Full wwPDB X-ray Structure Validation Report (i)

Mar 6, 2026 – 03:08 PM UTC

PDB ID	:	9GTQ / pdb_00009gtq
Title	:	NavMs F208L Apo
Authors	:	Hollingworth, D.; Wallace, B.A.
Deposited on	:	2024-09-18
Resolution	:	2.20 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 (i) 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 (i)) were used in the production of this report:

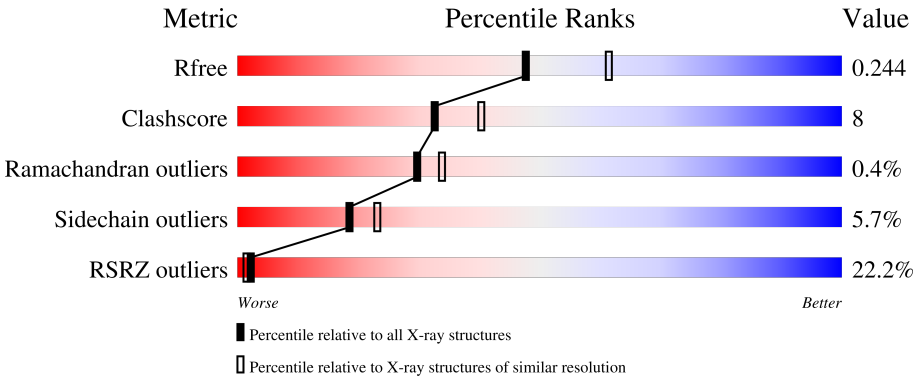
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 <=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	276	20% 67% 21% • 9%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2099 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.

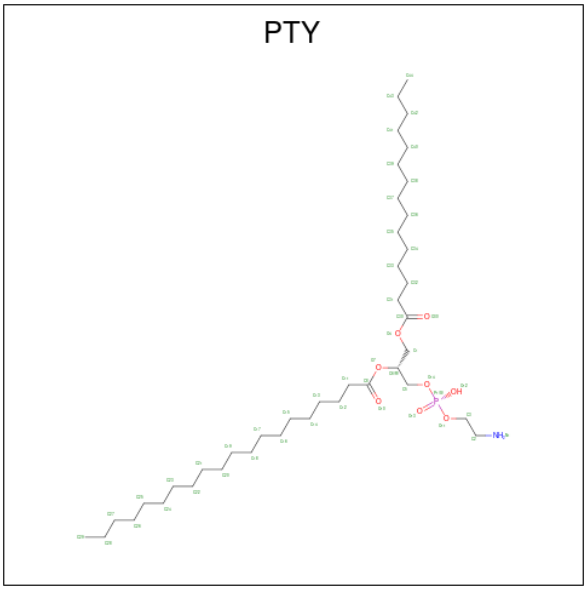
- Molecule 1 is a protein called Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	252	1960	1284	322	341	13	0	1	0

There are 3 discrepancies between the modelled and reference sequences:

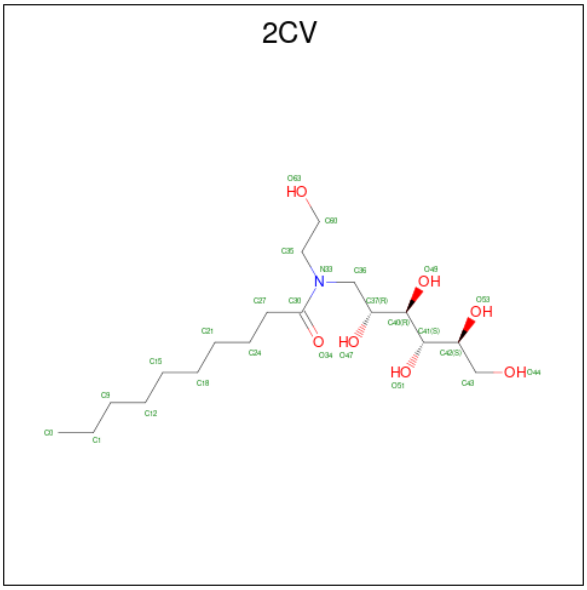
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP A0L5S6
A	0	HIS	-	expression tag	UNP A0L5S6
A	208	LEU	PHE	engineered mutation	UNP A0L5S6

- Molecule 2 is PHOSPHATIDYLETHANOLAMINE (CCD ID: PTY) (formula: $C_{40}H_{80}NO_8P$).



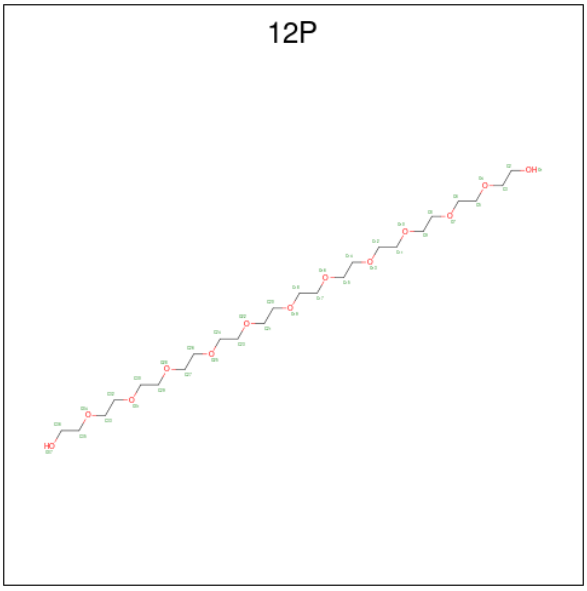
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	C		
2	A	1	7	7	0	0
			Total	C		
2	A	1	20	20	0	0

- Molecule 3 is HEGA-10 (CCD ID: 2CV) (formula: $C_{18}H_{37}NO_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 23 17 1 5	0	0
3	A	1	Total C 9 9	0	0
3	A	1	Total C 8 8	0	0

- Molecule 4 is DODECAETHYLENE GLYCOL (CCD ID: 12P) (formula: $C_{24}H_{50}O_{13}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			20	13	7		

- Molecule 5 is water.

