



# Full wwPDB EM Validation Report (i)

Nov 13, 2023 – 12:31 PM EST

PDB ID : 8SZC  
EMDB ID : EMD-40908  
Title : Heterodimeric ABC transporter BmrCD in the inward-facing conformation bound to substrate and ATP: BmrCD\_IF-1HT/ATP  
Authors : Tang, Q.; Mchaourab, H.  
Deposited on : 2023-05-29  
Resolution : 3.06 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](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 (i) 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 \(1\)](#)) were used in the production of this report:

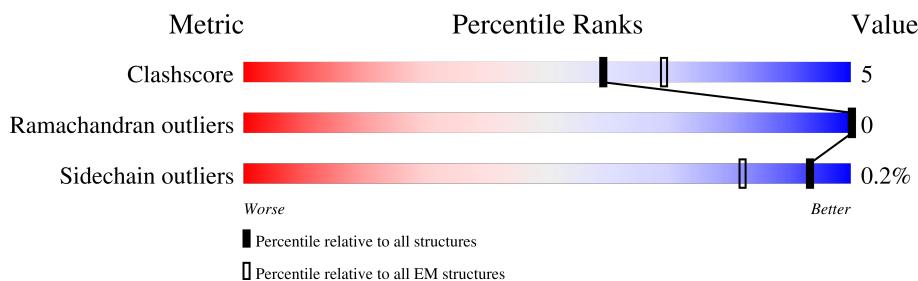
EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
**ELECTRON MICROSCOPY**

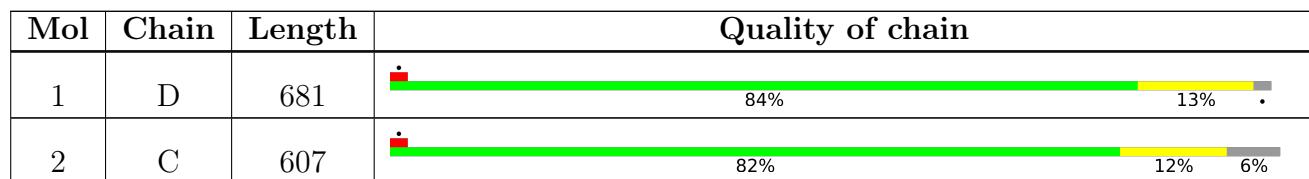
The reported resolution of this entry is 3.06 Å.

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 >=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%. 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.



## 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 21358 atoms, of which 10847 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 Probable multidrug resistance ABC transporter ATP-binding/permease protein YheH.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	D	664	10683	3415	5375	903	972	18	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	154	ALA	CYS	engineered mutation	UNP O07549
D	256	ALA	CYS	engineered mutation	UNP O07549
D	351	ALA	CYS	engineered mutation	UNP O07549
D	592	GLN	GLU	engineered mutation	UNP O07549
D	674	LEU	-	expression tag	UNP O07549
D	675	GLU	-	expression tag	UNP O07549
D	676	HIS	-	expression tag	UNP O07549
D	677	HIS	-	expression tag	UNP O07549
D	678	HIS	-	expression tag	UNP O07549
D	679	HIS	-	expression tag	UNP O07549
D	680	HIS	-	expression tag	UNP O07549
D	681	HIS	-	expression tag	UNP O07549

- Molecule 2 is a protein called Probable multidrug resistance ABC transporter ATP-binding/permease protein YheI.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	C	571	9074	2907	4576	751	817	23	0	0

There are 24 discrepancies between the modelled and reference sequences:

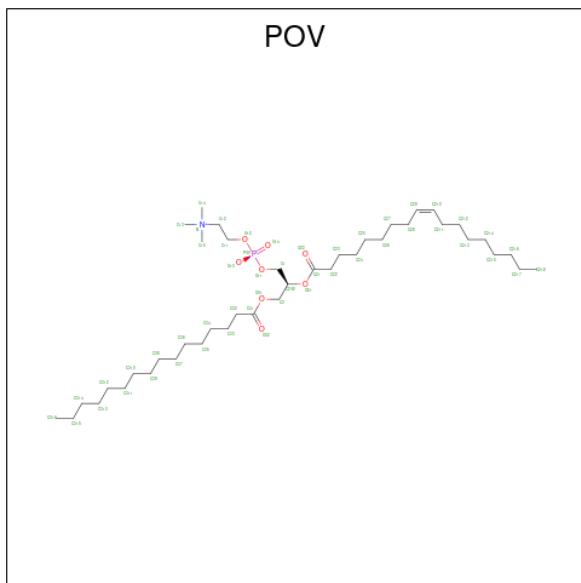
Chain	Residue	Modelled	Actual	Comment	Reference
C	-21	MET	-	initiating methionine	UNP O07550
C	-20	GLY	-	expression tag	UNP O07550
C	-19	SER	-	expression tag	UNP O07550

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	SER	-	expression tag	UNP O07550
C	-17	HIS	-	expression tag	UNP O07550
C	-16	HIS	-	expression tag	UNP O07550
C	-15	HIS	-	expression tag	UNP O07550
C	-14	HIS	-	expression tag	UNP O07550
C	-13	HIS	-	expression tag	UNP O07550
C	-12	HIS	-	expression tag	UNP O07550
C	-11	SER	-	expression tag	UNP O07550
C	-10	SER	-	expression tag	UNP O07550
C	-9	GLY	-	expression tag	UNP O07550
C	-8	LEU	-	expression tag	UNP O07550
C	-7	VAL	-	expression tag	UNP O07550
C	-6	PRO	-	expression tag	UNP O07550
C	-5	ARG	-	expression tag	UNP O07550
C	-4	GLY	-	expression tag	UNP O07550
C	-3	SER	-	expression tag	UNP O07550
C	-2	HIS	-	expression tag	UNP O07550
C	-1	MET	-	expression tag	UNP O07550
C	0	LEU	-	expression tag	UNP O07550
C	1	GLU	-	expression tag	UNP O07550
C	500	GLN	ASP	engineered mutation	UNP O07550

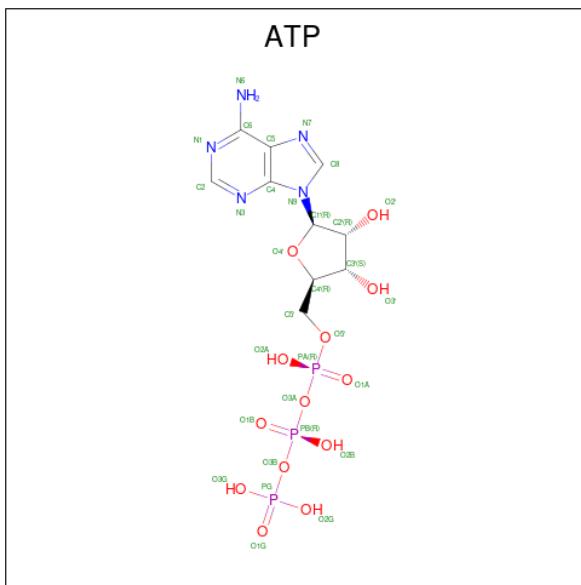
- Molecule 3 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enyloxy]propyl 2-(trimethylammonio)ethyl phosphate (three-letter code: POV) (formula: C<sub>42</sub>H<sub>82</sub>NO<sub>8</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	D	1	Total C H O P				0
3	D	1	83	29	54		
3	D	1	Total C H O P				0
3	D	1	115	37	69	8	1
3	D	1	Total C H O P				0
3	D	1	73	24	40	8	1
3	D	1	Total C H O P				0
3	D	1	50	17	26	6	1
3	D	1	Total C H O P				0
3	D	1	81	26	46	8	1
3	D	1	Total C H O P				0
3	D	1	79	26	44	8	1
3	D	1	Total C H O				0
3	D	1	106	36	66	4	
3	D	1	Total C H O				0
3	D	1	94	33	59	2	
3	D	1	Total C H O P				0
3	D	1	68	23	36	8	1
3	D	1	Total C H O P				0
3	D	1	115	37	69	8	1
3	C	1	Total C H				0
3	C	1	52	20	32		
3	C	1	Total C H O P				0
3	C	1	28	9	12	6	1
3	C	1	Total C H				0
3	C	1	44	15	29		
3	C	1	Total C H O P				0
3	C	1	63	21	33	8	1
3	C	1	Total C H O				0
3	C	1	58	20	35	3	
3	C	1	Total C H O P				0
3	C	1	44	15	20	8	1
3	C	1	Total C H O				0
3	C	1	44	17	24	3	
3	C	1	Total C H O				0
3	C	1	42	16	22	4	
3	C	1	Total C H				0
3	C	1	51	18	33		
3	C	1	Total C H O				0
3	C	1	58	20	35	3	
3	C	1	Total C H O P				0
3	C	1	106	35	62	8	1

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:

$C_{10}H_{16}N_5O_{13}P_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
4	D	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

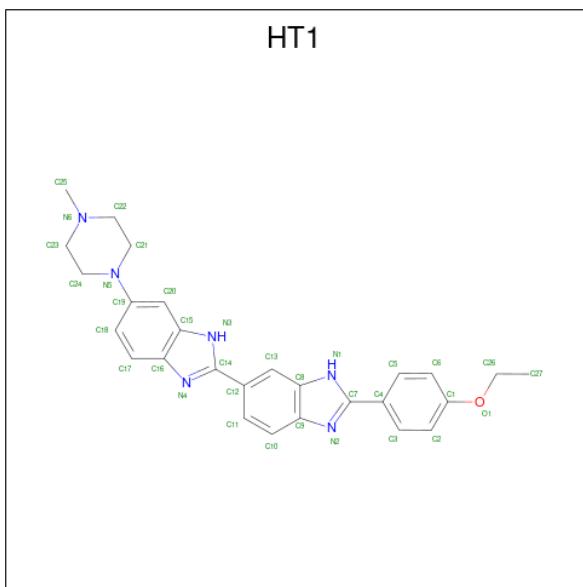
  

Mol	Chain	Residues	Atoms						AltConf
4	C	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms						AltConf
5	D	1	Total	Mg					0
			1	1					

- Molecule 6 is 2'-(4-ETHOXYPHENYL)-5-(4-METHYL-1-PIPERAZINYL)-2,5'-BI-BENZIMIDAZOLE (three-letter code: HT1) (formula:  $C_{27}H_{28}N_6O$ ) (labeled as "Ligand of Interest" by depositor).



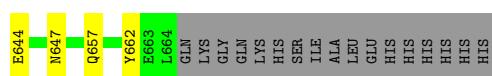
Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
6	C	1	60	27	26	6	1	0

### 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 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.

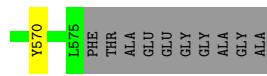
- Molecule 1: Probable multidrug resistance ABC transporter ATP-binding/permease protein YheH

Chain D: 



- Molecule 2: Probable multidrug resistance ABC transporter ATP-binding/permease protein YheI

Chain C: 



## 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	107639	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	15	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.296	Depositor
Minimum map value	-0.477	Depositor
Average map value	0.029	Depositor
Map value standard deviation	0.057	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	392.64, 392.64, 392.64	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.818, 0.818, 0.818	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: ATP, MG, HT1, POV

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	D	0.28	0/5409	0.48	0/7303
2	C	0.28	0/4590	0.49	0/6210
All	All	0.28	0/9999	0.49	0/13513

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	D	5308	5375	5375	60	0
2	C	4498	4576	4574	56	0
3	C	253	337	330	7	0
3	D	355	509	509	2	0
4	C	31	12	12	1	0
4	D	31	12	12	0	0
5	D	1	0	0	0	0
6	C	34	26	28	0	0
All	All	10511	10847	10840	102	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 5.

