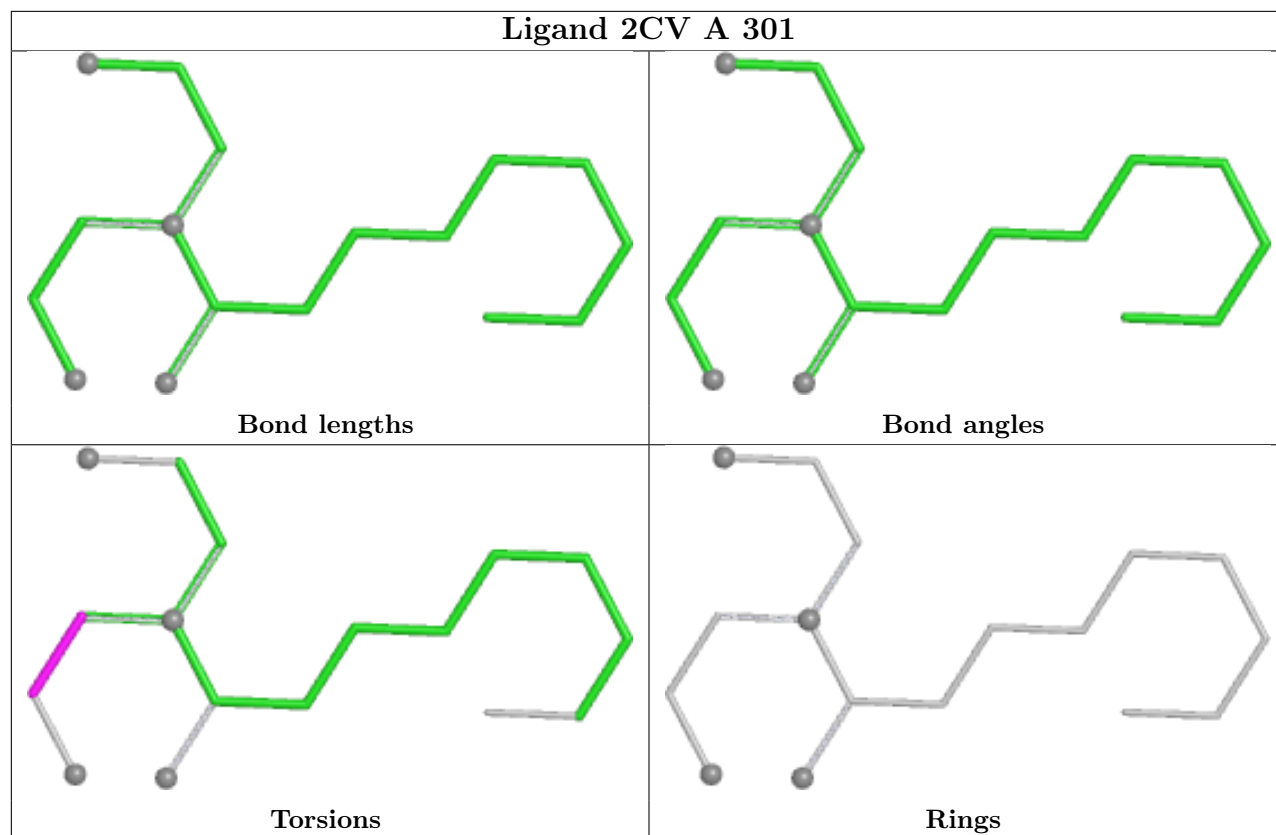
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	302	2CV	1	0
2	A	301	2CV	1	0

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	92/149 (61%)	2.18	47 (51%) 0 0	36, 51, 118, 157	0
1	B	92/149 (61%)	2.23	48 (52%) 0 0	37, 53, 121, 150	0
1	C	91/149 (61%)	2.45	52 (57%) 0 0	31, 53, 117, 166	1 (1%)
1	D	91/149 (61%)	2.50	54 (59%) 0 0	41, 53, 115, 152	1 (1%)
All	All	366/596 (61%)	2.34	201 (54%) 0 0	31, 53, 119, 166	2 (0%)

