



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2020 – 07:32 AM BST

PDB ID : 3RIF  
Title : C. elegans glutamate-gated chloride channel (GluCl) in complex with Fab, ivermectin and glutamate.  
Authors : Hibbs, R.E.; Gouaux, E.  
Deposited on : 2011-04-13  
Resolution : 3.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 : 2.13.1  
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) : 2.13.1

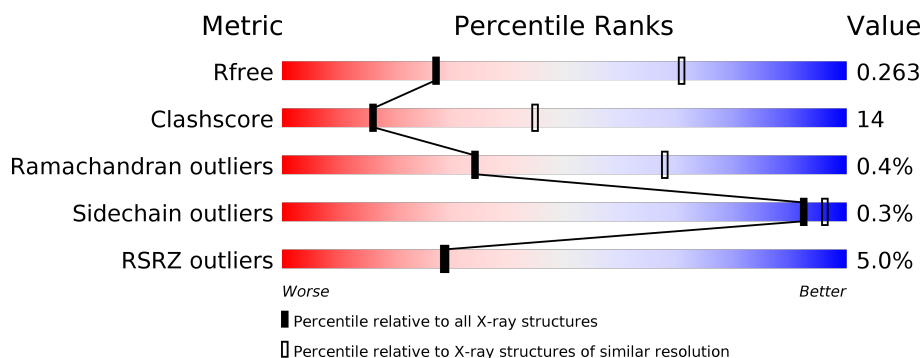
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.35 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	1060 (3.38-3.30)
Clashscore	141614	1111 (3.38-3.30)
Ramachandran outliers	138981	1090 (3.38-3.30)
Sidechain outliers	138945	1089 (3.38-3.30)
RSRZ outliers	127900	1028 (3.38-3.30)

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  $\geq 3$ , 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	347	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 68%, green 29%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>68%</span> <span>29%</span> <span>.</span> </div> </div>
1	B	347	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 67%, green 31%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>67%</span> <span>31%</span> <span>.</span> </div> </div>
1	C	347	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 4%, orange 1%, yellow 66%, green 31%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>4%</span> <span>66%</span> <span>31%</span> <span>.</span> </div> </div>
1	D	347	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 67%, green 30%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>67%</span> <span>30%</span> <span>.</span> </div> </div>
1	E	347	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 1%, yellow 68%, green 30%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>2%</span> <span>68%</span> <span>30%</span> <span>.</span> </div> </div>
2	F	221	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 9%, orange 1%, yellow 59%, green 18%, grey 23%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>9%</span> <span>59%</span> <span>18%</span> <span>23%</span> </div> </div>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	G	221	
2	H	221	
2	I	221	
2	J	221	
3	K	210	
3	L	210	
3	M	210	
3	N	210	
3	O	210	

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
10	UND	B	406	-	-	-	X
6	LMT	A	405	-	-	-	X

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 29020 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 Avermectin-sensitive glutamate-gated chloride channel GluCl alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2720	1771	442	492	15			
1	B	340	Total	C	N	O	S	0	0	0
			2720	1771	442	492	15			
1	C	339	Total	C	N	O	S	0	0	0
			2710	1765	439	491	15			
1	D	340	Total	C	N	O	S	0	0	0
			2720	1771	442	492	15			
1	E	340	Total	C	N	O	S	0	0	0
			2720	1771	442	492	15			

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	303	ALA	-	linker	UNP O17793
A	304	GLY	-	linker	UNP O17793
A	305	THR	-	linker	UNP O17793
A	340	HIS	-	expression tag	UNP O17793
A	341	HIS	-	expression tag	UNP O17793
A	342	HIS	-	expression tag	UNP O17793
A	343	HIS	-	expression tag	UNP O17793
A	344	HIS	-	expression tag	UNP O17793
A	345	HIS	-	expression tag	UNP O17793
A	346	HIS	-	expression tag	UNP O17793
A	347	HIS	-	expression tag	UNP O17793
B	303	ALA	-	linker	UNP O17793
B	304	GLY	-	linker	UNP O17793
B	305	THR	-	linker	UNP O17793
B	340	HIS	-	expression tag	UNP O17793
B	341	HIS	-	expression tag	UNP O17793
B	342	HIS	-	expression tag	UNP O17793
B	343	HIS	-	expression tag	UNP O17793

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	344	HIS	-	expression tag	UNP O17793
B	345	HIS	-	expression tag	UNP O17793
B	346	HIS	-	expression tag	UNP O17793
B	347	HIS	-	expression tag	UNP O17793
C	303	ALA	-	linker	UNP O17793
C	304	GLY	-	linker	UNP O17793
C	305	THR	-	linker	UNP O17793
C	340	HIS	-	expression tag	UNP O17793
C	341	HIS	-	expression tag	UNP O17793
C	342	HIS	-	expression tag	UNP O17793
C	343	HIS	-	expression tag	UNP O17793
C	344	HIS	-	expression tag	UNP O17793
C	345	HIS	-	expression tag	UNP O17793
C	346	HIS	-	expression tag	UNP O17793
C	347	HIS	-	expression tag	UNP O17793
D	303	ALA	-	linker	UNP O17793
D	304	GLY	-	linker	UNP O17793
D	305	THR	-	linker	UNP O17793
D	340	HIS	-	expression tag	UNP O17793
D	341	HIS	-	expression tag	UNP O17793
D	342	HIS	-	expression tag	UNP O17793
D	343	HIS	-	expression tag	UNP O17793
D	344	HIS	-	expression tag	UNP O17793
D	345	HIS	-	expression tag	UNP O17793
D	346	HIS	-	expression tag	UNP O17793
D	347	HIS	-	expression tag	UNP O17793
E	303	ALA	-	linker	UNP O17793
E	304	GLY	-	linker	UNP O17793
E	305	THR	-	linker	UNP O17793
E	340	HIS	-	expression tag	UNP O17793
E	341	HIS	-	expression tag	UNP O17793
E	342	HIS	-	expression tag	UNP O17793
E	343	HIS	-	expression tag	UNP O17793
E	344	HIS	-	expression tag	UNP O17793
E	345	HIS	-	expression tag	UNP O17793
E	346	HIS	-	expression tag	UNP O17793
E	347	HIS	-	expression tag	UNP O17793

- Molecule 2 is a protein called Mouse monoclonal Fab fragment, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	171	Total	C	N	O	S	0	0	0
			1324	846	213	259	6			

*Continued on next page...*

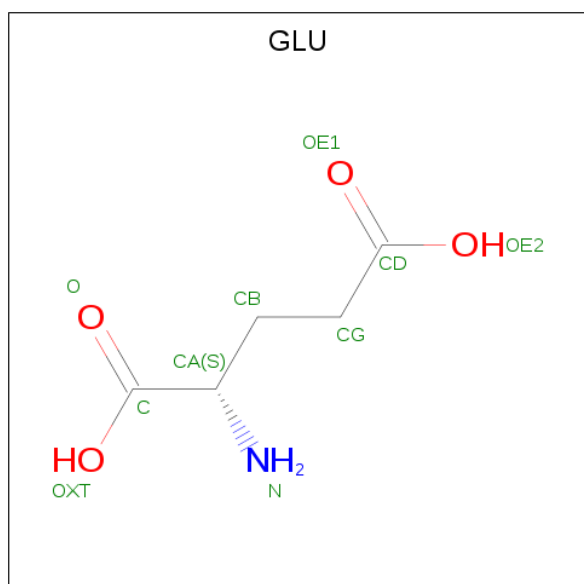
Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	214	Total	C	N	O	S	0	0	0
			1631	1038	263	323	7			
2	H	221	Total	C	N	O	S	0	0	0
			1675	1061	271	335	8			
2	I	192	Total	C	N	O	S	0	0	0
			1466	932	238	288	8			
2	J	200	Total	C	N	O	S	0	0	0
			1526	971	247	301	7			

- Molecule 3 is a protein called Mouse monoclonal Fab fragment, light chain.

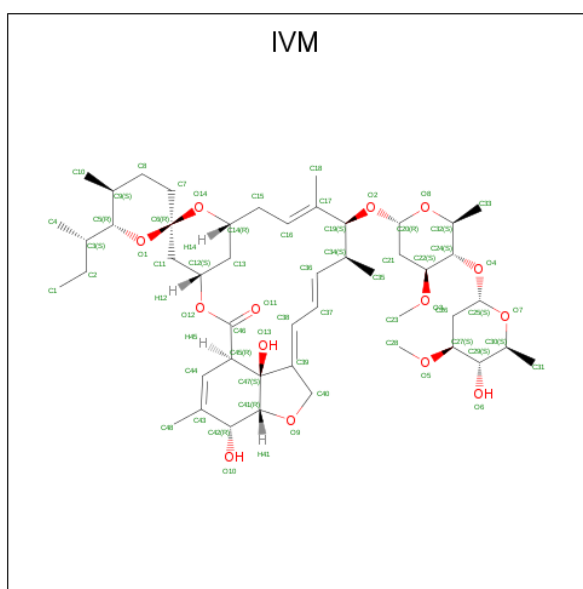
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	K	210	Total	C	N	O	S	0	0	0
			1579	993	260	320	6			
3	L	210	Total	C	N	O	S	0	0	0
			1591	999	266	320	6			
3	M	210	Total	C	N	O	S	0	0	0
			1576	991	262	317	6			
3	N	148	Total	C	N	O	S	0	0	0
			1075	678	180	214	3			
3	O	195	Total	C	N	O	S	0	0	0
			1470	927	243	294	6			

- Molecule 4 is GLUTAMIC ACID (three-letter code: GLU) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>4</sub>).



