



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:19 PM UTC

PDB ID : 8X43 / pdb_00008x43
EMDB ID : EMD-38041
Title : human KCNQ2-CaM-Ebio1-S1 complex in the presence of PIP2
Authors : Ma, D.; Guo, J.
Deposited on : 2023-11-15
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

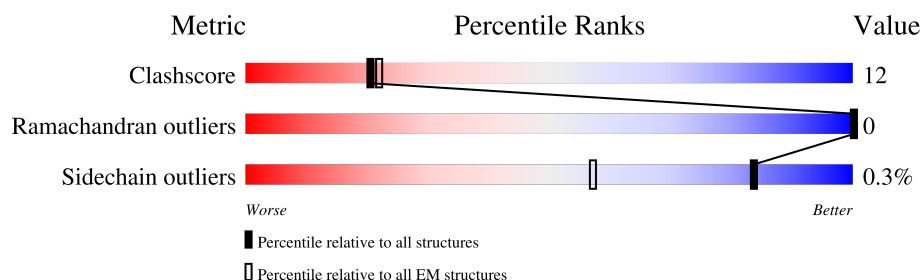
1 Overall quality at a glance

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	656	39% 11% 50%
1	C	656	38% 12% 50%
1	E	656	38% 11% 50%
1	G	656	38% 12% 50%
2	B	149	70% 26% .
2	D	149	68% 28% .
2	F	149	63% 33% .
2	H	149	68% 28% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 30224 atoms, of which 15044 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 Potassium voltage-gated channel subfamily KQT member 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	327	Total	C	H	N	O	S	0	0
			5389	1751	2723	463	439	13		
1	C	327	Total	C	H	N	O	S	0	0
			5389	1751	2723	463	439	13		
1	E	327	Total	C	H	N	O	S	0	0
			5389	1751	2723	463	439	13		
1	G	327	Total	C	H	N	O	S	0	0
			5389	1751	2723	463	439	13		

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	MET	-	initiating methionine	UNP O43526
A	703	VAL	-	expression tag	UNP O43526
A	704	GLU	-	expression tag	UNP O43526
A	705	GLY	-	expression tag	UNP O43526
A	706	GLY	-	expression tag	UNP O43526
A	707	SER	-	expression tag	UNP O43526
A	708	SER	-	expression tag	UNP O43526
A	709	GLY	-	expression tag	UNP O43526
A	710	GLY	-	expression tag	UNP O43526
A	711	TRP	-	expression tag	UNP O43526
A	712	SER	-	expression tag	UNP O43526
A	713	HIS	-	expression tag	UNP O43526
A	714	PRO	-	expression tag	UNP O43526
A	715	GLN	-	expression tag	UNP O43526
A	716	PHE	-	expression tag	UNP O43526
A	717	GLU	-	expression tag	UNP O43526
A	718	LYS	-	expression tag	UNP O43526
C	63	MET	-	initiating methionine	UNP O43526
C	703	VAL	-	expression tag	UNP O43526
C	704	GLU	-	expression tag	UNP O43526
C	705	GLY	-	expression tag	UNP O43526
C	706	GLY	-	expression tag	UNP O43526

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Chain	Residue	Modelled	Actual	Comment	Reference
C	707	SER	-	expression tag	UNP O43526
C	708	SER	-	expression tag	UNP O43526
C	709	GLY	-	expression tag	UNP O43526
C	710	GLY	-	expression tag	UNP O43526
C	711	TRP	-	expression tag	UNP O43526
C	712	SER	-	expression tag	UNP O43526
C	713	HIS	-	expression tag	UNP O43526
C	714	PRO	-	expression tag	UNP O43526
C	715	GLN	-	expression tag	UNP O43526
C	716	PHE	-	expression tag	UNP O43526
C	717	GLU	-	expression tag	UNP O43526
C	718	LYS	-	expression tag	UNP O43526
E	63	MET	-	initiating methionine	UNP O43526
E	703	VAL	-	expression tag	UNP O43526
E	704	GLU	-	expression tag	UNP O43526
E	705	GLY	-	expression tag	UNP O43526
E	706	GLY	-	expression tag	UNP O43526
E	707	SER	-	expression tag	UNP O43526
E	708	SER	-	expression tag	UNP O43526
E	709	GLY	-	expression tag	UNP O43526
E	710	GLY	-	expression tag	UNP O43526
E	711	TRP	-	expression tag	UNP O43526
E	712	SER	-	expression tag	UNP O43526
E	713	HIS	-	expression tag	UNP O43526
E	714	PRO	-	expression tag	UNP O43526
E	715	GLN	-	expression tag	UNP O43526
E	716	PHE	-	expression tag	UNP O43526
E	717	GLU	-	expression tag	UNP O43526
E	718	LYS	-	expression tag	UNP O43526
G	63	MET	-	initiating methionine	UNP O43526
G	703	VAL	-	expression tag	UNP O43526
G	704	GLU	-	expression tag	UNP O43526
G	705	GLY	-	expression tag	UNP O43526
G	706	GLY	-	expression tag	UNP O43526
G	707	SER	-	expression tag	UNP O43526
G	708	SER	-	expression tag	UNP O43526
G	709	GLY	-	expression tag	UNP O43526
G	710	GLY	-	expression tag	UNP O43526
G	711	TRP	-	expression tag	UNP O43526
G	712	SER	-	expression tag	UNP O43526
G	713	HIS	-	expression tag	UNP O43526
G	714	PRO	-	expression tag	UNP O43526