All (201) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	198	PHE	6.1
1	C	131	VAL	6.0
1	A	220	ASP	6.0
1	B	134	VAL	6.0
1	D	214	PHE	5.9
1	D	130	GLY	5.8
1	C	217	ILE	5.5
1	D	207	THR	5.5
1	C	198	PHE	5.5
1	C	132	GLY	5.4
1	D	131	VAL	5.4
1	D	220	ASP	5.3
1	D	212	ASN	5.3
1	D	217	ILE	5.3
1	C	183	GLY	5.3
1	C	212	ASN	5.1
1	D	218	ILE	5.1
1	C	207	THR	5.0
1	B	220	ASP	5.0
1	D	134	VAL	5.0
1	C	218	ILE	5.0

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Mol	Chain	Res	Type	RSRZ
1	D	143	TYR	5.0
1	D	183	GLY	4.9
1	C	214	PHE	4.9
1	B	222	MET	4.8
1	B	191	VAL	4.8
1	A	134	VAL	4.8
1	D	132	GLY	4.7
1	D	137	LEU	4.7
1	C	134	VAL	4.7
1	A	131	VAL	4.7
1	A	160	TRP	4.7
1	C	220	ASP	4.6
1	A	191	VAL	4.5
1	B	219	VAL	4.5
1	B	160	TRP	4.4
1	D	210	VAL	4.3
1	C	210	VAL	4.3
1	C	208	PHE	4.3
1	A	207	THR	4.2
1	B	207	THR	4.2
1	D	175	MET	4.1
1	A	143	TYR	4.1
1	C	135	ALA	4.1
1	D	208	PHE	4.0
1	B	131	VAL	4.0
1	C	181	SER	4.0
1	B	215	ILE	4.0
1	C	209	THR	3.9
1	A	133	SER	3.9
1	C	175	MET	3.8
1	D	135	ALA	3.8
1	A	144	ILE	3.8
1	A	195	ALA	3.8
1	A	217	ILE	3.7
1	D	138	LEU	3.7
1	D	202	PHE	3.7
1	C	130	GLY	3.6
1	C	137	LEU	3.6
1	C	202	PHE	3.6
1	A	188	VAL	3.6
1	B	169	TYR	3.6
1	B	188	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	195	ALA	3.5
1	B	210	VAL	3.5
1	D	211	LEU	3.5
1	B	206	THR	3.5
1	A	149	ALA	3.5
1	A	208	PHE	3.4
1	B	143	TYR	3.4
1	C	204	MET	3.4
1	A	206	THR	3.4
1	D	213	LEU	3.3
1	B	173	GLN	3.3
1	A	148	MET	3.3
1	C	213	LEU	3.2
1	B	217	ILE	3.2
1	D	215	ILE	3.2
1	A	210	VAL	3.2
1	D	178	GLU	3.2
1	C	138	LEU	3.2
1	B	141	VAL	3.2
1	C	143	TYR	3.2
1	C	215	ILE	3.2
1	B	202	PHE	3.1
1	C	219	VAL	3.1
1	B	184	ILE	3.1
1	D	184	ILE	3.1
1	D	209	THR	3.1
1	A	202	PHE	3.1
1	A	184	ILE	3.1
1	A	222	MET	3.1
1	C	184	ILE	3.0
1	C	205	LEU	3.0
1	D	205	LEU	3.0
1	B	149	ALA	3.0
1	D	204	MET	3.0
1	C	216	GLY	2.9
1	C	147	VAL	2.9
1	C	203	ILE	2.9
1	C	180	TRP	2.9
1	C	211	LEU	2.9
1	A	173	GLN	2.9
1	C	178	GLU	2.9
1	B	165	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	144	ILE	2.9
1	A	174	VAL	2.9
1	A	142	PHE	2.9
1	A	169	TYR	2.9
1	C	172	PHE	2.8
1	A	215	ILE	2.8
1	D	181	SER	2.8
