Full wwPDB X-ray Structure Validation Report (i)

Jan 20, 2024 – 07:53 pm GMT

PDB ID	:	6ZRY
Title	:	6-dimethylallyl tryptophan synthase
Authors	:	Ostertag, E.; Stehle, T.; Zocher, G.
Deposited on	:	2020-07-15
Resolution	:	1.65 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 (i) 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 (i)) were used in the production of this report:

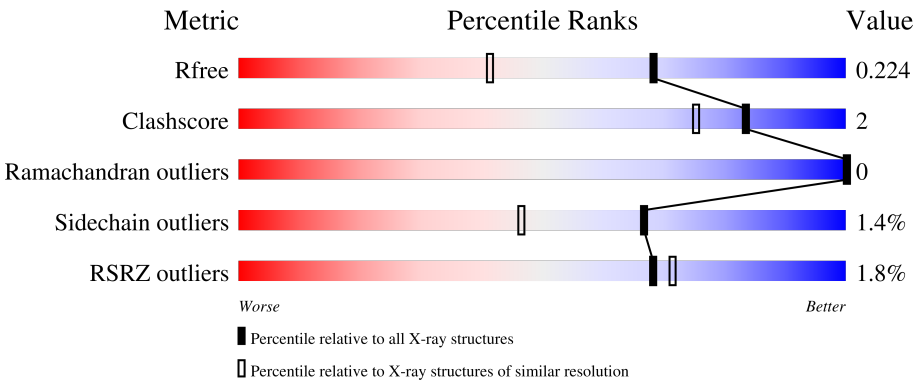
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

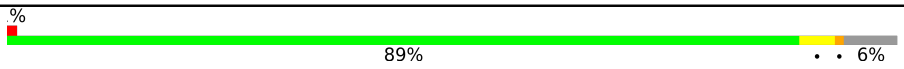
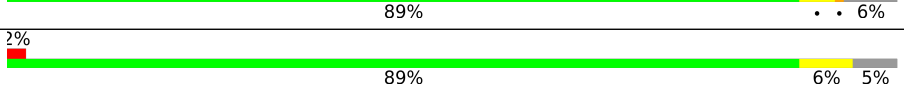
The reported resolution of this entry is 1.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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 <=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	AAA	373	
1	BBB	373	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6102 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 DMATS type aromatic prenyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	350	2717	1711	491	511	4	0	7	0
1	BBB	355	2720	1718	490	508	4	0	4	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	359	LEU	-	expression tag	UNP Q2MFY2
AAA	360	VAL	-	expression tag	UNP Q2MFY2
AAA	361	PRO	-	expression tag	UNP Q2MFY2
AAA	362	ARG	-	expression tag	UNP Q2MFY2
AAA	363	GLY	-	expression tag	UNP Q2MFY2
AAA	364	SER	-	expression tag	UNP Q2MFY2
AAA	365	SER	-	expression tag	UNP Q2MFY2
AAA	366	HIS	-	expression tag	UNP Q2MFY2
AAA	367	HIS	-	expression tag	UNP Q2MFY2
AAA	368	HIS	-	expression tag	UNP Q2MFY2
AAA	369	HIS	-	expression tag	UNP Q2MFY2
AAA	370	HIS	-	expression tag	UNP Q2MFY2
AAA	371	HIS	-	expression tag	UNP Q2MFY2
AAA	372	HIS	-	expression tag	UNP Q2MFY2
AAA	373	HIS	-	expression tag	UNP Q2MFY2
BBB	359	LEU	-	expression tag	UNP Q2MFY2
BBB	360	VAL	-	expression tag	UNP Q2MFY2
BBB	361	PRO	-	expression tag	UNP Q2MFY2
BBB	362	ARG	-	expression tag	UNP Q2MFY2
BBB	363	GLY	-	expression tag	UNP Q2MFY2
BBB	364	SER	-	expression tag	UNP Q2MFY2
BBB	365	SER	-	expression tag	UNP Q2MFY2
BBB	366	HIS	-	expression tag	UNP Q2MFY2
BBB	367	HIS	-	expression tag	UNP Q2MFY2
BBB	368	HIS	-	expression tag	UNP Q2MFY2

