



## wwPDB EM Validation Summary Report ⓘ

Jun 27, 2024 – 10:07 PM JST

PDB ID : 8YUV  
EMDB ID : EMD-39584  
Title : Cryo-EM structure of the immepip-bound H3R-Gi complex  
Authors : Shen, Q.; Tang, X.; Wen, X.; Cheng, S.; Xiao, P.; Zang, S.; Shen, D.; Jiang, L.; Zheng, Y.; Zhang, H.; Xu, H.; Mao, C.; Zhang, M.; Hu, W.; Sun, J.; Chen, Z.; Zhang, Y.  
Deposited on : 2024-03-27  
Resolution : 3.00 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

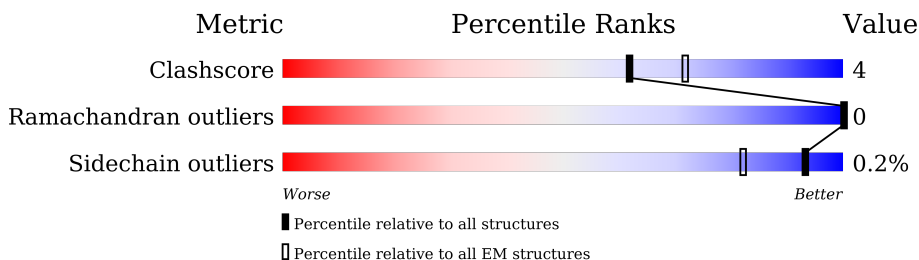
# 1 Overall quality at a glance i

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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	354	
2	B	358	
3	G	71	
4	S	269	
5	R	461	

## 2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 9102 atoms, of which 61 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 Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	225	1811	1150	301	346	14	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ASN	SER	conflict	UNP P63096
A	203	ALA	GLY	conflict	UNP P63096
A	245	ALA	GLU	conflict	UNP P63096
A	326	SER	ALA	conflict	UNP P63096

- 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
			Total	C	N	O	S		
2	B	339	2607	1607	468	511	21	0	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	MET	-	initiating methionine	UNP P62873
B	-16	HIS	-	expression tag	UNP P62873
B	-15	HIS	-	expression tag	UNP P62873
B	-14	HIS	-	expression tag	UNP P62873
B	-13	HIS	-	expression tag	UNP P62873
B	-12	HIS	-	expression tag	UNP P62873
B	-11	HIS	-	expression tag	UNP P62873
B	-10	LEU	-	expression tag	UNP P62873
B	-9	GLU	-	expression tag	UNP P62873
B	-8	VAL	-	expression tag	UNP P62873
B	-7	LEU	-	expression tag	UNP P62873
B	-6	PHE	-	expression tag	UNP P62873

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	GLN	-	expression tag	UNP P62873
B	-4	GLY	-	expression tag	UNP P62873
B	-3	PRO	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	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
			Total	C	N	O	S		
3	G	58	444	277	79	85	3	0	0

- Molecule 4 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	S	234	1795	1137	297	351	10	0	0

- Molecule 5 is a protein called Histamine H3 receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	R	289	2344	1559	389	384	12	0	0

There are 16 discrepancies between the modelled and reference sequences:

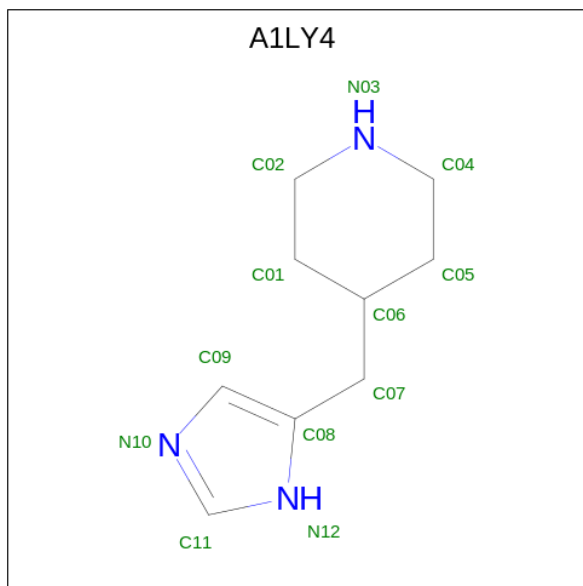
Chain	Residue	Modelled	Actual	Comment	Reference
R	-15	ASP	-	expression tag	UNP Q9Y5N1
R	-14	TYR	-	expression tag	UNP Q9Y5N1
R	-13	LYS	-	expression tag	UNP Q9Y5N1
R	-12	ASP	-	expression tag	UNP Q9Y5N1
R	-11	ASP	-	expression tag	UNP Q9Y5N1
R	-10	ASP	-	expression tag	UNP Q9Y5N1
R	-9	ASP	-	expression tag	UNP Q9Y5N1
R	-8	LYS	-	expression tag	UNP Q9Y5N1
R	-7	LEU	-	expression tag	UNP Q9Y5N1
R	-6	GLU	-	expression tag	UNP Q9Y5N1
R	-5	VAL	-	expression tag	UNP Q9Y5N1
R	-4	LEU	-	expression tag	UNP Q9Y5N1

