



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 02:05 AM EDT

PDB ID : 8QV7 / pdb_00008qv7
Title : Crystal structure of human TDO with alpha-methyl-L-tryptophan
Authors : Wicki, M.; Mac Sweeney, A.
Deposited on : 2023-10-17
Resolution : 2.93 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

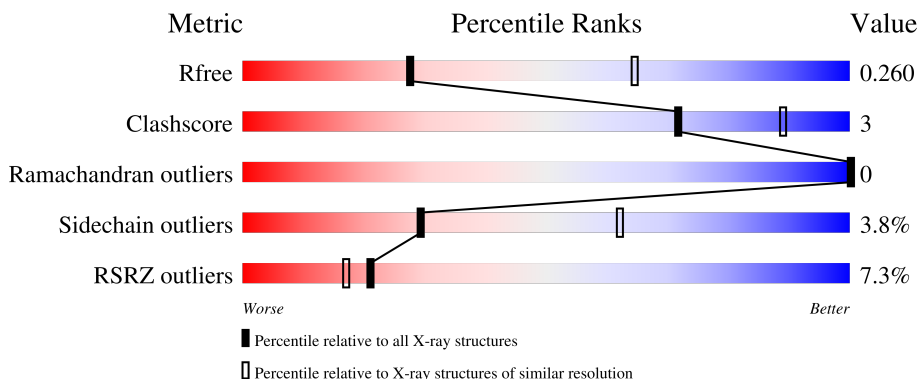
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

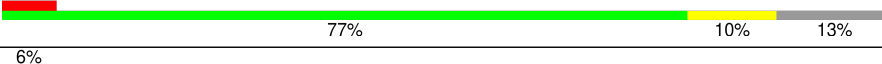
The reported resolution of this entry is 2.93 Å.

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	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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	355	
1	B	355	
1	C	355	
1	D	355	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10018 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.

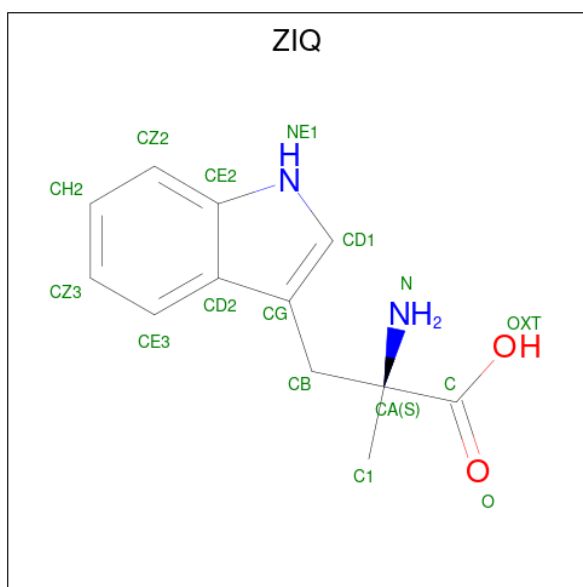
- Molecule 1 is a protein called Tryptophan 2,3-dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2526	1639	430	447	10			
1	B	310	Total	C	N	O	S	0	1	0
			2472	1607	426	429	10			
1	C	305	Total	C	N	O	S	0	0	0
			2420	1576	409	426	9			
1	D	313	Total	C	N	O	S	0	0	0
			2512	1632	427	443	10			

There are 16 discrepancies between the modelled and reference sequences:

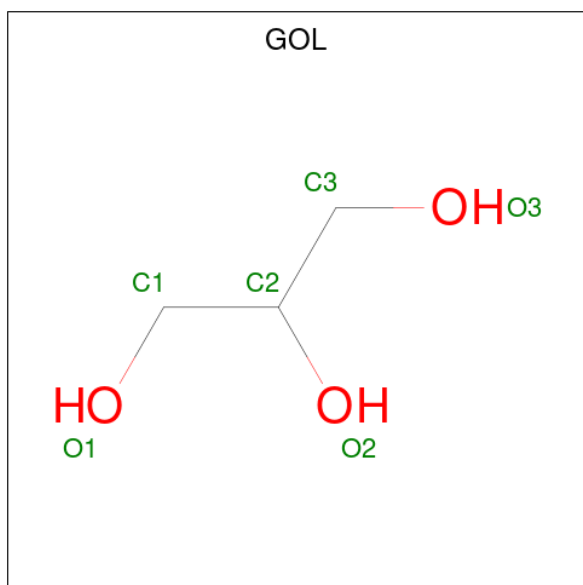
Chain	Residue	Modelled	Actual	Comment	Reference
A	390	GLU	-	expression tag	UNP P48775
A	391	HIS	-	expression tag	UNP P48775
A	392	HIS	-	expression tag	UNP P48775
A	393	HIS	-	expression tag	UNP P48775
B	390	GLU	-	expression tag	UNP P48775
B	391	HIS	-	expression tag	UNP P48775
B	392	HIS	-	expression tag	UNP P48775
B	393	HIS	-	expression tag	UNP P48775
C	390	GLU	-	expression tag	UNP P48775
C	391	HIS	-	expression tag	UNP P48775
C	392	HIS	-	expression tag	UNP P48775
C	393	HIS	-	expression tag	UNP P48775
D	390	GLU	-	expression tag	UNP P48775
D	391	HIS	-	expression tag	UNP P48775
D	392	HIS	-	expression tag	UNP P48775
D	393	HIS	-	expression tag	UNP P48775

- Molecule 2 is alpha-methyl-L-tryptophan (CCD ID: ZIQ) (formula: C₁₂H₁₄N₂O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			16	12	2	2		
2	B	1	Total	C	N	O	0	0
			16	12	2	2		
2	C	1	Total	C	N	O	0	0
			16	12	2	2		
2	D	1	Total	C	N	O	0	0
			16	12	2	2		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

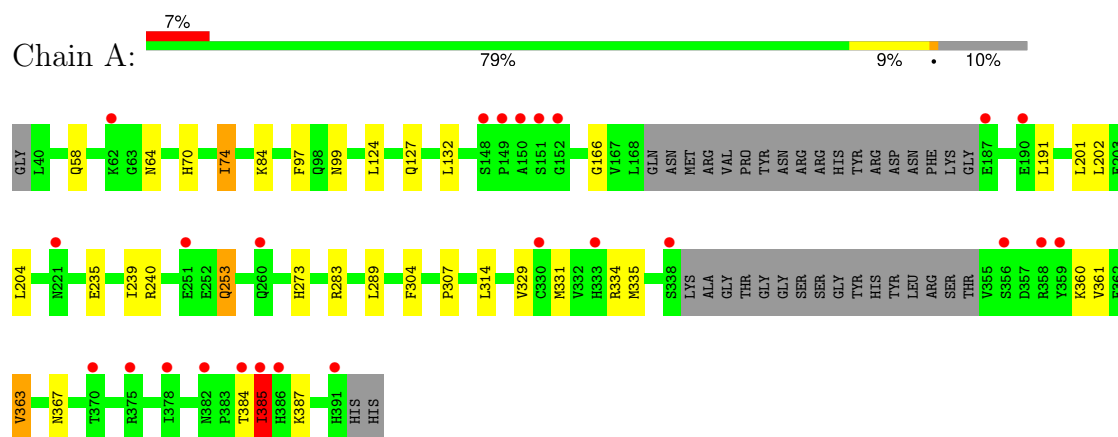
- Molecule 4 is water.