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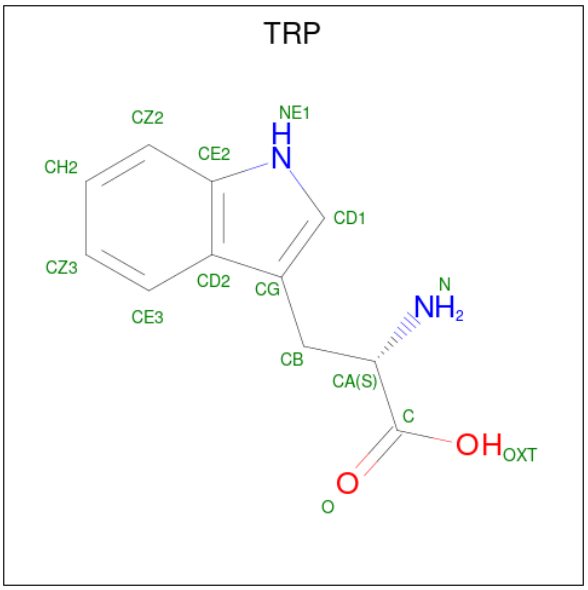
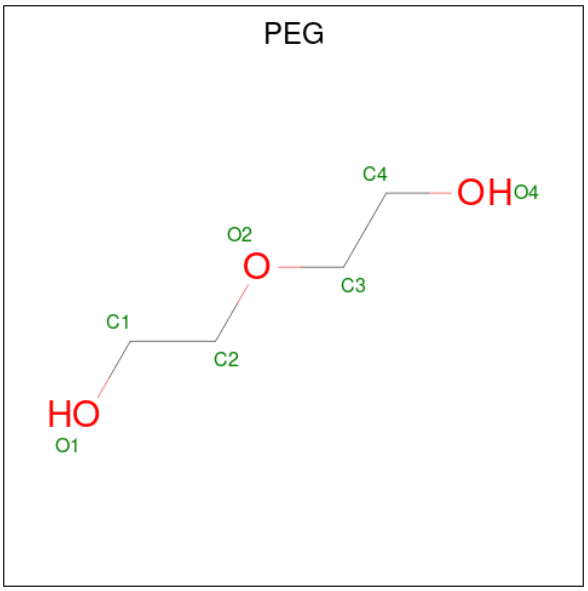
Chain	Residue	Modelled	Actual	Comment	Reference
BBB	369	HIS	-	expression tag	UNP Q2MFY2
BBB	370	HIS	-	expression tag	UNP Q2MFY2
BBB	371	HIS	-	expression tag	UNP Q2MFY2
BBB	372	HIS	-	expression tag	UNP Q2MFY2
BBB	373	HIS	-	expression tag	UNP Q2MFY2

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



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

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	AAA	1	6	4	2	0	0
			Total	C	O		
3	AAA	1	7	4	3	0	0
			Total	C	O		
3	AAA	1	7	4	3	0	0
			Total	C	O		
3	BBB	1	7	4	3	0	0
			Total	C	O		
3	BBB	1	7	4	3	0	0
			Total	C	O		
3	BBB	1	7	4	3	0	0
			Total	C	O		
3	BBB	1	7	4	3	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	BBB	1	1	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	AAA	296	296	296	0	0

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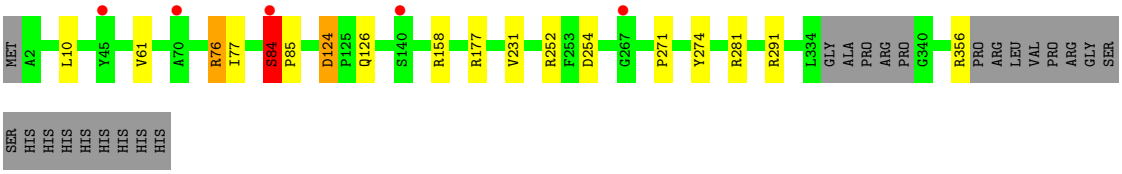
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	BBB	290	290	290	0	0

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.

