



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:40 AM UTC

PDB ID : 5VDH / pdb_00005vdh
Title : Crystal Structure of Human Glycine Receptor alpha-3 Bound to AM-3607, Glycine, and Ivermectin
Authors : Shaffer, P.L.; Huang, X.; Chen, H.
Deposited on : 2017-04-03
Resolution : 2.85 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

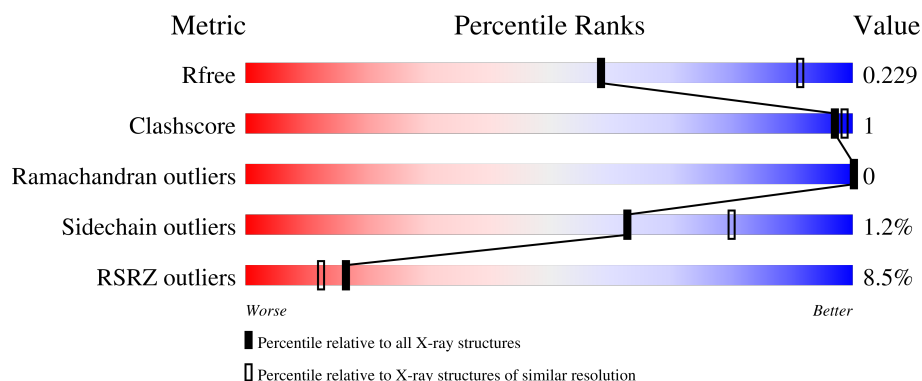
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	362	6% 90% 7%
1	B	362	7% 93% 5%
1	C	362	8% 90% 7%
1	D	362	13% 92% 5%
1	E	362	5% 90% 7%

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	GLY	A	402	-	X	-	-
3	GLY	C	402	-	X	-	-
3	GLY	D	402	-	X	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14064 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 Glycine receptor subunit alpha-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2696	1759	428	489	20			
1	B	343	Total	C	N	O	S	0	0	0
			2713	1771	430	492	20			
1	C	338	Total	C	N	O	S	0	0	0
			2686	1754	425	487	20			
1	D	343	Total	C	N	O	S	0	0	0
			2718	1772	433	494	19			
1	E	338	Total	C	N	O	S	0	0	0
			2700	1762	429	489	20			

There are 55 discrepancies between the modelled and reference sequences:

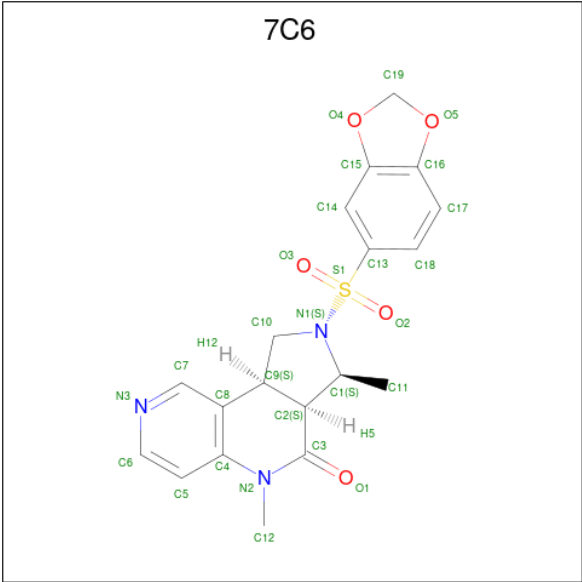
Chain	Residue	Modelled	Actual	Comment	Reference
A	310	ALA	-	linker	UNP O75311
A	311	GLY	-	linker	UNP O75311
A	312	THR	-	linker	UNP O75311
A	355	TRP	-	expression tag	UNP O75311
A	356	SER	-	expression tag	UNP O75311
A	357	HIS	-	expression tag	UNP O75311
A	358	PRO	-	expression tag	UNP O75311
A	359	GLN	-	expression tag	UNP O75311
A	360	PHE	-	expression tag	UNP O75311
A	361	GLU	-	expression tag	UNP O75311
A	362	LYS	-	expression tag	UNP O75311
B	310	ALA	-	linker	UNP O75311
B	311	GLY	-	linker	UNP O75311
B	312	THR	-	linker	UNP O75311
B	355	TRP	-	expression tag	UNP O75311
B	356	SER	-	expression tag	UNP O75311
B	357	HIS	-	expression tag	UNP O75311
B	358	PRO	-	expression tag	UNP O75311
B	359	GLN	-	expression tag	UNP O75311

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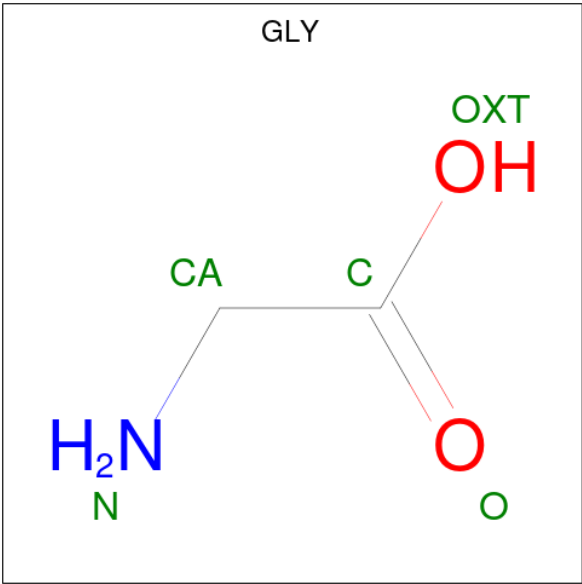
Chain	Residue	Modelled	Actual	Comment	Reference
B	360	PHE	-	expression tag	UNP O75311
B	361	GLU	-	expression tag	UNP O75311
B	362	LYS	-	expression tag	UNP O75311
C	310	ALA	-	linker	UNP O75311
C	311	GLY	-	linker	UNP O75311
C	312	THR	-	linker	UNP O75311
C	355	TRP	-	expression tag	UNP O75311
C	356	SER	-	expression tag	UNP O75311
C	357	HIS	-	expression tag	UNP O75311
C	358	PRO	-	expression tag	UNP O75311
C	359	GLN	-	expression tag	UNP O75311
C	360	PHE	-	expression tag	UNP O75311
C	361	GLU	-	expression tag	UNP O75311
C	362	LYS	-	expression tag	UNP O75311
D	310	ALA	-	linker	UNP O75311
D	311	GLY	-	linker	UNP O75311
D	312	THR	-	linker	UNP O75311
D	355	TRP	-	expression tag	UNP O75311
D	356	SER	-	expression tag	UNP O75311
D	357	HIS	-	expression tag	UNP O75311
D	358	PRO	-	expression tag	UNP O75311
D	359	GLN	-	expression tag	UNP O75311
D	360	PHE	-	expression tag	UNP O75311
D	361	GLU	-	expression tag	UNP O75311
D	362	LYS	-	expression tag	UNP O75311
E	310	ALA	-	linker	UNP O75311
E	311	GLY	-	linker	UNP O75311
E	312	THR	-	linker	UNP O75311
E	355	TRP	-	expression tag	UNP O75311
E	356	SER	-	expression tag	UNP O75311
E	357	HIS	-	expression tag	UNP O75311
E	358	PRO	-	expression tag	UNP O75311
E	359	GLN	-	expression tag	UNP O75311
E	360	PHE	-	expression tag	UNP O75311
E	361	GLU	-	expression tag	UNP O75311
E	362	LYS	-	expression tag	UNP O75311

- Molecule 2 is (3S,3aS,9bS)-2-[(2H-1,3-benzodioxol-5-yl)sulfonyl]-3,5-dimethyl-1,2,3,3a,5,9b-hexahydro-4H-pyrrolo[3,4-c][1,6]naphthyridin-4-one (CCD ID: 7C6) (formula: C₁₉H₁₉N₃O₅S).



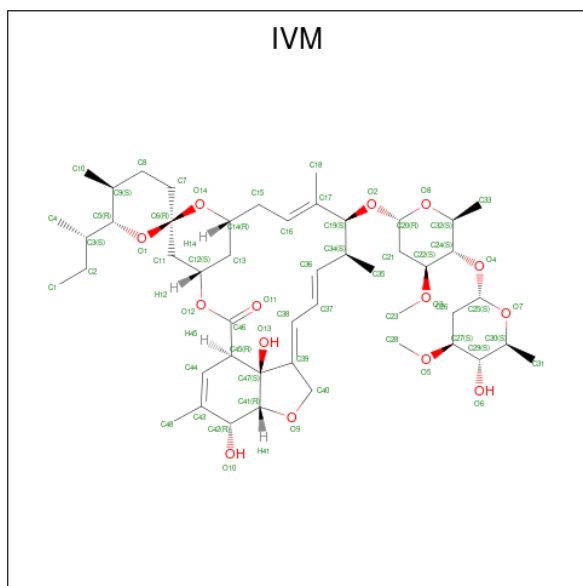
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			28	19	3	5	1		
2	B	1	Total	C	N	O	S	0	0
			28	19	3	5	1		
2	C	1	Total	C	N	O	S	0	0
			28	19	3	5	1		
2	D	1	Total	C	N	O	S	0	0
			28	19	3	5	1		
2	E	1	Total	C	N	O	S	0	0
			28	19	3	5	1		

- Molecule 3 is GLYCINE (CCD ID: GLY) (formula: C₂H₅NO₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 5 2 1 2	0	0
3	B	1	Total C N O 5 2 1 2	0	0
3	C	1	Total C N O 5 2 1 2	0	0
3	D	1	Total C N O 5 2 1 2	0	0
3	E	1	Total C N O 5 2 1 2	0	0

- Molecule 4 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 (CCD ID: IVM) (formula: C₄₈H₇₄O₁₄).



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

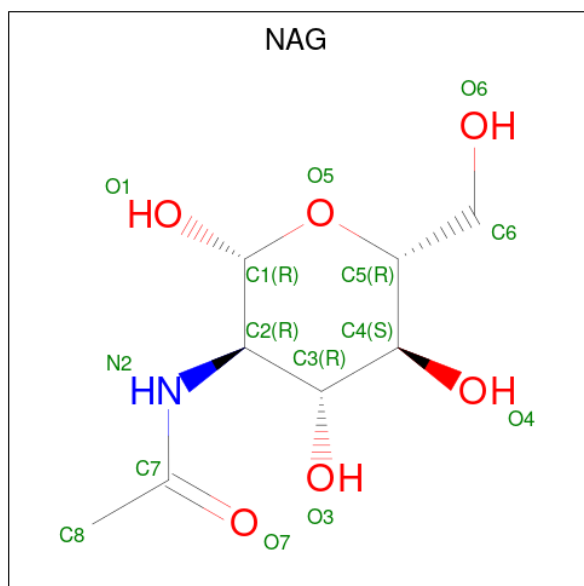
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		
5	B	1	Total	Zn	0	0
			1	1		
5	C	1	Total	Zn	0	0
			1	1		
5	D	1	Total	Zn	0	0
			1	1		
5	E	1	Total	Zn	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

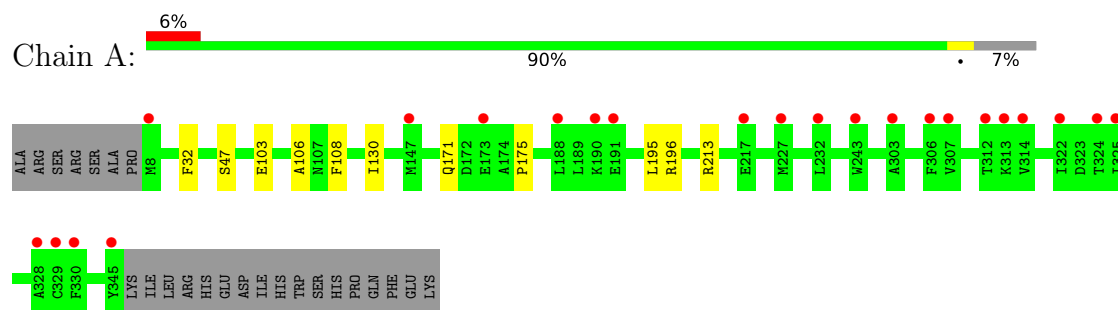
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	18	Total 18	O 18	0	0
8	B	11	Total 11	O 11	0	0
8	C	10	Total 10	O 10	0	0
8	D	8	Total 8	O 8	0	0
8	E	9	Total 9	O 9	0	0

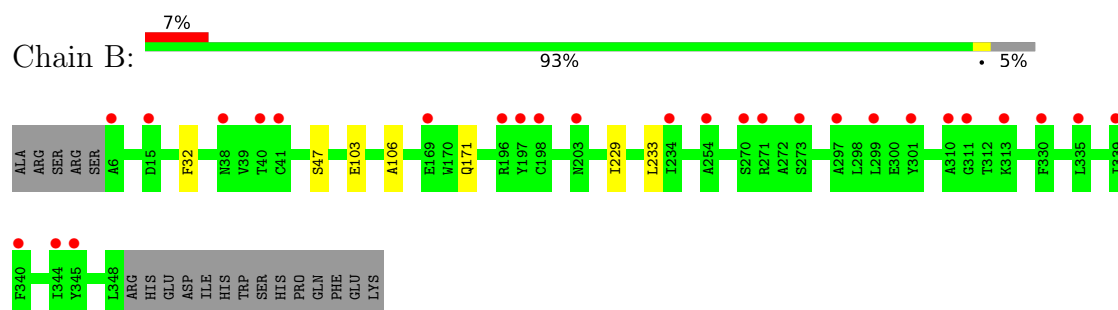
3 Residue-property plots [i](#)

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.

