



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 30, 2026 – 11:21 AM UTC

PDB ID : 8R5Q / pdb_00008r5q
Title : Structure of apo TDO with a bound inhibitor
Authors : Wicki, M.; Mac Sweeney, A.
Deposited on : 2023-11-17
Resolution : 2.62 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

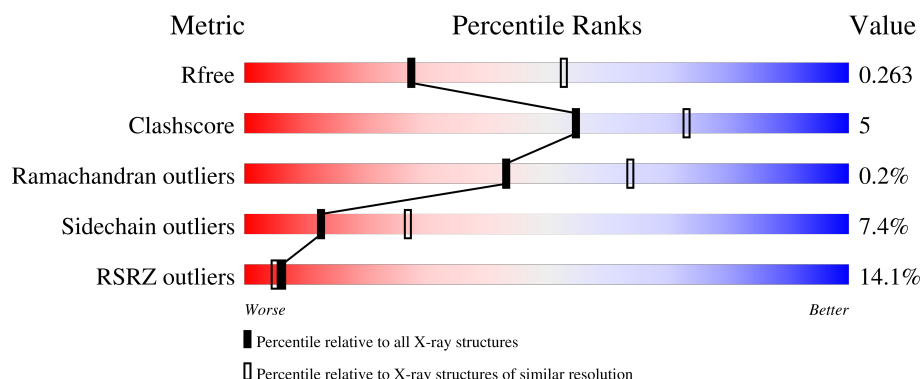
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	358	9% 72% 14% • 12%
1	B	358	12% 78% 10% • 11%
1	C	358	8% 74% 14% • 11%
1	D	358	21% 75% 11% • 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9960 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	314	Total	C	N	O	S	0	0	0
			2512	1628	428	446	10			
1	B	318	Total	C	N	O	S	0	0	0
			2513	1628	427	448	10			
1	C	317	Total	C	N	O	S	0	0	0
			2464	1591	424	439	10			
1	D	314	Total	C	N	O	S	0	0	0
			2310	1492	394	414	10			

There are 28 discrepancies between the modelled and reference sequences:

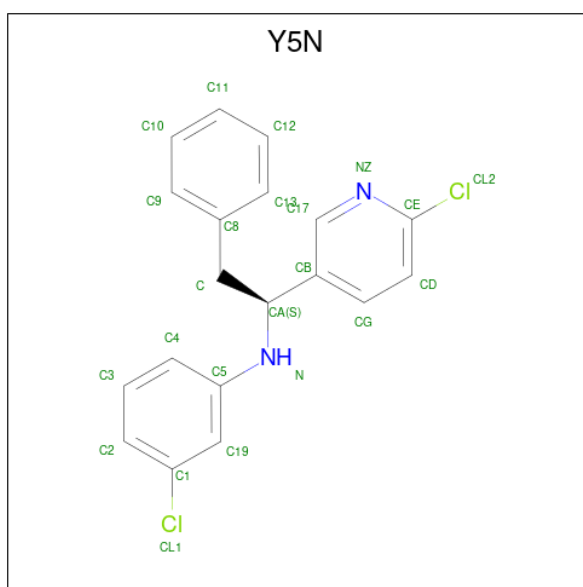
Chain	Residue	Modelled	Actual	Comment	Reference
A	390	GLU	-	expression tag	UNP P48775
A	391	HIS	-	expression tag	UNP P48775
A	392	HIS	-	expression tag	UNP P48775
A	393	HIS	-	expression tag	UNP P48775
A	394	HIS	-	expression tag	UNP P48775
A	395	HIS	-	expression tag	UNP P48775
A	396	HIS	-	expression tag	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
B	394	HIS	-	expression tag	UNP P48775
B	395	HIS	-	expression tag	UNP P48775
B	396	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
C	394	HIS	-	expression tag	UNP P48775
C	395	HIS	-	expression tag	UNP P48775
C	396	HIS	-	expression tag	UNP P48775

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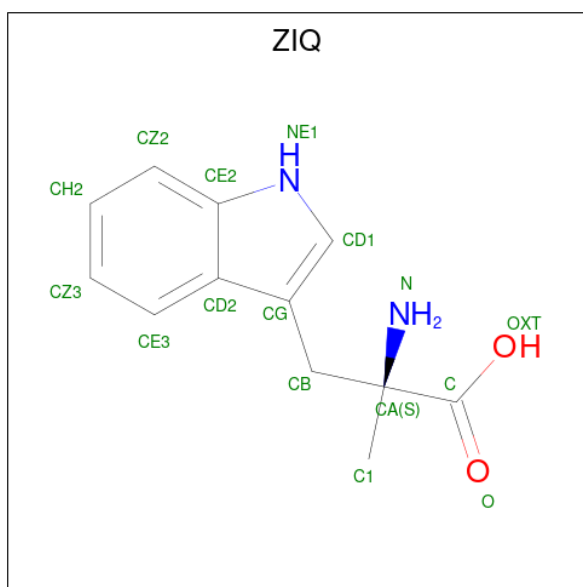
Chain	Residue	Modelled	Actual	Comment	Reference
D	390	GLU	-	expression tag	UNP P48775
D	391	HIS	-	expression tag	UNP P48775
D	392	HIS	-	expression tag	UNP P48775
D	393	HIS	-	expression tag	UNP P48775
D	394	HIS	-	expression tag	UNP P48775
D	395	HIS	-	expression tag	UNP P48775
D	396	HIS	-	expression tag	UNP P48775

- Molecule 2 is 3-chloranyl- {N}-[(1 {S})-1-(6-chloranypyridin-3-yl)-2-phenyl-ethyl]aniline (CCD ID: Y5N) (formula: C₁₉H₁₆Cl₂N₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	0	0
			23	19	2	2		
2	B	1	Total	C	Cl	N	0	0
			23	19	2	2		
2	C	1	Total	C	Cl	N	0	0
			23	19	2	2		
2	D	1	Total	C	Cl	N	0	0
			23	19	2	2		

- Molecule 3 is alpha-methyl-L-tryptophan (CCD ID: ZIQ) (formula: C₁₂H₁₄N₂O₂).



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

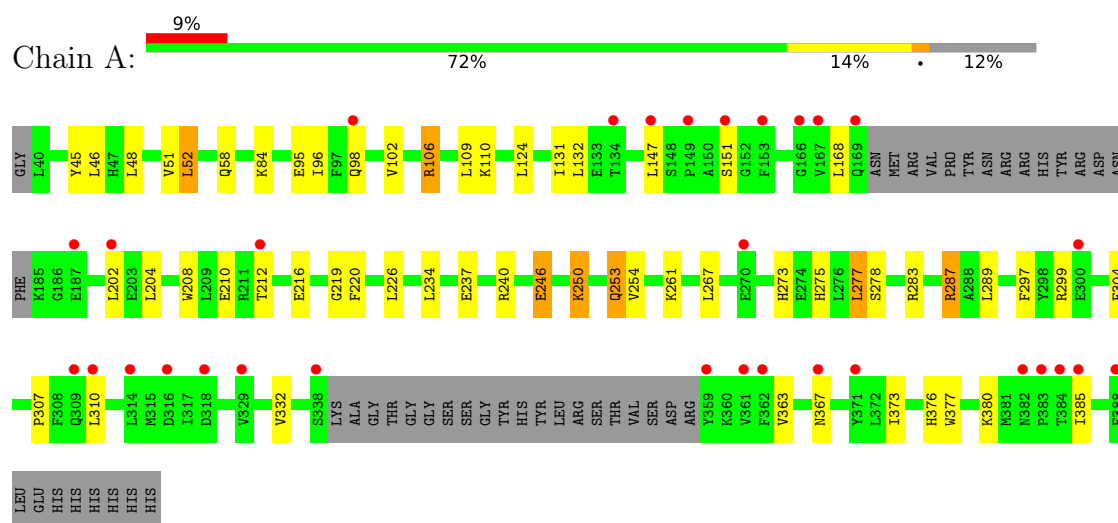
- Molecule 4 is water.

