



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 02:32 PM UTC

PDB ID : 8TEO / pdb_00008teo
EMDB ID : EMD-41193
Title : Shaker in low K⁺ (4mM K⁺)
Authors : Tan, X.; Swartz, K.J.
Deposited on : 2023-07-06
Resolution : 2.39 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 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

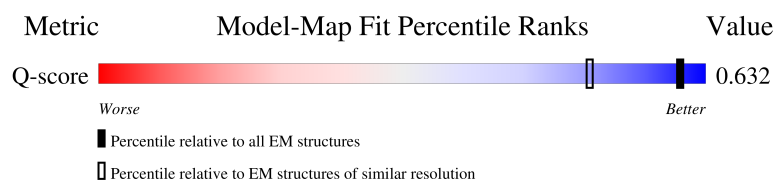
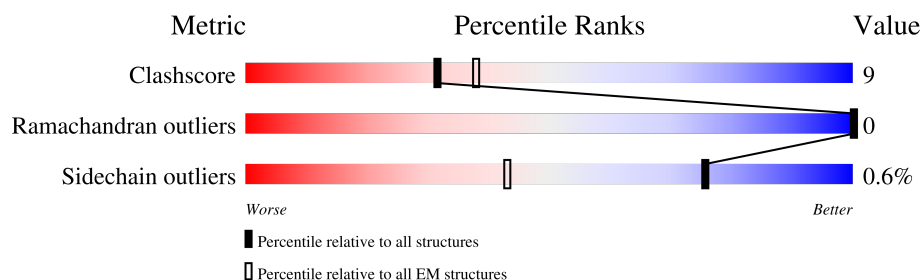
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.39 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	4884 (1.90 - 2.89)

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	658	
1	B	658	
1	C	658	
1	D	658	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6507 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.

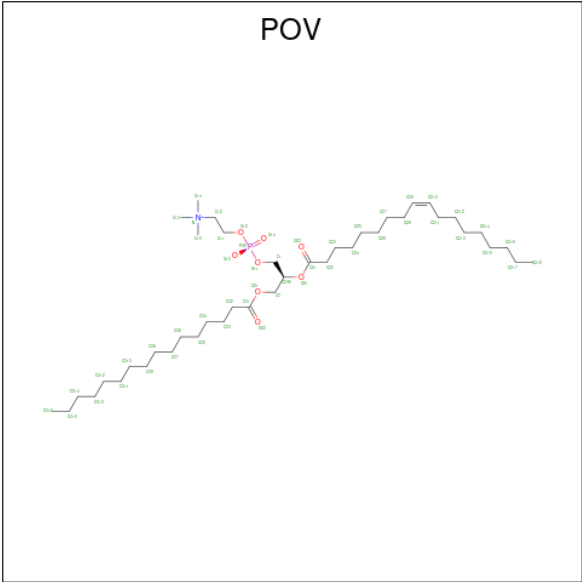
- Molecule 1 is a protein called Potassium voltage-gated channel protein Shaker.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	196	Total	C	N	O	S	0	0
			1536	1042	240	247	7		
1	B	196	Total	C	N	O	S	0	0
			1536	1042	240	247	7		
1	C	196	Total	C	N	O	S	0	0
			1536	1042	240	247	7		
1	D	196	Total	C	N	O	S	0	0
			1536	1042	240	247	7		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P08510
A	0	THR	-	expression tag	UNP P08510
A	513	VAL	-	insertion	UNP P08510
B	-1	GLY	-	expression tag	UNP P08510
B	0	THR	-	expression tag	UNP P08510
B	513	VAL	-	insertion	UNP P08510
C	-1	GLY	-	expression tag	UNP P08510
C	0	THR	-	expression tag	UNP P08510
C	513	VAL	-	insertion	UNP P08510
D	-1	GLY	-	expression tag	UNP P08510
D	0	THR	-	expression tag	UNP P08510
D	513	VAL	-	insertion	UNP P08510

- Molecule 2 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylamm onio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P).



Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total C O 21 17 4	0
2	A	1	Total C 6 6	0
2	A	1	Total C 8 8	0
2	A	1	Total C 12 12	0
2	A	1	Total C O 13 11 2	0
2	A	1	Total C O 11 9 2	0
2	A	1	Total C 10 10	0
2	A	1	Total C 7 7	0
2	B	1	Total C 10 10	0
2	B	1	Total C 7 7	0
2	B	1	Total C O 21 17 4	0
2	B	1	Total C 6 6	0
2	B	1	Total C 8 8	0
2	B	1	Total C 12 12	0