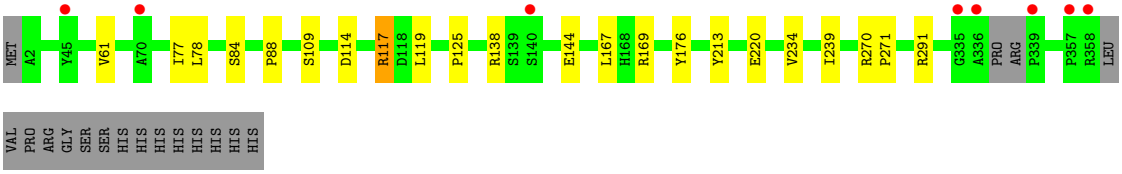
• Molecule 1: DMATS type aromatic prenyltransferase

Chain AAA:



• Molecule 1: DMATS type aromatic prenyltransferase

Chain BBB:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	53.35Å 85.68Å 74.54Å 90.00° 99.76° 90.00°	Depositor
Resolution (Å)	46.67 – 1.65 46.67 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.67-1.65) 99.8 (46.67-1.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.55 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.186 , 0.218 0.197 , 0.224	Depositor DCC
R_{free} test set	1580 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å^2)	21.2	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 43.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6102	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: CA, PEG

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	AAA	0.76	0/2780	0.80	0/3790
1	BBB	0.78	0/2794	0.79	0/3809
All	All	0.77	0/5574	0.79	0/7599

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AAA	0	1
1	BBB	0	2
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AAA	84	SER	Peptide
1	BBB	84	SER	Mainchain,Peptide

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	AAA	2717	0	2655	14	0
1	BBB	2720	0	2685	11	0
2	AAA	15	0	9	1	0
2	BBB	15	0	9	0	0
3	AAA	20	0	27	1	0
3	BBB	28	0	40	2	0
4	BBB	1	0	0	0	0
5	AAA	296	0	0	4	0
5	BBB	290	0	0	0	0
All	All	6102	0	5425	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 2.

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)
1:AAA:84:SER:HB3	1:AAA:85:PRO:HD3	1.75	0.69
1:AAA:76[B]:ARG:CZ	1:AAA:76[B]:ARG:HB2	2.23	0.68
1:AAA:84:SER:HA	5:AAA:865:HOH:O	1.95	0.65
1:AAA:10:LEU:HD13	1:AAA:61[A]:VAL:HG21	1.80	0.63
1:BBB:167:LEU:HD13	1:BBB:176:TYR:HB2	1.84	0.58
2:AAA:601:TRP:CZ2	3:AAA:604:PEG:H12	2.39	0.58
1:BBB:88:PRO:HB2	1:BBB:125:PRO:HG2	1.86	0.57
1:BBB:270:ARG:HB2	1:BBB:271:PRO:HD2	1.89	0.54
1:BBB:114:ASP:OD1	1:BBB:117:ARG:NH2	2.42	0.52
1:BBB:234:VAL:CG1	1:BBB:239:ILE:HD11	2.40	0.52
1:BBB:270:ARG:CZ	1:BBB:270:ARG:HB3	2.41	0.51
1:AAA:61[B]:VAL:HG13	1:AAA:77:ILE:HG23	1.92	0.51
1:BBB:61:VAL:HG13	1:BBB:77:ILE:HG23	1.94	0.48
1:BBB:78:LEU:HB2	3:BBB:506:PEG:H31	1.95	0.48
1:AAA:281:ARG:O	1:AAA:356:ARG:NH2	2.48	0.47
1:AAA:10:LEU:HD13	1:AAA:61[A]:VAL:CG2	2.45	0.47
1:AAA:177[A]:ARG:HG3	5:AAA:824:HOH:O	2.15	0.46
1:BBB:138:ARG:NH1	1:BBB:144:GLU:OE1	2.48	0.46
1:AAA:231:VAL:HG22	1:AAA:271:PRO:HB2	1.97	0.46
1:AAA:124:ASP:HB2	5:AAA:816:HOH:O	2.16	0.46
1:AAA:124:ASP:O	1:AAA:126:GLN:NE2	2.41	0.45
1:AAA:252:ARG:NH2	1:AAA:254:ASP:OD1	2.50	0.45
1:AAA:231:VAL:HG21	1:AAA:274:TYR:HB2	1.99	0.44
1:BBB:119:LEU:HD21	1:BBB:169:ARG:NH2	2.33	0.44
1:AAA:158:ARG:HG3	5:AAA:916:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:213:TYR:CE2	3:BBB:506:PEG:H11	2.56	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	AAA	353/373 (95%)	344 (98%)	9 (2%)	0	100	100
1	BBB	355/373 (95%)	349 (98%)	6 (2%)	0	100	100
All	All	708/746 (95%)	693 (98%)	15 (2%)	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	AAA	283/300 (94%)	278 (98%)	5 (2%)	59	36
1	BBB	285/300 (95%)	281 (99%)	4 (1%)	67	46
All	All	568/600 (95%)	559 (98%)	9 (2%)	67	41