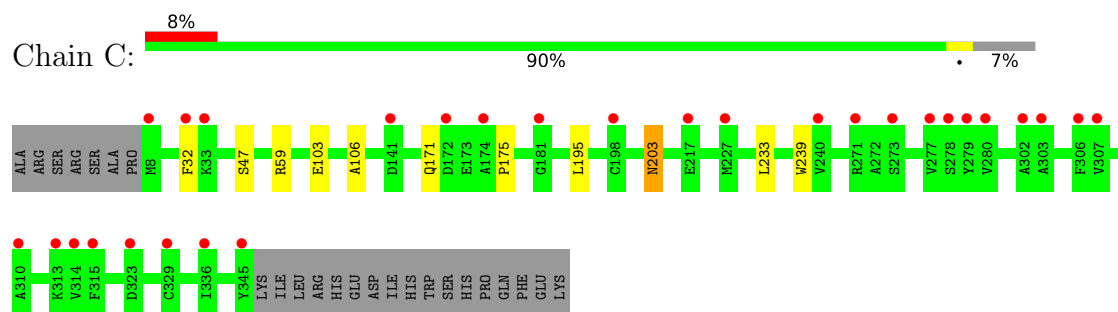
- Molecule 1: Glycine receptor subunit alpha-3



- Molecule 1: Glycine receptor subunit alpha-3

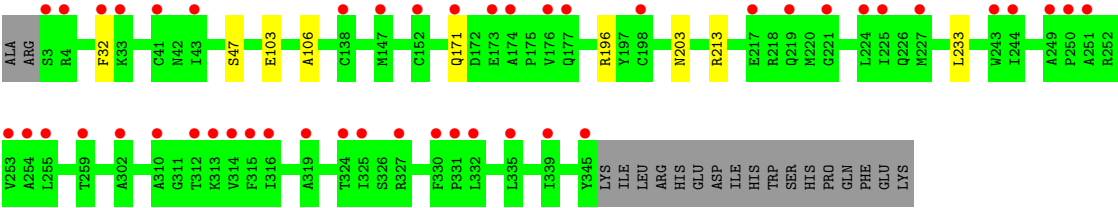


- Molecule 1: Glycine receptor subunit alpha-3

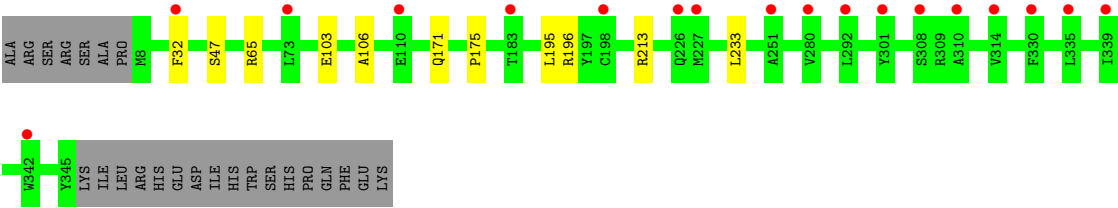
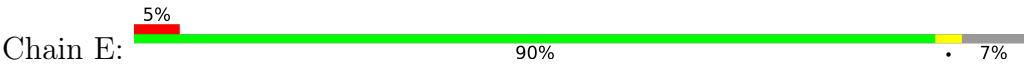


- Molecule 1: Glycine receptor subunit alpha-3





● Molecule 1: Glycine receptor subunit alpha-3



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	119.06Å 119.06Å 429.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.85 50.00 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.85) 99.8 (50.00-2.85)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.226 , 0.236 0.223 , 0.229	Depositor DCC
R_{free} test set	3666 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	71.3	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 62.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14064	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IVM, ZN, NAG, 7C6, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/2767	0.66	0/3769
1	B	0.39	0/2785	0.65	0/3797
1	C	0.39	0/2757	0.66	0/3757
1	D	0.38	0/2790	0.65	0/3803
1	E	0.39	0/2771	0.65	0/3773
All	All	0.39	0/13870	0.65	0/18899

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	2696	0	2640	4	0
1	B	2713	0	2643	4	0
1	C	2686	0	2624	6	0
1	D	2718	0	2653	5	0
1	E	2700	0	2651	6	0
2	A	28	0	0	0	0
2	B	28	0	0	0	0
2	C	28	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	28	0	0	0	0
2	E	28	0	0	0	0
3	A	5	0	2	0	0
3	B	5	0	2	1	0
3	C	5	0	2	0	0
3	D	5	0	2	0	0
3	E	5	0	2	0	0
4	A	62	0	74	3	0
4	B	62	0	74	3	0
4	C	62	0	74	2	0
4	D	62	0	74	2	0
4	E	62	0	74	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
6	A	1	0	0	0	0
7	C	14	0	13	0	0
8	A	18	0	0	0	0
8	B	11	0	0	0	0
8	C	10	0	0	2	0
8	D	8	0	0	0	0
8	E	9	0	0	0	0
All	All	14064	0	13604	26	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 (26) 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)
3:B:402:GLY:N	8:C:501:HOH:O	2.37	0.56
4:B:403:IVM:H30	4:B:403:IVM:H33	1.90	0.54
4:D:403:IVM:H8	1:E:233:LEU:HD13	1.93	0.51
4:B:403:IVM:H8	1:C:233:LEU:HD13	1.93	0.50
1:A:103:GLU:HG3	1:A:106:ALA:HB2	1.96	0.48
1:C:103:GLU:HG3	1:C:106:ALA:HB2	1.95	0.48
1:B:103:GLU:HG3	1:B:106:ALA:HB2	1.96	0.47
4:B:403:IVM:H8	1:C:233:LEU:CD1	2.44	0.47
1:E:103:GLU:HG3	1:E:106:ALA:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:103:GLU:HG3	1:D:106:ALA:HB2	1.95	0.47
4:A:403:IVM:H8	1:B:233:LEU:HD13	1.96	0.46
1:C:203:ASN:C	1:C:203:ASN:HD22	2.23	0.46
4:C:403:IVM:H8	1:D:233:LEU:HD13	1.97	0.46
1:E:196:ARG:HD2	1:E:213:ARG:HE	1.83	0.44
1:D:196:ARG:HD2	1:D:213:ARG:HE	1.83	0.44
4:D:403:IVM:H8	1:E:233:LEU:CD1	2.49	0.43
1:A:196:ARG:HD2	1:A:213:ARG:HE	1.83	0.43
4:A:403:IVM:H23A	1:B:229:ILE:HD11	2.01	0.42
4:A:403:IVM:H8	1:B:233:LEU:CD1	2.49	0.42
4:C:403:IVM:H8	1:D:233:LEU:CD1	2.50	0.41
1:A:175:PRO:HG2	1:A:195:LEU:HD11	2.03	0.41
1:D:203:ASN:HD21	1:E:65:ARG:NH1	2.19	0.41
1:C:175:PRO:HG2	1:C:195:LEU:HD11	2.03	0.41
1:E:175:PRO:HG2	1:E:195:LEU:HD11	2.03	0.41
1:A:108:PHE:CD1	1:A:130:ILE:HD11	2.57	0.40
1:C:239:TRP:NE1	8:C:502:HOH:O	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	336/362 (93%)	330 (98%)	6 (2%)	0	100	100
1	B	341/362 (94%)	335 (98%)	6 (2%)	0	100	100
1	C	336/362 (93%)	330 (98%)	6 (2%)	0	100	100
1	D	341/362 (94%)	335 (98%)	6 (2%)	0	100	100
1	E	336/362 (93%)	330 (98%)	6 (2%)	0	100	100
All	All	1690/1810 (93%)	1660 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	295/326 (90%)	292 (99%)	3 (1%)	68	83
1	B	294/326 (90%)	291 (99%)	3 (1%)	68	83
1	C	293/326 (90%)	288 (98%)	5 (2%)	53	75
1	D	296/326 (91%)	293 (99%)	3 (1%)	68	83
1	E	296/326 (91%)	293 (99%)	3 (1%)	68	83
All	All	1474/1630 (90%)	1457 (99%)	17 (1%)	63	80

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	PHE
1	A	47	SER
1	A	171	GLN
1	B	32	PHE
1	B	47	SER
1	B	171	GLN
1	C	32	PHE
1	C	47	SER
1	C	59	ARG
1	C	171	GLN
1	C	203	ASN
1	D	32	PHE
1	D	47	SER
1	D	171	GLN
1	E	32	PHE
1	E	47	SER
1	E	171	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	219	GLN
1	A	226	GLN
1	B	66	GLN
1	B	219	GLN
1	C	66	GLN
1	C	203	ASN
1	C	219	GLN
1	C	226	GLN
1	D	66	GLN
1	D	203	ASN
1	D	219	GLN
1	D	226	GLN
1	E	66	GLN
1	E	219	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 6 are monoatomic - leaving 16 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
4	IVM	D	403	-	67,68,68	1.84	7 (10%)	87,102,102	1.32	12 (13%)
3	GLY	A	402	-	4,4,4	1.17	1 (25%)	3,4,4	1.71	2 (66%)
4	IVM	C	403	-	67,68,68	1.82	8 (11%)	87,102,102	1.31	9 (10%)
2	7C6	C	401	-	31,32,32	1.92	4 (12%)	41,50,50	1.96	9 (21%)
3	GLY	E	402	-	4,4,4	1.14	1 (25%)	3,4,4	1.83	2 (66%)
7	NAG	C	405	1	14,14,15	0.51	0	17,19,21	1.14	2 (11%)
3	GLY	D	402	-	4,4,4	1.22	1 (25%)	3,4,4	1.67	1 (33%)
4	IVM	B	403	-	67,68,68	1.83	7 (10%)	87,102,102	1.29	9 (10%)
2	7C6	B	401	-	31,32,32	1.90	4 (12%)	41,50,50	2.09	12 (29%)
4	IVM	E	403	-	67,68,68	1.80	7 (10%)	87,102,102	1.28	9 (10%)
3	GLY	C	402	-	4,4,4	1.20	1 (25%)	3,4,4	1.73	1 (33%)
3	GLY	B	402	-	4,4,4	1.28	1 (25%)	3,4,4	1.49	0
4	IVM	A	403	-	67,68,68	1.85	7 (10%)	87,102,102	1.23	10 (11%)
2	7C6	A	401	-	31,32,32	2.03	6 (19%)	41,50,50	1.98	10 (24%)
2	7C6	D	401	-	31,32,32	2.05	5 (16%)	41,50,50	2.05	12 (29%)
2	7C6	E	401	-	31,32,32	1.99	5 (16%)	41,50,50	1.96	10 (24%)