1	D	203	ILE	2.8
1	B	167	SER	2.8
1	C	179	SER	2.8
1	D	180	TRP	2.7
1	A	139	THR	2.7
1	A	141	VAL	2.7
1	B	174	VAL	2.7
1	B	142	PHE	2.7
1	C	174	VAL	2.7
1	B	208	PHE	2.7
1	D	195	ALA	2.7
1	C	160	TRP	2.7
1	D	219	VAL	2.7
1	D	133	SER	2.7
1	A	186	ARG	2.6
1	B	139	THR	2.6
1	C	199	PHE	2.6
1	A	137	LEU	2.6
1	D	216	GLY	2.6
1	B	151	ASN	2.6
1	A	167	SER	2.6
1	A	211	LEU	2.6
1	B	211	LEU	2.5
1	D	206	THR	2.5
1	C	169	TYR	2.5
1	C	195	ALA	2.5
1	D	156	THR	2.5
1	D	179	SER	2.5
1	D	147	VAL	2.5
1	D	172	PHE	2.5
1	C	145	ALA	2.5
1	B	137	LEU	2.4
1	B	148	MET	2.4
1	A	219	VAL	2.4
1	C	141	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	199	PHE	2.4
1	D	169	TYR	2.4
1	B	168	LEU	2.4
1	B	181	SER	2.4
1	C	142	PHE	2.4
1	D	200	ILE	2.4
1	A	151	ASN	2.3
1	B	183	GLY	2.3
1	D	148	MET	2.3
1	B	213	LEU	2.3
1	C	171	LEU	2.3
1	D	176	THR	2.3
1	B	147	VAL	2.3
1	D	141	VAL	2.3
1	D	190	ASN	2.3
1	A	181	SER	2.3
1	D	152	LEU	2.3
1	C	206	THR	2.3
1	A	165	SER	2.3
1	C	176	THR	2.3
1	A	168	LEU	2.3
1	C	177	LEU	2.3
1	A	135	ALA	2.2
1	A	218	ILE	2.2
1	A	147	VAL	2.2
1	B	133	SER	2.2
1	C	197	VAL	2.2
1	D	177	LEU	2.2
1	A	180	TRP	2.2
1	C	144	ILE	2.2
1	A	176	THR	2.2
1	B	204	MET	2.2
1	D	145	ALA	2.2
1	B	176	THR	2.2
1	A	179	SER	2.2
1	B	214	PHE	2.2
1	B	135	ALA	2.2
1	C	200	ILE	2.1
1	A	216	GLY	2.1
1	A	213	LEU	2.1
1	B	179	SER	2.1
1	D	197	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	216	GLY	2.1
1	A	221	ALA	2.1
1	D	153	TYR	2.1
1	B	178	GLU	2.1
1	A	194	ASN	2.1
1	B	190	ASN	2.1
1	B	198	PHE	2.1
1	C	148[A]	MET	2.0
1	B	161	PHE	2.0
1	D	174	VAL	2.0
1	D	201	PRO	2.0
1	A	183	GLY	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	2CV	A	302	17/26	0.65	0.30	53,65,77,77	0
4	BR	C	305[A]	1/1	0.67	0.80	70,70,70,70	1
4	BR	C	305[B]	1/1	0.67	0.80	49,49,49,49	1
2	2CV	A	301	17/26	0.76	0.24	58,63,74,77	0
3	NA	A	303	1/1	0.78	0.75	78,78,78,78	1
2	2CV	C	302	17/26	0.79	0.24	37,71,76,77	0
4	BR	A	304[A]	1/1	0.82	0.72	66,66,66,66	1
4	BR	A	304[B]	1/1	0.82	0.72	44,44,44,44	1
2	2CV	C	301	17/26	0.84	0.20	42,66,72,75	0
3	NA	B	402	1/1	0.91	0.49	55,55,55,55	1
3	NA	C	303	1/1	0.93	0.86	78,78,78,78	1