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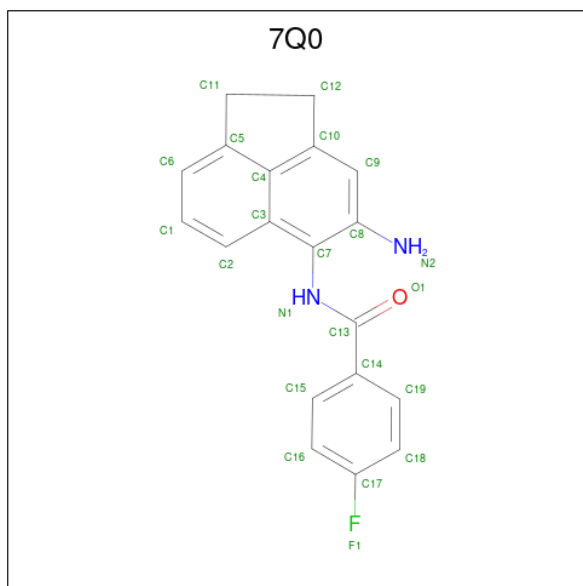
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Chain	Residue	Modelled	Actual	Comment	Reference
G	715	GLN	-	expression tag	UNP O43526
G	716	PHE	-	expression tag	UNP O43526
G	717	GLU	-	expression tag	UNP O43526
G	718	LYS	-	expression tag	UNP O43526

- Molecule 2 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	143	Total	C	H	N	O	S	0	0
			2129	681	1023	178	238	9		
2	D	143	Total	C	H	N	O	S	0	0
			2129	681	1023	178	238	9		
2	F	143	Total	C	H	N	O	S	0	0
			2129	681	1023	178	238	9		
2	H	143	Total	C	H	N	O	S	0	0
			2129	681	1023	178	238	9		

- Molecule 3 is N-(4-azanyl-1,2-dihydroacenaphthylen-5-yl)-4-fluoranyl-benzamide (CCD ID: 7Q0) (formula: C₁₉H₁₅FN₂O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
3	A	1	Total	C	F	H	N	O	0
			38	19	1	15	2	1	
3	C	1	Total	C	F	H	N	O	0
			38	19	1	15	2	1	
3	E	1	Total	C	F	H	N	O	0
			38	19	1	15	2	1	

