



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 04:05 AM UTC

PDB ID : 6UL2 / pdb_00006ul2
Title : Crystal structure of tryptophan-6-halogenase BorH complexed with L-tryptophan
Authors : Lingkon, K.; Bellizzi, J.J.
Deposited on : 2019-10-06
Resolution : 1.98 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

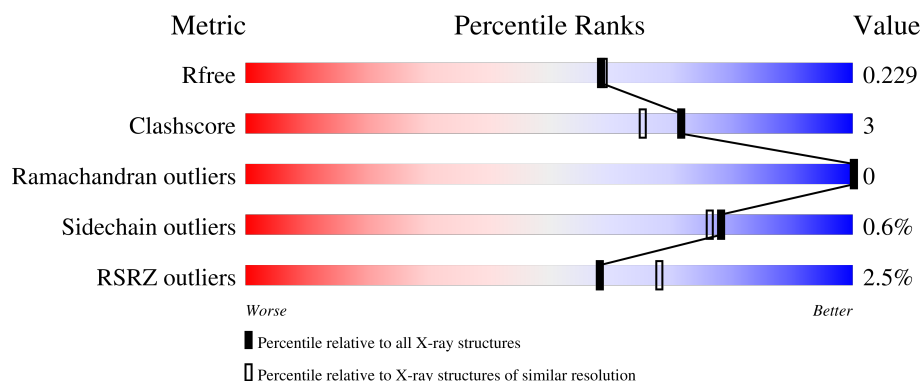
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	529	2% 91% 9%
1	B	529	3% 90% 8%
1	C	529	% 88% 10%
1	D	529	3% 90% 8%

2 Entry composition [i](#)

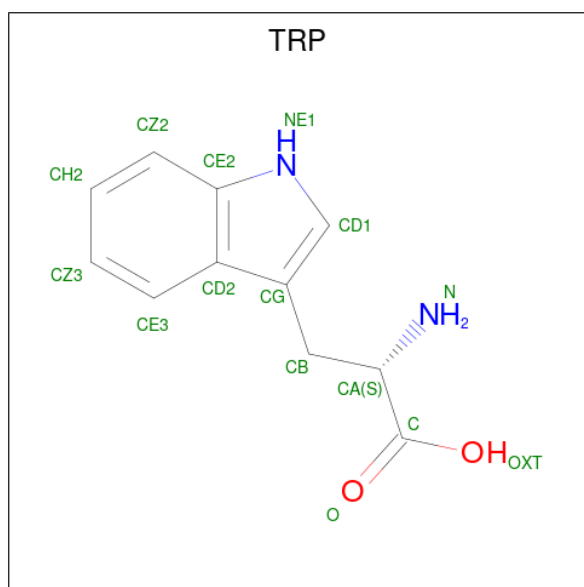
There are 4 unique types of molecules in this entry. The entry contains 18160 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 6-halogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	526	Total	C	N	O	S	0	1	0
			4222	2693	744	763	22			
1	B	520	Total	C	N	O	S	0	1	0
			4174	2663	734	755	22			
1	C	519	Total	C	N	O	S	0	1	0
			4161	2654	732	753	22			
1	D	516	Total	C	N	O	S	0	1	0
			4132	2639	728	743	22			

- Molecule 2 is TRYPTOPHAN (CCD ID: TRP) (formula: $C_{11}H_{12}N_2O_2$) (labeled as "Ligand of Interest" by depositor).



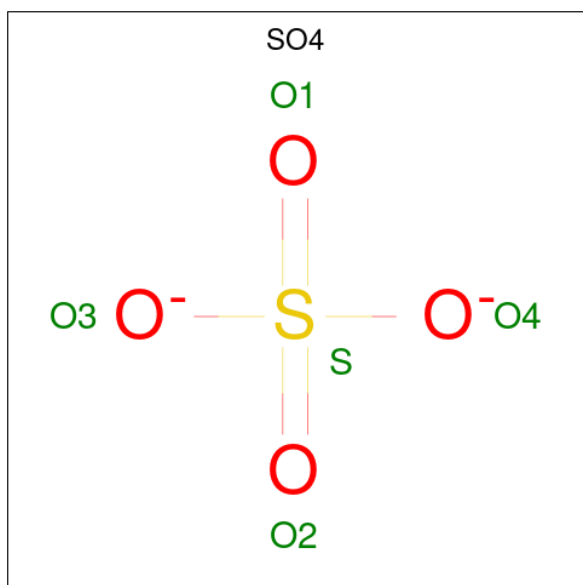
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	11	2	2		
2	B	1	Total	C	N	O	0	0
			15	11	2	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			15	11	2	2		
2	D	1	Total	C	N	O	0	0
			15	11	2	2		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	376	Total	O	0	0
			376	376		

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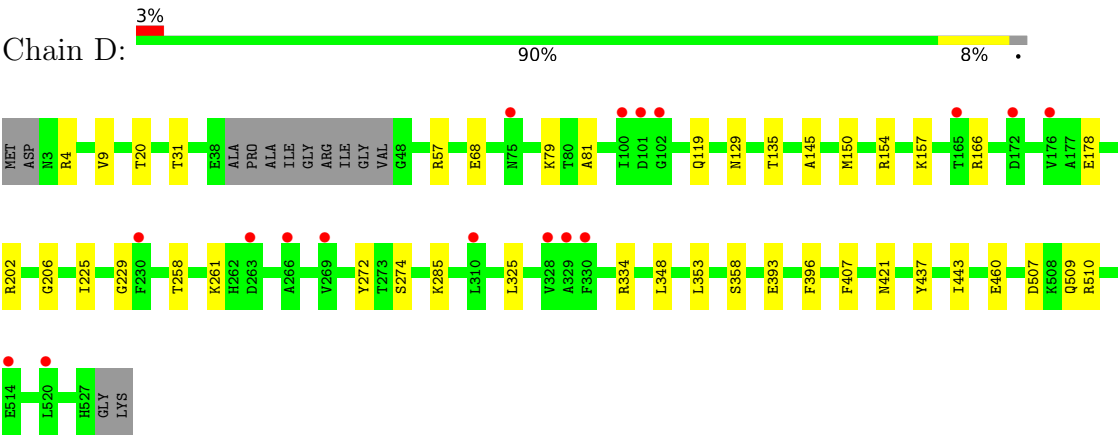
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	319	Total 319	O 319	0	0
4	C	310	Total 310	O 310	0	0
4	D	271	Total 271	O 271	0	0

