WORLDWIDE wwPDB
PROTEIN DATA BANK

wwPDB EM Validation Summary Report (i)

Mar 31, 2025 – 07:09 PM JST

PDB ID	:	6JZO / pdb_00006jzo
EMDB ID	:	EMD-9898
Title	:	Structure of the mouse TRPC4 ion channel
Authors	:	Duan, J.; Li, Z.; Li, J.; Zhang, J.
Deposited on	:	2019-05-03
Resolution	:	3.28 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 (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:

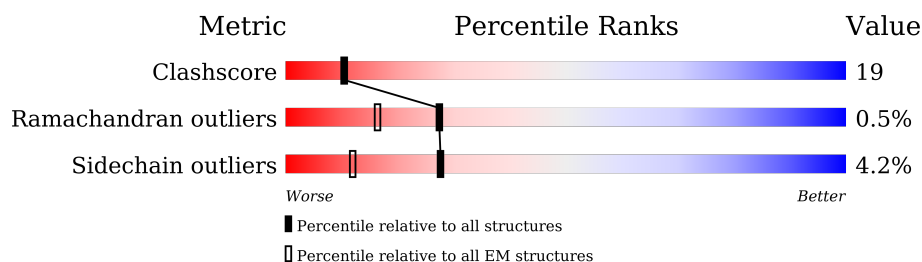|		
EMDB validation analysis	:	0.0.1.dev117
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

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 3.28 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	Percentile Ranks	Value
Clashscore		19
Ramachandran outliers		0.5%
Sidechain outliers		4.2%

Worse   *Better*

■ Percentile relative to all structures
◻ Percentile relative to all EM structures

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	755	64% 22% • 12%
1	B	755	66% 20% • 12%
1	C	755	69% 17% • 12%
1	D	755	66% 21% • 12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	Y01	B	801	-	-	X	-
2	Y01	C	801	-	-	X	-

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| Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	Y01	D	801	-	-	X	-
3	LPP	A	802	-	-	X	-
3	LPP	A	803	-	-	X	-
3	LPP	C	802	-	-	X	-
3	LPP	D	802	-	-	X	-

2   Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 21405 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 Short transient receptor potential channel 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	668	Total	C	N	O	S	0	0
			5296	3457	885	932	22		
1	B	663	Total	C	N	O	S	0	0
			5268	3439	880	927	22		
1	C	663	Total	C	N	O	S	0	0
			5266	3440	880	924	22		
1	D	663	Total	C	N	O	S	0	0
			5255	3437	879	917	22		

- Molecule 2 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula: $C_{31}H_{50}O_4$) (labeled as "Ligand of Interest" by depositor).
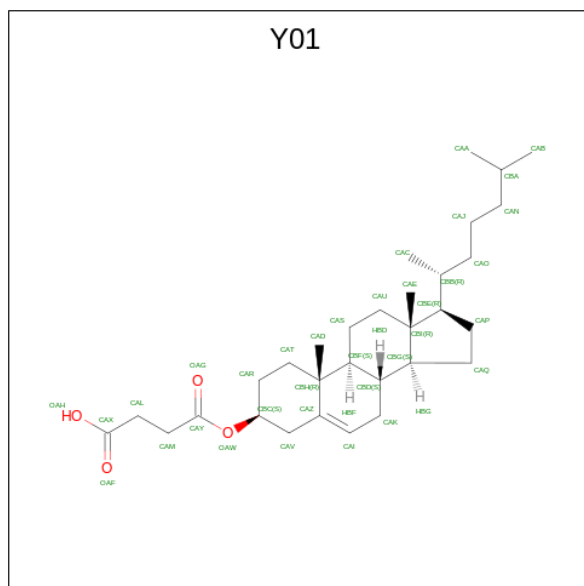
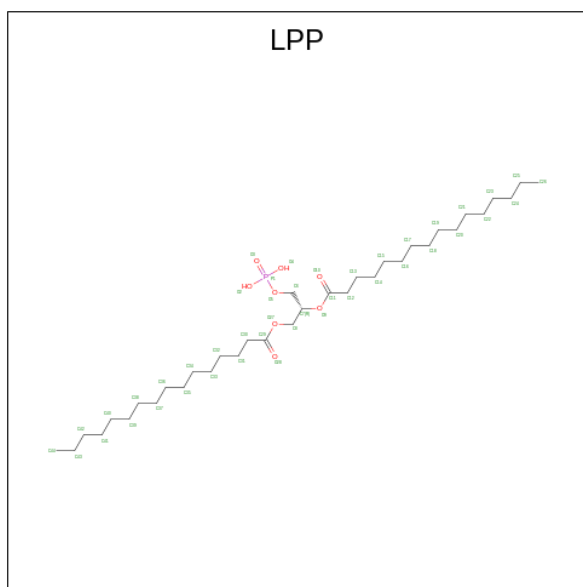| Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total	C	O	0
			35	31	4	
2	B	1	Total	C	O	0
			35	31	4	