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

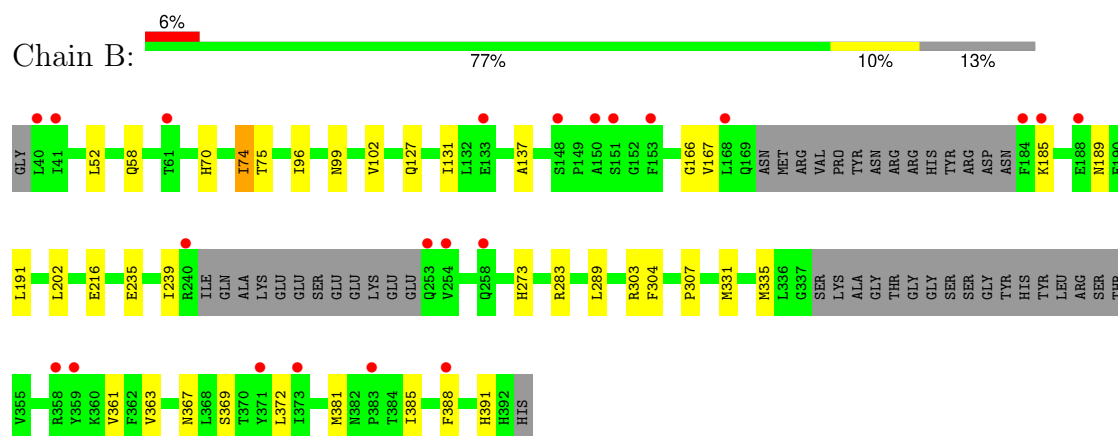
3 Residue-property plots [i](#)

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.

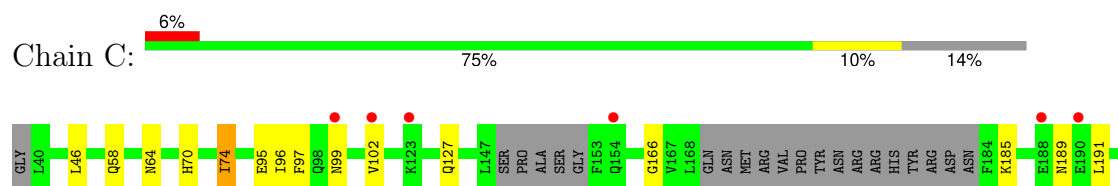
- Molecule 1: Tryptophan 2,3-dioxygenase

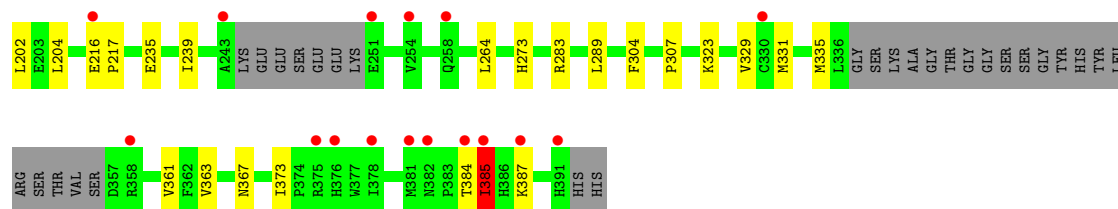


- Molecule 1: Tryptophan 2,3-dioxygenase

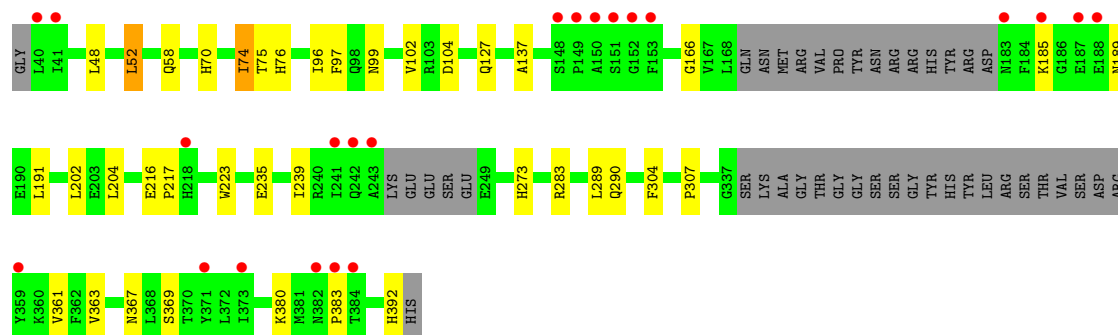
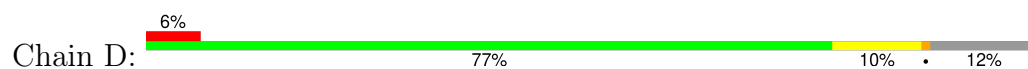


- Molecule 1: Tryptophan 2,3-dioxygenase





- Molecule 1: Tryptophan 2,3-dioxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	181.28Å 90.76Å 132.77Å 90.00° 120.75° 90.00°	Depositor
Resolution (Å)	41.35 – 2.93 41.35 – 2.93	Depositor EDS
% Data completeness (in resolution range)	94.1 (41.35-2.93) 77.3 (41.35-2.93)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.65Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.246 , 0.273 0.231 , 0.260	Depositor DCC
R_{free} test set	1590 reflections (2.98%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	10018	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZIQ, GOL