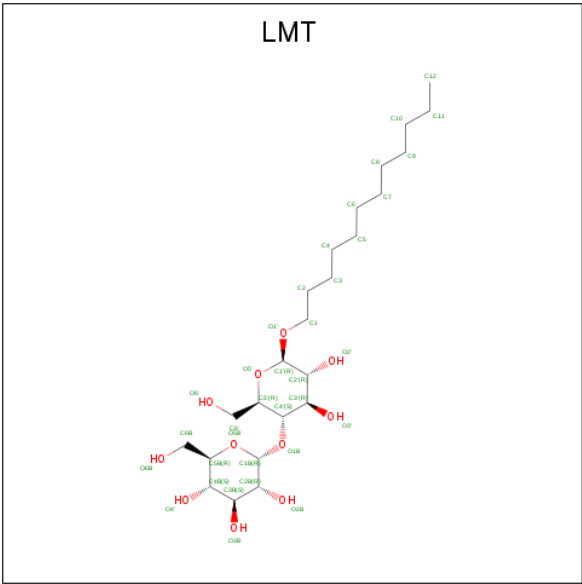
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	5	1	4		
4	B	1	Total	C	N	O	0	0
			10	5	1	4		
4	C	1	Total	C	N	O	0	0
			10	5	1	4		
4	D	1	Total	C	N	O	0	0
			10	5	1	4		
4	E	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 5 is (2aE,4E,5'S,6S,6'R,7S,8E,11R,13R,15S,17aR,20R,20aR,20bS)-6'-[(2S)-butan-2-yl]-20,20b-dihydroxy-5',6,8,19-tetramethyl-17-oxo-3',4',5',6,6',10,11,14,15,17,17a,20,20a,20b-tetradecahydro-2H,7H-spiro[11,15-methanofuro[4,3,2-pq][2,6]benzodioxacy cloctadecine-13,2'-pyran]-7-yl 2,6-dideoxy-4-O-(2,6-dideoxy-3-O-methyl-alpha-L-arabino-hexopyranosyl)-3-O-methyl-alpha-L-arabino-hexopyranoside (three-letter code: IVM) (formula: C<sub>48</sub>H<sub>74</sub>O<sub>14</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			62	48	14		
5	A	1	Total	C	O	0	0
			62	48	14		
5	B	1	Total	C	O	0	0
			62	48	14		
5	D	1	Total	C	O	0	0
			62	48	14		
5	E	1	Total	C	O	0	0
			62	48	14		

- Molecule 6 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: C<sub>24</sub>H<sub>46</sub>O<sub>11</sub>).



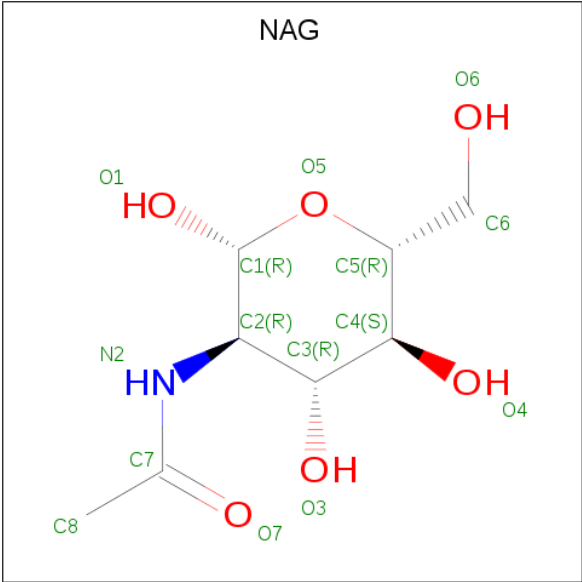
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			26	15	11		
6	A	1	Total	C	O	0	0
			27	16	11		
6	B	1	Total	C	O	0	0
			26	15	11		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Cl	0	0
			1	1		

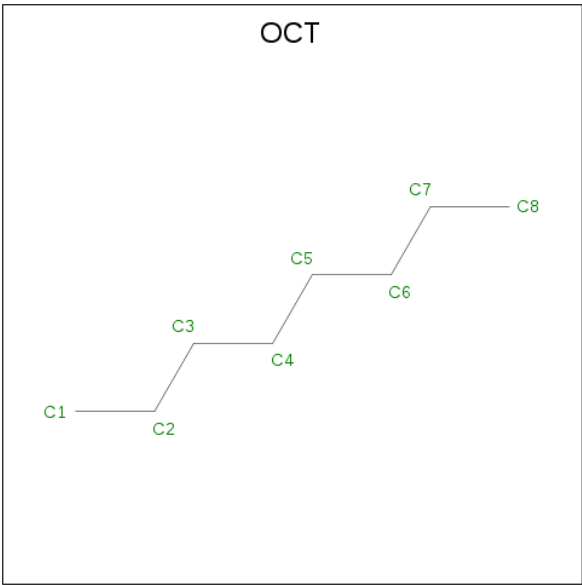
- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	C	1	Total	C	N	O	0	0
			14	8	1	5		
8	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is N-OCTANE (three-letter code: OCT) (formula: C<sub>8</sub>H<sub>18</sub>).



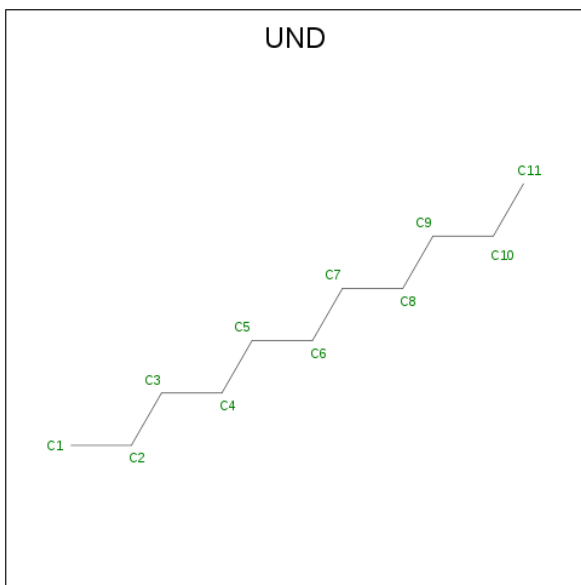
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	C	0	0
			8	8		

Continued on next page...

*Continued from previous page...*

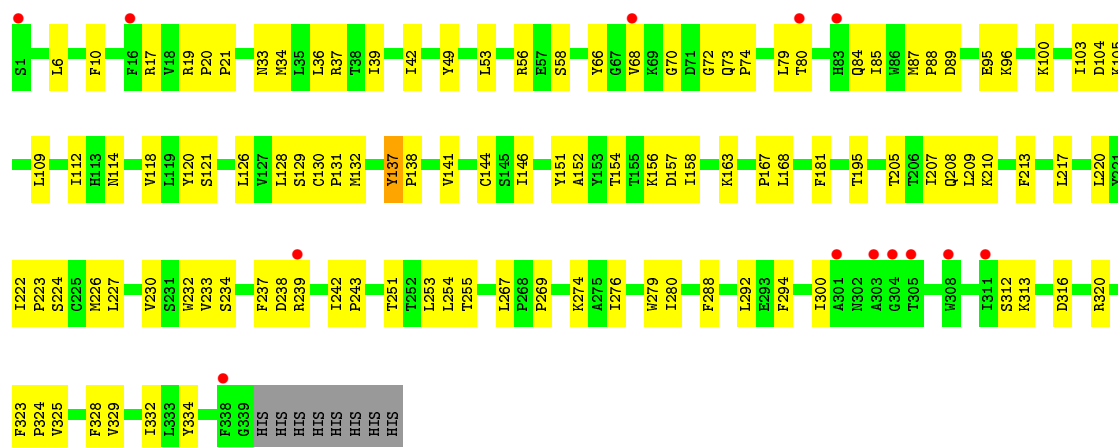
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	D	1	Total C 8 8	0	0
9	E	1	Total C 8 8	0	0

- Molecule 10 is UNDECANE (three-letter code: UND) (formula:  $C_{11}H_{24}$ ).

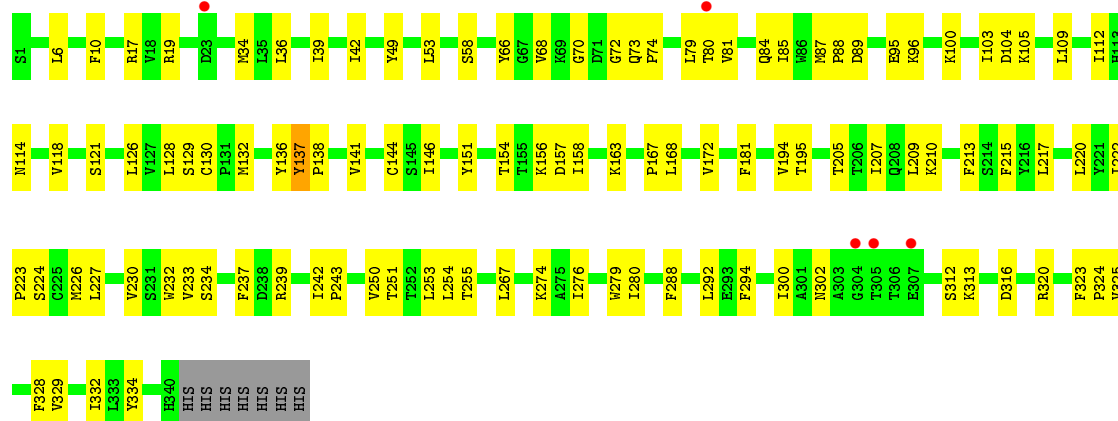


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total C 11 11	0	0

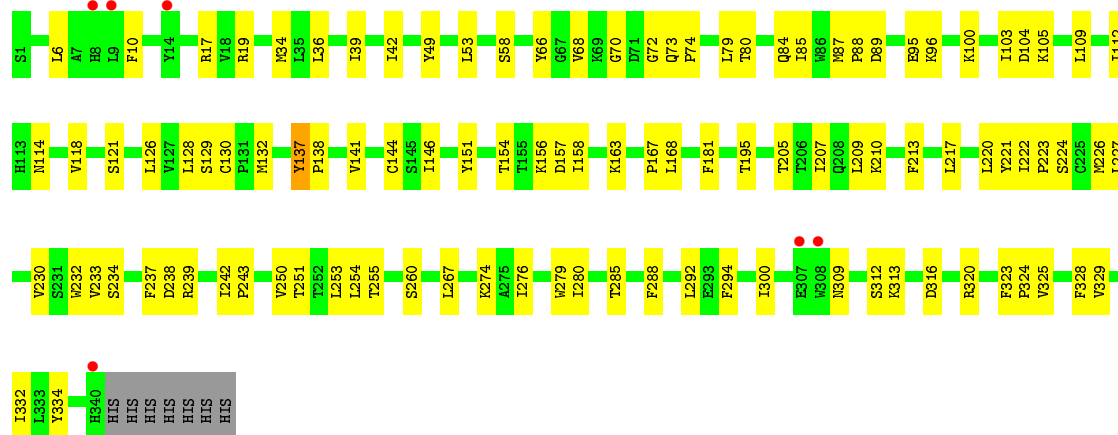




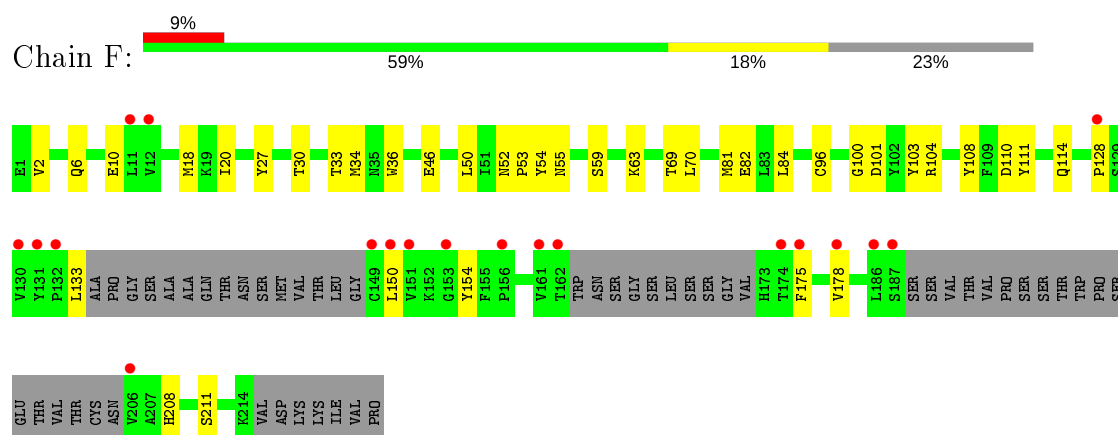
- Molecule 1: Avermectin-sensitive glutamate-gated chloride channel GluCl alpha