All (102) 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:D:242:PHE:HB3	3:D:708:POV:H29	1.73	0.70
1:D:486:ASP:OD1	1:D:487:VAL:N	2.29	0.66
1:D:266:TRP:HH2	1:D:341:VAL:HG23	1.60	0.66
3:C:610:POV:H210	3:C:610:POV:H26	1.78	0.65
1:D:66:GLN:N	1:D:66:GLN:OE1	2.30	0.64
2:C:462:SER:O	2:C:465:GLU:N	2.31	0.64
1:D:194:GLN:NE2	2:C:220:ASP:OD2	2.31	0.63
2:C:75:SER:HA	2:C:78:TRP:CD1	2.34	0.62
2:C:310:ASP:O	2:C:314:GLU:N	2.34	0.60
2:C:558:GLU:N	2:C:558:GLU:OE1	2.35	0.59
1:D:34:THR:HG21	1:D:159:LEU:HD13	1.85	0.58
2:C:26:LEU:HD13	2:C:140:VAL:HG11	1.86	0.58
1:D:176:MET:HA	2:C:236:MET:HE3	1.86	0.56
2:C:521:ARG:NH1	2:C:526:THR:OG1	2.37	0.56
1:D:420:GLU:OE1	1:D:420:GLU:N	2.38	0.56
1:D:28:ALA:HB1	1:D:167:GLN:HG3	1.87	0.56
2:C:375:SER:N	4:C:612:ATP:O1B	2.39	0.56
1:D:74:ARG:NH2	1:D:145:GLU:OE2	2.38	0.56
1:D:76:ASP:OD1	1:D:77:ARG:N	2.39	0.55
1:D:61:ASP:OD1	1:D:77:ARG:NH2	2.38	0.55
1:D:612:VAL:O	1:D:616:ARG:NH1	2.39	0.55
1:D:644:GLU:OE2	1:D:657:GLN:N	2.36	0.55
3:C:609:POV:H21D	3:C:609:POV:H210	1.88	0.54
2:C:26:LEU:HD21	2:C:78:TRP:CZ2	2.43	0.54
1:D:176:MET:HA	2:C:236:MET:CE	2.37	0.53
1:D:110:ARG:NH2	2:C:48:LYS:O	2.41	0.53
2:C:537:GLU:OE2	2:C:556:HIS:NE2	2.42	0.53
2:C:26:LEU:CD1	2:C:140:VAL:HG11	2.39	0.52
1:D:611:VAL:O	1:D:611:VAL:HG12	2.11	0.51
2:C:146:MET:HE2	2:C:291:PRO:HB2	1.93	0.51
1:D:107:ASP:OD1	1:D:108:GLY:N	2.42	0.50
2:C:58:LEU:HD21	3:C:601:POV:H24A	1.93	0.50
1:D:360:SER:OG	2:C:47:MET:SD	2.63	0.49
1:D:88:ALA:O	1:D:89:HIS:ND1	2.45	0.49
1:D:164:VAL:HG21	2:C:251:LEU:HB2	1.94	0.49
1:D:223:LEU:HB2	1:D:399:ALA:HB1	1.93	0.49
1:D:252:LEU:HB3	1:D:375:PHE:CE2	2.47	0.49
2:C:143:THR:HG23	2:C:144:MET:N	2.27	0.49
1:D:266:TRP:CH2	1:D:341:VAL:HG23	2.44	0.49
2:C:139:LEU:O	2:C:143:THR:HG22	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:459:MET:SD	2:C:479:GLN:NE2	2.87	0.48
2:C:479:GLN:O	2:C:483:ILE:HG22	2.14	0.48
1:D:33:LEU:O	1:D:378:TYR:OH	2.23	0.47
2:C:332:LYS:N	2:C:332:LYS:HD3	2.29	0.47
1:D:632:ASP:O	1:D:647:ASN:ND2	2.47	0.47
2:C:201:VAL:O	2:C:205:VAL:HG23	2.14	0.47
1:D:431:GLU:OE2	1:D:433:ARG:NE	2.46	0.47
1:D:72:TYR:OH	1:D:101:ASP:OD2	2.30	0.47
1:D:334:SER:HA	2:C:79:MET:CE	2.44	0.47
2:C:536:VAL:O	2:C:542:ILE:HD11	2.14	0.47
1:D:457:GLU:N	1:D:457:GLU:OE1	2.48	0.47
2:C:167:ILE:N	2:C:168:PRO:HD2	2.30	0.47
1:D:265:LEU:HD11	3:D:705:POV:H31C	1.97	0.46
1:D:298:GLY:HA2	2:C:422:LEU:HD21	1.97	0.46
1:D:360:SER:CB	2:C:47:MET:SD	3.03	0.46
1:D:34:THR:HG21	1:D:159:LEU:CD1	2.46	0.46
1:D:216:ASP:HB3	1:D:406:VAL:HG23	1.98	0.46
1:D:350:VAL:CG2	2:C:64:PHE:HB3	2.47	0.45
1:D:367:VAL:HG13	1:D:368:SER:N	2.32	0.45
1:D:541:ARG:NH1	1:D:608:ALA:O	2.50	0.45
1:D:546:GLU:O	1:D:549:LEU:N	2.50	0.45
2:C:295:ILE:HG21	3:C:607:POV:H210	2.00	0.44
1:D:398:LEU:O	1:D:401:VAL:HG22	2.17	0.44
1:D:543:VAL:O	1:D:547:PRO:HD2	2.16	0.44
2:C:264:GLY:O	2:C:268:VAL:HG23	2.17	0.44
1:D:606:GLN:OE1	1:D:627:THR:HG23	2.18	0.44
1:D:44:ASP:OD1	1:D:370:GLY:N	2.44	0.43
1:D:156:TYR:CG	2:C:258:LEU:HD13	2.52	0.43
2:C:566:TYR:HA	2:C:570:TYR:HD2	1.84	0.43
1:D:98:TYR:HA	1:D:131:GLU:O	2.19	0.43
2:C:344:PHE:O	2:C:353:ASN:HB3	2.19	0.43
1:D:288:ILE:HG23	1:D:315:PHE:HE1	1.84	0.43
1:D:541:ARG:HE	1:D:577:PHE:HB3	1.84	0.43
1:D:153:ILE:HG23	2:C:258:LEU:HD11	2.00	0.43
2:C:75:SER:HA	2:C:78:TRP:NE1	2.34	0.43
1:D:32:GLU:OE2	1:D:237:TYR:OH	2.36	0.43
2:C:118:MET:O	2:C:122:THR:HG22	2.19	0.42
2:C:154:GLY:HA3	2:C:159:TRP:CZ3	2.55	0.42
2:C:106:PRO:N	2:C:107:PRO:CD	2.83	0.42
2:C:36:PRO:N	2:C:37:PRO:HD2	2.35	0.42
1:D:186:ARG:HH12	2:C:231:VAL:HG11	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:320:GLU:OE2	2:C:91:LYS:HD2	2.19	0.41
2:C:433:LEU:O	2:C:437:GLN:N	2.53	0.41
2:C:58:LEU:HD21	3:C:601:POV:C24	2.50	0.41
1:D:189:VAL:HG22	1:D:410:LEU:HG	2.02	0.41
1:D:303:GLN:NE2	2:C:104:MET:O	2.44	0.41
1:D:543:VAL:O	1:D:545:ALA:N	2.54	0.41
1:D:417:GLU:N	1:D:417:GLU:OE1	2.54	0.41
1:D:441:GLU:O	1:D:443:GLU:N	2.48	0.41
2:C:34:MET:HB3	3:C:603:POV:H25	2.02	0.41
2:C:304:ARG:O	2:C:305:GLY:C	2.59	0.41
1:D:302:ILE:HA	2:C:434:TYR:OH	2.20	0.41
2:C:28:ALA:O	2:C:32:ILE:HG12	2.20	0.41
2:C:38:LYS:NZ	2:C:42:ASN:OD1	2.54	0.41
1:D:461:LEU:HD12	1:D:635:LEU:O	2.21	0.40
2:C:164:ALA:HB1	3:C:604:POV:H35	2.02	0.40
2:C:331:LEU:HD11	2:C:398:SER:HB2	2.03	0.40
2:C:298:LEU:O	2:C:299:ILE:C	2.58	0.40
1:D:167:GLN:O	1:D:170:GLN:HG3	2.20	0.40
1:D:425:ARG:NH2	1:D:584:ASP:OD2	2.54	0.40
2:C:124:ASP:OD1	2:C:311:ARG:NH1	2.54	0.40
2:C:200:ARG:NH2	2:C:220:ASP:OD1	2.55	0.40

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	D	662/681 (97%)	608 (92%)	54 (8%)	0	100 100
2	C	567/607 (93%)	533 (94%)	34 (6%)	0	100 100
All	All	1229/1288 (95%)	1141 (93%)	88 (7%)	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	D	566/581 (97%)	564 (100%)	2 (0%)	91 95
2	C	483/508 (95%)	483 (100%)	0	100 100
All	All	1049/1089 (96%)	1047 (100%)	2 (0%)	93 97

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

Mol	Chain	Res	Type
1	D	42	MET
1	D	662	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	278	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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 25 ligands modelled in this entry, 1 is monoatomic - leaving 24 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$
3	POV	C	608	-	19,19,51	1.24	2 (10%)	20,20,59	1.09	2 (10%)
3	POV	C	610	-	22,22,51	1.15	2 (9%)	22,22,59	0.95	1 (4%)
3	POV	D	710	-	45,45,51	1.28	6 (13%)	49,50,59	1.27	3 (6%)
3	POV	D	705	-	34,34,51	1.28	5 (14%)	38,39,59	1.17	4 (10%)
3	POV	D	701	-	27,27,51	0.80	1 (3%)	25,25,59	0.81	0
3	POV	C	605	-	22,22,51	1.18	2 (9%)	22,22,59	1.06	1 (4%)
3	POV	C	607	-	19,19,51	1.25	2 (10%)	19,19,59	0.96	1 (5%)
6	HT1	C	613	-	37,39,39	3.11	12 (32%)	34,56,56	1.57	5 (14%)
4	ATP	C	612	-	26,33,33	0.63	0	31,52,52	1.09	2 (6%)
3	POV	D	707	-	39,39,51	1.09	3 (7%)	40,40,59	1.02	2 (5%)
3	POV	D	708	-	33,33,51	0.77	1 (3%)	31,31,59	0.88	0
3	POV	D	706	-	34,34,51	1.43	6 (17%)	38,39,59	1.14	3 (7%)
3	POV	C	601	-	18,18,51	1.02	1 (5%)	15,16,59	0.89	0
3	POV	D	709	-	31,31,51	1.48	6 (19%)	35,36,59	1.35	4 (11%)
3	POV	C	602	-	15,15,51	1.48	3 (20%)	18,18,59	1.23	2 (11%)
3	POV	D	703	-	32,32,51	1.44	7 (21%)	36,37,59	1.32	4 (11%)
4	ATP	D	711	5	26,33,33	0.63	0	31,52,52	1.09	2 (6%)
3	POV	C	609	-	17,17,51	0.98	1 (5%)	16,16,59	0.68	0
3	POV	D	704	-	23,23,51	1.44	4 (17%)	26,26,59	1.08	2 (7%)
3	POV	C	606	-	23,23,51	1.58	6 (26%)	27,28,59	1.37	3 (11%)
3	POV	D	702	-	45,45,51	1.26	7 (15%)	49,50,59	1.13	3 (6%)
3	POV	C	604	-	29,29,51	1.35	5 (17%)	33,34,59	1.26	3 (9%)
3	POV	C	603	-	14,14,51	1.10	1 (7%)	13,13,59	1.09	2 (15%)
3	POV	C	611	-	43,43,51	1.26	6 (13%)	47,48,59	1.30	5 (10%)

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	POV	C	608	-	-	4/19/19/55	-
3	POV	C	610	-	-	8/21/21/55	-
3	POV	D	710	-	-	25/47/47/55	-
3	POV	D	705	-	-	20/36/36/55	-
3	POV	D	701	-	-	4/23/23/55	-
3	POV	C	605	-	-	7/21/21/55	-
3	POV	C	607	-	-	5/18/18/55	-
6	HT1	C	613	-	-	3/7/25/25	0/6/6/6
4	ATP	C	612	-	-	6/18/38/38	0/3/3/3
3	POV	D	707	-	-	8/39/39/55	-
3	POV	D	708	-	-	10/29/29/55	-
3	POV	D	706	-	-	18/36/36/55	-
3	POV	C	601	-	-	2/14/14/55	-
3	POV	D	709	-	-	15/33/33/55	-
3	POV	C	602	-	-	4/14/14/55	-
3	POV	D	703	-	-	15/34/34/55	-
4	ATP	D	711	5	-	6/18/38/38	0/3/3/3
3	POV	C	609	-	-	5/15/15/55	-
3	POV	D	704	-	-	7/22/22/55	-
3	POV	C	606	-	-	12/24/24/55	-
3	POV	D	702	-	-	21/47/47/55	-
3	POV	C	604	-	-	7/31/31/55	-
3	POV	C	603	-	-	3/12/12/55	-
3	POV	C	611	-	-	24/45/45/55	-

All (89) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	613	HT1	C23-N6	-8.60	1.27	1.46
6	C	613	HT1	C5-C6	8.09	1.53	1.36
6	C	613	HT1	C2-C1	6.49	1.51	1.38
6	C	613	HT1	C25-N6	-5.40	1.34	1.46
6	C	613	HT1	C22-N6	-5.38	1.34	1.46
6	C	613	HT1	C3-C4	4.50	1.52	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	613	HT1	C19-N5	4.38	1.50	1.38
6	C	613	HT1	C5-C4	-4.02	1.32	1.41
3	C	601	POV	C29-C210	3.91	1.54	1.31
3	C	603	POV	C29-C210	3.85	1.54	1.31
3	D	702	POV	C29-C210	3.81	1.53	1.31
3	C	605	POV	C29-C210	3.80	1.53	1.31
3	D	706	POV	C29-C210	3.80	1.53	1.31
3	D	707	POV	C29-C210	3.75	1.53	1.31
3	D	710	POV	C29-C210	3.75	1.53	1.31
3	D	708	POV	C29-C210	3.74	1.53	1.31
3	C	607	POV	C29-C210	3.72	1.53	1.31
3	C	609	POV	C29-C210	3.68	1.53	1.31
3	D	704	POV	C29-C210	3.67	1.53	1.31
3	D	701	POV	C29-C210	3.66	1.53	1.31
3	D	709	POV	C210-C29	3.66	1.53	1.28
3	D	703	POV	C29-C210	3.61	1.52	1.31
3	C	610	POV	C29-C210	3.60	1.52	1.31
3	C	611	POV	C29-C210	3.59	1.52	1.31
3	C	606	POV	C210-C29	3.52	1.52	1.28
3	D	710	POV	O31-C31	3.12	1.42	1.33
6	C	613	HT1	O1-C1	3.06	1.44	1.37
6	C	613	HT1	C10-C9	-2.96	1.36	1.41
3	C	604	POV	O31-C31	2.91	1.41	1.33
3	D	705	POV	O31-C31	2.91	1.41	1.33
3	D	710	POV	P-O12	2.89	1.66	1.54
3	D	702	POV	P-O12	2.88	1.65	1.54
3	D	706	POV	O31-C31	2.87	1.41	1.33
3	C	604	POV	P-O12	2.87	1.65	1.54
3	C	608	POV	O31-C31	2.87	1.41	1.33
3	D	702	POV	O31-C31	2.87	1.41	1.33
3	D	709	POV	O31-C31	2.87	1.41	1.33
3	D	705	POV	P-O12	2.86	1.65	1.54
3	D	703	POV	P-O12	2.86	1.65	1.54
3	C	611	POV	P-O12	2.86	1.65	1.54
3	D	709	POV	P-O12	2.85	1.65	1.54
3	D	706	POV	P-O12	2.85	1.65	1.54
3	C	602	POV	P-O12	2.84	1.65	1.54
3	D	707	POV	O31-C31	2.84	1.41	1.33
3	D	704	POV	P-O12	2.83	1.65	1.54
3	C	606	POV	P-O12	2.83	1.65	1.54
3	D	703	POV	O31-C31	2.80	1.41	1.33
3	C	611	POV	O31-C31	2.74	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	704	POV	O21-C21	2.61	1.41	1.33
3	C	607	POV	O21-C21	2.60	1.40	1.33
3	C	611	POV	O21-C21	2.60	1.41	1.34
3	C	608	POV	O21-C21	2.58	1.40	1.33
3	C	602	POV	O21-C21	2.58	1.40	1.33
3	D	707	POV	O21-C21	2.57	1.40	1.33
3	C	610	POV	O21-C21	2.54	1.40	1.33
3	C	605	POV	O21-C21	2.54	1.40	1.33
3	D	709	POV	O21-C21	2.53	1.41	1.34
3	D	710	POV	O21-C21	2.52	1.41	1.34
3	D	703	POV	O21-C21	2.50	1.41	1.34
3	C	604	POV	O21-C2	-2.49	1.40	1.46
3	C	606	POV	O21-C21	2.48	1.41	1.34
3	D	705	POV	O21-C21	2.47	1.41	1.34
3	D	702	POV	O21-C2	-2.47	1.40	1.46
3	D	706	POV	O21-C2	-2.45	1.40	1.46
3	D	706	POV	O21-C21	2.44	1.41	1.34
3	D	702	POV	O21-C21	2.41	1.41	1.34
3	D	709	POV	O21-C2	-2.40	1.40	1.46
3	D	703	POV	O21-C2	-2.40	1.40	1.46
3	C	604	POV	O21-C21	2.39	1.41	1.34
6	C	613	HT1	C17-C18	2.34	1.41	1.36
3	D	705	POV	O21-C2	-2.34	1.40	1.46
6	C	613	HT1	C6-C1	-2.33	1.33	1.38
3	D	710	POV	O21-C2	-2.33	1.40	1.46
3	C	611	POV	O21-C2	-2.31	1.40	1.46
3	D	703	POV	P-O13	-2.23	1.46	1.54
3	C	606	POV	O21-C2	-2.23	1.41	1.46
3	D	705	POV	P-O13	-2.22	1.46	1.54
3	D	702	POV	P-O13	-2.21	1.46	1.54
3	D	710	POV	P-O13	-2.20	1.46	1.54
3	D	704	POV	P-O13	-2.20	1.46	1.54
3	C	602	POV	P-O13	-2.20	1.46	1.54
3	C	604	POV	P-O13	-2.19	1.46	1.54
3	D	709	POV	P-O13	-2.18	1.46	1.54
3	C	611	POV	P-O13	-2.18	1.46	1.54
3	D	706	POV	P-O13	-2.18	1.46	1.54
3	C	606	POV	P-O13	-2.17	1.46	1.54
3	C	606	POV	O31-C3	-2.04	1.40	1.45
3	D	703	POV	O31-C3	-2.04	1.40	1.45
3	D	702	POV	O31-C3	-2.01	1.40	1.45