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

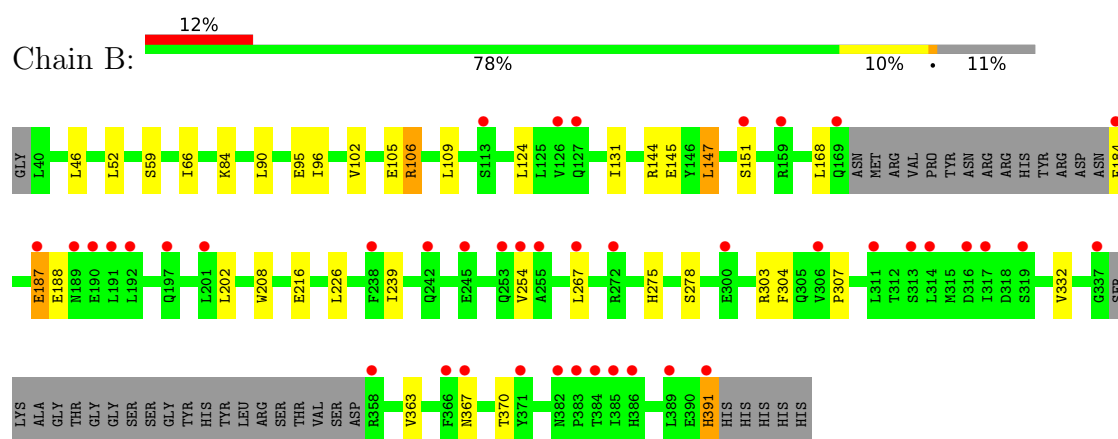
3 Residue-property plots [i](#)

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.

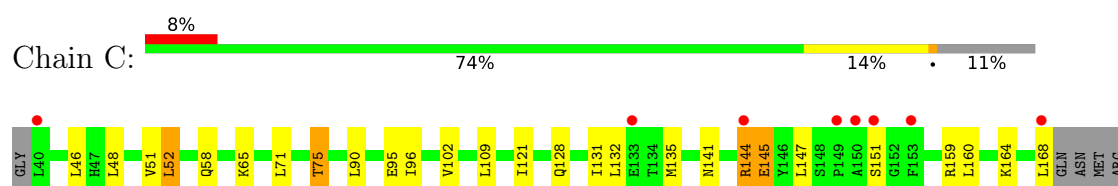
• Molecule 1: Tryptophan 2,3-dioxygenase

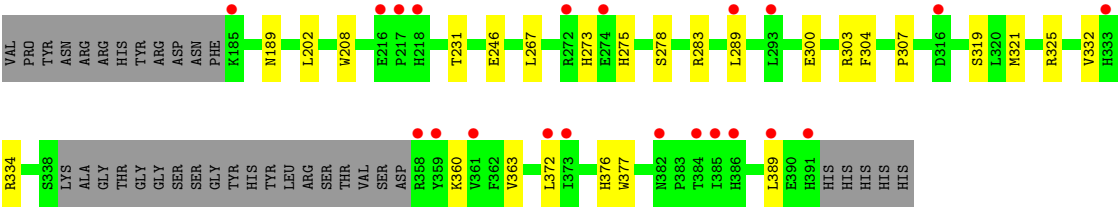


• Molecule 1: Tryptophan 2,3-dioxygenase

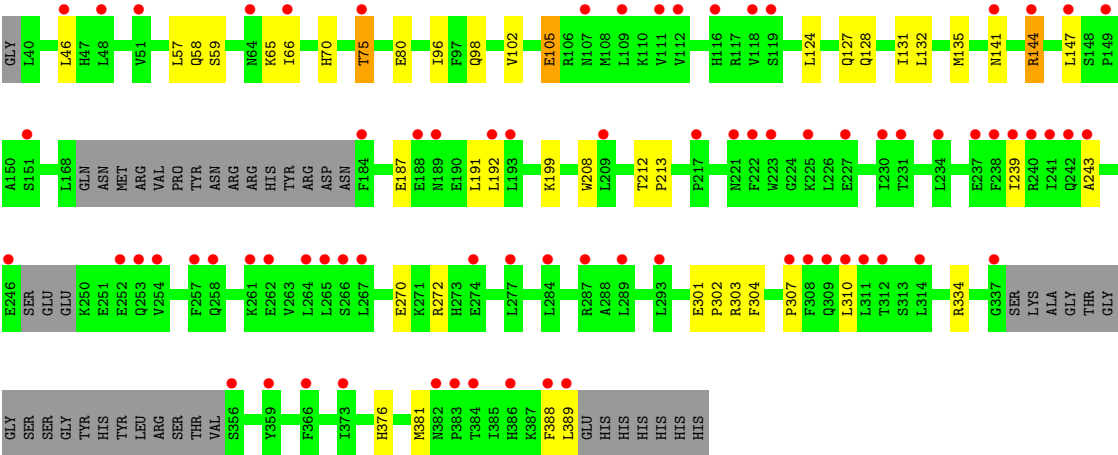
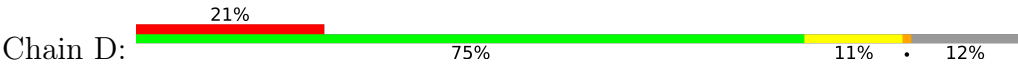


• Molecule 1: Tryptophan 2,3-dioxygenase





● Molecule 1: Tryptophan 2,3-dioxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.33Å 132.49Å 135.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	75.75 – 2.62 75.75 – 2.62	Depositor EDS
% Data completeness (in resolution range)	79.2 (75.75-2.62) 79.2 (75.75-2.62)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 2.62Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.254 , 0.267 0.248 , 0.263	Depositor DCC
R_{free} test set	1876 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	74.3	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 68.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.002 for -h,l,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9960	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% 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, Y5N

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	0.68	0/2568	1.06	1/3475 (0.0%)
1	B	0.71	0/2570	1.11	6/3479 (0.2%)
1	C	0.68	0/2521	1.07	1/3422 (0.0%)
1	D	0.71	1/2364 (0.0%)	1.09	2/3217 (0.1%)
All	All	0.69	1/10023 (0.0%)	1.08	10/13593 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	243	ALA	CA-C	5.39	1.59	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	367	ASN	CA-CB-CG	6.86	119.46	112.60
1	C	144	ARG	N-CA-C	-5.88	100.42	109.76
1	A	367	ASN	CA-CB-CG	5.80	118.40	112.60
1	D	388	PHE	CA-CB-CG	5.63	119.43	113.80
1	B	168	LEU	CA-C-N	5.32	131.27	121.70
1	B	168	LEU	C-N-CA	5.32	131.27	121.70
1	D	270	GLU	CB-CG-CD	5.17	121.39	112.60
1	B	187	GLU	CA-C-N	5.16	128.16	120.31
1	B	187	GLU	C-N-CA	5.16	128.16	120.31
1	B	184	PHE	CA-CB-CG	5.12	118.92	113.80

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	2512	0	2404	31	0
1	B	2513	0	2365	20	0
1	C	2464	0	2258	31	0
1	D	2310	0	1957	22	0
2	A	23	0	0	1	0
2	B	23	0	0	1	0
2	C	23	0	0	1	0
2	D	23	0	0	1	0
3	A	16	0	0	1	0
3	B	16	0	0	0	0
3	C	16	0	0	0	0
3	D	16	0	0	1	0
4	A	2	0	0	0	0
4	B	3	0	0	0	0
All	All	9960	0	8984	90	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 5.