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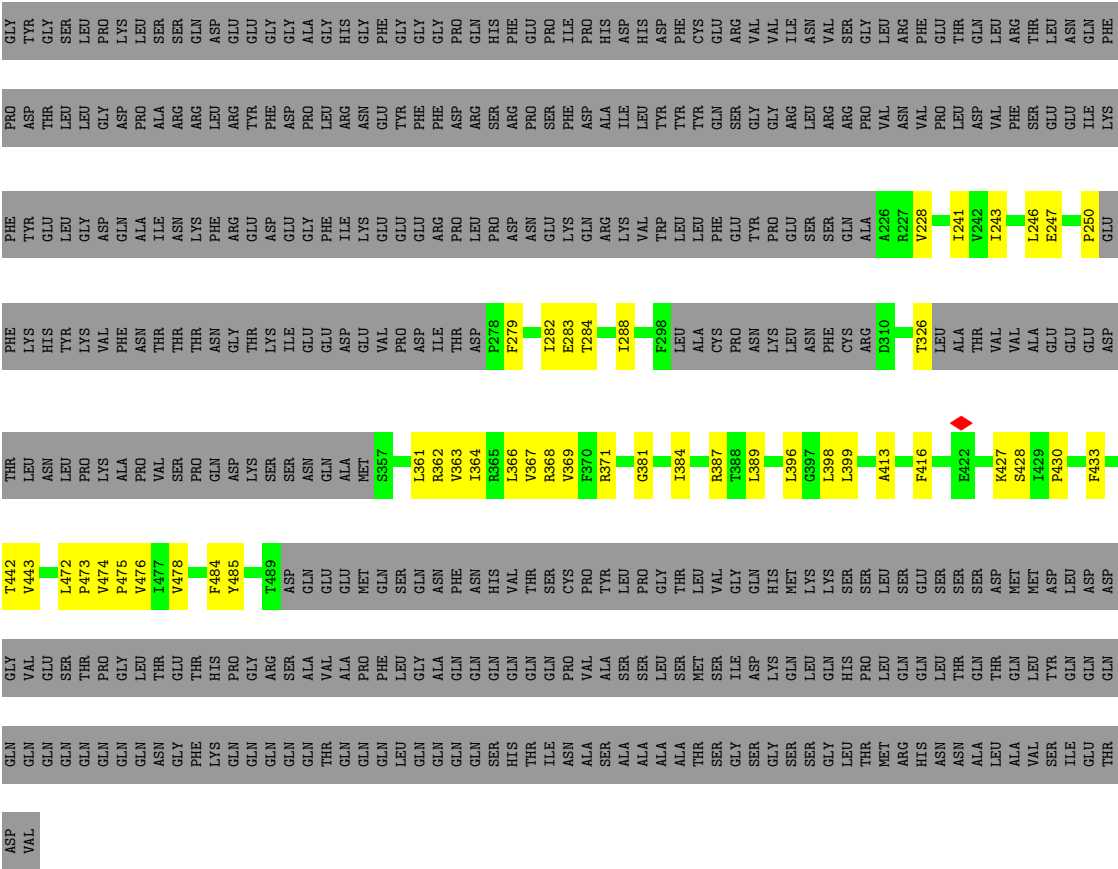
Mol	Chain	Residues	Atoms	AltConf
2	B	1	Total C O 13 11 2	0
2	B	1	Total C O 11 9 2	0
2	C	1	Total C O 11 9 2	0
2	C	1	Total C O 21 17 4	0
2	C	1	Total C 6 6	0
2	C	1	Total C 8 8	0
2	C	1	Total C 12 12	0
2	C	1	Total C O 13 11 2	0
2	C	1	Total C 10 10	0
2	C	1	Total C 7 7	0
2	D	1	Total C 10 10	0
2	D	1	Total C 7 7	0
2	D	1	Total C O 11 9 2	0
2	D	1	Total C O 21 17 4	0
2	D	1	Total C 6 6	0
2	D	1	Total C 8 8	0
2	D	1	Total C 12 12	0
2	D	1	Total C O 13 11 2	0

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

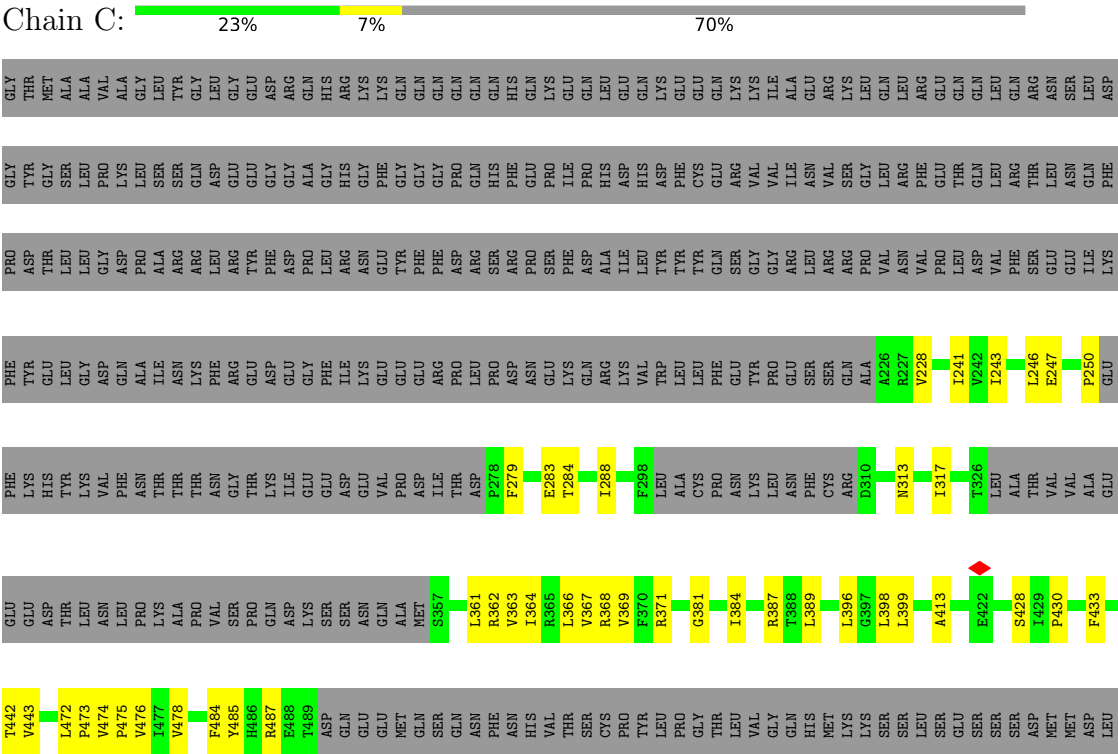
Mol	Chain	Residues	Atoms	AltConf
3	A	2	Total K 2 2	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total 2	O 2	0
4	B	2	Total 2	O 2	0
4	C	3	Total 3	O 3	0
4	D	2	Total 2	O 2	0