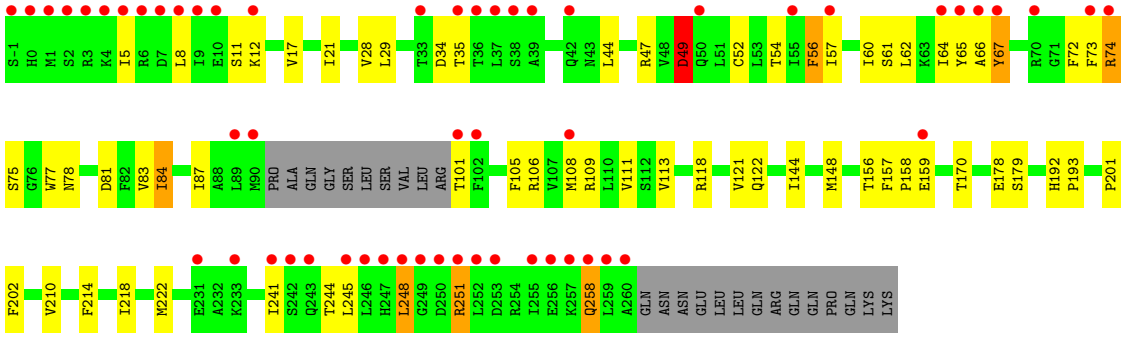
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	52	Total	O	0	0
			52	52		

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

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α, β, γ	108.93Å 108.93Å 209.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.95 – 2.20 39.95 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (39.95-2.20) 100.0 (39.95-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.87 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.217 , 0.244 0.217 , 0.244	Depositor DCC
R_{free} test set	1665 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å^2)	41.6	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 61.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	2099	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.61% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: PTY, 12P, 2CV

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	0.83	2/1999 (0.1%)	1.49	19/2719 (0.7%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	201	PRO	CA-CB	7.38	1.64	1.53
1	A	158	PRO	CA-CB	6.57	1.63	1.53

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	157	PHE	CA-CB-CG	-7.55	106.25	113.80
1	A	159	GLU	CB-CG-CD	7.22	124.88	112.60
1	A	113	VAL	CA-C-N	-6.03	118.50	122.60
1	A	113	VAL	C-N-CA	-6.03	118.50	122.60
1	A	67	TYR	N-CA-CB	6.00	120.62	110.49
1	A	251	ARG	CA-CB-CG	5.79	125.68	114.10
1	A	29	LEU	CA-C-N	5.35	125.77	119.94
1	A	29	LEU	C-N-CA	5.35	125.77	119.94
1	A	202	PHE	CA-CB-CG	-5.34	108.46	113.80
1	A	56	PHE	N-CA-CB	5.32	118.52	110.28
1	A	193	PRO	CA-C-N	-5.26	114.26	122.73
1	A	193	PRO	C-N-CA	-5.26	114.26	122.73
1	A	170	THR	CA-CB-OG1	-5.26	101.71	109.60
1	A	214	PHE	N-CA-CB	5.16	117.50	110.01
1	A	49	ASP	CA-CB-CG	5.16	117.76	112.60
1	A	67	TYR	CB-CA-C	-5.12	100.23	110.42
1	A	52	CYS	CA-C-N	-5.04	113.02	120.28
1	A	52	CYS	C-N-CA	-5.04	113.02	120.28
1	A	258	GLN	N-CA-CB	5.04	117.27	109.91

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	1960	0	2000	31	0
2	A	27	0	52	1	0
3	A	40	0	64	0	0
4	A	20	0	24	1	0
5	A	52	0	0	0	0
All	All	2099	0	2140	33	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 8.