- Molecule 1: Tryptophan 6-halogenase



● Molecule 1: Tryptophan 6-halogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.48Å 157.92Å 113.25Å 90.00° 104.06° 90.00°	Depositor
Resolution (Å)	31.89 – 1.98 31.89 – 1.98	Depositor EDS
% Data completeness (in resolution range)	98.2 (31.89-1.98) 98.1 (31.89-1.98)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 1.98Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.193 , 0.229 0.195 , 0.229	Depositor DCC
R_{free} test set	2001 reflections (1.17%)	wwPDB-VP
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.505	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18160	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.52% 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: SO4

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	0.44	0/4344	0.72	0/5899
1	B	0.42	0/4294	0.73	2/5831 (0.0%)
1	C	0.40	0/4281	0.71	0/5813
1	D	0.38	0/4252	0.71	0/5774
All	All	0.41	0/17171	0.72	2/23317 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	162	ARG	CA-C-N	5.79	125.69	119.85
1	B	162	ARG	C-N-CA	5.79	125.69	119.85

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4222	0	4070	25	0
1	B	4174	0	4010	27	0
1	C	4161	0	3988	34	0
1	D	4132	0	3966	23	0
2	A	15	0	9	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	15	0	9	0	0
2	C	15	0	9	0	0
2	D	15	0	9	1	0
3	A	40	0	0	1	0
3	B	40	0	0	2	0
3	C	25	0	0	0	0
3	D	30	0	0	1	0
4	A	376	0	0	2	0
4	B	319	0	0	2	0
4	C	310	0	0	8	0
4	D	271	0	0	2	0
All	All	18160	0	16070	108	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 (108) 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:D:81:ALA:HB3	1:D:150:MET:HE1	1.61	0.81
1:B:456:ARG:NH1	4:B:702:HOH:O	2.24	0.70
1:D:274:SER:HB2	1:D:285:LYS:HB3	1.74	0.69
1:C:4:ARG:NE	4:C:702:HOH:O	2.22	0.66
1:B:2:ASP:O	1:B:378:ARG:NH2	2.28	0.66
1:D:507:ASP:OD1	1:D:510:ARG:NH2	2.29	0.66
1:A:491:ARG:NH1	4:A:704:HOH:O	2.30	0.64
1:C:202:ARG:NE	4:C:704:HOH:O	2.31	0.64
1:C:141:TYR:HA	1:C:147:THR:HG21	1.79	0.64
1:D:150:MET:HE3	1:D:272:TYR:HB3	1.81	0.62
1:C:203:ASP:OD2	1:C:205:ARG:NH1	2.34	0.61
1:D:437:TYR:HB2	1:D:443:ILE:HD11	1.83	0.60
1:C:75:ASN:HB3	4:C:940:HOH:O	2.04	0.58
1:D:68:GLU:OE1	1:D:68:GLU:N	2.32	0.58
1:A:426:LEU:N	3:A:608:SO4:O1	2.35	0.57
1:A:359:THR:HG21	1:A:399:THR:HG21	1.87	0.57
1:A:229:GLY:HA2	1:A:348:LEU:HB2	1.86	0.55
1:B:7:ARG:HB2	1:B:221:GLY:HA2	1.88	0.55
1:C:353:LEU:HG	1:C:396:PHE:CE1	2.43	0.54
1:D:119:GLN:NE2	4:D:701:HOH:O	2.15	0.53
1:D:258:THR:HB	1:D:325:LEU:HD23	1.90	0.53
1:C:129:ASN:HB3	1:C:135:THR:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:334:ARG:CZ	1:C:393:GLU:HG3	2.39	0.53
1:B:239:MET:HE1	1:B:341:LYS:HD2	1.91	0.53
1:C:166:ARG:NH1	4:C:701:HOH:O	2.21	0.52
1:C:252:CYS:HB3	1:C:297:VAL:HG12	1.93	0.51
1:A:200:VAL:HG11	1:A:238:ALA:HB2	1.93	0.51
1:D:202:ARG:HD2	1:D:206:GLY:O	2.11	0.50
1:B:447:VAL:HG12	1:B:448:THR:HG23	1.93	0.49
1:A:356:LEU:HB3	1:A:403:ILE:HD12	1.93	0.49
1:C:157:LYS:HB3	1:C:163:PRO:HA	1.94	0.49
1:D:129:ASN:HB3	1:D:135:THR:HG22	1.94	0.49
1:D:157:LYS:NZ	4:D:712:HOH:O	2.45	0.49
1:A:57:ARG:NH1	1:A:454:TYR:O	2.46	0.49
1:A:460:GLU:OE2	2:A:601:TRP:N	2.46	0.48
1:B:20:THR:HG21	1:B:225:ILE:HG21	1.94	0.48
1:C:66:ARG:HH21	1:C:68:GLU:CD	2.21	0.48
1:C:198:GLN:HB2	1:C:214:VAL:HG12	1.94	0.48
1:B:294:THR:HG23	1:B:312:PHE:CZ	2.48	0.48
1:D:334:ARG:CZ	1:D:393:GLU:HG3	2.44	0.48
1:D:145:ALA:HA	1:D:509:GLN:HG3	1.95	0.48
1:C:422:LYS:N	1:C:422:LYS:HD3	2.28	0.48
