



Full wwPDB EM Validation Report ⓘ

Jan 26, 2025 – 02:14 PM JST

PDB ID : 9ITB
EMDB ID : EMD-60857
Title : LPA-bound LPAR6 in complex with miniGq
Authors : He, Y.; Duan, Y.
Deposited on : 2024-07-19
Resolution : 2.89 Å(reported)

This is a Full wwPDB EM 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/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	: FAILED
Mogul	: 1.8.5 (274361), CSD as541be (2020)
MolProbity	: 4.02b-467
buster-report	: 1.1.7 (2018)
Percentile statistics	: 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	: FAILED
Ideal geometry (proteins)	: Engh & Huber (2001)
Ideal geometry (DNA, RNA)	: Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: 2.40

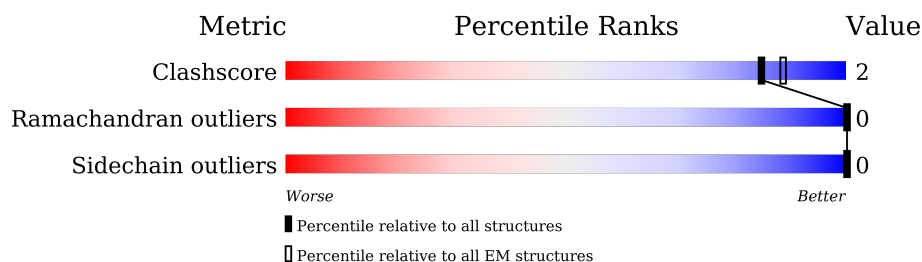
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	362	
2	B	345	
3	N	161	
4	R	294	
5	G	71	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7980 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 engineered miniGaq.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	228	Total	C	N	O	S	0	0
			1818	1151	319	341	7		

- 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	B	334	Total	C	N	O	S	0	0
			2514	1559	439	495	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	initiating methionine	UNP P62873
B	-3	GLY	-	expression tag	UNP P62873
B	-2	SER	-	expression tag	UNP P62873
B	-1	LEU	-	expression tag	UNP P62873
B	0	LEU	-	expression tag	UNP P62873
B	1	GLN	-	expression tag	UNP P62873

- Molecule 3 is a protein called Nb35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	128	Total	C	N	O	S	0	0
			963	600	167	190	6		

- Molecule 4 is a protein called Lysophosphatidic acid receptor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	271	Total	C	N	O	S	0	0
			2147	1441	327	355	24		

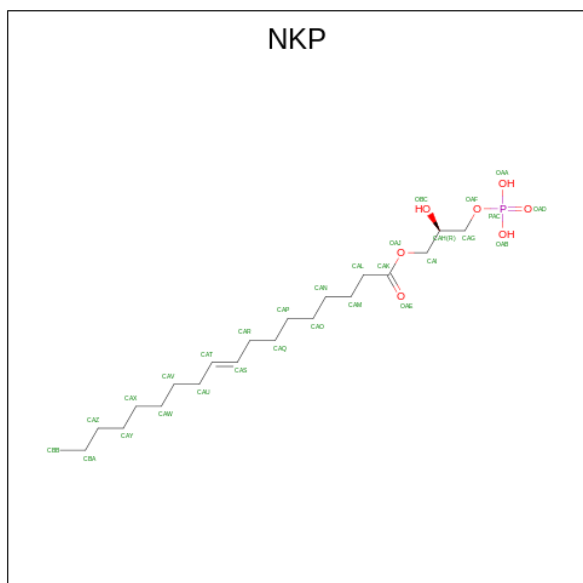
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	43	ALA	ILE	conflict	UNP P43657
R	166	ARG	GLU	conflict	UNP P43657

- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

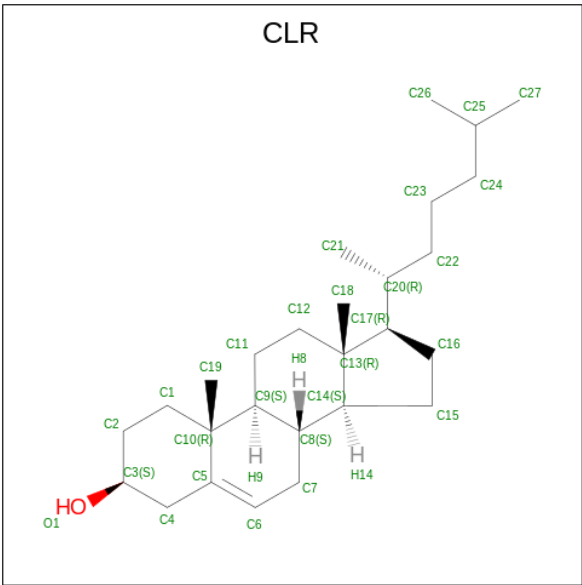
Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	56	Total 407	C 258	N 68	O 78	S 3	0	0

- Molecule 6 is (2R)-2-hydroxy-3-(phosphonoxy)propyl (9E)-octadec-9-enoate (three-letter code: NKP) (formula: C₂₁H₄₁O₇P).



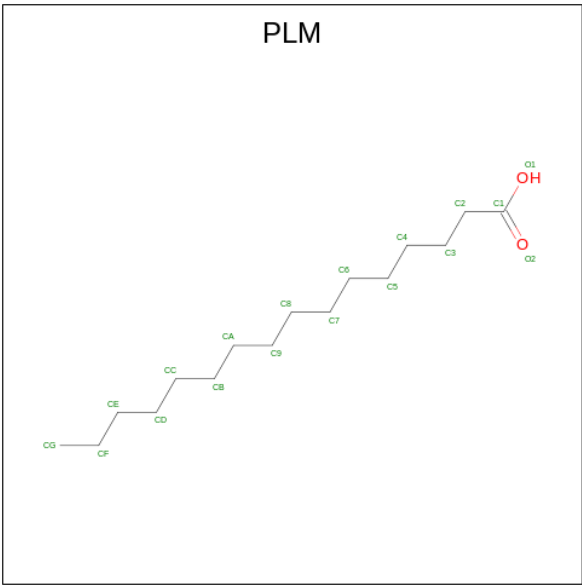
Mol	Chain	Residues	Atoms				AltConf
6	R	1	Total	C	O	P	0
			29	21	7	1	

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



Mol	Chain	Residues	Atoms			AltConf
7	R	1	Total	C	O	0
			28	27	1	
7	R	1	Total	C	O	0
			28	27	1	
7	R	1	Total	C	O	0
			28	27	1	

- Molecule 8 is PALMITIC ACID (three-letter code: PLM) (formula: C₁₆H₃₂O₂).

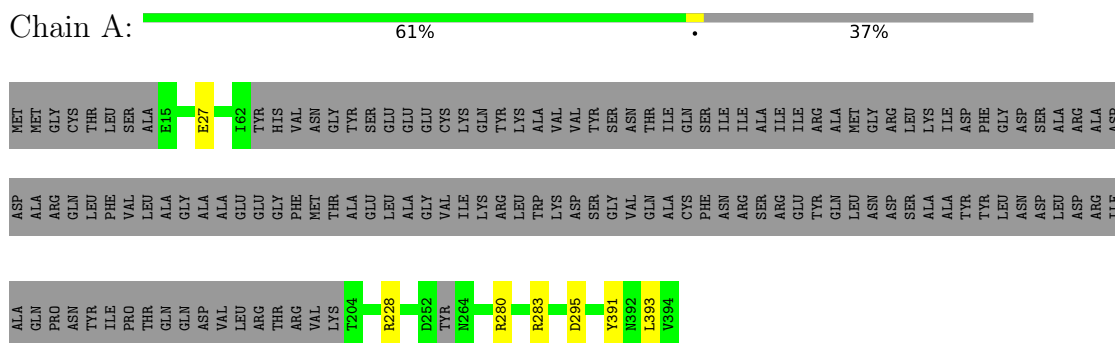


Mol	Chain	Residues	Atoms			AltConf
8	R	1	Total	C	O	0
			18	16	2	

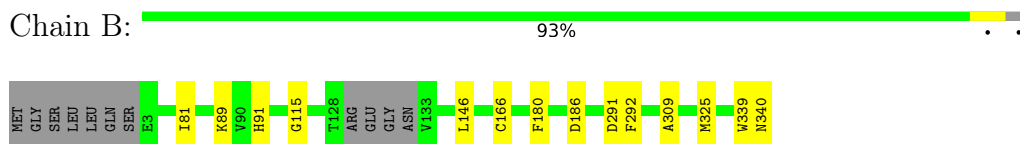
3 Residue-property plots [i](#)

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. 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.