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
4	IVM	D	403	-	-	3/45/141/141	0/7/7/7
3	GLY	A	402	-	-	2/2/2/2	-
4	IVM	C	403	-	-	5/45/141/141	1/7/7/7
2	7C6	C	401	-	-	0/12/50/50	0/5/5/5
3	GLY	E	402	-	-	0/2/2/2	-
7	NAG	C	405	1	-	1/6/23/26	0/1/1/1
3	GLY	D	402	-	-	2/2/2/2	-
4	IVM	B	403	-	-	3/45/141/141	0/7/7/7
2	7C6	B	401	-	-	0/12/50/50	0/5/5/5
4	IVM	E	403	-	-	5/45/141/141	0/7/7/7
3	GLY	C	402	-	-	2/2/2/2	-
3	GLY	B	402	-	-	2/2/2/2	-
4	IVM	A	403	-	-	4/45/141/141	1/7/7/7
2	7C6	A	401	-	-	0/12/50/50	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	7C6	D	401	-	-	0/12/50/50	0/5/5/5
2	7C6	E	401	-	-	0/12/50/50	0/5/5/5

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	401	7C6	O3-S1	7.50	1.51	1.43
2	D	401	7C6	O3-S1	6.94	1.50	1.43
2	D	401	7C6	O2-S1	6.91	1.50	1.43
2	A	401	7C6	O3-S1	6.74	1.50	1.43
2	B	401	7C6	O3-S1	6.68	1.50	1.43
2	C	401	7C6	O3-S1	6.62	1.50	1.43
2	E	401	7C6	O2-S1	6.43	1.50	1.43
4	A	403	IVM	C44-C43	6.40	1.40	1.33
4	C	403	IVM	C40-C39	-6.39	1.40	1.50
4	D	403	IVM	C40-C39	-6.36	1.40	1.50
2	B	401	7C6	O2-S1	6.33	1.50	1.43
4	A	403	IVM	C40-C39	-6.31	1.40	1.50
4	B	403	IVM	C44-C43	6.29	1.40	1.33
2	C	401	7C6	O2-S1	6.27	1.50	1.43
4	B	403	IVM	C40-C39	-6.17	1.40	1.50
4	E	403	IVM	C40-C39	-6.13	1.40	1.50
4	E	403	IVM	C44-C43	6.12	1.40	1.33
2	A	401	7C6	O2-S1	6.11	1.50	1.43
4	C	403	IVM	C44-C43	6.08	1.40	1.33
4	D	403	IVM	C44-C43	6.08	1.40	1.33
4	D	403	IVM	C15-C16	-5.70	1.39	1.50
4	A	403	IVM	C15-C16	-5.67	1.39	1.50
4	E	403	IVM	C15-C16	-5.64	1.39	1.50
4	B	403	IVM	C15-C16	-5.62	1.39	1.50
4	C	403	IVM	C15-C16	-5.61	1.39	1.50
4	D	403	IVM	C16-C17	4.89	1.39	1.33
4	E	403	IVM	C16-C17	4.81	1.39	1.33
4	B	403	IVM	C16-C17	4.80	1.39	1.33
4	A	403	IVM	C16-C17	4.79	1.39	1.33
4	C	403	IVM	C16-C17	4.63	1.39	1.33
4	A	403	IVM	C45-C44	3.94	1.55	1.50
4	B	403	IVM	C45-C44	3.93	1.55	1.50
4	C	403	IVM	C38-C39	3.87	1.39	1.33
4	B	403	IVM	C38-C39	3.84	1.39	1.33
4	D	403	IVM	C38-C39	3.82	1.39	1.33
4	A	403	IVM	C38-C39	3.76	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	403	IVM	C45-C44	3.71	1.55	1.50
4	E	403	IVM	C38-C39	3.70	1.39	1.33
4	D	403	IVM	C45-C44	3.65	1.54	1.50
4	E	403	IVM	C45-C44	3.52	1.54	1.50
2	A	401	7C6	S1-N1	3.51	1.68	1.63
2	A	401	7C6	C13-S1	-2.62	1.72	1.76
2	D	401	7C6	C13-S1	-2.56	1.73	1.76
2	B	401	7C6	C2-C3	2.49	1.55	1.51
3	B	402	GLY	OXT-C	-2.46	1.22	1.30
2	A	401	7C6	C2-C3	2.40	1.55	1.51
3	D	402	GLY	OXT-C	-2.37	1.23	1.30
2	D	401	7C6	C3-N2	2.33	1.40	1.36
3	C	402	GLY	OXT-C	-2.33	1.23	1.30
2	C	401	7C6	C3-N2	2.32	1.40	1.36
4	E	403	IVM	O9-C40	2.31	1.47	1.43
2	A	401	7C6	C3-N2	2.29	1.40	1.36
3	A	402	GLY	OXT-C	-2.25	1.23	1.30
2	C	401	7C6	C2-C3	2.24	1.54	1.51
3	E	402	GLY	OXT-C	-2.23	1.23	1.30
4	A	403	IVM	O9-C40	2.19	1.47	1.43
2	B	401	7C6	C3-N2	2.18	1.40	1.36
2	E	401	7C6	C2-C3	2.16	1.54	1.51
4	C	403	IVM	O9-C40	2.14	1.47	1.43
4	D	403	IVM	O9-C40	2.10	1.47	1.43
4	C	403	IVM	C41-C42	2.05	1.55	1.52
2	E	401	7C6	S1-N1	2.04	1.66	1.63
2	E	401	7C6	C3-N2	2.03	1.40	1.36
4	B	403	IVM	O9-C40	2.02	1.46	1.43
2	D	401	7C6	C2-C3	2.01	1.54	1.51

All (110) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	7C6	O3-S1-O2	-6.38	109.63	119.59
2	E	401	7C6	O3-S1-O2	-6.33	109.72	119.59
2	C	401	7C6	O3-S1-O2	-5.83	110.49	119.59
2	D	401	7C6	O3-S1-O2	-5.74	110.63	119.59
4	D	403	IVM	O12-C46-C45	5.05	118.57	110.91
2	A	401	7C6	O3-S1-O2	-5.04	111.73	119.59
4	C	403	IVM	O12-C46-C45	4.97	118.45	110.91
4	B	403	IVM	O12-C46-C45	4.91	118.36	110.91
2	D	401	7C6	C1-N1-S1	-4.82	111.79	120.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	7C6	C1-N1-S1	-4.76	111.90	120.13
2	A	401	7C6	C7-C8-C9	-4.62	120.36	125.03
4	E	403	IVM	O12-C46-C45	4.60	117.90	110.91
4	A	403	IVM	O12-C46-C45	4.54	117.80	110.91
2	C	401	7C6	C1-N1-S1	-4.53	112.30	120.13
2	D	401	7C6	C7-C8-C9	-4.43	120.55	125.03
2	D	401	7C6	C10-N1-S1	-4.26	110.32	118.80
2	B	401	7C6	C10-N1-S1	-4.22	110.39	118.80
2	E	401	7C6	C7-C8-C9	-4.20	120.79	125.03
2	B	401	7C6	C7-C8-C9	-4.17	120.81	125.03
2	C	401	7C6	C7-C8-C9	-4.12	120.86	125.03
2	A	401	7C6	C10-N1-S1	-4.07	110.70	118.80
2	C	401	7C6	C10-N1-S1	-4.07	110.71	118.80
2	E	401	7C6	C1-N1-S1	-3.98	113.25	120.13
2	A	401	7C6	C1-N1-S1	-3.98	113.25	120.13
2	A	401	7C6	O1-C3-N2	-3.76	118.69	122.35
2	B	401	7C6	O1-C3-N2	-3.73	118.72	122.35
2	C	401	7C6	O1-C3-N2	-3.47	118.97	122.35
2	E	401	7C6	C10-N1-S1	-3.44	111.95	118.80
2	E	401	7C6	O1-C3-N2	-3.20	119.23	122.35
2	D	401	7C6	O1-C3-N2	-3.19	119.24	122.35
4	C	403	IVM	O14-C14-C15	3.17	110.22	106.53
7	C	405	NAG	C1-O5-C5	3.14	116.39	112.19
4	D	403	IVM	C37-C38-C39	-3.02	121.09	125.87
4	C	403	IVM	C13-C14-C15	-3.00	109.49	113.05
4	E	403	IVM	C34-C36-C37	-2.99	119.93	126.11
4	B	403	IVM	O11-C46-C45	-2.94	120.60	125.06
2	B	401	7C6	C6-N3-C7	2.90	121.93	116.85
4	E	403	IVM	O11-C46-C45	-2.89	120.68	125.06
4	D	403	IVM	O11-C46-C45	-2.85	120.74	125.06
4	E	403	IVM	C37-C38-C39	-2.85	121.36	125.87
4	C	403	IVM	C34-C36-C37	-2.85	120.23	126.11
2	D	401	7C6	C6-N3-C7	2.82	121.79	116.85
4	D	403	IVM	C34-C36-C37	-2.82	120.28	126.11
4	C	403	IVM	O11-C46-C45	-2.79	120.83	125.06
2	E	401	7C6	C6-N3-C7	2.78	121.73	116.85
2	D	401	7C6	O4-C15-C14	2.75	131.52	127.86
2	A	401	7C6	C6-N3-C7	2.74	121.65	116.85
4	A	403	IVM	O11-C46-C45	-2.70	120.97	125.06
4	B	403	IVM	C8-C9-C5	2.69	112.06	108.33
4	D	403	IVM	O1-C5-C3	2.64	110.24	106.29
4	A	403	IVM	C37-C38-C39	-2.62	121.72	125.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	7C6	O4-C15-C14	2.62	131.35	127.86
4	B	403	IVM	C13-C14-C15	-2.62	109.94	113.05
4	E	403	IVM	C34-C19-C17	-2.59	108.46	113.19
4	B	403	IVM	C38-C37-C36	-2.59	118.42	124.43
2	A	401	7C6	C10-N1-C1	-2.59	107.36	110.68
4	C	403	IVM	C37-C38-C39	-2.55	121.83	125.87
2	D	401	7C6	O5-C19-O4	-2.55	104.10	108.09
4	A	403	IVM	C34-C36-C37	-2.54	120.86	126.11
2	C	401	7C6	C6-N3-C7	2.54	121.30	116.85
4	B	403	IVM	C37-C38-C39	-2.53	121.86	125.87
2	B	401	7C6	O4-C15-C14	2.51	131.19	127.86
2	C	401	7C6	O4-C15-C14	2.49	131.17	127.86
4	A	403	IVM	C8-C9-C5	2.49	111.78	108.33
4	A	403	IVM	C38-C37-C36	-2.47	118.69	124.43
4	B	403	IVM	C34-C36-C37	-2.46	121.02	126.11
4	D	403	IVM	C38-C37-C36	-2.46	118.73	124.43
2	B	401	7C6	C12-N2-C3	2.46	120.02	117.69
4	E	403	IVM	O14-C14-C15	2.44	109.37	106.53
4	E	403	IVM	C8-C9-C5	2.43	111.70	108.33
2	E	401	7C6	O4-C15-C14	2.40	131.06	127.86
4	B	403	IVM	O14-C14-C15	2.40	109.32	106.53
4	D	403	IVM	C8-C9-C5	2.40	111.66	108.33
2	B	401	7C6	O3-S1-N1	2.36	111.09	106.97
3	E	402	GLY	OXT-C-O	-2.34	117.31	123.33
4	D	403	IVM	C34-C19-C17	-2.34	108.93	113.19
4	C	403	IVM	C38-C37-C36	-2.30	119.10	124.43
3	C	402	GLY	OXT-C-O	-2.29	117.45	123.33
7	C	405	NAG	O5-C1-C2	-2.28	107.76	111.29
2	B	401	7C6	C10-N1-C1	-2.28	107.77	110.68
2	E	401	7C6	C13-S1-N1	2.26	111.31	107.36
4	A	403	IVM	C47-C45-C46	2.26	111.38	109.05
2	D	401	7C6	C12-N2-C3	2.24	119.81	117.69
3	D	402	GLY	OXT-C-O	-2.23	117.61	123.33
4	C	403	IVM	C8-C9-C5	2.22	111.41	108.33
4	D	403	IVM	O1-C6-C11	2.22	109.28	106.26
2	D	401	7C6	C8-C7-N3	-2.20	120.90	124.41
2	B	401	7C6	C13-S1-N1	2.19	111.18	107.36
4	A	403	IVM	C20-O2-C19	-2.19	111.02	116.45
4	C	403	IVM	C34-C19-C17	-2.19	109.21	113.19
4	E	403	IVM	C38-C37-C36	-2.14	119.46	124.43
2	A	401	7C6	C8-C7-N3	-2.13	121.01	124.41
3	A	402	GLY	OXT-C-O	-2.13	117.86	123.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	401	7C6	C12-N2-C3	2.12	119.70	117.69
2	C	401	7C6	C10-N1-C1	-2.12	107.97	110.68
3	E	402	GLY	OXT-C-CA	2.11	121.79	113.38
2	C	401	7C6	C13-S1-N1	2.11	111.04	107.36
4	E	403	IVM	O12-C12-C11	2.11	113.03	107.64
2	B	401	7C6	C8-C7-N3	-2.10	121.07	124.41
2	E	401	7C6	C8-C7-N3	-2.08	121.09	124.41
4	B	403	IVM	C20-O2-C19	-2.07	111.30	116.45
4	A	403	IVM	C34-C19-C17	-2.04	109.48	113.19
4	D	403	IVM	C20-O2-C19	-2.03	111.39	116.45
3	A	402	GLY	OXT-C-CA	2.02	121.40	113.38
4	A	403	IVM	C13-C14-C15	-2.01	110.67	113.05
2	A	401	7C6	O5-C19-O4	-2.01	104.94	108.09
2	D	401	7C6	C10-N1-C1	-2.01	108.11	110.68
4	D	403	IVM	C12-O12-C46	-2.01	114.57	117.72
2	D	401	7C6	C13-S1-N1	2.00	110.86	107.36
4	D	403	IVM	C47-C45-C44	-2.00	110.41	112.74