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Mol	Chain	Residues	Atoms			AltConf
2	C	1	Total 35	C 31	O 4	0
2	D	1	Total 35	C 31	O 4	0

- Molecule 3 is 2-(HEXADECANOYLOXY)-1-[(PHOSPHONOOXY)METHYL]ETH YL HEXADECANOATE (CCD ID: LPP) (formula: $C_{35}H_{69}O_8P$) (labeled as "Ligand of Interest" by depositor).

LPP

Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total 44	C 35	O 8	P 1	0
3	A	1	Total 44	C 35	O 8	P 1	0
3	C	1	Total 44	C 35	O 8	P 1	0
3	D	1	Total 44	C 35	O 8	P 1	0

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total 1	Na 1	0
4	B	1	Total 1	Na 1	0

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Mol	Chain	Residues	Atoms		AltConf
4	C	1	Total 1	Na 1	0
4	D	1	Total 1	Na 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.
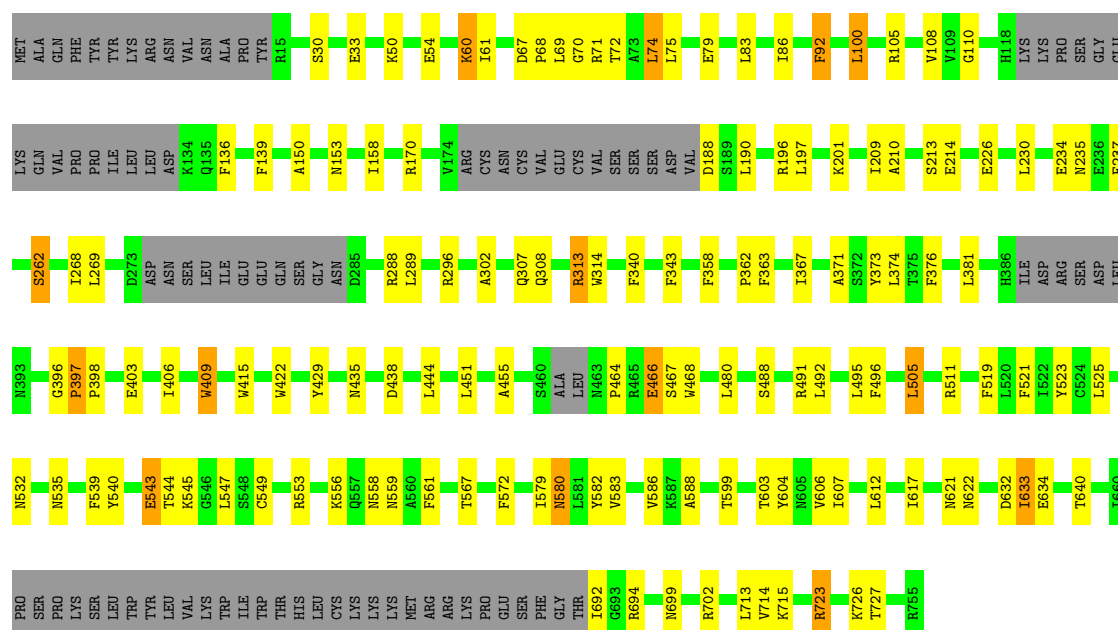
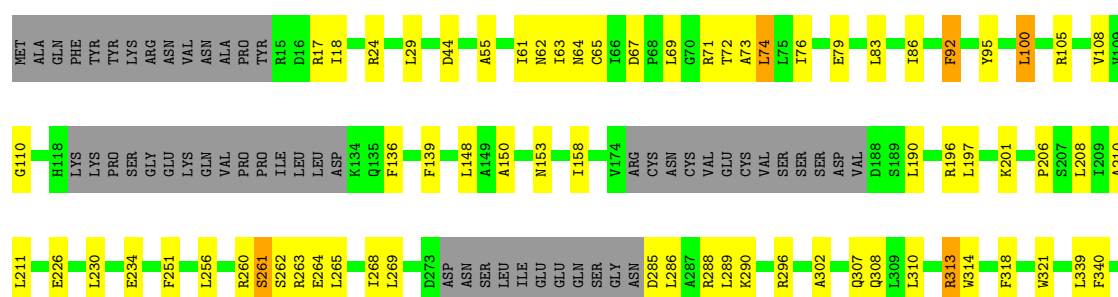- Molecule 1: Short transient receptor potential channel 4