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	611	POV	O21-C21-C22	5.18	122.66	111.50
6	C	613	HT1	C23-N6-C22	4.53	115.86	109.52
3	D	710	POV	O21-C21-C22	4.45	121.08	111.50
6	C	613	HT1	C21-C22-N6	4.07	115.40	110.80
3	D	709	POV	O21-C21-C22	3.98	120.09	111.50
3	C	606	POV	O21-C21-C22	3.82	119.72	111.50
3	D	705	POV	O21-C21-C22	3.76	119.60	111.50
3	D	702	POV	O21-C21-C22	3.74	119.55	111.50
3	D	703	POV	O21-C21-C22	3.69	119.46	111.50
3	C	604	POV	O21-C21-C22	3.55	119.15	111.50
3	D	703	POV	O31-C31-C32	3.22	119.82	111.38
3	D	706	POV	O21-C21-C22	3.08	118.14	111.50
3	D	710	POV	O31-C31-C32	3.06	121.52	111.91
3	C	604	POV	O31-C31-C32	2.99	121.28	111.91
3	D	709	POV	O31-C31-C32	2.82	120.75	111.91
3	C	605	POV	O21-C21-C22	2.81	120.72	111.91
3	D	707	POV	O31-C31-C32	2.61	120.11	111.91
3	D	705	POV	O31-C31-C32	2.59	120.04	111.91
3	C	608	POV	O31-C31-C32	2.56	119.96	111.91
3	D	702	POV	O31-C31-C32	2.53	119.84	111.91
3	C	611	POV	O31-C31-C32	2.50	119.75	111.91
3	C	611	POV	O21-C21-O22	-2.47	117.72	123.70
3	C	607	POV	O21-C21-C22	2.42	119.50	111.91
3	D	707	POV	O21-C21-C22	2.42	119.50	111.91
6	C	613	HT1	C25-N6-C23	2.42	114.28	110.66
3	D	706	POV	O31-C31-C32	2.41	119.47	111.91
6	C	613	HT1	C24-C23-N6	2.41	113.52	110.80
4	D	711	ATP	C5-C6-N6	2.40	124.00	120.35
3	D	710	POV	O13-P-O14	-2.39	101.33	110.68
3	D	704	POV	O21-C21-C22	2.36	119.31	111.91
4	C	612	ATP	C5-C6-N6	2.36	123.93	120.35
3	C	602	POV	O21-C21-C22	2.34	119.27	111.91
3	C	608	POV	O21-C21-C22	2.33	119.21	111.91
3	C	602	POV	O13-P-O14	-2.32	101.61	110.68
3	C	606	POV	C28-C29-C210	-2.31	111.13	126.84
3	D	709	POV	O13-P-O14	-2.31	101.64	110.68
3	C	610	POV	O21-C21-C22	2.28	119.05	111.91
3	D	703	POV	O13-P-O14	-2.27	101.78	110.68
3	D	705	POV	O13-P-O14	-2.27	101.79	110.68
3	D	706	POV	O13-P-O14	-2.26	101.84	110.68
3	C	611	POV	O13-P-O14	-2.25	101.86	110.68
3	D	704	POV	O13-P-O14	-2.25	101.87	110.68
3	C	606	POV	O13-P-O14	-2.23	101.94	110.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	702	POV	O13-P-O14	-2.23	101.97	110.68
6	C	613	HT1	C24-N5-C21	2.22	116.42	111.52
3	D	703	POV	C211-C210-C29	-2.22	107.67	124.73
3	C	604	POV	O13-P-O14	-2.21	102.03	110.68
3	C	603	POV	C28-C29-C210	-2.19	107.91	124.73
4	C	612	ATP	O2'-C2'-C1'	-2.15	102.93	110.85
3	D	709	POV	O11-P-O14	2.14	112.47	106.47
3	C	611	POV	C28-C29-C210	-2.09	108.65	124.73
4	D	711	ATP	O4'-C1'-C2'	-2.05	103.94	106.93
3	C	603	POV	C211-C210-C29	-2.02	109.22	124.73
3	D	705	POV	O11-P-O14	2.02	112.14	106.47

There are no chirality outliers.

All (239) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	705	POV	C1-O11-P-O12
3	D	705	POV	C1-O11-P-O13
3	D	705	POV	C1-O11-P-O14
3	D	705	POV	O21-C2-C3-O31
3	D	706	POV	C211-C210-C29-C28
3	D	709	POV	C1-O11-P-O12
3	D	709	POV	C1-O11-P-O13
3	D	709	POV	C1-O11-P-O14
3	D	710	POV	C1-O11-P-O12
3	D	710	POV	C32-C31-O31-C3
3	C	602	POV	C1-O11-P-O12
3	C	602	POV	C2-C1-O11-P
3	C	602	POV	C22-C21-O21-C2
3	C	602	POV	O22-C21-O21-C2
3	C	611	POV	C1-O11-P-O12
3	C	611	POV	C1-O11-P-O13
3	C	611	POV	O11-C1-C2-O21
3	C	611	POV	O21-C2-C3-O31
3	C	611	POV	C22-C21-O21-C2
3	C	611	POV	O22-C21-O21-C2
4	D	711	ATP	PB-O3B-PG-O2G
4	C	612	ATP	O4'-C4'-C5'-O5'
4	C	612	ATP	C3'-C4'-C5'-O5'
3	D	710	POV	O32-C31-O31-C3
3	C	604	POV	O32-C31-O31-C3
3	C	608	POV	O32-C31-O31-C3

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Mol	Chain	Res	Type	Atoms
3	D	709	POV	C2-C3-O31-C31
3	C	604	POV	C32-C31-O31-C3
3	C	608	POV	C32-C31-O31-C3
3	D	702	POV	O32-C31-O31-C3
3	D	703	POV	O32-C31-O31-C3
3	D	707	POV	O32-C31-O31-C3
3	D	709	POV	O32-C31-O31-C3
3	D	702	POV	C32-C31-O31-C3
3	D	703	POV	C32-C31-O31-C3
3	D	707	POV	C32-C31-O31-C3
3	D	709	POV	C32-C31-O31-C3
3	D	704	POV	C211-C210-C29-C28
3	D	710	POV	C211-C210-C29-C28
3	C	606	POV	O32-C31-O31-C3
3	C	606	POV	C32-C31-O31-C3
3	C	606	POV	C22-C21-O21-C2
6	C	613	HT1	C27-C26-O1-C1
3	D	705	POV	C39-C310-C311-C312
3	D	710	POV	C211-C212-C213-C214
3	C	606	POV	O22-C21-O21-C2
3	D	702	POV	C211-C212-C213-C214
3	D	709	POV	C23-C24-C25-C26
3	C	608	POV	O21-C2-C3-O31
3	C	611	POV	O32-C31-O31-C3
3	D	707	POV	O21-C2-C3-O31
3	D	706	POV	C32-C31-O31-C3
3	C	611	POV	C32-C31-O31-C3
3	D	706	POV	C21-C22-C23-C24
3	D	710	POV	C21-C22-C23-C24
3	D	709	POV	C21-C22-C23-C24
3	D	709	POV	C31-C32-C33-C34
3	D	702	POV	C211-C210-C29-C28
3	D	708	POV	C211-C210-C29-C28
3	C	601	POV	C211-C210-C29-C28
4	D	711	ATP	C3'-C4'-C5'-O5'
3	D	703	POV	C2-C1-O11-P
3	D	710	POV	C31-C32-C33-C34
6	C	613	HT1	C2-C1-O1-C26
3	D	706	POV	O32-C31-O31-C3
3	C	611	POV	C31-C32-C33-C34
3	D	707	POV	C211-C210-C29-C28
3	D	702	POV	C22-C21-O21-C2

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Mol	Chain	Res	Type	Atoms
6	C	613	HT1	C6-C1-O1-C26
3	D	702	POV	O22-C21-O21-C2
3	D	710	POV	C22-C21-O21-C2
4	D	711	ATP	O4'-C4'-C5'-O5'
3	D	706	POV	C211-C212-C213-C214
3	D	710	POV	C311-C312-C313-C314
3	C	611	POV	C37-C38-C39-C310
3	D	710	POV	O22-C21-O21-C2
3	D	702	POV	C35-C36-C37-C38
3	D	705	POV	C34-C35-C36-C37
3	D	703	POV	C212-C213-C214-C215
3	C	610	POV	C24-C25-C26-C27
3	D	706	POV	C31-C32-C33-C34
3	C	605	POV	C23-C24-C25-C26
3	D	710	POV	C24-C25-C26-C27
3	D	709	POV	C35-C36-C37-C38
3	C	605	POV	C26-C27-C28-C29
3	C	611	POV	C21-C22-C23-C24
3	D	705	POV	C35-C36-C37-C38
3	C	603	POV	C25-C26-C27-C28
3	C	606	POV	C22-C23-C24-C25
3	D	710	POV	C214-C215-C216-C217
3	D	703	POV	C211-C212-C213-C214
3	D	710	POV	C23-C24-C25-C26
3	D	710	POV	C1-C2-C3-O31
3	D	703	POV	C211-C210-C29-C28
3	D	702	POV	C36-C37-C38-C39
3	D	707	POV	C39-C310-C311-C312
3	D	706	POV	C210-C211-C212-C213
3	D	706	POV	C26-C27-C28-C29
3	D	709	POV	C26-C27-C28-C29
3	D	701	POV	C213-C214-C215-C216
3	C	611	POV	C22-C23-C24-C25
3	D	702	POV	C215-C216-C217-C218
3	D	704	POV	C25-C26-C27-C28
3	D	703	POV	C22-C21-O21-C2
3	D	710	POV	C35-C36-C37-C38
3	D	702	POV	C26-C27-C28-C29
3	D	705	POV	C32-C31-O31-C3
3	D	710	POV	C36-C37-C38-C39
3	C	604	POV	C35-C36-C37-C38
3	C	611	POV	C23-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
3	D	706	POV	C22-C21-O21-C2
3	C	609	POV	C22-C23-C24-C25
3	D	710	POV	C212-C213-C214-C215
3	D	703	POV	C213-C214-C215-C216
3	D	702	POV	C213-C214-C215-C216
3	D	703	POV	O22-C21-O21-C2
3	D	706	POV	O22-C21-O21-C2
3	C	606	POV	O11-C1-C2-C3
3	C	610	POV	C21-C22-C23-C24
3	D	709	POV	C25-C26-C27-C28
3	D	705	POV	C31-C32-C33-C34
3	D	707	POV	C35-C36-C37-C38
3	D	702	POV	C1-C2-C3-O31
3	D	705	POV	C1-C2-C3-O31
3	C	611	POV	C1-C2-C3-O31
3	D	705	POV	O32-C31-O31-C3
3	D	706	POV	C25-C26-C27-C28
3	C	604	POV	C22-C23-C24-C25
3	D	708	POV	C26-C27-C28-C29
3	C	607	POV	C22-C21-O21-C2
3	C	606	POV	C3-C2-O21-C21
3	D	702	POV	C33-C34-C35-C36
3	D	710	POV	C1-O11-P-O14
3	C	611	POV	C1-O11-P-O14
3	D	710	POV	C215-C216-C217-C218
3	D	710	POV	C29-C210-C211-C212
4	C	612	ATP	PB-O3A-PA-O1A
3	D	704	POV	C212-C213-C214-C215
3	C	611	POV	C35-C36-C37-C38
3	D	710	POV	C313-C314-C315-C316
3	C	609	POV	C211-C210-C29-C28
3	C	606	POV	C21-C22-C23-C24
3	D	705	POV	C22-C23-C24-C25
3	C	603	POV	C24-C25-C26-C27
3	C	606	POV	C25-C26-C27-C28
3	D	704	POV	C22-C21-O21-C2
3	C	607	POV	C211-C210-C29-C28
3	C	608	POV	C32-C33-C34-C35
3	C	606	POV	O11-C1-C2-O21
3	C	607	POV	O22-C21-O21-C2
3	D	702	POV	O21-C2-C3-O31
3	D	710	POV	O21-C2-C3-O31