All (90) 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:C:141:ASN:HA	1:C:144:ARG:HG2	1.49	0.94
1:A:273:HIS:CE1	1:A:289:LEU:HD11	2.04	0.93
1:C:273:HIS:CE1	1:C:289:LEU:HD11	2.07	0.88
1:D:141:ASN:HA	1:D:144:ARG:HG2	1.73	0.68
1:A:212:THR:HG22	3:A:502:ZIQ:CZ2	2.26	0.66
1:D:96:ILE:HG22	1:D:102:VAL:HG23	1.76	0.66
1:B:144:ARG:NH2	1:C:372:LEU:HD22	2.11	0.65
1:B:96:ILE:HG22	1:B:102:VAL:HG23	1.78	0.64
1:A:48:LEU:HB3	1:A:52:LEU:HD22	1.79	0.64
1:C:202:LEU:HD21	1:C:283:ARG:HB3	1.79	0.63
1:C:96:ILE:HG22	1:C:102:VAL:HG23	1.79	0.63
1:C:48:LEU:HB3	1:C:52:LEU:HD22	1.80	0.62
1:A:168:LEU:HD11	1:A:283:ARG:HD3	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ILE:HG22	1:A:102:VAL:HG23	1.81	0.62
1:B:106:ARG:HG2	1:D:302:PRO:HD3	1.81	0.61
1:D:212:THR:HG22	3:D:502:ZIQ:CZ2	2.30	0.61
1:A:210:GLU:HG2	1:A:287:ARG:HB3	1.82	0.60
1:C:376:HIS:CD2	1:C:377:TRP:HD1	2.21	0.59
1:C:46:LEU:HD21	2:D:501:Y5N:CL1	2.41	0.58
1:A:131:ILE:CD1	1:B:124:LEU:HD22	2.35	0.57
1:B:144:ARG:O	1:B:144:ARG:HG2	2.03	0.57
1:D:141:ASN:HA	1:D:144:ARG:CG	2.36	0.56
1:A:376:HIS:CD2	1:A:377:TRP:HD1	2.24	0.56
1:B:59:SER:HB3	1:B:66:ILE:HD12	1.88	0.55
1:A:240:ARG:HH22	1:A:253:GLN:HG2	1.71	0.55
1:C:376:HIS:CD2	1:C:377:TRP:CD1	2.95	0.54
1:A:151:SER:HB2	1:A:332:VAL:HG11	1.89	0.54
1:D:213:PRO:HB2	1:D:389:LEU:HD21	1.89	0.54
1:C:75:THR:HG22	1:C:128:GLN:HE21	1.72	0.53
1:C:151:SER:HB2	1:C:332:VAL:HG11	1.91	0.52
1:A:131:ILE:HD11	1:B:124:LEU:HD22	1.92	0.52
1:A:45:TYR:CE1	1:B:147:LEU:HD22	2.45	0.52
1:A:376:HIS:CD2	1:A:377:TRP:CD1	2.98	0.52
1:D:102:VAL:CG1	1:D:208:TRP:CD1	2.93	0.51
1:C:51:VAL:HG12	1:C:52:LEU:HD13	1.93	0.50
1:B:151:SER:HB2	1:B:332:VAL:HG11	1.93	0.50
1:B:144:ARG:NH2	1:C:372:LEU:HD13	2.27	0.50
1:A:51:VAL:HG12	1:A:52:LEU:HD13	1.93	0.50
1:A:102:VAL:CG1	1:A:208:TRP:CD1	2.94	0.49
1:B:144:ARG:HH21	1:C:372:LEU:HD22	1.76	0.49
1:C:121:ILE:HG12	1:D:131:ILE:HD13	1.93	0.49
1:D:135:MET:O	1:D:334:ARG:NH2	2.44	0.48
1:B:102:VAL:CG1	1:B:208:TRP:CD1	2.97	0.48
1:C:141:ASN:HA	1:C:144:ARG:CG	2.33	0.48
1:D:105:GLU:OE1	1:D:303:ARG:HD2	2.14	0.48
1:B:391:HIS:HD2	1:D:303:ARG:HG2	1.79	0.48
1:C:102:VAL:CG1	1:C:208:TRP:CD1	2.97	0.47
1:C:144:ARG:O	1:C:145:GLU:CB	2.62	0.47
1:D:144:ARG:HG2	1:D:144:ARG:HH21	1.79	0.47
1:A:273:HIS:NE2	1:A:277:LEU:CD1	2.78	0.47
2:A:501:Y5N:CL1	1:B:46:LEU:HD21	2.52	0.47
1:A:275:HIS:O	1:A:278:SER:OG	2.33	0.46
1:B:105:GLU:OE1	1:B:303:ARG:HD2	2.16	0.46
1:A:124:LEU:HD22	1:B:131:ILE:CD1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:HIS:CE1	1:A:277:LEU:CD1	2.99	0.46
1:A:273:HIS:NE2	1:A:277:LEU:HD13	2.31	0.46
1:A:250:LYS:O	1:A:254:VAL:HG23	2.16	0.46
1:C:304:PHE:C	1:C:307:PRO:HD2	2.41	0.45
1:D:57:LEU:HD21	1:D:70:HIS:HA	1.99	0.45
1:D:301:GLU:HG3	1:D:381:MET:HE2	1.99	0.45
1:C:275:HIS:O	1:C:278:SER:OG	2.30	0.44
1:C:319:SER:HB3	1:C:360:LYS:NZ	2.32	0.44
2:C:501:Y5N:CL1	1:D:46:LEU:HD21	2.54	0.44
1:A:84:LYS:HD2	1:B:52:LEU:HD22	1.98	0.44
1:C:303:ARG:HD3	1:C:389:LEU:HA	2.00	0.44
1:A:304:PHE:C	1:A:307:PRO:HD2	2.42	0.44
1:D:132:LEU:HD23	1:D:132:LEU:HA	1.89	0.44
1:B:144:ARG:HH22	1:C:372:LEU:HB3	1.82	0.44
1:B:304:PHE:C	1:B:307:PRO:HD2	2.44	0.43
1:D:75:THR:HG22	1:D:128:GLN:HE21	1.82	0.43
1:B:275:HIS:O	1:B:278:SER:OG	2.36	0.43
1:C:321:MET:HE3	1:C:325:ARG:HH21	1.84	0.43
1:D:59:SER:HB2	1:D:66:ILE:HD12	2.01	0.43
1:D:304:PHE:C	1:D:307:PRO:HD2	2.43	0.43
1:D:212:THR:HA	1:D:213:PRO:HD3	1.94	0.42
1:C:135:MET:O	1:C:334:ARG:NH2	2.46	0.42
1:A:46:LEU:HD21	2:B:501:Y5N:CL1	2.56	0.42
1:C:132:LEU:HD23	1:C:132:LEU:HA	1.92	0.42
1:A:297:PHE:HZ	1:A:373:ILE:HD12	1.84	0.41
1:C:376:HIS:NE2	1:C:377:TRP:CD1	2.88	0.41
1:C:168:LEU:HD21	1:C:283:ARG:HD3	2.02	0.41
1:A:376:HIS:NE2	1:A:377:TRP:CD1	2.87	0.41
1:A:106:ARG:NH1	1:C:300:GLU:OE1	2.54	0.41
1:D:98:GLN:HE21	1:D:199:LYS:HB2	1.86	0.41
1:A:98:GLN:HG3	1:A:204:LEU:HD21	2.03	0.41
1:A:234:LEU:HD13	1:A:261:LYS:HG3	2.02	0.41
1:C:131:ILE:CD1	1:D:124:LEU:HD22	2.51	0.41
1:C:160:LEU:O	1:C:164:LYS:HG3	2.21	0.41
1:A:132:LEU:HD23	1:A:132:LEU:HA	1.94	0.40
1:A:220:PHE:HB2	1:A:385:ILE:HG13	2.02	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	308/358 (86%)	298 (97%)	8 (3%)	2 (1%)	21	39
1	B	312/358 (87%)	297 (95%)	15 (5%)	0	100	100
1	C	311/358 (87%)	301 (97%)	9 (3%)	1 (0%)	36	56
1	D	306/358 (86%)	291 (95%)	15 (5%)	0	100	100
All	All	1237/1432 (86%)	1187 (96%)	47 (4%)	3 (0%)	43	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	145	GLU
1	A	246	GLU
1	A	219	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	255/330 (77%)	234 (92%)	21 (8%)	10	22
1	B	250/330 (76%)	232 (93%)	18 (7%)	13	28
1	C	236/330 (72%)	221 (94%)	15 (6%)	16	33
1	D	191/330 (58%)	176 (92%)	15 (8%)	11	24
All	All	932/1320 (71%)	863 (93%)	69 (7%)	13	27