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-3	PHE	-	expression tag	UNP Q9Y5N1
R	-2	GLN	-	expression tag	UNP Q9Y5N1
R	-1	GLY	-	expression tag	UNP Q9Y5N1
R	0	PRO	-	expression tag	UNP Q9Y5N1

- Molecule 6 is 4-(1H-imidazol-5-ylmethyl)piperidine (three-letter code: A1LY4) (formula:  $C_9H_{15}N_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	H	N	
6	R	1	27	9	15	3	0

- Molecule 7 is CHOLESTEROL (three-letter code: CLR) (formula:  $C_{27}H_{46}O$ ).

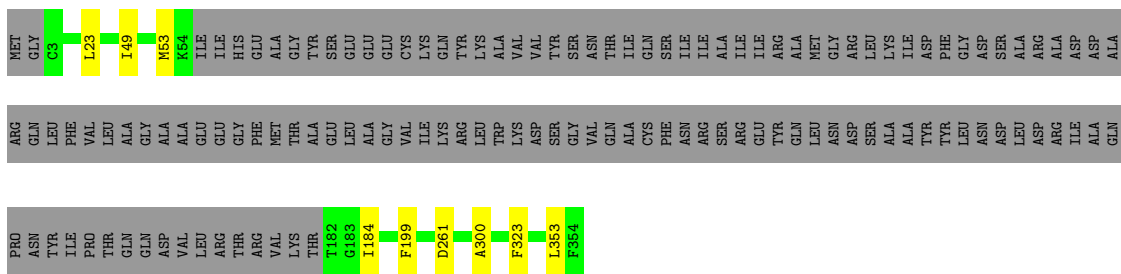


Mol	Chain	Residues	Atoms				AltConf
			Total	C	H	O	
7	R	1	74	27	46	1	0

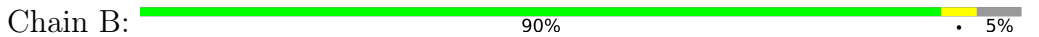
### 3 Residue-property plots

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.

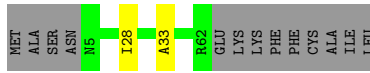
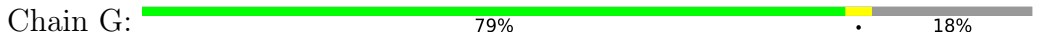
- Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1



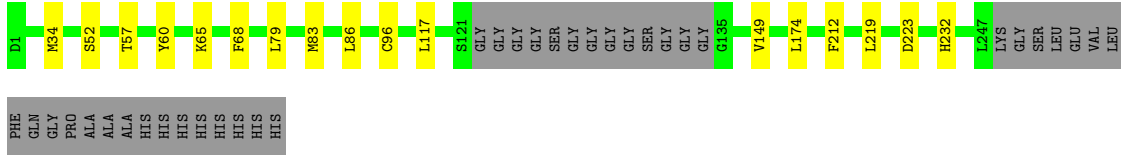
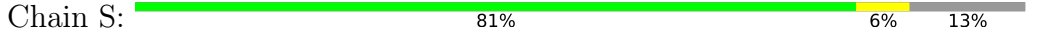
- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



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



- Molecule 4: scFv16



- Molecule 5: Histamine H3 receptor



HIS	SER	MET	ASP
SER	ALA	PRO	TYR
ALA	SER	LEU	LYS
LEU	SER	LEU	ASP
GLU	HIS	ARG	ASP
LYS	TYR	GLY	ASP
ARG	GLY	VAL	LEU
MET	VAL	GLY	GLU
LYS	MET	GLU	VAL
VAL	SER	ALA	LEU
GLN	SER	VAL	PHE
S3943	GLN	GLY	GLN
Q3946	ALA	ALA	GLY
L3960	ALA	ALA	PRO
T3963	GLY	GLU	MET
W3971	LEU	THR	GLU
Y3992	GLY	LEU	GLY
K3993	GLY	GLY	ASP
F3998	GLY	GLY	GLY
L401	GLY	GLY	LEU
M404	SER	SER	ALA
S405	VAL	VAL	ALA
A406	ALA	ALA	LEU
V407	SER	PRO	ALA
M408	THR	THR	GLY
P409	SER	PRO	ALA
V410	SER	SER	ALA
L411	SER	SER	ALA
Y412	GLY	GLU	ALA
P413	SER	ALA	ALA
L414	SER	SER	GLY
S418	SER	ARG	ALA
R421	GLY	PRO	GLY
A422	THR	THR	ARG
F423	GLU	THR	PHE
T424	ARG	ARG	SER
K425	PRO	PRO	SER
L426	SER	PRO	ALA
L427	SER	GLY	ALA
CYS	LEU	TRP	A32
PRO	LYS	GLY	L37
GLN	ARG	CYS	L44
LYS	THR	TRP	M56
GLN	GLY	GLN	L57
LYS	SER	LYS	A58
LEU	LYS	GLY	L65
LYS	PRO	HIS	Q68
ILE	SER	GLY	
GLN	ALA	GLU	
PRO	SER	SER	