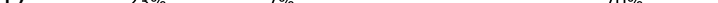


● Molecule 1: Potassium voltage-gated channel protein Shaker



GLU
THR
ASP
VAL

- Molecule 1: Potassium voltage-gated channel protein Shaker

Chain D:  23% 7% 70%

GLY	TYR	GLY	LEU	SER	LEU	PRO	LYS	LEU	SER	SER	GLN	ASP	GLU	GLU	GLY	GLY	GLY	PHE	GLY	GLY	GLY	GLY	PRO	PRO	GLN	HIS	PHE	GLU	GLU	PRO	PRO	ILE	GLY	GLY	ASP	HIS	ASP	PHE	PHE	CYS	GLU	GLU	ARG	VAL	VAL	ILE	ASN	ASN	VAL	VAL	SER	SER	GLY	GLY	LEU	ARG	LEU	LEU	THR	THR	LEU	LEU	ASN	ASN	GLN	GLN	PHE
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PRO	ASP	THR	LEU	LEU	GLY	ASP	PRO	ALA	ALA	ARG	ARG	LEU	PRO	LEU	LEU	ASN	GLY	THR	PHE	PHE	ASP	ARG	SER	SER	PRO	SER	PHE	ASP	ALA	ILE	LEU	TYR	TYR	GLN	SER	SER	GLY	GLY	ARG	LEU	ARG	ARG	PRO	VAL	ASN	VAL	PRO	PRO	LEU	LEU	ASP	VAL	PHE	SER	GLU	GLU	ILE	YS
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PHE	TYR	GLU	LEU	GLY	ASP	GLN	ALA	ILE	ASN	LYS	PHE	ARG	GLU	ASP	GLY	GLY	PHE	ILE	LYS	GLU	GLU	GLY	ARG	GLU	PRO	PRO	PRO	ASP	ASN	GLU	GLY	LYS	LYS	VAL	TRP	TRP	LEU	LEU	PHE	GLU	GLU	TYR	PRO	GLU	SER	SER	GLN	ALA	I226	I227	V228	I241	V242	I243	I244	C245	I246	E247	P250
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GLU	PHE	LYS	HIS	TYR	LYS	VAL	PHE	ASN	THR	THR	THR	ASP	THR	GLY	GLU	LYS	ILE	GLU	GLU	ASP	VAL	GLU	PRO	ASP	ILE	THR	THR	ASP	P278	P279	E283	T284	I288	F298	LEU	ALA	CYS	PRO	ASN	LYS	LEU	ASN	PHE	CYS	ARG	D310	N313	I317	T326	LEU	ALA	THR	VAL	VAL
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GLU	GLU	GLU	ASP	THR	LEU	ASN	LEU	PRO	PRO	LYS	ALA	PRO	VAL	SER	PRO	GLN	ASP	LYS	SER	SER	SER	GLN	GLN	MET	S367	L361	R362	V363	L364	R365	L366	V367	R368	V369	F370	R371	G381	L384	R387	L388	L389	L396	G397	L398	L399	A413	E422	S428	I429	P430
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[illegible]

ASP	GLY	VAL	GLU	SER	THR	PRO	GLY	LEU	THR	GLU	THR	HIS	PRO	GLY	ARG	SER	ALA	VAL	ALA	ALA	ALA	PRO	PHE	LEU	GLY	GLN	GLN	GLN	GLN	PRO	VAL	VAL	SER	SER	LEU	SER	MET	SER	ILE	ASP	LYS	GLN	LEU	GLN	HIS	PRO	LEU	GLN	GLN	GLN	THR	LEU	TYR	GLN	GLN
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[illegible]

THR
ASP
VAL

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	663447	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 ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.103	Depositor
Minimum map value	-0.033	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.006	Depositor
Map size ($\text{\AA}$)	249.0, 249.0, 249.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	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: K, 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	A	0.13	0/1573	0.31	0/2140
1	B	0.13	0/1573	0.31	0/2140
1	C	0.13	0/1573	0.31	0/2140
1	D	0.13	0/1573	0.31	0/2140
All	All	0.13	0/6292	0.31	0/8560

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	1536	0	1606	34	0
1	B	1536	0	1606	35	0
1	C	1536	0	1606	33	0
1	D	1536	0	1606	35	0
2	A	88	0	117	3	0
2	B	88	0	117	2	0
2	C	88	0	117	2	0
2	D	88	0	117	2	0
3	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	3	0	0	0	0
4	D	2	0	0	0	0
All	All	6507	0	6892	116	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 9.