1:C:198:GLN:HG2	1:C:199:GLN:HG3	1.96	0.48
1:C:20:THR:HG21	1:C:225:ILE:HG21	1.96	0.47
1:C:438:LYS:HA	1:C:481:PRO:HA	1.97	0.47
1:A:353:LEU:HG	1:A:396:PHE:CE1	2.50	0.47
1:C:7:ARG:HB2	1:C:221:GLY:HA2	1.97	0.47
1:A:203:ASP:OD1	1:A:205:ARG:HG2	2.15	0.47
1:B:35:THR:HG22	1:B:191:GLU:HB3	1.95	0.47
1:B:339:TRP:CG	1:B:344:VAL:HG22	2.51	0.46
1:C:205:ARG:NH2	4:C:717:HOH:O	2.48	0.46
1:B:154:ARG:NH2	3:B:604:SO4:O3	2.30	0.46
1:D:20:THR:HG21	1:D:225:ILE:HG21	1.97	0.46
1:C:79:LYS:NZ	1:C:358:SER:OG	2.48	0.46
1:A:86:ASN:HA	1:A:105:ASP:OD2	2.15	0.46
1:B:88:ARG:HD3	1:B:477:LEU:C	2.41	0.46
1:C:251:LEU:HD13	1:C:302:PHE:HE2	1.80	0.46
1:D:353:LEU:HG	1:D:396:PHE:CE1	2.51	0.46
1:C:437:TYR:HB2	1:C:443:ILE:HD11	1.99	0.45
1:C:243:PHE:CZ	1:C:331:ARG:HG2	2.51	0.45
1:B:294:THR:HG23	1:B:312:PHE:HZ	1.81	0.45
1:B:438:LYS:HA	1:B:481:PRO:HA	1.98	0.45
1:D:4:ARG:NH1	1:D:31:THR:O	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:GLN:HG3	4:A:900:HOH:O	2.18	0.44
1:B:56:GLN:HB2	1:B:169:TRP:CH2	2.53	0.44
1:C:57:ARG:NH1	4:C:724:HOH:O	2.50	0.43
1:B:129:ASN:HB3	1:B:135:THR:HG22	2.00	0.43
1:B:419:LYS:HB2	1:B:419:LYS:HE3	1.82	0.43
1:A:158:TRP:HB2	1:A:162:ARG:HB2	2.00	0.43
1:B:79:LYS:NZ	1:B:358:SER:OG	2.51	0.43
1:A:243:PHE:CZ	1:A:331:ARG:HG2	2.53	0.43
1:C:215:GLU:OE2	1:D:261:LYS:NZ	2.43	0.43
1:A:28:LEU:HD13	1:A:32:VAL:HG21	2.00	0.43
1:D:166:ARG:NH2	3:D:604:SO4:O1	2.39	0.43
1:A:205:ARG:HG3	1:A:207:PHE:CD1	2.54	0.43
1:A:239:MET:HE1	1:A:341:LYS:HD2	2.01	0.43
1:B:230:PHE:CZ	1:B:348:LEU:HD13	2.54	0.43
1:B:3:ASN:O	1:B:377:ASP:HB2	2.18	0.42
1:A:8:ILE:HB	1:A:34:ILE:HD13	2.02	0.42
1:B:353:LEU:HG	1:B:396:PHE:CE1	2.54	0.42
1:B:20:THR:OG1	1:B:368:ILE:HD11	2.19	0.42
1:B:239:MET:CE	1:B:341:LYS:HD2	2.49	0.42
1:A:241:GLU:HA	1:A:242:PRO:HD3	1.90	0.42
1:A:20:THR:HG21	1:A:225:ILE:HG21	2.02	0.42
1:B:68:GLU:N	3:B:606:SO4:O4	2.33	0.42
1:B:448:THR:HB	1:B:452:THR:HB	2.02	0.42
1:C:453:TYR:CZ	1:C:460:GLU:HG3	2.54	0.42
1:A:331:ARG:O	1:A:352:PHE:HB3	2.20	0.41
1:C:202:ARG:CZ	4:C:704:HOH:O	2.64	0.41
1:B:229:GLY:HA2	1:B:348:LEU:HB2	2.02	0.41
1:D:229:GLY:HA2	1:D:348:LEU:HB2	2.02	0.41
1:A:157:LYS:HG2	1:A:163:PRO:HA	2.02	0.41
1:D:407:PHE:HB3	1:D:421:ASN:HD22	1.85	0.41
1:C:157:LYS:HE3	1:C:522:PHE:CZ	2.55	0.41
1:A:445:ALA:HA	1:A:446:PRO:HD3	1.91	0.41
1:C:68:GLU:OE1	1:C:68:GLU:N	2.54	0.41
1:C:187:ARG:NE	4:C:731:HOH:O	2.54	0.41
1:C:408:TYR:CE2	1:C:426:LEU:HD22	2.55	0.41
1:B:331:ARG:HD3	4:B:757:HOH:O	2.21	0.40
1:C:116:GLU:HG2	1:C:121:PRO:HA	2.03	0.40
1:C:274:SER:HB2	1:C:285:LYS:HB3	2.03	0.40
1:B:88:ARG:HD3	1:B:477:LEU:O	2.21	0.40
1:D:79:LYS:NZ	1:D:358:SER:OG	2.53	0.40
1:A:18:TRP:CZ2	1:A:181:ARG:HG3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:GLN:HB2	1:A:169:TRP:CH2	2.57	0.40
1:D:154:ARG:HA	1:D:154:ARG:HD3	1.90	0.40
1:D:460:GLU:OE1	2:D:601:TRP:N	2.55	0.40
1:C:229:GLY:HA2	1:C:348:LEU:HB2	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	525/529 (99%)	512 (98%)	13 (2%)	0	100	100
1	B	517/529 (98%)	500 (97%)	17 (3%)	0	100	100
1	C	516/529 (98%)	502 (97%)	14 (3%)	0	100	100
1	D	513/529 (97%)	497 (97%)	16 (3%)	0	100	100
All	All	2071/2116 (98%)	2011 (97%)	60 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	434/436 (100%)	431 (99%)	3 (1%)	76	73
1	B	429/436 (98%)	425 (99%)	4 (1%)	70	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	426/436 (98%)	425 (100%)	1 (0%)	87	88
1	D	422/436 (97%)	419 (99%)	3 (1%)	76	73
All	All	1711/1744 (98%)	1700 (99%)	11 (1%)	78	76