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	402	GLY	O-C-CA-N
3	B	402	GLY	OXT-C-CA-N
3	D	402	GLY	O-C-CA-N
3	D	402	GLY	OXT-C-CA-N
4	B	403	IVM	C1-C2-C3-C5
3	A	402	GLY	OXT-C-CA-N
4	D	403	IVM	O7-C25-O4-C24
3	A	402	GLY	O-C-CA-N
4	D	403	IVM	C21-C22-O3-C23
4	E	403	IVM	C26-C25-O4-C24
4	A	403	IVM	O7-C25-O4-C24
4	E	403	IVM	O7-C25-O4-C24
4	C	403	IVM	C1-C2-C3-C4
3	C	402	GLY	O-C-CA-N
4	A	403	IVM	C26-C25-O4-C24
4	D	403	IVM	C26-C25-O4-C24
4	B	403	IVM	C1-C2-C3-C4
4	C	403	IVM	C26-C25-O4-C24
4	C	403	IVM	O7-C25-O4-C24
4	C	403	IVM	C1-C2-C3-C5

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Mol	Chain	Res	Type	Atoms
4	E	403	IVM	C1-C2-C3-C5
4	E	403	IVM	C1-C2-C3-C4
3	C	402	GLY	OXT-C-CA-N
4	A	403	IVM	C21-C22-O3-C23
4	A	403	IVM	C19-C34-C36-C37
4	C	403	IVM	C19-C34-C36-C37
4	E	403	IVM	C19-C34-C36-C37
7	C	405	NAG	O5-C5-C6-O6
4	B	403	IVM	C19-C34-C36-C37

All (2) ring outliers are listed below:

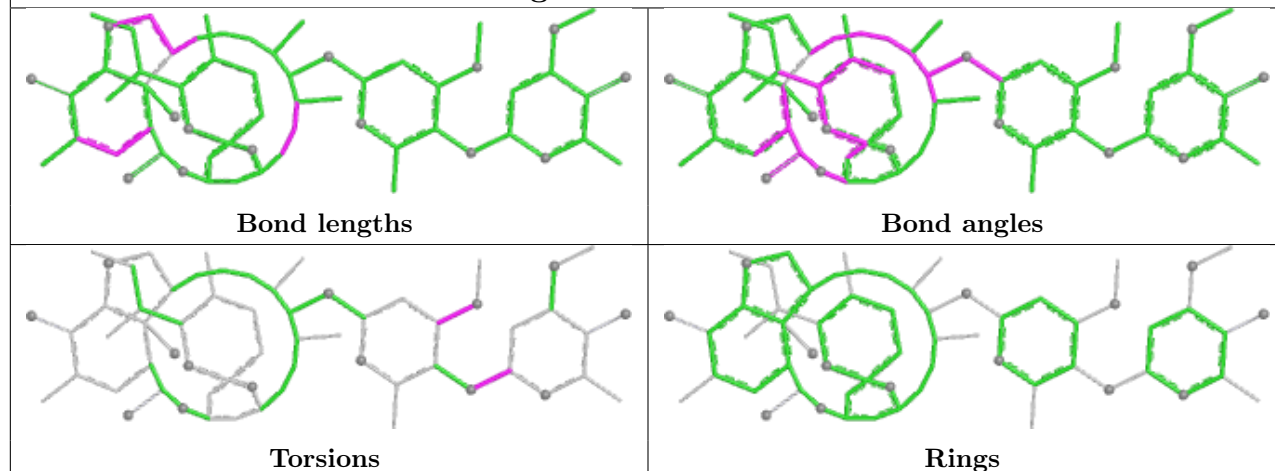
Mol	Chain	Res	Type	Atoms
4	A	403	IVM	C5-C6-C7-C8-C9-O1
4	C	403	IVM	C5-C6-C7-C8-C9-O1

5 monomers are involved in 11 short contacts:

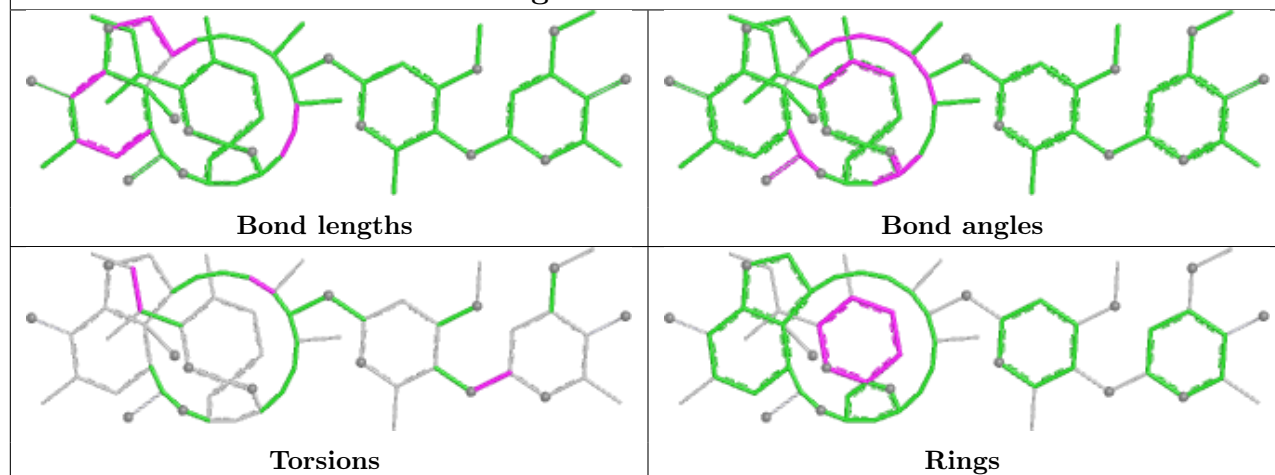
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	403	IVM	2	0
4	C	403	IVM	2	0
4	B	403	IVM	3	0
3	B	402	GLY	1	0
4	A	403	IVM	3	0