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	0.67	1/2584 (0.0%)	1.13	6/3500 (0.2%)
1	B	0.66	0/2533	1.12	5/3428 (0.1%)
1	C	0.68	1/2473 (0.0%)	1.12	4/3347 (0.1%)
1	D	0.66	0/2570	1.11	3/3477 (0.1%)
All	All	0.67	2/10160 (0.0%)	1.12	18/13752 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	385	ILE	CA-C	8.31	1.61	1.52
1	A	385	ILE	CA-C	7.38	1.60	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	385	ILE	CA-C-N	8.02	133.43	120.60
1	A	385	ILE	C-N-CA	8.02	133.43	120.60
1	C	385	ILE	CA-C-N	7.68	132.89	120.60
1	C	385	ILE	C-N-CA	7.68	132.89	120.60
1	B	381	MET	CA-C-N	6.78	132.55	121.57
1	B	381	MET	C-N-CA	6.78	132.55	121.57
1	D	99	ASN	CA-CB-CG	5.80	118.40	112.60
1	D	383	PRO	CA-C-N	5.68	131.71	123.13
1	D	383	PRO	C-N-CA	5.68	131.71	123.13
1	B	99	ASN	CA-CB-CG	5.57	118.17	112.60
1	A	99	ASN	CA-CB-CG	5.48	118.08	112.60
1	C	384	THR	N-CA-C	-5.45	102.07	109.54
1	A	384	THR	N-CA-C	-5.35	102.22	109.54
1	A	64	ASN	CA-CB-CG	5.28	117.88	112.60
1	B	167	VAL	CA-C-N	5.23	128.27	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	167	VAL	C-N-CA	5.23	128.27	120.90
1	C	64	ASN	CA-CB-CG	5.14	117.74	112.60
1	A	385	ILE	N-CA-CB	-5.01	104.04	112.06

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	2526	0	2372	19	0
1	B	2472	0	2346	15	0
1	C	2420	0	2279	18	0
1	D	2512	0	2375	16	0
2	A	16	0	0	0	0
2	B	16	0	0	0	0
2	C	16	0	0	1	0
2	D	16	0	0	0	0
3	A	6	0	8	1	0
3	B	6	0	8	0	0
4	A	3	0	0	0	0
4	B	5	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
All	All	10018	0	9388	64	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 3.

All (64) 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:334:ARG:HE	1:A:335:MET:HE2	1.44	0.80
1:A:334:ARG:HE	1:A:335:MET:CE	1.97	0.76
3:A:402:GOL:H12	1:C:323:LYS:HD3	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:273:HIS:CE1	1:B:289:LEU:HD13	2.38	0.59
1:A:273:HIS:CE1	1:A:289:LEU:HD13	2.39	0.57
1:C:273:HIS:CE1	1:C:289:LEU:HD13	2.39	0.57
1:D:273:HIS:CE1	1:D:289:LEU:HD13	2.40	0.57
1:A:70:HIS:CE1	1:A:74:ILE:HD13	2.40	0.56
1:D:48:LEU:HB3	1:D:52:LEU:HD22	1.88	0.56
1:A:240:ARG:HH22	1:A:253:GLN:NE2	2.04	0.56
1:B:70:HIS:CE1	1:B:74:ILE:HD13	2.41	0.55
1:C:70:HIS:CE1	1:C:74:ILE:HD13	2.40	0.55
1:B:303:ARG:NH2	1:B:391:HIS:CD2	2.75	0.55
1:D:166:GLY:O	1:D:283:ARG:NH1	2.40	0.55
1:A:360:LYS:HB2	1:A:363:VAL:HG13	1.87	0.54
1:B:137:ALA:HB3	1:D:369:SER:HB3	1.89	0.54
1:C:331:MET:HE1	1:C:335:MET:HE2	1.90	0.54
1:C:46:LEU:HD21	1:D:76:HIS:HB3	1.89	0.54
1:A:166:GLY:O	1:A:283:ARG:NH1	2.42	0.53
1:C:166:GLY:O	1:C:283:ARG:NH1	2.42	0.52
1:A:334:ARG:NE	1:A:335:MET:HE2	2.19	0.52
1:C:96:ILE:HG22	1:C:102:VAL:HG13	1.92	0.52
1:D:70:HIS:CE1	1:D:74:ILE:HD13	2.46	0.51
1:B:166:GLY:O	1:B:283:ARG:NH1	2.43	0.51
1:D:96:ILE:HG22	1:D:102:VAL:HG13	1.93	0.51
1:C:185:LYS:HA	1:C:189:ASN:HB2	1.94	0.50
1:C:202:LEU:HD13	1:C:361:VAL:HG12	1.95	0.49
1:B:96:ILE:HG22	1:B:102:VAL:HG13	1.95	0.49
1:B:331:MET:HE1	1:B:335:MET:HE2	1.96	0.48
1:A:235:GLU:O	1:A:239:ILE:HG12	2.13	0.48
1:D:104:ASP:HA	1:D:392:HIS:HA	1.96	0.47
1:D:185:LYS:HA	1:D:189:ASN:HB2	1.97	0.47
1:B:385:ILE:HA	1:B:388[B]:PHE:CE1	2.50	0.47
1:C:235:GLU:O	1:C:239:ILE:HG12	2.16	0.46
1:D:202:LEU:HD13	1:D:361:VAL:HG12	1.97	0.46
1:C:95:GLU:O	1:C:99:ASN:HB2	2.16	0.45
1:A:331:MET:HE1	1:A:335:MET:HE3	1.99	0.45
1:B:185:LYS:HA	1:B:189:ASN:HB2	1.98	0.45
1:B:202:LEU:HD13	1:B:361:VAL:HG12	1.98	0.45
1:A:202:LEU:HD13	1:A:361:VAL:HG12	1.98	0.44
1:A:385:ILE:HG22	1:A:387:LYS:CG	2.48	0.44
1:D:216:GLU:HA	1:D:217:PRO:HD3	1.92	0.44
1:C:385:ILE:HG22	1:C:387:LYS:HG3	1.98	0.44
1:C:385:ILE:HG22	1:C:387:LYS:CG	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:HIS:CE1	1:A:74:ILE:CD1	3.02	0.43
1:A:84:LYS:HD2	1:B:52:LEU:HD22	1.99	0.43
1:D:97:PHE:HB3	1:D:204:LEU:HB3	2.01	0.43
1:B:304:PHE:C	1:B:307:PRO:HD2	2.44	0.43
1:B:369:SER:HB3	1:D:137:ALA:HB3	2.00	0.43
1:C:216:GLU:HA	1:C:217:PRO:HD3	1.91	0.43
1:B:235:GLU:O	1:B:239:ILE:HG12	2.19	0.43
1:C:304:PHE:C	1:C:307:PRO:HD2	2.44	0.42
1:C:70:HIS:CE1	1:C:74:ILE:CD1	3.03	0.42
1:C:264:LEU:HD22	1:C:373:ILE:HD11	2.02	0.41
1:D:223:TRP:CD1	1:D:290:GLN:HE21	2.38	0.41
1:D:304:PHE:C	1:D:307:PRO:HD2	2.45	0.41
1:A:132:LEU:HD13	1:A:331:MET:HE2	2.03	0.41
1:A:240:ARG:HH22	1:A:253:GLN:HE21	1.67	0.41
2:C:401:ZIQ:CD1	2:C:401:ZIQ:C	2.98	0.41
1:D:235:GLU:O	1:D:239:ILE:HG13	2.21	0.41
1:C:97:PHE:HB3	1:C:204:LEU:HB3	2.02	0.40
1:A:97:PHE:HB3	1:A:204:LEU:HB3	2.02	0.40
1:A:124:LEU:HD22	1:B:131:ILE:CD1	2.51	0.40
1:A:304:PHE:C	1:A:307:PRO:HD2	2.47	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	312/355 (88%)	303 (97%)	9 (3%)	0	100	100
1	B	303/355 (85%)	297 (98%)	6 (2%)	0	100	100
1	C	295/355 (83%)	287 (97%)	8 (3%)	0	100	100
1	D	305/355 (86%)	298 (98%)	7 (2%)	0	100	100
All	All	1215/1420 (86%)	1185 (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	249/327 (76%)	238 (96%)	11 (4%)	25	57
1	B	247/327 (76%)	238 (96%)	9 (4%)	31	63
1	C	238/327 (73%)	230 (97%)	8 (3%)	32	65
1	D	251/327 (77%)	242 (96%)	9 (4%)	31	63
All	All	985/1308 (75%)	948 (96%)	37 (4%)	29	62