All (116) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:398:LEU:HD11	1:D:381:GLY:HA3	1.65	0.79
1:C:381:GLY:HA3	1:D:398:LEU:HD11	1.65	0.79
1:A:381:GLY:HA3	1:C:398:LEU:HD11	1.66	0.78
1:A:398:LEU:HD11	1:B:381:GLY:HA3	1.65	0.78
1:C:389:LEU:HD22	1:C:396:LEU:HD11	1.75	0.68
1:B:389:LEU:HD22	1:B:396:LEU:HD11	1.75	0.68
1:D:389:LEU:HD22	1:D:396:LEU:HD11	1.75	0.68
1:A:283:GLU:OE2	1:A:368:ARG:NH1	2.27	0.67
1:A:389:LEU:HD22	1:A:396:LEU:HD11	1.75	0.67
1:D:283:GLU:OE2	1:D:368:ARG:NH1	2.27	0.67
1:C:283:GLU:OE2	1:C:368:ARG:NH1	2.27	0.67
1:B:283:GLU:OE2	1:B:368:ARG:NH1	2.27	0.67
1:C:399:LEU:HD13	1:C:473:PRO:HG2	1.80	0.63
1:D:399:LEU:HD13	1:D:473:PRO:HG2	1.80	0.63
1:B:399:LEU:HD13	1:B:473:PRO:HG2	1.80	0.62
1:A:399:LEU:HD13	1:A:473:PRO:HG2	1.80	0.62
1:A:243:ILE:HG23	1:A:279:PHE:HD1	1.66	0.61
1:C:243:ILE:HG23	1:C:279:PHE:HD1	1.66	0.61
1:B:243:ILE:HG23	1:B:279:PHE:HD1	1.66	0.60
1:D:243:ILE:HG23	1:D:279:PHE:HD1	1.66	0.60
1:A:366:LEU:HD11	1:C:413:ALA:HA	1.85	0.58
1:C:363:VAL:O	1:C:367:VAL:HG13	2.04	0.57
1:B:363:VAL:O	1:B:367:VAL:HG13	2.04	0.57
1:A:363:VAL:O	1:A:367:VAL:HG13	2.04	0.57
1:D:363:VAL:O	1:D:367:VAL:HG13	2.04	0.57
1:A:430:PRO:HA	1:A:433:PHE:CE2	2.40	0.56
1:D:430:PRO:HA	1:D:433:PHE:CE2	2.40	0.56
1:B:430:PRO:HA	1:B:433:PHE:CE2	2.40	0.56
1:C:366:LEU:HD11	1:D:413:ALA:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:GLU:OE2	1:A:371:ARG:NH2	2.26	0.56
1:B:413:ALA:HA	1:D:366:LEU:HD11	1.87	0.56
1:D:362:ARG:HG2	1:D:362:ARG:HH11	1.72	0.55
1:A:362:ARG:HH11	1:A:362:ARG:HG2	1.71	0.55
1:C:430:PRO:HA	1:C:433:PHE:CE2	2.40	0.55
1:D:283:GLU:OE2	1:D:371:ARG:NH2	2.26	0.55
1:B:283:GLU:OE2	1:B:371:ARG:NH2	2.26	0.55
1:B:362:ARG:HH11	1:B:362:ARG:HG2	1.71	0.55
1:C:362:ARG:HG2	1:C:362:ARG:HH11	1.71	0.55
1:A:413:ALA:HA	1:B:366:LEU:HD11	1.88	0.54
1:A:243:ILE:O	1:A:247:GLU:HG2	2.08	0.54
1:C:243:ILE:O	1:C:247:GLU:HG2	2.08	0.54
1:D:243:ILE:O	1:D:247:GLU:HG2	2.08	0.53
1:B:243:ILE:O	1:B:247:GLU:HG2	2.08	0.53
1:C:284:THR:O	1:C:288:ILE:HG13	2.09	0.52
1:A:241:ILE:HG22	2:A:708:POV:H36A	1.92	0.52
1:D:284:THR:O	1:D:288:ILE:HG13	2.09	0.52
1:A:284:THR:O	1:A:288:ILE:HG13	2.09	0.52
1:B:284:THR:O	1:B:288:ILE:HG13	2.09	0.51
1:C:241:ILE:HG22	2:C:708:POV:H36A	1.92	0.51
1:D:474:VAL:C	1:D:476:VAL:H	2.19	0.51
1:B:474:VAL:C	1:B:476:VAL:H	2.19	0.51
1:D:361:LEU:O	1:D:364:ILE:HG13	2.11	0.51
1:A:361:LEU:O	1:A:364:ILE:HG13	2.11	0.51
1:C:283:GLU:OE2	1:C:371:ARG:NH2	2.26	0.51
1:B:241:ILE:HG22	2:B:702:POV:H36A	1.93	0.51
1:B:361:LEU:O	1:B:364:ILE:HG13	2.11	0.51
1:A:472:LEU:HB2	1:A:473:PRO:HD3	1.94	0.50