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	200	VAL
1	A	508	LYS
1	B	187	ARG
1	B	248	ASP
1	B	359	THR
1	B	447	VAL
1	C	299	SER
1	D	9	VAL
1	D	57	ARG
1	D	178	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	GLN
1	A	247	ASN
1	A	249	GLN
1	A	322	ASN
1	B	249	GLN
1	B	390	HIS
1	C	483	ASN
1	D	236	ASN
1	D	335	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

31 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	$\# Z > 2$
3	SO4	B	602	-	4,4,4	0.23	0	6,6,6	0.10	0
2	TRP	D	601	-	15,16,16	0.75	1 (6%)	18,22,22	0.81	1 (5%)
3	SO4	D	606	-	4,4,4	0.24	0	6,6,6	0.09	0
3	SO4	B	609	-	4,4,4	0.24	0	6,6,6	0.06	0
3	SO4	D	603	-	4,4,4	0.26	0	6,6,6	0.08	0
3	SO4	D	602	-	4,4,4	0.25	0	6,6,6	0.07	0
3	SO4	A	606	-	4,4,4	0.22	0	6,6,6	0.07	0
3	SO4	A	609	-	4,4,4	0.29	0	6,6,6	0.23	0
3	SO4	B	608	-	4,4,4	0.24	0	6,6,6	0.14	0
2	TRP	B	601	-	15,16,16	0.81	1 (6%)	18,22,22	0.90	2 (11%)
3	SO4	C	602	-	4,4,4	0.23	0	6,6,6	0.13	0
3	SO4	A	608	-	4,4,4	0.22	0	6,6,6	0.12	0
3	SO4	B	605	-	4,4,4	0.23	0	6,6,6	0.09	0
2	TRP	C	601	-	15,16,16	0.78	1 (6%)	18,22,22	0.83	1 (5%)
3	SO4	B	603	-	4,4,4	0.25	0	6,6,6	0.07	0
3	SO4	A	603	-	4,4,4	0.21	0	6,6,6	0.20	0
2	TRP	A	601	-	15,16,16	0.73	1 (6%)	18,22,22	0.95	2 (11%)
3	SO4	B	607	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	C	606	-	4,4,4	0.25	0	6,6,6	0.16	0
3	SO4	D	607	-	4,4,4	0.22	0	6,6,6	0.18	0
3	SO4	D	605	-	4,4,4	0.24	0	6,6,6	0.12	0
3	SO4	C	604	-	4,4,4	0.23	0	6,6,6	0.12	0
3	SO4	C	603	-	4,4,4	0.25	0	6,6,6	0.08	0
3	SO4	A	602	-	4,4,4	0.26	0	6,6,6	0.14	0
3	SO4	B	604	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	D	604	-	4,4,4	0.23	0	6,6,6	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	607	-	4,4,4	0.25	0	6,6,6	0.09	0
3	SO4	A	605	-	4,4,4	0.24	0	6,6,6	0.05	0
3	SO4	C	605	-	4,4,4	0.24	0	6,6,6	0.11	0
3	SO4	A	604	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	B	606	-	4,4,4	0.23	0	6,6,6	0.10	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	TRP	A	601	-	-	2/8/8/8	0/2/2/2
2	TRP	C	601	-	-	2/8/8/8	0/2/2/2
2	TRP	B	601	-	-	2/8/8/8	0/2/2/2
2	TRP	D	601	-	-	2/8/8/8	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	TRP	OXT-C	-2.23	1.23	1.30
2	C	601	TRP	OXT-C	-2.21	1.23	1.30
2	A	601	TRP	OXT-C	-2.18	1.23	1.30
2	D	601	TRP	OXT-C	-2.16	1.23	1.30

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	TRP	OXT-C-O	-2.91	117.47	124.08
2	A	601	TRP	OXT-C-O	-2.88	117.54	124.08
2	B	601	TRP	OXT-C-O	-2.67	118.01	124.08
2	D	601	TRP	OXT-C-O	-2.67	118.02	124.08
2	A	601	TRP	CA-CB-CG	2.16	117.58	113.49
2	B	601	TRP	CA-CB-CG	2.10	117.47	113.49

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	TRP	OXT-C-CA-N

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Mol	Chain	Res	Type	Atoms
2	B	601	TRP	OXT-C-CA-N
2	C	601	TRP	OXT-C-CA-N
2	D	601	TRP	OXT-C-CA-N
2	A	601	TRP	O-C-CA-N
2	B	601	TRP	O-C-CA-N
2	C	601	TRP	O-C-CA-N
2	D	601	TRP	O-C-CA-N