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Mol	Chain	Res	Type	Atoms
3	C	610	POV	C27-C28-C29-C210
3	D	702	POV	C312-C313-C314-C315
3	D	702	POV	C311-C312-C313-C314
3	D	702	POV	C311-C310-C39-C38
3	D	709	POV	C33-C34-C35-C36
3	C	610	POV	O11-C1-C2-O21
3	D	705	POV	C22-C21-O21-C2
3	C	609	POV	C24-C25-C26-C27
3	D	708	POV	C313-C314-C315-C316
3	C	611	POV	O11-C1-C2-C3
3	C	606	POV	C1-O11-P-O12
3	D	702	POV	C31-C32-C33-C34
3	D	705	POV	C23-C24-C25-C26
3	D	708	POV	C35-C36-C37-C38
3	D	705	POV	C37-C38-C39-C310
3	D	706	POV	C1-C2-C3-O31
3	D	706	POV	C214-C215-C216-C217
3	D	705	POV	O22-C21-O21-C2
3	D	704	POV	O22-C21-O21-C2
3	D	706	POV	O21-C2-C3-O31
3	C	611	POV	C211-C212-C213-C214
3	D	705	POV	C2-C1-O11-P
3	D	709	POV	C2-C1-O11-P
3	D	706	POV	O11-C1-C2-C3
3	D	703	POV	C214-C215-C216-C217
3	C	603	POV	C211-C210-C29-C28
3	D	706	POV	O11-C1-C2-O21
3	C	610	POV	C213-C214-C215-C216
3	D	708	POV	C311-C312-C313-C314
3	C	610	POV	C22-C23-C24-C25
3	D	706	POV	C213-C214-C215-C216
3	C	610	POV	C25-C26-C27-C28
3	D	708	POV	C39-C310-C311-C312
3	C	611	POV	C25-C26-C27-C28
3	D	708	POV	C21-C22-C23-C24
3	D	703	POV	C25-C26-C27-C28
3	C	611	POV	C312-C313-C314-C315
3	C	604	POV	C31-C32-C33-C34
3	D	710	POV	C26-C27-C28-C29
3	D	709	POV	C37-C38-C39-C310
3	D	703	POV	C27-C28-C29-C210
3	D	705	POV	C24-C25-C26-C27

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Mol	Chain	Res	Type	Atoms
3	D	702	POV	C24-C25-C26-C27
3	D	707	POV	C212-C213-C214-C215
3	D	704	POV	O11-C1-C2-O21
3	C	606	POV	C23-C24-C25-C26
3	C	604	POV	O21-C2-C3-O31
3	C	605	POV	C211-C210-C29-C28
3	D	708	POV	C32-C33-C34-C35
4	C	612	ATP	PA-O3A-PB-O1B
4	C	612	ATP	PB-O3A-PA-O2A
3	C	601	POV	C29-C210-C211-C212
3	D	708	POV	C213-C214-C215-C216
3	D	710	POV	C310-C311-C312-C313
3	D	703	POV	O31-C31-C32-C33
3	D	710	POV	C1-O11-P-O13
3	C	605	POV	C211-C212-C213-C214
4	D	711	ATP	PB-O3B-PG-O1G
3	D	702	POV	C32-C33-C34-C35
3	D	702	POV	C29-C210-C211-C212
3	D	704	POV	C29-C210-C211-C212
3	C	609	POV	C211-C212-C213-C214
3	D	703	POV	C29-C210-C211-C212
3	D	701	POV	C39-C310-C311-C312
3	C	607	POV	C22-C23-C24-C25
3	D	701	POV	C27-C28-C29-C210
3	C	607	POV	C27-C28-C29-C210
4	D	711	ATP	PB-O3B-PG-O3G
3	C	611	POV	C313-C314-C315-C316
4	D	711	ATP	C5'-O5'-PA-O3A
3	C	605	POV	C22-C23-C24-C25
3	C	609	POV	C29-C210-C211-C212
3	C	605	POV	C25-C26-C27-C28
4	C	612	ATP	PA-O3A-PB-O2B
3	D	708	POV	C22-C23-C24-C25
3	D	707	POV	O22-C21-O21-C2
3	D	703	POV	C1-C2-C3-O31
3	D	706	POV	C24-C25-C26-C27
3	C	605	POV	C24-C25-C26-C27
3	D	705	POV	O31-C31-C32-C33
3	C	604	POV	O22-C21-O21-C2
3	C	611	POV	C310-C311-C312-C313
3	D	705	POV	O32-C31-C32-C33
3	C	611	POV	C213-C214-C215-C216

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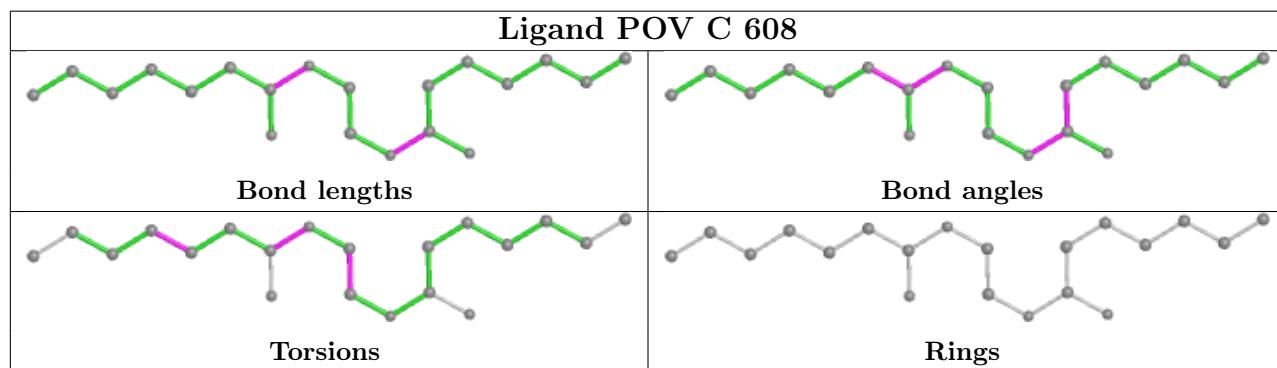
Mol	Chain	Res	Type	Atoms
3	C	611	POV	O31-C31-C32-C33
3	C	610	POV	O22-C21-O21-C2
3	D	701	POV	C310-C311-C312-C313

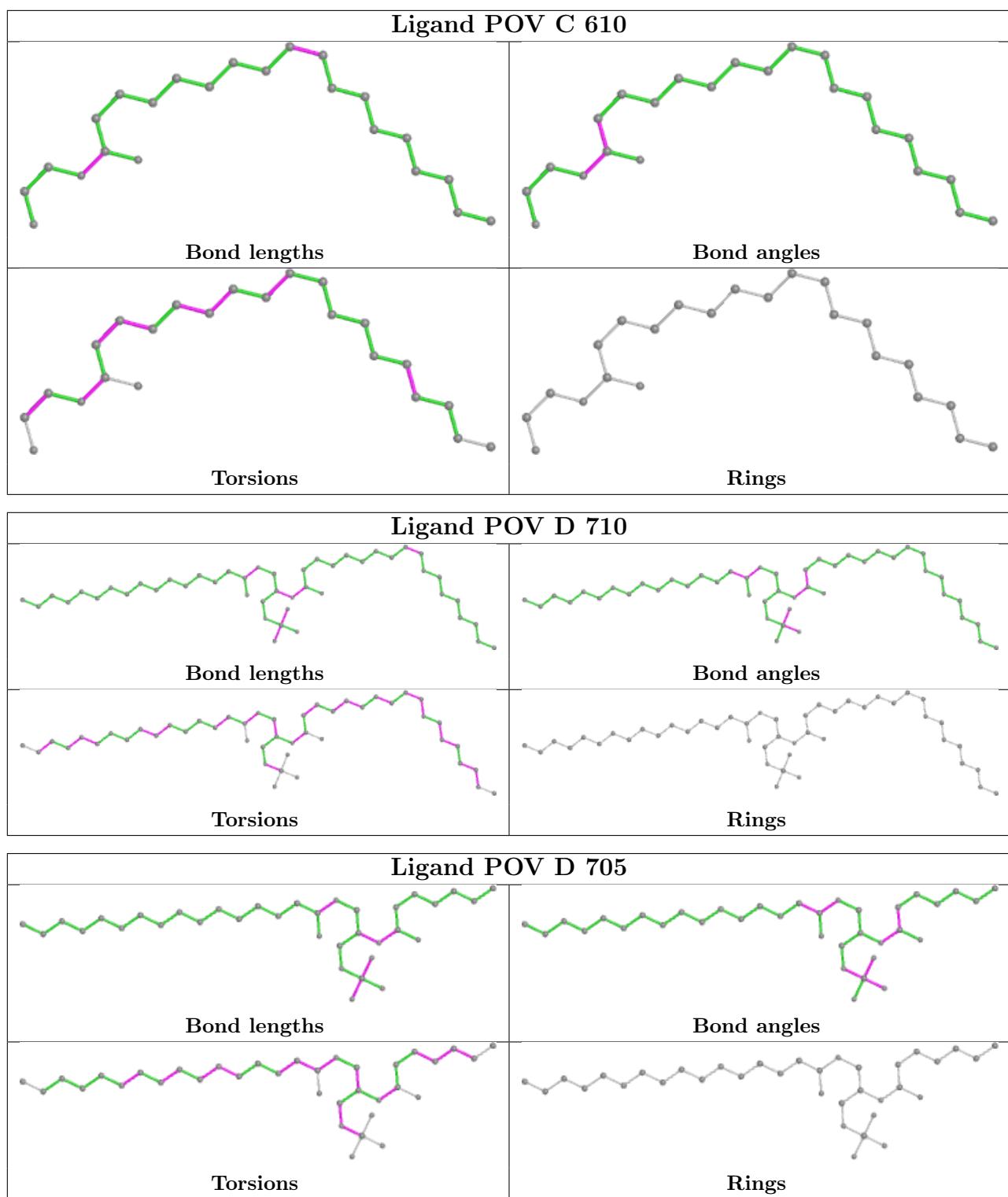
There are no ring outliers.

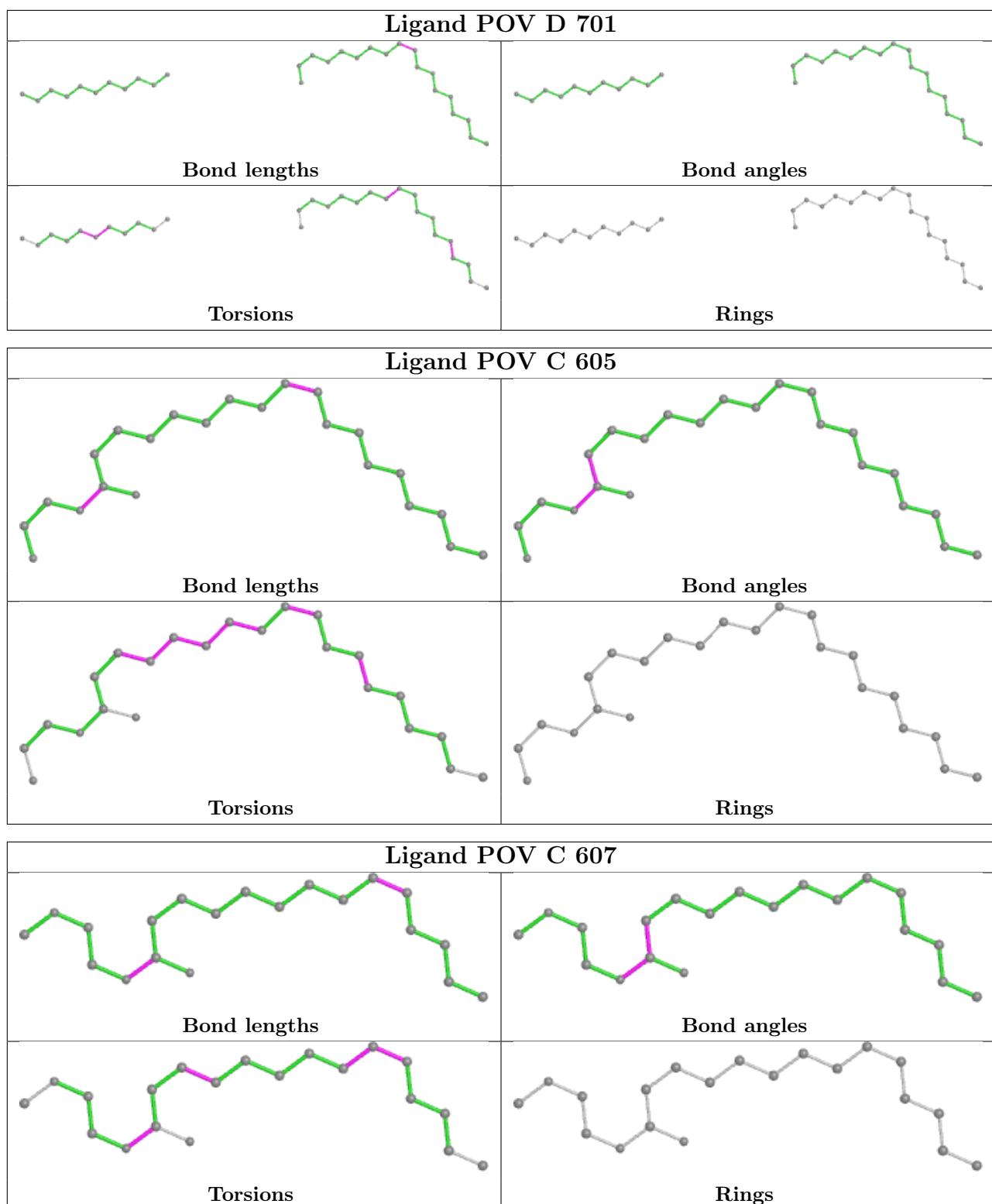
9 monomers are involved in 10 short contacts:

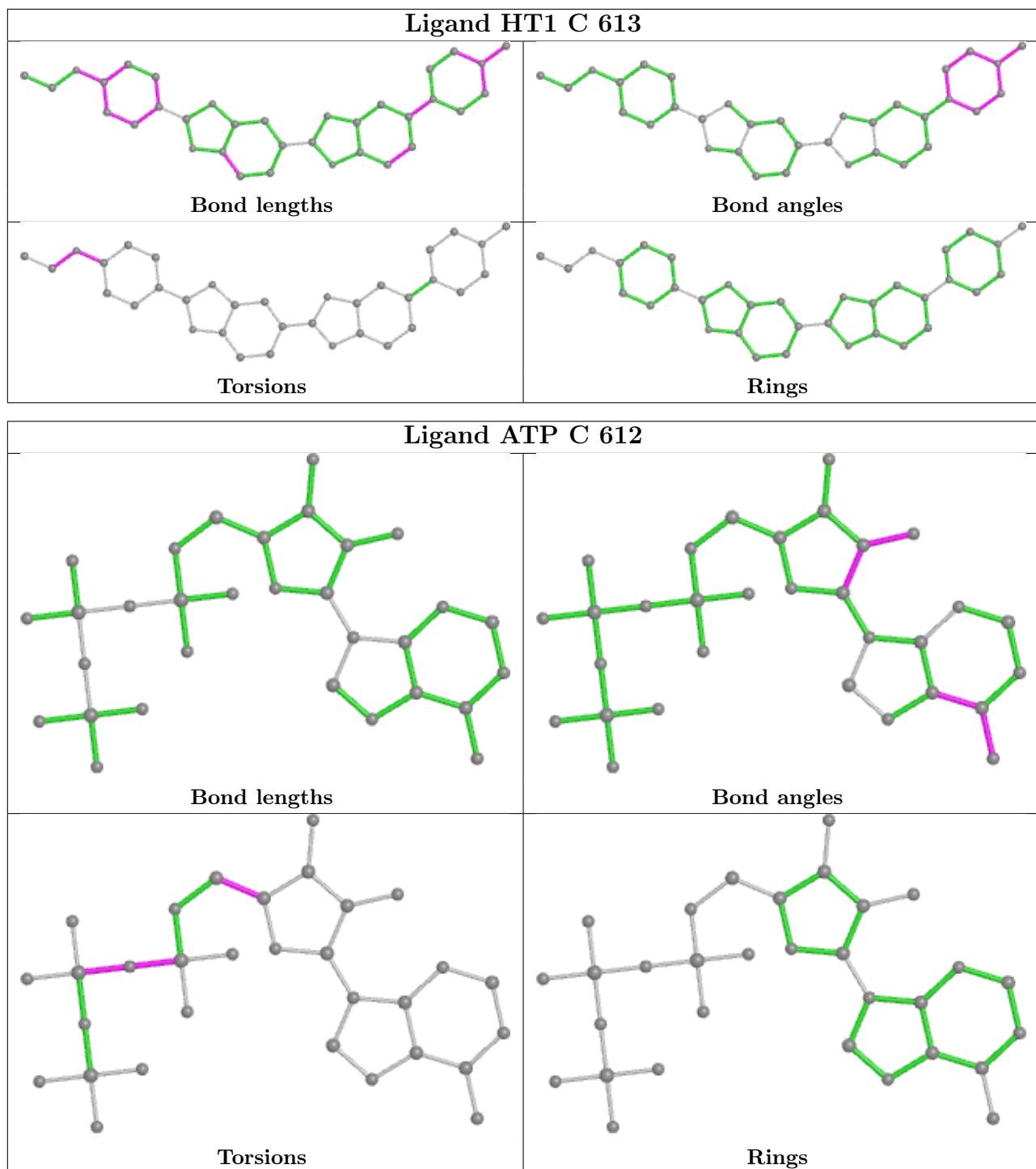
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	610	POV	1	0
3	D	705	POV	1	0
3	C	607	POV	1	0
4	C	612	ATP	1	0
3	D	708	POV	1	0
3	C	601	POV	2	0
3	C	609	POV	1	0
3	C	604	POV	1	0
3	C	603	POV	1	0

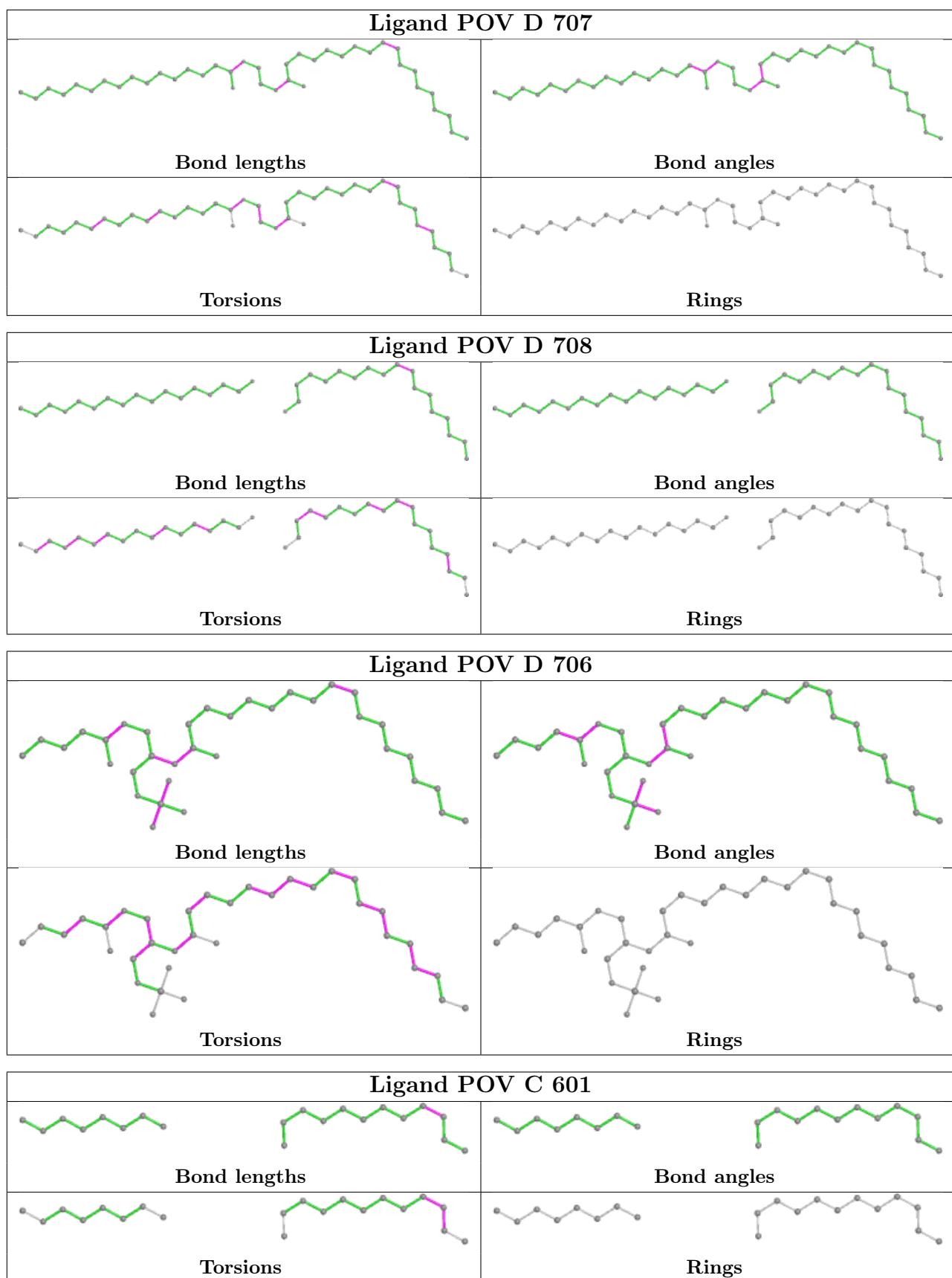
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