1:C:361:LEU:O	1:C:364:ILE:HG13	2.11	0.50
1:D:241:ILE:HG22	2:D:702:POV:H36A	1.93	0.50
1:C:474:VAL:C	1:C:476:VAL:H	2.19	0.50
1:A:474:VAL:C	1:A:476:VAL:H	2.19	0.50
1:B:472:LEU:HB2	1:B:473:PRO:HD3	1.94	0.50
1:C:472:LEU:HB2	1:C:473:PRO:HD3	1.94	0.50
1:D:472:LEU:HB2	1:D:473:PRO:HD3	1.94	0.49
1:A:474:VAL:O	1:A:476:VAL:N	2.44	0.48
1:B:474:VAL:O	1:B:476:VAL:N	2.44	0.48
1:A:366:LEU:O	1:A:369:VAL:HG12	2.14	0.48
1:C:366:LEU:O	1:C:369:VAL:HG12	2.14	0.48
1:B:366:LEU:O	1:B:369:VAL:HG12	2.14	0.48
1:A:384:ILE:HD13	1:A:485:TYR:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:384:ILE:HD13	1:C:485:TYR:HA	1.96	0.47
1:D:474:VAL:O	1:D:476:VAL:N	2.44	0.47
1:D:384:ILE:HD13	1:D:485:TYR:HA	1.96	0.47
1:B:384:ILE:HD13	1:B:485:TYR:HA	1.96	0.47
1:D:366:LEU:O	1:D:369:VAL:HG12	2.14	0.46
1:C:474:VAL:O	1:C:476:VAL:N	2.44	0.46
1:A:246:LEU:HD21	2:A:708:POV:H32	1.97	0.46
1:D:326:THR:O	1:D:326:THR:OG1	2.33	0.45
1:C:487:ARG:HE	1:C:487:ARG:HB3	1.63	0.44
1:A:443:VAL:HG22	1:C:442:THR:HA	1.99	0.44
1:A:475:PRO:HG2	1:B:478:VAL:HG11	1.99	0.43
1:A:428:SER:HB3	1:B:250:PRO:HD3	2.00	0.43
1:A:487:ARG:HE	1:A:487:ARG:HB3	1.63	0.43
1:A:442:THR:HA	1:B:443:VAL:HG22	2.00	0.42
1:C:246:LEU:HD21	2:C:708:POV:H32	2.00	0.42
1:B:326:THR:O	1:B:326:THR:OG1	2.32	0.42
1:C:443:VAL:HG22	1:D:442:THR:HA	2.00	0.42
1:A:243:ILE:HD11	2:A:707:POV:H39A	2.00	0.42
1:B:475:PRO:HG2	1:D:478:VAL:HG11	2.01	0.42
1:C:250:PRO:HD3	1:D:428:SER:HB3	2.01	0.42
1:A:250:PRO:HD3	1:C:428:SER:HB3	2.00	0.42
1:C:478:VAL:HG11	1:D:475:PRO:HG2	2.02	0.42
1:D:247:GLU:CD	1:D:368:ARG:HH22	2.27	0.42
1:B:428:SER:HB3	1:D:250:PRO:HD3	2.00	0.41
1:A:474:VAL:HB	1:A:475:PRO:HD3	2.02	0.41
1:B:246:LEU:HD21	2:B:702:POV:H32	2.02	0.41
1:D:246:LEU:HD21	2:D:702:POV:H32	2.01	0.41
1:A:387:ARG:HD2	1:A:484:PHE:CE1	2.56	0.41
1:B:474:VAL:HB	1:B:475:PRO:HD3	2.03	0.41
1:D:313:ASN:O	1:D:317:ILE:HG12	2.21	0.41
1:B:416:PHE:HE2	1:D:244:PHE:HZ	1.69	0.41
1:C:313:ASN:O	1:C:317:ILE:HG12	2.21	0.41
1:B:427:LYS:HA	1:B:427:LYS:HD3	1.83	0.41
1:A:313:ASN:O	1:A:317:ILE:HG12	2.21	0.41
1:C:247:GLU:CD	1:C:368:ARG:HH22	2.27	0.41
1:C:474:VAL:HB	1:C:475:PRO:HD3	2.02	0.41
1:B:442:THR:HA	1:D:443:VAL:HG22	2.01	0.41
1:A:247:GLU:CD	1:A:368:ARG:HH22	2.27	0.40
1:A:478:VAL:HG11	1:C:475:PRO:HG2	2.03	0.40
1:B:366:LEU:HD12	1:B:366:LEU:HA	1.90	0.40
1:B:387:ARG:HD2	1:B:484:PHE:CE1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:366:LEU:HD12	1:D:366:LEU:HA	1.90	0.40
1:C:387:ARG:HD2	1:C:484:PHE:CE1	2.56	0.40
1:D:474:VAL:HB	1:D:475:PRO:HD3	2.02	0.40
1:B:243:ILE:HG13	1:B:282:ILE:HG21	2.03	0.40
1:D:387:ARG:HD2	1:D:484:PHE:CE1	2.56	0.40