All (33) 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:8:LEU:O	1:A:11:SER:OG	2.08	0.72
1:A:111:VAL:HG11	1:A:121:VAL:HG21	1.76	0.68
1:A:72:PHE:HD2	1:A:73:PHE:CD1	2.15	0.64
1:A:118:ARG:O	1:A:122:GLN:HG3	1.98	0.63
1:A:65:TYR:O	1:A:67:TYR:N	2.35	0.60
1:A:5:ILE:O	1:A:8:LEU:HB3	2.06	0.56
1:A:156:THR:OG1	1:A:192:HIS:HE1	1.88	0.56
1:A:56:PHE:O	1:A:60:ILE:HG12	2.09	0.52
1:A:17:VAL:O	1:A:21:ILE:HG12	2.09	0.52
1:A:81:ASP:CG	1:A:109:ARG:HH21	2.18	0.51
1:A:61:SER:HA	1:A:64:ILE:HG13	1.91	0.51
1:A:144:ILE:O	1:A:148:MET:HG3	2.11	0.50
1:A:49:ASP:OD1	1:A:106:ARG:NH1	2.44	0.50
1:A:34:ASP:OD1	1:A:34:ASP:C	2.56	0.48
1:A:65:TYR:C	1:A:67:TYR:H	2.22	0.48
1:A:105:PHE:HB3	1:A:108[A]:MET:HE2	1.94	0.48
1:A:5:ILE:O	1:A:8:LEU:N	2.48	0.44
1:A:64:ILE:HD12	1:A:65:TYR:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:THR:O	1:A:248:LEU:HB2	2.17	0.44
1:A:83:VAL:O	1:A:84:ILE:C	2.61	0.44
1:A:75:SER:HB3	1:A:78:ASN:ND2	2.33	0.43
1:A:77:TRP:CE2	1:A:118:ARG:HG3	2.53	0.43
1:A:47:ARG:HD3	1:A:47:ARG:HA	1.87	0.43
4:A:303:12P:H271	4:A:303:12P:H301	1.71	0.43
2:A:301:PTY:H392	2:A:301:PTY:H422	1.75	0.43
1:A:61:SER:O	1:A:62:LEU:C	2.61	0.43
1:A:178:GLU:OE2	1:A:179:SER:OG	2.29	0.42
1:A:44:LEU:O	1:A:47:ARG:N	2.50	0.42
1:A:218:ILE:O	1:A:222:MET:HG3	2.20	0.42
1:A:74:ARG:HB3	1:A:74:ARG:NH1	2.35	0.41
1:A:241:ILE:O	1:A:245:LEU:HG	2.20	0.41
1:A:77:TRP:CZ2	1:A:118:ARG:HG3	2.55	0.41
1:A:54:THR:HA	1:A:57:ILE:HD12	2.03	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	249/276 (90%)	228 (92%)	20 (8%)	1 (0%)	30 34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	66	ALA

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	210/242 (87%)	198 (94%)	12 (6%)	18 23

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LYS
1	A	28	VAL
1	A	35	THR
1	A	49	ASP
1	A	74	ARG
1	A	84	ILE
1	A	87	ILE
1	A	101	THR
1	A	210	VAL
1	A	248	LEU
1	A	251	ARG
1	A	258	GLN

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

Mol	Chain	Res	Type
1	A	192	HIS
1	A	194	ASN
1	A	237	HIS
1	A	247	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

6 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	$\#\|Z\| > 2$
2	PTY	A	301	-	6,6,49	0.46	0	5,5,54	0.40	0
3	2CV	A	302	-	22,22,25	1.35	2 (9%)	25,26,30	1.87	4 (16%)
4	12P	A	303	-	19,19,36	0.30	0	18,18,35	0.34	0
3	2CV	A	305	-	7,7,25	0.65	0	6,6,30	0.54	0
3	2CV	A	304	-	8,8,25	0.14	0	7,7,30	0.16	0
2	PTY	A	306	-	19,19,49	0.40	0	18,18,54	0.30	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	PTY	A	301	-	-	3/4/4/53	-
3	2CV	A	302	-	-	11/28/28/34	-
4	12P	A	303	-	-	13/17/17/34	-
3	2CV	A	305	-	-	1/5/5/34	-
3	2CV	A	304	-	-	3/6/6/34	-
2	PTY	A	306	-	-	13/17/17/53	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	2CV	O51-C41	4.42	1.54	1.43
3	A	302	2CV	C37-C40	3.65	1.59	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	302	2CV	C37-C40-C41	6.57	122.60	112.48
3	A	302	2CV	O51-C41-C40	4.04	116.46	109.77
3	A	302	2CV	C36-C37-C40	3.56	119.30	109.66
3	A	302	2CV	C42-C41-C40	2.18	114.78	112.11

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	2CV	N33-C36-C37-C40
3	A	302	2CV	N33-C36-C37-O47
3	A	302	2CV	C36-C37-C40-C41
3	A	302	2CV	C36-C37-C40-O49
3	A	302	2CV	O47-C37-C40-C41
3	A	302	2CV	O47-C37-C40-O49
4	A	303	12P	C30-C29-O28-C27
3	A	302	2CV	O49-C40-C41-O51
4	A	303	12P	O31-C32-C33-O34
2	A	306	PTY	C18-C19-C20-C21
3	A	305	2CV	C15-C12-C9-C1
4	A	303	12P	O28-C29-C30-O31
2	A	301	PTY	C39-C40-C41-C42
4	A	303	12P	O16-C17-C18-O19
2	A	301	PTY	C40-C41-C42-C43
2	A	306	PTY	C16-C17-C18-C19
3	A	304	2CV	C12-C15-C18-C21
2	A	306	PTY	C17-C18-C19-C20
2	A	306	PTY	C14-C15-C16-C17
2	A	306	PTY	C13-C14-C15-C16
2	A	306	PTY	C26-C27-C28-C29
3	A	304	2CV	C15-C18-C21-C24
4	A	303	12P	C32-C33-O34-C35
3	A	304	2CV	C9-C12-C15-C18
3	A	302	2CV	C37-C36-N33-C35
3	A	302	2CV	C37-C40-C41-O51
4	A	303	12P	C33-C32-O31-C30
4	A	303	12P	C21-C20-O19-C18
4	A	303	12P	C27-C26-O25-C24
2	A	306	PTY	C25-C26-C27-C28
2	A	301	PTY	C38-C39-C40-C41
4	A	303	12P	O22-C23-C24-O25