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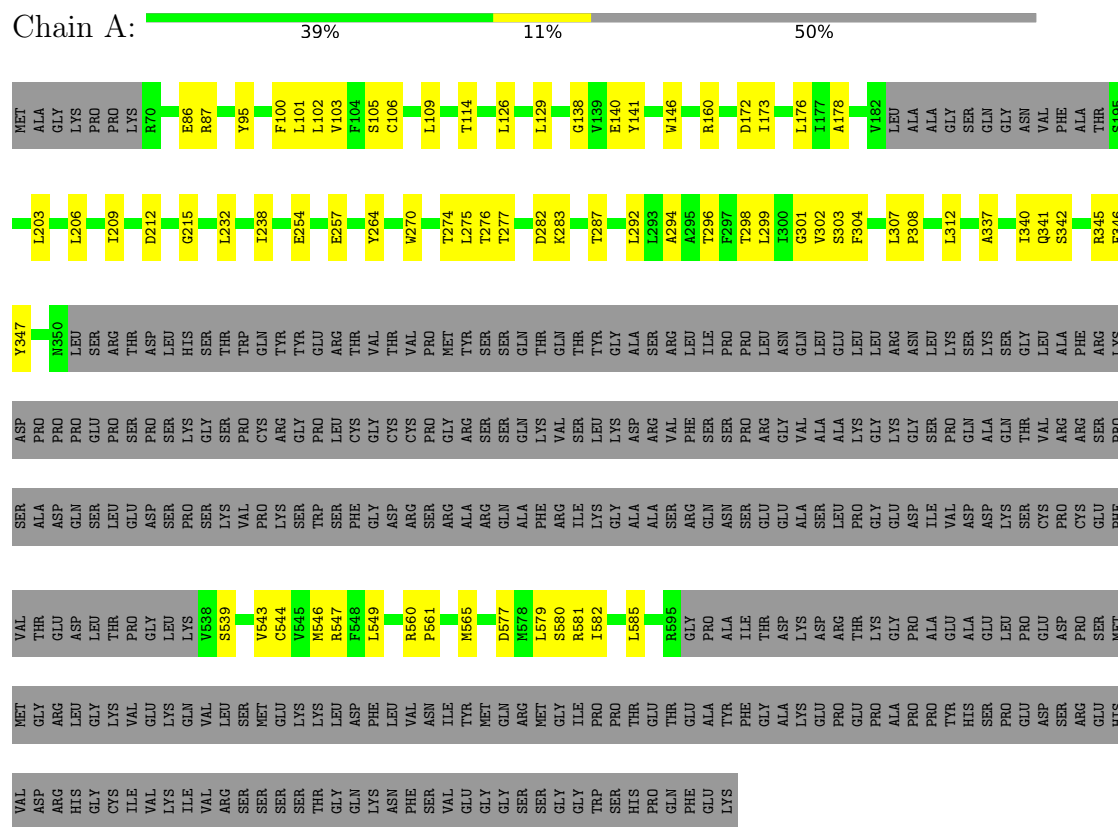
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Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	H	N	O	
3	G	1	38	19	1	15	2	1	0

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: Potassium voltage-gated channel subfamily KQT member 2



PRO	SER	LYS	GLY	SER	PRO	VAL	PRO	CYS	ARG	GLY	TRP	SER	LEU	CYS	GLY	CYS	CYS	PRO	GLY	ALA	ARG	SER	GLN	ALA	VAL	SER	LEU	LYS	ASP	ALA	ARG	VAL	ILE	SER	ASP	LEU	LYS	PRO	GLY	GLY	ASP	ILE	VAL	PRO	GLN	ALA	ALA	PRO	GLY	GLY	ASP	ILE	THR	ASP	LYS	ASP	ARG	THR	CYS	PRO	ARG	ARG	CYS	PRO	PHE	PRO	ALA	VAL	SER	THR	ALA	THR	ASP	GLN	SER	LEU	PRO	THR	LEU	GLU	ASP	SER	
ASP	SER	PRO	SER	GLY	VAL	VAL	PRO	CYS	ARG	GLY	TRP	SER	PHE	GLY	CYS	ASP	ARG	PRO	SER	ARG	ALA	ARG	GLN	ALA	GLN	VAL	SER	LEU	LYS	ASP	ALA	ARG	VAL	ILE	SER	ASP	LEU	LYS	PRO	GLY	GLY	ASP	ILE	VAL	PRO	GLN	ALA	ALA	PRO	GLY	GLY	ASP	ILE	THR	ASP	LYS	ASP	ARG	THR	CYS	PRO	ARG	ARG	CYS	PRO	PHE	PRO	ALA	VAL	SER	THR	ALA	THR	ASP	GLN	SER	LEU	PRO	THR	LEU	GLU	ASP	SER
GLY	LEU	LYS	V538	S539	A542	V543	C544	V545	M546	L549	K552	K556	R560	P561	M565	H575	L576	D577	N578	S580	R581	I582	L585	R588	Q591	R595	GLY	PRO	ALA	ALA	ASP	ILE	THR	ASP	LYS	ASP	ARG	THR	LYS	GLY	PRO	GLU	ASP	ILE	THR	ASP	LYS	ASP	ARG	THR	LYS	PRO	ALA	VAL	SER	THR	ALA	THR	ASP	GLN	SER	LEU	PRO	THR	LEU	GLU	ASP	SER															
PRO	SER	MET	MET	GLY	ARG	LEU	GLY	GLY	VAL	GLU	LYS	GLN	VAL	LEU	ASP	PHE	LEU	VAL	ASN	ILE	TYR	MET	GLN	GLY	SER	ARG	MET	GLY	ILE	PRO	PRO	PRO	THR	GLU	THR	ALA	TYR	PHE	GLY	ALA	LYS	GLU	PRO	GLU	ALA	TYR	PHE	GLY	ALA	PRO	ALA	PRO	PRO	PRO	TYR	THR	GLU	SER	PRO	GLU	ASP	SER																					
ARG	GLU	HIS	VAL	ASP	ARG	HIS	GLY	CYS	ILE	VAL	LYS	ILE	VAL	ARG	SER	SER	SER	THR	GLY	GLN	LYS	ASN	PHE	VAL	SER	SER	GLY	GLY	TRP	SER	HIS	PRO	GLN	PHE	LYS																																																