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	188/658 (29%)	183 (97%)	5 (3%)	0	100	100
1	B	188/658 (29%)	183 (97%)	5 (3%)	0	100	100
1	C	188/658 (29%)	183 (97%)	5 (3%)	0	100	100
1	D	188/658 (29%)	183 (97%)	5 (3%)	0	100	100
All	All	752/2632 (29%)	732 (97%)	20 (3%)	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	A	166/579 (29%)	165 (99%)	1 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	166/579 (29%)	165 (99%)	1 (1%)	78	89
1	C	166/579 (29%)	165 (99%)	1 (1%)	78	89
1	D	166/579 (29%)	165 (99%)	1 (1%)	78	89
All	All	664/2316 (29%)	660 (99%)	4 (1%)	76	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	228	VAL
1	B	228	VAL
1	C	228	VAL
1	D	228	VAL

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

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 34 ligands modelled in this entry, 2 are monoatomic - leaving 32 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	POV	C	708	-	6,6,51	0.72	0	5,5,59	0.71	0
2	POV	C	704	-	7,7,51	0.81	0	6,6,59	0.75	0
2	POV	A	703	-	7,7,51	0.81	0	6,6,59	0.75	0
2	POV	A	705	-	12,12,51	1.43	2 (16%)	12,12,59	1.19	0
2	POV	C	702	-	20,20,51	1.52	4 (20%)	22,22,59	1.38	2 (9%)
2	POV	D	707	-	11,11,51	0.76	0	10,10,59	0.83	0
2	POV	C	706	-	12,12,51	1.44	2 (16%)	12,12,59	1.19	0
2	POV	B	704	-	5,5,51	0.65	0	4,4,59	0.61	0
2	POV	A	704	-	11,11,51	0.77	0	10,10,59	0.83	0
2	POV	A	708	-	6,6,51	0.72	0	5,5,59	0.71	0
2	POV	D	703	-	10,10,51	1.50	1 (10%)	10,10,59	1.09	1 (10%)
2	POV	D	705	-	5,5,51	0.65	0	4,4,59	0.61	0
2	POV	C	701	-	10,10,51	1.50	1 (10%)	10,10,59	1.09	1 (10%)
2	POV	C	707	-	9,9,51	0.78	0	8,8,59	0.81	0
2	POV	D	704	-	20,20,51	1.51	3 (15%)	22,22,59	1.38	2 (9%)
2	POV	D	702	-	6,6,51	0.72	0	5,5,59	0.71	0
2	POV	D	706	-	7,7,51	0.81	0	6,6,59	0.75	0
2	POV	A	707	-	9,9,51	0.78	0	8,8,59	0.81	0
2	POV	B	708	-	10,10,51	1.50	1 (10%)	10,10,59	1.09	1 (10%)
2	POV	D	701	-	9,9,51	0.78	0	8,8,59	0.81	0
2	POV	B	705	-	7,7,51	0.81	0	6,6,59	0.75	0
2	POV	C	705	-	11,11,51	0.77	0	10,10,59	0.83	0
2	POV	D	708	-	12,12,51	1.42	2 (16%)	12,12,59	1.20	0
2	POV	B	702	-	6,6,51	0.72	0	5,5,59	0.71	0
2	POV	B	703	-	20,20,51	1.51	3 (15%)	22,22,59	1.38	2 (9%)
2	POV	A	702	-	5,5,51	0.65	0	4,4,59	0.61	0
2	POV	B	706	-	11,11,51	0.77	0	10,10,59	0.83	0
2	POV	B	701	-	9,9,51	0.78	0	8,8,59	0.81	0
2	POV	A	701	-	20,20,51	1.51	4 (20%)	22,22,59	1.38	2 (9%)
2	POV	C	703	-	5,5,51	0.66	0	4,4,59	0.62	0
2	POV	B	707	-	12,12,51	1.43	2 (16%)	12,12,59	1.19	0
2	POV	A	706	-	10,10,51	1.50	1 (10%)	10,10,59	1.08	1 (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
2	POV	C	708	-	-	2/4/4/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	POV	C	704	-	-	4/5/5/55	-
2	POV	A	703	-	-	4/5/5/55	-
2	POV	A	705	-	-	4/10/10/55	-
2	POV	C	702	-	-	12/21/21/55	-
2	POV	D	707	-	-	3/9/9/55	-
2	POV	C	706	-	-	4/10/10/55	-
2	POV	B	704	-	-	3/3/3/55	-
2	POV	A	704	-	-	3/9/9/55	-
2	POV	A	708	-	-	2/4/4/55	-
2	POV	D	703	-	-	6/9/9/55	-
2	POV	D	705	-	-	3/3/3/55	-
2	POV	C	701	-	-	6/9/9/55	-
2	POV	C	707	-	-	2/7/7/55	-
2	POV	D	704	-	-	12/21/21/55	-
2	POV	D	702	-	-	2/4/4/55	-
2	POV	D	706	-	-	4/5/5/55	-
2	POV	A	707	-	-	2/7/7/55	-
2	POV	B	708	-	-	6/9/9/55	-
2	POV	D	701	-	-	2/7/7/55	-
2	POV	B	705	-	-	4/5/5/55	-
2	POV	C	705	-	-	3/9/9/55	-
2	POV	D	708	-	-	4/10/10/55	-
2	POV	B	702	-	-	2/4/4/55	-
2	POV	B	703	-	-	12/21/21/55	-
2	POV	A	702	-	-	3/3/3/55	-
2	POV	B	706	-	-	3/9/9/55	-
2	POV	B	701	-	-	2/7/7/55	-
2	POV	A	701	-	-	12/21/21/55	-
2	POV	C	703	-	-	3/3/3/55	-
2	POV	B	707	-	-	4/10/10/55	-
2	POV	A	706	-	-	6/9/9/55	-

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	POV	O31-C31	3.87	1.44	1.33
2	B	703	POV	O31-C31	3.87	1.44	1.33
2	C	702	POV	O31-C31	3.87	1.44	1.33
2	D	704	POV	O31-C31	3.87	1.44	1.33
2	A	706	POV	O31-C31	3.68	1.44	1.33
2	C	701	POV	O31-C31	3.68	1.44	1.33
2	D	703	POV	O31-C31	3.68	1.44	1.33
2	B	708	POV	O31-C31	3.65	1.44	1.33
2	C	706	POV	O21-C21	3.35	1.41	1.30
2	A	705	POV	O21-C21	3.34	1.41	1.30
2	B	707	POV	O21-C21	3.34	1.41	1.30
2	D	708	POV	O21-C21	3.32	1.41	1.30
2	B	703	POV	O21-C21	2.97	1.42	1.34
2	D	704	POV	O21-C21	2.97	1.42	1.34
2	C	702	POV	O21-C21	2.96	1.42	1.34
2	A	701	POV	O21-C21	2.95	1.42	1.34
2	C	706	POV	C22-C21	2.62	1.56	1.50
2	A	705	POV	C22-C21	2.60	1.56	1.50
2	B	707	POV	C22-C21	2.60	1.56	1.50
2	D	708	POV	C22-C21	2.58	1.56	1.50
2	A	701	POV	O21-C2	-2.18	1.43	1.47
2	B	703	POV	O21-C2	-2.18	1.43	1.47
2	C	702	POV	O21-C2	-2.18	1.43	1.47
2	D	704	POV	O21-C2	-2.18	1.43	1.47
2	C	702	POV	C22-C21	2.02	1.56	1.50
2	A	701	POV	C22-C21	2.01	1.56	1.50

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	POV	O21-C21-C22	3.50	119.06	111.48
2	B	703	POV	O21-C21-C22	3.50	119.06	111.48
2	C	702	POV	O21-C21-C22	3.50	119.05	111.48
2	D	704	POV	O21-C21-C22	3.49	119.03	111.48
2	B	703	POV	O31-C31-C32	2.76	120.25	111.83
2	D	704	POV	O31-C31-C32	2.76	120.25	111.83
2	A	701	POV	O31-C31-C32	2.76	120.25	111.83
2	C	702	POV	O31-C31-C32	2.76	120.25	111.83
2	B	708	POV	O31-C31-C32	2.16	120.30	112.14
2	D	703	POV	O31-C31-C32	2.16	120.30	112.14
2	C	701	POV	O31-C31-C32	2.15	120.27	112.14
2	A	706	POV	O31-C31-C32	2.14	120.24	112.14

There are no chirality outliers.