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

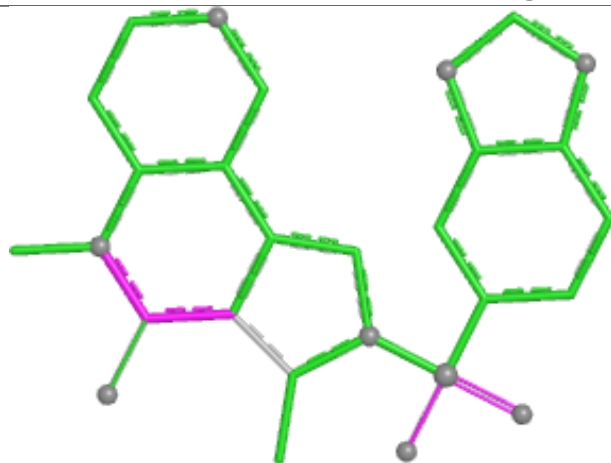
Ligand IVM D 403



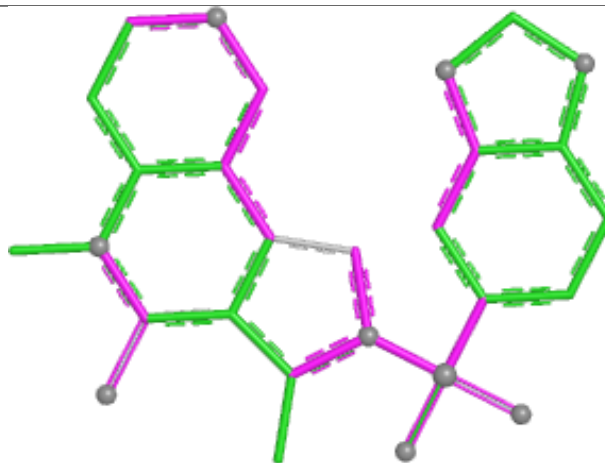
Ligand IVM C 403



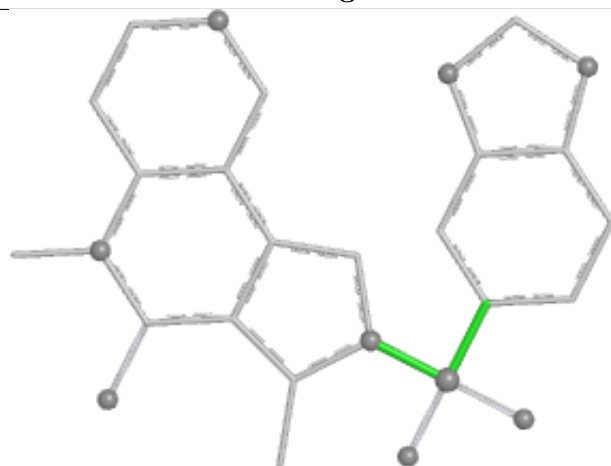
Ligand 7C6 C 401



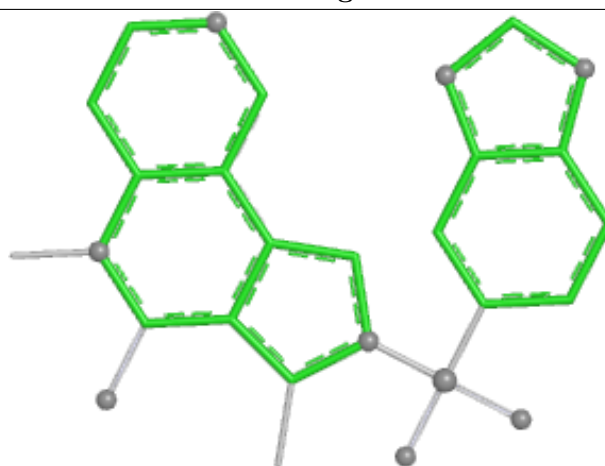
Bond lengths



Bond angles

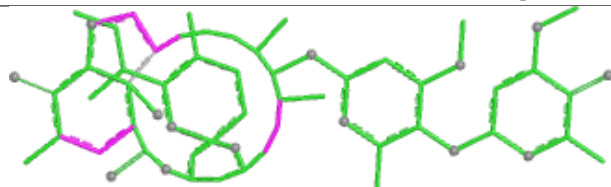


Torsions



Rings

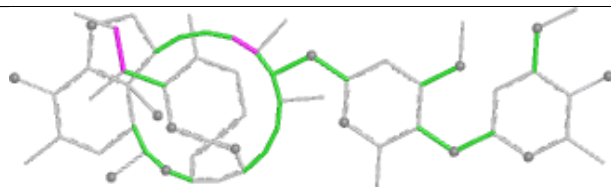
Ligand IVM B 403



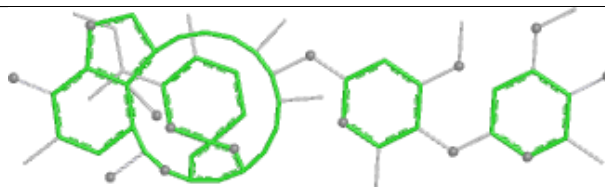
Bond lengths



Bond angles

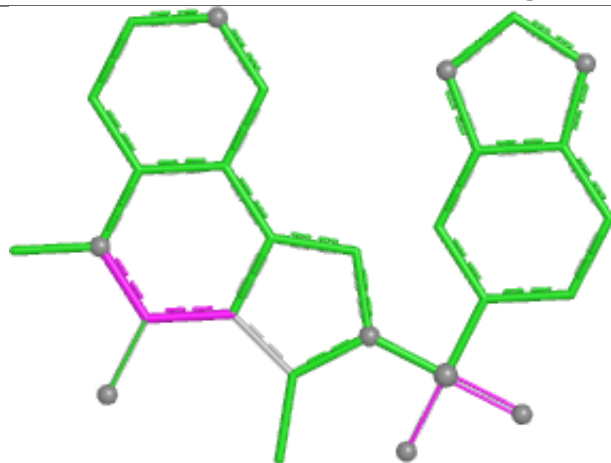


Torsions

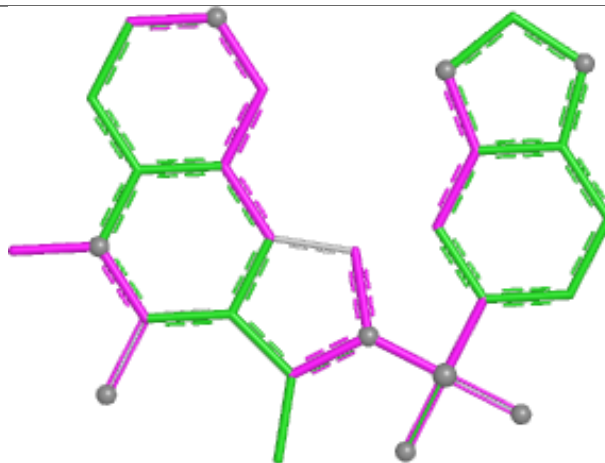


Rings

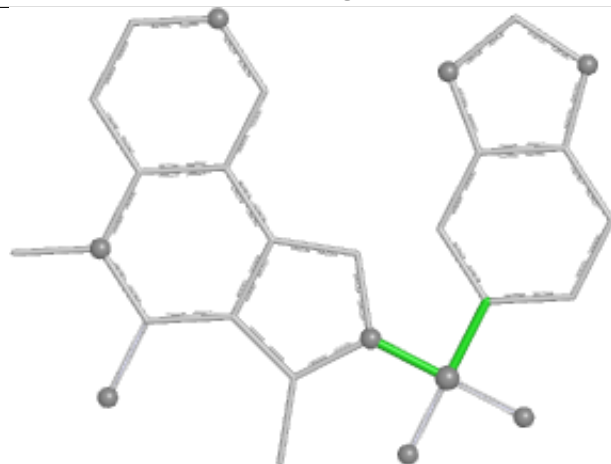
Ligand 7C6 B 401



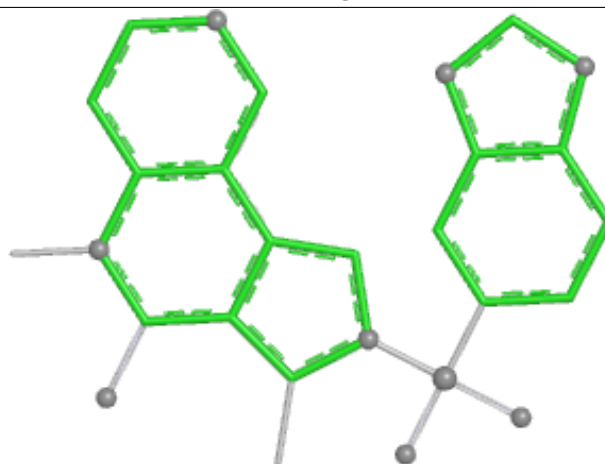
Bond lengths



Bond angles

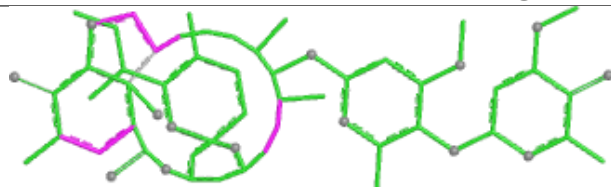


Torsions



Rings

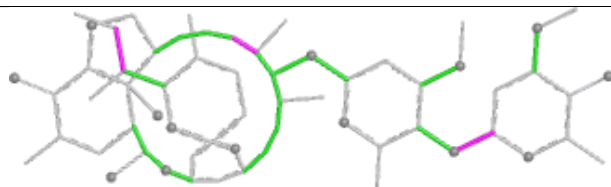
Ligand IVM E 403



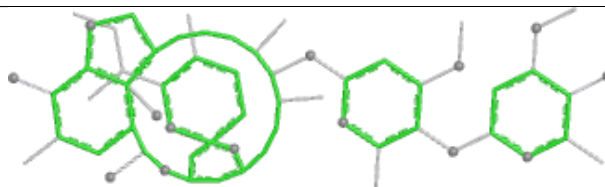
Bond lengths



Bond angles

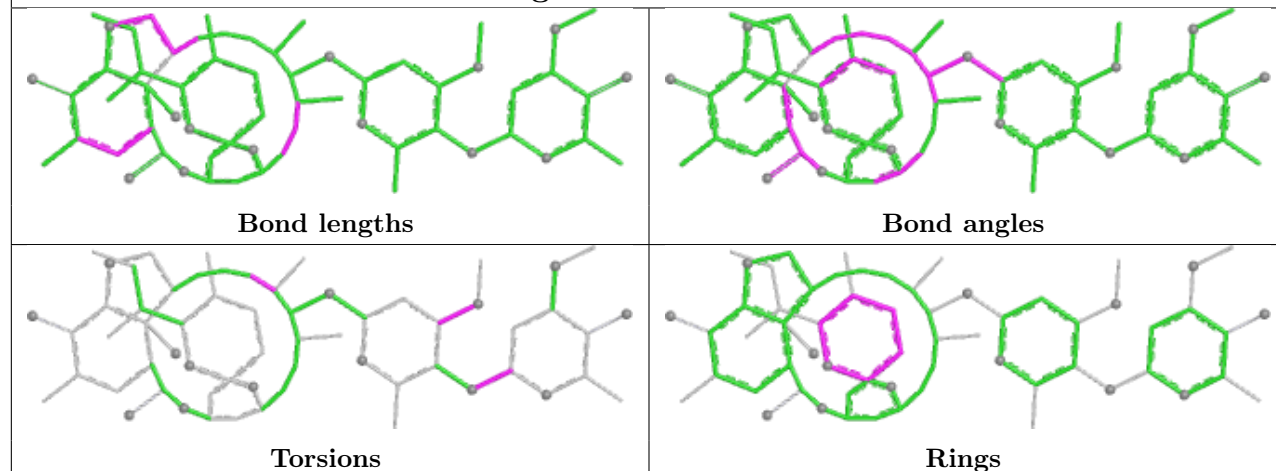


Torsions

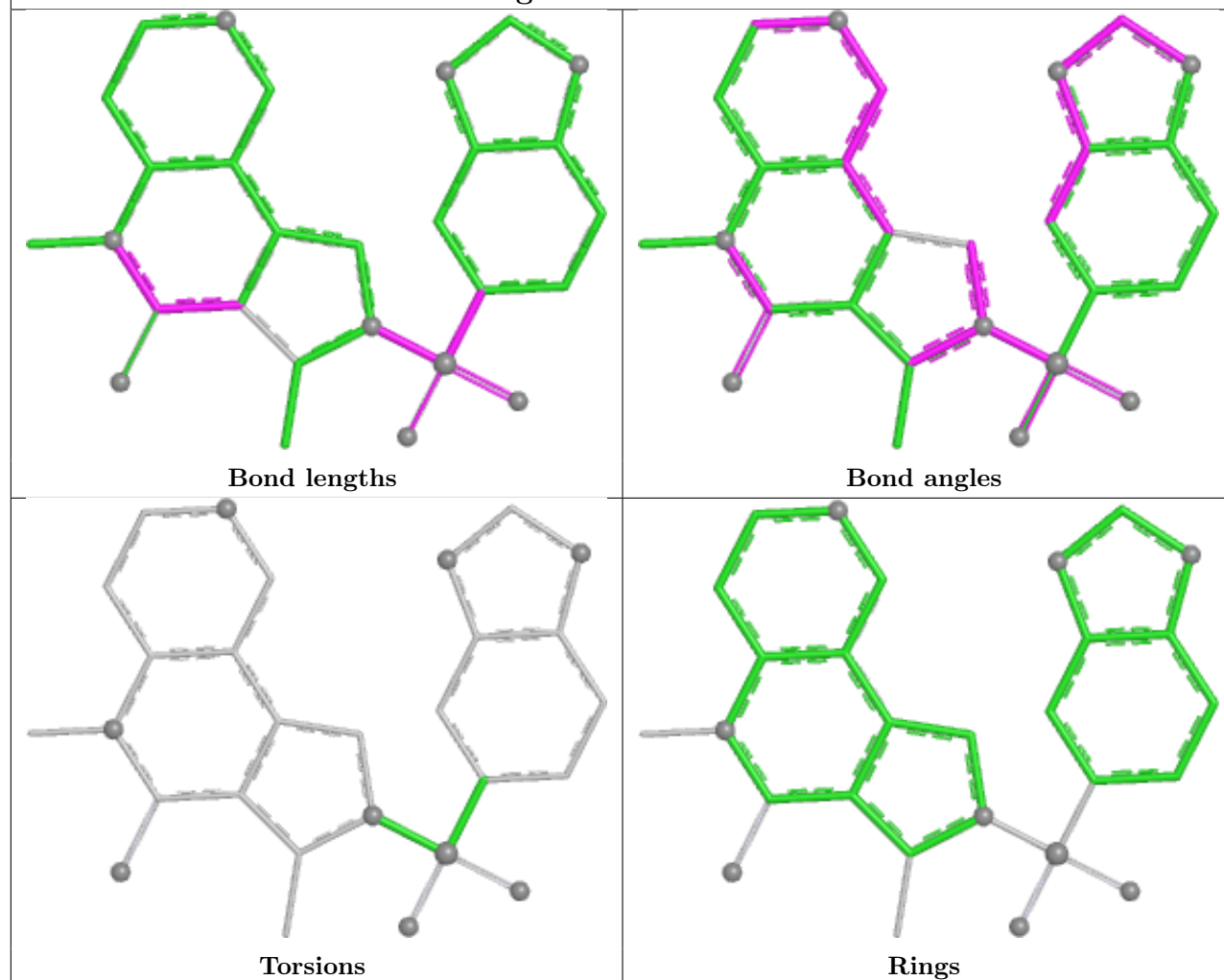


Rings

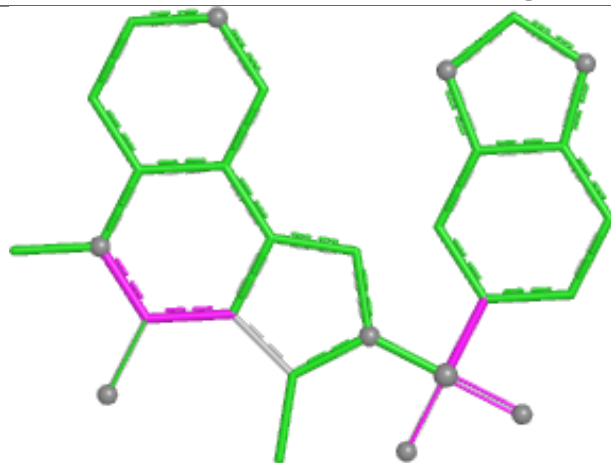
Ligand IVM A 403



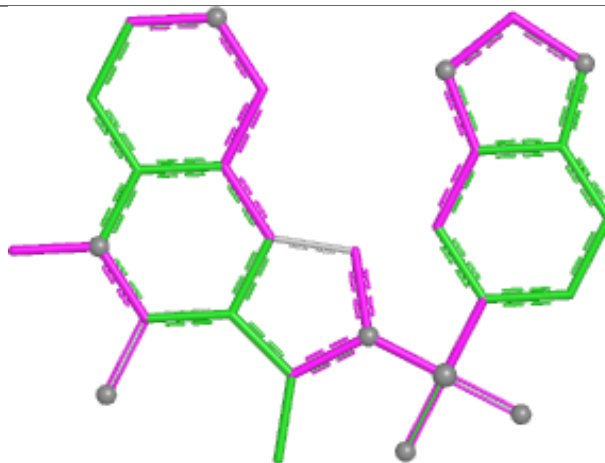
Ligand 7C6 A 401



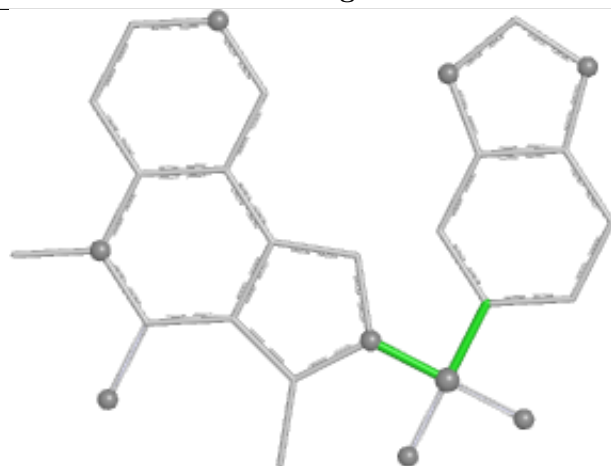
Ligand 7C6 D 401



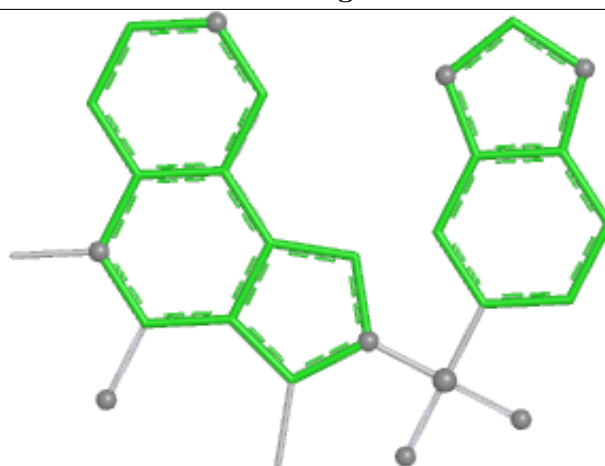
Bond lengths



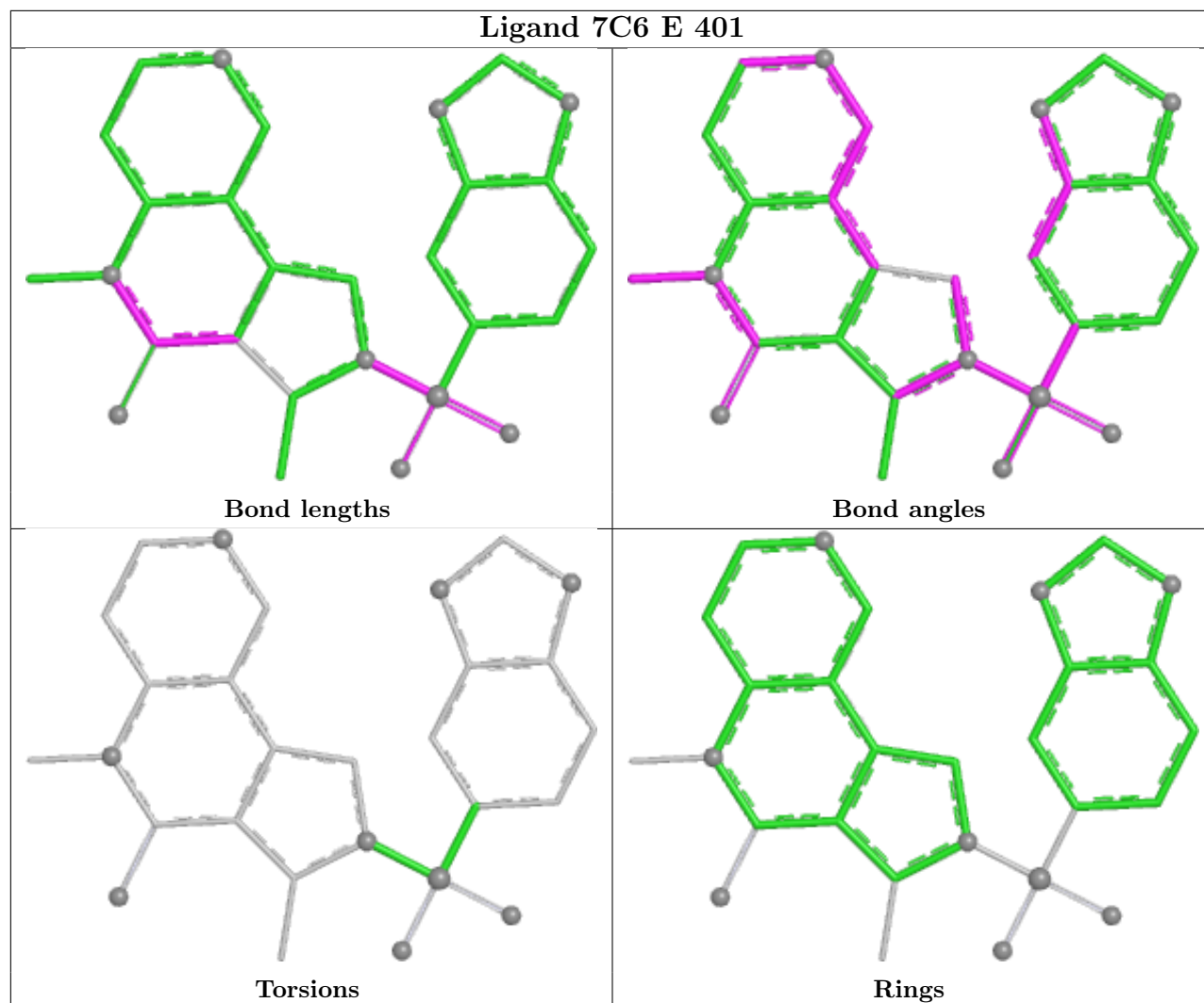
Bond angles



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, 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	338/362 (93%)	0.34	23 (6%)	23	17	41, 75, 136, 173	0
1	B	343/362 (94%)	0.49	27 (7%)	18	14	42, 78, 144, 188	0
1	C	338/362 (93%)	0.55	29 (8%)	16	12	46, 88, 171, 224	0
1	D	343/362 (94%)	0.77	47 (13%)	6	5	50, 94, 173, 217	0
1	E	338/362 (93%)	0.45	18 (5%)	32	24	50, 87, 152, 195	0
All	All	1700/1810 (93%)	0.52	144 (8%)	16	12	41, 85, 162, 224	0

All (144) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	280	VAL	5.8
1	D	312	THR	5.4
1	B	169	GLU	4.7
1	B	203	ASN	4.6
1	A	217	GLU	4.4
1	C	306	PHE	4.2
1	B	310	ALA	4.2
1	D	330	PHE	4.2
1	D	254	ALA	4.0
1	D	177	GLN	4.0
1	C	303	ALA	3.9
1	D	174	ALA	3.9
1	B	197	TYR	3.9
1	D	310	ALA	3.8
1	D	324	THR	3.8
1	B	345	TYR	3.5
1	B	234	ILE	3.4
1	D	253	VAL	3.3
1	D	224	LEU	3.2