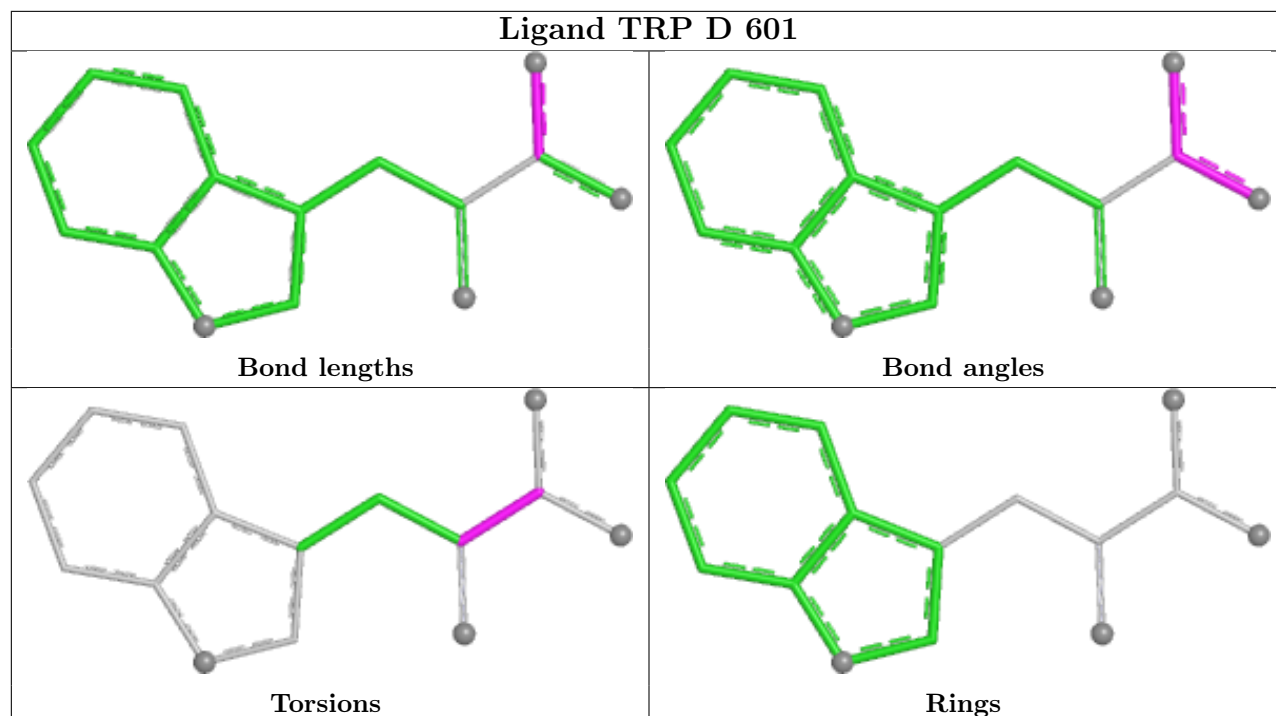
There are no ring outliers.

6 monomers are involved in 6 short contacts:

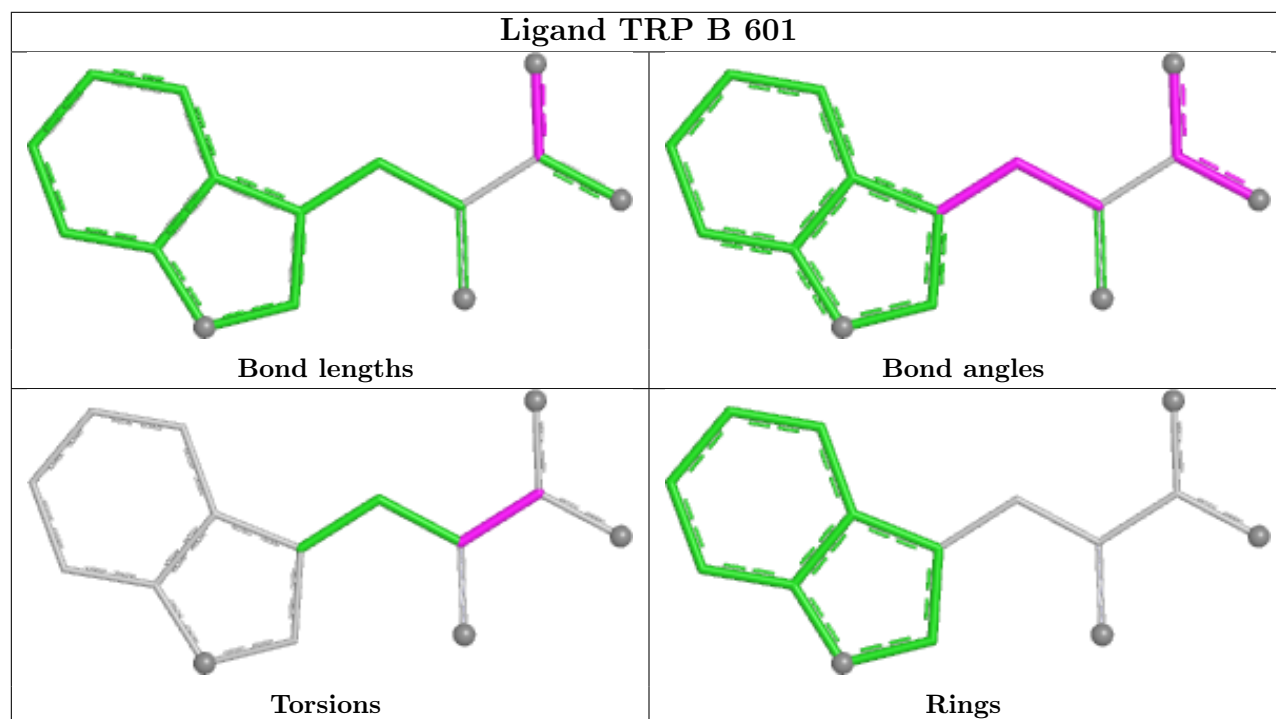
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	601	TRP	1	0
3	A	608	SO4	1	0
2	A	601	TRP	1	0
3	B	604	SO4	1	0
3	D	604	SO4	1	0
3	B	606	SO4	1	0