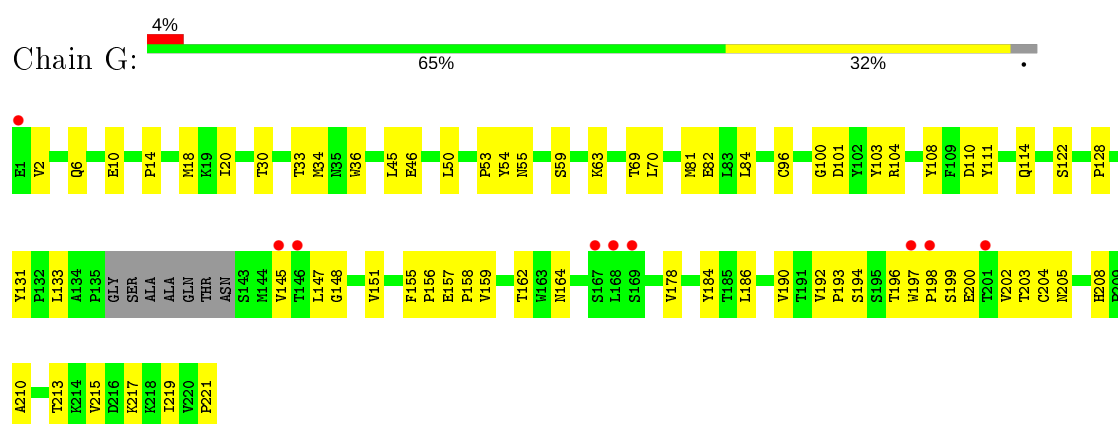
- Molecule 1: Avermectin-sensitive glutamate-gated chloride channel GluCl alpha



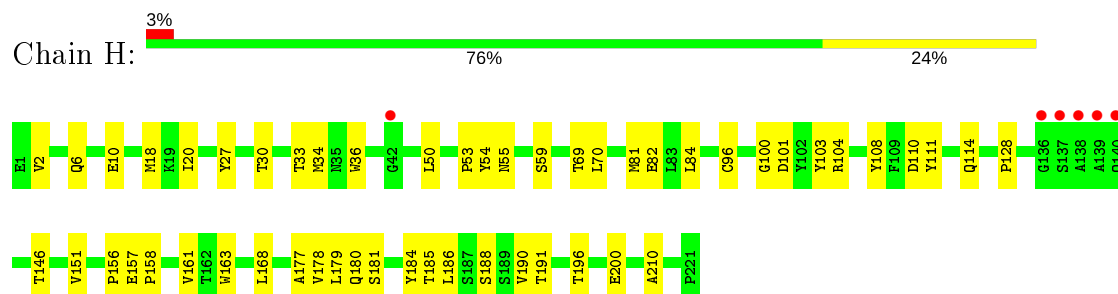
- Molecule 2: Mouse monoclonal Fab fragment, heavy chain



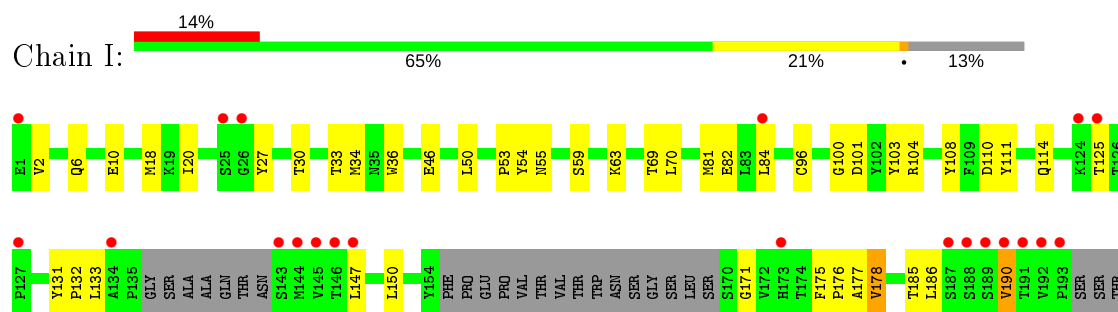
- Molecule 2: Mouse monoclonal Fab fragment, heavy chain

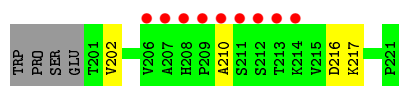


- Molecule 2: Mouse monoclonal Fab fragment, heavy chain

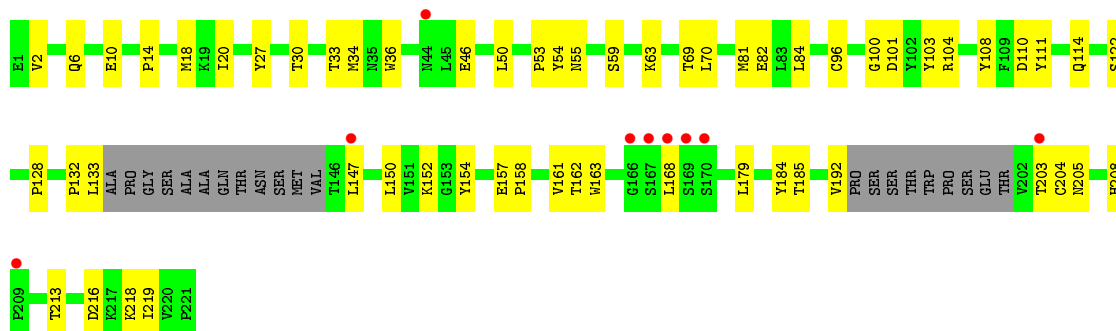


- Molecule 2: Mouse monoclonal Fab fragment, heavy chain

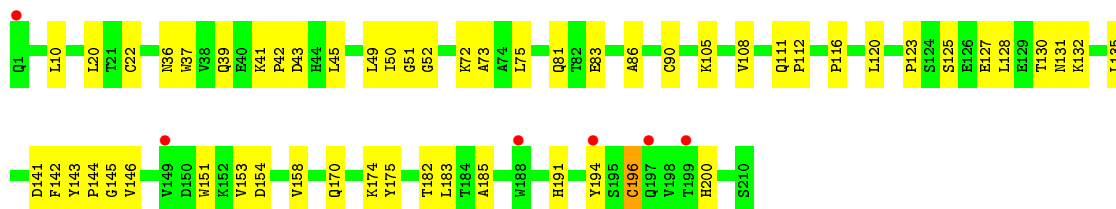
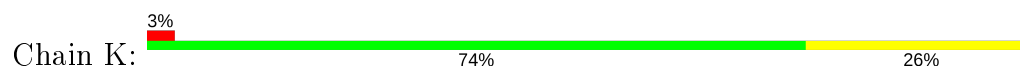




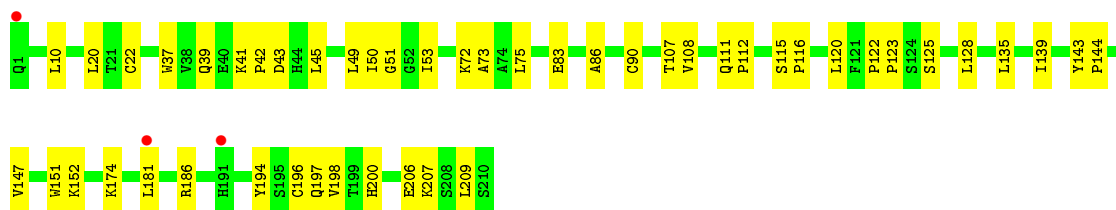
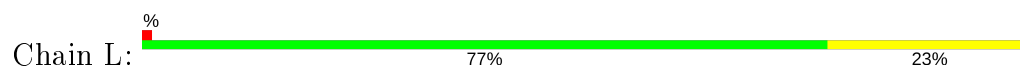
- Molecule 2: Mouse monoclonal Fab fragment, heavy chain



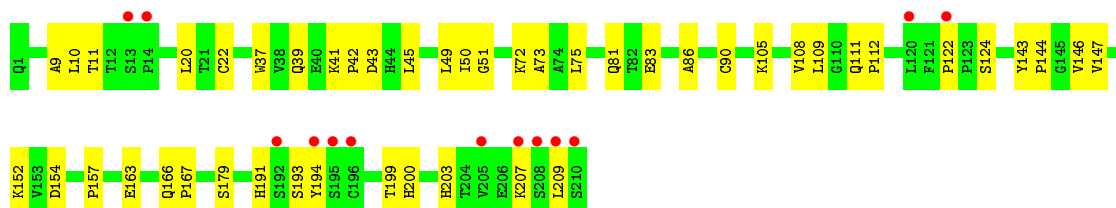
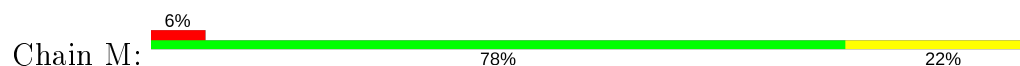
- Molecule 3: Mouse monoclonal Fab fragment, light chain