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LEU
1	A	58	GLN
1	A	95	GLU
1	A	106	ARG
1	A	109	LEU
1	A	110	LYS
1	A	147	LEU
1	A	202	LEU
1	A	216	GLU
1	A	226	LEU
1	A	237	GLU
1	A	246	GLU
1	A	250	LYS
1	A	253	GLN
1	A	267	LEU
1	A	277	LEU
1	A	287	ARG
1	A	299	ARG
1	A	310	LEU
1	A	363	VAL
1	A	380	LYS
1	B	84	LYS
1	B	90	LEU
1	B	95	GLU
1	B	106	ARG
1	B	109	LEU
1	B	145	GLU
1	B	147	LEU
1	B	187	GLU
1	B	188	GLU
1	B	202	LEU
1	B	216	GLU
1	B	226	LEU
1	B	239	ILE
1	B	254	VAL
1	B	267	LEU
1	B	363	VAL
1	B	370	THR
1	B	391	HIS
1	C	52	LEU
1	C	58	GLN
1	C	65	LYS
1	C	71	LEU

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Mol	Chain	Res	Type
1	C	75	THR
1	C	90	LEU
1	C	95	GLU
1	C	109	LEU
1	C	147	LEU
1	C	159	ARG
1	C	189	ASN
1	C	231	THR
1	C	246	GLU
1	C	267	LEU
1	C	363	VAL
1	D	58	GLN
1	D	65	LYS
1	D	75	THR
1	D	80	GLU
1	D	105	GLU
1	D	127	GLN
1	D	144	ARG
1	D	147	LEU
1	D	187	GLU
1	D	191	LEU
1	D	192	LEU
1	D	239	ILE
1	D	272	ARG
1	D	310	LEU
1	D	376	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	154	GLN
1	A	275	HIS
1	A	309	GLN
1	A	328	HIS
1	B	154	GLN
1	B	221	ASN
1	B	391	HIS
1	C	128	GLN
1	C	309	GLN
1	C	333	HIS
1	C	391	HIS
1	D	55	GLN

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Mol	Chain	Res	Type
1	D	58	GLN
1	D	77	GLN
1	D	98	GLN
1	D	154	GLN
1	D	275	HIS
1	D	333	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

8 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	Y5N	C	501	-	25,25,25	0.28	0	31,33,33	0.34	0
2	Y5N	A	501	-	25,25,25	0.41	0	31,33,33	0.49	0
2	Y5N	B	501	-	25,25,25	0.27	0	31,33,33	0.33	0
3	ZIQ	C	502	-	14,17,17	1.44	2 (14%)	20,25,25	1.35	4 (20%)
3	ZIQ	A	502	-	14,17,17	1.39	3 (21%)	20,25,25	1.53	4 (20%)
3	ZIQ	B	502	-	14,17,17	1.44	1 (7%)	20,25,25	1.45	4 (20%)
3	ZIQ	D	502	-	14,17,17	1.49	3 (21%)	20,25,25	1.49	4 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	Y5N	D	501	-	25,25,25	0.29	0	31,33,33	0.33	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	Y5N	C	501	-	-	0/12/12/12	0/3/3/3
2	Y5N	A	501	-	-	0/12/12/12	0/3/3/3
2	Y5N	B	501	-	-	0/12/12/12	0/3/3/3
3	ZIQ	C	502	-	-	4/11/11/11	0/2/2/2
3	ZIQ	A	502	-	-	4/11/11/11	0/2/2/2
3	ZIQ	B	502	-	-	5/11/11/11	0/2/2/2
3	ZIQ	D	502	-	-	3/11/11/11	0/2/2/2
2	Y5N	D	501	-	-	0/12/12/12	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	502	ZIQ	CD2-CG	-3.32	1.38	1.44
3	B	502	ZIQ	CD2-CG	-3.05	1.39	1.44
3	C	502	ZIQ	CD2-CG	-2.93	1.39	1.44
3	A	502	ZIQ	CD2-CG	-2.74	1.39	1.44
3	C	502	ZIQ	CD2-CE2	-2.52	1.38	1.41
3	D	502	ZIQ	CD2-CE2	-2.36	1.38	1.41
3	A	502	ZIQ	CD1-CG	2.21	1.40	1.36
3	A	502	ZIQ	CD2-CE2	-2.12	1.38	1.41
3	D	502	ZIQ	CB-CA	-2.10	1.52	1.55

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	ZIQ	CZ2-CE2-CD2	-3.89	118.42	122.19
3	B	502	ZIQ	CZ2-CE2-CD2	-3.41	118.89	122.19
3	D	502	ZIQ	CZ2-CE2-CD2	-3.37	118.92	122.19
3	C	502	ZIQ	CZ2-CE2-CD2	-3.13	119.16	122.19
3	B	502	ZIQ	CE3-CD2-CE2	2.94	121.88	118.84
3	D	502	ZIQ	CE3-CD2-CE2	2.80	121.74	118.84
3	B	502	ZIQ	CE3-CD2-CG	-2.71	129.82	133.85
3	A	502	ZIQ	CE3-CD2-CE2	2.69	121.63	118.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	502	ZIQ	CE3-CD2-CG	-2.65	129.89	133.85
3	A	502	ZIQ	CE3-CD2-CG	-2.62	129.95	133.85
3	D	502	ZIQ	O-C-CA	-2.50	118.30	122.78
3	C	502	ZIQ	CE3-CD2-CG	-2.48	130.15	133.85
3	C	502	ZIQ	CE3-CD2-CE2	2.38	121.30	118.84
3	B	502	ZIQ	O-C-CA	-2.22	118.80	122.78
3	C	502	ZIQ	O-C-CA	-2.17	118.88	122.78
3	A	502	ZIQ	O-C-CA	-2.14	118.94	122.78

There are no chirality outliers.

All (16) torsion outliers are listed below:

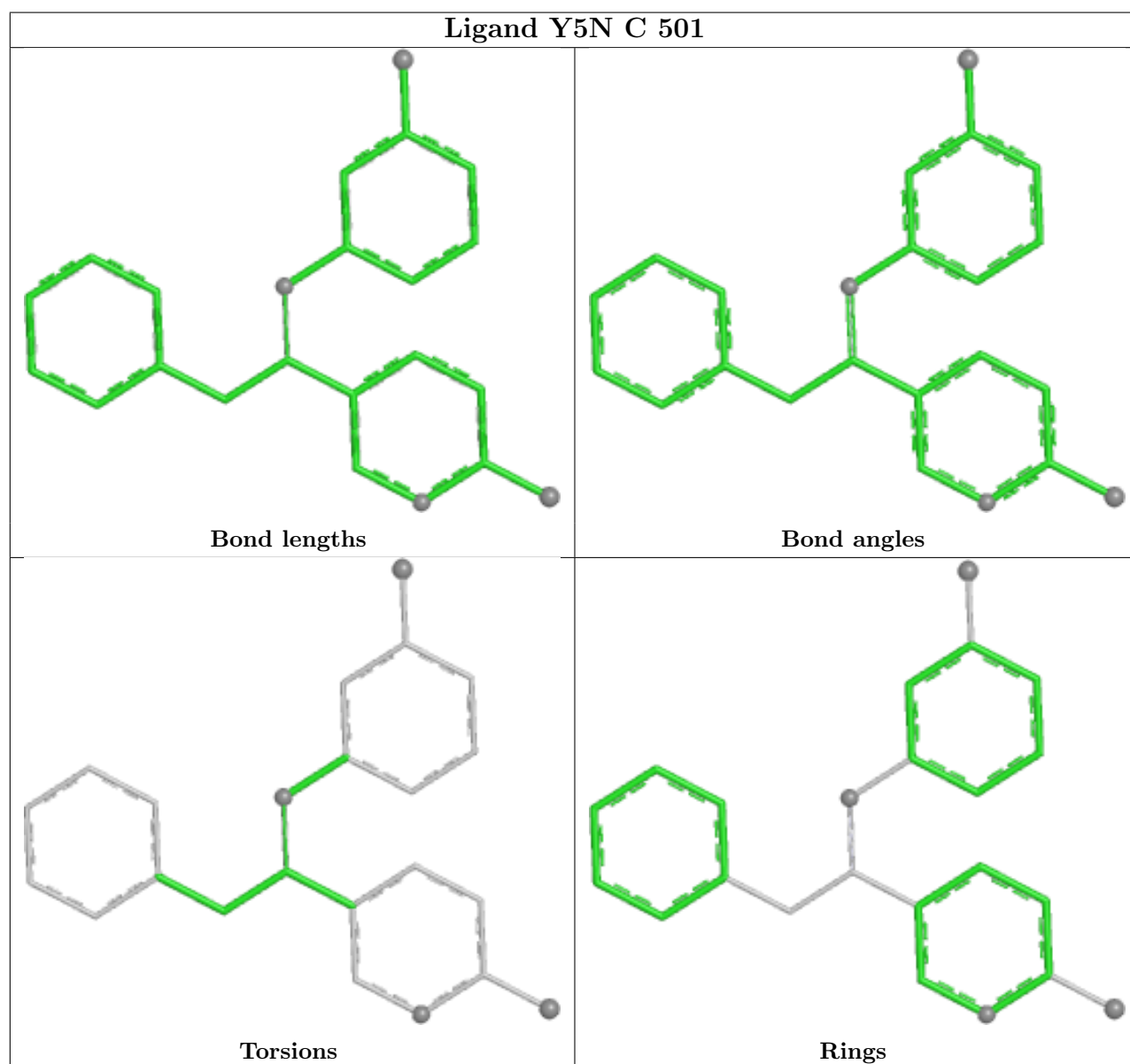
Mol	Chain	Res	Type	Atoms
3	A	502	ZIQ	OXT-C-CA-C1
3	B	502	ZIQ	OXT-C-CA-C1
3	A	502	ZIQ	O-C-CA-C1
3	B	502	ZIQ	O-C-CA-C1
3	C	502	ZIQ	OXT-C-CA-C1
3	A	502	ZIQ	OXT-C-CA-CB
3	B	502	ZIQ	OXT-C-CA-CB
3	C	502	ZIQ	OXT-C-CA-CB
3	B	502	ZIQ	CA-CB-CG-CD2
3	C	502	ZIQ	O-C-CA-C1
3	D	502	ZIQ	OXT-C-CA-C1
3	A	502	ZIQ	O-C-CA-CB
3	B	502	ZIQ	O-C-CA-CB
3	C	502	ZIQ	O-C-CA-CB
3	D	502	ZIQ	O-C-CA-CB
3	D	502	ZIQ	OXT-C-CA-CB

There are no ring outliers.

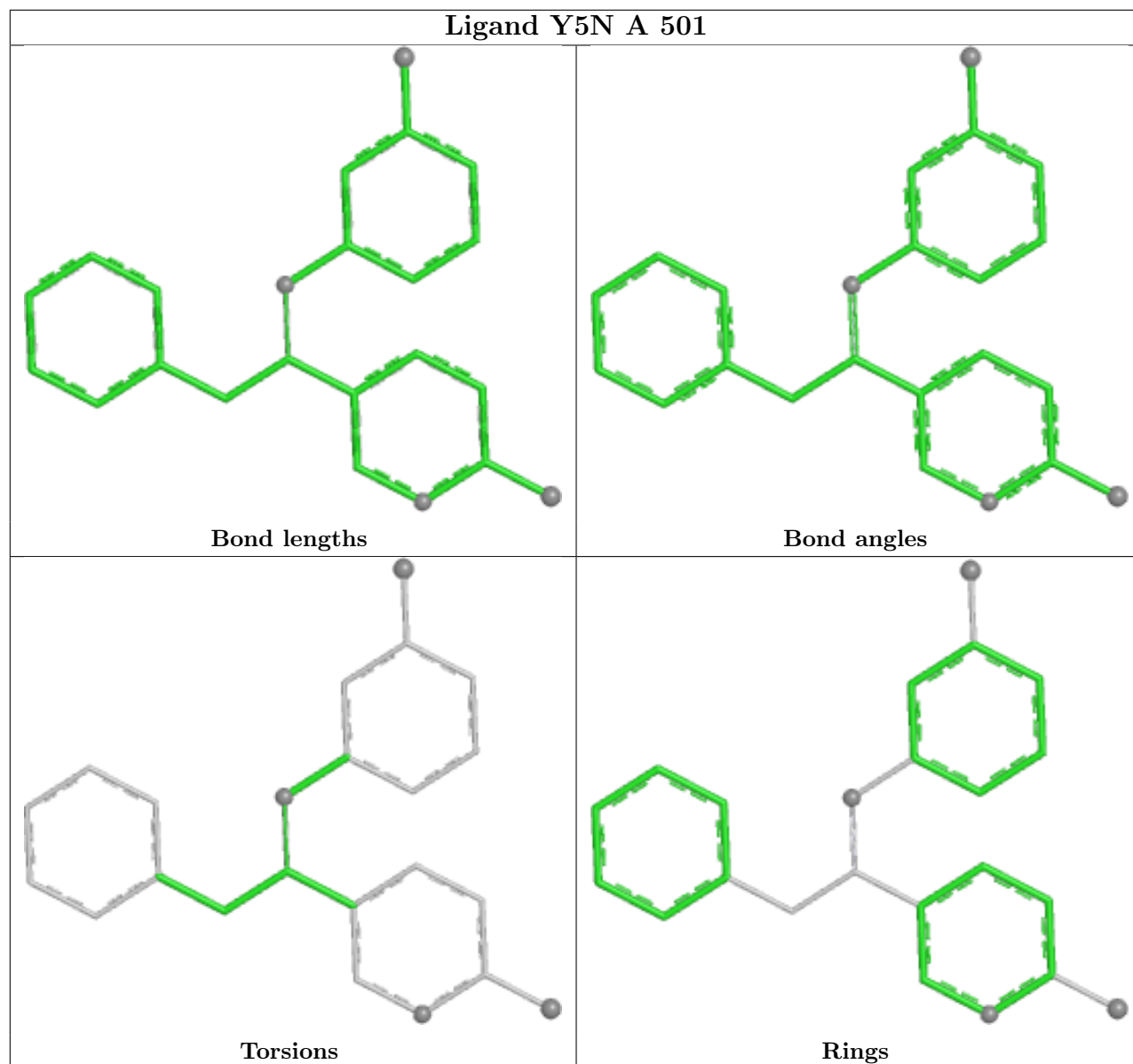
6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	Y5N	1	0
2	A	501	Y5N	1	0
2	B	501	Y5N	1	0
3	A	502	ZIQ	1	0
3	D	502	ZIQ	1	0
2	D	501	Y5N	1	0