• Molecule 2: Calmodulin-1

Chain B:  70% 26%

MET	ALA	ASP	GLN	LEU	T6	L19	K22	E32	M37	M52	V56	D59	G60	D65	F66	P67	M72	R75	K76	M77	E83	E84	E85	E88	A89	F90	R91	V92	F93	D94	N98	G99	Y100	M110	T111	E115	K116	L117	T118	D119	E120	V122
M125	I126	R127	E128	E140	E141	F142	V143	M146	T147	A148	LYS																															

• Molecule 2: Calmodulin-1

Chain D:  68% 28%

MET	ALA	ASP	GLN	LEU	T6	L19	K22	D23	E32	M37	M52	E55	V56	D59	G60	D65	F69	M72	R75	K76	M77	E83	E84	E85	I86	R87	E88	A89	F90	R91	V92	F93	D94	N98	G99	Y100	M110	T111	E115	K116	L117	T118	D119	E120
E121	V122	M125	I126	R127	E128	F142	V143	Q144	M145	M146	T147	A148	LYS																															

• Molecule 2: Calmodulin-1

Chain F:  63% 33%

MET	ALA	ASP	GLN	LEU	T6	L19	K22	D23	I28	E32	M37	M52	V56	D59	G60	D65	F69	M72	R75	K76	M77	E83	E84	E85	I86	R87	E88	A89	F90	R91	V92	F93	D94	N98	G99	Y100	I101	S102	E105	L106	M110	T111
E115	K116	L117	T118	D119	E120	E121	V122	M125	E128	Q136	E140	E141	F142	V143	Q144	M145	M146	T147	A148	LYS																						

• Molecule 2: Calmodulin-1

Chain H:  68% 28%

MET	ALA	ASP	GLN	LEU	T6	L19	K22	D23	E32	M37	M52	V56	D65	F69	M72	M73	A74	R75	E83	E84	E85	I86	R87	E88	A89	F90	R91	V92	F93	D94	N98	G99	Y100	L106	R107	H108	V109	M112	L113	G114	E115	K116	L117	T118	D119	E120
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E121	V122	M125	E128	E140	E141	F142	V143	Q144	M145	M146	T147	A148	LYS
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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	151312	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 ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (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: 7Q0

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	0.23	0/2732	0.32	0/3688
1	C	0.23	0/2732	0.33	0/3688
1	E	0.23	0/2732	0.33	0/3688
1	G	0.22	0/2732	0.33	0/3688
2	B	0.12	0/1118	0.30	0/1502
2	D	0.11	0/1118	0.29	0/1502
2	F	0.11	0/1118	0.30	0/1502
2	H	0.11	0/1118	0.28	0/1502
All	All	0.20	0/15400	0.32	0/20760

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	2666	2723	2722	62	0
1	C	2666	2723	2722	64	0
1	E	2666	2723	2722	62	0
1	G	2666	2723	2722	61	0
2	B	1106	1023	1023	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1106	1023	1023	42	0
2	F	1106	1023	1023	48	0
2	H	1106	1023	1023	41	0
3	A	23	15	0	2	0
3	C	23	15	0	2	0
3	E	23	15	0	2	0
3	G	23	15	0	2	0
All	All	15180	15044	14980	365	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 12.