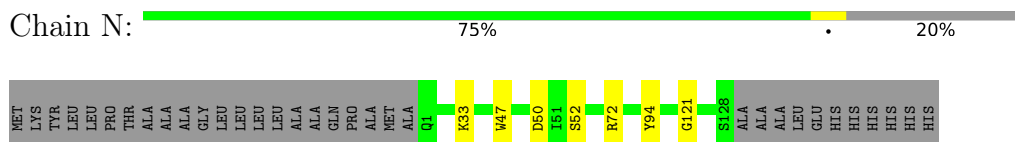
- Molecule 1: engineered miniGaq



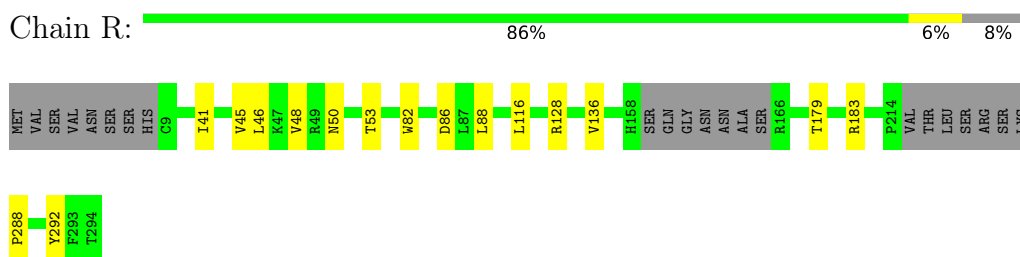
- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



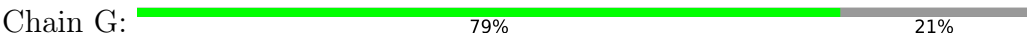
- Molecule 3: Nb35



- Molecule 4: Lysophosphatidic acid receptor 6



- Molecule 5: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



MET	ALA	SER	ASN	ASN	THR	47	R62	GLU	LYS	LYS	PHE	PHE	CYS	ALA	ILE	LEU
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	211505	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NKP, PLM, 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	0.28	0/1850	0.45	0/2500
2	B	0.28	0/2560	0.56	0/3479
3	N	0.30	0/983	0.51	0/1333
4	R	0.31	0/2203	0.47	0/3000
5	G	0.26	0/413	0.40	0/561
All	All	0.29	0/8009	0.50	0/10873