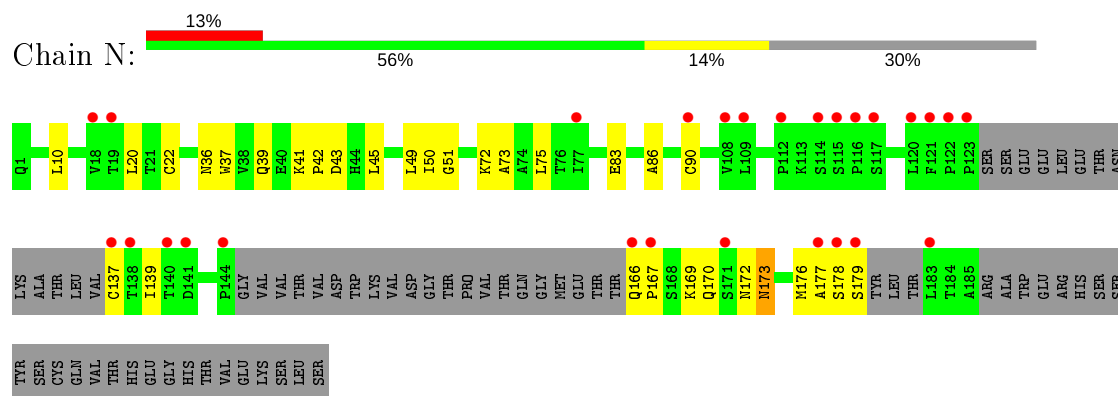
- Molecule 3: Mouse monoclonal Fab fragment, light chain



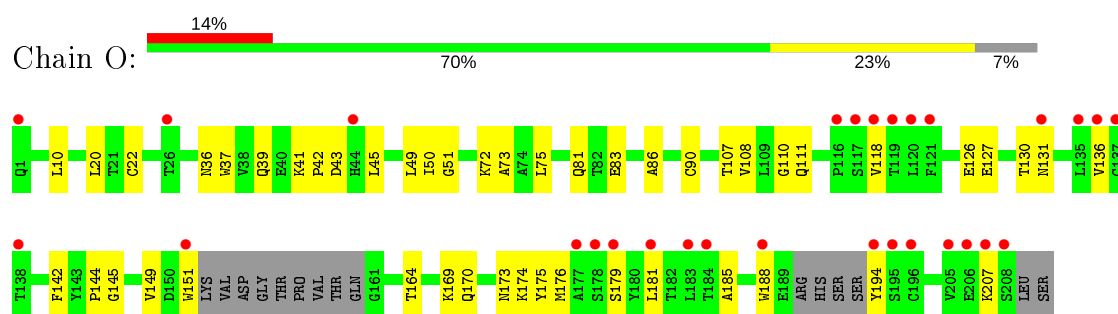
- Molecule 3: Mouse monoclonal Fab fragment, light chain



- Molecule 3: Mouse monoclonal Fab fragment, light chain



- Molecule 3: Mouse monoclonal Fab fragment, light chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	155.44Å 155.44Å 575.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.73 – 3.35 39.73 – 3.34	Depositor EDS
% Data completeness (in resolution range)	93.0 (39.73-3.35) 99.4 (39.73-3.34)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.52 (at 3.32Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.248 , 0.271 0.243 , 0.263	Depositor DCC
$R_{free}$ test set	5136 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	87.8	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 44.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	29020	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.63% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: NAG, CL, IVM, LMT, UND, OCT

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	0.25	0/2793	0.39	0/3813
1	B	0.25	0/2793	0.39	0/3813
1	C	0.25	0/2782	0.39	0/3798
1	D	0.25	0/2793	0.39	0/3813
1	E	0.26	0/2793	0.39	0/3813
2	F	0.26	0/1359	0.41	0/1849
2	G	0.26	0/1676	0.44	0/2290
2	H	0.25	0/1721	0.42	0/2352
2	I	0.25	0/1501	0.41	0/2040
2	J	0.25	0/1565	0.41	0/2133
3	K	0.26	0/1617	0.43	0/2212
3	L	0.24	0/1629	0.43	0/2226
3	M	0.25	0/1614	0.42	0/2210
3	N	0.27	0/1098	0.42	0/1503
3	O	0.25	0/1504	0.42	0/2056
All	All	0.25	0/29238	0.41	0/39921

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 ⓘ

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	2720	0	2720	105	0
1	B	2720	0	2719	110	0
1	C	2710	0	2712	111	0
1	D	2720	0	2720	105	0
1	E	2720	0	2719	103	0
2	F	1324	0	1265	31	0
2	G	1631	0	1574	58	0
2	H	1675	0	1610	42	0
2	I	1466	0	1428	37	0
2	J	1526	0	1468	41	0
3	K	1579	0	1520	41	0
3	L	1591	0	1542	36	0
3	M	1576	0	1518	33	0
3	N	1075	0	1026	25	0
3	O	1470	0	1412	35	0
4	A	10	0	5	0	0
4	B	10	0	5	2	0
4	C	10	0	5	1	0
4	D	10	0	5	1	0
4	E	10	0	5	1	0
5	A	124	0	148	11	0
5	B	62	0	74	5	0
5	D	62	0	74	3	0
5	E	62	0	74	3	0
6	A	53	0	52	13	0
6	B	26	0	25	7	0
7	B	1	0	0	0	0
8	B	14	0	13	1	0
8	C	14	0	13	1	0
8	E	14	0	13	0	0
9	B	8	0	18	0	0
9	D	8	0	18	0	0
9	E	8	0	18	3	0
10	B	11	0	24	0	0
All	All	29020	0	28542	831	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 14.

The worst 5 of 831 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:299:HIS:CD2	6:A:404:LMT:H12	1.75	1.21
1:A:299:HIS:HD2	6:A:404:LMT:H12	1.25	0.97
1:B:100:LYS:HE2	1:C:104:ASP:H	1.27	0.96
1:D:89:ASP:HA	1:E:105:LYS:HG3	1.49	0.95
1:C:100:LYS:HE2	1:D:104:ASP:H	1.31	0.93

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	338/347 (97%)	317 (94%)	19 (6%)	2 (1%)	25	60
1	B	338/347 (97%)	317 (94%)	19 (6%)	2 (1%)	25	60
1	C	337/347 (97%)	316 (94%)	19 (6%)	2 (1%)	25	60
1	D	338/347 (97%)	317 (94%)	19 (6%)	2 (1%)	25	60
1	E	338/347 (97%)	317 (94%)	19 (6%)	2 (1%)	25	60
2	F	163/221 (74%)	150 (92%)	12 (7%)	1 (1%)	25	60
2	G	210/221 (95%)	196 (93%)	13 (6%)	1 (0%)	29	63
2	H	219/221 (99%)	206 (94%)	13 (6%)	0	100	100
2	I	184/221 (83%)	172 (94%)	10 (5%)	2 (1%)	14	47
2	J	194/221 (88%)	180 (93%)	14 (7%)	0	100	100
3	K	208/210 (99%)	189 (91%)	19 (9%)	0	100	100
3	L	208/210 (99%)	195 (94%)	13 (6%)	0	100	100
3	M	208/210 (99%)	194 (93%)	14 (7%)	0	100	100
3	N	140/210 (67%)	128 (91%)	11 (8%)	1 (1%)	22	57
3	O	189/210 (90%)	168 (89%)	20 (11%)	1 (0%)	29	63
All	All	3612/3890 (93%)	3362 (93%)	234 (6%)	16 (0%)	34	68

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	137	TYR
1	B	137	TYR
1	C	137	TYR
1	D	137	TYR
1	E	137	TYR

### 5.3.2 Protein sidechains ⓘ

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	308/316 (98%)	307 (100%)	1 (0%)	92	96
1	B	308/316 (98%)	307 (100%)	1 (0%)	92	96
1	C	307/316 (97%)	306 (100%)	1 (0%)	92	96
1	D	308/316 (98%)	307 (100%)	1 (0%)	92	96
1	E	308/316 (98%)	307 (100%)	1 (0%)	92	96
2	F	145/190 (76%)	145 (100%)	0	100	100
2	G	184/190 (97%)	182 (99%)	2 (1%)	73	86
2	H	188/190 (99%)	188 (100%)	0	100	100
2	I	164/190 (86%)	164 (100%)	0	100	100
2	J	170/190 (90%)	170 (100%)	0	100	100
3	K	176/178 (99%)	174 (99%)	2 (1%)	73	86
3	L	178/178 (100%)	178 (100%)	0	100	100
3	M	175/178 (98%)	175 (100%)	0	100	100
3	N	115/178 (65%)	115 (100%)	0	100	100
3	O	162/178 (91%)	162 (100%)	0	100	100
All	All	3196/3420 (94%)	3187 (100%)	9 (0%)	92	96

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	95	GLU
3	K	196	CYS
2	G	194	SER
1	C	95	GLU
2	G	45	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	46	ASN
2	F	5	GLN
3	L	197	GLN
1	E	84	GLN
1	E	169	GLN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 1 is monoatomic - leaving 20 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
8	NAG	B	400	1	14,14,15	0.58	0	17,19,21	0.88	1 (5%)
6	LMT	A	405	-	28,28,36	1.43	5 (17%)	39,39,47	1.39	5 (12%)
9	OCT	E	403	-	7,7,7	0.25	0	6,6,6	0.48	0
8	NAG	C	400	1	14,14,15	0.48	0	17,19,21	1.67	2 (11%)
8	NAG	E	400	1	14,14,15	0.46	0	17,19,21	1.20	2 (11%)
6	LMT	A	404	-	27,27,36	1.48	4 (14%)	37,38,47	1.76	11 (29%)
9	OCT	B	405	-	7,7,7	0.25	0	6,6,6	0.42	0
5	IVM	A	403	-	65,68,68	0.81	1 (1%)	82,102,102	1.65	16 (19%)
5	IVM	E	402	-	65,68,68	0.80	1 (1%)	82,102,102	1.65	16 (19%)
5	IVM	D	402	-	65,68,68	0.80	1 (1%)	82,102,102	1.64	16 (19%)
10	UND	B	406	-	10,10,10	0.26	0	9,9,9	0.46	0
6	LMT	B	404	-	27,27,36	1.45	4 (14%)	37,38,47	1.45	7 (18%)
5	IVM	A	402	-	65,68,68	0.80	1 (1%)	82,102,102	1.65	16 (19%)
9	OCT	D	403	-	7,7,7	0.25	0	6,6,6	0.42	0
5	IVM	B	403	-	65,68,68	0.80	1 (1%)	82,102,102	1.63	16 (19%)

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
8	NAG	B	400	1	-	0/6/23/26	0/1/1/1
6	LMT	A	405	-	-	5/13/53/61	0/2/2/2
9	OCT	E	403	-	-	0/5/5/5	-
8	NAG	C	400	1	-	0/6/23/26	0/1/1/1
8	NAG	E	400	1	-	4/6/23/26	0/1/1/1
6	LMT	A	404	-	-	9/12/52/61	0/2/2/2
9	OCT	B	405	-	-	0/5/5/5	-
5	IVM	A	403	-	-	6/45/141/141	0/6/7/7
5	IVM	E	402	-	-	6/45/141/141	0/6/7/7
5	IVM	D	402	-	-	7/45/141/141	0/6/7/7
10	UND	B	406	-	-	0/8/8/8	-
6	LMT	B	404	-	-	5/12/52/61	0/2/2/2
5	IVM	A	402	-	-	7/45/141/141	0/6/7/7
9	OCT	D	403	-	-	0/5/5/5	-
5	IVM	B	403	-	-	7/45/141/141	0/6/7/7

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	402	IVM	O12-C46	4.84	1.45	1.34
5	B	403	IVM	O12-C46	4.83	1.45	1.34
5	A	402	IVM	O12-C46	4.83	1.45	1.34
5	A	403	IVM	O12-C46	4.81	1.45	1.34
5	D	402	IVM	O12-C46	4.77	1.45	1.34

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	403	IVM	O12-C46-C45	6.80	120.81	110.97
5	E	402	IVM	O12-C46-C45	6.76	120.75	110.97
5	A	402	IVM	O12-C46-C45	6.68	120.64	110.97
5	B	403	IVM	O12-C46-C45	6.63	120.56	110.97
5	D	402	IVM	O12-C46-C45	6.62	120.56	110.97

There are no chirality outliers.