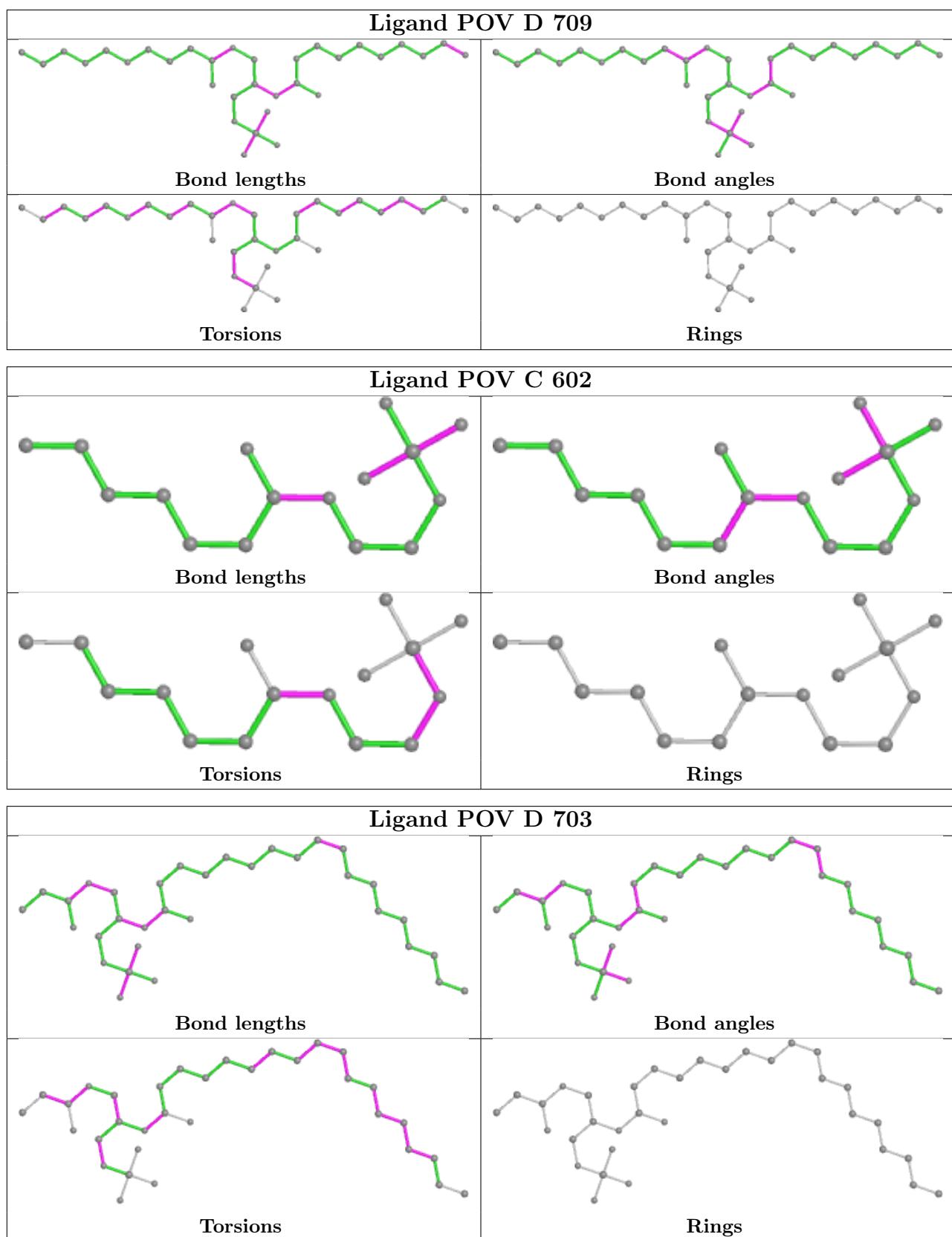


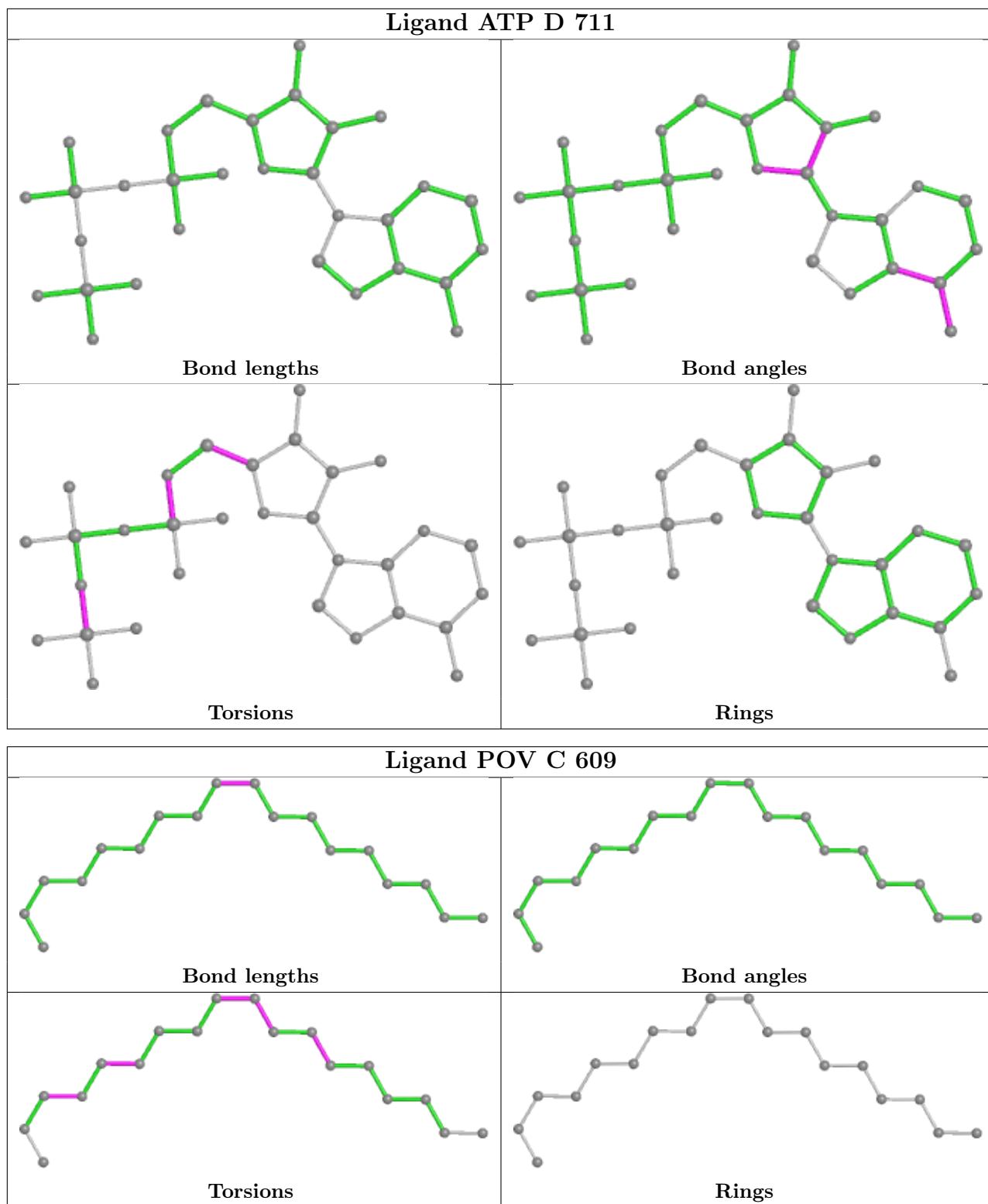


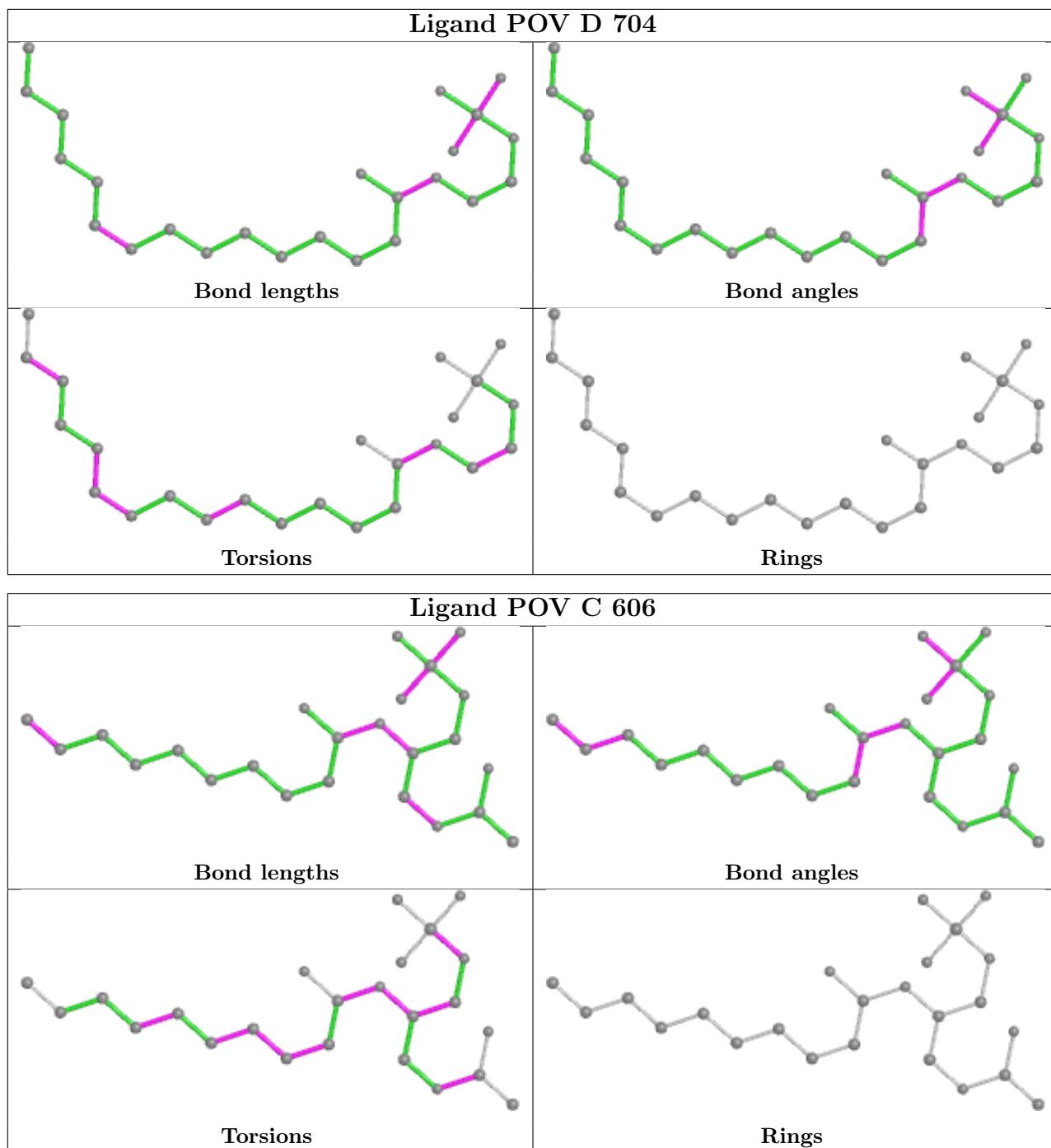


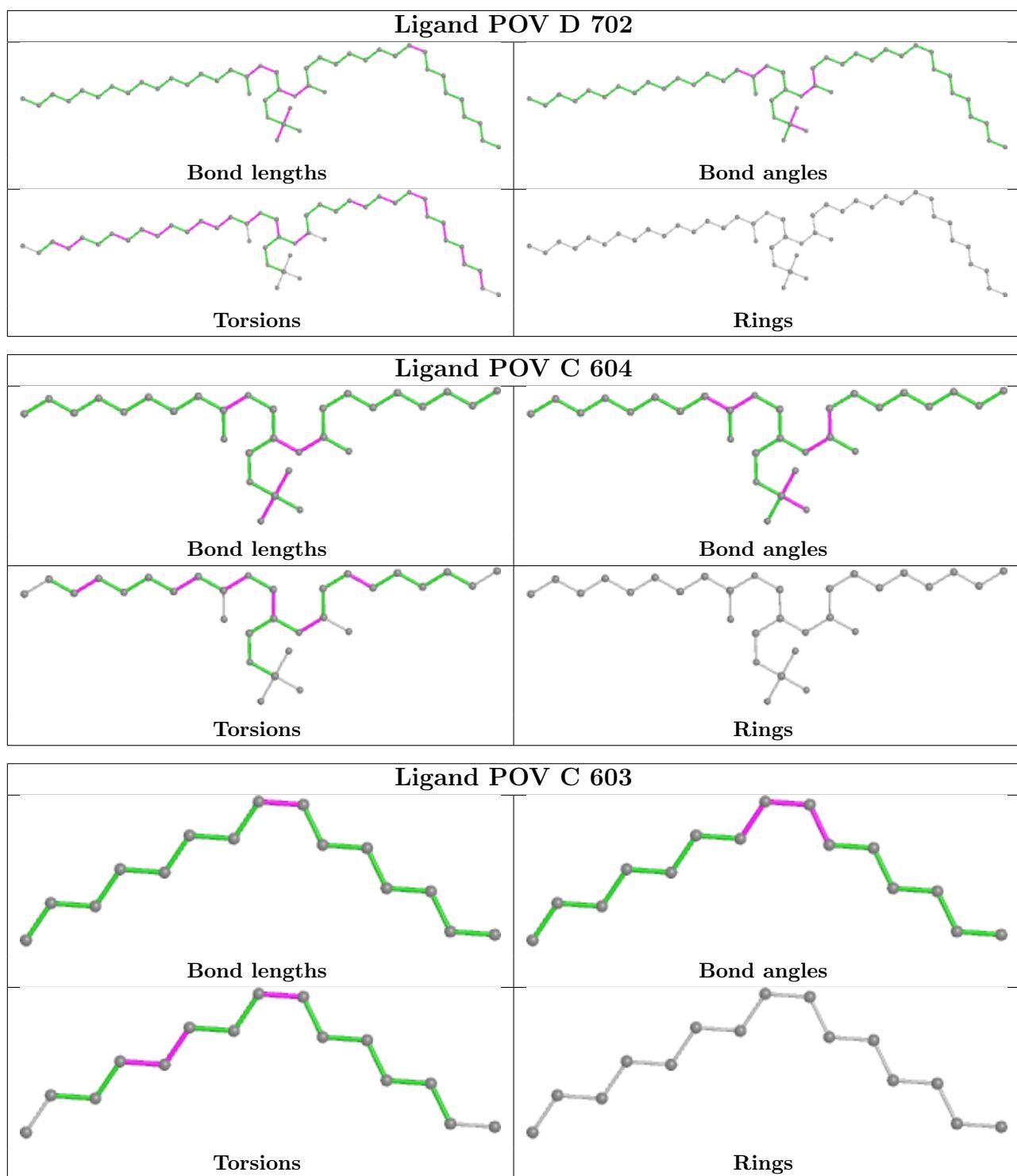


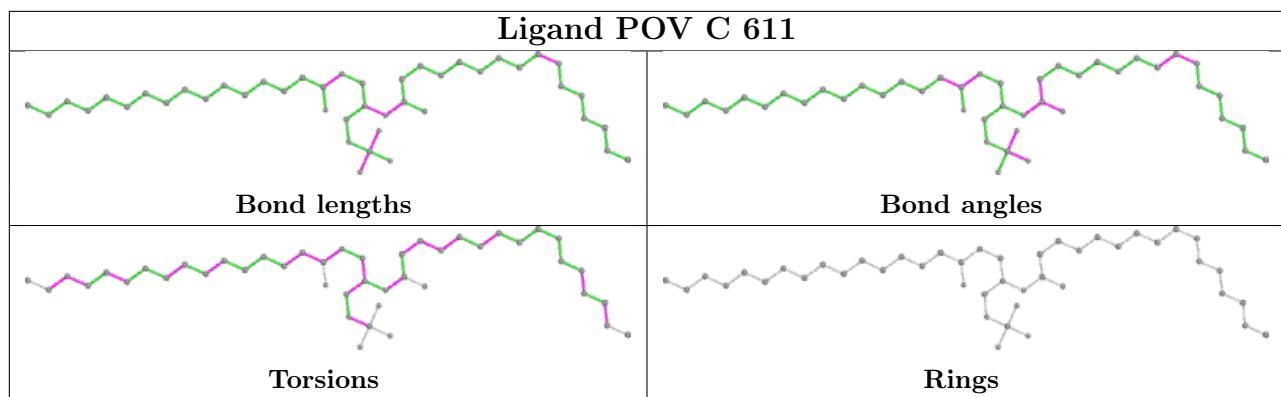












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

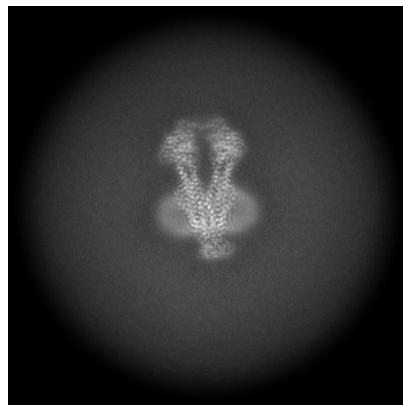
## 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-40908. These allow visual inspection of the internal detail of the map and identification of artifacts.