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

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	1818	0	1753	7	0
2	B	2514	0	2383	8	0
3	N	963	0	927	4	0
4	R	2147	0	2181	14	0
5	G	407	0	402	0	0
6	R	29	0	39	1	0
7	R	84	0	138	4	0
8	R	18	0	31	1	0
All	All	7980	0	7854	33	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 (33) 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)
7:R:402:CLR:H211	7:R:403:CLR:H14	1.73	0.70
4:R:179:THR:O	4:R:183:ARG:NH1	2.27	0.67
2:B:115:GLY:HA3	2:B:146:LEU:HD23	1.77	0.67
4:R:116:LEU:HD21	7:R:402:CLR:H112	1.77	0.66
4:R:82:TRP:CD1	4:R:82:TRP:O	2.52	0.63
4:R:50:ASN:O	4:R:53:THR:OG1	2.15	0.61
1:A:391:TYR:OH	4:R:128:ARG:NH2	2.34	0.61
4:R:288:PRO:HA	4:R:292:TYR:HD2	1.67	0.59
3:N:52:SER:O	3:N:72:ARG:NH1	2.35	0.59
4:R:46:LEU:HD12	4:R:48:VAL:H	1.69	0.57
4:R:82:TRP:O	4:R:82:TRP:CG	2.56	0.56
3:N:94:TYR:O	3:N:121:GLY:HA2	2.05	0.56
1:A:295:ASP:N	1:A:295:ASP:OD1	2.40	0.55
4:R:288:PRO:HA	4:R:292:TYR:CD2	2.41	0.55
4:R:82:TRP:HZ2	4:R:88:LEU:HB3	1.70	0.55
4:R:136:VAL:HG21	7:R:403:CLR:H191	1.89	0.54
1:A:280:ARG:HA	1:A:283:ARG:HH21	1.74	0.53
1:A:393:LEU:HD22	4:R:227:VAL:HG23	1.91	0.52
3:N:33:LYS:HG2	3:N:52:SER:HA	1.92	0.51
2:B:81:ILE:HB	2:B:91:HIS:HB2	1.94	0.50
1:A:280:ARG:HA	1:A:283:ARG:HE	1.76	0.49
2:B:166:CYS:HB2	2:B:180:PHE:HB2	1.93	0.49
4:R:86:ASP:OD1	4:R:86:ASP:N	2.44	0.48
2:B:309:ALA:O	2:B:339:TRP:HH2	1.96	0.48
2:B:325:MET:O	2:B:340:ASN:ND2	2.46	0.48
8:R:405:PLM:HD1	8:R:405:PLM:HA2	1.70	0.47
3:N:47:TRP:HZ2	3:N:50:ASP:HB2	1.82	0.44
2:B:291:ASP:O	2:B:292:PHE:CD1	2.70	0.44
4:R:41:ILE:HG23	4:R:45:VAL:HG22	1.99	0.44
7:R:402:CLR:H241	7:R:403:CLR:H161	1.98	0.44
1:A:27:GLU:OE2	2:B:89:LYS:NZ	2.31	0.43
6:R:401:NKP:HARA	6:R:401:NKP:HAU	1.64	0.43
1:A:228:ARG:NH1	2:B:186:ASP:OD1	2.53	0.42

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	222/362 (61%)	217 (98%)	5 (2%)	0	100	100
2	B	330/345 (96%)	316 (96%)	14 (4%)	0	100	100
3	N	126/161 (78%)	121 (96%)	5 (4%)	0	100	100
4	R	265/294 (90%)	253 (96%)	12 (4%)	0	100	100
5	G	54/71 (76%)	52 (96%)	2 (4%)	0	100	100
All	All	997/1233 (81%)	959 (96%)	38 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	192/317 (61%)	192 (100%)	0	100	100
2	B	267/287 (93%)	267 (100%)	0	100	100
3	N	104/128 (81%)	104 (100%)	0	100	100
4	R	240/272 (88%)	240 (100%)	0	100	100
5	G	40/58 (69%)	40 (100%)	0	100	100
All	All	843/1062 (79%)	843 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

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 ⓘ

5 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	NKP	R	401	-	28,28,28	1.51	2 (7%)	31,32,32	1.25	3 (9%)
7	CLR	R	404	-	31,31,31	0.58	0	48,48,48	1.13	3 (6%)
7	CLR	R	402	-	31,31,31	0.70	0	48,48,48	1.46	8 (16%)
7	CLR	R	403	-	31,31,31	0.84	1 (3%)	48,48,48	1.29	4 (8%)
8	PLM	R	405	-	17,17,17	0.55	0	17,17,17	1.16	1 (5%)

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	NKP	R	401	-	-	7/28/28/28	-
7	CLR	R	404	-	-	6/10/68/68	0/4/4/4
7	CLR	R	402	-	-	2/10/68/68	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	CLR	R	403	-	-	2/10/68/68	0/4/4/4
8	PLM	R	405	-	-	6/15/15/15	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R	401	NKP	PAC-OAF	6.84	1.82	1.60
6	R	401	NKP	OAF-CAG	-2.62	1.34	1.44
7	R	403	CLR	C10-C9	-2.35	1.52	1.56