5 of 56 torsion outliers are listed below:

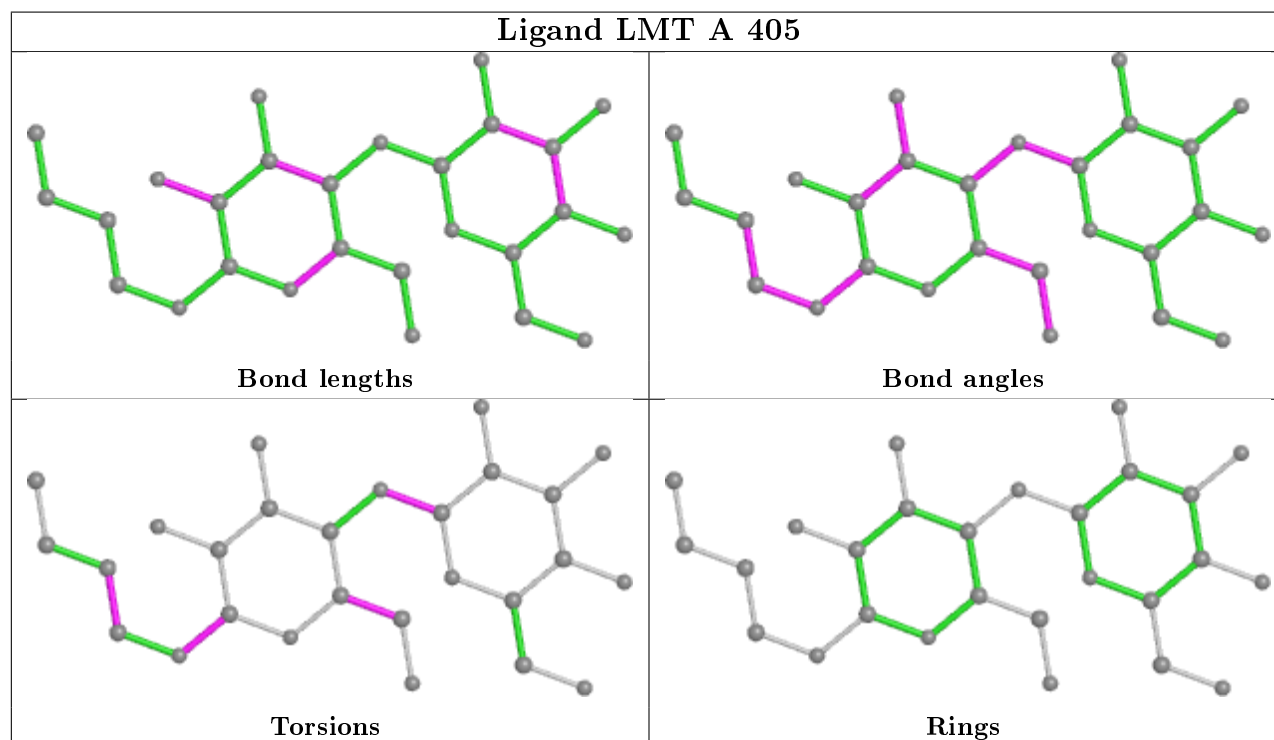
Mol	Chain	Res	Type	Atoms
6	A	405	LMT	C2'-C1'-O1'-C1
6	A	405	LMT	O5'-C1'-O1'-C1
5	A	403	IVM	O7-C25-O4-C24
5	A	403	IVM	C26-C25-O4-C24
5	E	402	IVM	O7-C25-O4-C24

There are no ring outliers.

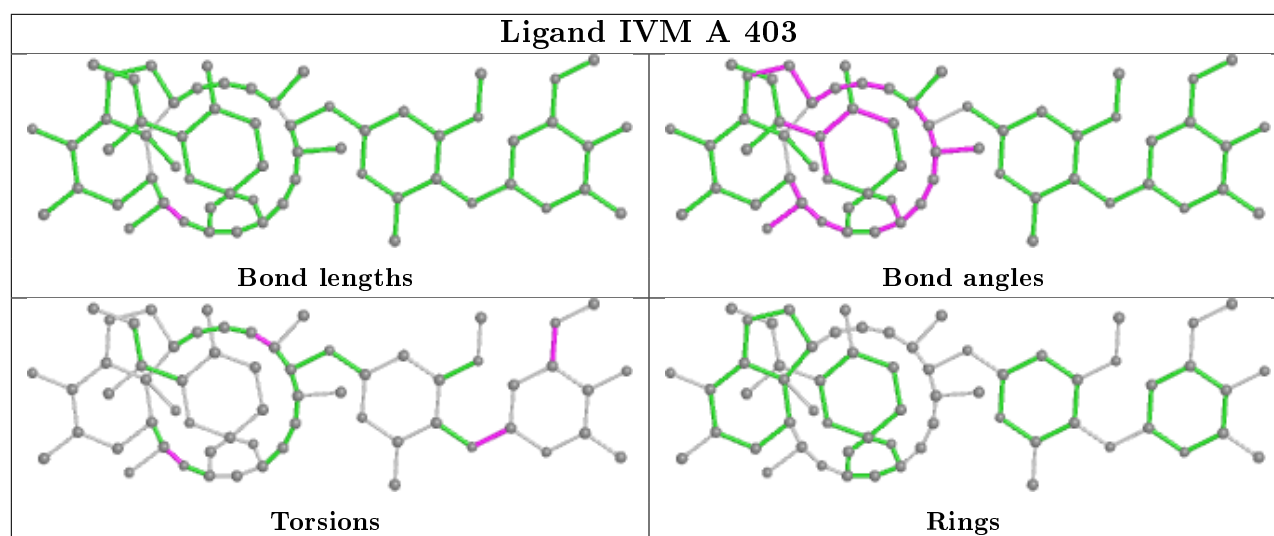
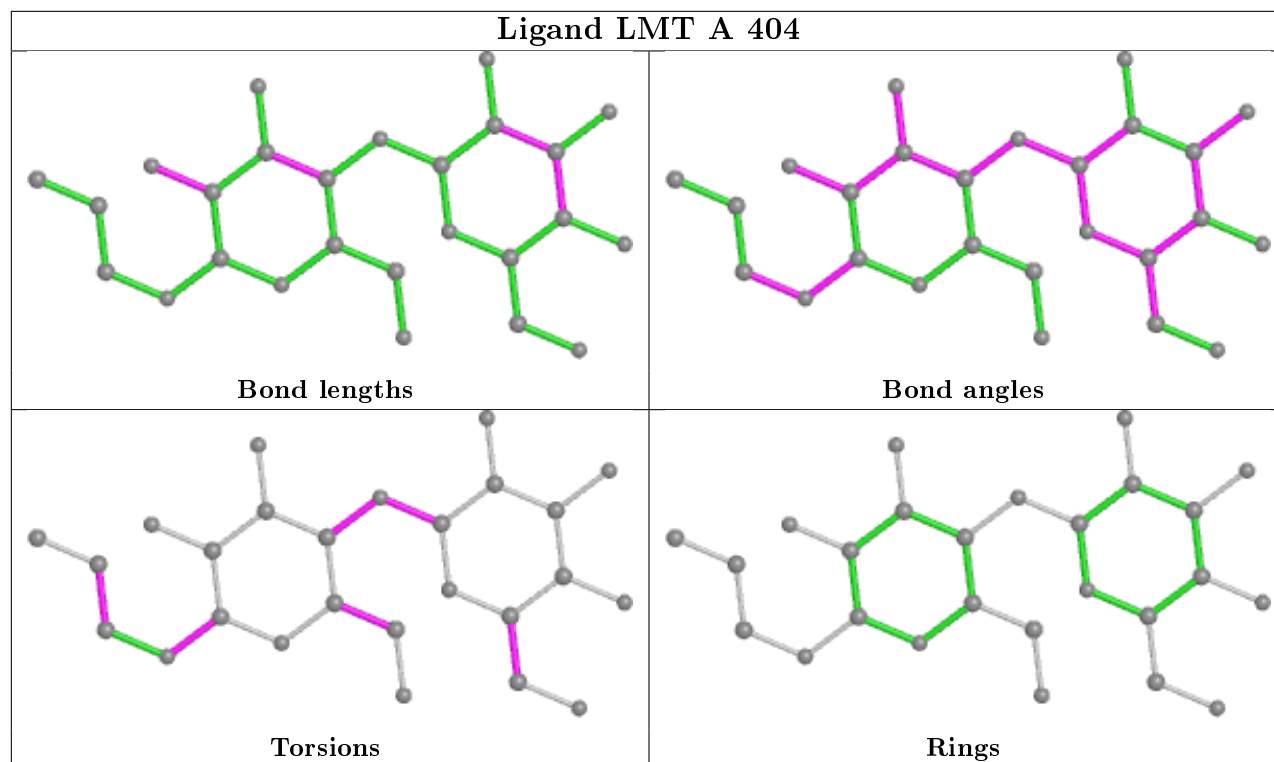
11 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	400	NAG	1	0
6	A	405	LMT	3	0
9	E	403	OCT	3	0
8	C	400	NAG	1	0
6	A	404	LMT	10	0
5	A	403	IVM	7	0
5	E	402	IVM	3	0
5	D	402	IVM	3	0
6	B	404	LMT	7	0
5	A	402	IVM	4	0
5	B	403	IVM	5	0

