



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:19 PM UTC

PDB ID : 6KZO / pdb_00006kzo
EMDB ID : EMD-0791
Title : membrane protein
Authors : Yan, N.
Deposited on : 2019-09-25
Resolution : 3.30 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 : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

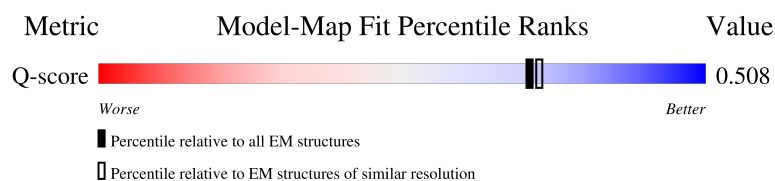
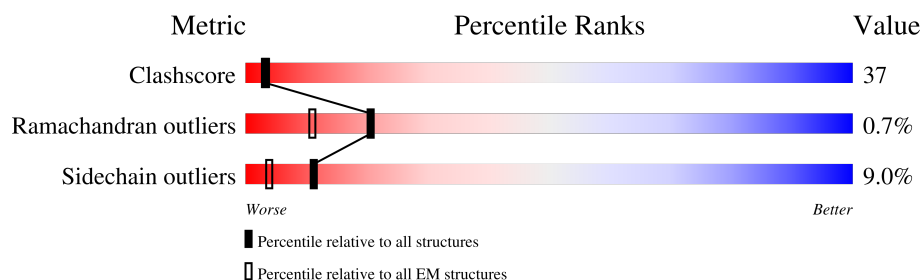
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2261	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8238 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.

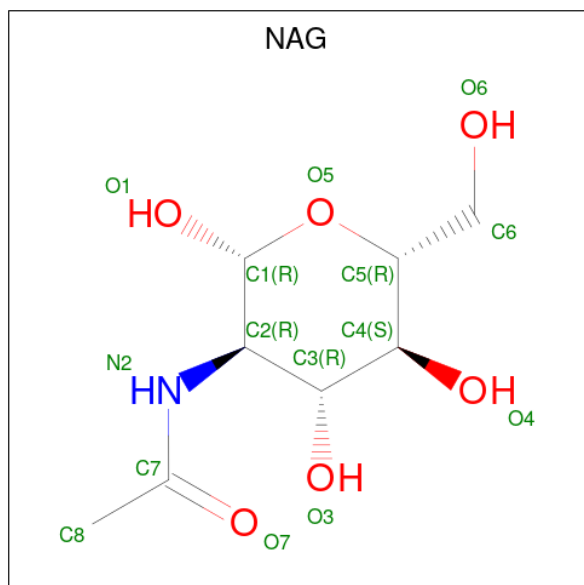
- Molecule 1 is a protein called Voltage-dependent T-type calcium channel subunit alpha-1G.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	967	7739	5114	1248	1313	64	0	0

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
2	A	2	Total	Ca	0
			2	2	

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



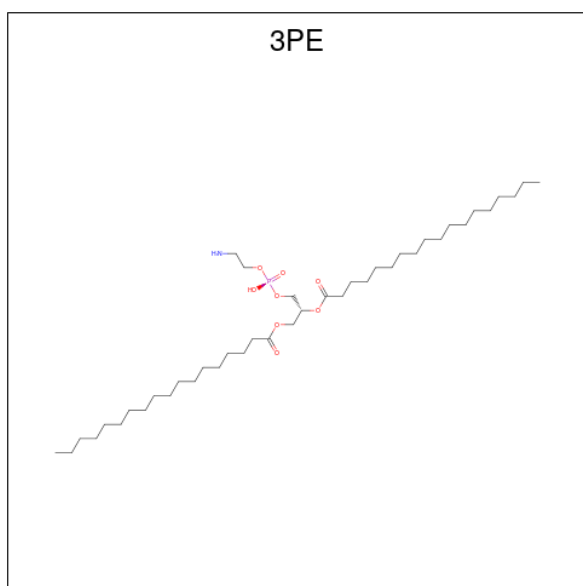
Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 4 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



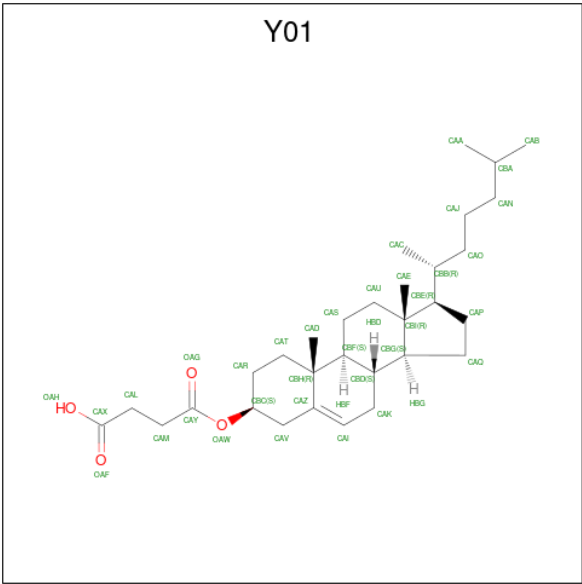
Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			31	21	1	8	1	
4	A	1	Total	C	N	O	P	0
			38	28	1	8	1	
4	A	1	Total	C	N	O	P	0
			35	25	1	8	1	
4	A	1	Total	C				0
			17	17				
4	A	1	Total	C	N	O	P	0
			44	34	1	8	1	
4	A	1	Total	C	N	O	P	0
			35	25	1	8	1	
4	A	1	Total	C	N	O	P	0
			37	27	1	8	1	
4	A	1	Total	C	N	O	P	0
			39	29	1	8	1	

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Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	C	0
			17	17	
4	A	1	Total	C	0
			17	17	
4	A	1	Total	C	0
			14	14	
4	A	1	Total	C	0
			16	16	
4	A	1	Total	C	0
			17	17	

- Molecule 5 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula: C₃₁H₅₀O₄).

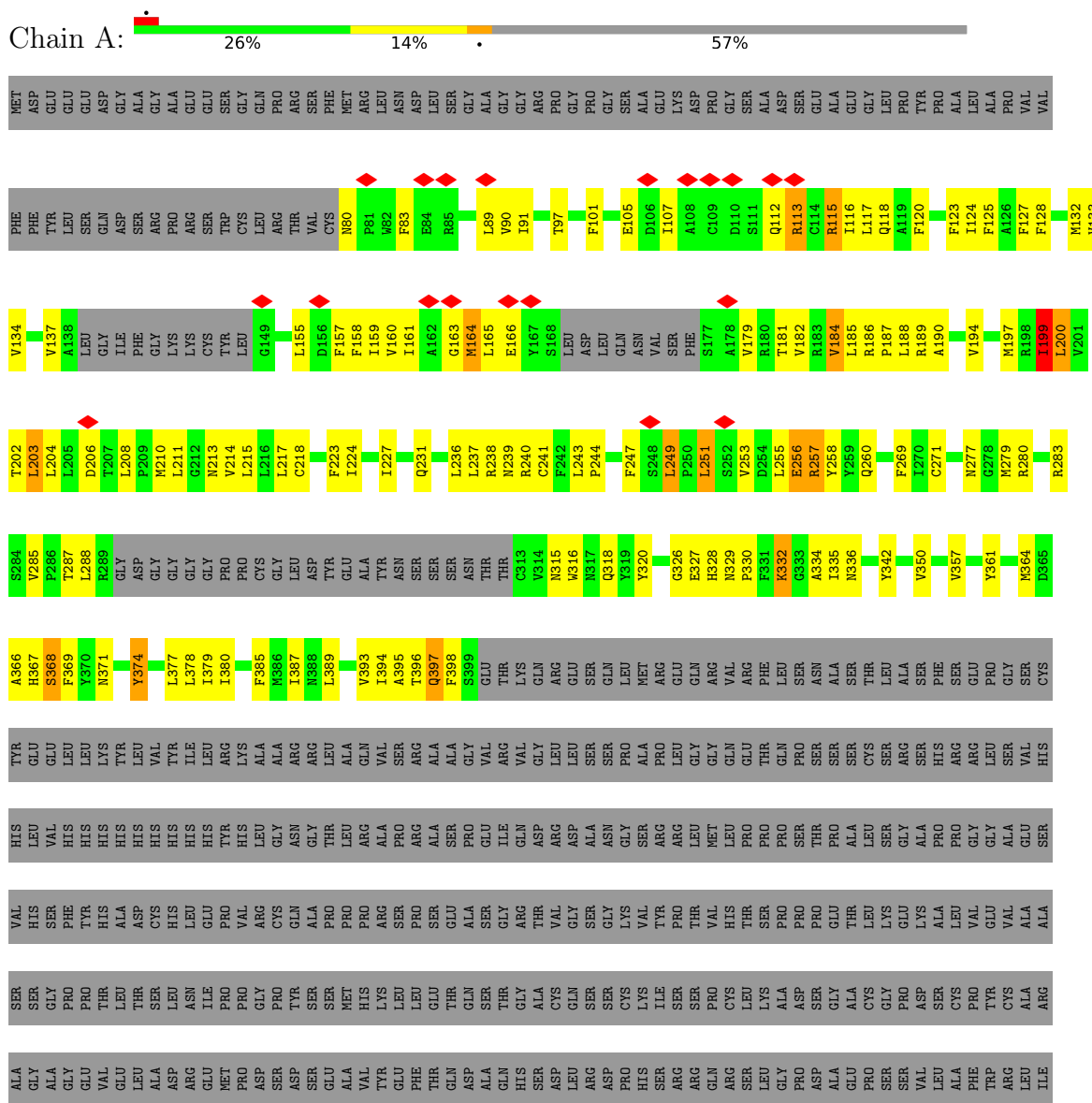


Mol	Chain	Residues	Atoms			AltConf
5	A	1	Total	C	O	0
			35	31	4	
5	A	1	Total	C	O	0
			35	31	4	