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	R	402	CLR	C14-C8-C9	-4.54	103.01	109.09
7	R	403	CLR	C10-C9-C8	-3.70	107.18	112.73
6	R	401	NKP	OAF-PAC-OAD	-3.53	96.59	106.47
7	R	403	CLR	C11-C9-C10	-2.99	109.14	113.08
6	R	401	NKP	OAB-PAC-OAA	2.83	118.44	107.64
7	R	402	CLR	C2-C3-C4	-2.76	106.52	110.31
7	R	402	CLR	C13-C17-C20	-2.70	115.26	119.49
7	R	404	CLR	C13-C17-C20	-2.57	115.46	119.49
7	R	402	CLR	C7-C8-C9	2.53	112.77	109.71
7	R	402	CLR	C13-C14-C8	-2.48	110.70	114.38
7	R	403	CLR	C19-C10-C9	-2.37	108.85	111.68
7	R	403	CLR	C13-C14-C8	-2.35	110.90	114.38
7	R	402	CLR	C8-C7-C6	-2.29	109.45	112.73
7	R	402	CLR	C16-C15-C14	-2.25	100.68	105.13
7	R	404	CLR	C11-C12-C13	-2.19	109.03	112.78
6	R	401	NKP	OAB-PAC-OAF	-2.17	100.97	106.73
7	R	404	CLR	C10-C9-C8	-2.12	109.56	112.73
8	R	405	PLM	C3-C2-C1	-2.08	109.22	114.47
7	R	402	CLR	C11-C9-C8	-2.00	108.87	111.75

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	R	401	NKP	OAF-CAG-CAH-CAI
6	R	401	NKP	OAF-CAG-CAH-OBC
7	R	402	CLR	C17-C20-C22-C23
7	R	402	CLR	C21-C20-C22-C23

