



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:10 AM UTC

PDB ID : 7YS6 / pdb_00007ys6
EMDB ID : EMD-34073
Title : Cryo-EM structure of the Serotonin 6 (5-HT6) receptor-DNGs-scFv16 complex
Authors : Zhao, Q.Y.; Wang, Y.F.; He, L.; Wang, S.; Cong, Y.
Deposited on : 2022-08-11
Resolution : 3.00 Å(reported)

This is a wwPDB EM Validation Summary 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

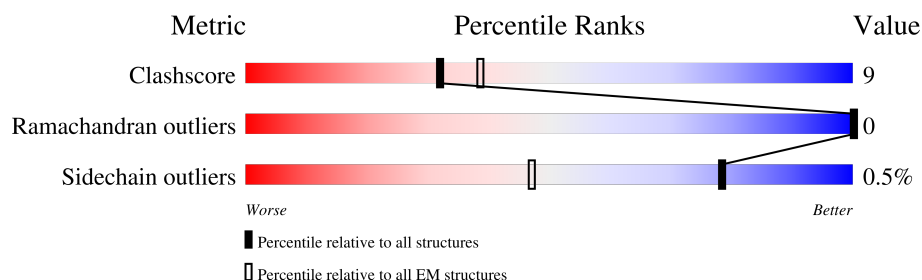
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	304	73% 14% • 12%
2	C	357	84% 11% 5%
3	D	71	75% 6% 20%
4	E	266	76% 12% 12%
5	B	373	52% 10% • 38%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8794 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 5-hydroxytryptamine receptor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	269	Total	C	N	O	S	0	0
			2037	1348	338	331	20		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	SER	deletion	UNP P50406
A	?	-	GLN	deletion	UNP P50406
A	?	-	ALA	deletion	UNP P50406
A	?	-	SER	deletion	UNP P50406
A	?	-	GLU	deletion	UNP P50406
A	?	-	THR	deletion	UNP P50406
A	?	-	LEU	deletion	UNP P50406
A	?	-	GLN	deletion	UNP P50406
A	?	-	VAL	deletion	UNP P50406
A	?	-	PRO	deletion	UNP P50406
A	?	-	ARG	deletion	UNP P50406
A	?	-	THR	deletion	UNP P50406
A	?	-	PRO	deletion	UNP P50406
A	?	-	ARG	deletion	UNP P50406
A	?	-	PRO	deletion	UNP P50406
A	?	-	GLY	deletion	UNP P50406
A	?	-	VAL	deletion	UNP P50406
A	?	-	GLU	deletion	UNP P50406

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	338	Total	C	N	O	S	0	0
			2601	1604	467	509	21		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	MET	-	initiating methionine	UNP P62873
C	2	HIS	-	expression tag	UNP P62873
C	3	HIS	-	expression tag	UNP P62873
C	4	HIS	-	expression tag	UNP P62873
C	5	HIS	-	expression tag	UNP P62873
C	6	HIS	-	expression tag	UNP P62873
C	7	HIS	-	expression tag	UNP P62873
C	8	GLU	-	expression tag	UNP P62873
C	9	ASN	-	expression tag	UNP P62873
C	10	LEU	-	expression tag	UNP P62873
C	11	TYR	-	expression tag	UNP P62873
C	12	PHE	-	expression tag	UNP P62873
C	13	GLN	-	expression tag	UNP P62873
C	14	GLY	-	expression tag	UNP P62873
C	15	GLY	-	expression tag	UNP P62873
C	16	SER	-	expression tag	UNP P62873
C	17	SER	-	expression tag	UNP P62873
C	18	GLY	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	57	Total	C	N	O	S	0	0
			436	273	77	83	3		

- Molecule 4 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	233	Total	C	N	O	S	0	0
			1787	1133	296	348	10		

- Molecule 5 is a protein called Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	232	Total	C	N	O	S	0	0
			1920	1216	347	349	8		

There are 18 discrepancies between the modelled and reference sequences:

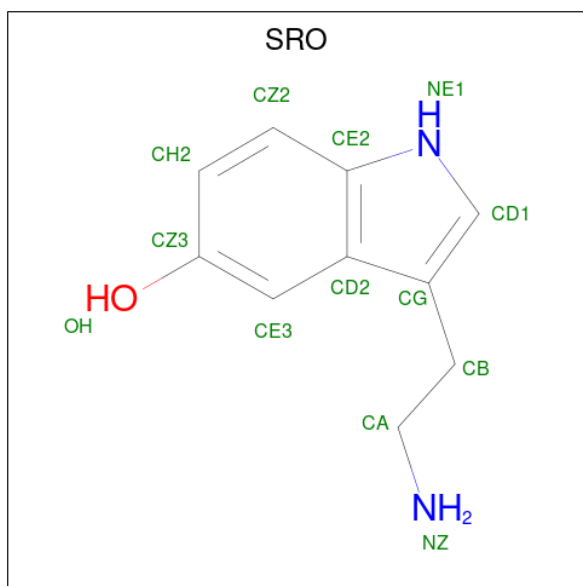
Chain	Residue	Modelled	Actual	Comment	Reference
B	8	MET	-	initiating methionine	UNP P63092-2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	9	GLY	-	expression tag	UNP P63092-2
B	10	CYS	-	expression tag	UNP P63092-2
B	11	THR	-	expression tag	UNP P63092-2
B	12	LEU	-	expression tag	UNP P63092-2
B	13	SER	-	expression tag	UNP P63092-2
B	14	ALA	-	expression tag	UNP P63092-2
B	15	GLU	-	expression tag	UNP P63092-2
B	16	ASP	-	expression tag	UNP P63092-2
B	17	LYS	-	expression tag	UNP P63092-2
B	18	ALA	-	expression tag	UNP P63092-2
B	19	ALA	-	expression tag	UNP P63092-2
B	20	VAL	-	expression tag	UNP P63092-2
B	21	GLU	-	expression tag	UNP P63092-2
B	22	ARG	-	expression tag	UNP P63092-2
B	23	SER	-	expression tag	UNP P63092-2
B	24	LYS	-	expression tag	UNP P63092-2
B	25	MET	-	expression tag	UNP P63092-2

- Molecule 6 is SEROTONIN (CCD ID: SRO) (formula: $C_{10}H_{12}N_2O$) (labeled as "Ligand of Interest" by depositor).

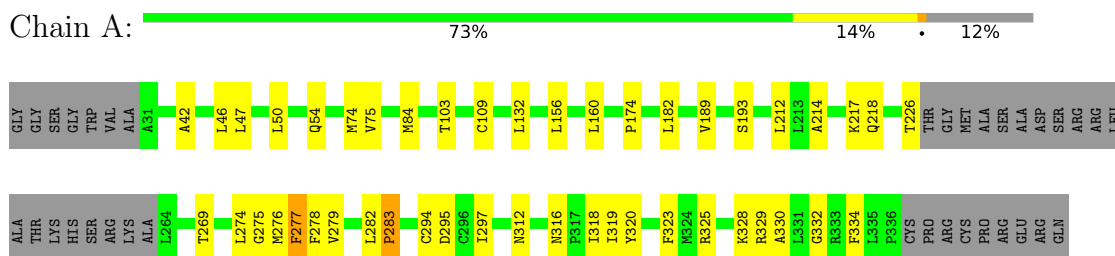


Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			13	10	2	1	

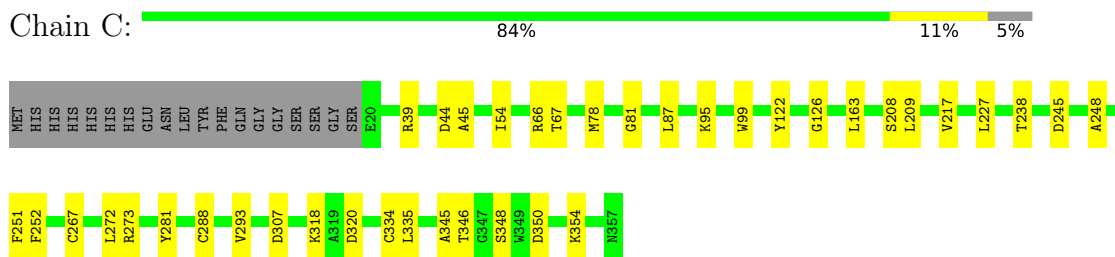
3 Residue-property plots

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. 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. 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.

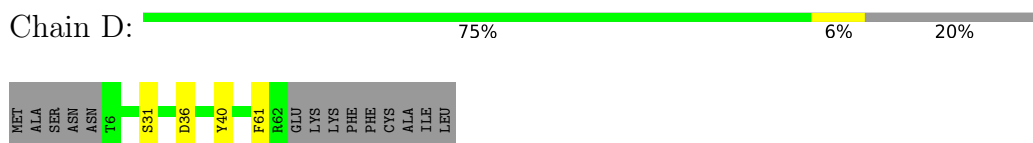
- Molecule 1: 5-hydroxytryptamine receptor 6