Chain A:

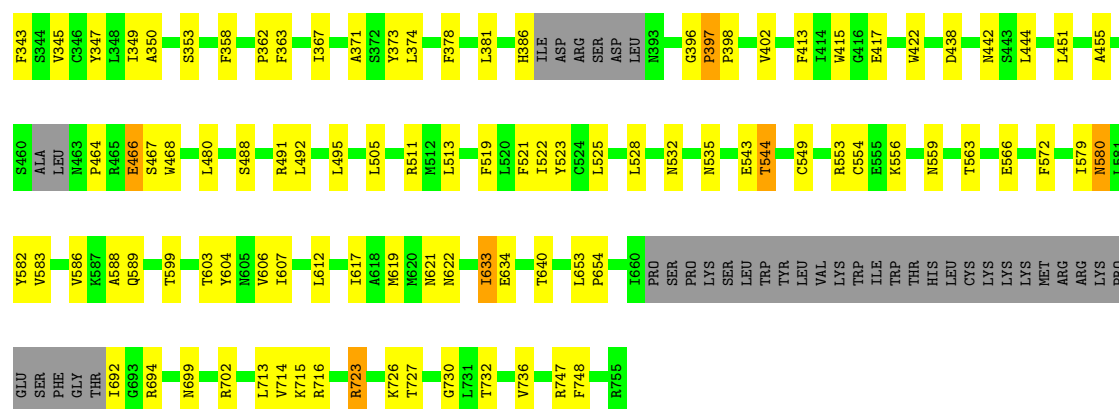- Molecule 1: Short transient receptor potential channel 4

Chain B:

F318 W321 F340 P362 F363 I367 A371 S372 Y373 L374 L377 F378 L381 H386 ILE ASP ARG SER ASP LEU N393 P397 P398 E403 I406 W409 W415 W422 D423 I430 D438 L444 L451 A455 S460 ALA LEU N463 P464 R465

E466 S467 W468 L480 S488 R491 L492 L495 L505 R511 F519 L520 F521 I522 Y523 C524 L525 N532 N535 T544 L547 S548 C549 I552 R553 C554 E555 K556 Q557 N558 N559 A560 F561 E566 T567 F572 F576 I579 N580 L581 Y582 V583 V586

K587 A588 T599 T603 Y604 N605 V606 I607 S608 L609 V610 V611 I617 A618 M619 M620 N621 N622 D632 I633 E634 T640 I660 PRO SER PRO LYS SER LEU TRP TYR LEU VAL LYS TRP ILE TRP THR HIS LEU CYS LYS LYS MET ARG LYS PRO GLU SER PHE GLY THR

I692 G693 R694 N699 R702 R711 N712 L713 V714 K715 R723 T727 T732 D742 F748 E749 R755

• Molecule 1: Short transient receptor potential channel 4

Chain C:

69%   17%   •   12%

MET ALA GLN PHE TYR TYR LYS ARG ASN VAL ASN ALA PRO TYR R15 S30 E33 K50 E54 K60 I61 D67 P68 L69 G70 R71 T72 A73 L74 L75 E79 L83 I86 F92 L100 R105 V108 V109 G110 H118 LYS LYS PRO SER GLY GLU

LYS GLN VAL PRO PRO ILE LEU LEU ASP K134 Q135 F136 F139 A150 N153 I158 R170 V174 ARG CYS ASN CYS VAL GLU CYS VAL SER SER ASP VAL D188 S189 L190 R196 L197 K201 I209 A210 S213 E214 E226 L230 E234 N235 E236 F237

S262 I268 L269 D273 ASP ASN SER LEU ILE GLU GLU GLN SER GLY ASN D285 R288 L289 R296 A302 Q307 Q308 R313 W314 F340 F343 F358 P362 F363 I367 A371 S372 Y373 L374 T375 F376 L381 H386 ILE ASP ARG SER ASP LEU