1	B	40	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	329	CYS	3.1
1	D	314	VAL	3.1
1	B	273	SER	3.1
1	B	330	PHE	3.0
1	E	330	PHE	3.0
1	D	33	LYS	3.0
1	D	249	ALA	3.0
1	C	181	GLY	2.9
1	D	255	LEU	2.9
1	C	141	ASP	2.9
1	C	278	SER	2.9
1	A	188	LEU	2.9
1	A	173	GLU	2.9
1	D	345	TYR	2.9
1	D	217	GLU	2.8
1	D	4	ARG	2.8
1	D	173	GLU	2.8
1	C	314	VAL	2.8
1	A	306	PHE	2.8
1	E	292	LEU	2.8
1	D	176	VAL	2.7
1	A	190	LYS	2.7
1	D	32	PHE	2.7
1	C	345	TYR	2.7
1	E	280	VAL	2.7
1	E	251	ALA	2.7
1	D	43	ILE	2.6
1	B	339	ILE	2.6
1	E	310	ALA	2.6
1	B	271	ARG	2.6
1	C	279	TYR	2.6
1	E	301	TYR	2.6
1	A	329	CYS	2.6
1	D	259	THR	2.5
1	E	110	GLU	2.5
1	D	250	PRO	2.5
1	B	301	TYR	2.5
1	E	314	VAL	2.5
1	A	312	THR	2.5
1	C	227	MET	2.5
1	D	225	ILE	2.5
1	E	183	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	198	CYS	2.5
1	D	315	PHE	2.5
1	A	324	THR	2.5
1	C	310	ALA	2.5
1	B	198	CYS	2.5
1	D	243	TRP	2.4
1	A	330	PHE	2.4
1	A	8	MET	2.4
1	D	147	MET	2.4
1	C	198	CYS	2.4
1	A	322	ILE	2.4
1	A	314	VAL	2.4
1	A	303	ALA	2.4
1	A	147	MET	2.4
1	E	198	CYS	2.4
1	D	221	GLY	2.4
1	E	32	PHE	2.4
1	B	311	GLY	2.4
1	B	41	CYS	2.4
1	D	227	MET	2.4
1	D	319	ALA	2.3
1	B	335	LEU	2.3
1	B	344	ILE	2.3
1	C	307	VAL	2.3
1	D	327	ARG	2.3
1	A	191	GLU	2.3
1	D	152	CYS	2.3
1	E	335	LEU	2.3
1	C	32	PHE	2.3
1	C	273	SER	2.3
1	C	313	LYS	2.3
1	C	323	ASP	2.3
1	D	3	SER	2.3
1	B	299	LEU	2.2
1	E	226	GLN	2.2
1	A	325	ILE	2.2
1	C	277	VAL	2.2
1	E	308	SER	2.2
1	C	217	GLU	2.2
1	D	335	LEU	2.2
1	E	73	LEU	2.2
1	A	243	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	8	MET	2.2
1	C	315	PHE	2.2
1	A	232	LEU	2.2
1	B	38	ASN	2.2
1	C	336	ILE	2.2
1	B	270	SER	2.2
1	B	313	LYS	2.2
1	A	328	ALA	2.2
1	B	297	ALA	2.2
1	A	227	MET	2.2
1	D	325	ILE	2.1
1	D	219	GLN	2.1
1	A	313	LYS	2.1
1	B	340	PHE	2.1
1	C	174	ALA	2.1
1	D	302	ALA	2.1
1	C	271	ARG	2.1
1	D	316	ILE	2.1
1	B	6	ALA	2.1
1	B	196	ARG	2.1
1	D	41	CYS	2.1
1	D	339	ILE	2.1
1	D	331	PRO	2.1
1	B	15	ASP	2.1
1	B	254	ALA	2.1
1	D	138	CYS	2.1
1	D	171	GLN	2.1
1	C	240	VAL	2.1
1	C	172	ASP	2.1
1	C	302	ALA	2.1
1	D	244	ILE	2.0
1	C	33	LYS	2.0
1	A	307	VAL	2.0
1	D	332	LEU	2.0
1	E	339	ILE	2.0
1	D	251	ALA	2.0
1	D	313	LYS	2.0
1	E	227	MET	2.0
1	E	342	TRP	2.0
1	A	345	TYR	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 ⓘ