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	74	ILE
1	A	127	GLN
1	A	191	LEU
1	A	201	LEU
1	A	253	GLN
1	A	314	LEU
1	A	329	VAL
1	A	363	VAL
1	A	367	ASN
1	A	385	ILE
1	B	58	GLN
1	B	74	ILE
1	B	75	THR
1	B	127	GLN
1	B	191	LEU
1	B	216	GLU
1	B	363	VAL
1	B	367	ASN
1	B	372	LEU
1	C	58	GLN
1	C	74	ILE

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Mol	Chain	Res	Type
1	C	127	GLN
1	C	191	LEU
1	C	329	VAL
1	C	363	VAL
1	C	367	ASN
1	C	385	ILE
1	D	52	LEU
1	D	58	GLN
1	D	74	ILE
1	D	75	THR
1	D	127	GLN
1	D	191	LEU
1	D	363	VAL
1	D	367	ASN
1	D	380	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	77	GLN
1	A	127	GLN
1	A	253	GLN
1	A	309	GLN
1	A	327	ASN
1	B	64	ASN
1	B	141	ASN
1	B	309	GLN
1	B	386	HIS
1	B	391	HIS
1	C	55	GLN
1	C	77	GLN
1	C	309	GLN
1	C	327	ASN
1	D	141	ASN
1	D	258	GLN
1	D	309	GLN
1	D	327	ASN
1	D	386	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	ZIQ	A	401	-	14,17,17	1.36	3 (21%)	20,25,25	1.26	3 (15%)
2	ZIQ	B	401	-	14,17,17	1.41	1 (7%)	20,25,25	1.46	4 (20%)
3	GOL	A	402	-	5,5,5	0.25	0	5,5,5	0.06	0
3	GOL	B	402	-	5,5,5	0.33	0	5,5,5	0.22	0
2	ZIQ	D	401	-	14,17,17	1.29	2 (14%)	20,25,25	1.35	3 (15%)
2	ZIQ	C	401	-	14,17,17	1.42	3 (21%)	20,25,25	1.28	4 (20%)

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	ZIQ	A	401	-	-	2/11/11/11	0/2/2/2
2	ZIQ	B	401	-	-	3/11/11/11	0/2/2/2
3	GOL	A	402	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	402	-	-	0/4/4/4	-
2	ZIQ	D	401	-	-	0/11/11/11	0/2/2/2
2	ZIQ	C	401	-	-	6/11/11/11	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	ZIQ	CD2-CG	-3.10	1.38	1.44
2	C	401	ZIQ	CD2-CG	-2.98	1.39	1.44
2	A	401	ZIQ	CD2-CG	-2.83	1.39	1.44
2	D	401	ZIQ	CD2-CG	-2.71	1.39	1.44
2	D	401	ZIQ	CD1-CG	2.32	1.40	1.36
2	C	401	ZIQ	CD2-CE2	-2.27	1.38	1.41
2	A	401	ZIQ	CE2-NE1	-2.22	1.34	1.37
2	A	401	ZIQ	CD2-CE2	-2.06	1.38	1.41
2	C	401	ZIQ	CE2-NE1	-2.06	1.34	1.37

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	ZIQ	CZ2-CE2-CD2	-3.51	118.79	122.19
2	D	401	ZIQ	CZ2-CE2-CD2	-3.29	119.01	122.19
2	A	401	ZIQ	CE3-CD2-CG	-2.75	129.76	133.85
2	C	401	ZIQ	CZ2-CE2-CD2	-2.67	119.61	122.19
2	B	401	ZIQ	CE3-CD2-CE2	2.65	121.59	118.84
2	B	401	ZIQ	CE3-CD2-CG	-2.65	129.89	133.85
2	A	401	ZIQ	CZ2-CE2-CD2	-2.63	119.64	122.19
2	C	401	ZIQ	CE3-CD2-CG	-2.62	129.95	133.85
2	C	401	ZIQ	CE3-CD2-CE2	2.56	121.49	118.84
2	D	401	ZIQ	CE3-CD2-CE2	2.54	121.47	118.84
2	D	401	ZIQ	CE3-CD2-CG	-2.53	130.08	133.85
2	A	401	ZIQ	CE3-CD2-CE2	2.37	121.29	118.84
2	B	401	ZIQ	O-C-CA	-2.19	118.84	122.78
2	C	401	ZIQ	O-C-CA	-2.07	119.07	122.78

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	401	ZIQ	O-C-CA-C1
2	C	401	ZIQ	OXT-C-CA-C1