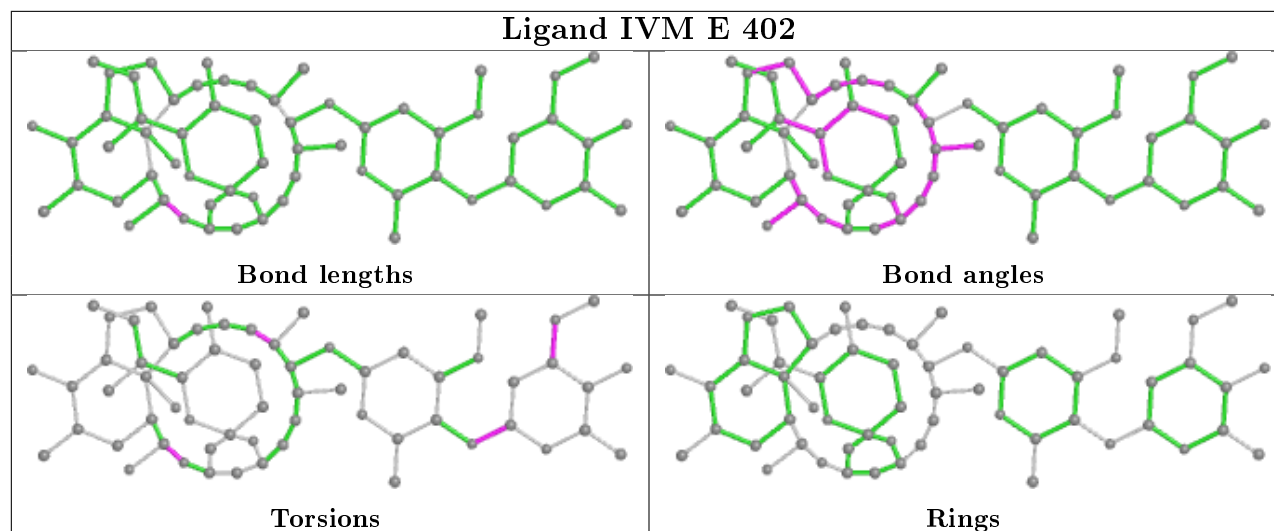
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



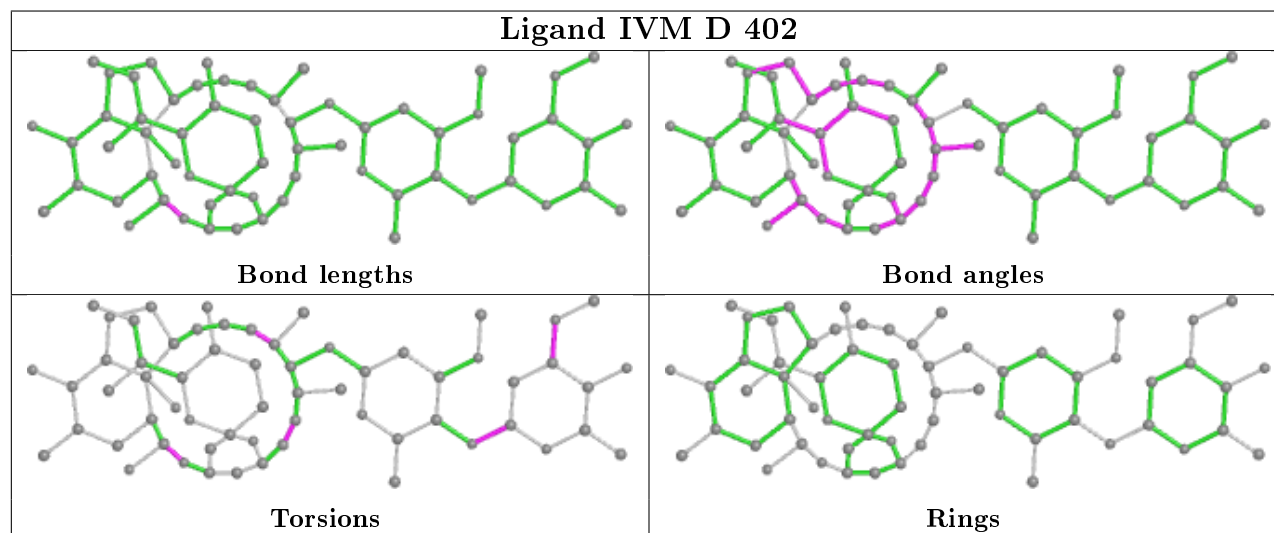


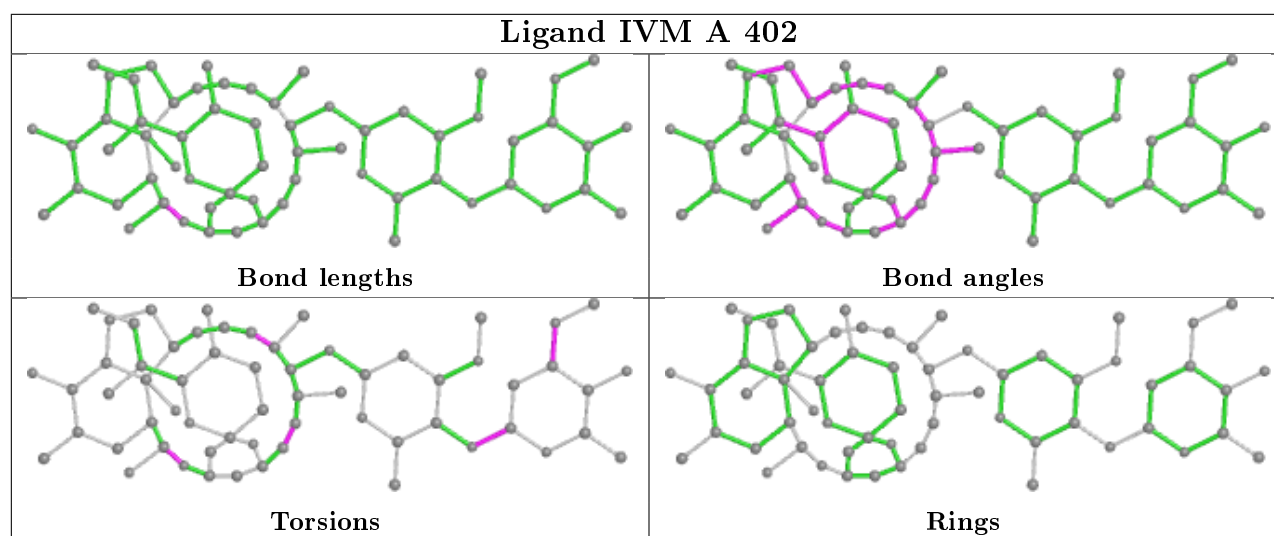
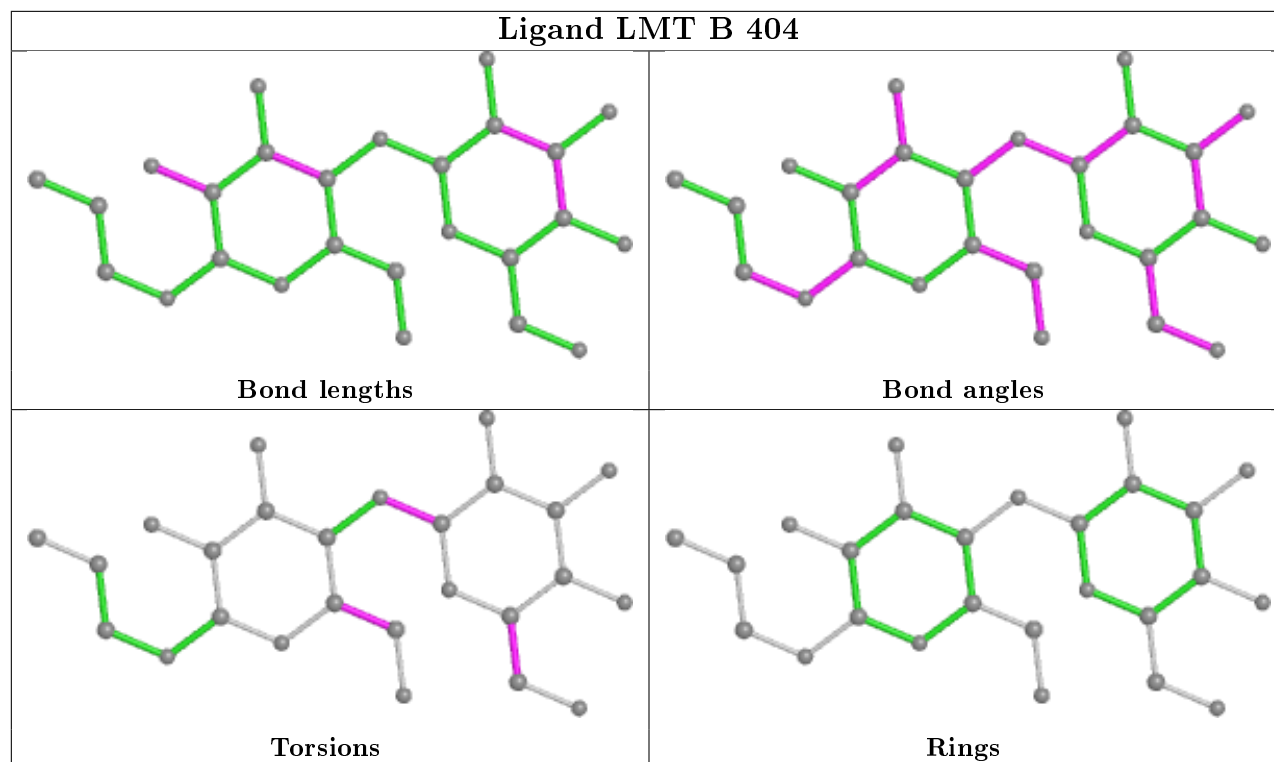