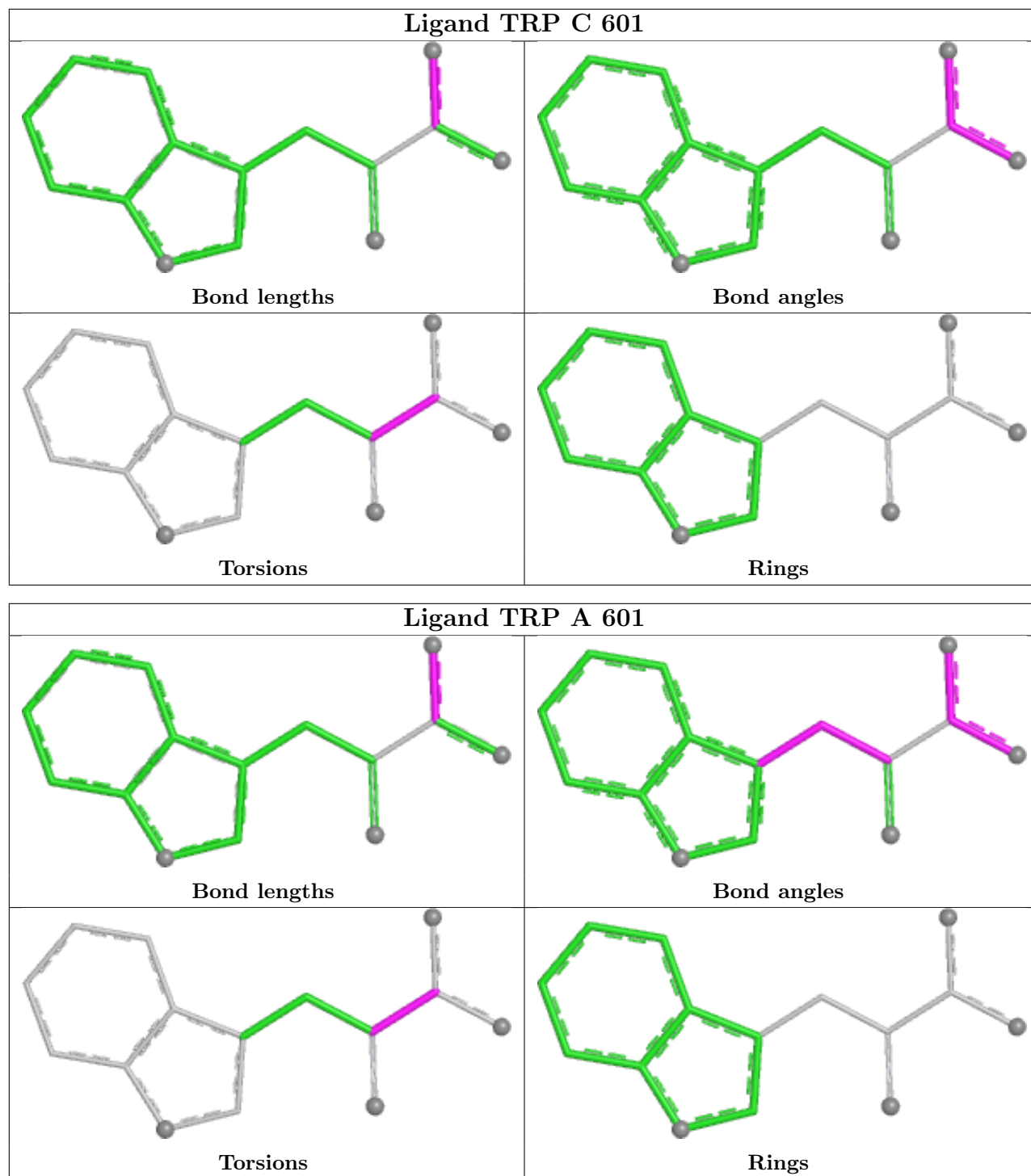
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 TRP D 601



Ligand TRP B 601





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	526/529 (99%)	0.03	12 (2%) 61 70	16, 27, 48, 65	1 (0%)
1	B	520/529 (98%)	0.22	17 (3%) 49 59	15, 31, 60, 87	1 (0%)
1	C	519/529 (98%)	0.27	5 (0%) 79 86	17, 33, 55, 76	1 (0%)
1	D	516/529 (97%)	0.55	17 (3%) 49 59	22, 39, 63, 82	1 (0%)
All	All	2081/2116 (98%)	0.27	51 (2%) 58 68	15, 33, 59, 87	4 (0%)

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	40	PRO	4.0
1	D	100	ILE	4.0
1	B	214	VAL	3.8
1	C	447	VAL	3.6
1	D	330	PHE	3.5
1	A	45	ILE	3.5
1	D	102	GLY	3.4
1	A	42	ILE	3.4
1	D	165	THR	3.1
1	B	190	VAL	3.1
1	B	330	PHE	2.9
1	B	189	ASN	2.8
1	B	134	THR	2.8
1	B	45	ILE	2.8
1	D	514	GLU	2.6
1	C	330	PHE	2.6
1	D	263	ASP	2.6
1	B	47	VAL	2.6
1	A	39	ALA	2.5
1	A	43	GLY	2.4
1	B	193	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	176	VAL	2.4
1	D	230	PHE	2.4
1	A	330	PHE	2.4
1	A	447	VAL	2.3
1	C	100	ILE	2.3
1	C	102	GLY	2.3
1	D	172	ASP	2.3
1	D	310	LEU	2.2
1	B	172	ASP	2.2
1	A	267	HIS	2.2
1	B	213	THR	2.2
1	B	199	GLN	2.2
1	A	266	ALA	2.2
1	D	75	ASN	2.2
1	B	195	GLY	2.2
1	B	382	LEU	2.2
1	D	101	ASP	2.1
1	B	182	ARG	2.1
1	B	216	GLY	2.1
1	B	513	VAL	2.1
1	D	266	ALA	2.1
1	D	269	VAL	2.1
1	B	198	GLN	2.1
1	C	321	GLU	2.0
1	D	328	VAL	2.0
1	D	520	LEU	2.0
1	D	329	ALA	2.0
1	A	2	ASP	2.0
1	A	248	ASP	2.0
1	A	44	ARG	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 ⓘ