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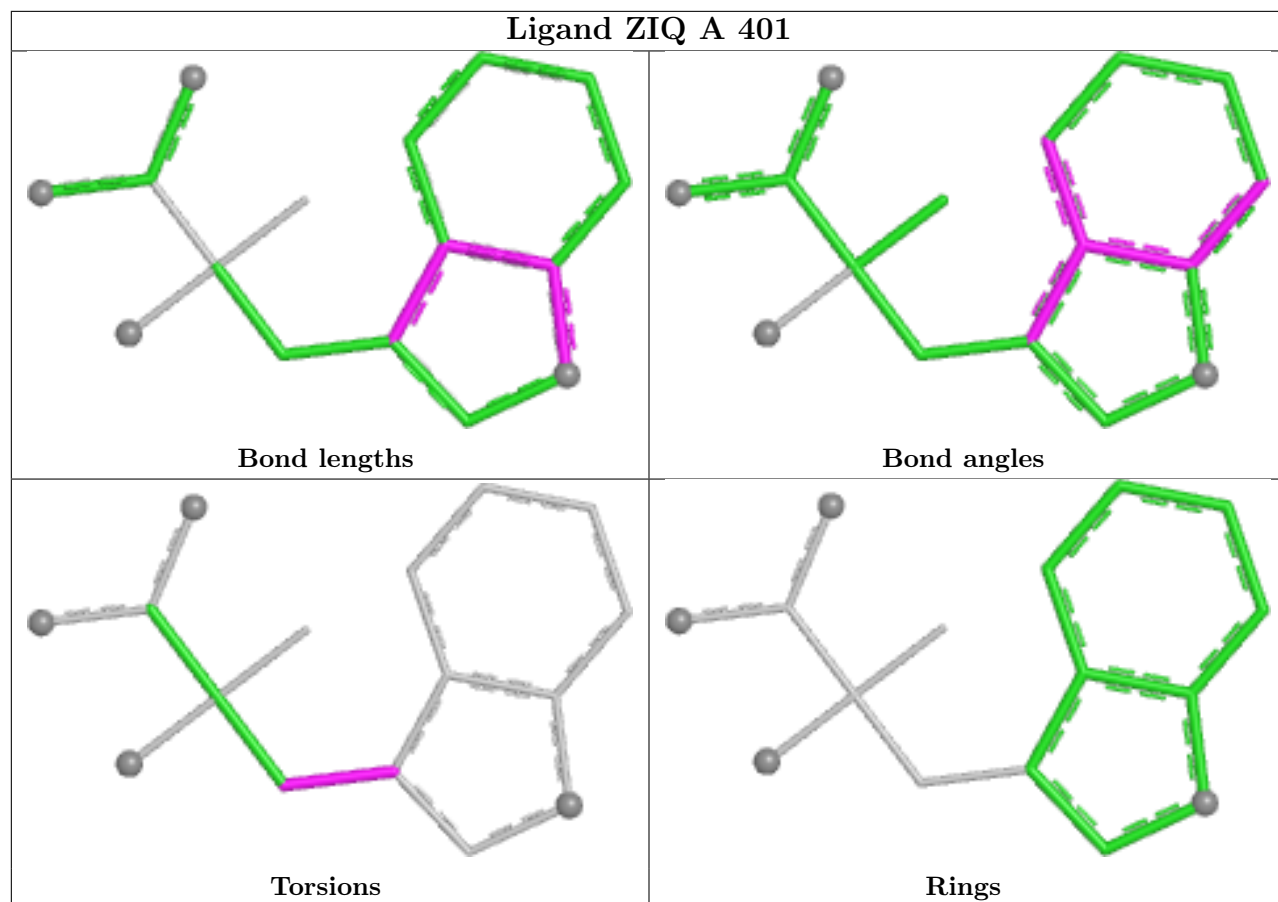
Mol	Chain	Res	Type	Atoms
3	A	402	GOL	C1-C2-C3-O3
3	A	402	GOL	O2-C2-C3-O3
2	C	401	ZIQ	O-C-CA-CB
2	C	401	ZIQ	OXT-C-CA-CB
2	A	401	ZIQ	CA-CB-CG-CD2
2	C	401	ZIQ	CA-CB-CG-CD2
2	A	401	ZIQ	CA-CB-CG-CD1
2	C	401	ZIQ	CA-CB-CG-CD1
2	B	401	ZIQ	O-C-CA-CB
2	B	401	ZIQ	OXT-C-CA-CB
2	B	401	ZIQ	O-C-CA-N

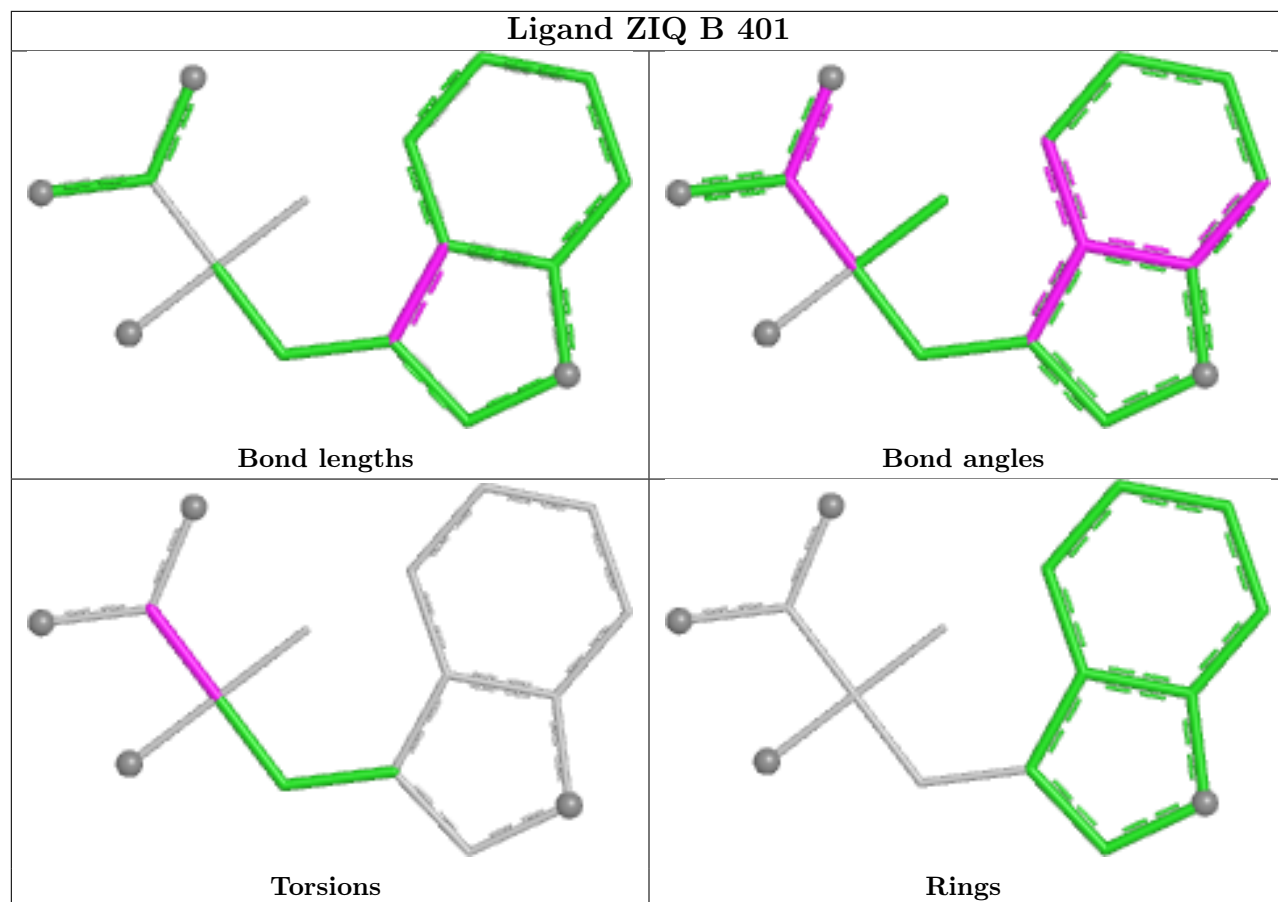
There are no ring outliers.