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	76[A]	ARG
1	AAA	76[B]	ARG
1	AAA	84	SER
1	AAA	124	ASP
1	AAA	291	ARG
1	BBB	109	SER
1	BBB	117	ARG
1	BBB	220	GLU
1	BBB	291	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	$\#\|Z\| > 2$
2	TRP	AAA	601	-	14,16,16	0.72	0	16,22,22	1.05	2 (12%)
3	PEG	BBB	504	-	6,6,6	0.15	0	5,5,5	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	PEG	AAA	602	-	5,5,6	0.16	0	4,4,5	0.21	0
3	PEG	AAA	603	-	6,6,6	0.16	0	5,5,5	0.11	0
3	PEG	BBB	506	-	6,6,6	0.27	0	5,5,5	0.18	0
3	PEG	AAA	604	-	6,6,6	0.19	0	5,5,5	0.16	0
3	PEG	BBB	501	-	6,6,6	0.13	0	5,5,5	0.12	0
3	PEG	BBB	505	-	6,6,6	0.13	0	5,5,5	0.19	0
2	TRP	BBB	502	-	14,16,16	0.70	0	16,22,22	1.06	2 (12%)

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	AAA	601	-	-	0/7/8/8	0/2/2/2
3	PEG	BBB	504	-	-	2/4/4/4	-
3	PEG	AAA	602	-	-	1/3/3/4	-
3	PEG	AAA	603	-	-	2/4/4/4	-
3	PEG	BBB	506	-	-	4/4/4/4	-
3	PEG	AAA	604	-	-	2/4/4/4	-
3	PEG	BBB	501	-	-	2/4/4/4	-
3	PEG	BBB	505	-	-	3/4/4/4	-
2	TRP	BBB	502	-	-	0/7/8/8	0/2/2/2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	BBB	502	TRP	OXT-C-CA	2.20	120.87	113.38
2	AAA	601	TRP	OXT-C-CA	2.14	120.68	113.38
2	AAA	601	TRP	CH2-CZ2-CE2	-2.04	117.15	120.08
2	BBB	502	TRP	OXT-C-O	-2.01	119.52	124.09

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	BBB	501	PEG	O1-C1-C2-O2
3	AAA	604	PEG	O2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
3	BBB	501	PEG	O2-C3-C4-O4
3	BBB	506	PEG	O2-C3-C4-O4
3	AAA	603	PEG	O1-C1-C2-O2
3	BBB	505	PEG	O1-C1-C2-O2
3	BBB	505	PEG	O2-C3-C4-O4
3	AAA	602	PEG	O2-C3-C4-O4
3	BBB	506	PEG	C1-C2-O2-C3
3	BBB	505	PEG	C4-C3-O2-C2
3	AAA	603	PEG	C1-C2-O2-C3
3	AAA	604	PEG	C4-C3-O2-C2
3	BBB	506	PEG	O1-C1-C2-O2
3	BBB	506	PEG	C4-C3-O2-C2
3	BBB	504	PEG	O1-C1-C2-O2
3	BBB	504	PEG	C1-C2-O2-C3