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 and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: Voltage-dependent T-type calcium channel subunit alpha-1G





PRO	SER	GLY	GLU	GLN	LYS	HIS	SER
SER	GLY	ALA	ALA	ALA	LEU	LEU	PRO
PRO	PRO	GLN	GLN	GLN	PRO	SER	LYS
LYS	SER	HIS	HIS	PRO	PRO	GLY	THR
ASP	ARG	SER	ARG	SER	GLY	ALA	GLY
VAL	ASP	PRO	ASP	ARG	GLY	LEU	ALA
LEU	LYS	LYS	LEU	SER	PRO	HIS	HIS
SER	LYS	LYS	LYS	SER	PRO	LEU	ALA
LEU	LEU	LEU	CYS	SER	ALA	GLY	ALA
SER	GLY	SER	TYR	ILE	GLN	ARG	HIS
LEU	PRO	SER	VAL	SER	ARG	GLY	ALA
SER	PRO	PRO	VAL	LYS	PRO	TRP	ARG
SER	ILE	GLU	ALA	HIS	SER	GLY	ALA
ASP	THR	THR	ALA	GLN	ARG	LEU	ALA
PRO	THR	ILE	SER	PRO	PRO	LYS	HIS
ALA	ASP	ILE	CYS	PRO	ALA	ALA	PHE
ASP	PRO	PRO	ARG	GLN	ALA	SER	SER
ASP	GLU	GLU	ARG	PRO	ILE	GLY	LEU
PRO	SER	GLN	THR	GLY	THR	VAL	THR
GLY	GLY	GLY	THR	PRO	ASP	GLY	THR
PRO	PRO	PRO	TRP	SER	LEU	SER	MET
ARG	ARG	LEU	LEU	PRO	SER	LEU	THR
THR	THR	LEU	LEU	ASP	VAL	GLN	PRO
PRO	PRO	PRO	GLU	GLY	HIS	HIS	PRO
SER	SER	SER	ARG	LYS	PRO	THR	THR
PRO	PRO	ARG	ARG	GLY	ALA	GLU	GLU
GLY	GLY	HIS	HIS	PRO	ASP	ASP	LEU
ILE	ILE	SER	SER	PRO	THR	THR	PRO
CYS	CYS	ILE	ILE	PRO	GLY	GLY	SER
LEU	LEU	ALA	THR	ALA	TYR	PRO	PRO
ARG	ARG	VAL	VAL	ARG	ILE	ASP	ASP
ARG	ARG	SER	SER	SER	LEU	LEU	LEU
ARG	ARG	CYS	CYS	SER	ALA	GLN	THR
ALA	ALA	LEU	LEU	LEU	VAL	PRO	THR
PRO	PRO	ASP	ASP	GLY	LYS	ARG	ARG
SER	SER	GLN	GLN	THR	ALA	LYS	SER
LYS	LYS	PRO	PRO	GLU	PRO	GLY	GLY
ASP	ASP	THR	THR	THR	SER	VAL	VAL
PRO	PRO	LEU	LEU	TRP	LEU	HIS	SER
ALA	ALA	THR	THR	ILE	ALA	GLN	THR
ASP	ASP	ASP	ASP	GLY	ARG	PRO	HIS
LEU	LEU	SER	SER	ASP	ALA	HIS	SER
ASP	ASP	PRO	PRO	TYR	SER	LEU	LEU
PRO	PRO	LEU	LEU	GLY	PRO	ALA	ASN
PRO	PRO	GLY	GLY	PRO	TRP	THR	ASP
PRO	PRO	ALA	ALA	GLY	GLY	GLY	SER
PRO	PRO	SER	SER	GLN	SER	THR	TYR
PRO	PRO	THR	THR	GLU	THR	ILE	MET
PRO	PRO	SER	SER	GLY	GLY	CYS	CYS
PRO	PRO	LEU	LEU	THR	THR	PRO	ARG

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	105559	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.163	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	349.12, 349.12, 349.12	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.091, 1.091, 1.091	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: 3PE, Y01, CA, NAG

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	0.53	0/7904	0.86	14/10711 (0.1%)

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	334	ALA	N-CA-C	9.91	122.16	111.36
1	A	1674	VAL	N-CA-C	7.67	117.74	110.53
1	A	1447	ASP	N-CA-C	7.42	119.16	111.14
1	A	256	GLU	N-CA-C	7.31	119.25	111.28
1	A	327	GLU	N-CA-C	7.20	119.13	111.28

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	7739	0	7919	592	0
2	A	2	0	0	0	0
3	A	70	0	65	7	0
4	A	357	0	508	52	0
5	A	70	0	98	17	0
All	All	8238	0	8590	620	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 37.

The worst 5 of 620 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:1420:GLY:HA3	1:A:1437:TYR:CD2	1.55	1.42
1:A:1672:ILE:HD12	1:A:1676:ALA:CB	1.64	1.26
1:A:1418:CYS:HB3	1:A:1439:TRP:CZ3	1.75	1.21
1:A:1672:ILE:CD1	1:A:1676:ALA:HB3	1.70	1.21
1:A:210:MET:HG2	1:A:397:GLN:NE2	1.57	1.19

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	941/2261 (42%)	903 (96%)	31 (3%)	7 (1%)	18	49

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	257	ARG
1	A	907	ASP
1	A	765	HIS
1	A	837	ARG
1	A	107	ILE

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	855/1946 (44%)	778 (91%)	77 (9%)	9	31

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1600	LEU
1	A	1723	LEU
1	A	1620	LEU
1	A	1684	ILE
1	A	1828	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1409	GLN
1	A	1448	ASN
1	A	1442	HIS
1	A	1486	HIS
1	A	773	ASN

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](#)

Of 22 ligands modelled in this entry, 2 are monoatomic - leaving 20 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$
4	3PE	A	2310	-	34,34,50	1.19	2 (5%)	37,39,55	1.22	4 (10%)
3	NAG	A	2304	1	14,14,15	0.23	0	17,19,21	0.53	0
3	NAG	A	2306	1	14,14,15	0.43	0	17,19,21	1.59	4 (23%)
4	3PE	A	2312	-	43,43,50	1.05	2 (4%)	46,48,55	1.03	4 (8%)
4	3PE	A	2313	-	34,34,50	1.14	2 (5%)	37,39,55	1.11	2 (5%)
4	3PE	A	2318	-	13,13,50	0.23	0	12,12,55	0.61	0
4	3PE	A	2308	-	30,30,50	1.24	2 (6%)	33,35,55	1.09	3 (9%)
5	Y01	A	2321	-	38,38,38	4.24	12 (31%)	57,57,57	2.37	20 (35%)
4	3PE	A	2309	-	37,37,50	1.10	2 (5%)	40,42,55	1.07	3 (7%)
3	NAG	A	2305	1	14,14,15	0.29	0	17,19,21	0.57	0
4	3PE	A	2320	-	16,16,50	0.24	0	15,15,55	0.56	0
5	Y01	A	2322	-	38,38,38	4.17	12 (31%)	57,57,57	1.96	14 (24%)
4	3PE	A	2311	-	16,16,50	0.28	0	15,15,55	0.50	0
3	NAG	A	2303	1	14,14,15	0.40	0	17,19,21	0.44	0
3	NAG	A	2307	1	14,14,15	0.37	0	17,19,21	0.48	0
4	3PE	A	2315	-	38,38,50	1.11	2 (5%)	41,43,55	0.94	3 (7%)
4	3PE	A	2314	-	36,36,50	1.11	2 (5%)	39,41,55	1.25	3 (7%)
4	3PE	A	2316	-	16,16,50	0.24	0	15,15,55	0.57	0
4	3PE	A	2319	-	15,15,50	0.26	0	14,14,55	0.51	0
4	3PE	A	2317	-	16,16,50	0.35	0	15,15,55	0.39	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
4	3PE	A	2310	-	-	15/38/38/54	-
3	NAG	A	2304	1	-	2/6/23/26	0/1/1/1
3	NAG	A	2306	1	-	6/6/23/26	0/1/1/1
4	3PE	A	2312	-	-	11/47/47/54	-
4	3PE	A	2313	-	-	5/38/38/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	3PE	A	2318	-	-	0/11/11/54	-
4	3PE	A	2308	-	-	5/34/34/54	-
5	Y01	A	2321	-	-	8/19/77/77	0/4/4/4
4	3PE	A	2309	-	-	13/41/41/54	-
3	NAG	A	2305	1	-	0/6/23/26	0/1/1/1
4	3PE	A	2320	-	-	0/14/14/54	-
5	Y01	A	2322	-	-	4/19/77/77	0/4/4/4
4	3PE	A	2311	-	-	0/14/14/54	-
3	NAG	A	2303	1	-	0/6/23/26	0/1/1/1
3	NAG	A	2307	1	-	2/6/23/26	0/1/1/1
4	3PE	A	2315	-	-	5/42/42/54	-
4	3PE	A	2314	-	-	10/40/40/54	-
4	3PE	A	2316	-	-	0/14/14/54	-
4	3PE	A	2319	-	-	0/13/13/54	-
4	3PE	A	2317	-	-	0/14/14/54	-