All (144) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	POV	C1-C2-O21-C21
2	B	703	POV	C1-C2-O21-C21
2	C	702	POV	C1-C2-O21-C21
2	D	704	POV	C1-C2-O21-C21
2	A	701	POV	O32-C31-O31-C3
2	B	703	POV	O32-C31-O31-C3
2	C	702	POV	O32-C31-O31-C3
2	D	704	POV	O32-C31-O31-C3
2	A	701	POV	C32-C31-O31-C3
2	B	703	POV	C32-C31-O31-C3
2	C	702	POV	C32-C31-O31-C3
2	D	704	POV	C32-C31-O31-C3
2	A	706	POV	C32-C31-O31-C3
2	B	708	POV	C32-C31-O31-C3
2	C	701	POV	C32-C31-O31-C3
2	D	703	POV	C32-C31-O31-C3
2	A	706	POV	O32-C31-O31-C3
2	B	708	POV	O32-C31-O31-C3
2	C	701	POV	O32-C31-O31-C3
2	D	703	POV	O32-C31-O31-C3
2	A	701	POV	C21-C22-C23-C24
2	B	703	POV	C21-C22-C23-C24
2	C	702	POV	C21-C22-C23-C24
2	D	704	POV	C21-C22-C23-C24
2	A	705	POV	C23-C24-C25-C26
2	B	707	POV	C23-C24-C25-C26
2	D	708	POV	C23-C24-C25-C26
2	C	706	POV	C23-C24-C25-C26
2	D	706	POV	C33-C34-C35-C36
2	A	703	POV	C33-C34-C35-C36
2	B	705	POV	C33-C34-C35-C36
2	C	704	POV	C33-C34-C35-C36
2	C	701	POV	C33-C34-C35-C36
2	D	703	POV	C33-C34-C35-C36
2	A	706	POV	C33-C34-C35-C36
2	B	708	POV	C33-C34-C35-C36
2	A	704	POV	C35-C36-C37-C38
2	B	706	POV	C35-C36-C37-C38
2	C	705	POV	C35-C36-C37-C38
2	D	707	POV	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
2	A	708	POV	C33-C34-C35-C36
2	B	702	POV	C33-C34-C35-C36
2	C	708	POV	C33-C34-C35-C36
2	D	702	POV	C33-C34-C35-C36
2	A	701	POV	C22-C21-O21-C2
2	B	703	POV	C22-C21-O21-C2
2	C	702	POV	C22-C21-O21-C2
2	D	704	POV	C22-C21-O21-C2
2	A	701	POV	O22-C21-O21-C2
2	B	703	POV	O22-C21-O21-C2
2	C	702	POV	O22-C21-O21-C2
2	D	704	POV	O22-C21-O21-C2
2	A	701	POV	C26-C27-C28-C29
2	B	703	POV	C26-C27-C28-C29
2	C	702	POV	C26-C27-C28-C29
2	D	704	POV	C26-C27-C28-C29
2	A	704	POV	C32-C33-C34-C35
2	B	706	POV	C32-C33-C34-C35
2	D	707	POV	C32-C33-C34-C35
2	C	705	POV	C32-C33-C34-C35
2	A	704	POV	C33-C34-C35-C36
2	B	706	POV	C33-C34-C35-C36
2	C	705	POV	C33-C34-C35-C36
2	D	707	POV	C33-C34-C35-C36
2	A	705	POV	C21-C22-C23-C24
2	B	707	POV	C21-C22-C23-C24
2	C	706	POV	C21-C22-C23-C24
2	D	708	POV	C21-C22-C23-C24
2	A	703	POV	C35-C36-C37-C38
2	B	705	POV	C35-C36-C37-C38
2	C	704	POV	C35-C36-C37-C38
2	D	706	POV	C35-C36-C37-C38
2	A	702	POV	C32-C33-C34-C35
2	B	704	POV	C32-C33-C34-C35
2	C	703	POV	C32-C33-C34-C35
2	D	705	POV	C32-C33-C34-C35
2	A	707	POV	C33-C34-C35-C36
2	B	701	POV	C33-C34-C35-C36
2	C	707	POV	C33-C34-C35-C36
2	D	701	POV	C33-C34-C35-C36
2	A	701	POV	C23-C24-C25-C26
2	C	702	POV	C23-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
2	B	703	POV	C23-C24-C25-C26
2	D	704	POV	C23-C24-C25-C26
2	A	702	POV	C33-C34-C35-C36
2	B	704	POV	C33-C34-C35-C36
2	C	703	POV	C33-C34-C35-C36
2	D	705	POV	C33-C34-C35-C36
2	A	707	POV	C35-C36-C37-C38
2	B	701	POV	C35-C36-C37-C38
2	C	707	POV	C35-C36-C37-C38
2	D	701	POV	C35-C36-C37-C38
2	A	701	POV	C25-C26-C27-C28
2	B	703	POV	C25-C26-C27-C28
2	C	702	POV	C25-C26-C27-C28
2	D	704	POV	C25-C26-C27-C28
2	B	707	POV	C24-C25-C26-C27
2	A	705	POV	C24-C25-C26-C27
2	C	706	POV	C24-C25-C26-C27
2	D	708	POV	C24-C25-C26-C27
2	A	701	POV	C3-C2-O21-C21
2	B	703	POV	C3-C2-O21-C21
2	C	702	POV	C3-C2-O21-C21
2	D	704	POV	C3-C2-O21-C21
2	A	706	POV	C35-C36-C37-C38
2	B	708	POV	C35-C36-C37-C38
2	C	701	POV	C35-C36-C37-C38
2	D	703	POV	C35-C36-C37-C38
2	B	705	POV	C36-C37-C38-C39
2	C	704	POV	C36-C37-C38-C39
2	A	703	POV	C36-C37-C38-C39
2	D	706	POV	C36-C37-C38-C39
2	D	702	POV	C31-C32-C33-C34
2	A	708	POV	C31-C32-C33-C34
2	B	702	POV	C31-C32-C33-C34
2	C	708	POV	C31-C32-C33-C34
2	D	704	POV	C24-C25-C26-C27
2	C	702	POV	C24-C25-C26-C27
2	A	701	POV	C24-C25-C26-C27
2	B	703	POV	C24-C25-C26-C27
2	A	701	POV	C31-C32-C33-C34
2	B	703	POV	C31-C32-C33-C34
2	C	702	POV	C31-C32-C33-C34
2	D	704	POV	C31-C32-C33-C34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	A	703	POV	C32-C33-C34-C35
2	B	705	POV	C32-C33-C34-C35
2	C	704	POV	C32-C33-C34-C35
2	D	706	POV	C32-C33-C34-C35
2	A	705	POV	C27-C28-C29-C210
2	B	707	POV	C27-C28-C29-C210
2	C	706	POV	C27-C28-C29-C210
2	D	708	POV	C27-C28-C29-C210
2	A	706	POV	O31-C31-C32-C33
2	B	708	POV	O31-C31-C32-C33
2	C	701	POV	O31-C31-C32-C33
2	D	703	POV	O31-C31-C32-C33
2	D	703	POV	O32-C31-C32-C33
2	A	706	POV	O32-C31-C32-C33
2	B	708	POV	O32-C31-C32-C33
2	C	701	POV	O32-C31-C32-C33
2	C	703	POV	C31-C32-C33-C34
2	D	705	POV	C31-C32-C33-C34
2	A	702	POV	C31-C32-C33-C34
2	B	704	POV	C31-C32-C33-C34