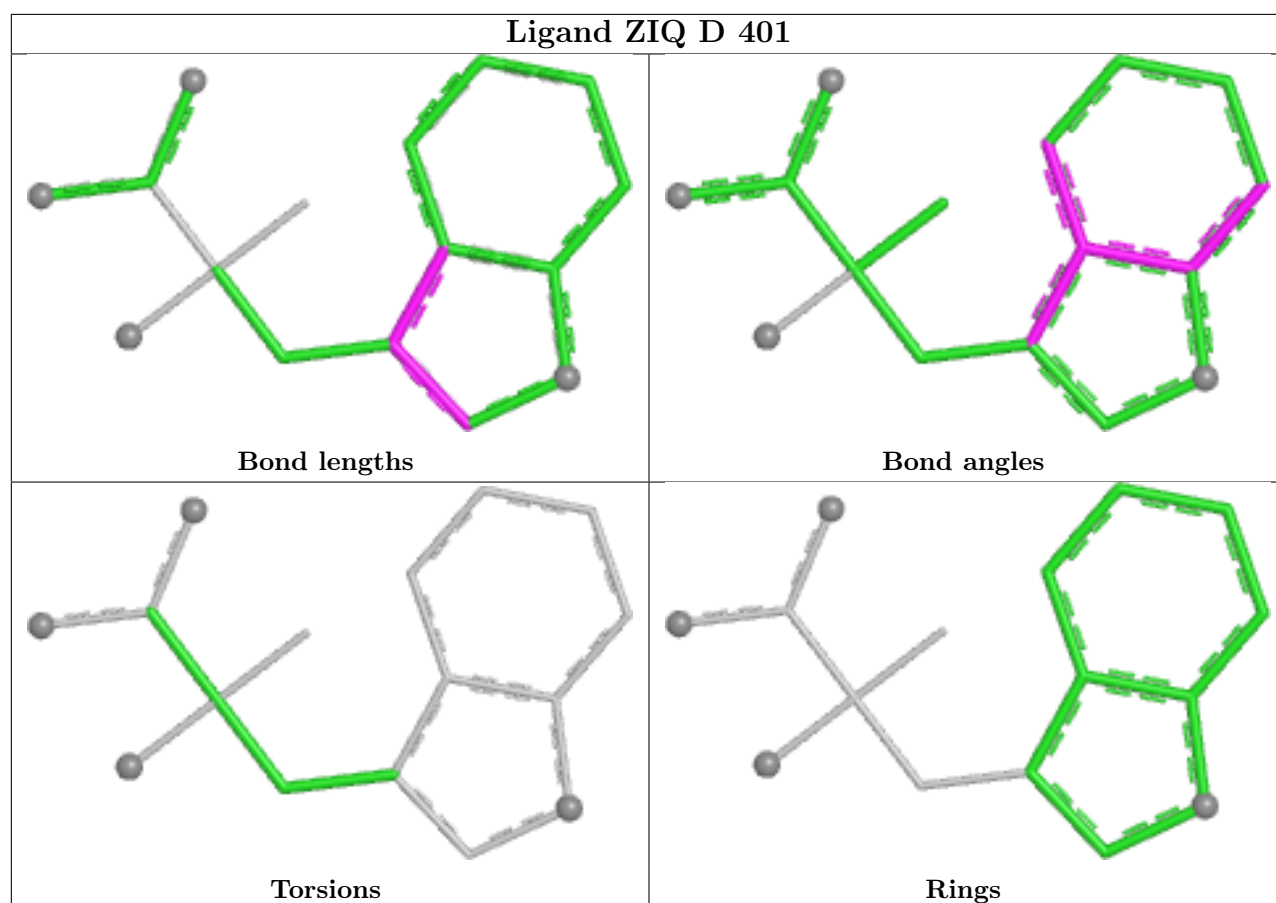
2 monomers are involved in 2 short contacts:

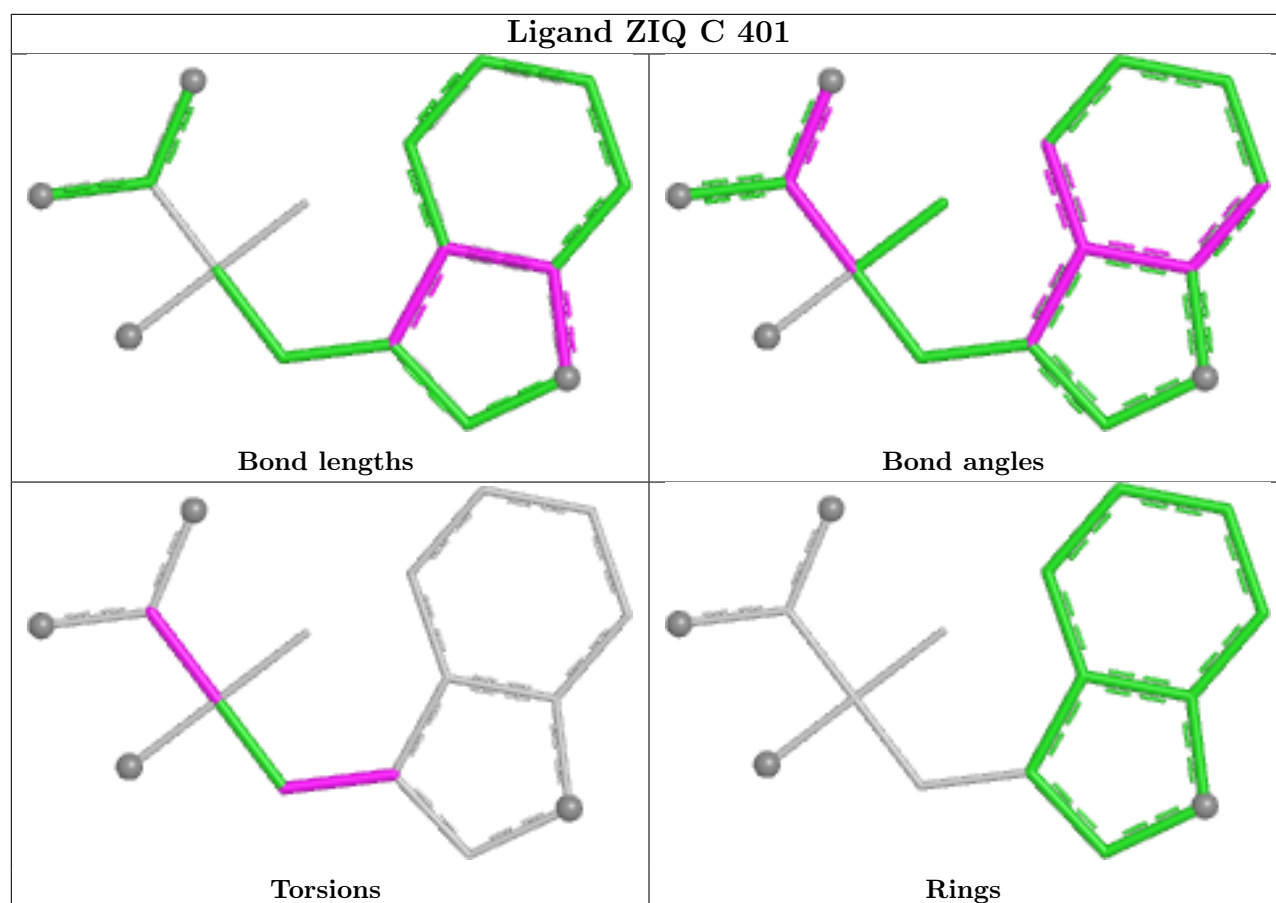
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	GOL	1	0
2	C	401	ZIQ	1	0