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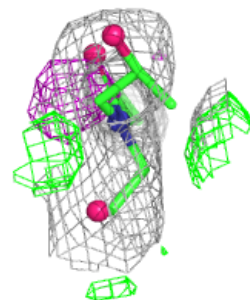
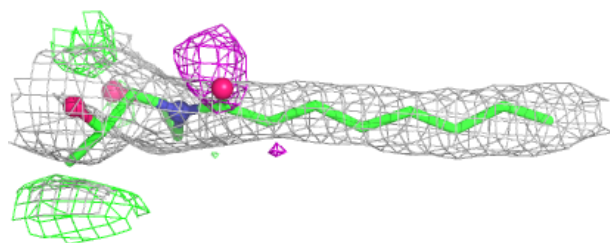
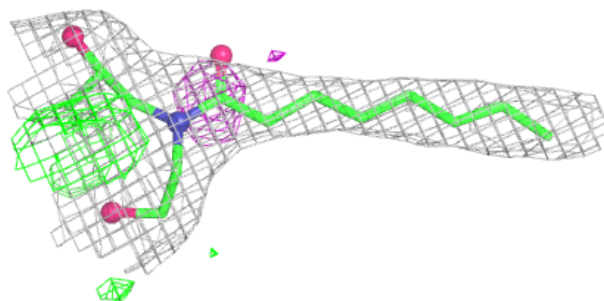
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NA	B	401	1/1	0.96	1.07	93,93,93,93	1
3	NA	C	304	1/1	0.97	0.40	63,63,63,63	1
3	NA	D	401	1/1	0.97	0.44	39,39,39,39	1

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.

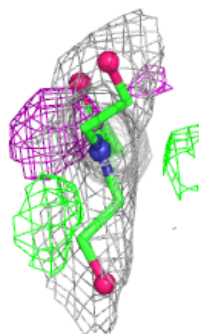
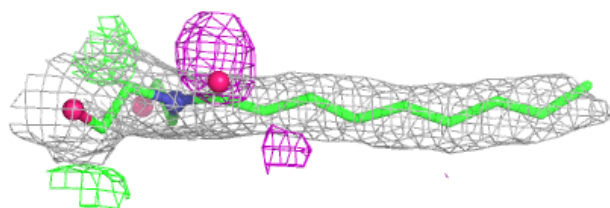
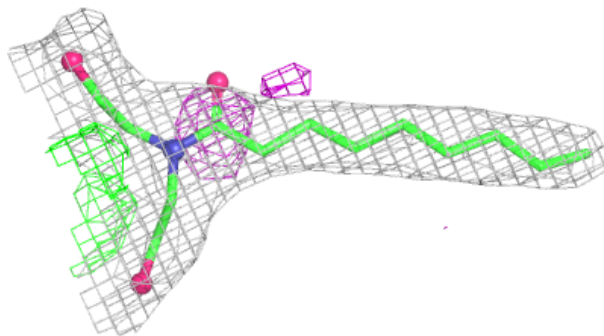
Electron density around 2CV A 302:

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

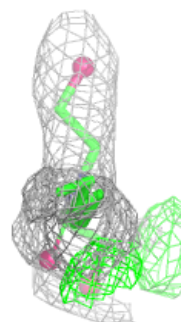
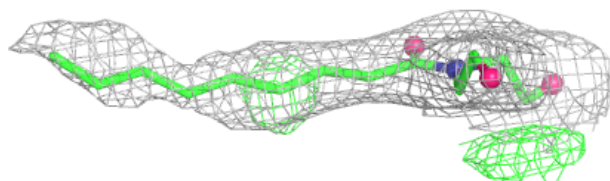
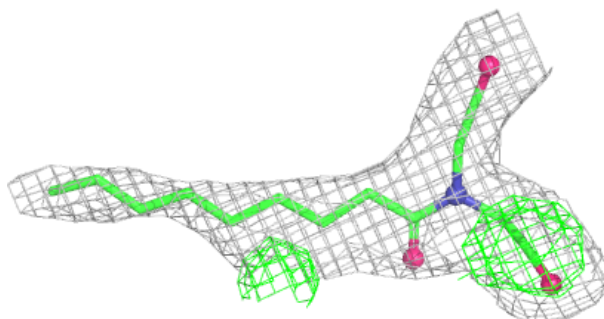