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	330449	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	62	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k 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: A1LY4, CLR

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	0.90	0/1841	0.66	0/2471
2	B	0.83	0/2654	0.78	0/3597
3	G	0.80	0/450	0.65	0/608
4	S	0.64	0/1839	0.67	0/2493
5	R	0.81	0/2414	0.74	0/3292
All	All	0.80	0/9198	0.72	0/12461

There are no bond length outliers.

There are no bond angle outliers.

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	1811	0	1799	6	0
2	B	2607	0	2510	11	0
3	G	444	0	454	1	0
4	S	1795	0	1727	24	0
5	R	2344	0	2367	40	0
6	R	12	15	0	4	0
7	R	28	46	46	2	0
All	All	9041	61	8903	80	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 4.

The worst 5 of 80 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)
2:B:254:ASP:HB2	2:B:261:LEU:HD11	1.35	1.05
5:R:119:THR:HG23	5:R:206:GLU:HG3	1.36	1.05
2:B:254:ASP:HB2	2:B:261:LEU:CD1	1.99	0.92
4:S:68:PHE:CZ	4:S:83:MET:HE2	2.07	0.89
5:R:412:TYR:HB2	5:R:413:PRO:HD3	1.54	0.88

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 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	221/354 (62%)	215 (97%)	6 (3%)	0	100	100
2	B	337/358 (94%)	324 (96%)	13 (4%)	0	100	100
3	G	56/71 (79%)	56 (100%)	0	0	100	100
4	S	230/269 (86%)	228 (99%)	2 (1%)	0	100	100
5	R	285/461 (62%)	276 (97%)	9 (3%)	0	100	100
All	All	1129/1513 (75%)	1099 (97%)	30 (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 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	200/305 (66%)	200 (100%)	0	100	100
2	B	282/298 (95%)	280 (99%)	2 (1%)	84	94
3	G	47/58 (81%)	47 (100%)	0	100	100
4	S	198/217 (91%)	198 (100%)	0	100	100
5	R	249/372 (67%)	249 (100%)	0	100	100
All	All	976/1250 (78%)	974 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	105	TYR
2	B	234	PHE

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](#)

2 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
6	A1LY4	R	501	-	9,13,13	0.50	0	11,16,16	1.88	2 (18%)
7	CLR	R	502	-	31,31,31	1.21	1 (3%)	48,48,48	1.53	9 (18%)

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	A1LY4	R	501	-	-	2/3/12/12	1/2/2/2
7	CLR	R	502	-	-	3/10/68/68	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	R	502	CLR	C16-C17	3.20	1.61	1.54

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	R	501	A1LY4	C01-C06-C07	3.57	120.24	111.88
6	R	501	A1LY4	C02-C01-C06	-3.51	106.71	112.14
7	R	502	CLR	C12-C11-C9	3.44	119.07	113.11
7	R	502	CLR	C15-C14-C13	3.28	107.79	103.84
7	R	502	CLR	C1-C2-C3	3.07	114.40	110.47

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	R	501	A1LY4	C01-C06-C07-C08
7	R	502	CLR	C17-C20-C22-C23
7	R	502	CLR	C21-C20-C22-C23
6	R	501	A1LY4	C05-C06-C07-C08
7	R	502	CLR	C23-C24-C25-C27