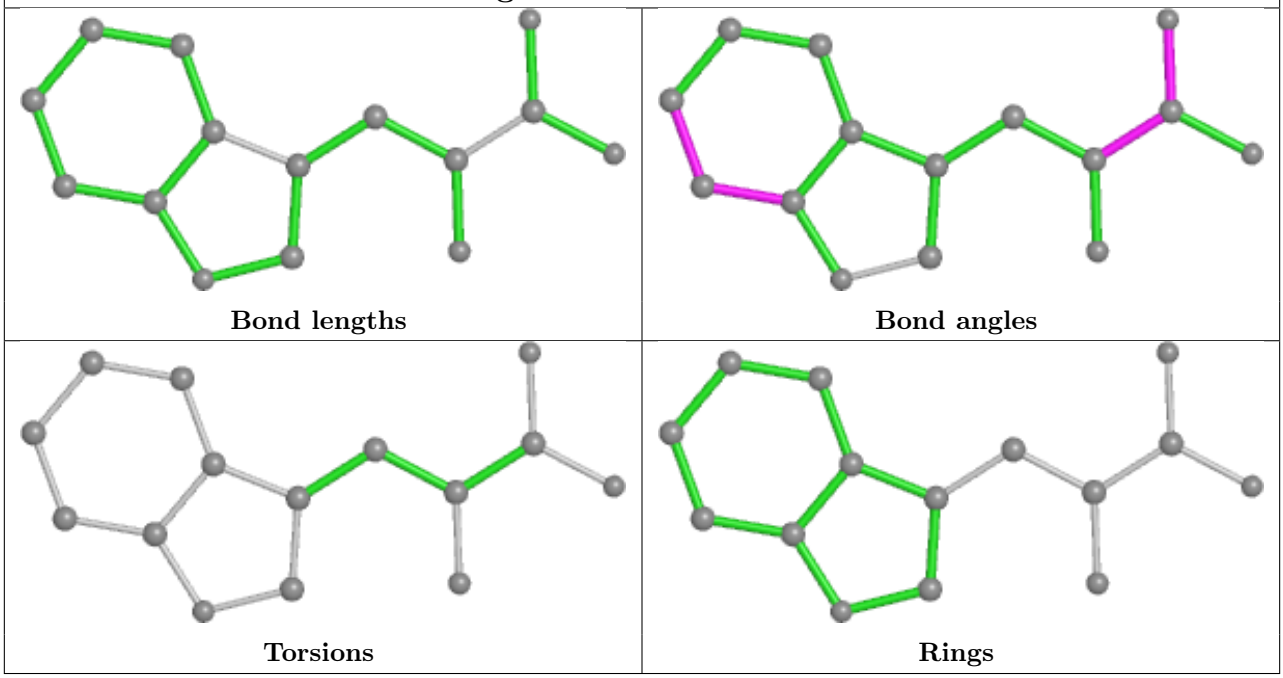
There are no ring outliers.

3 monomers are involved in 3 short contacts:

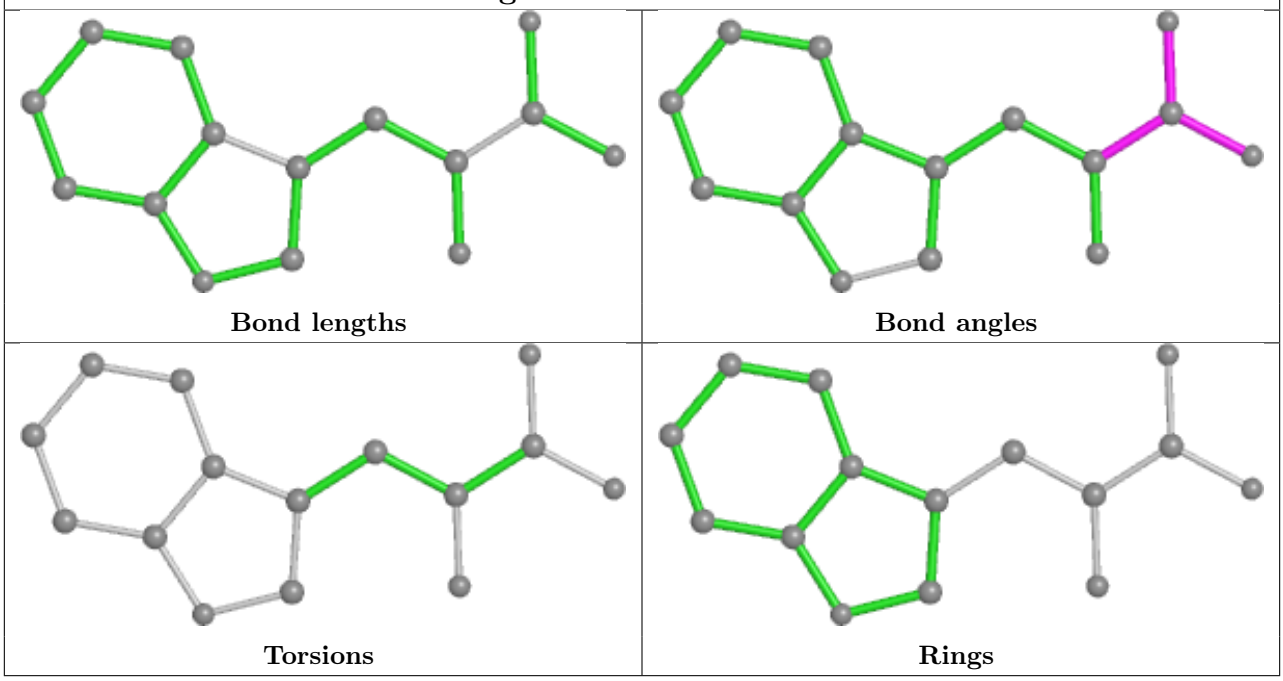
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	601	TRP	1	0
3	BBB	506	PEG	2	0
3	AAA	604	PEG	1	0

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 then 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 AAA 601



Ligand TRP BBB 502



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 (i)

6.1 Protein, DNA and RNA chains (i)

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	AAA	350/373 (93%)	-0.11	5 (1%)	75	79	14, 23, 39, 52	0
1	BBB	355/373 (95%)	-0.01	8 (2%)	60	61	13, 23, 42, 68	0
All	All	705/746 (94%)	-0.06	13 (1%)	68	71	13, 23, 40, 68	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	339	PRO	6.0
1	AAA	84	SER	5.1
1	BBB	70	ALA	3.9
1	BBB	335	GLY	3.8
1	BBB	45	TYR	3.6
1	AAA	70	ALA	3.2
1	BBB	336	ALA	3.2
1	BBB	357	PRO	3.0
1	AAA	45	TYR	2.9
1	AAA	140	SER	2.8
1	BBB	140	SER	2.7
1	AAA	267	GLY	2.5
1	BBB	358	ARG	2.2

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 monosaccharides in this entry.

6.4 Ligands (i)

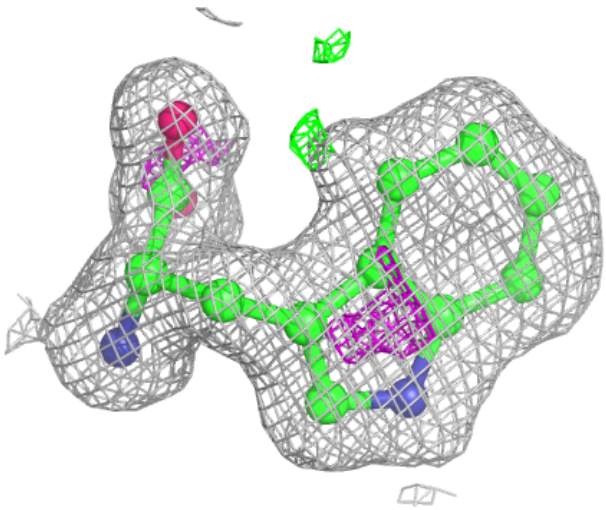
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