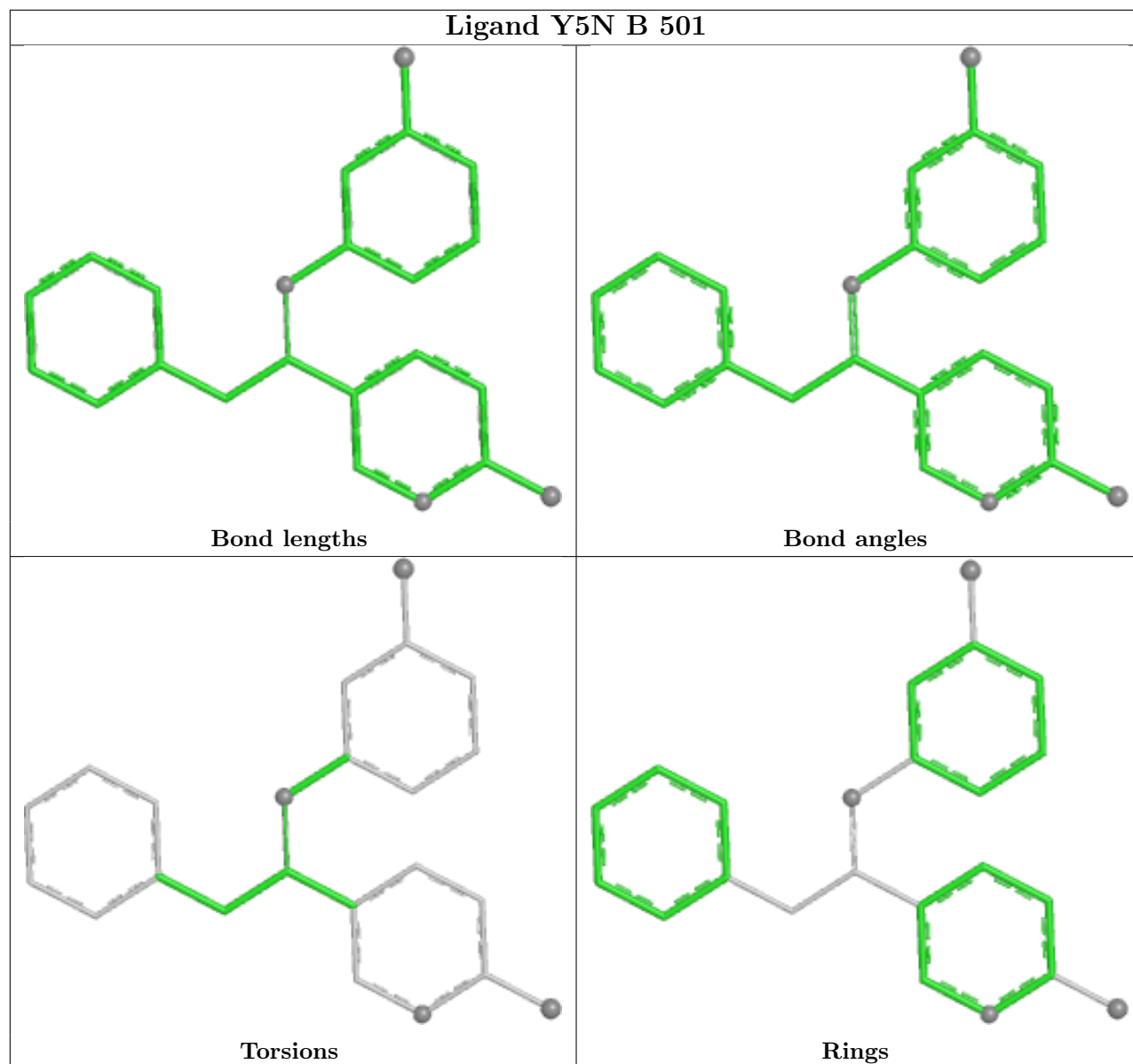
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

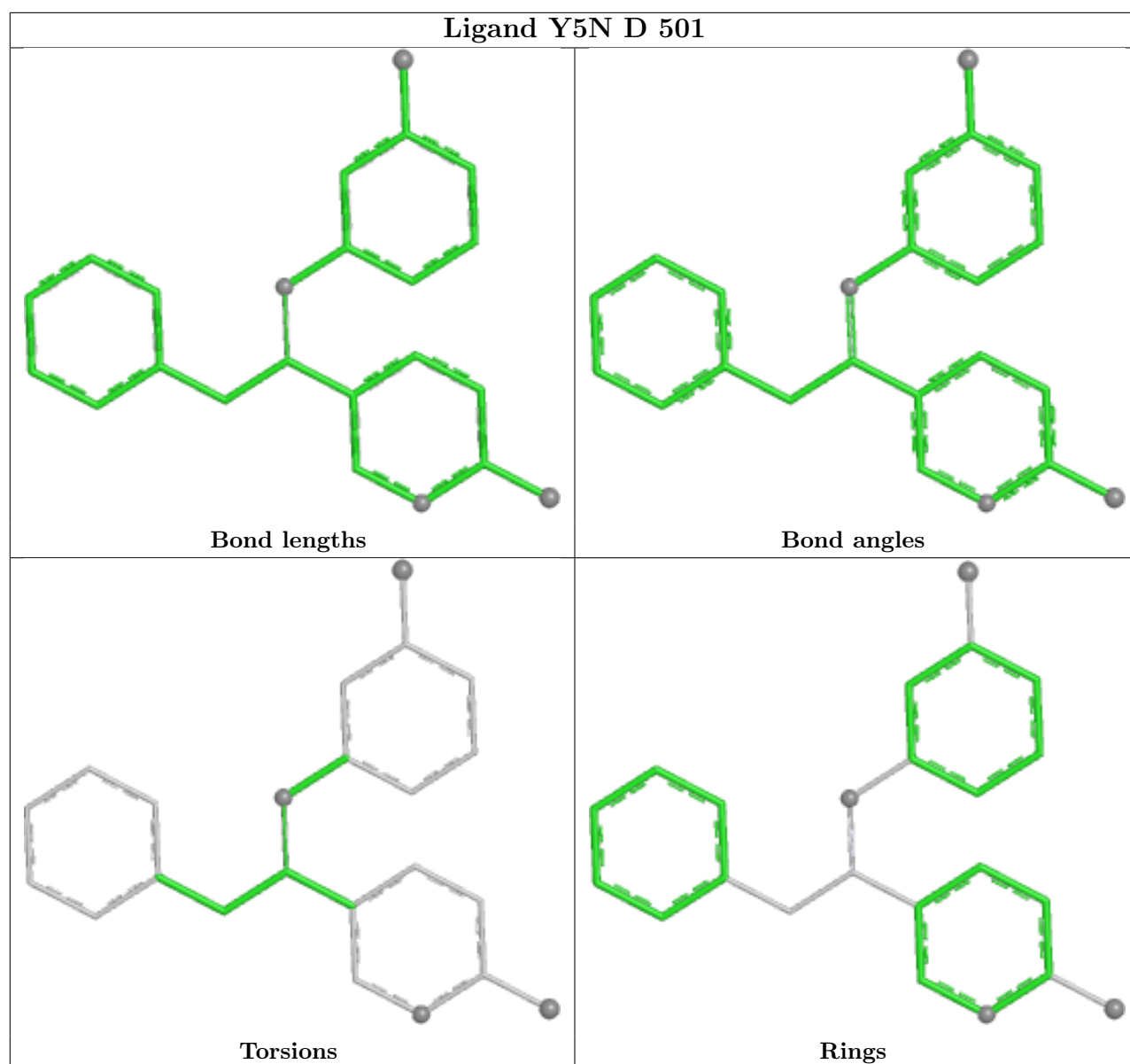


Ligand Y5N A 501



Ligand Y5N B 501





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	314/358 (87%)	0.71	31 (9%) 13 10	47, 73, 105, 122	0
1	B	318/358 (88%)	0.85	42 (13%) 7 5	47, 73, 114, 132	0
1	C	317/358 (88%)	0.83	29 (9%) 15 11	50, 78, 108, 124	0
1	D	314/358 (87%)	1.33	76 (24%) 2 1	55, 87, 125, 135	0
All	All	1263/1432 (88%)	0.93	178 (14%) 6 5	47, 77, 116, 135	0