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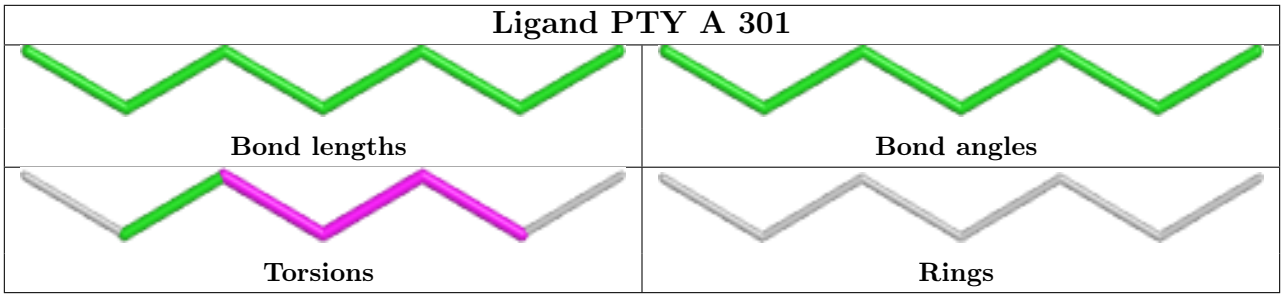
Mol	Chain	Res	Type	Atoms
2	A	306	PTY	C19-C20-C21-C22
2	A	306	PTY	C21-C22-C23-C24
2	A	306	PTY	C12-C13-C14-C15
2	A	306	PTY	C22-C23-C24-C25
4	A	303	12P	O25-C26-C27-O28
4	A	303	12P	C29-C30-O31-C32
2	A	306	PTY	C11-C12-C13-C14
4	A	303	12P	C23-C24-O25-C26
4	A	303	12P	O19-C20-C21-O22
3	A	302	2CV	C12-C15-C18-C21
2	A	306	PTY	C8-C11-C12-C13
3	A	302	2CV	C37-C40-C41-C42

There are no ring outliers.

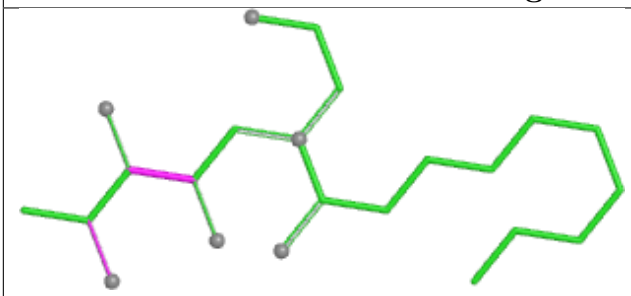
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	PTY	1	0
4	A	303	12P	1	0

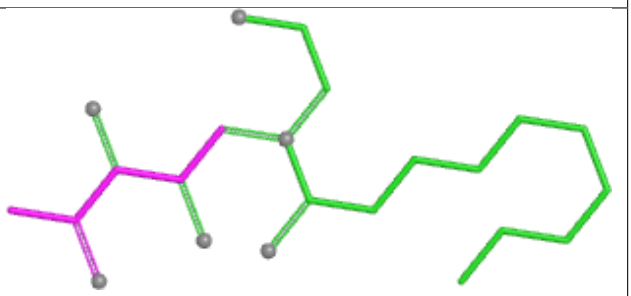
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