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









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	318/355 (89%)	0.70	25 (7%) 18 15	34, 57, 77, 91	0
1	B	310/355 (87%)	0.57	22 (7%) 22 18	31, 50, 79, 96	1 (0%)
1	C	305/355 (85%)	0.71	22 (7%) 21 17	32, 56, 73, 86	0
1	D	313/355 (88%)	0.48	22 (7%) 22 18	33, 50, 75, 83	0
All	All	1246/1420 (87%)	0.61	91 (7%) 21 17	31, 53, 76, 96	1 (0%)

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	359	TYR	5.4
1	B	148	SER	4.9
1	A	385	ILE	4.7
1	D	148	SER	4.5
1	D	151	SER	4.2
1	A	384	THR	4.2
1	A	382	ASN	4.1
1	D	183	ASN	3.9
1	A	358	ARG	3.8
1	A	356	SER	3.7
1	D	188	GLU	3.7
1	A	152	GLY	3.6
1	B	151	SER	3.5
1	B	40	LEU	3.5
1	B	388[A]	PHE	3.5
1	C	375	ARG	3.4
1	C	387	LYS	3.3
1	C	251	GLU	3.3
1	A	359	TYR	3.3
1	C	382	ASN	3.3
1	C	385	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	330	CYS	3.3
1	A	148	SER	3.3
1	C	384	THR	3.2
1	A	333	HIS	3.2
1	B	358	ARG	3.1
1	A	150	ALA	3.0
1	B	150	ALA	3.0
1	D	359	TYR	3.0
1	C	358	ARG	2.9
1	C	154	GLN	2.9
1	A	187	GLU	2.9
1	B	383	PRO	2.8
1	A	62	LYS	2.8
1	D	383	PRO	2.8
1	C	381	MET	2.8
1	A	151	SER	2.7
1	A	375	ARG	2.7
1	C	243	ALA	2.7
1	B	371	TYR	2.7
1	D	371	TYR	2.6
1	B	240	ARG	2.6
1	D	187	GLU	2.6
1	B	41	ILE	2.6
1	C	188	GLU	2.6
1	D	41	ILE	2.6
1	A	338	SER	2.6
1	A	149	PRO	2.6
1	D	153	PHE	2.5
1	B	188	GLU	2.4
1	B	258	GLN	2.4
1	D	243	ALA	2.4
1	D	382	ASN	2.4
1	B	184	PHE	2.4
1	B	253	GLN	2.4
1	D	149	PRO	2.4
1	A	378	ILE	2.4
1	A	330	CYS	2.3
1	B	153	PHE	2.3
1	B	168	LEU	2.3
1	C	102	VAL	2.3
1	C	378	ILE	2.3
1	C	376	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	152	GLY	2.3
1	C	391	HIS	2.3
1	D	384	THR	2.3
1	B	185	LYS	2.2
1	C	99	ASN	2.2
1	A	260	GLN	2.2
1	A	251	GLU	2.2
1	D	242	GLN	2.2
1	D	185	LYS	2.2
1	B	133	GLU	2.2
1	D	150	ALA	2.2
1	A	370	THR	2.2
1	A	190	GLU	2.2
1	B	373	ILE	2.1
1	A	221	ASN	2.1
1	D	218	HIS	2.1
1	D	373	ILE	2.1
1	C	258	GLN	2.1
1	A	391	HIS	2.1
1	C	123	LYS	2.1
1	B	61	THR	2.1
1	B	254	VAL	2.1
1	D	40	LEU	2.1
1	D	241	ILE	2.0
1	C	190	GLU	2.0
1	C	216	GLU	2.0
1	A	386	HIS	2.0
1	C	254	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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,

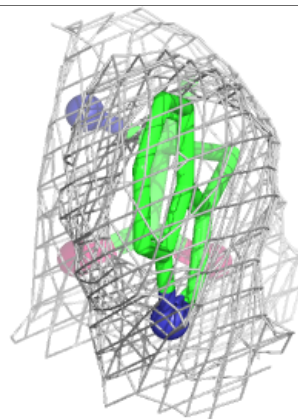
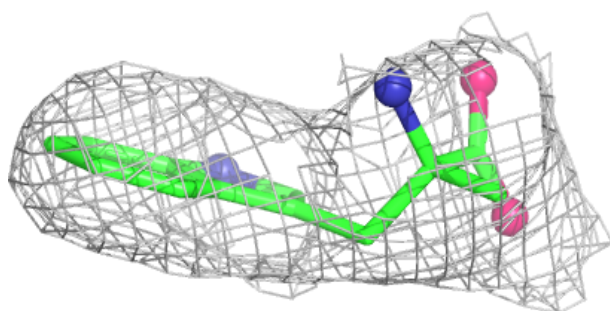
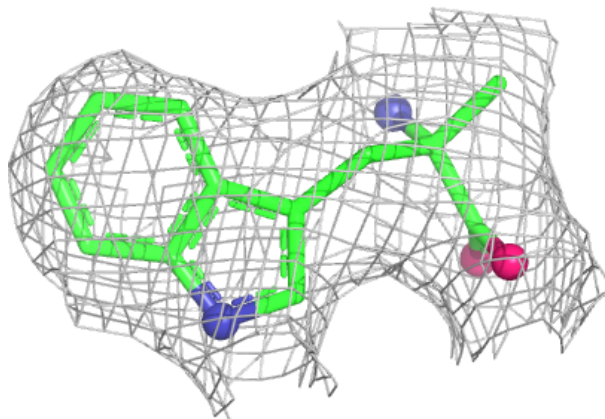
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	B	402	6/6	0.84	0.21	34,34,35,36	0
3	GOL	A	402	6/6	0.93	0.13	18,19,19,19	0
2	ZIQ	D	401	16/16	0.94	0.10	41,42,42,42	0
2	ZIQ	A	401	16/16	0.95	0.10	46,46,47,47	0
2	ZIQ	B	401	16/16	0.95	0.11	51,51,52,52	0
2	ZIQ	C	401	16/16	0.95	0.10	53,53,54,55	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.