The worst 5 of 365 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:A:95:TYR:OH	1:A:140:GLU:OE1	1.97	0.83
1:C:95:TYR:OH	1:C:140:GLU:OE1	1.97	0.82
1:E:95:TYR:OH	1:E:140:GLU:OE1	1.97	0.82
1:G:95:TYR:OH	1:G:140:GLU:OE1	1.97	0.82
1:C:565:MET:HE3	1:C:565:MET:O	1.80	0.81

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	321/656 (49%)	306 (95%)	15 (5%)	0	100	100
1	C	321/656 (49%)	305 (95%)	16 (5%)	0	100	100
1	E	321/656 (49%)	307 (96%)	14 (4%)	0	100	100
1	G	321/656 (49%)	307 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	141/149 (95%)	138 (98%)	3 (2%)	0	100	100
2	D	141/149 (95%)	139 (99%)	2 (1%)	0	100	100
2	F	141/149 (95%)	138 (98%)	3 (2%)	0	100	100
2	H	141/149 (95%)	138 (98%)	3 (2%)	0	100	100
All	All	1848/3220 (57%)	1778 (96%)	70 (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	278/558 (50%)	277 (100%)	1 (0%)	84	90
1	C	278/558 (50%)	277 (100%)	1 (0%)	84	90
1	E	261/558 (47%)	259 (99%)	2 (1%)	73	86
1	G	278/558 (50%)	277 (100%)	1 (0%)	84	90
2	B	118/127 (93%)	118 (100%)	0	100	100
2	D	48/127 (38%)	48 (100%)	0	100	100
2	F	118/127 (93%)	118 (100%)	0	100	100
2	H	118/127 (93%)	118 (100%)	0	100	100
All	All	1497/2740 (55%)	1492 (100%)	5 (0%)	84	91

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

Mol	Chain	Res	Type
1	A	342	SER
1	C	342	SER
1	E	176	LEU
1	E	342	SER
1	G	342	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	575	HIS
1	E	575	HIS

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](#)

4 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	$\# Z > 2$
3	7Q0	A	801	-	26,26,26	1.53	5 (19%)	36,38,38	1.28	1 (2%)
3	7Q0	C	801	-	26,26,26	1.53	5 (19%)	36,38,38	1.30	3 (8%)
3	7Q0	E	801	-	26,26,26	1.52	5 (19%)	36,38,38	1.29	3 (8%)
3	7Q0	G	801	-	26,26,26	1.52	5 (19%)	36,38,38	1.29	3 (8%)

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
3	7Q0	A	801	-	-	4/8/13/13	0/4/4/4
3	7Q0	C	801	-	-	4/8/13/13	0/4/4/4
3	7Q0	E	801	-	-	4/8/13/13	0/4/4/4
3	7Q0	G	801	-	-	4/8/13/13	0/4/4/4

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	801	7Q0	C12-C11	-3.59	1.49	1.55
3	C	801	7Q0	C12-C11	-3.59	1.49	1.55
3	G	801	7Q0	C12-C11	-3.58	1.49	1.55
3	E	801	7Q0	C12-C11	-3.57	1.49	1.55
3	C	801	7Q0	C3-C4	-3.22	1.36	1.42

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	801	7Q0	C12-C10-C4	-2.33	105.94	108.80
3	E	801	7Q0	C12-C10-C4	-2.30	105.98	108.80
3	G	801	7Q0	C12-C10-C4	-2.27	106.02	108.80
3	A	801	7Q0	C12-C10-C4	-2.24	106.05	108.80
3	C	801	7Q0	C11-C12-C10	2.15	106.58	105.02