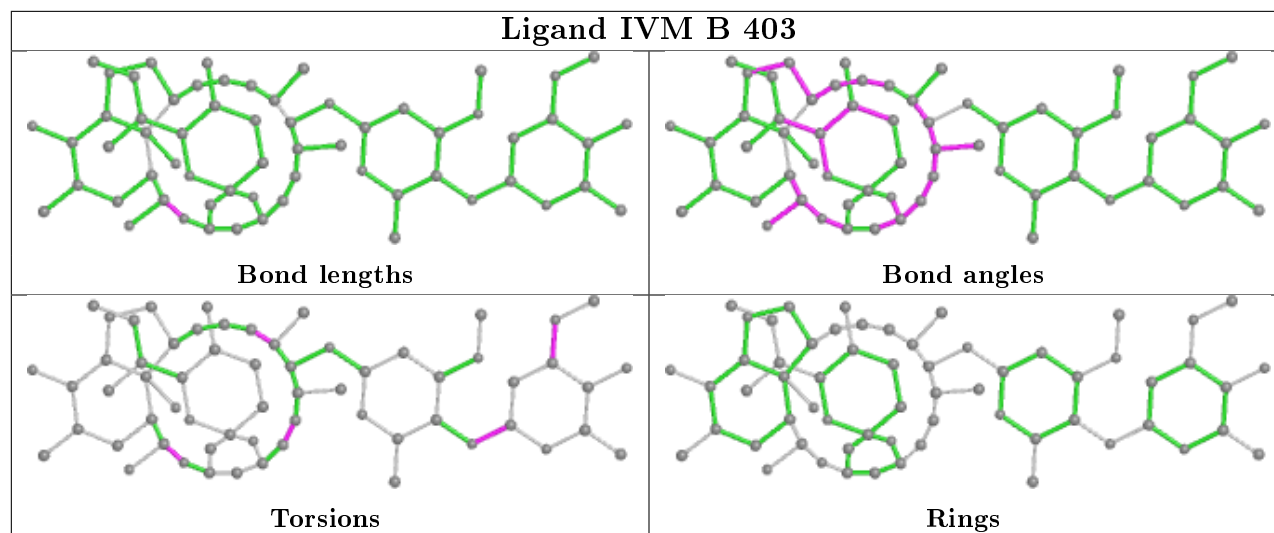
## Ligand IVM E 402



## Ligand IVM D 402







## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	340/347 (97%)	0.04	3 (0%) 84 85	32, 66, 123, 196	0
1	B	340/347 (97%)	-0.09	5 (1%) 73 72	38, 68, 125, 199	0
1	C	339/347 (97%)	0.08	13 (3%) 40 39	41, 71, 153, 279	0
1	D	340/347 (97%)	-0.12	5 (1%) 73 72	39, 72, 159, 243	0
1	E	340/347 (97%)	-0.00	6 (1%) 68 67	36, 69, 142, 210	0
2	F	171/221 (77%)	0.56	19 (11%) 5 5	58, 106, 163, 192	0
2	G	214/221 (96%)	0.29	9 (4%) 36 36	40, 89, 142, 182	0
2	H	221/221 (100%)	-0.10	6 (2%) 54 53	42, 76, 131, 201	0
2	I	192/221 (86%)	0.75	30 (15%) 2 1	57, 110, 171, 201	0
2	J	200/221 (90%)	0.09	9 (4%) 33 34	49, 90, 158, 182	0
3	K	210/210 (100%)	0.12	6 (2%) 51 51	50, 95, 139, 209	0
3	L	210/210 (100%)	0.00	3 (1%) 75 75	38, 73, 114, 159	0
3	M	210/210 (100%)	0.18	13 (6%) 20 21	49, 93, 143, 165	0
3	N	148/210 (70%)	0.85	27 (18%) 1 1	58, 119, 178, 202	0
3	O	195/210 (92%)	0.67	29 (14%) 2 2	63, 113, 167, 190	0
All	All	3670/3890 (94%)	0.16	183 (4%) 28 29	32, 82, 155, 279	0

The worst 5 of 183 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	O	208	SER	8.2
2	I	212	SER	7.3
2	I	188	SER	6.6
2	I	189	SER	6.5
2	I	213	THR	6.4

## 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 monosaccharides in this entry.

## 6.4 Ligands ⓘ

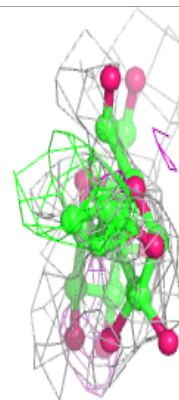
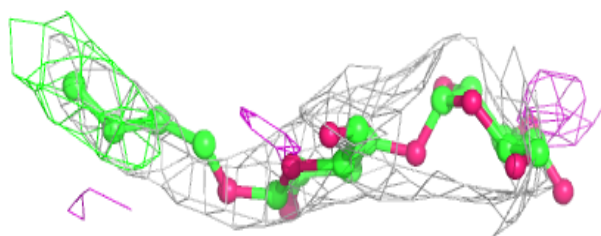
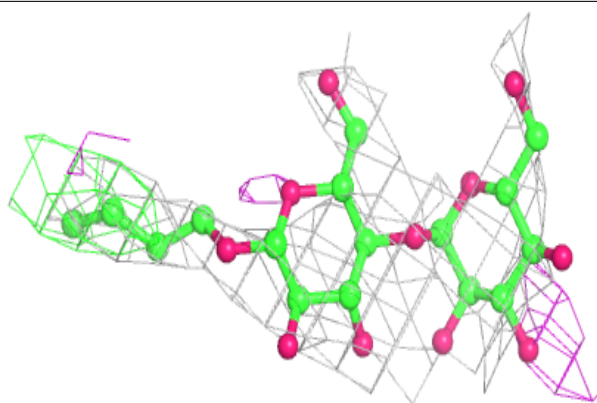
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	LMT	A	405	27/35	0.58	0.59	143,143,143,143	0
10	UND	B	406	11/11	0.59	0.49	60,60,60,60	0
9	OCT	E	403	8/8	0.73	0.39	79,79,79,79	0
8	NAG	C	400	14/15	0.76	0.37	128,132,137,137	0
6	LMT	B	404	26/35	0.76	0.38	145,145,145,145	0
8	NAG	E	400	14/15	0.82	0.35	172,176,179,180	0
9	OCT	D	403	8/8	0.82	0.60	59,59,59,59	0
7	CL	B	402	1/1	0.83	1.01	72,72,72,72	0
8	NAG	B	400	14/15	0.84	0.60	138,141,143,145	0
9	OCT	B	405	8/8	0.84	0.32	60,60,60,60	0
6	LMT	A	404	26/35	0.86	0.25	106,106,106,106	0
5	IVM	A	402	62/62	0.87	0.25	55,58,69,70	0
5	IVM	B	403	62/62	0.89	0.30	60,68,83,84	0
4	GLU	A	401	10/10	0.90	0.35	73,74,77,78	0
5	IVM	D	402	62/62	0.90	0.23	61,70,84,85	0
5	IVM	A	403	62/62	0.90	0.24	70,73,80,81	0
4	GLU	B	401	10/10	0.90	0.27	67,68,71,71	0
5	IVM	E	402	62/62	0.91	0.30	65,69,73,75	0
4	GLU	D	401	10/10	0.92	0.33	66,67,69,69	0
4	GLU	C	401	10/10	0.92	0.23	74,76,79,80	0
4	GLU	E	401	10/10	0.95	0.20	66,67,69,70	0

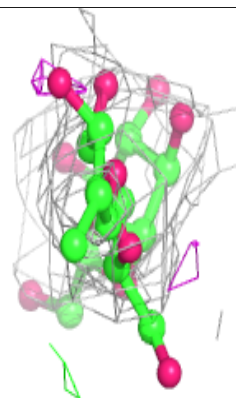
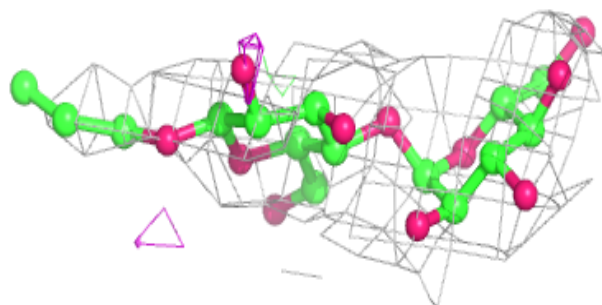
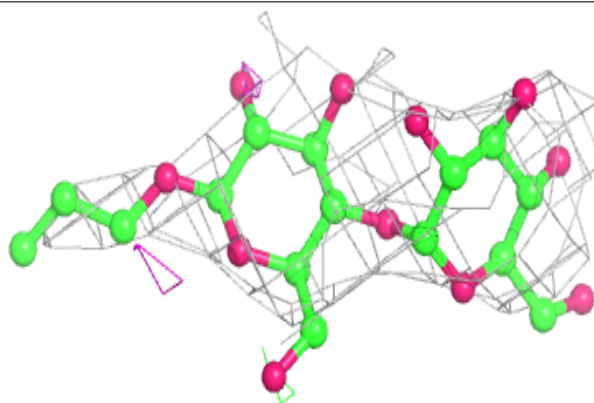
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around LMT A 405:**

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

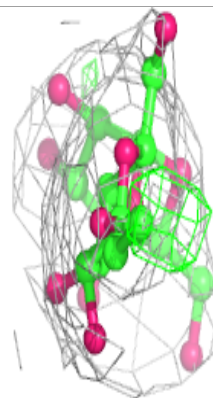
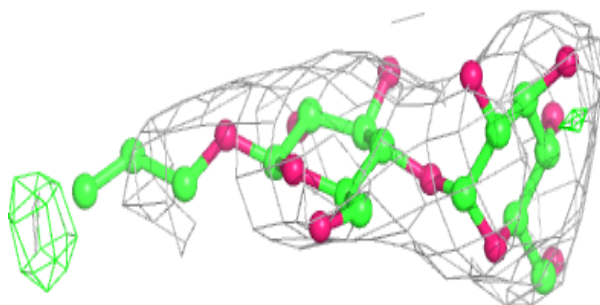
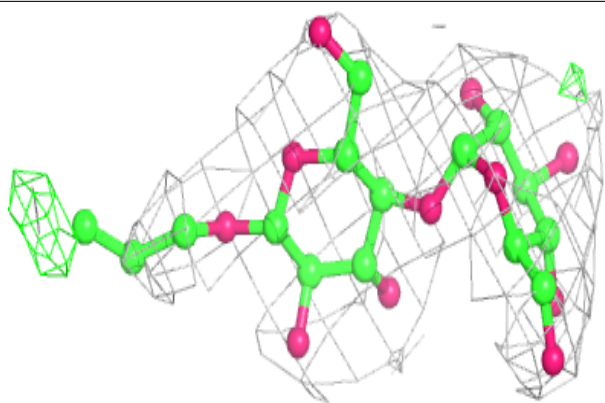
**Electron density around LMT B 404:**