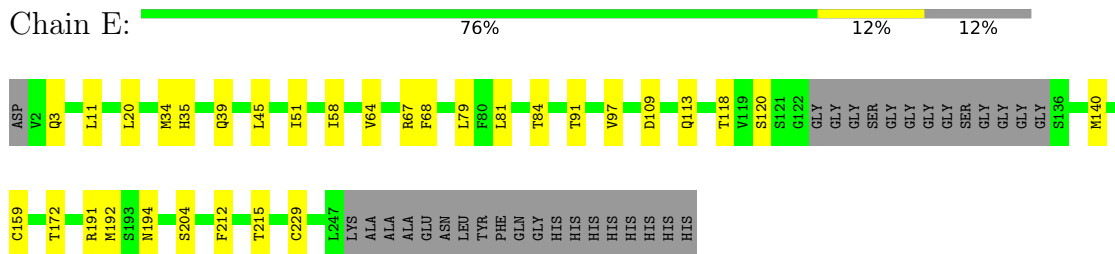
- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

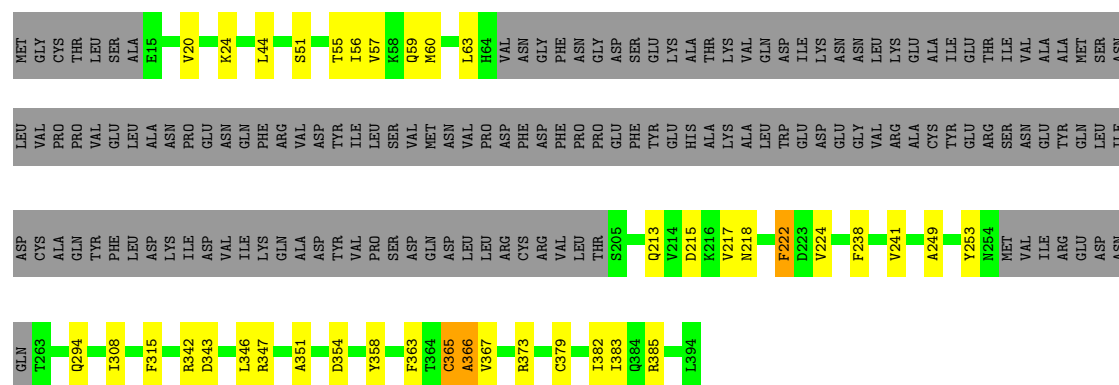


- Molecule 4: scFv16



- Molecule 5: Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

Device Type	Percentage
Smartphones	52%
Tablets	10%
Other mobile devices	38%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	388504	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.2	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

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: SRO

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	0.56	1/2087 (0.0%)	0.83	6/2851 (0.2%)
2	C	0.33	2/2648 (0.1%)	0.59	0/3589
3	D	0.46	1/442 (0.2%)	0.60	0/597
4	E	0.33	1/1831 (0.1%)	0.58	2/2482 (0.1%)
5	B	0.50	1/1957 (0.1%)	0.71	4/2630 (0.2%)
All	All	0.44	6/8965 (0.1%)	0.68	12/12149 (0.1%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	40	TYR	CA-C	-6.63	1.44	1.52
5	B	363	PHE	CA-C	-6.60	1.46	1.53
1	A	320	TYR	N-CA	6.37	1.52	1.46
2	C	245	ASP	CA-C	-5.62	1.45	1.53
2	C	252	PHE	CA-C	-5.48	1.46	1.53

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	365	CYS	N-CA-C	-6.98	98.81	109.41
5	B	222	PHE	N-CA-C	6.42	118.91	107.80
4	E	191	ARG	CA-C-N	5.99	132.97	121.54
4	E	191	ARG	C-N-CA	5.99	132.97	121.54
1	A	312	ASN	N-CA-C	-5.54	104.87	111.69

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	2037	0	2121	46	0
2	C	2601	0	2505	37	0
3	D	436	0	448	3	0
4	E	1787	0	1722	18	0
5	B	1920	0	1912	52	0
6	A	13	0	11	0	0
All	All	8794	0	8719	150	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 9.

The worst 5 of 150 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)
5:B:253:TYR:CZ	5:B:308:ILE:HG21	1.27	1.66
2:C:208:SER:C	2:C:251:PHE:HE2	1.10	1.49
2:C:208:SER:O	2:C:251:PHE:CE2	1.63	1.49
5:B:253:TYR:CZ	5:B:308:ILE:CG2	2.04	1.39
2:C:208:SER:C	2:C:251:PHE:CE2	2.02	1.31

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	265/304 (87%)	252 (95%)	13 (5%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	336/357 (94%)	325 (97%)	11 (3%)	0	100	100
3	D	55/71 (78%)	53 (96%)	2 (4%)	0	100	100
4	E	229/266 (86%)	218 (95%)	11 (5%)	0	100	100
5	B	226/373 (61%)	220 (97%)	6 (3%)	0	100	100
All	All	1111/1371 (81%)	1068 (96%)	43 (4%)	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 PDB entries followed by that with respect to all EM entries.