N393 G396 P397 P398 E403 I406 W409 W415 W422 Y429 N435 D438 L444 L451 A455 S460 ALA LEU N463 P464 R465 E466 S467 W468 L480 S488 R491 L492 L495 F496 L505 R511 F519 L520 F521 I522 Y523 C524 L525

N532 N535 F539 Y540 E543 T544 K545 G546 L547 S548 C549 R553 K556 Q557 N558 N559 A560 F561 T567 F572 I579 N580 L581 Y582 V583 V586 K587 A588 T599 T603 Y604 N605 V606 I607 L612 I617 N621 N622 D632 I633 E634 T640 I660

PRO SER PRO LYS SER LEU TRP TYR LEU VAL LYS TRP ILE TRP THR HIS LEU CYS LYS LYS LYS MET ARG ARG LYS PRO GLU SER PHE GLY THR I692 G693 R694 N699 R702 L713 V714 K715 R723 K726 T727 R755

• Molecule 1: Short transient receptor potential channel 4

Chain D:

66%   21%   •   12%

MET ALA GLN PHE TYR TYR LYS ARG ASN VAL ASN ALA PRO TYR R15 D16 R17 I18 R24 L29 D44 A55 I61 N62 I63 N64 C65 I66 D67 P68 L69 G70 R71 T72 A73 L74 L75 I76 E79 L83 I86 F92 Y95 L100 R105 V108 V109

G110 H118 LYS LYS PRO SER GLY GLU LYS GLN VAL PRO PRO ILE LEU LEU ASP K134 Q135 F136 F139 L148 A149 A150 N153 I158 V174 ARG CYS ASN CYS VAL GLU CYS VAL SER SER ASP VAL D188 S189 L190 R196 L197 K201 P206 S207 L208 I209 A210

I211 E226 L230 E234 F251 L256 R260 S261 S262 R263 E264 L265 I268 L269 D273 ASP ASN SER LEU ILE GLU GLU SER GLY ASN D285 L286 A287 R288 L289 K290 R296 A302 Q307 Q308 L310 R313 W314 F318 W321 L339 F340

F343 S344 V345 C346 Y347 L348 I349 A350 S353 F358 P362 F363 I367 A371 S372 Y373 L374 F378 L381 H386 ILE ASP ARG SER ASP LEU N393 G396 P397 P398 V402 F413 I414 W415 G416 E417 W422 D438 N442 S443 L444 L451 A455

S460 ALA LEU N463 P464 R465 E466 S467 W468 L480 S488 R491 L492 L495 L505 R511 M512 L513 F519 L520 F521 I522 Y523 C524 L525 L528 N532 N535 E543 T544 C549 R553 C554 E555 K556 N559 T563 E566 F572 I579 N580 L581

Y582 V583 V586 K587 A588 Q589 T599 T603 Y604 N605 V606 I607 L612 I617 A618 M619 M620 N621 N622 I633 E634 T640 L653 P654 I660 PRO SER PRO LYS SER LEU TRP TYR LEU VAL LYS TRP ILE TRP THR HIS LEU CYS LYS LYS LYS MET ARG ARG LYS PRO

GLU SER PHE GLY THR I692 G693 R694 N699 R702 L713 V714 K715 R716 R723 K726 T727 G730 L731 T732 V736 R747 F748 R755

4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	232858	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/Å^2)$	56	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
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: Y01, LPP, NA

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	0.41	0/5419	0.61	5/7357 (0.1%)
1	B	0.38	0/5389	0.58	0/7313
1	C	0.38	0/5389	0.58	1/7315 (0.0%)
1	D	0.38	0/5378	0.59	1/7301 (0.0%)
All	All	0.39	0/21575	0.59	7/29286 (0.0%)

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	B	0	2
1	C	0	2
1	D	0	2
All	All	0	6

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	656	PRO	CA-N-CD	-9.19	98.64	111.50
1	D	29	LEU	CA-CB-CG	8.76	135.45	115.30
1	C	60	LYS	N-CA-C	5.99	127.16	111.00
1	A	57	ILE	N-CA-C	-5.78	95.38	111.00
1	A	398	PRO	N-CA-C	-5.55	97.66	112.10

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	397	PRO	Peptide
1	B	398	PRO	Peptide
1	C	397	PRO	Peptide
1	C	398	PRO	Peptide
1	D	397	PRO	Peptide

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	5296	0	5238	246	0
1	B	5268	0	5215	206	0
1	C	5266	0	5217	154	0
1	D	5255	0	5212	229	0
2	A	35	0	47	19	0
2	B	35	0	49	26	0
2	C	35	0	49	21	0
2	D	35	0	49	22	0
3	A	88	0	134	51	0
3	C	44	0	67	21	0
3	D	44	0	67	25	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	21405	0	21344	797	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 19.