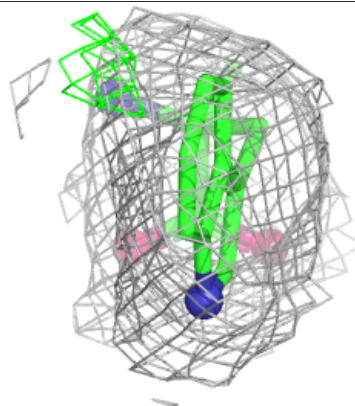
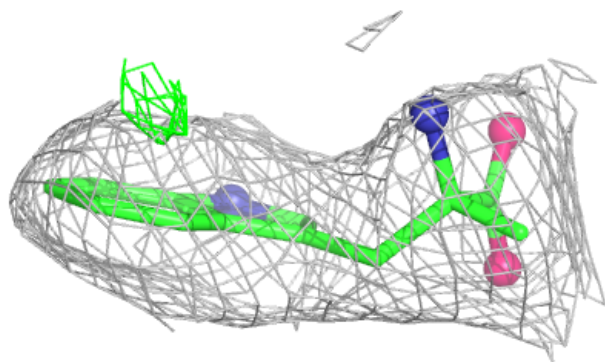
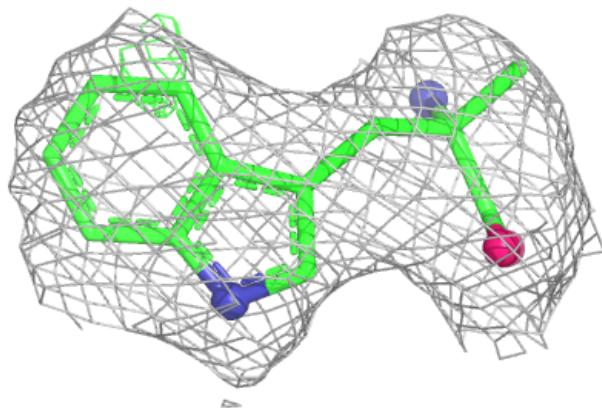
Electron density around ZIQ D 401:

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



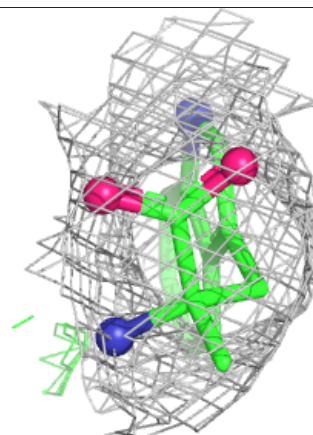
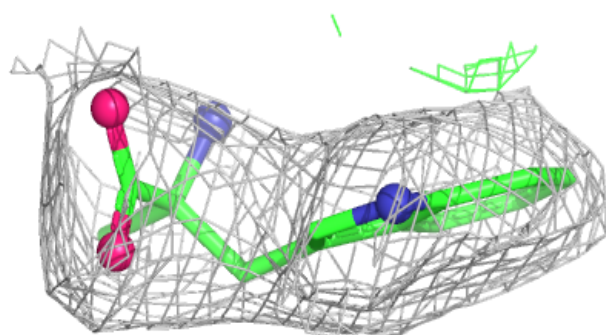
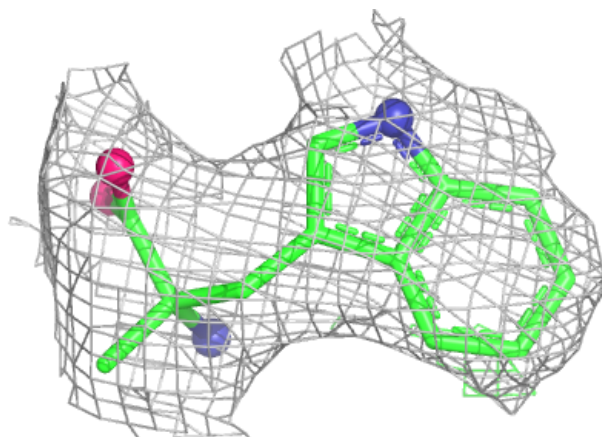
Electron density around ZIQ A 401:

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

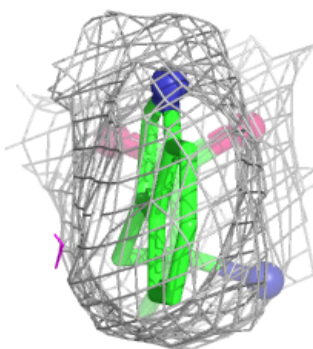
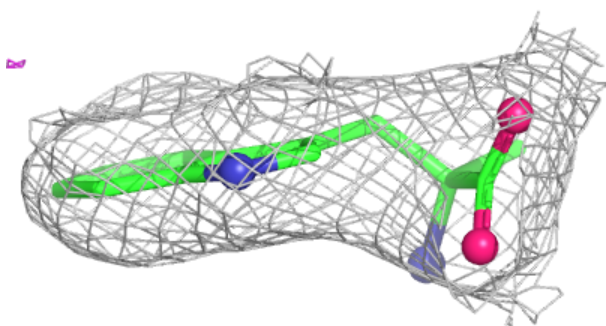
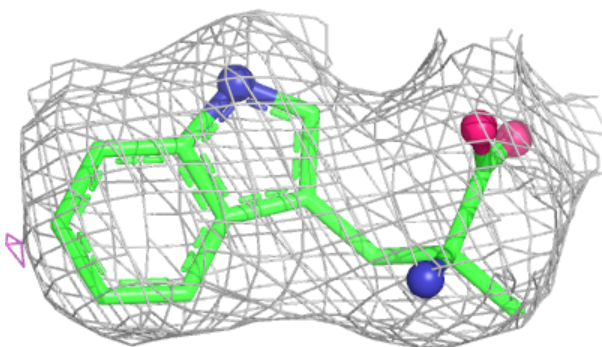


Electron density around ZIQ B 401:

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

**Electron density around ZIQ 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.