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

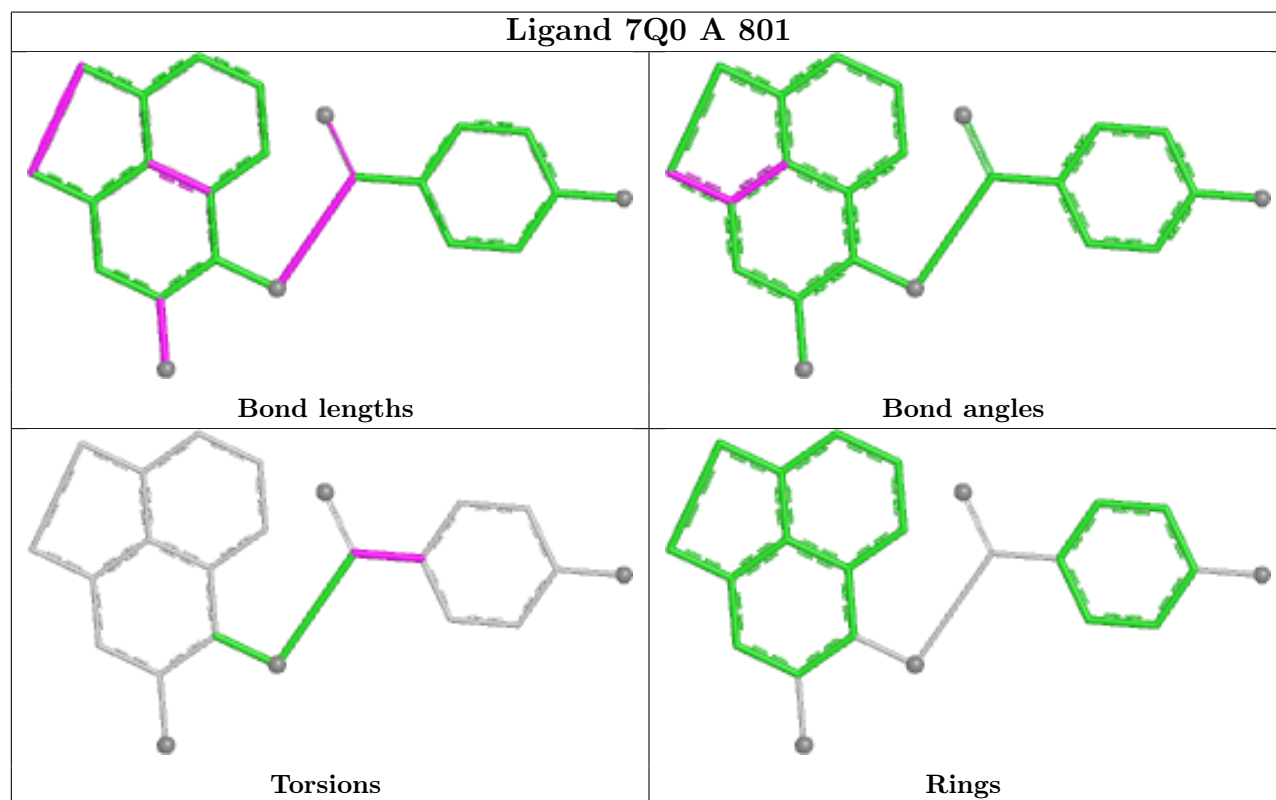
Mol	Chain	Res	Type	Atoms
3	E	801	7Q0	O1-C13-C14-C19
3	A	801	7Q0	O1-C13-C14-C19
3	C	801	7Q0	O1-C13-C14-C19
3	G	801	7Q0	O1-C13-C14-C19
3	E	801	7Q0	N1-C13-C14-C19

There are no ring outliers.