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	216/250 (86%)	213 (99%)	3 (1%)	59	80
2	C	281/297 (95%)	280 (100%)	1 (0%)	84	90
3	D	46/58 (79%)	46 (100%)	0	100	100
4	E	197/215 (92%)	197 (100%)	0	100	100
5	B	208/334 (62%)	207 (100%)	1 (0%)	81	89
All	All	948/1154 (82%)	943 (100%)	5 (0%)	78	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	212	LEU
1	A	283	PRO
1	A	297	ILE
2	C	163	LEU
5	B	224	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
5	B	29	GLN
5	B	59	GLN
4	E	13	GLN
4	E	39	GLN
4	E	142	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
6	SRO	A	401	-	14,14,14	0.56	0	19,19,19	0.56	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
6	SRO	A	401	-	-	0/3/3/3	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

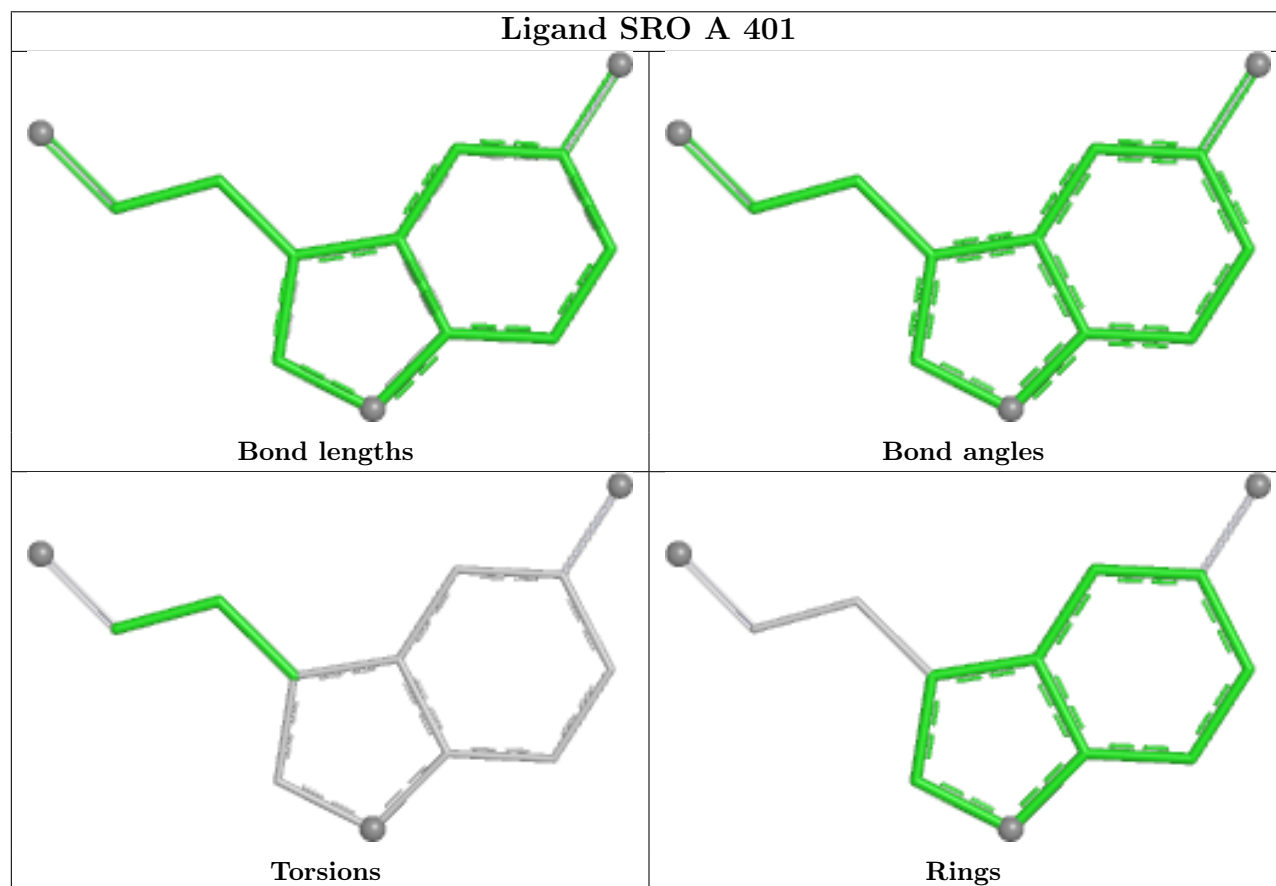
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-34073. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.