The worst 5 of 797 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:B:378:PHE:CE1	2:B:801:Y01:HAB1	1.45	1.52
1:B:378:PHE:CZ	2:B:801:Y01:HAB1	1.47	1.48
1:D:378:PHE:CZ	2:D:801:Y01:HAB1	1.51	1.44
1:B:378:PHE:CE1	2:B:801:Y01:CAB	2.01	1.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:386:HIS:HE1	1:D:402:VAL:CG2	1.31	1.41

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	654/755 (87%)	632 (97%)	19 (3%)	3 (0%)	25	56
1	B	649/755 (86%)	629 (97%)	17 (3%)	3 (0%)	25	56
1	C	649/755 (86%)	628 (97%)	18 (3%)	3 (0%)	25	56
1	D	649/755 (86%)	631 (97%)	15 (2%)	3 (0%)	25	56
All	All	2601/3020 (86%)	2520 (97%)	69 (3%)	12 (0%)	27	56

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	397	PRO
1	C	543	GLU
1	C	544	THR
1	D	544	THR
1	D	261	SER

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	555/677 (82%)	522 (94%)	33 (6%)	16	43
1	B	552/677 (82%)	527 (96%)	25 (4%)	23	51
1	C	552/677 (82%)	533 (97%)	19 (3%)	32	58
1	D	549/677 (81%)	533 (97%)	16 (3%)	37	62
All	All	2208/2708 (82%)	2115 (96%)	93 (4%)	27	53

5 of 93 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	723	ARG
1	C	559	ASN
1	C	92	PHE
1	C	340	PHE
1	C	633	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	258	GLN
1	C	625	GLN
1	C	308	GLN
1	C	559	ASN
1	D	80	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 ⓘ

There are no oligosaccharides in this entry.

5.6   Ligand geometry   ⓘ

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	Y01	B	801	-	38,38,38	1.74	5 (13%)	57,57,57	1.79	12 (21%)
2	Y01	C	801	-	38,38,38	1.77	6 (15%)	57,57,57	1.80	13 (22%)
3	LPP	A	803	-	43,43,43	0.97	2 (4%)	47,48,48	1.18	2 (4%)
2	Y01	A	801	1	38,38,38	1.75	5 (13%)	57,57,57	1.71	12 (21%)
3	LPP	A	802	-	43,43,43	0.97	2 (4%)	47,48,48	1.18	2 (4%)
2	Y01	D	801	-	38,38,38	1.75	5 (13%)	57,57,57	1.78	12 (21%)
3	LPP	C	802	-	43,43,43	0.97	2 (4%)	47,48,48	1.18	2 (4%)
3	LPP	D	802	-	43,43,43	0.97	2 (4%)	47,48,48	1.18	2 (4%)

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	Y01	B	801	-	-	7/19/77/77	0/4/4/4
2	Y01	C	801	-	-	8/19/77/77	0/4/4/4
3	LPP	A	803	-	-	25/45/45/45	-
2	Y01	A	801	1	-	9/19/77/77	0/4/4/4
3	LPP	A	802	-	-	25/45/45/45	-
2	Y01	D	801	-	-	8/19/77/77	0/4/4/4
3	LPP	C	802	-	-	25/45/45/45	-
3	LPP	D	802	-	-	25/45/45/45	-

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	Y01	CAV-CAZ	-5.46	1.39	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	Y01	CAV-CAZ	-5.43	1.39	1.51
2	D	801	Y01	CAV-CAZ	-5.42	1.39	1.51
2	A	801	Y01	CAV-CAZ	-5.35	1.40	1.51
2	A	801	Y01	CBH-CAZ	-5.24	1.42	1.52

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	801	Y01	CBI-CBE-CBB	-5.54	110.82	119.49
2	C	801	Y01	CBI-CBE-CBB	-5.51	110.85	119.49
2	D	801	Y01	CBI-CBE-CBB	-5.40	111.03	119.49
3	A	802	LPP	O9-C11-C12	4.25	120.66	111.50
3	A	803	LPP	O9-C11-C12	4.25	120.66	111.50

There are no chirality outliers.