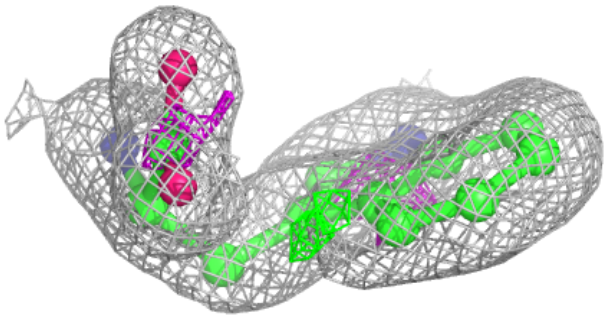
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	PEG	AAA	604	7/7	0.78	0.16	38,42,43,45	0
3	PEG	AAA	603	7/7	0.85	0.15	50,51,52,52	0
2	TRP	AAA	601	15/15	0.85	0.12	20,23,23,24	0
3	PEG	BBB	506	7/7	0.85	0.14	36,38,39,41	0
3	PEG	BBB	501	7/7	0.86	0.11	46,47,48,50	0
3	PEG	AAA	602	6/7	0.86	0.13	40,40,42,45	0
3	PEG	BBB	505	7/7	0.87	0.28	36,37,42,44	0
3	PEG	BBB	504	7/7	0.89	0.11	50,52,52,53	0
2	TRP	BBB	502	15/15	0.90	0.09	21,22,23,23	0
4	CA	BBB	503	1/1	0.96	0.09	30,30,30,30	0

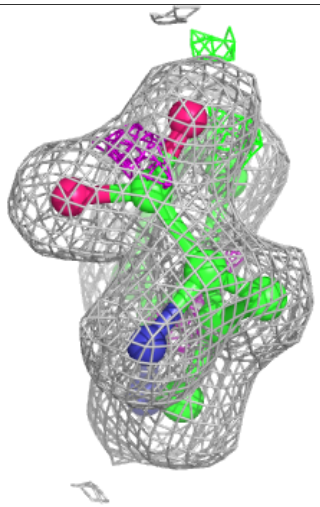
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TRP AAA 601:

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

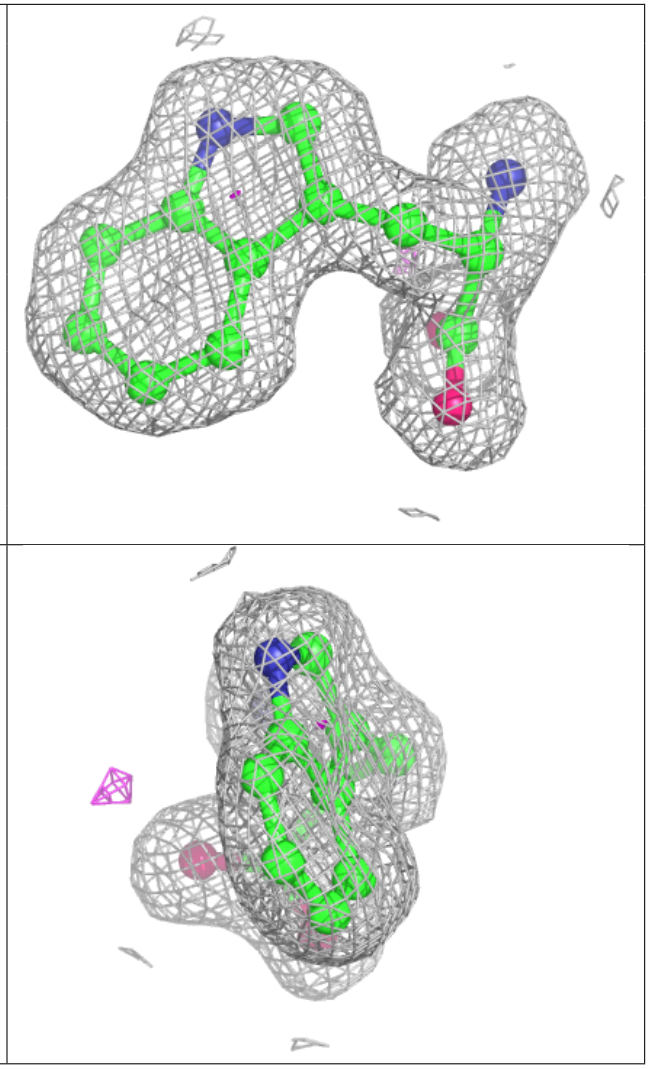






Electron density around TRP BBB 502:

$2mF_o$-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.