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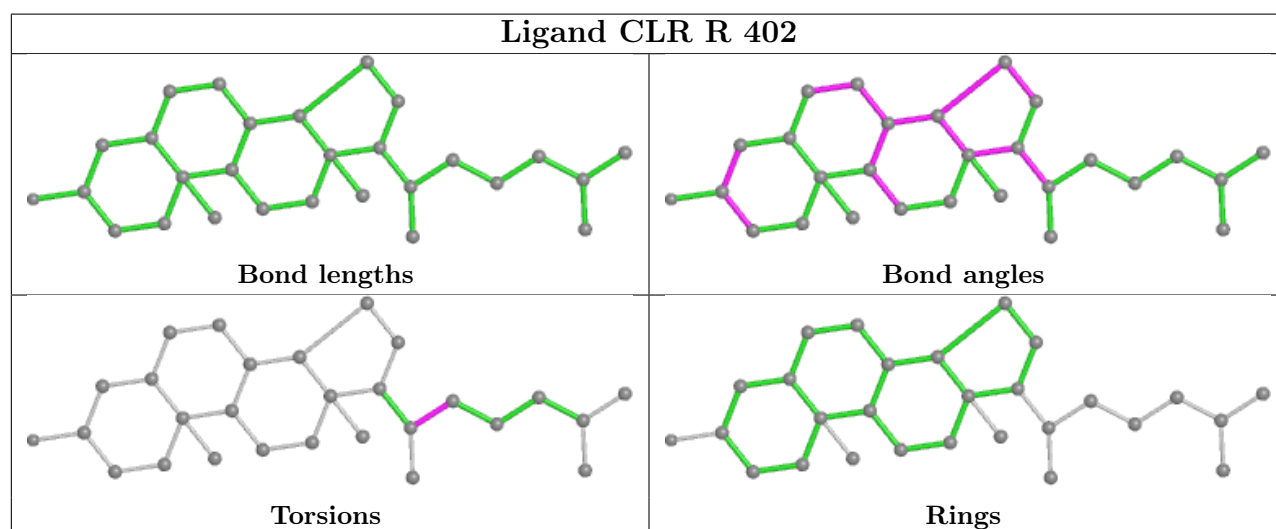
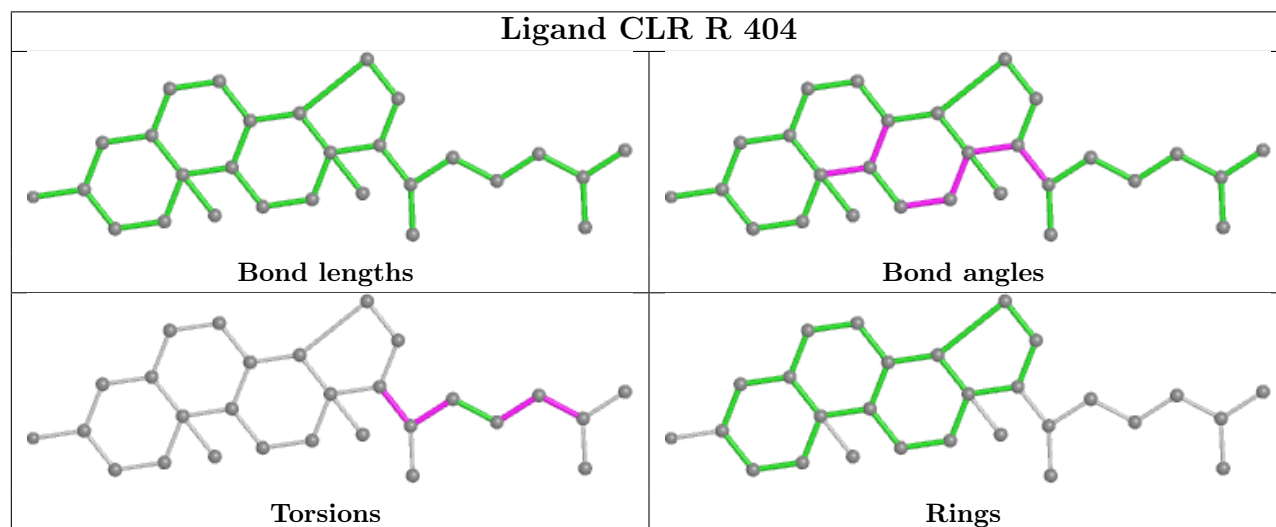
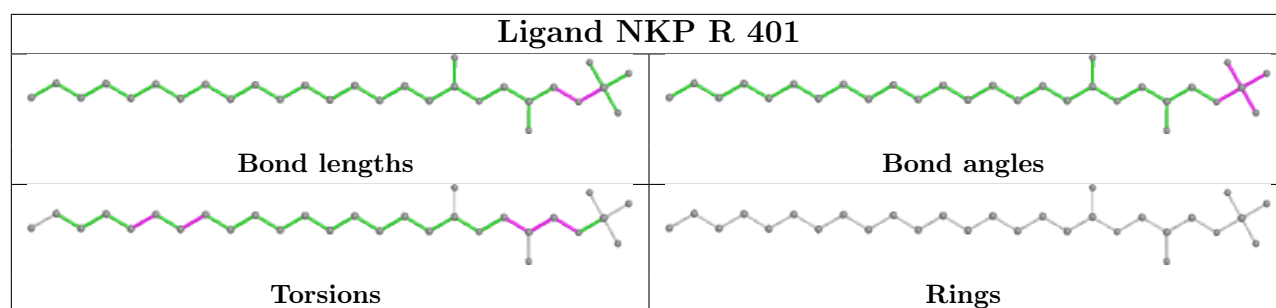
Mol	Chain	Res	Type	Atoms
7	R	404	CLR	C21-C20-C22-C23
7	R	404	CLR	C22-C23-C24-C25
6	R	401	NKP	OBC-CAH-CAI-OAJ
8	R	405	PLM	C4-C5-C6-C7
8	R	405	PLM	C2-C3-C4-C5
7	R	403	CLR	C21-C20-C22-C23
7	R	403	CLR	C17-C20-C22-C23
6	R	401	NKP	CAH-CAG-OAF-PAC
6	R	401	NKP	CAT-CAU-CAV-CAW
6	R	401	NKP	CAG-CAH-CAI-OAJ
8	R	405	PLM	C3-C4-C5-C6
7	R	404	CLR	C13-C17-C20-C21
6	R	401	NKP	CAV-CAW-CAX-CAY
8	R	405	PLM	O2-C1-C2-C3
7	R	404	CLR	C23-C24-C25-C27
8	R	405	PLM	O1-C1-C2-C3
8	R	405	PLM	CA-CB-CC-CD
7	R	404	CLR	C23-C24-C25-C26
7	R	404	CLR	C13-C17-C20-C22