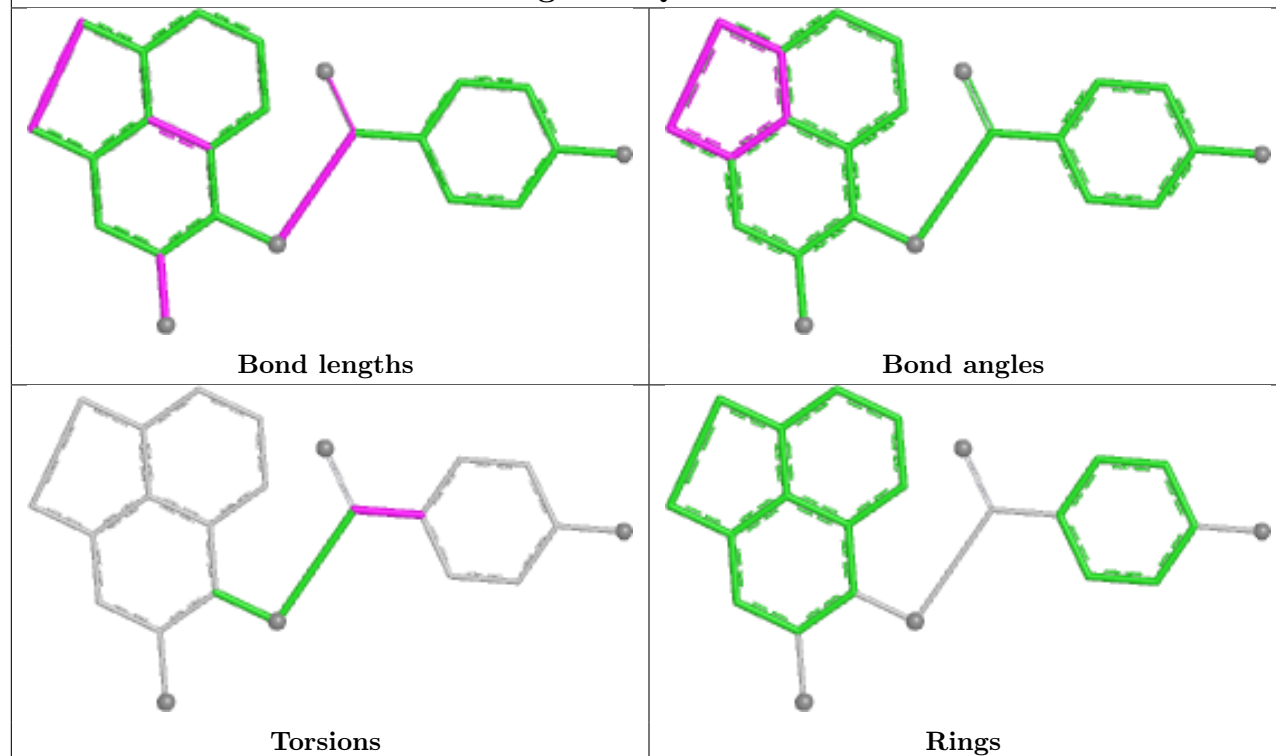
4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	7Q0	2	0
3	C	801	7Q0	2	0
3	E	801	7Q0	2	0
3	G	801	7Q0	2	0

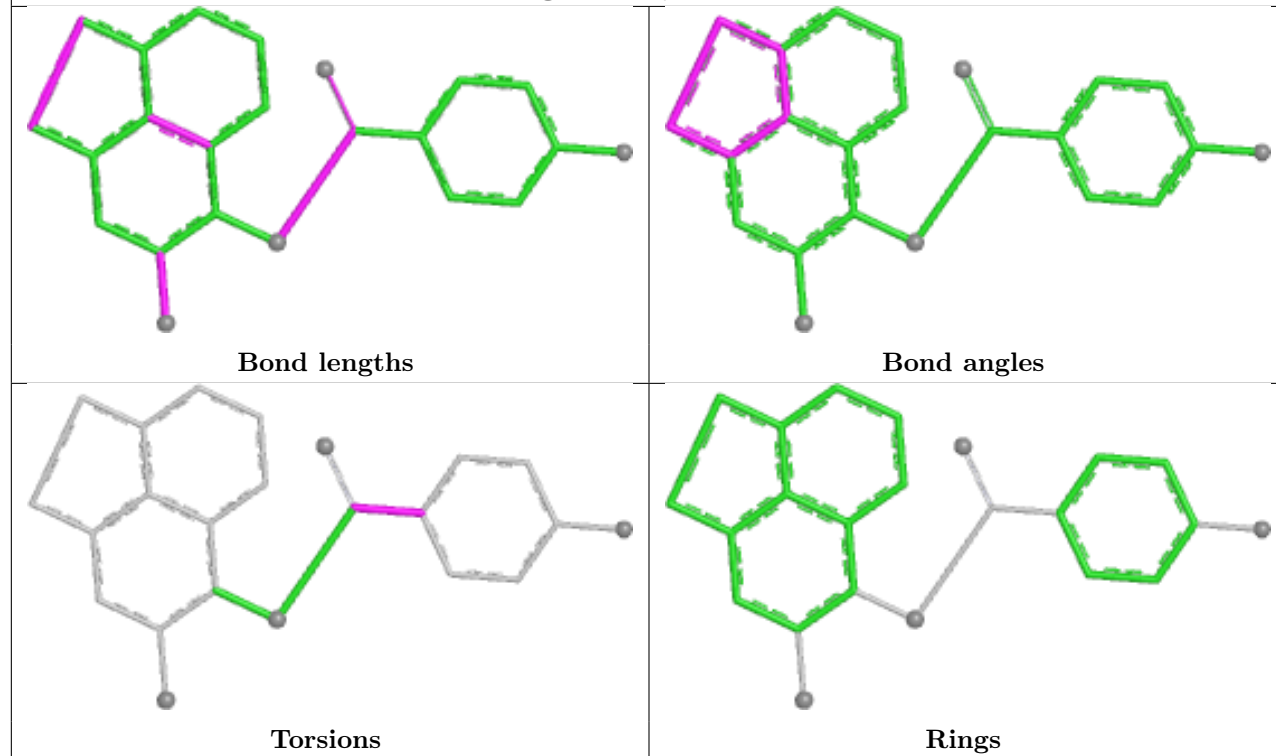
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