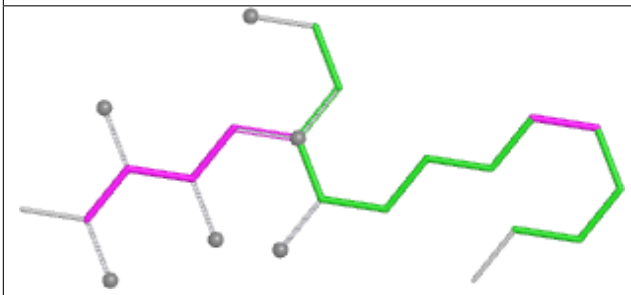
Ligand 2CV A 302



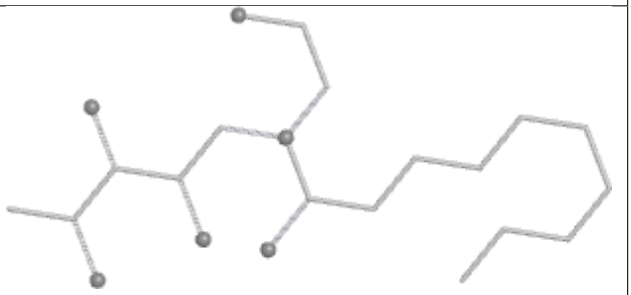
Bond lengths



Bond angles



Torsions



Rings

Ligand 12P A 303

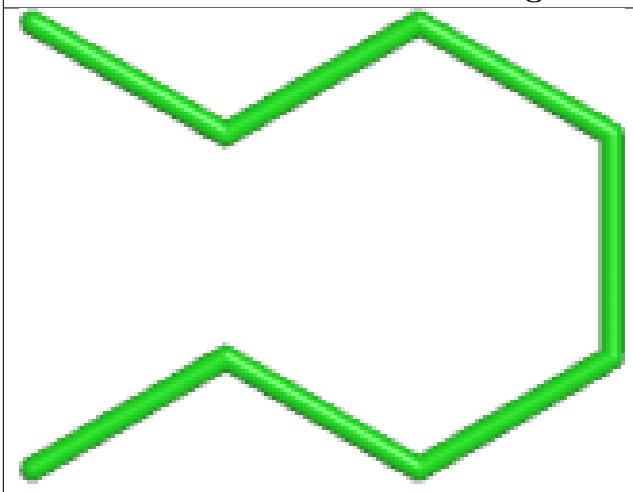
Bond lengths

Bond angles

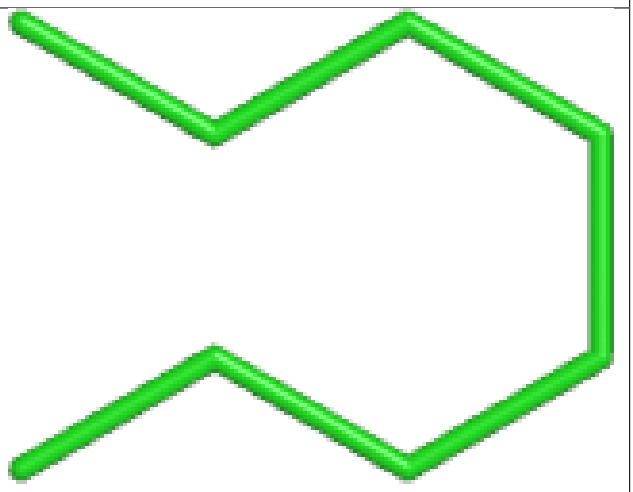
Torsions

Rings

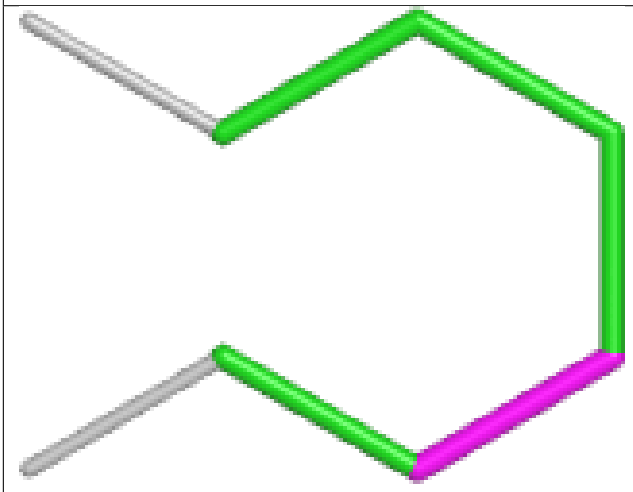
Ligand 2CV A 305



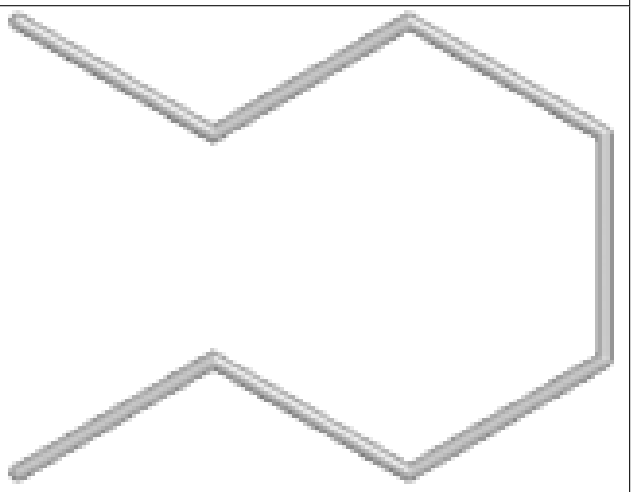
Bond lengths



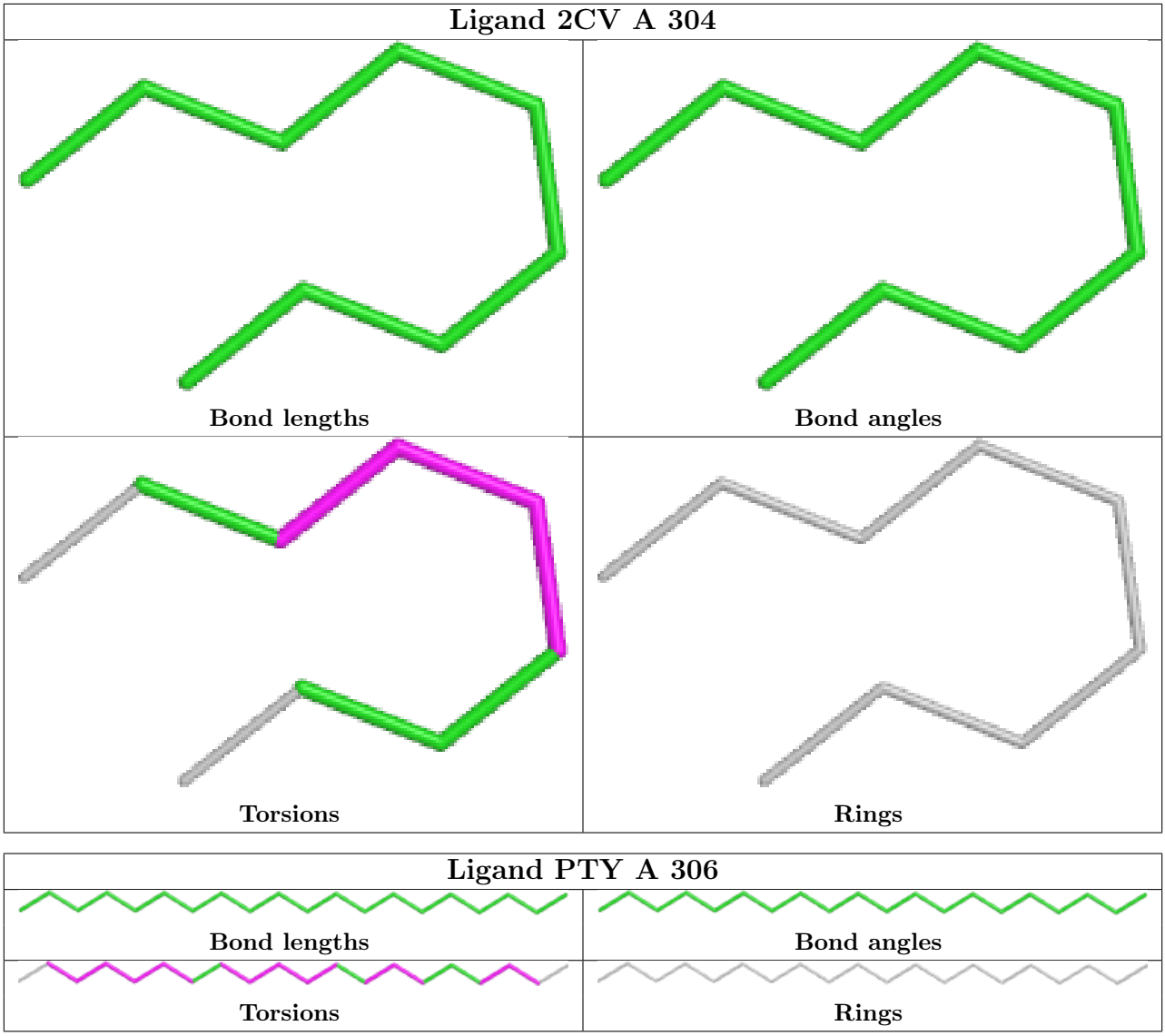
Bond angles



Torsions



Rings



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, 95^{th} 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	252/276 (91%)	1.11	56 (22%) 2 1	24, 56, 135, 192	1 (0%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	246	LEU	9.2
1	A	260	ALA	7.5
1	A	248	LEU	6.8
1	A	259	LEU	6.7
1	A	7	ASP	6.1
1	A	250	ASP	6.0