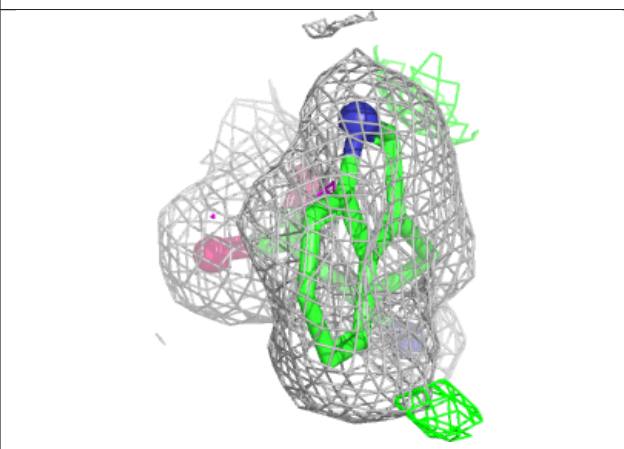
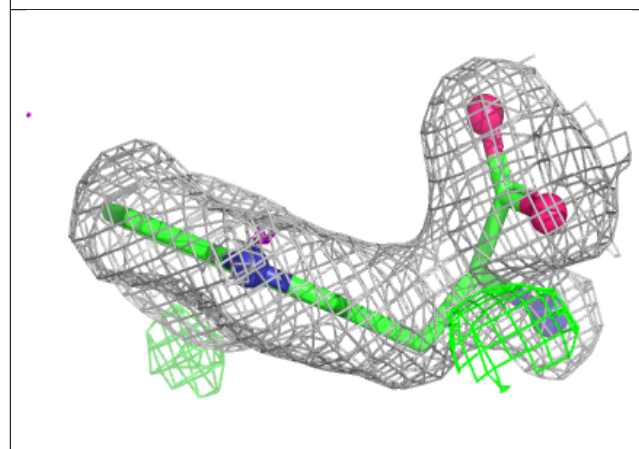
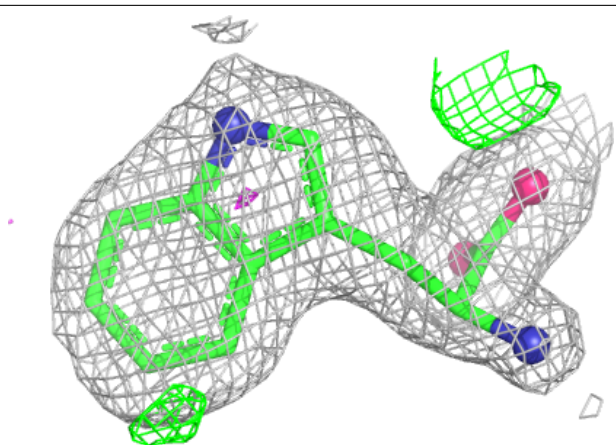
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	D	605	5/5	0.67	0.11	92,92,93,94	0
3	SO4	A	607	5/5	0.68	0.24	95,96,97,99	5
3	SO4	D	606	5/5	0.68	0.19	117,118,118,118	0
3	SO4	C	605	5/5	0.75	0.16	92,93,93,93	0
3	SO4	B	607	5/5	0.80	0.18	101,102,102,102	0
3	SO4	A	604	5/5	0.80	0.13	77,79,80,80	0
3	SO4	A	606	5/5	0.81	0.18	62,63,64,66	5
3	SO4	A	608	5/5	0.81	0.17	49,50,51,51	5
3	SO4	C	604	5/5	0.83	0.11	80,80,81,81	0
3	SO4	B	609	5/5	0.84	0.13	61,64,65,68	5
3	SO4	C	606	5/5	0.84	0.17	36,40,42,43	5
3	SO4	B	606	5/5	0.85	0.17	33,37,42,43	5
3	SO4	A	605	5/5	0.85	0.12	70,71,72,72	5
3	SO4	B	604	5/5	0.87	0.08	79,79,80,81	0
3	SO4	B	605	5/5	0.89	0.09	51,52,53,54	5
3	SO4	B	608	5/5	0.89	0.14	32,33,40,42	5
3	SO4	D	604	5/5	0.91	0.11	48,49,51,54	5
2	TRP	D	601	15/15	0.92	0.08	30,32,35,36	0
3	SO4	C	603	5/5	0.92	0.11	51,54,55,57	5
3	SO4	D	607	5/5	0.93	0.10	27,29,32,34	5
3	SO4	B	602	5/5	0.94	0.07	54,54,55,55	5
3	SO4	D	603	5/5	0.94	0.08	40,41,43,43	5
3	SO4	A	609	5/5	0.94	0.12	22,23,32,35	5
3	SO4	B	603	5/5	0.95	0.09	35,35,37,37	5
2	TRP	C	601	15/15	0.95	0.07	22,26,30,30	0
2	TRP	B	601	15/15	0.96	0.05	20,21,23,24	0
3	SO4	A	602	5/5	0.96	0.07	34,34,38,43	5
3	SO4	D	602	5/5	0.96	0.06	41,44,46,48	0
2	TRP	A	601	15/15	0.96	0.06	20,22,26,27	0
3	SO4	C	602	5/5	0.97	0.06	38,39,40,43	0
3	SO4	A	603	5/5	0.98	0.06	21,22,24,25	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.

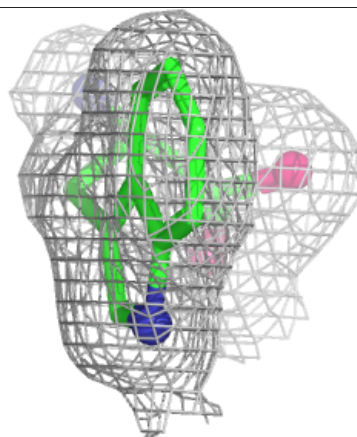
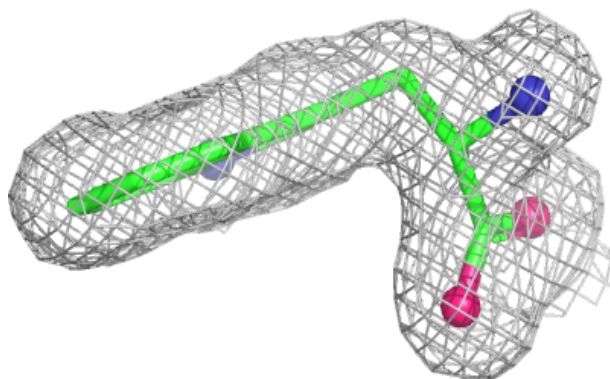
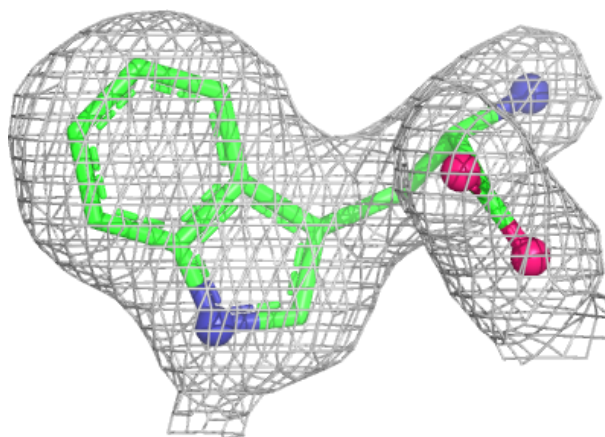
Electron density around TRP D 601:

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



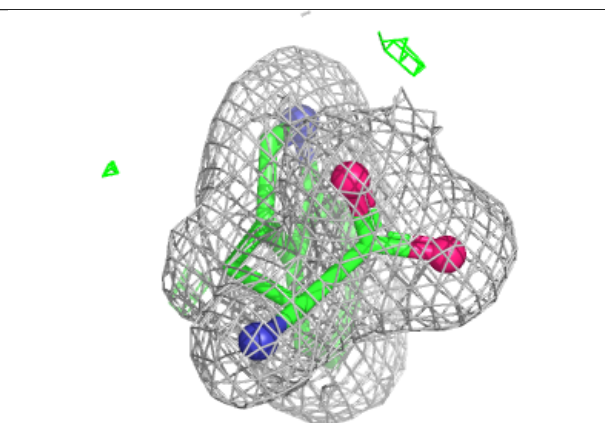
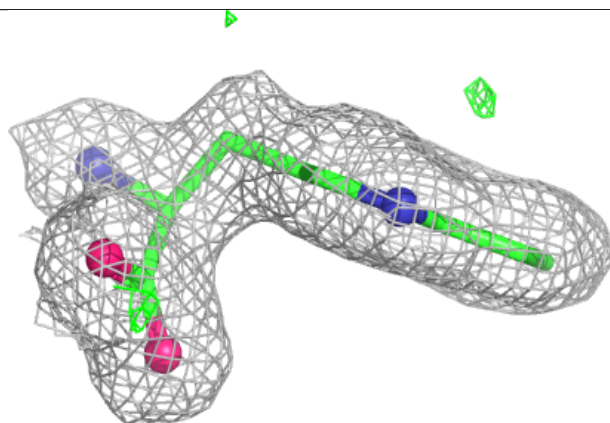
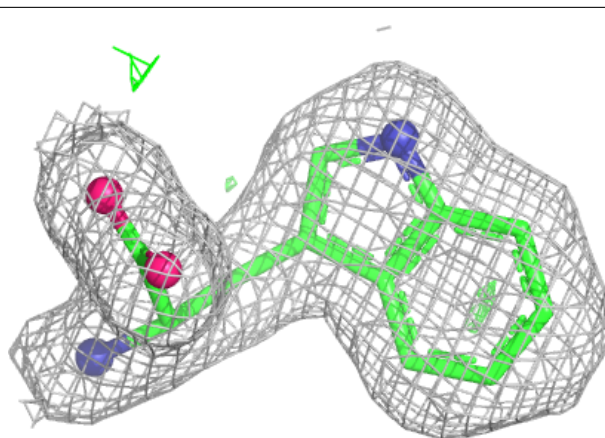
Electron density around TRP C 601:

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

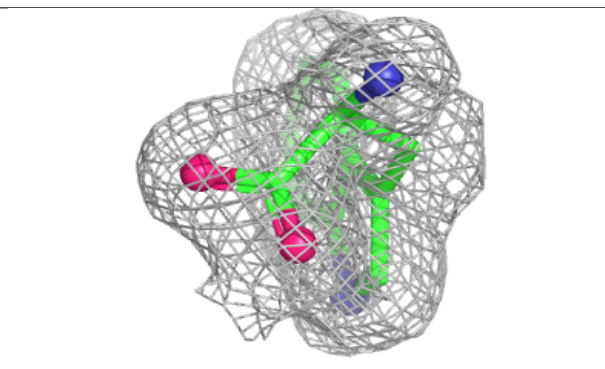
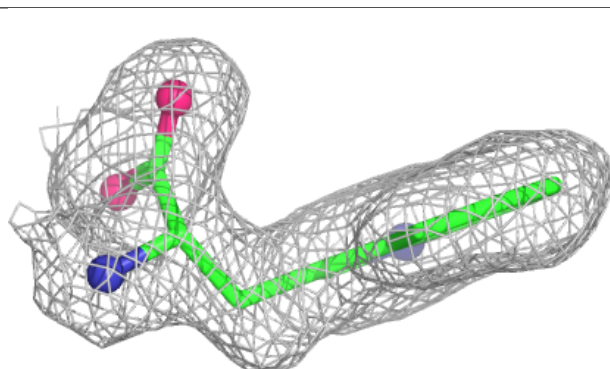
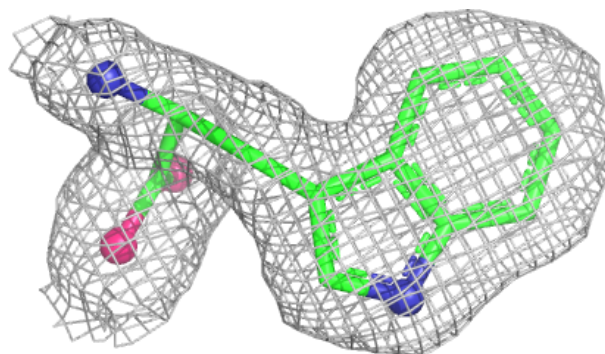


Electron density around TRP B 601:

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

**Electron density around TRP A 601:**

$2mF_o-DF_c$ (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.