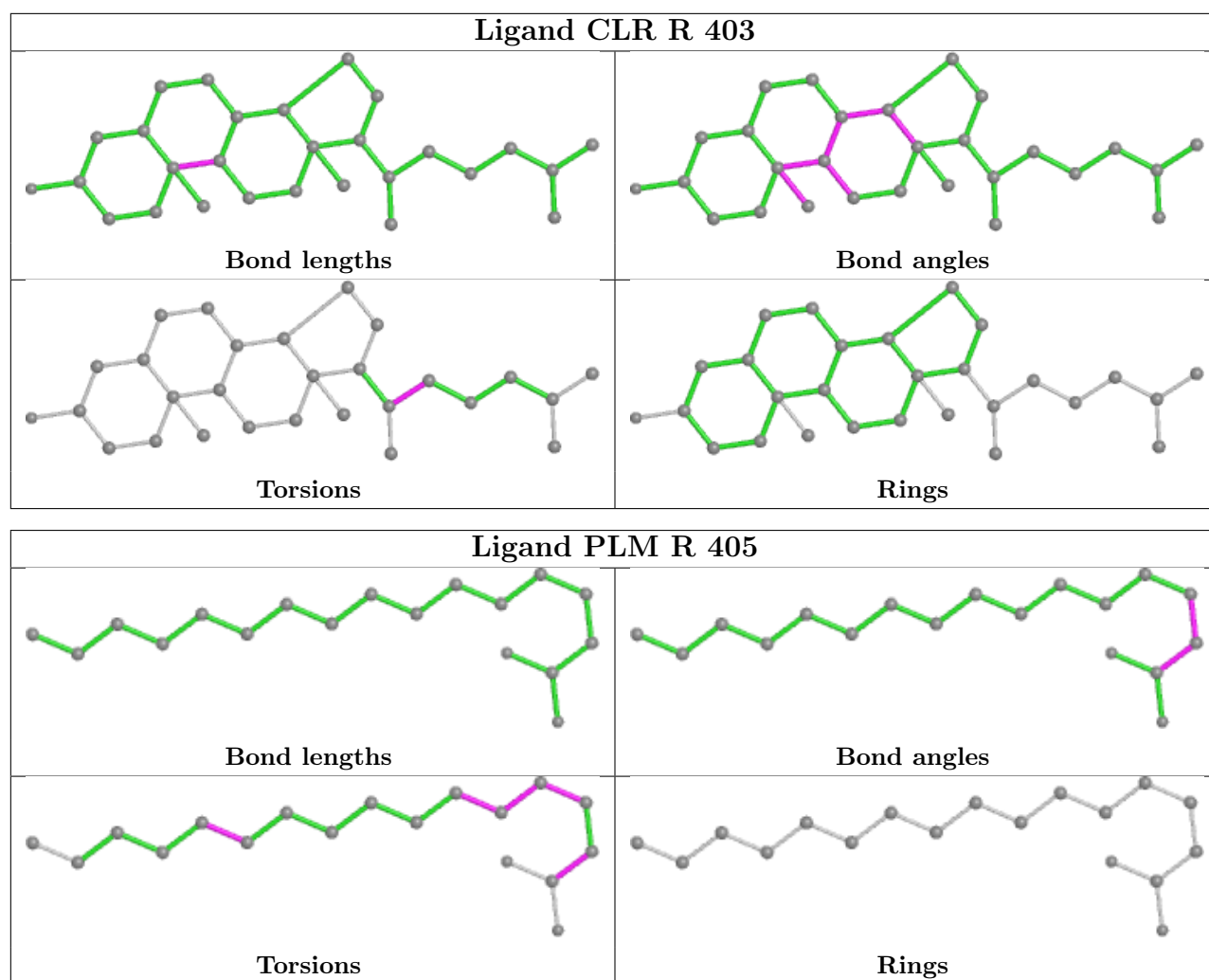
There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	R	401	NKP	1	0
7	R	402	CLR	3	0
7	R	403	CLR	3	0
8	R	405	PLM	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.





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.