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



**Electron density around LMT A 404:**

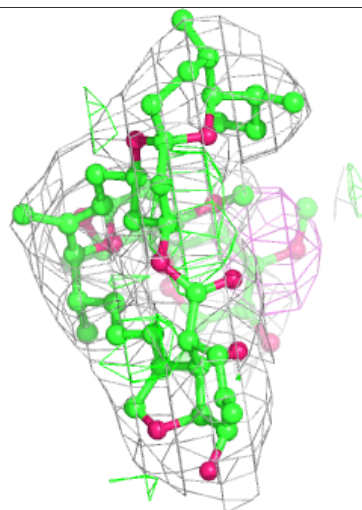
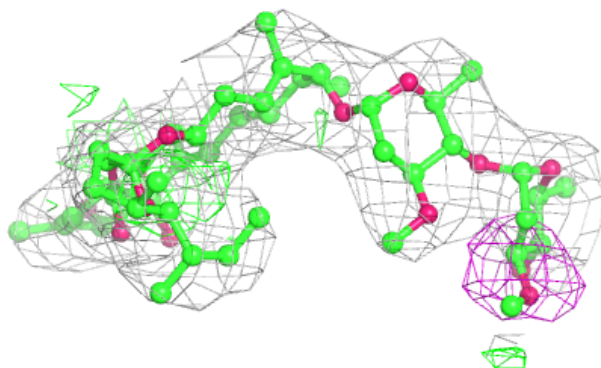
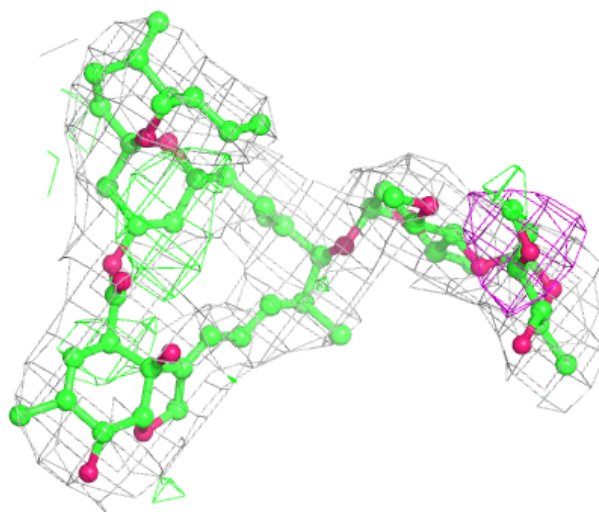
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





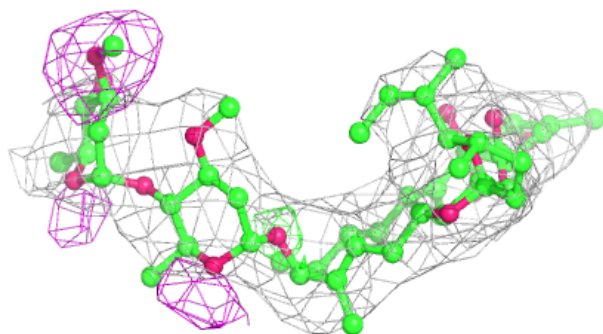
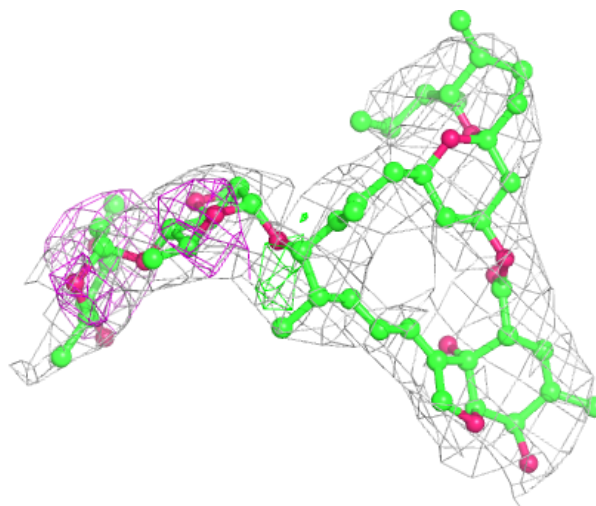
**Electron density around IVM A 402:**

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



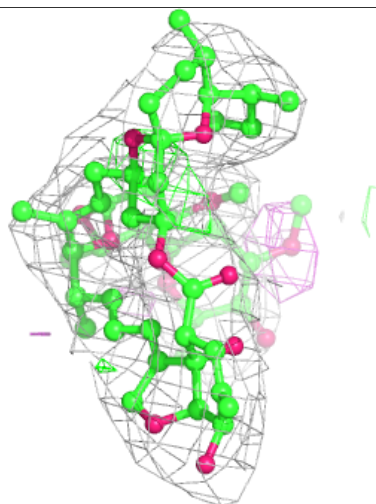
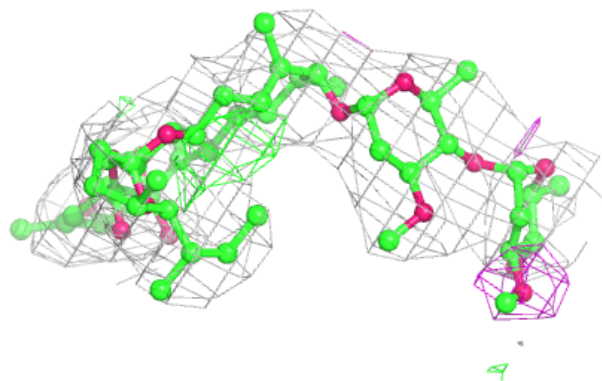
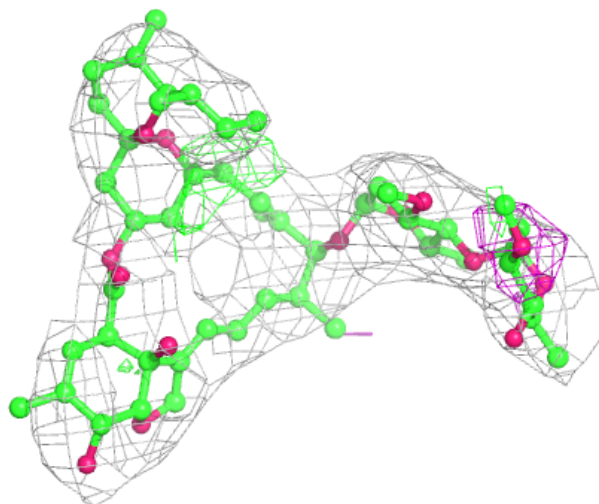
**Electron density around IVM B 403:**

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



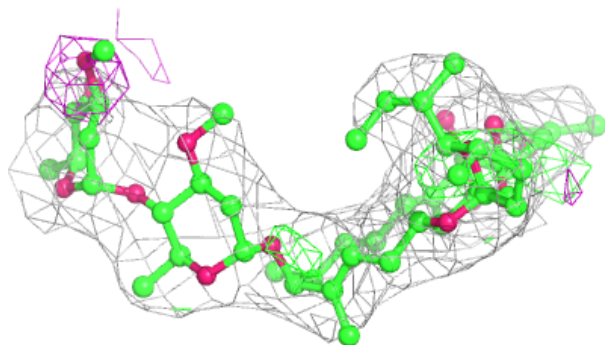
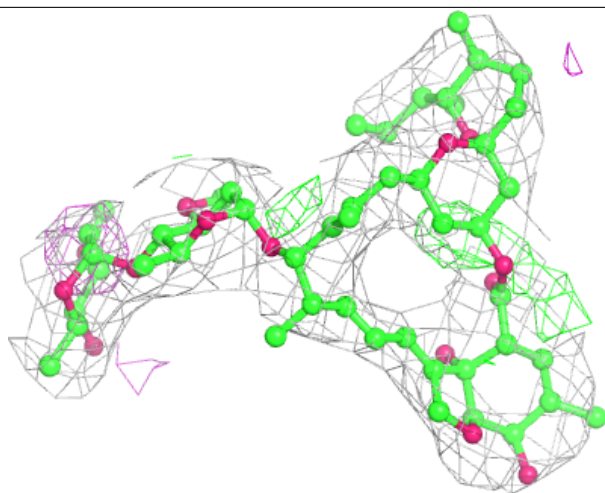
**Electron density around IVM D 402:**

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



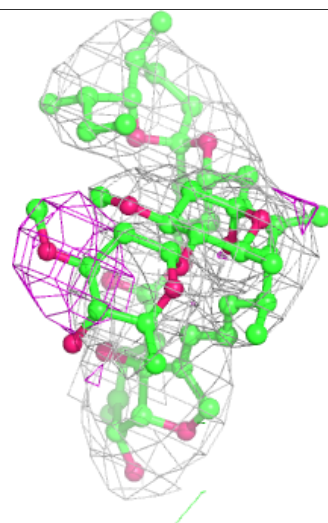
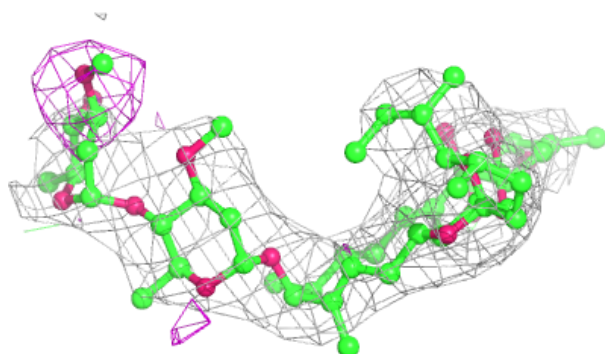
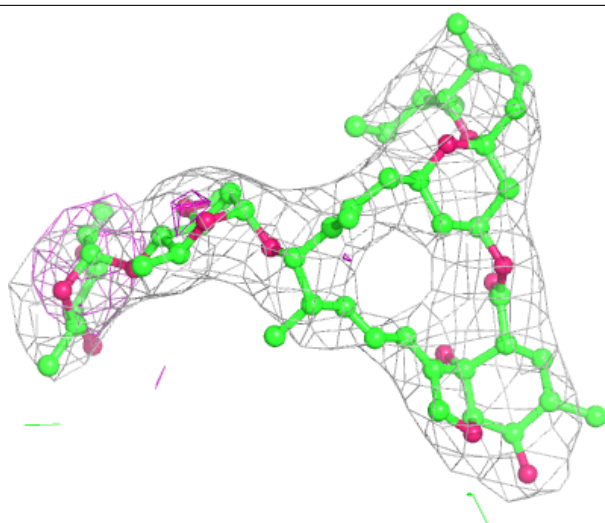
**Electron density around IVM A 403:**

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



**Electron density around IVM E 402:**

$2mF_o-DF_c$  (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.