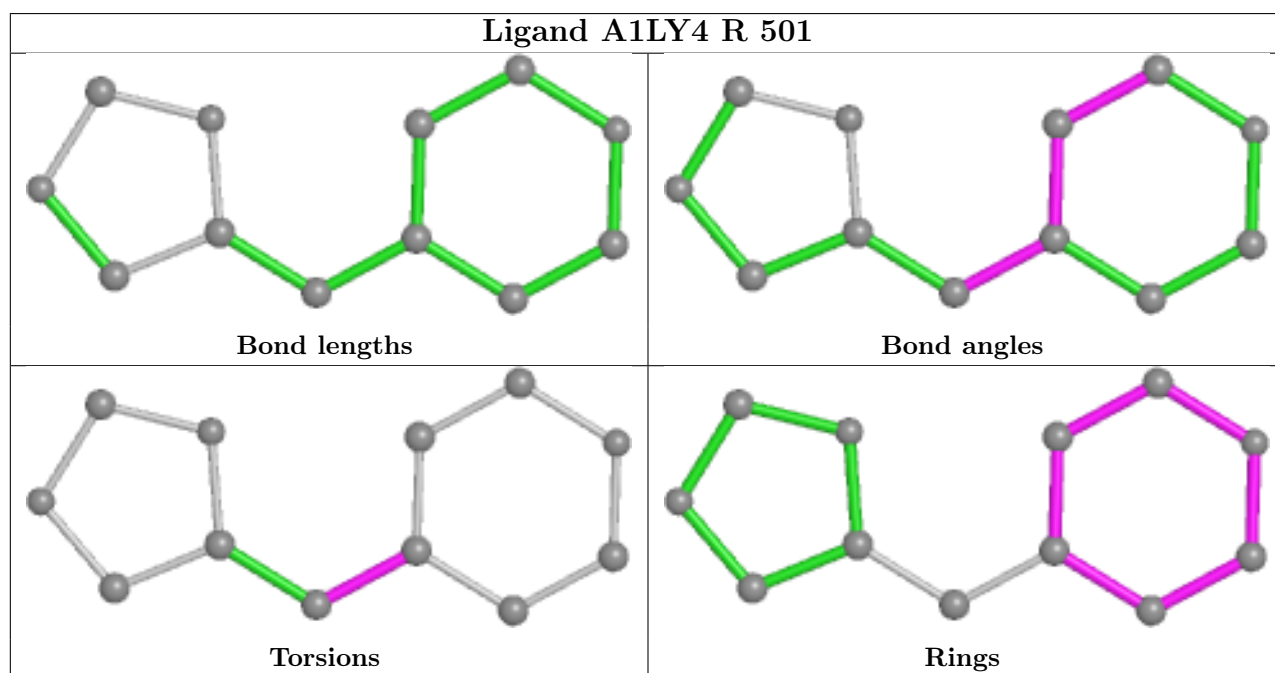
All (1) ring outliers are listed below:

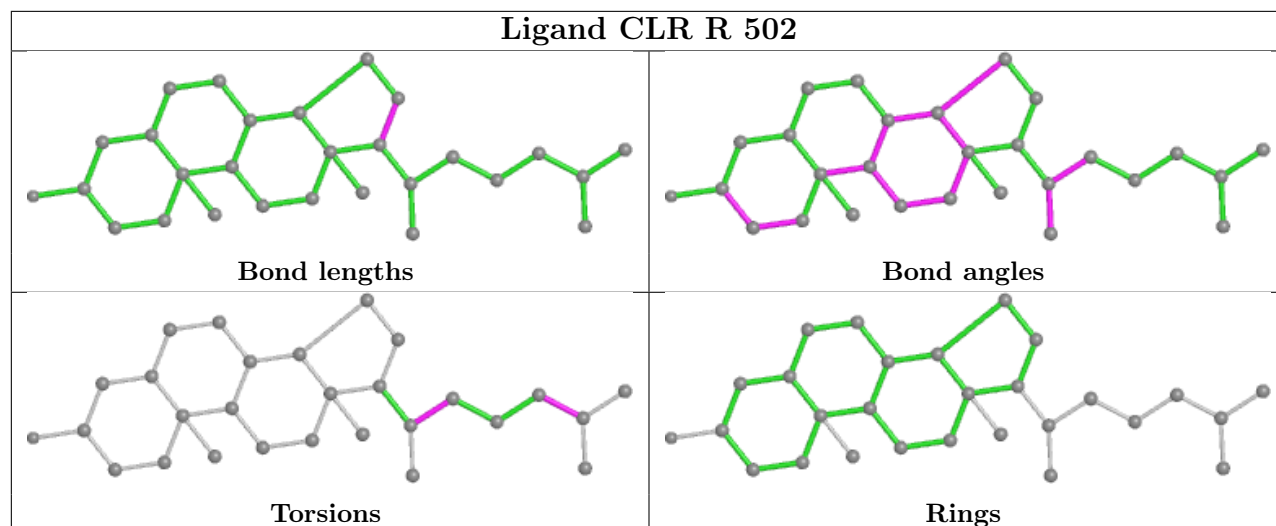
Mol	Chain	Res	Type	Atoms
6	R	501	A1LY4	C01-C02-C04-C05-C06-N03

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	R	501	A1LY4	4	0
7	R	502	CLR	2	0

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





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.