1	A	90	MET	5.7
1	A	247	HIS	5.5
1	A	5	ILE	5.4
1	A	249	GLY	5.4
1	A	65	TYR	5.3
1	A	1	MET	5.2
1	A	8	LEU	4.9
1	A	102	PHE	4.8
1	A	2	SER	4.6
1	A	6	ARG	4.4
1	A	9	ILE	4.4
1	A	57	ILE	4.2
1	A	10	GLU	4.1
1	A	251	ARG	4.1
1	A	35	THR	4.1
1	A	64	ILE	3.8
1	A	-1	SER	3.8
1	A	66	ALA	3.8
1	A	67	TYR	3.7
1	A	258	GLN	3.5
1	A	74	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	253	ASP	3.4
1	A	252	LEU	3.3
1	A	255	ILE	3.2
1	A	0	HIS	3.0
1	A	4	LYS	3.0
1	A	243	GLN	3.0
1	A	70	ARG	2.9
1	A	55	ILE	2.9
1	A	101	THR	2.9
1	A	42	GLN	2.8
1	A	33	THR	2.7
1	A	242	SER	2.7
1	A	233	LYS	2.7
1	A	12	LYS	2.6
1	A	36	THR	2.6
1	A	245	LEU	2.6
1	A	50	GLN	2.6
1	A	256	GLU	2.6
1	A	241	ILE	2.6
1	A	3	ARG	2.5
1	A	73	PHE	2.5
1	A	108[A]	MET	2.5
1	A	159	GLU	2.5
1	A	231	GLU	2.4
1	A	257	LYS	2.4
1	A	37	LEU	2.3
1	A	38	SER	2.3
1	A	89	LEU	2.3
1	A	39	ALA	2.1