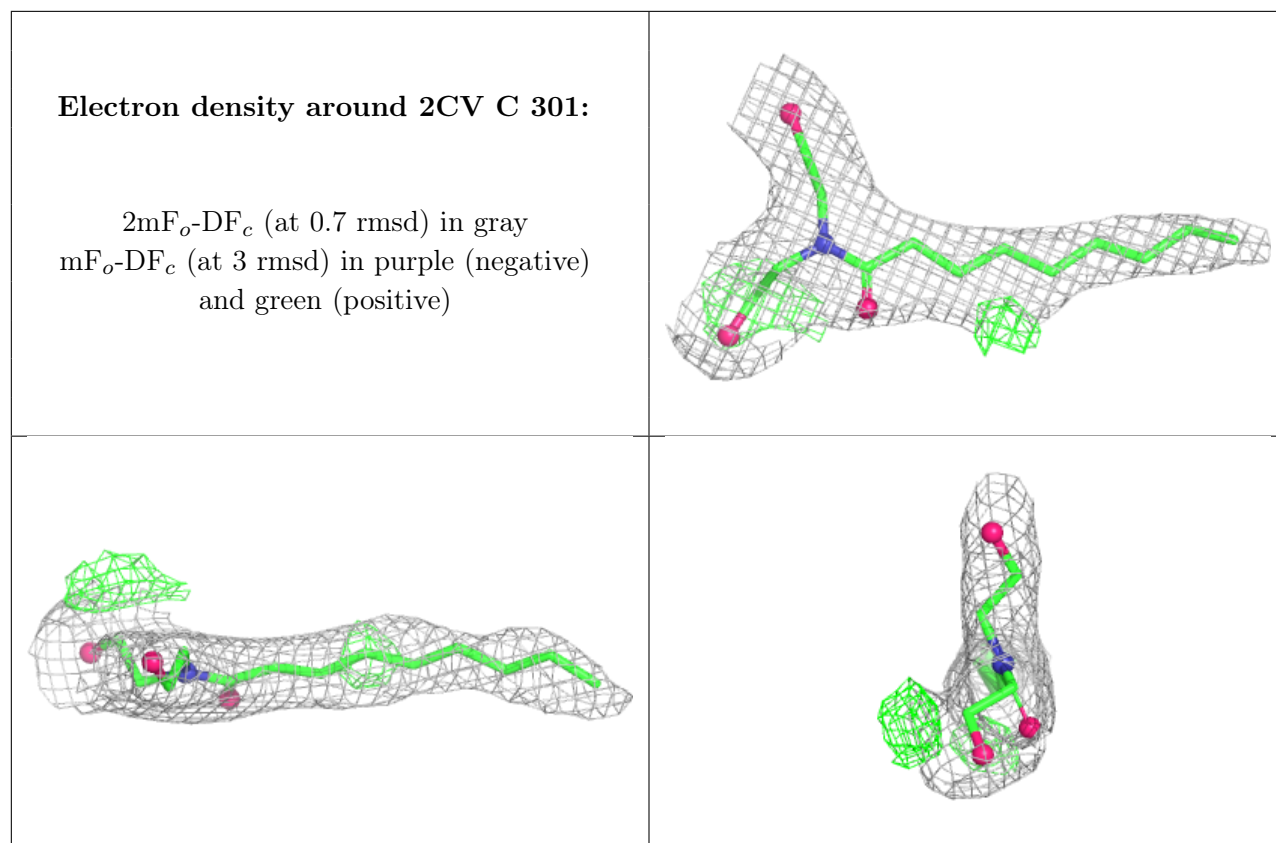
Electron density around 2CV A 301:

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

**Electron density around 2CV C 302:**

$2mF_o-DF_c$ (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.