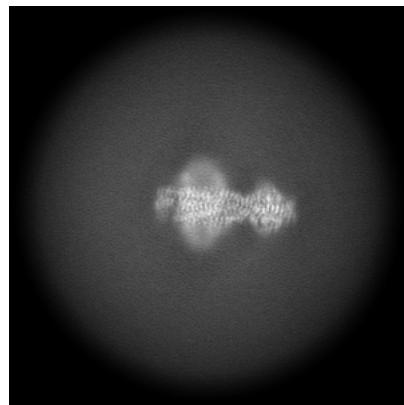
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections (i)

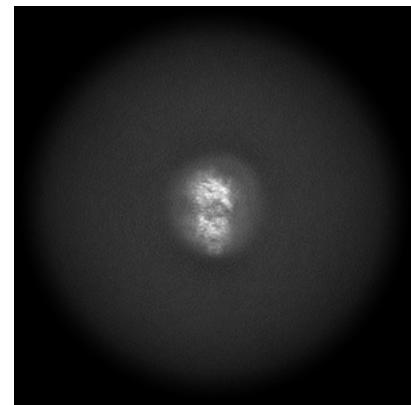
#### 6.1.1 Primary map



X



Y

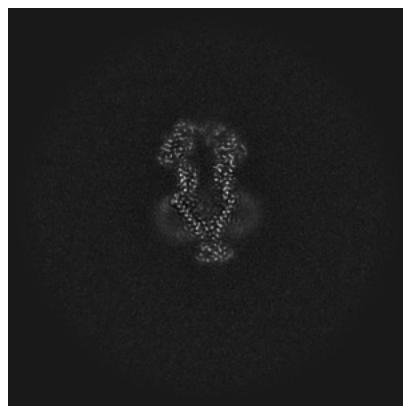


Z

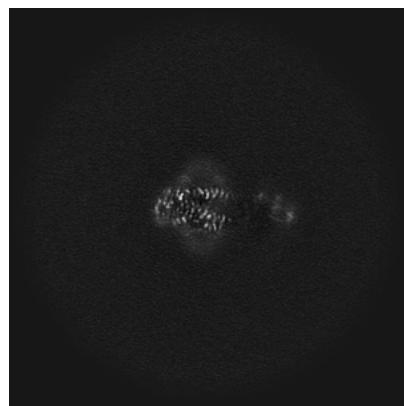
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices (i)

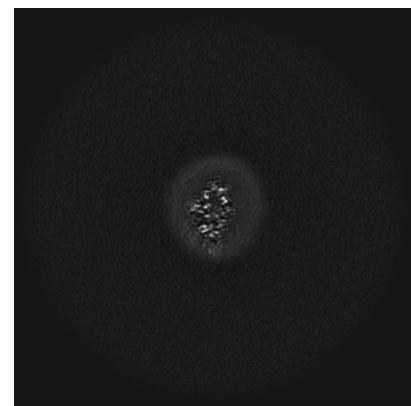
#### 6.2.1 Primary map



X Index: 240



Y Index: 240

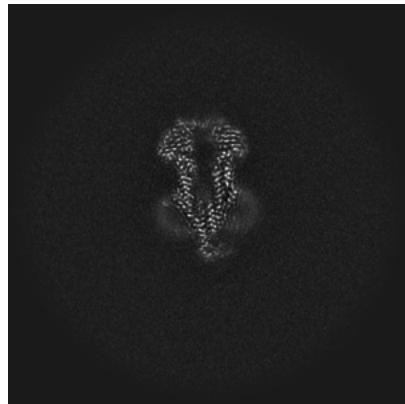


Z Index: 240

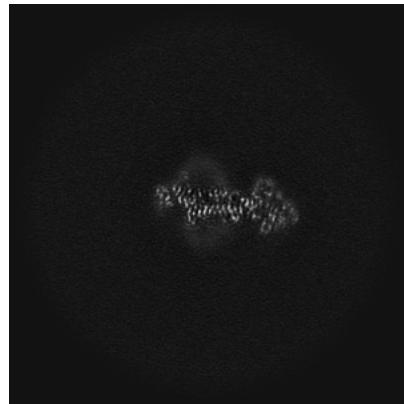
The images above show central slices of the map in three orthogonal directions.

### 6.3 Largest variance slices [\(i\)](#)

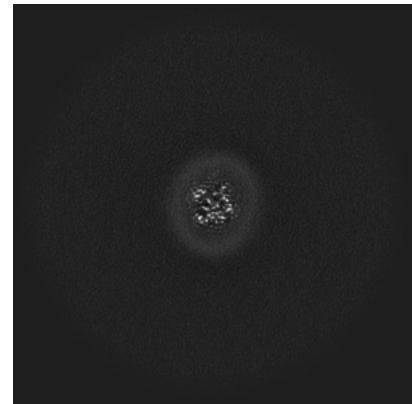
#### 6.3.1 Primary map



X Index: 235



Y Index: 253

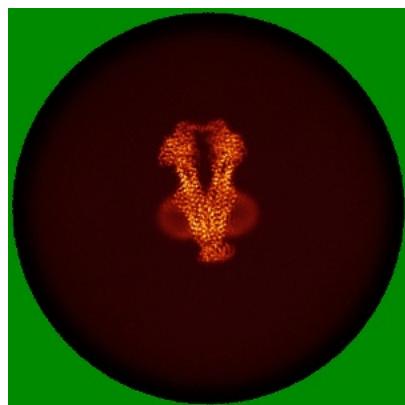


Z Index: 221

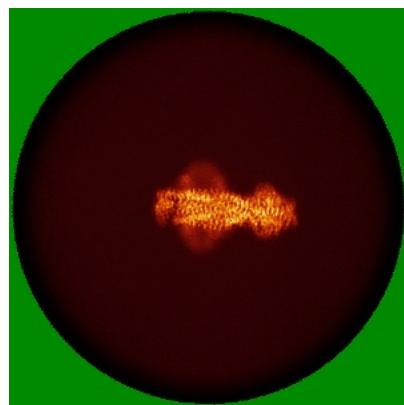
The images above show the largest variance slices of the map in three orthogonal directions.

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

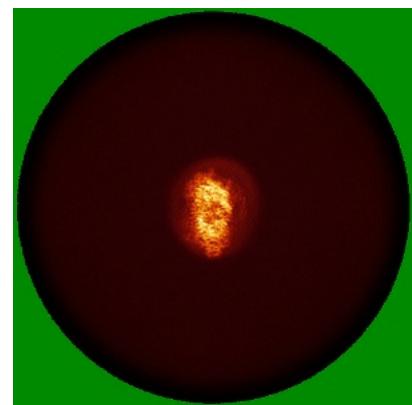
#### 6.4.1 Primary map



X



Y

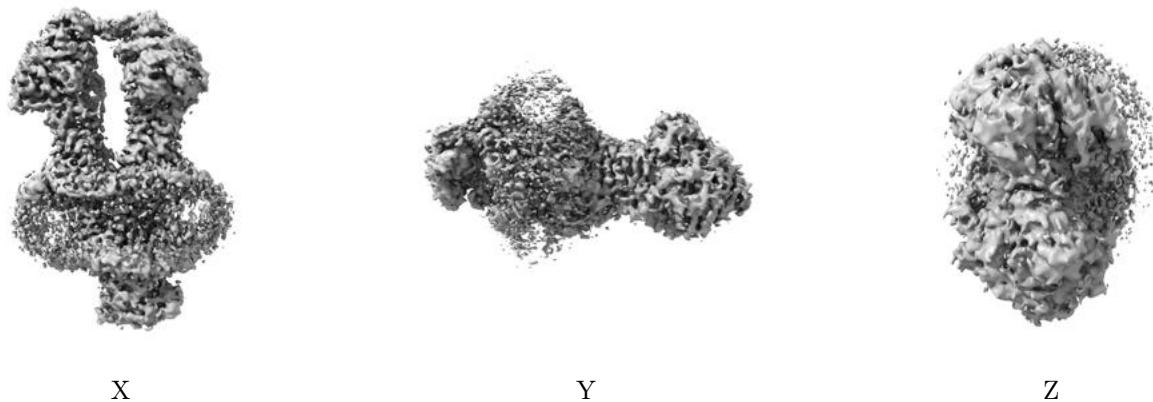


Z

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 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

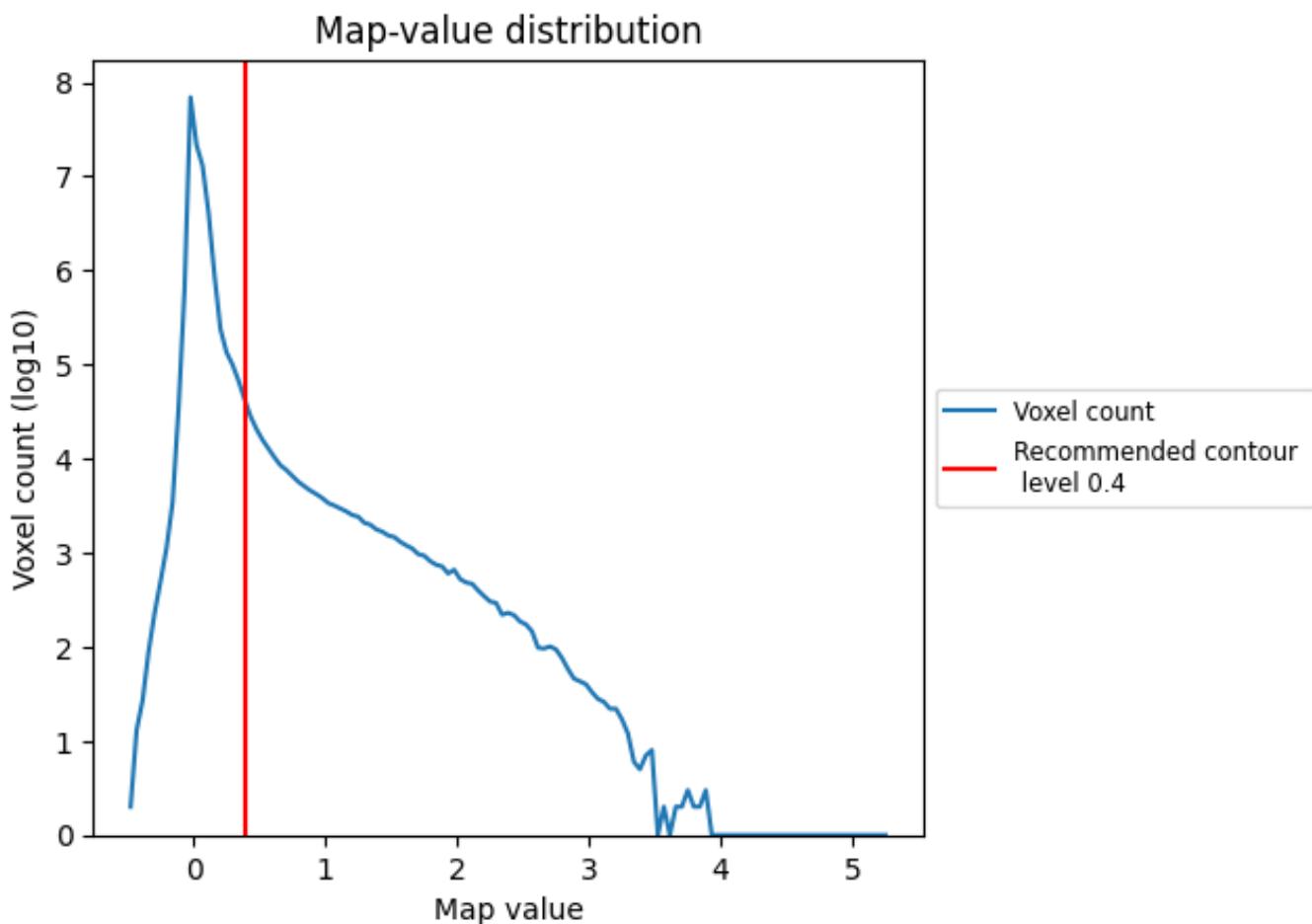
## 6.6 Mask visualisation [\(i\)](#)

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

## 7 Map analysis (i)

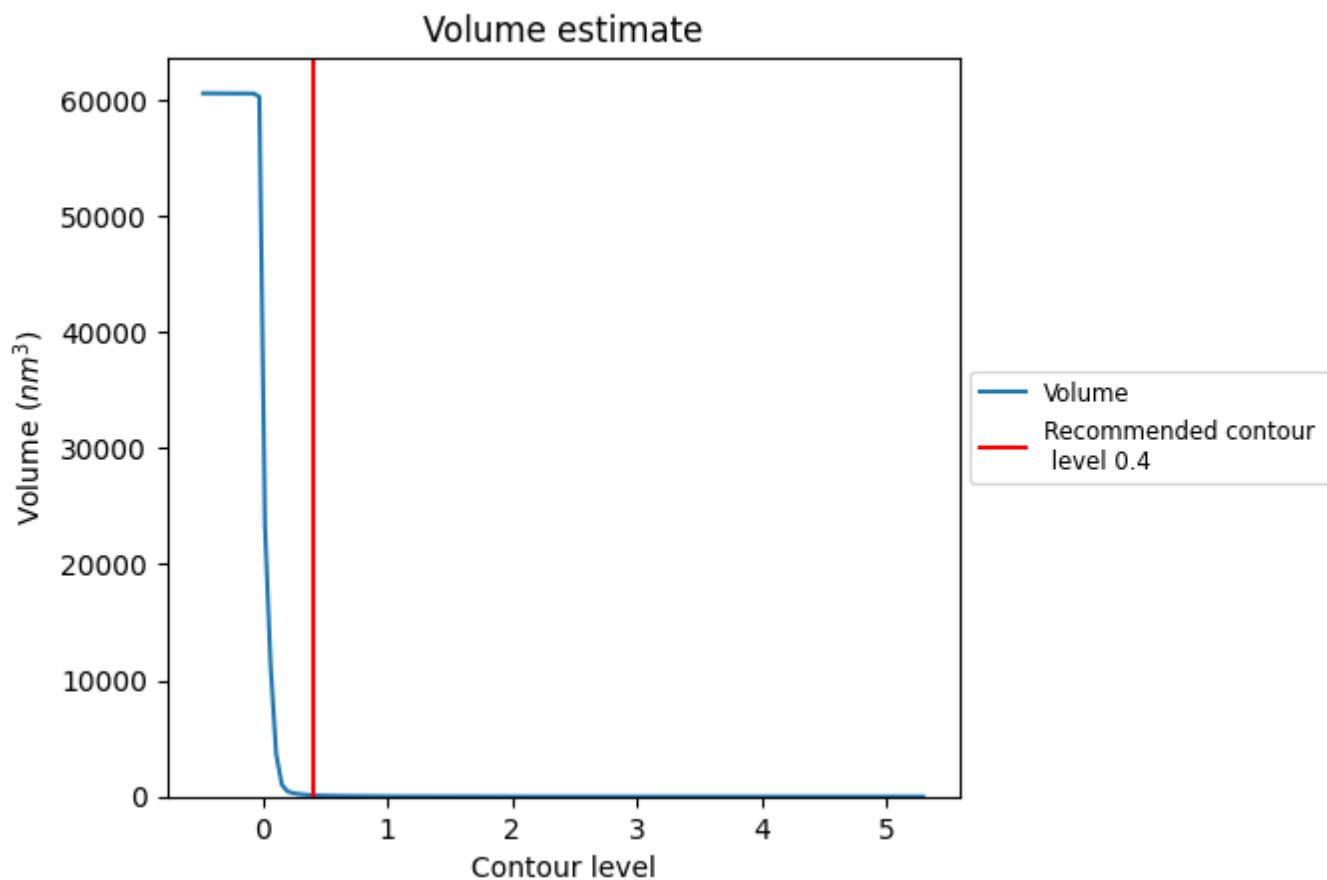
This section contains the results of statistical analysis of the map.