All (178) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	316	ASP	5.5
1	A	382	ASN	5.2
1	A	151	SER	5.1
1	D	192	LEU	5.1
1	D	116	HIS	5.1
1	C	151	SER	5.1
1	C	149	PRO	4.9
1	B	371	TYR	4.5
1	D	258	GLN	4.4
1	D	189	ASN	4.3
1	C	359	TYR	4.1
1	C	133	GLU	4.1
1	D	389	LEU	4.0
1	D	227	GLU	3.7
1	B	192	LEU	3.7
1	B	382	ASN	3.7
1	D	310	LEU	3.6
1	A	359	TYR	3.6
1	C	168	LEU	3.6
1	C	389	LEU	3.6
1	D	293	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	267	LEU	3.5
1	A	385	ILE	3.4
1	A	383	PRO	3.4
1	D	111	VAL	3.4
1	A	338	SER	3.4
1	B	151	SER	3.4
1	B	337	GLY	3.4
1	D	384	THR	3.4
1	A	314	LEU	3.4
1	D	222	PHE	3.4
1	D	188	GLU	3.3
1	B	197	GLN	3.3
1	A	371	TYR	3.3
1	B	300	GLU	3.3
1	B	314	LEU	3.3
1	D	147	LEU	3.3
1	A	329	VAL	3.3
1	D	382	ASN	3.3
1	D	144	ARG	3.2
1	B	311	LEU	3.2
1	C	150	ALA	3.2
1	D	386	HIS	3.2
1	D	308	PHE	3.2
1	B	389	LEU	3.1
1	D	193	LEU	3.1
1	D	312	THR	3.1
1	B	189	ASN	3.1
1	B	191	LEU	3.1
1	A	384	THR	3.1
1	B	367	ASN	3.1
1	B	385	ILE	3.0
1	C	144	ARG	3.0
1	A	310	LEU	3.0
1	D	48	LEU	3.0
1	D	231	THR	3.0
1	A	362	PHE	3.0
1	B	313	SER	2.9
1	D	242	GLN	2.9
1	D	184	PHE	2.9
1	D	223	TRP	2.9
1	D	141	ASN	2.9
1	B	386	HIS	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	356	SER	2.9
1	C	361	VAL	2.8
1	A	316	ASP	2.8
1	D	314	LEU	2.8
1	D	112	VAL	2.8
1	B	245	GLU	2.8
1	D	246	GLU	2.8
1	B	184	PHE	2.8
1	A	309	GLN	2.8
1	D	230	ILE	2.8
1	A	147	LEU	2.8
1	A	388	PHE	2.8
1	D	262	GLU	2.8
1	D	221	ASN	2.7
1	A	167	VAL	2.7
1	C	382	ASN	2.7
1	D	238	PHE	2.7
1	C	185	LYS	2.7
1	C	385	ILE	2.7
1	D	284	LEU	2.6
1	B	358	ARG	2.6
1	D	274	GLU	2.6
1	C	316	ASP	2.6
1	C	293	LEU	2.6
1	C	386	HIS	2.6
1	D	261	LYS	2.6
1	D	289	LEU	2.6
1	D	51	VAL	2.6
1	C	40	LEU	2.6
1	D	240	ARG	2.6
1	C	333	HIS	2.6
1	A	187	GLU	2.6
1	D	257	PHE	2.5
1	D	287	ARG	2.5
1	A	202	LEU	2.5
1	C	272	ARG	2.5
1	D	239	ILE	2.5
1	D	237	GLU	2.5
1	B	272	ARG	2.4
1	B	391	HIS	2.4
1	D	265	LEU	2.4
1	D	151	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	169	GLN	2.4
1	D	64	ASN	2.4
1	B	190	GLU	2.4
1	D	66	ILE	2.4
1	B	113	SER	2.4
1	D	252	GLU	2.4
1	D	383	PRO	2.4
1	B	242	GLN	2.4
1	D	309	GLN	2.4
1	C	153	PHE	2.4
1	C	274	GLU	2.3
1	D	119	SER	2.3
1	D	225	LYS	2.3
1	B	254	VAL	2.3
1	D	254	VAL	2.3
1	B	366	PHE	2.3
1	A	318	ASP	2.3
1	D	307	PRO	2.3
1	D	75	THR	2.3
1	D	359	TYR	2.3
1	A	300	GLU	2.3
1	D	366	PHE	2.3
1	D	241	ILE	2.3
1	B	187	GLU	2.3
1	B	159	ARG	2.3
1	D	217	PRO	2.3
1	A	169	GLN	2.2
1	D	277	LEU	2.2
1	A	134	THR	2.2
1	B	383	PRO	2.2
1	D	253	GLN	2.2
1	D	311	LEU	2.2
1	C	373	ILE	2.2
1	D	373	ILE	2.2
1	A	212	THR	2.2
1	D	266	SER	2.2
1	B	126	VAL	2.2
1	D	118	VAL	2.2
1	B	238	PHE	2.2
1	A	149	PRO	2.1
1	A	367	ASN	2.1
1	B	253	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	234	LEU	2.1
1	A	166	GLY	2.1
1	B	317	ILE	2.1
1	C	391	HIS	2.1
1	B	384	THR	2.1
1	D	337	GLY	2.1
1	B	255	ALA	2.1
1	C	384	THR	2.1
1	A	98	GLN	2.1
1	B	201	LEU	2.1
1	D	209	LEU	2.1
1	A	153	PHE	2.1
1	D	149	PRO	2.1
1	D	46	LEU	2.1
1	C	218	HIS	2.1
1	A	361	VAL	2.1
1	A	270	GLU	2.0
1	C	358	ARG	2.0
1	B	319	SER	2.0
1	D	243	ALA	2.0
1	B	127	GLN	2.0
1	C	289	LEU	2.0
1	C	372	LEU	2.0
1	D	264	LEU	2.0
1	D	267	LEU	2.0
1	B	306	VAL	2.0
1	C	216	GLU	2.0
1	D	388	PHE	2.0
1	C	217	PRO	2.0
1	D	109	LEU	2.0
1	D	107	ASN	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

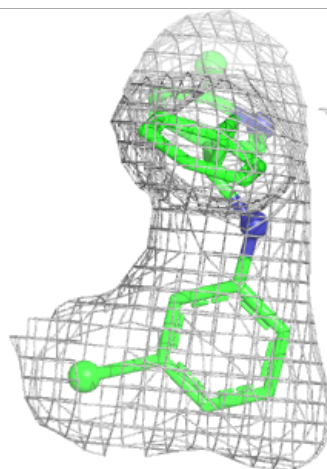
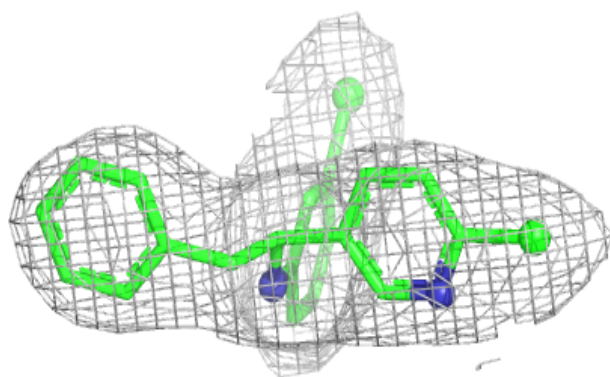
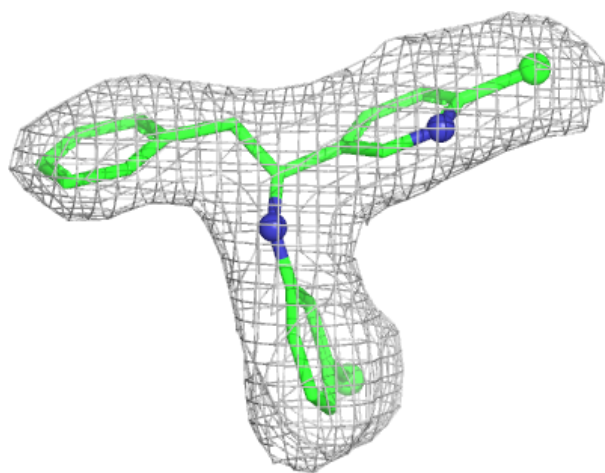
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ZIQ	A	502	16/16	0.87	0.14	89,89,90,90	0
2	Y5N	B	501	23/23	0.92	0.11	66,68,69,71	0
3	ZIQ	D	502	16/16	0.92	0.15	101,101,103,103	0
2	Y5N	A	501	23/23	0.93	0.10	68,69,75,77	0
2	Y5N	C	501	23/23	0.94	0.09	70,71,76,77	0
3	ZIQ	C	502	16/16	0.94	0.09	69,71,76,76	0
2	Y5N	D	501	23/23	0.94	0.10	72,75,76,77	0
3	ZIQ	B	502	16/16	0.96	0.07	67,67,69,70	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.