5 of 132 torsion outliers are listed below:

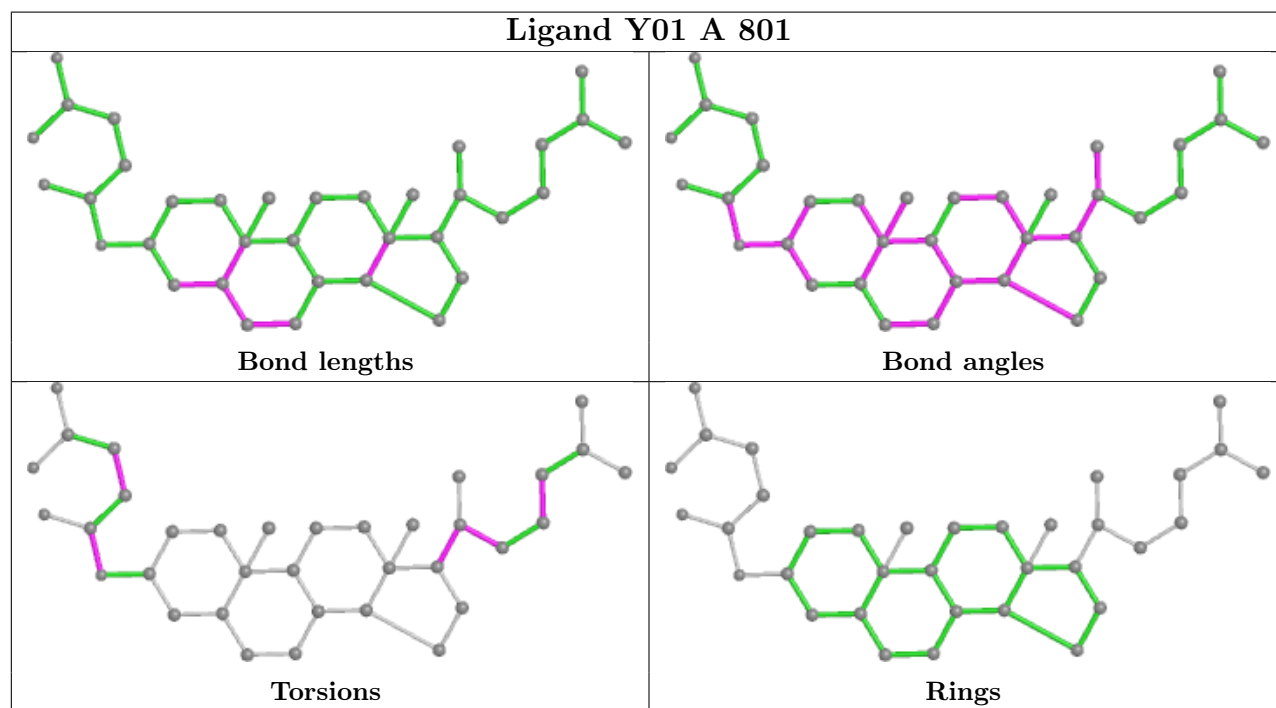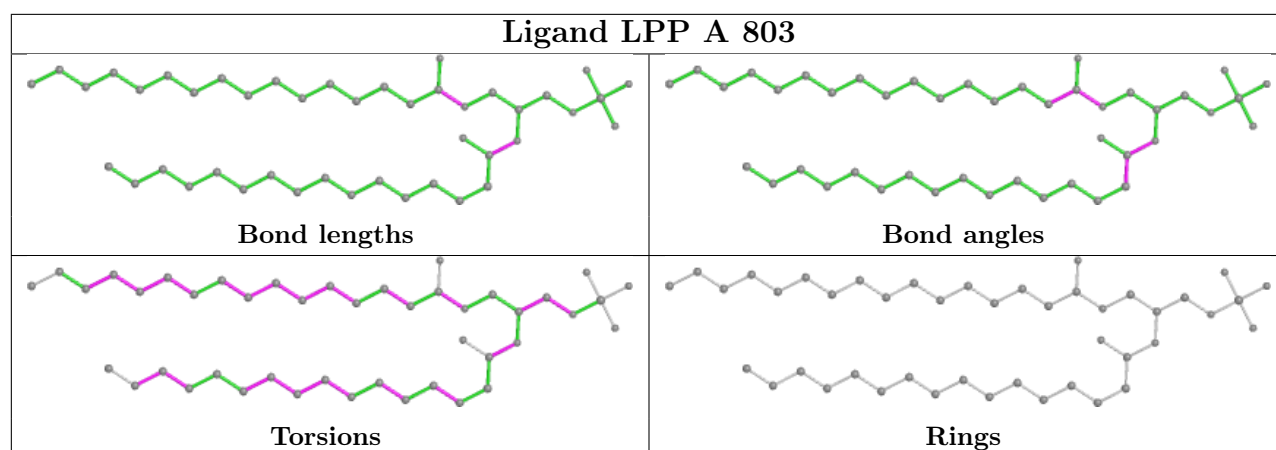| Mol	Chain	Res	Type	Atoms
3	A	802	LPP	C7-C6-O5-P1
3	A	803	LPP	C7-C6-O5-P1
3	C	802	LPP	C7-C6-O5-P1
3	D	802	LPP	C7-C6-O5-P1
3	A	802	LPP	O10-C11-O9-C7