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2321	Y01	CAI-CAZ	17.68	1.69	1.33
5	A	2322	Y01	CAI-CAZ	17.59	1.69	1.33
5	A	2322	Y01	CBH-CBF	7.40	1.67	1.56
5	A	2321	Y01	CBH-CBF	7.16	1.67	1.56
5	A	2321	Y01	CAU-CBI	-7.14	1.41	1.54

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2321	Y01	CBI-CBE-CBB	-5.81	110.53	119.50
5	A	2321	Y01	CBG-CBI-CBE	5.47	106.38	100.10
5	A	2322	Y01	CAD-CBH-CBF	-5.18	105.85	111.66
5	A	2322	Y01	CAK-CAI-CAZ	-4.82	116.89	125.02
5	A	2321	Y01	CAV-CAZ-CBH	-4.80	110.28	116.42

There are no chirality outliers.

5 of 86 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2306	NAG	C8-C7-N2-C2
3	A	2306	NAG	O7-C7-N2-C2

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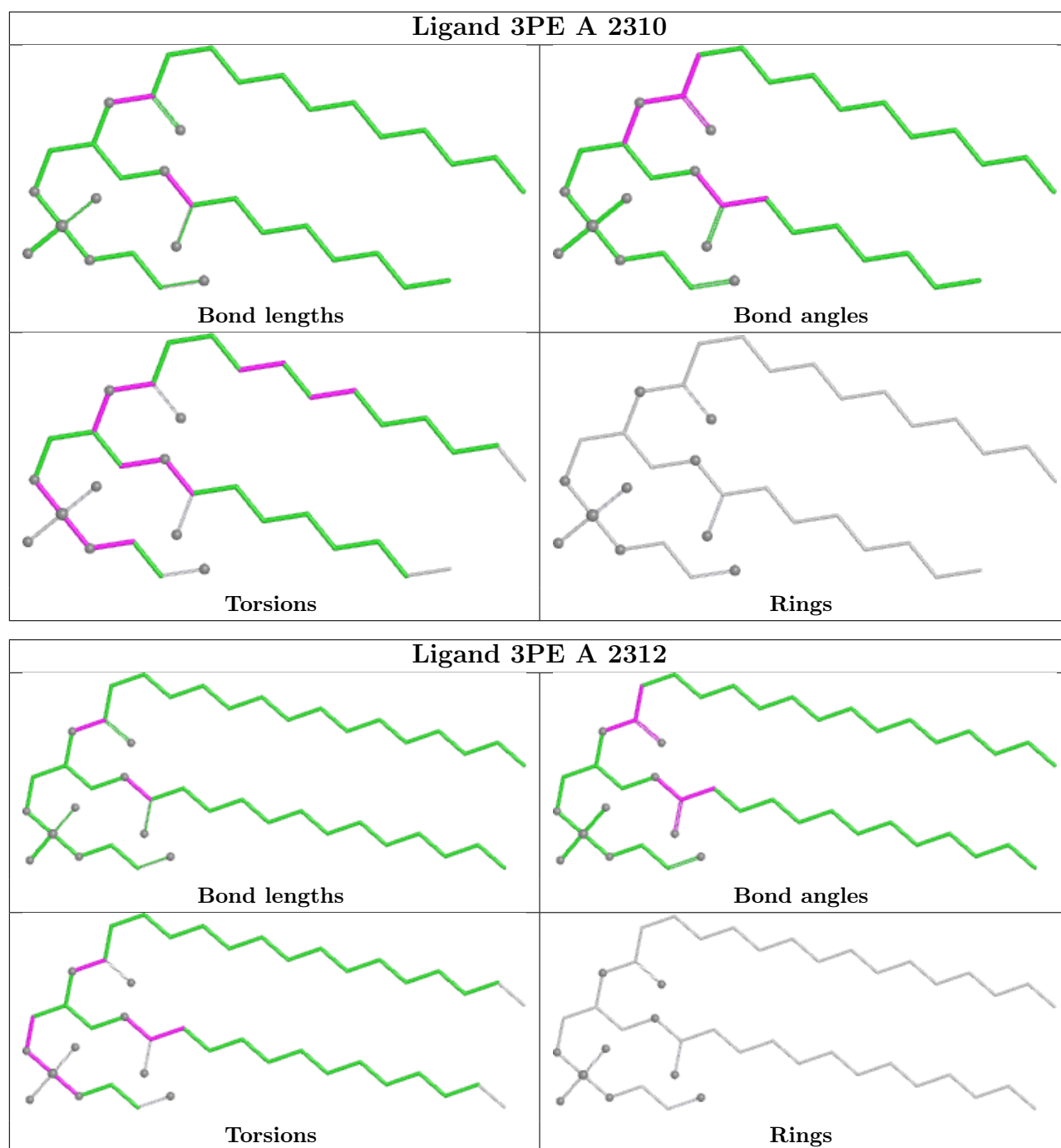
Mol	Chain	Res	Type	Atoms
4	A	2308	3PE	C1-O11-P-O13
4	A	2308	3PE	C1-O11-P-O14
4	A	2309	3PE	C11-O13-P-O11