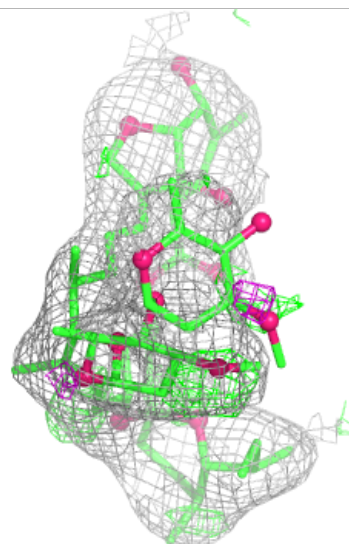
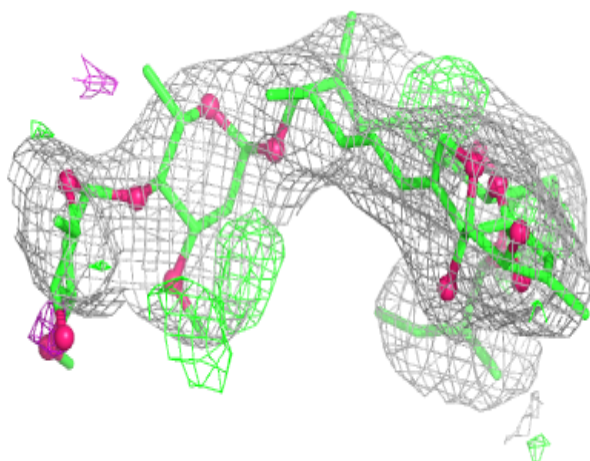
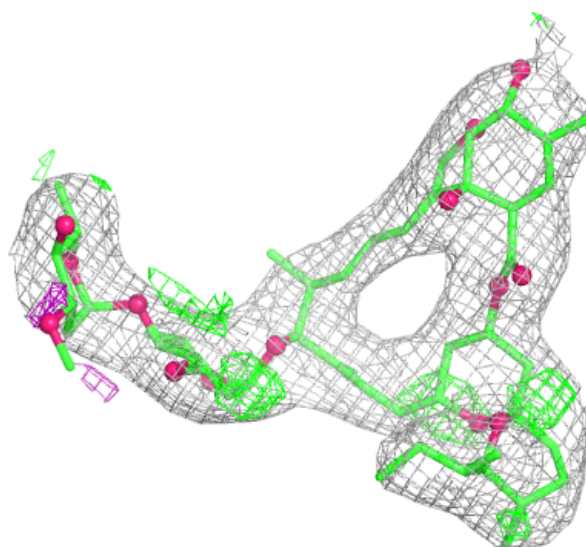
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	CL	A	405	1/1	0.62	0.26	102,102,102,102	0
5	ZN	E	404	1/1	0.67	0.13	104,104,104,104	1
7	NAG	C	405	14/15	0.67	0.15	115,123,127,127	0
5	ZN	C	404	1/1	0.75	0.08	123,123,123,123	1
5	ZN	D	404	1/1	0.80	0.13	122,122,122,122	1
5	ZN	A	404	1/1	0.85	0.11	85,85,85,85	1
5	ZN	B	404	1/1	0.87	0.14	110,110,110,110	1
4	IVM	E	403	62/62	0.88	0.20	86,101,121,128	0
4	IVM	D	403	62/62	0.89	0.18	106,132,149,154	0
4	IVM	C	403	62/62	0.90	0.17	109,135,156,162	0
4	IVM	A	403	62/62	0.90	0.17	80,99,122,128	0
4	IVM	B	403	62/62	0.92	0.14	91,114,132,134	0
3	GLY	A	402	5/5	0.93	0.13	64,64,65,65	0
3	GLY	E	402	5/5	0.93	0.11	63,63,64,65	0
3	GLY	C	402	5/5	0.94	0.12	74,75,75,77	0
2	7C6	E	401	28/28	0.95	0.09	69,74,79,81	0
3	GLY	D	402	5/5	0.95	0.13	72,73,73,74	0
2	7C6	C	401	28/28	0.95	0.09	64,72,79,81	0
3	GLY	B	402	5/5	0.96	0.09	71,72,72,73	0
2	7C6	A	401	28/28	0.96	0.09	50,61,67,69	0
2	7C6	B	401	28/28	0.97	0.07	64,71,79,81	0
2	7C6	D	401	28/28	0.97	0.07	71,78,85,87	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.

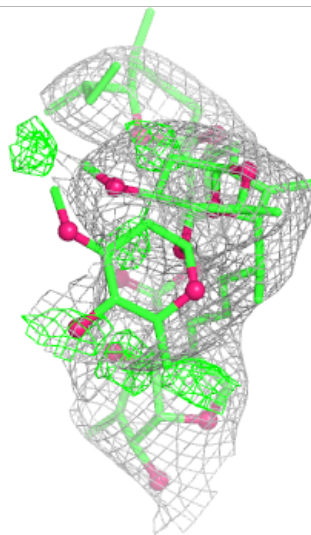
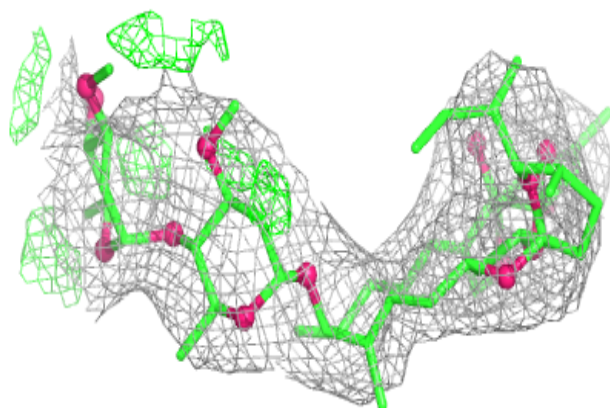
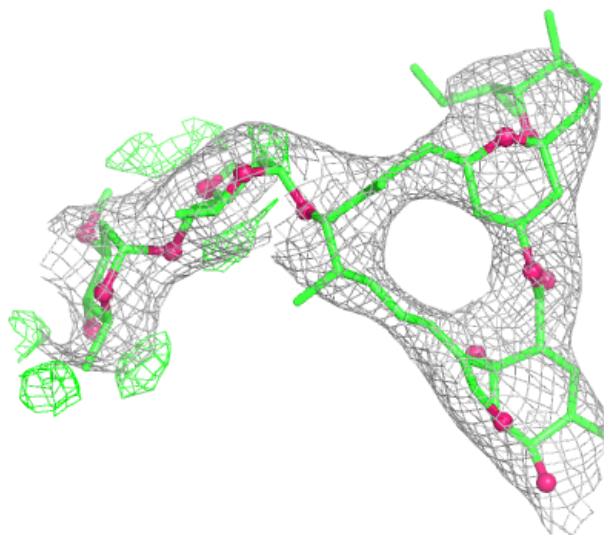
Electron density around IVM E 403:

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



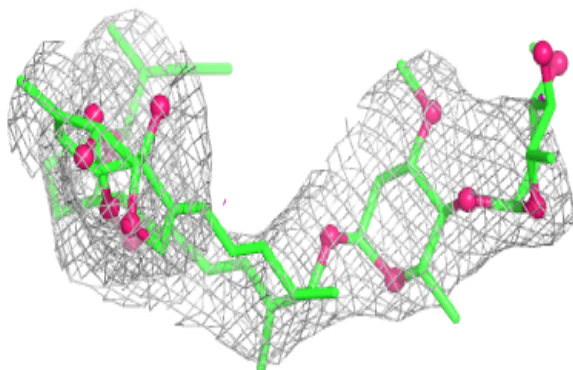
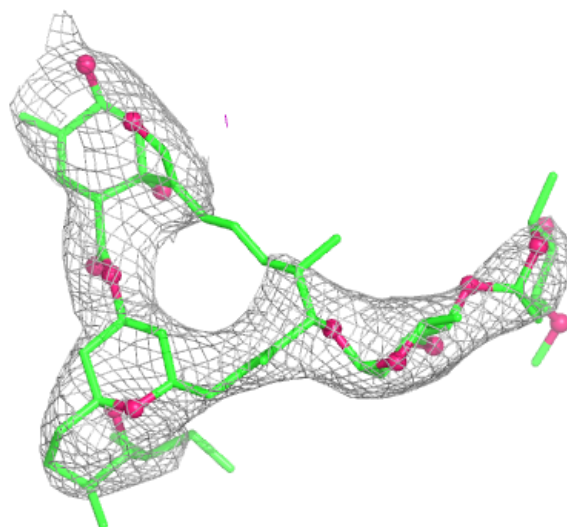
Electron density around IVM D 403:

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



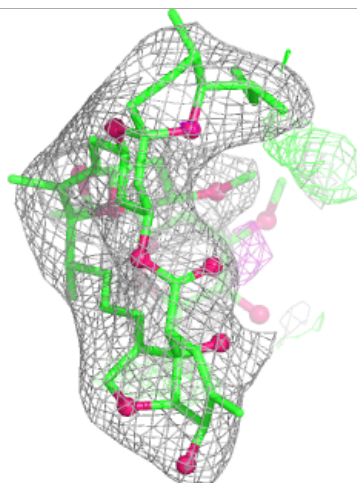
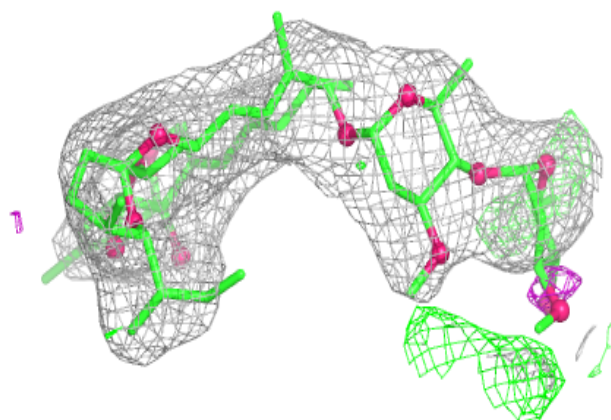
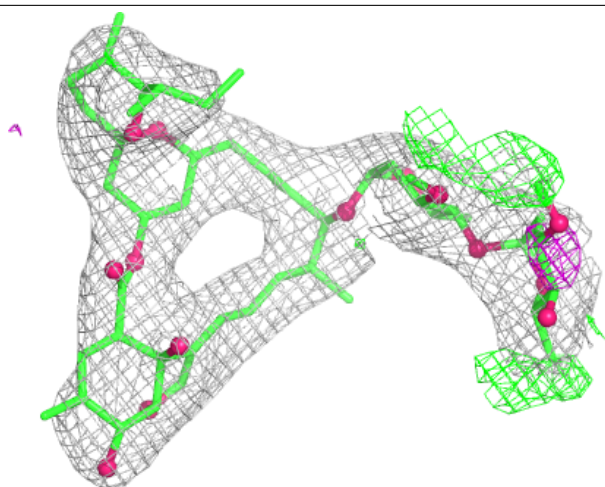
Electron density around IVM C 403:

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



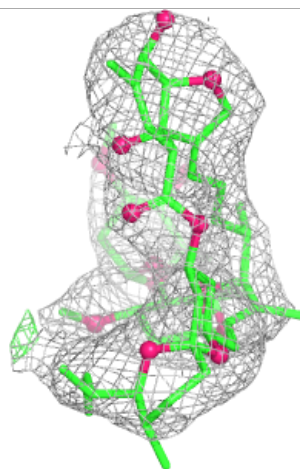
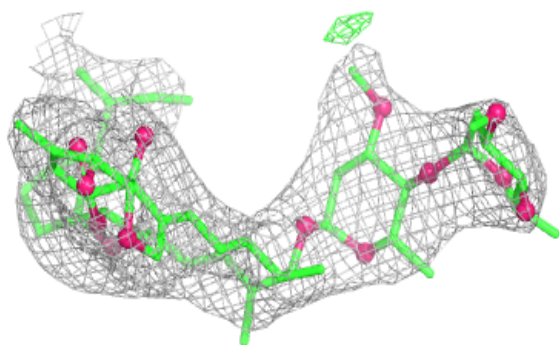
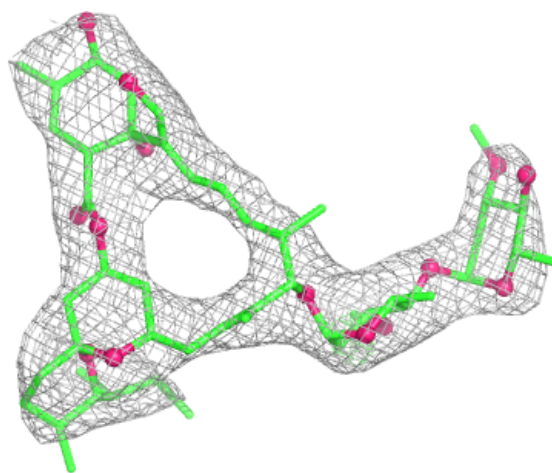
Electron density around IVM A 403:

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



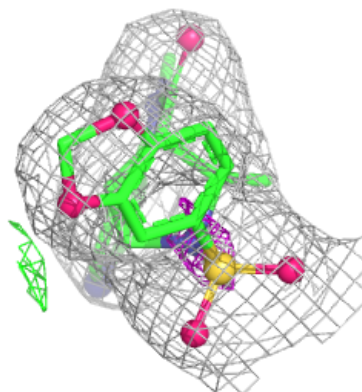
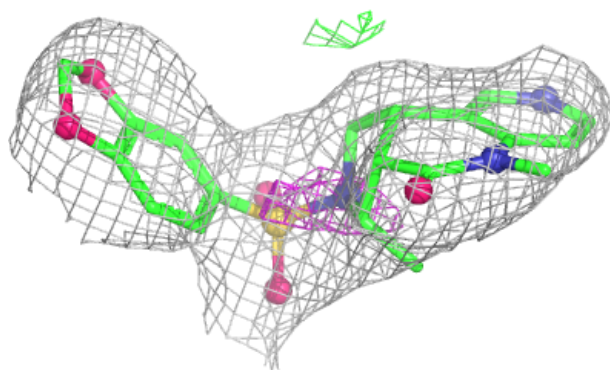
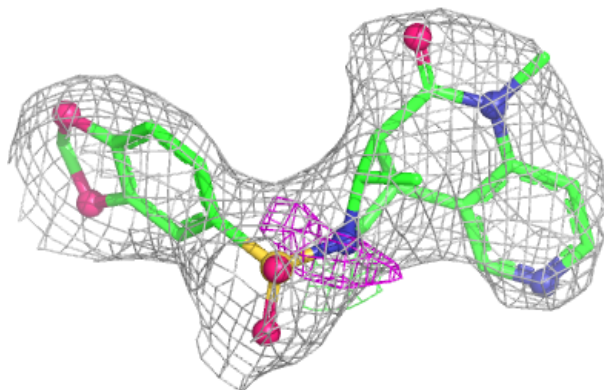
Electron density around IVM B 403:

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

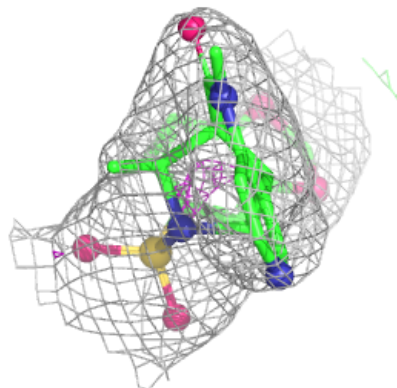
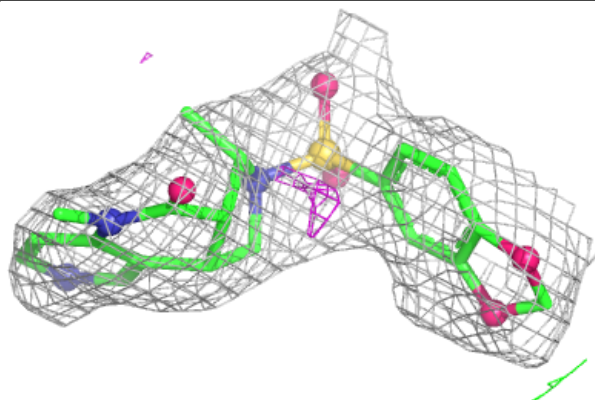
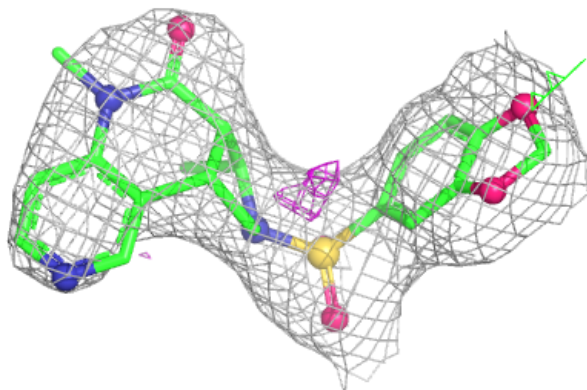


Electron density around 7C6 E 401:

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

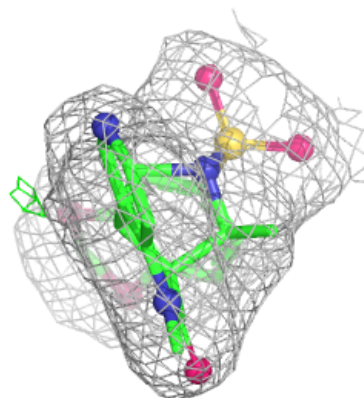
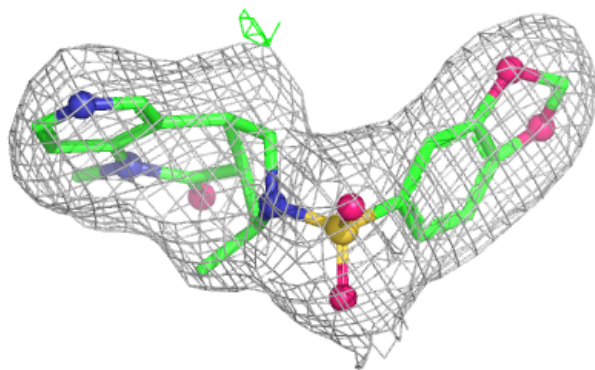
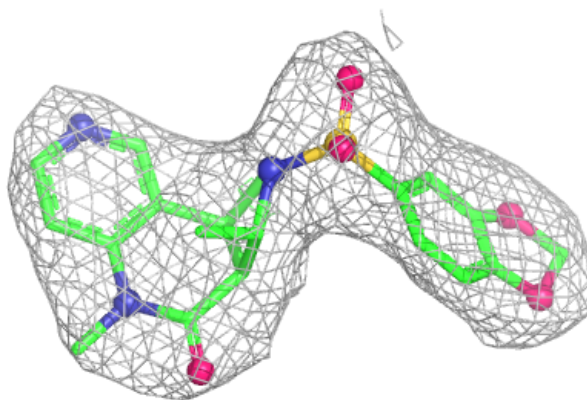
**Electron density around 7C6 C 401:**

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

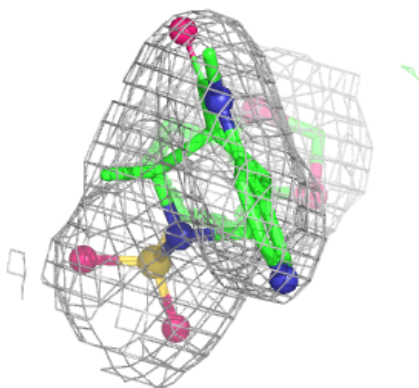
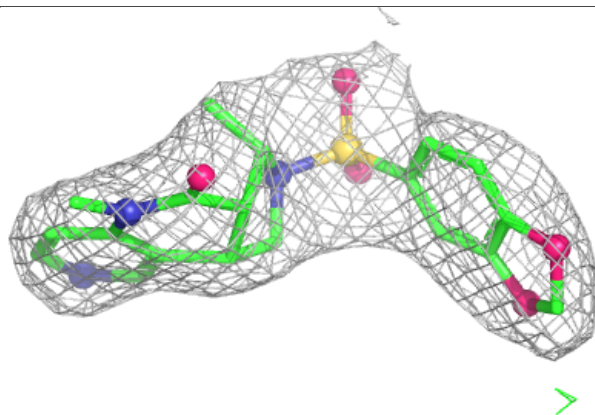
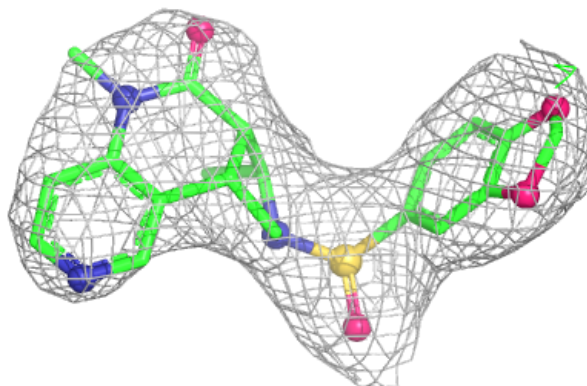


Electron density around 7C6 A 401:

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

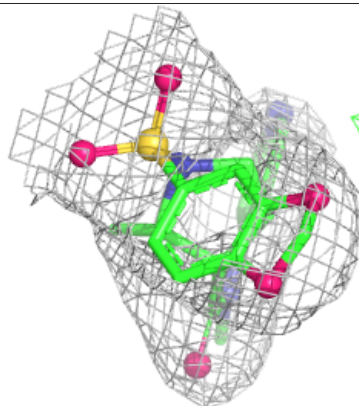
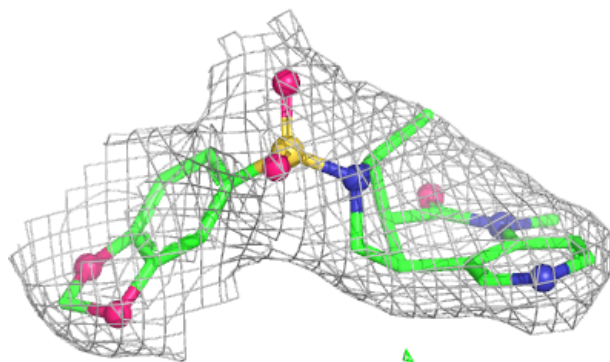
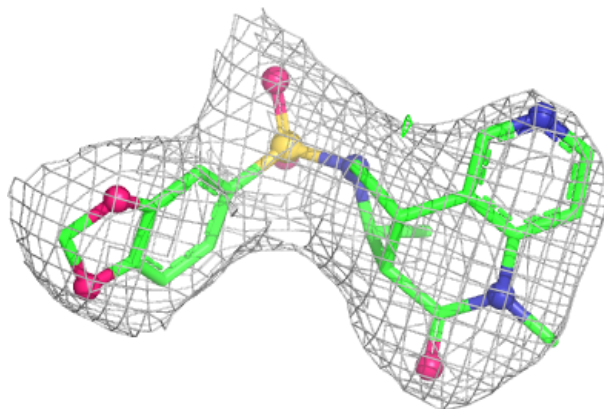
**Electron density around 7C6 B 401:**

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



Electron density around 7C6 D 401:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.