### 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.

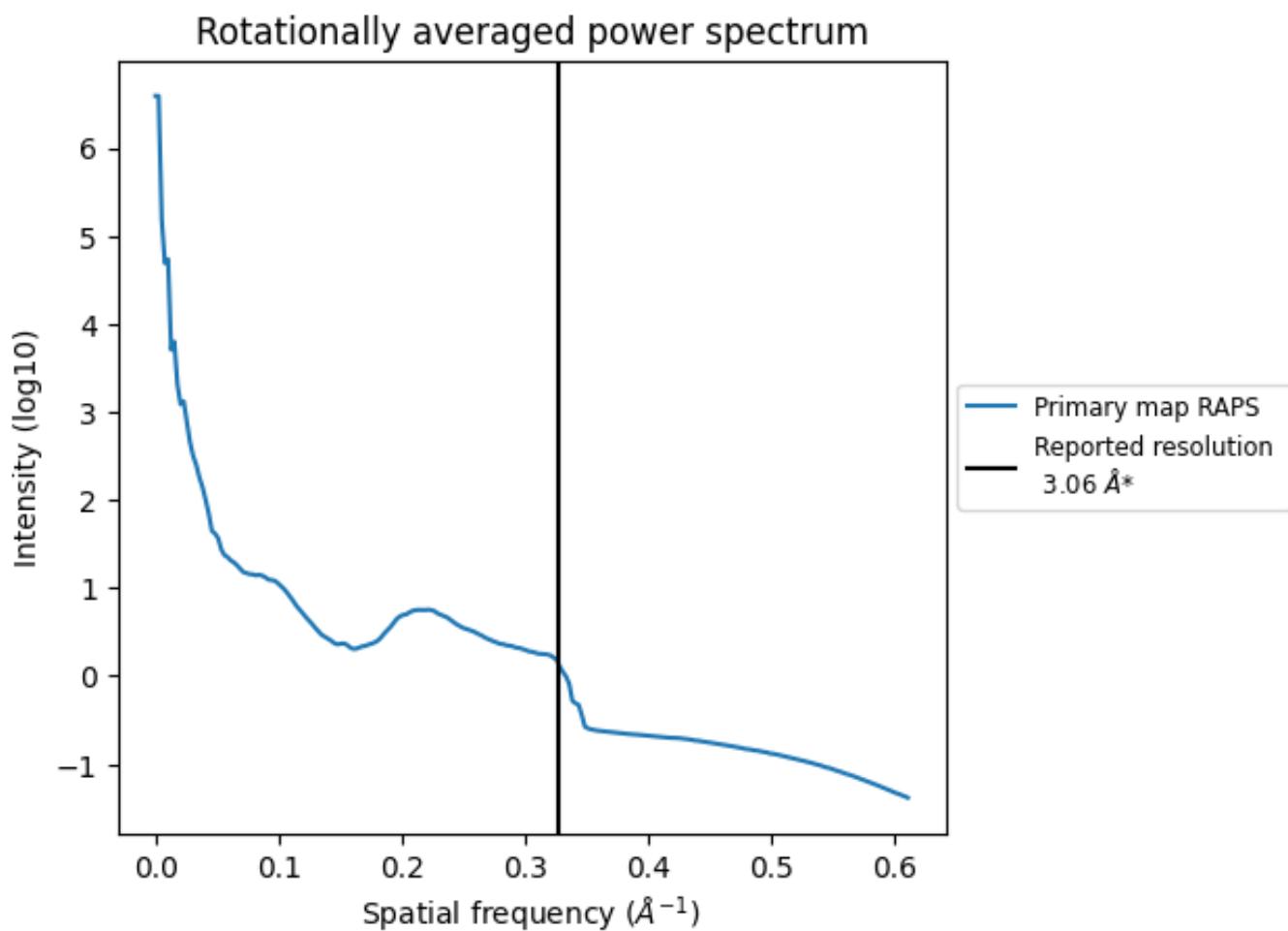
## 7.2 Volume estimate (i)



The volume at the recommended contour level is  $113 \text{ nm}^3$ ; this corresponds to an approximate mass of 102 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 [\(i\)](#)



\*Reported resolution corresponds to spatial frequency of  $0.327 \text{ \AA}^{-1}$

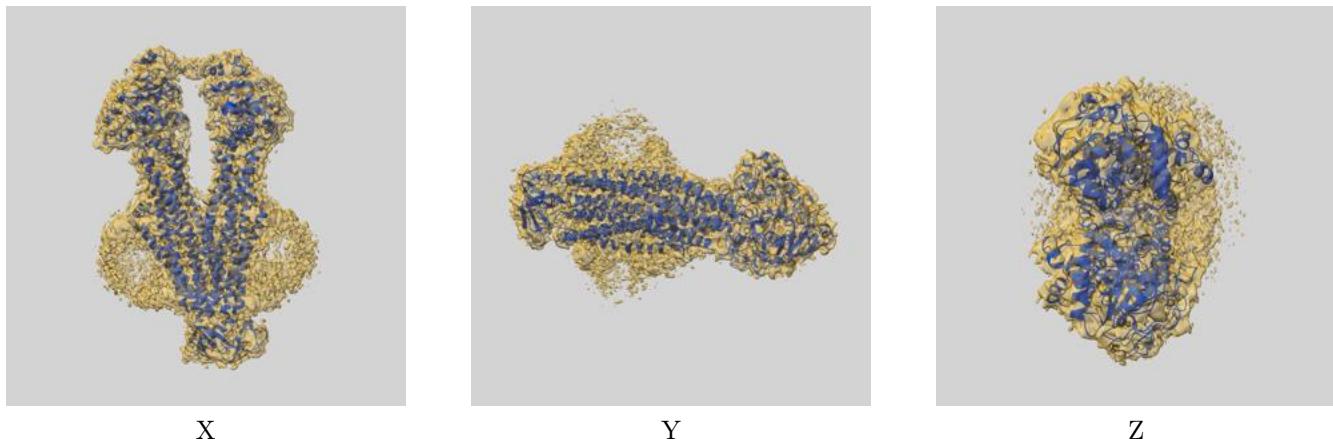
## 8 Fourier-Shell correlation

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

## 9 Map-model fit (i)

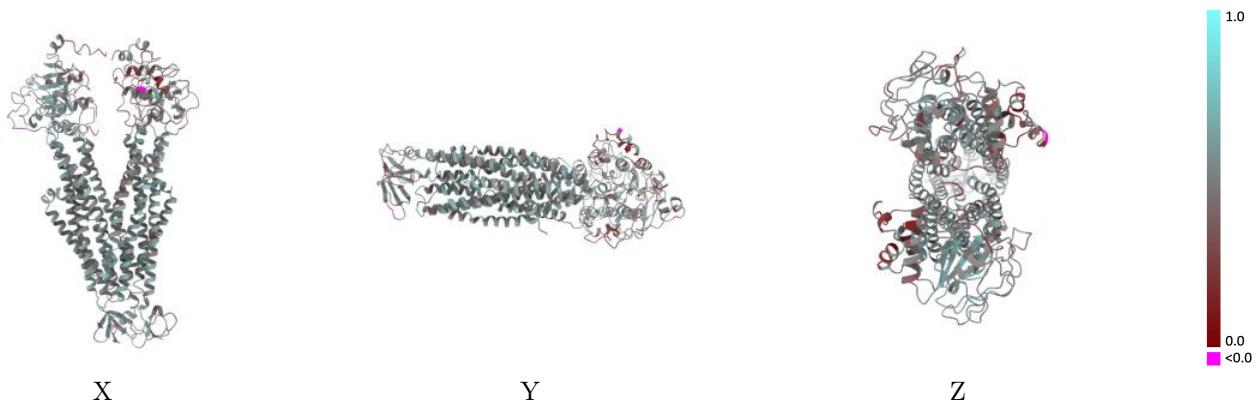
This section contains information regarding the fit between EMDB map EMD-40908 and PDB model 8SXC. Per-residue inclusion information can be found in section 3 on page 8.

### 9.1 Map-model overlay (i)



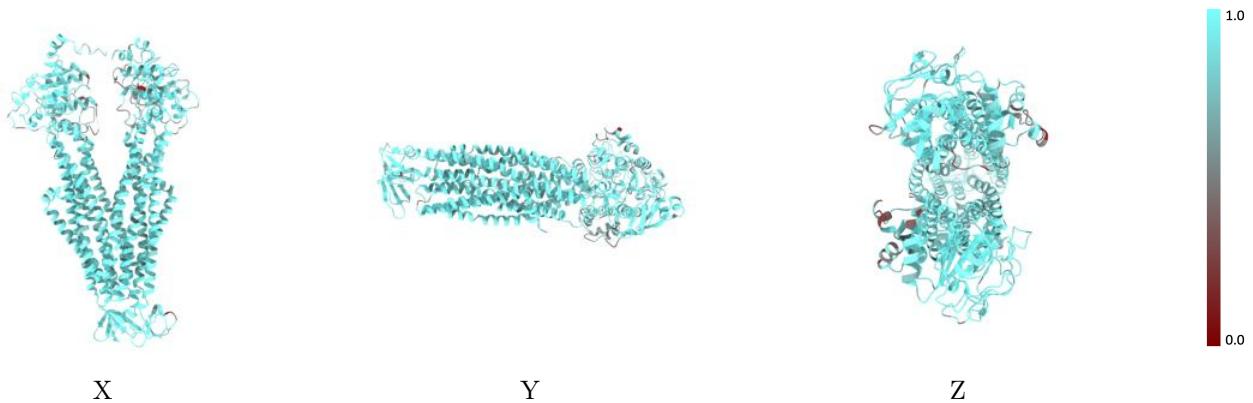
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



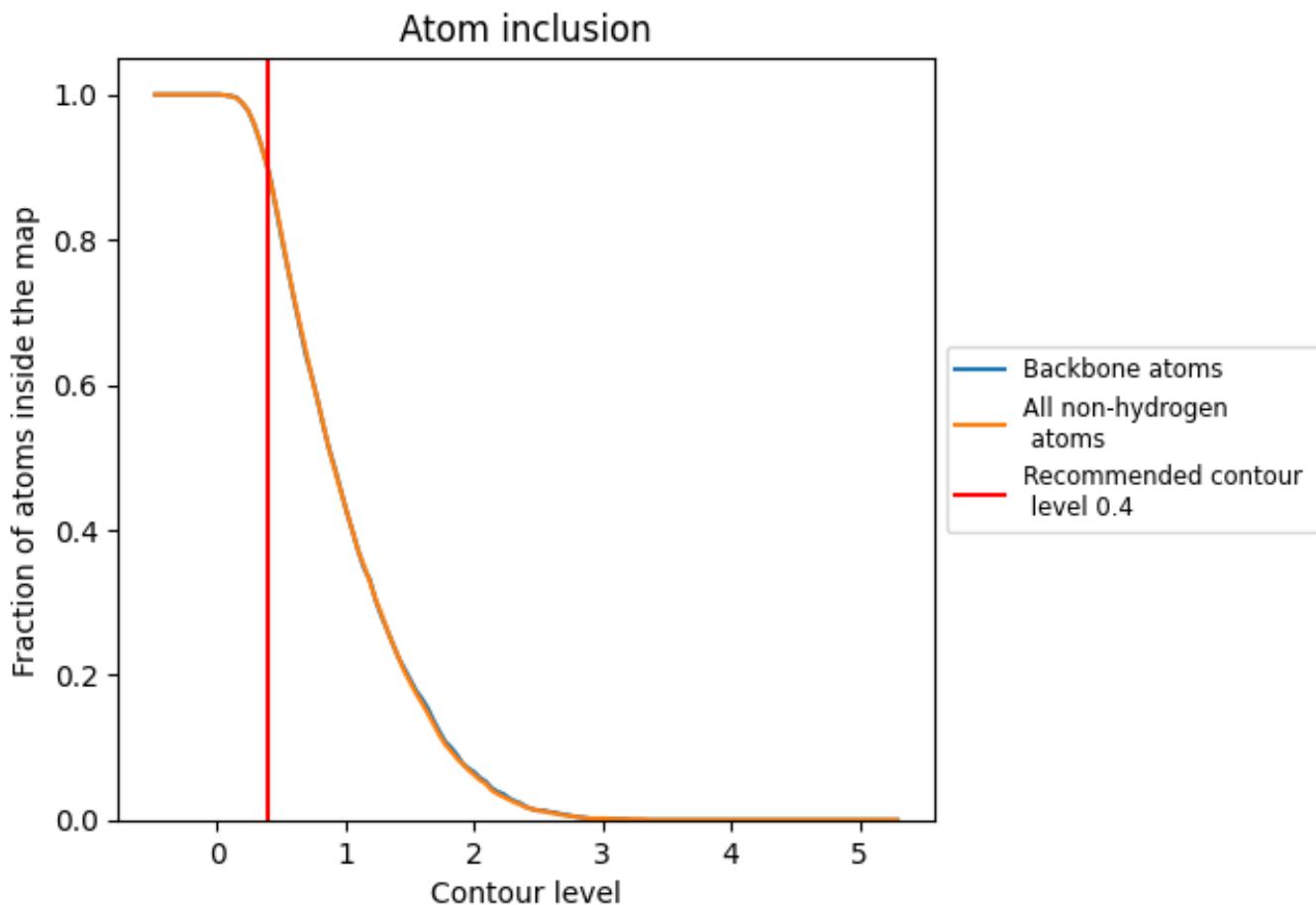
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

## 9.4 Atom inclusion [\(i\)](#)



At the recommended contour level, 90% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [\(i\)](#)

The table lists the average atom inclusion at the recommended contour level (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8970	0.4940
C	0.8950	0.4990
D	0.8990	0.4900