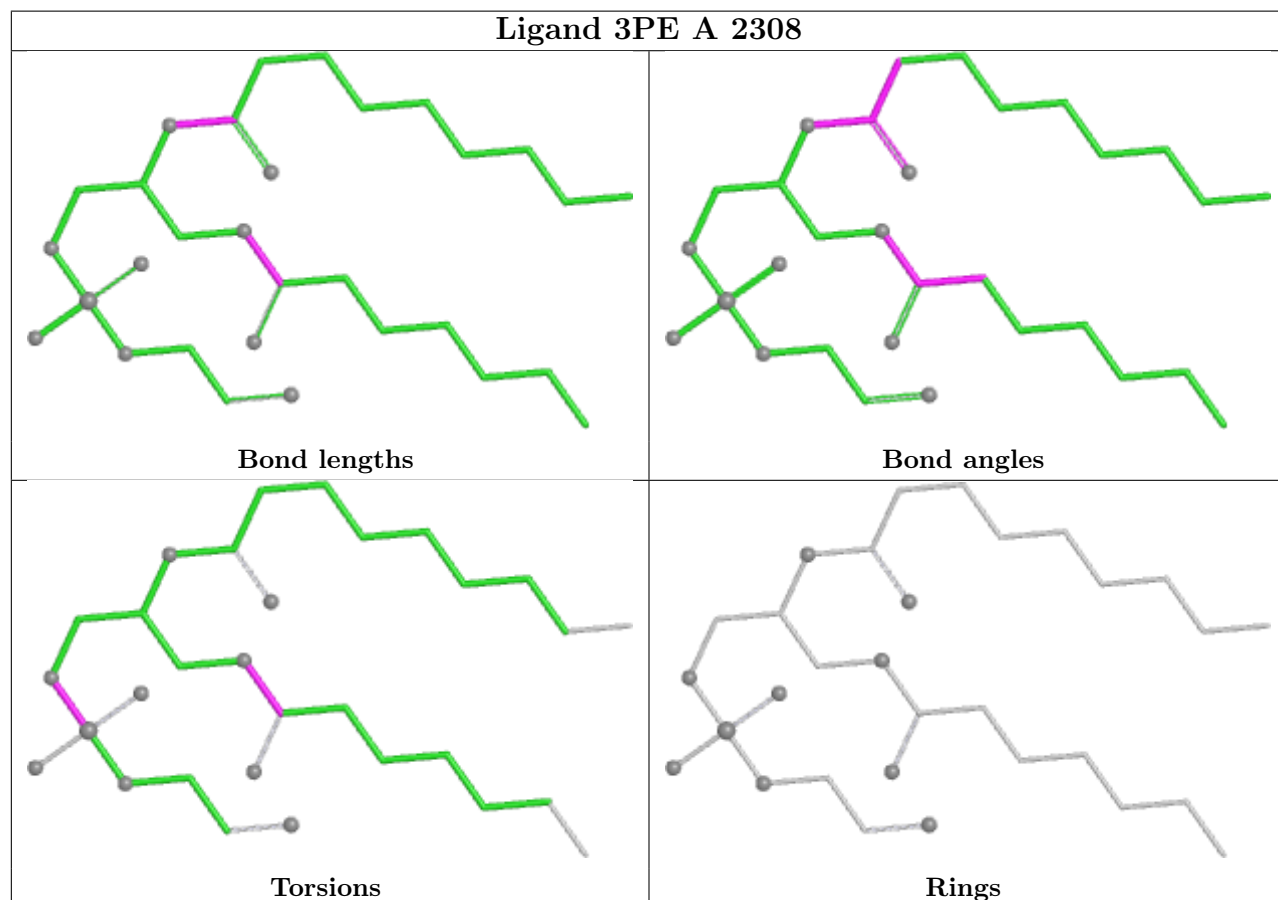
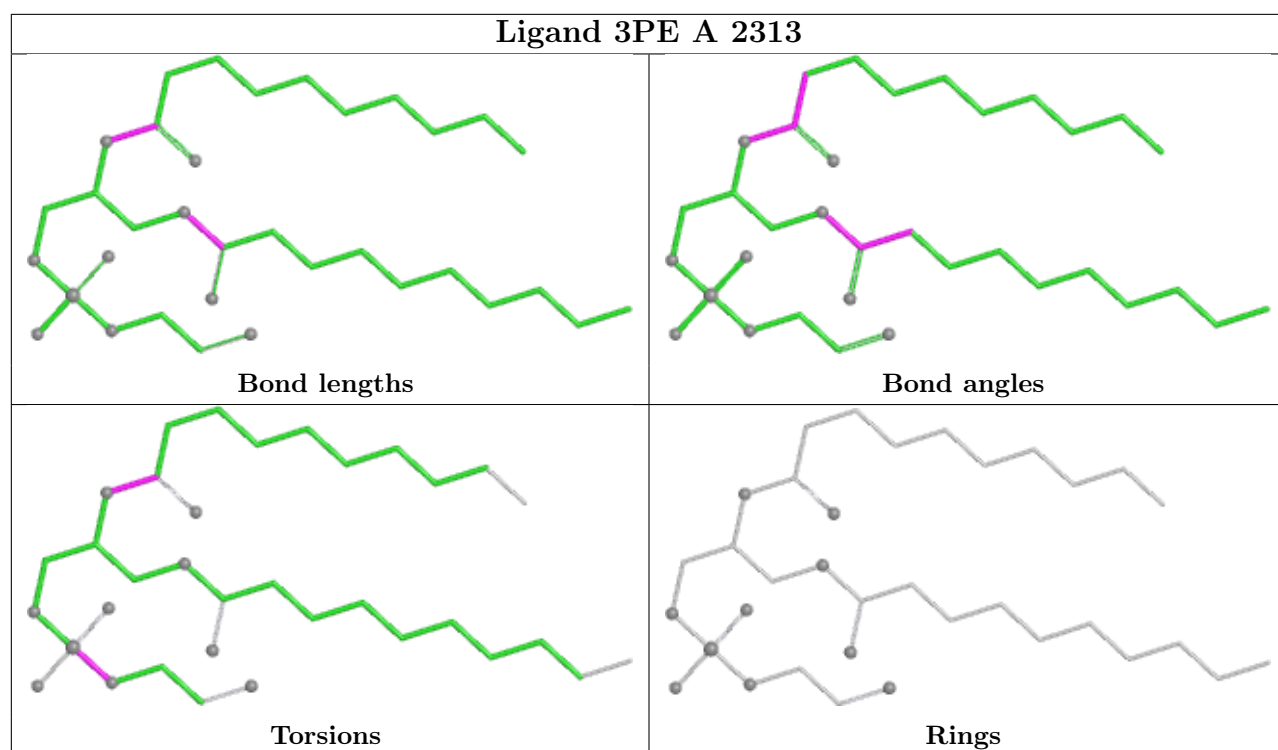
There are no ring outliers.

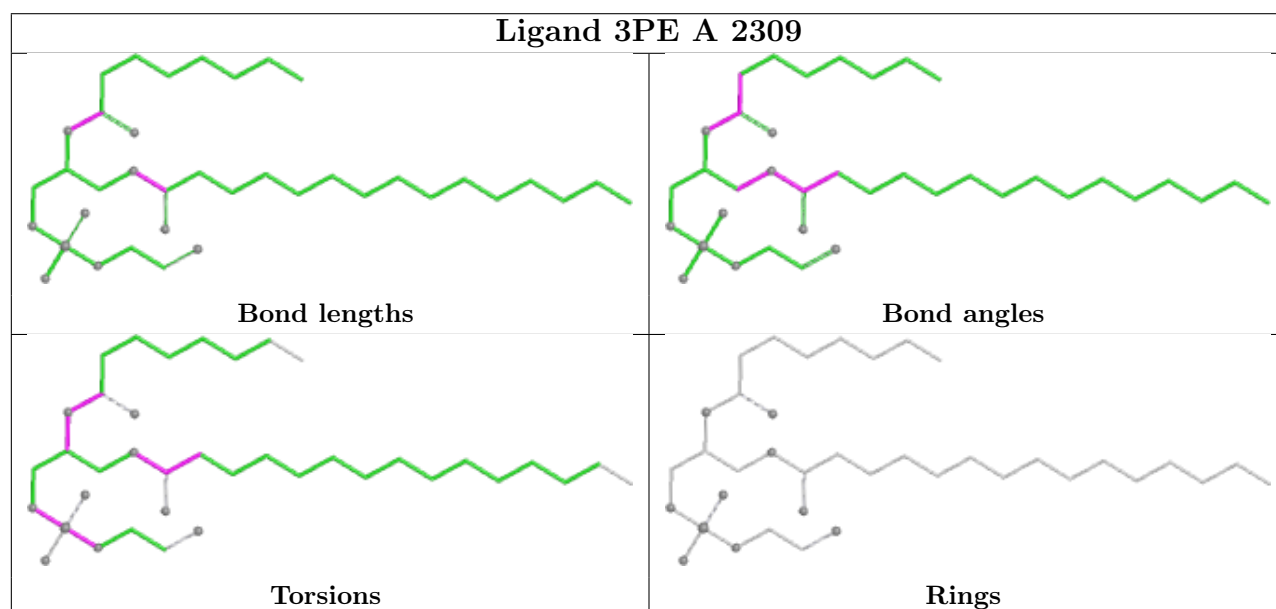
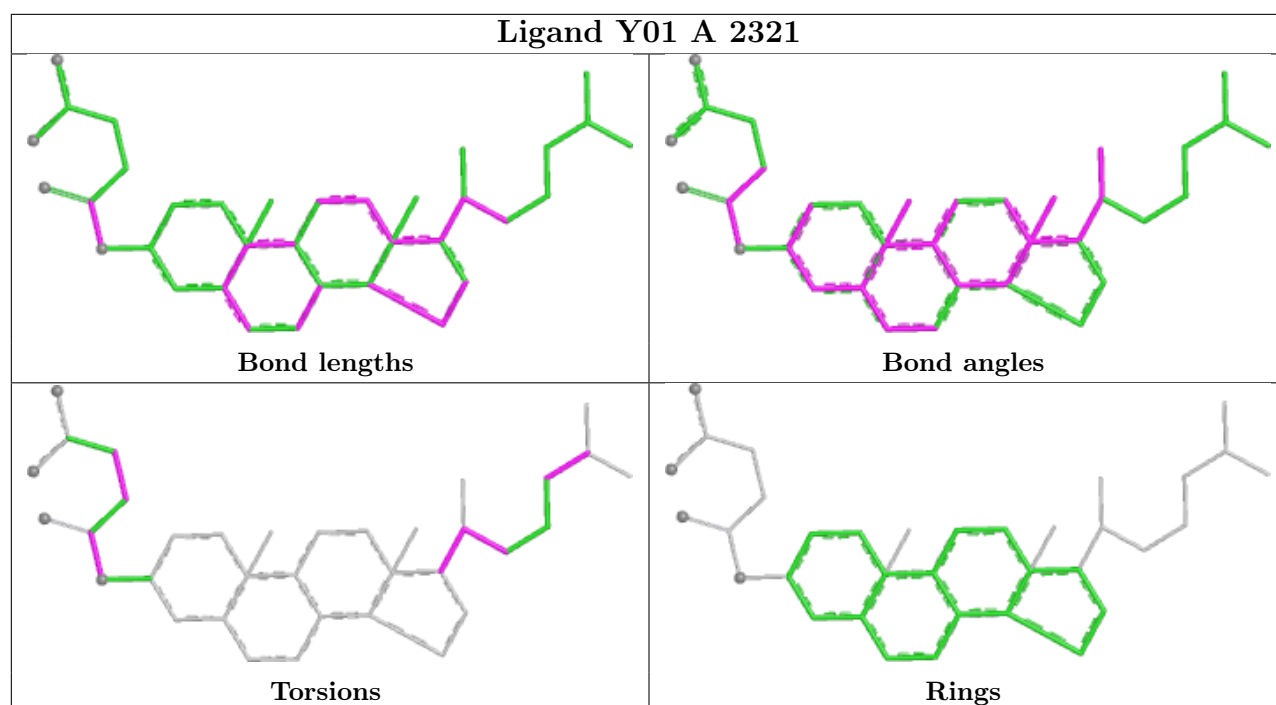
17 monomers are involved in 73 short contacts:

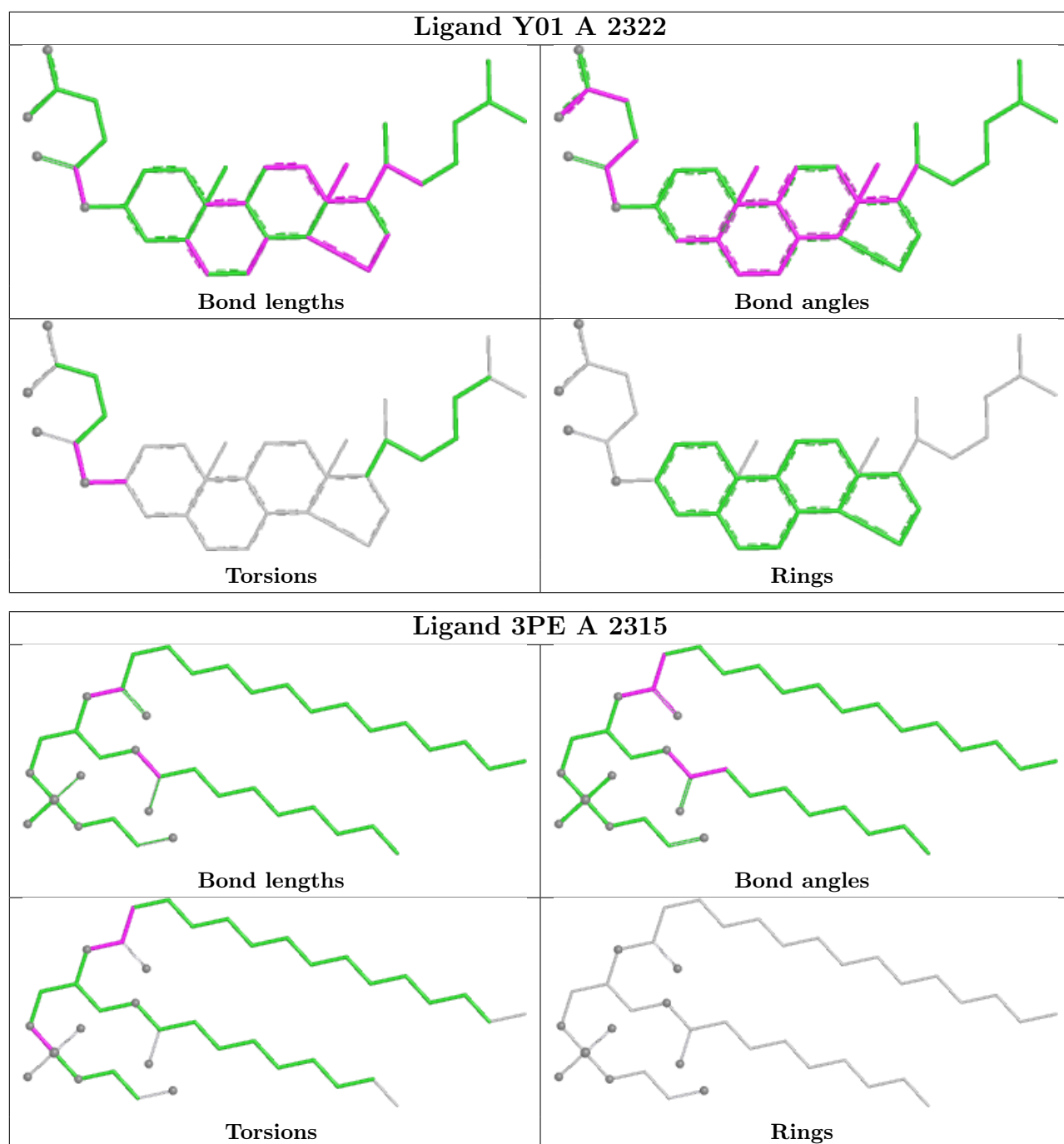
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2310	3PE	4	0
3	A	2306	NAG	6	0
4	A	2312	3PE	9	0
4	A	2313	3PE	3	0
4	A	2318	3PE	3	0
4	A	2308	3PE	5	0
5	A	2321	Y01	15	0
4	A	2309	3PE	7	0
3	A	2305	NAG	1	0
4	A	2320	3PE	6	0
5	A	2322	Y01	2	0
4	A	2311	3PE	1	0
4	A	2315	3PE	4	0
4	A	2314	3PE	5	0
4	A	2316	3PE	6	0
4	A	2319	3PE	6	0
4	A	2317	3PE	2	0

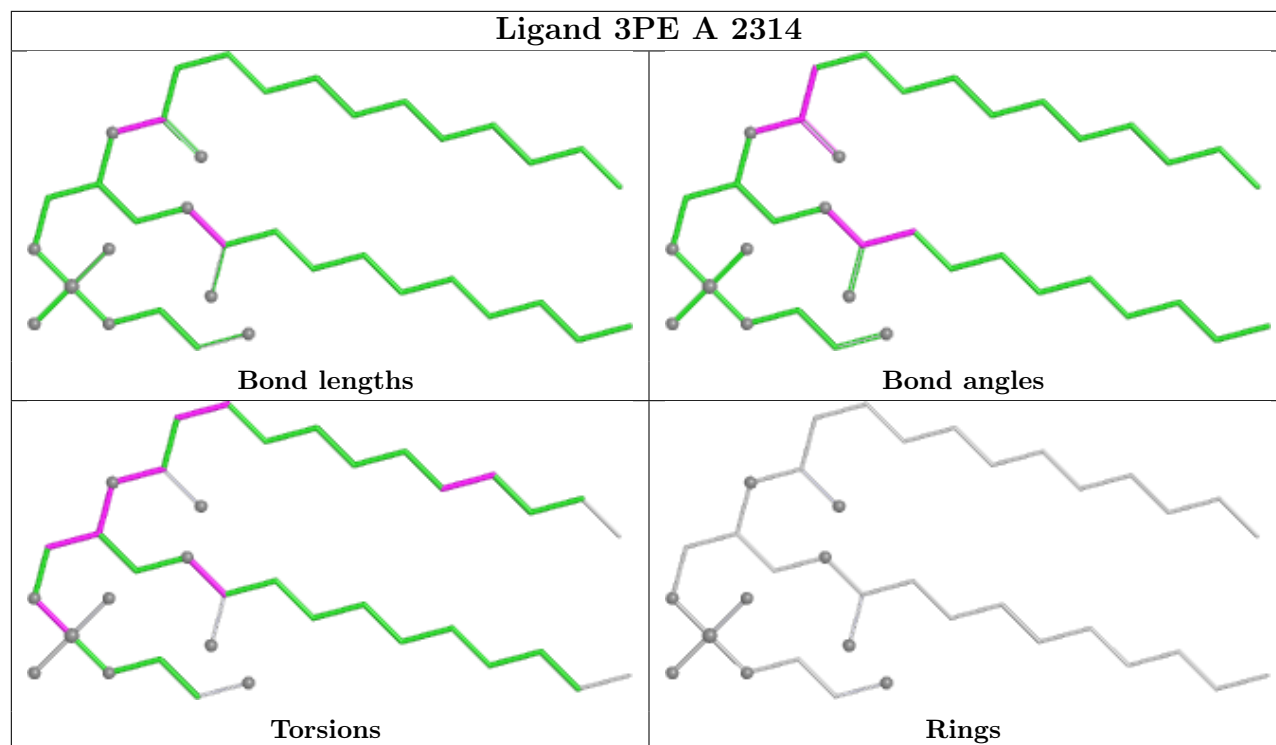
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

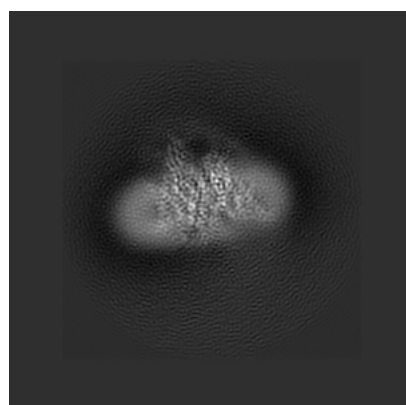
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0791. These allow visual inspection of the internal detail of the map and identification of artifacts.