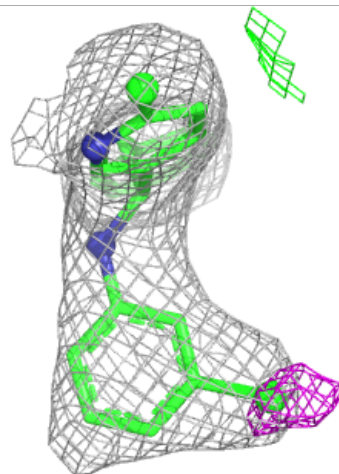
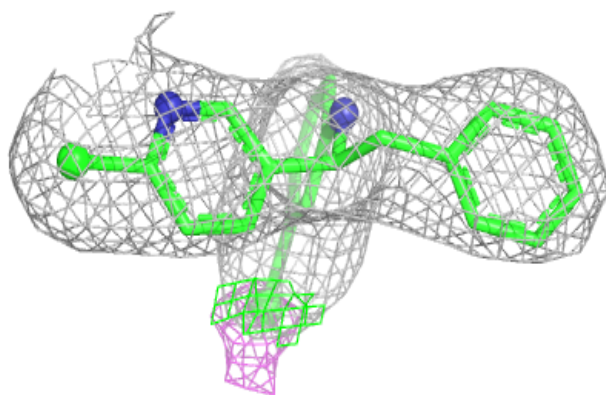
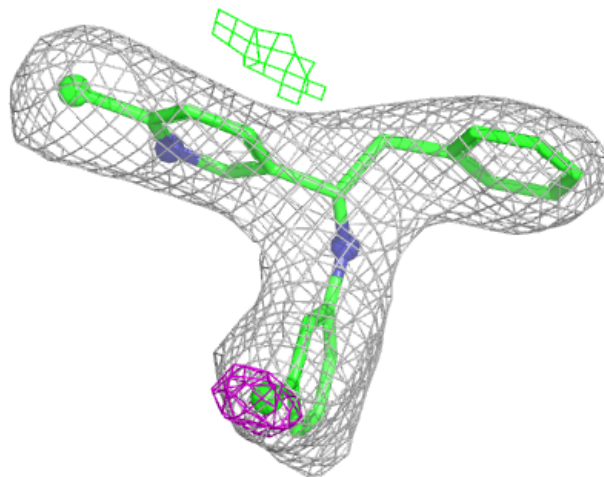
Electron density around Y5N B 501:

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



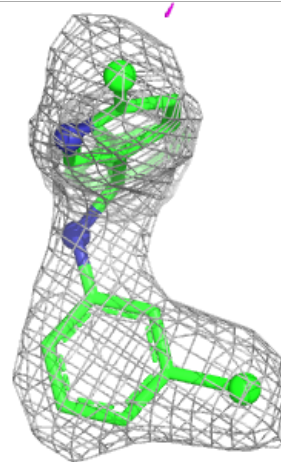
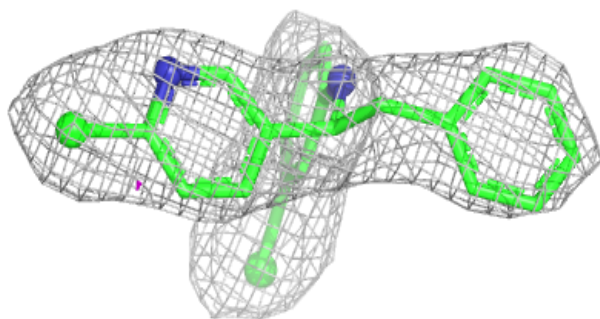
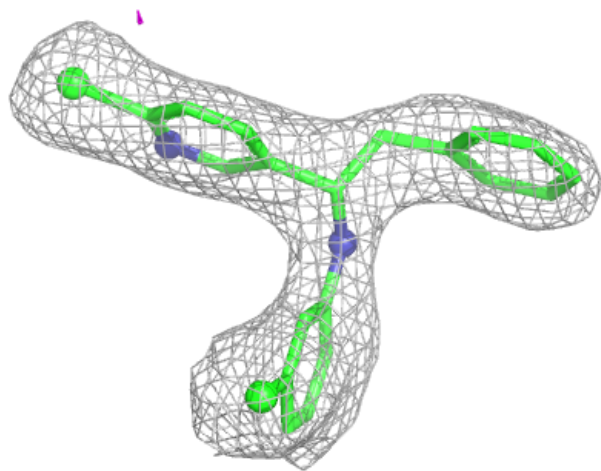
Electron density around Y5N A 501:

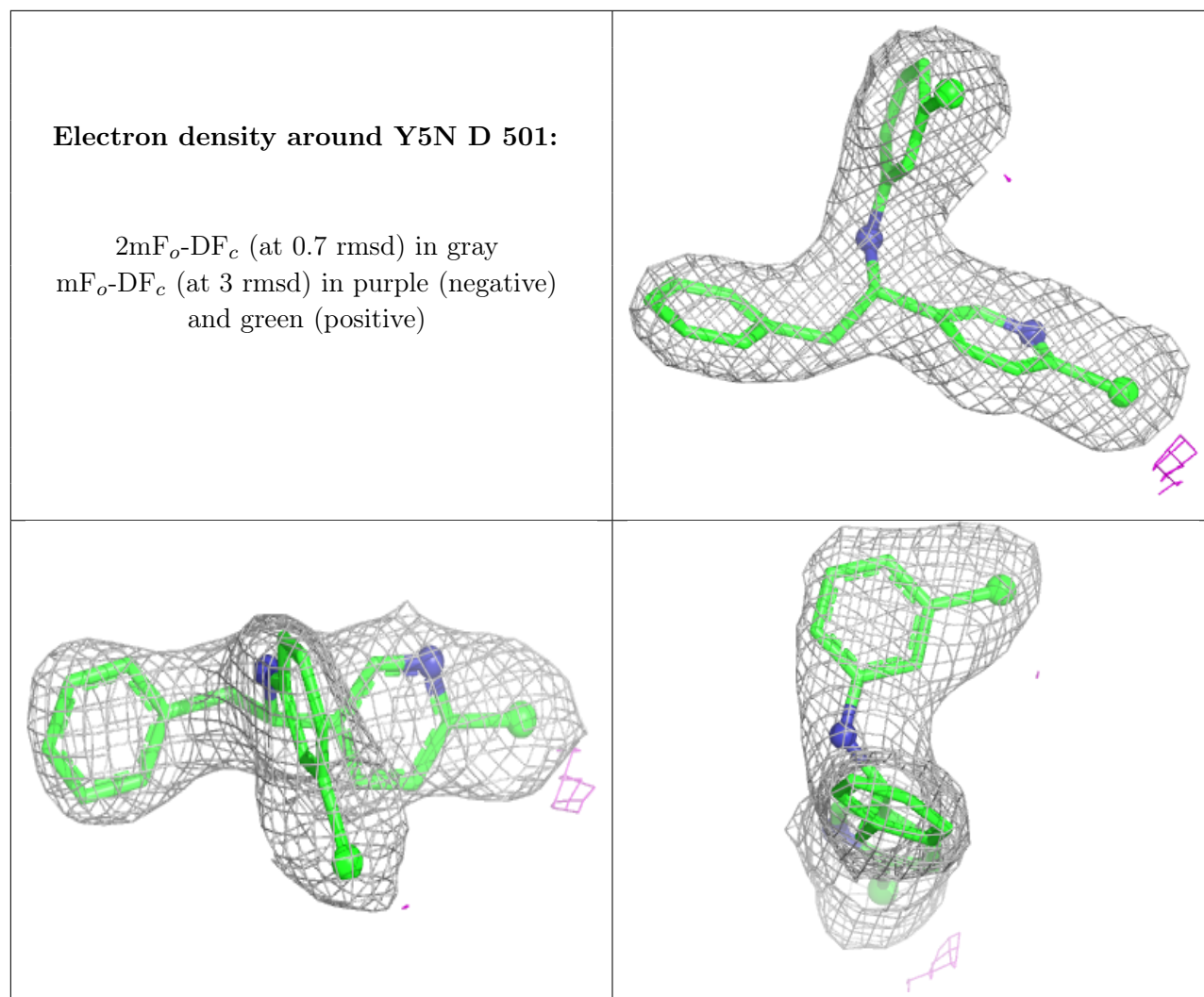
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Y5N C 501:

$2mF_o-DF_c$ (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.