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

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

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

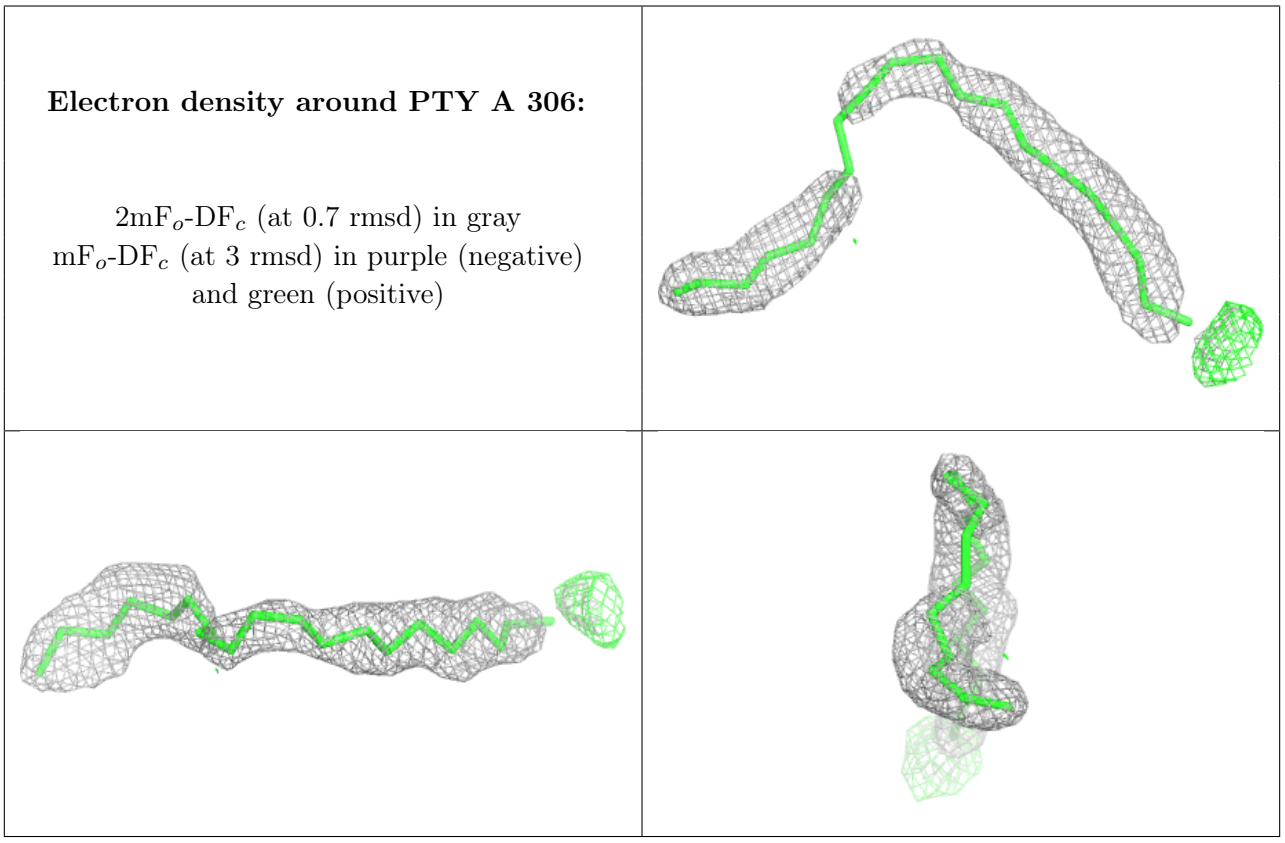
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	PTY	A	306	20/50	0.77	0.33	61,76,102,102	0
3	2CV	A	304	9/26	0.78	0.37	64,71,104,105	0
3	2CV	A	302	23/26	0.83	0.22	34,55,88,106	0
2	PTY	A	301	7/50	0.86	0.26	53,59,86,88	0
4	12P	A	303	20/37	0.88	0.21	46,77,112,115	0
3	2CV	A	305	8/26	0.89	0.21	37,62,69,72	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.

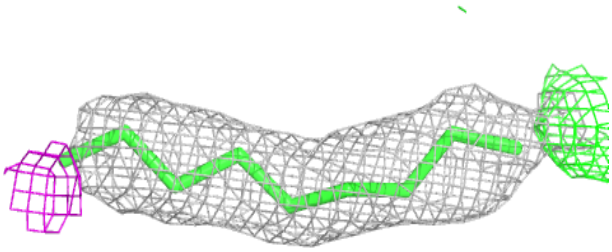
Electron density around PTY A 306:

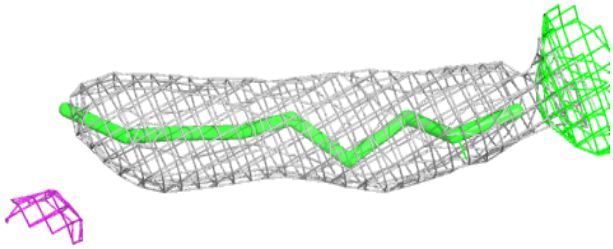
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

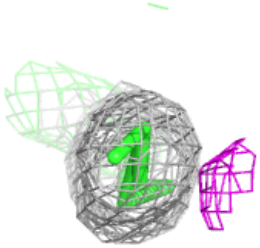


Electron density around 2CV A 304:

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

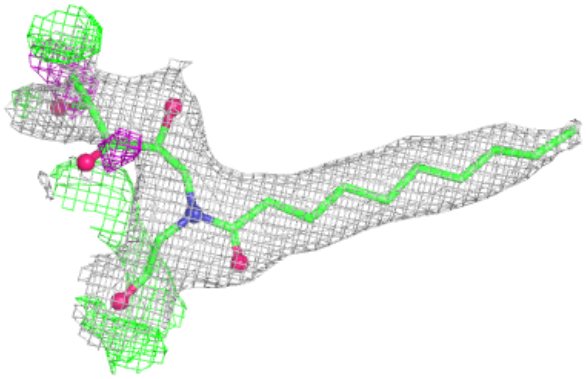


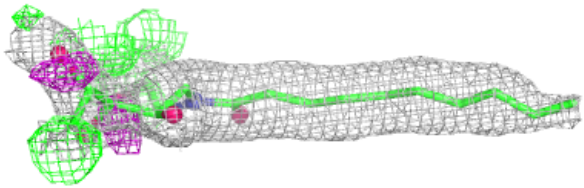


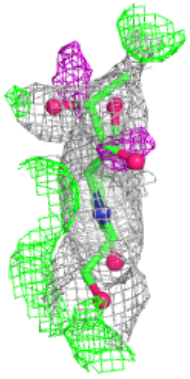


Electron density around 2CV A 302:

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

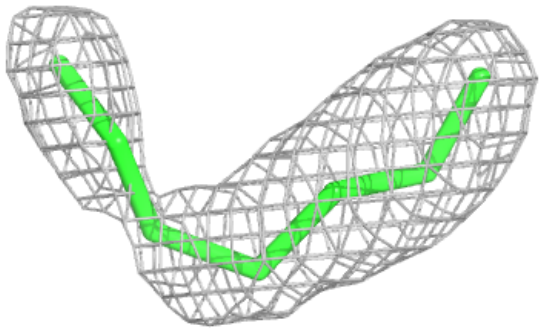


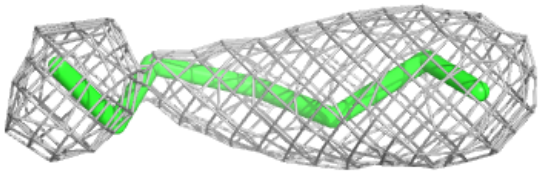


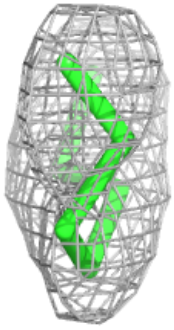


Electron density around PTY A 301:

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

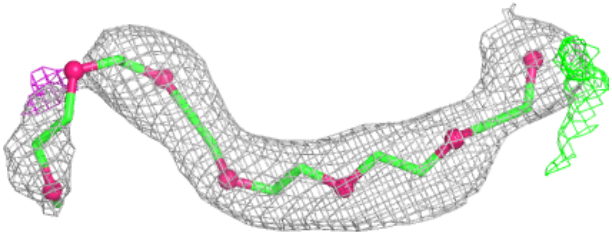


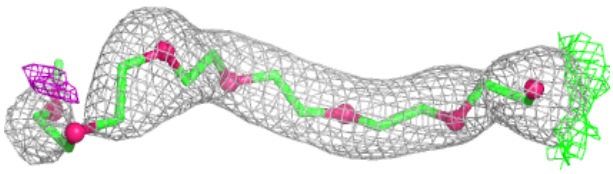


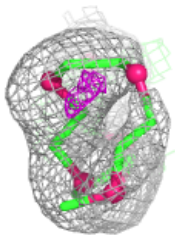


Electron density around 12P A 303:

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

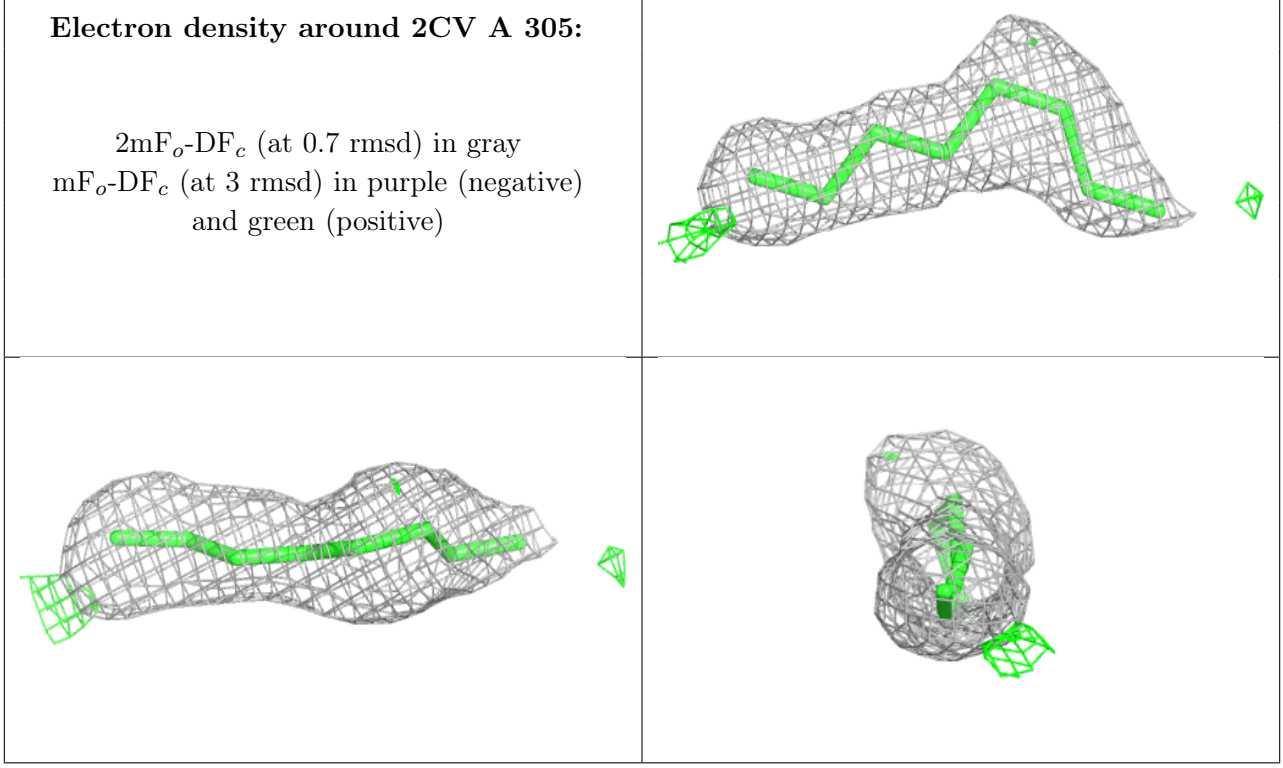






Electron density around 2CV A 305:

$2mF_o$-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.