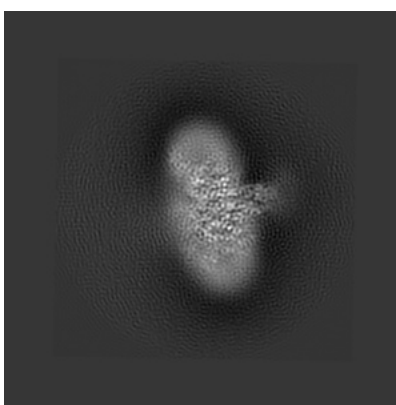
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

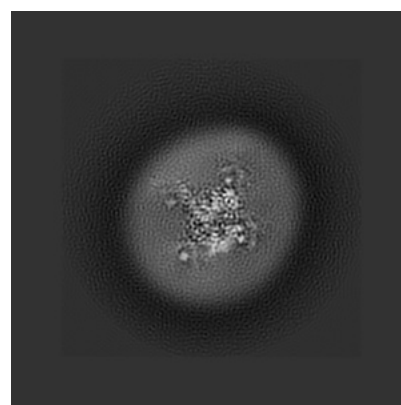
6.1.1 Primary map



X



Y

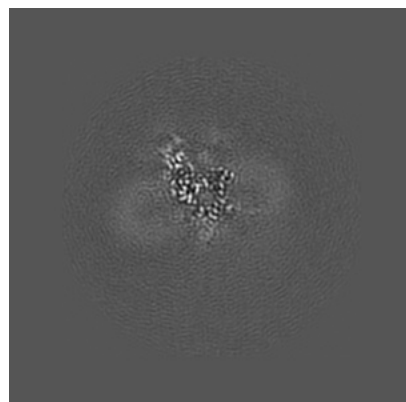


Z

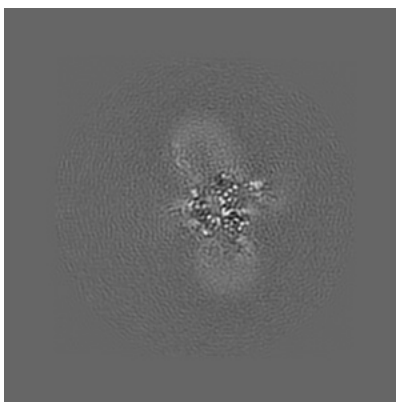
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

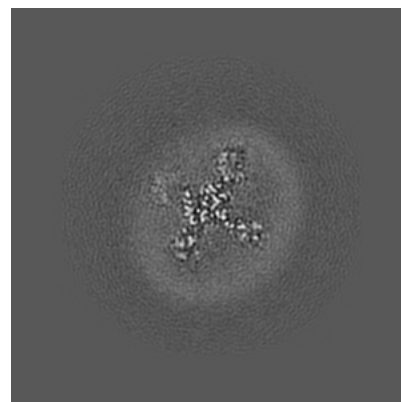
6.2.1 Primary map



X Index: 160



Y Index: 160

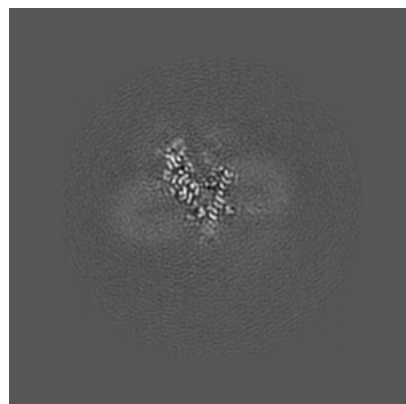


Z Index: 160

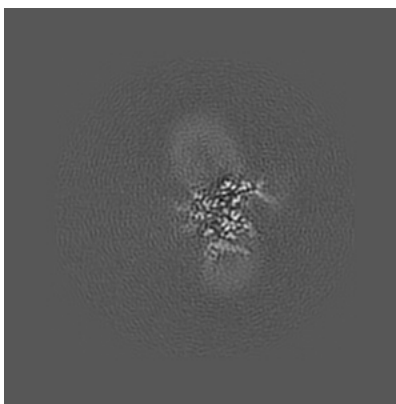
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

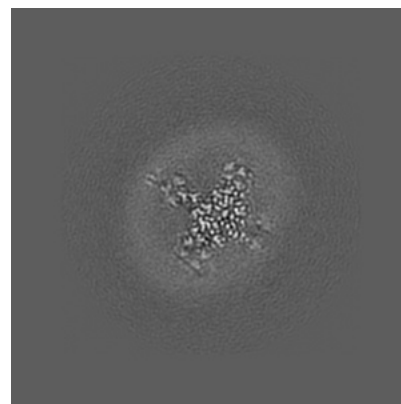
6.3.1 Primary map



X Index: 161



Y Index: 166

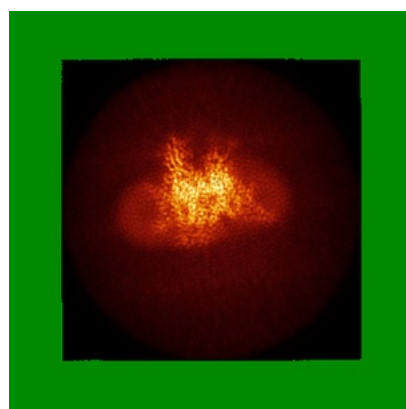


Z Index: 175

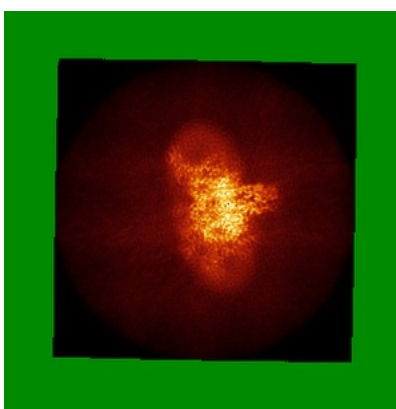
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

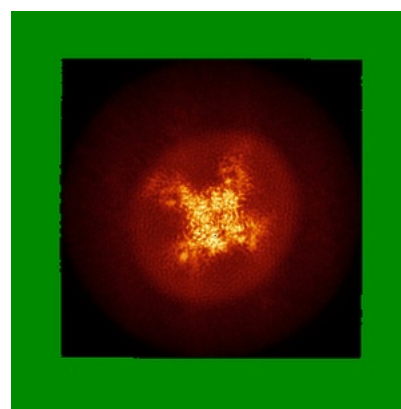
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