There are no ring outliers.

8 monomers are involved in 185 short contacts:

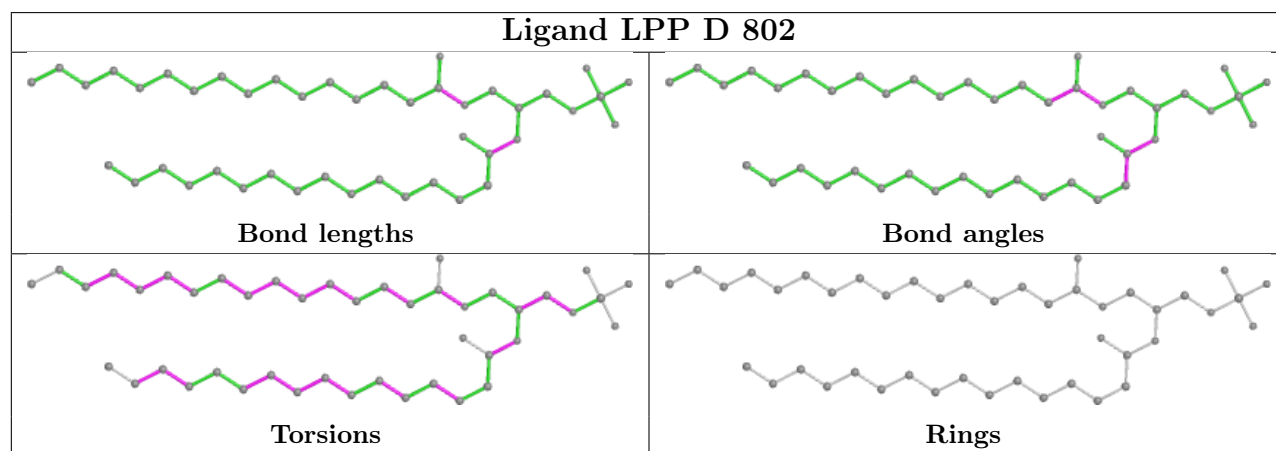| Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	Y01	26	0
2	C	801	Y01	21	0
3	A	803	LPP	28	0
2	A	801	Y01	19	0
3	A	802	LPP	23	0
2	D	801	Y01	22	0
3	C	802	LPP	21	0
3	D	802	LPP	25	0

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 Y01 B 801

Bond lengths

Bond angles

Torsions

Rings

Ligand Y01 C 801

Bond lengths

Bond angles

Torsions

Rings

Ligand LPP A 803

Bond lengths

Bond angles

Torsions

Rings

Ligand Y01 A 801

Bond lengths

Bond angles

Torsions

Rings

Ligand LPP A 802

Bond lengths

Bond angles

Torsions

Rings

Ligand Y01 D 801

Bond lengths

Bond angles

Torsions

Rings

Ligand LPP C 802

Bond lengths

Bond angles

Torsions

Rings

Ligand LPP D 802

Bond lengths

Bond angles

Torsions

Rings

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-9898. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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 (i)

This section was not generated.