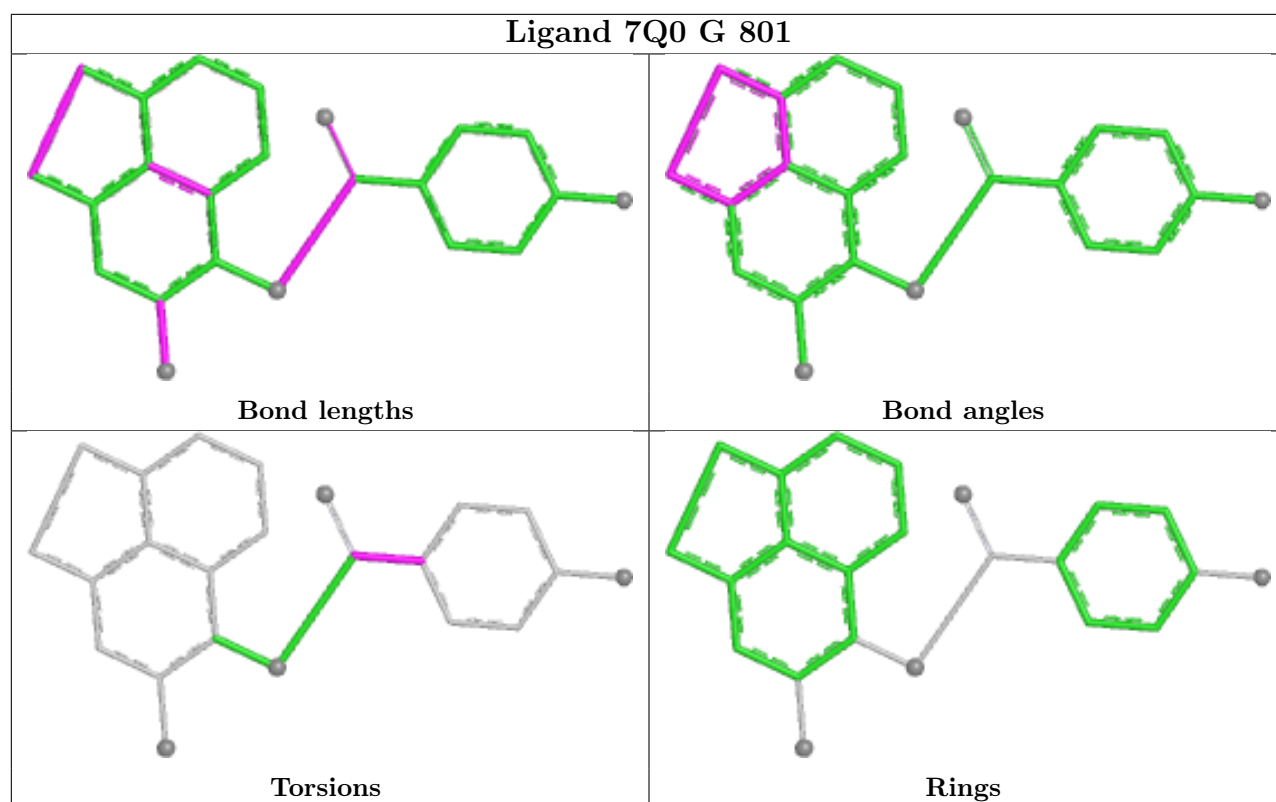


Ligand 7Q0 C 801



Ligand 7Q0 E 801





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-38041. 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.