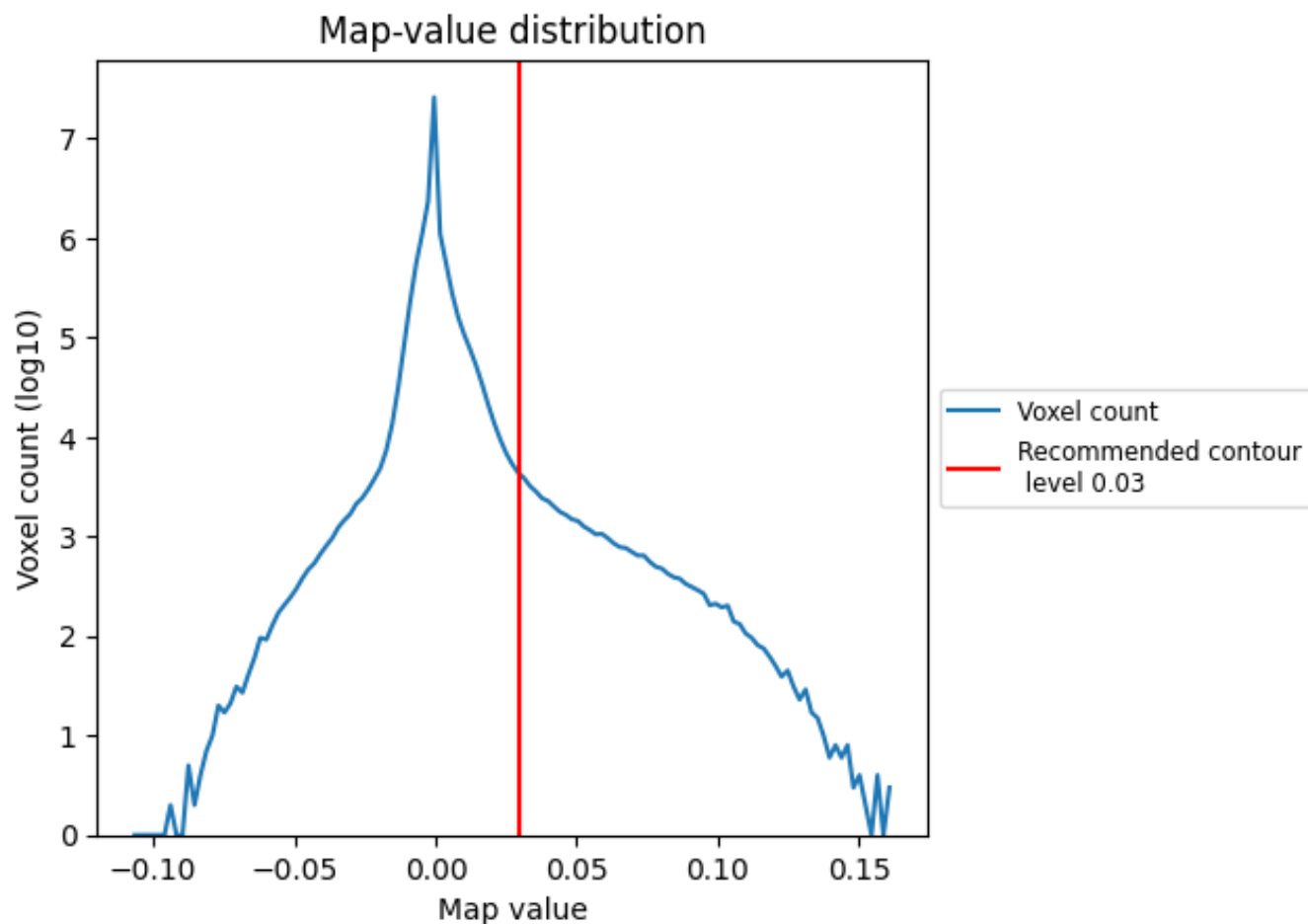
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

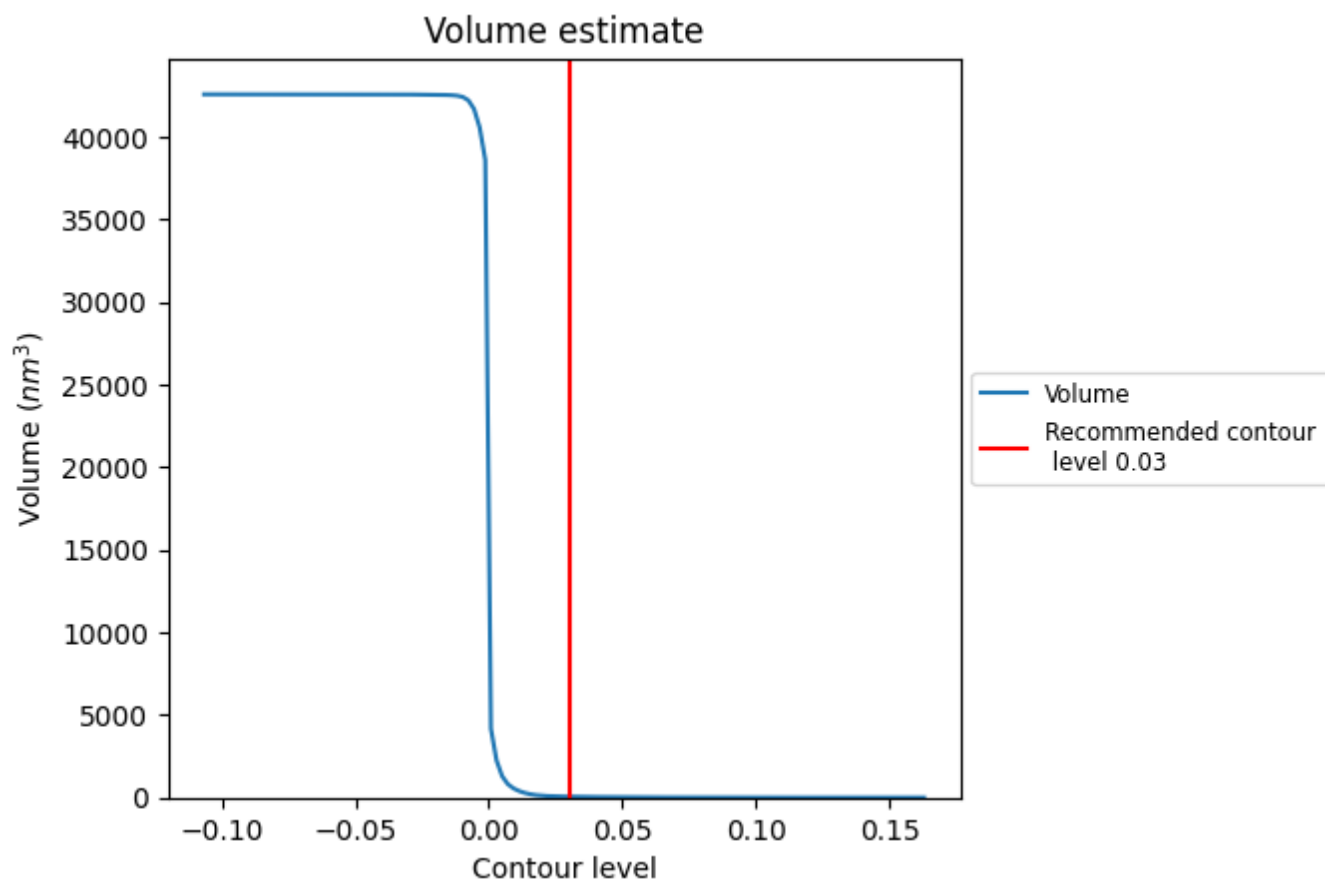
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

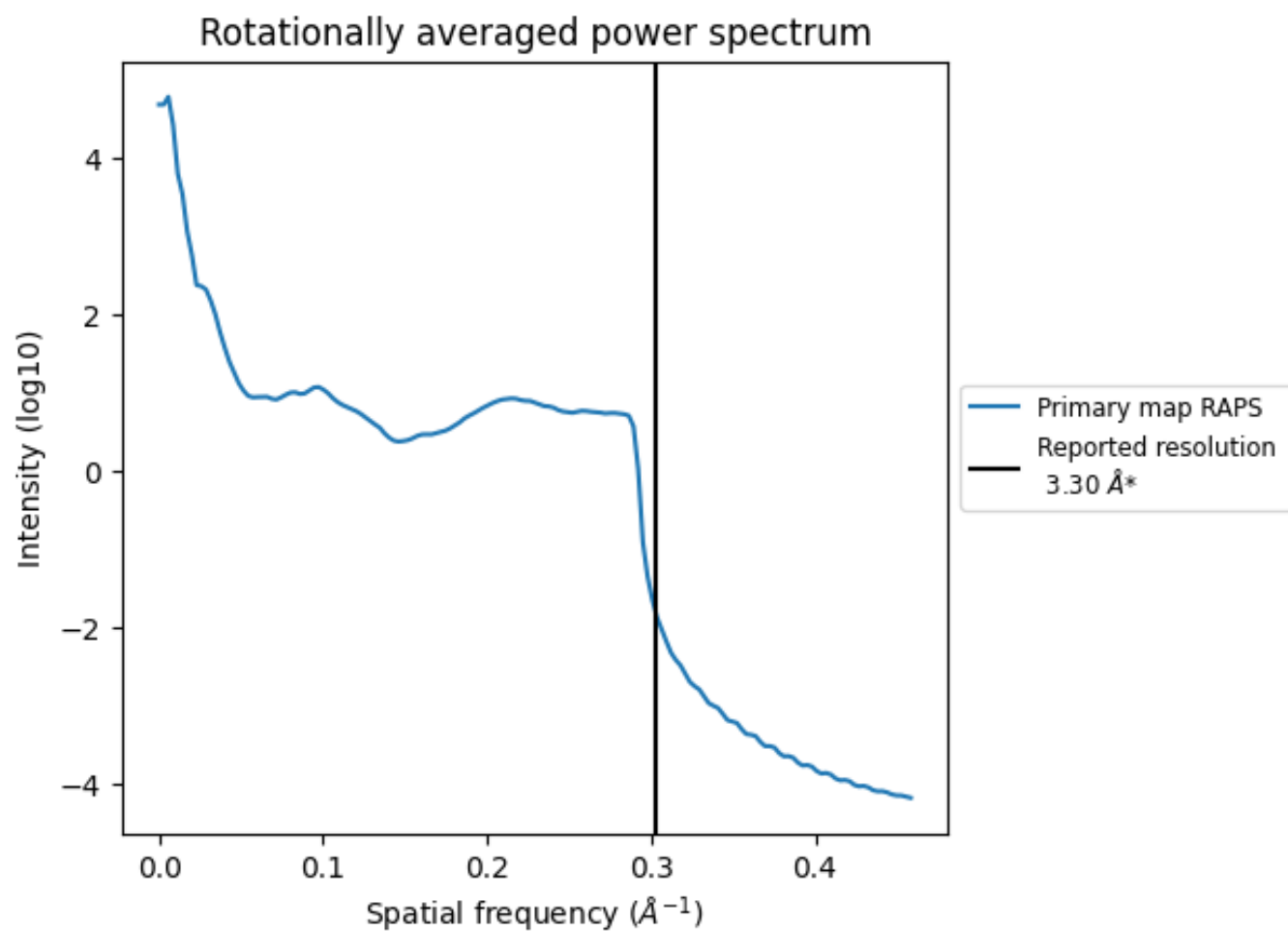
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 54 nm^3 ; this corresponds to an approximate mass of 48 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation

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

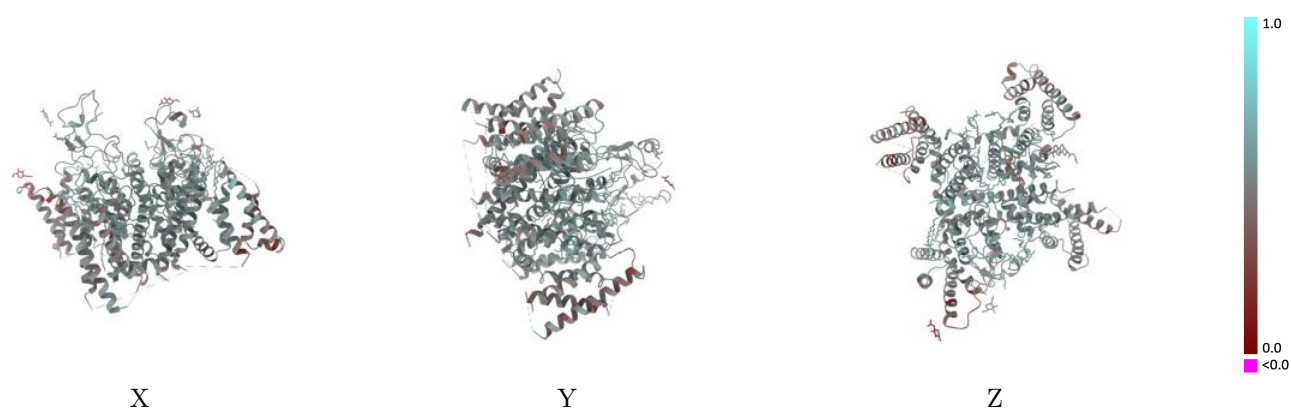
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0791 and PDB model 6KZO. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

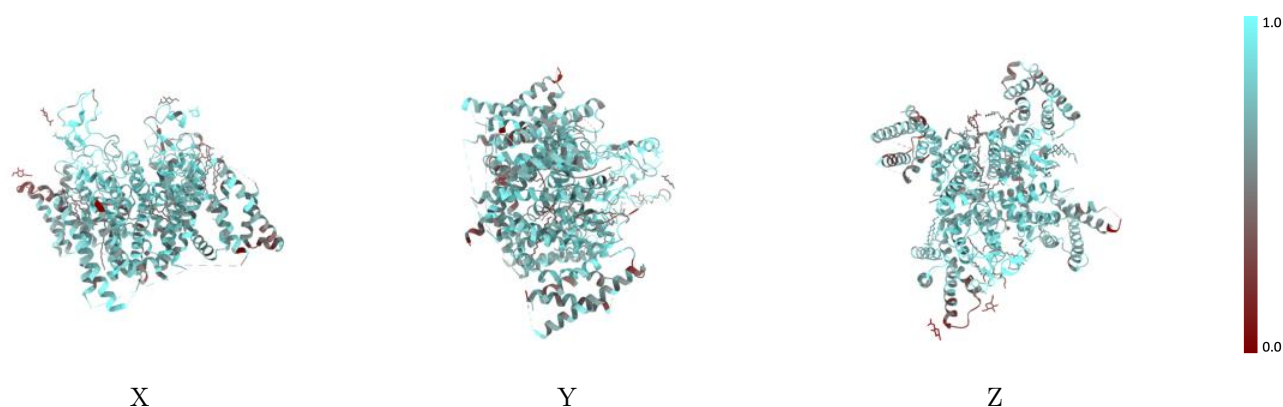
This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)



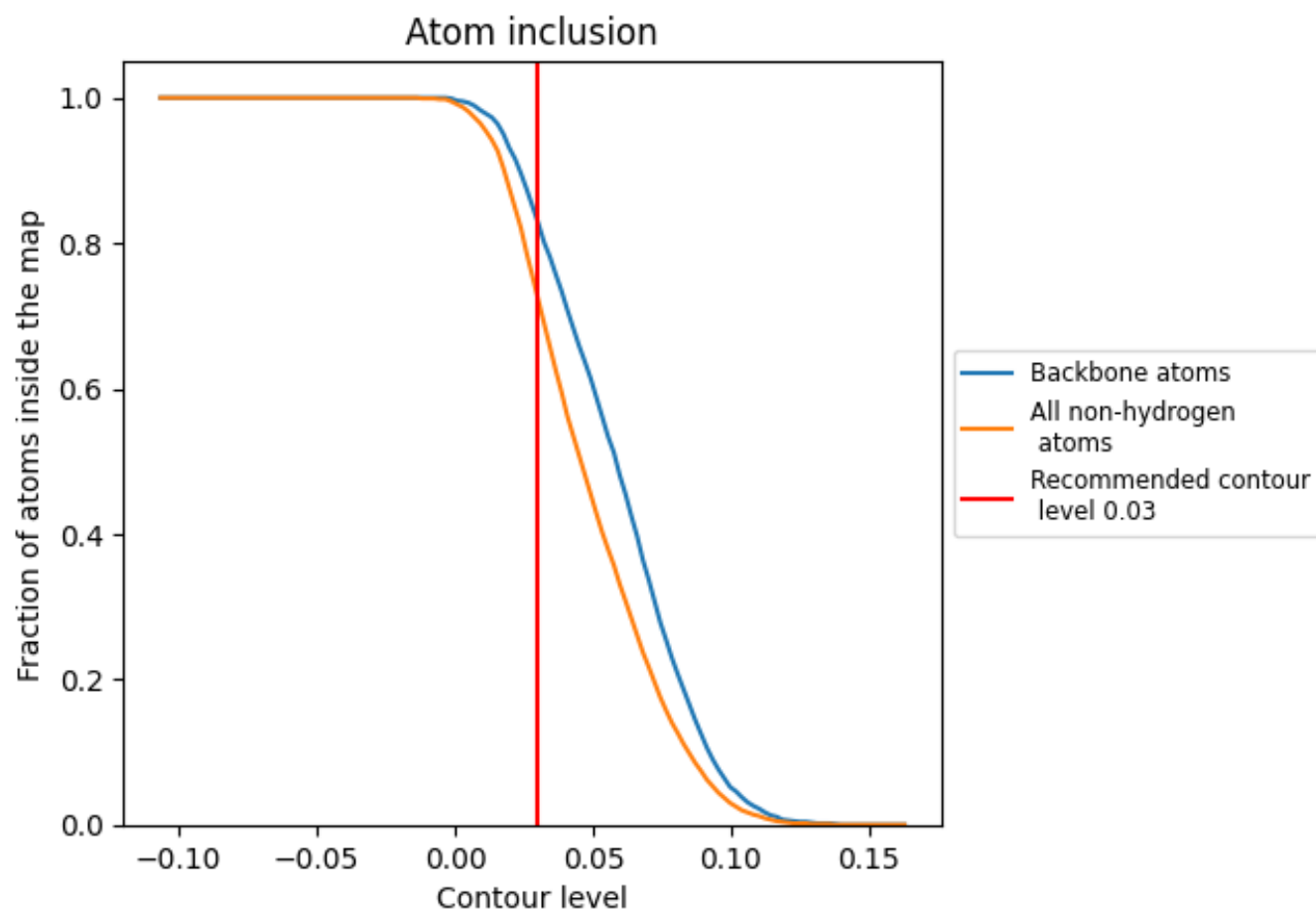
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7250	0.5080
A	0.7250	0.5080