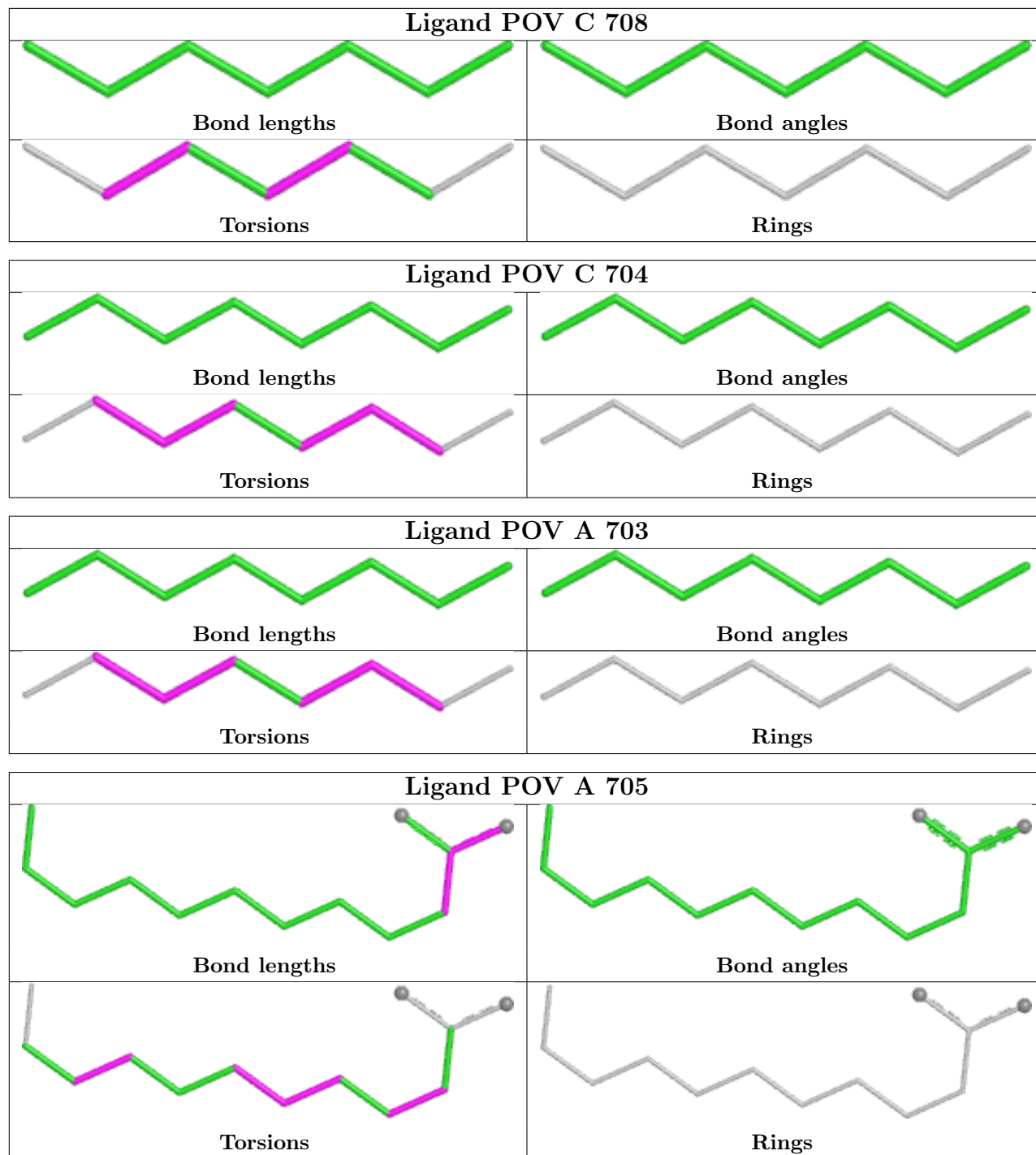
There are no ring outliers.

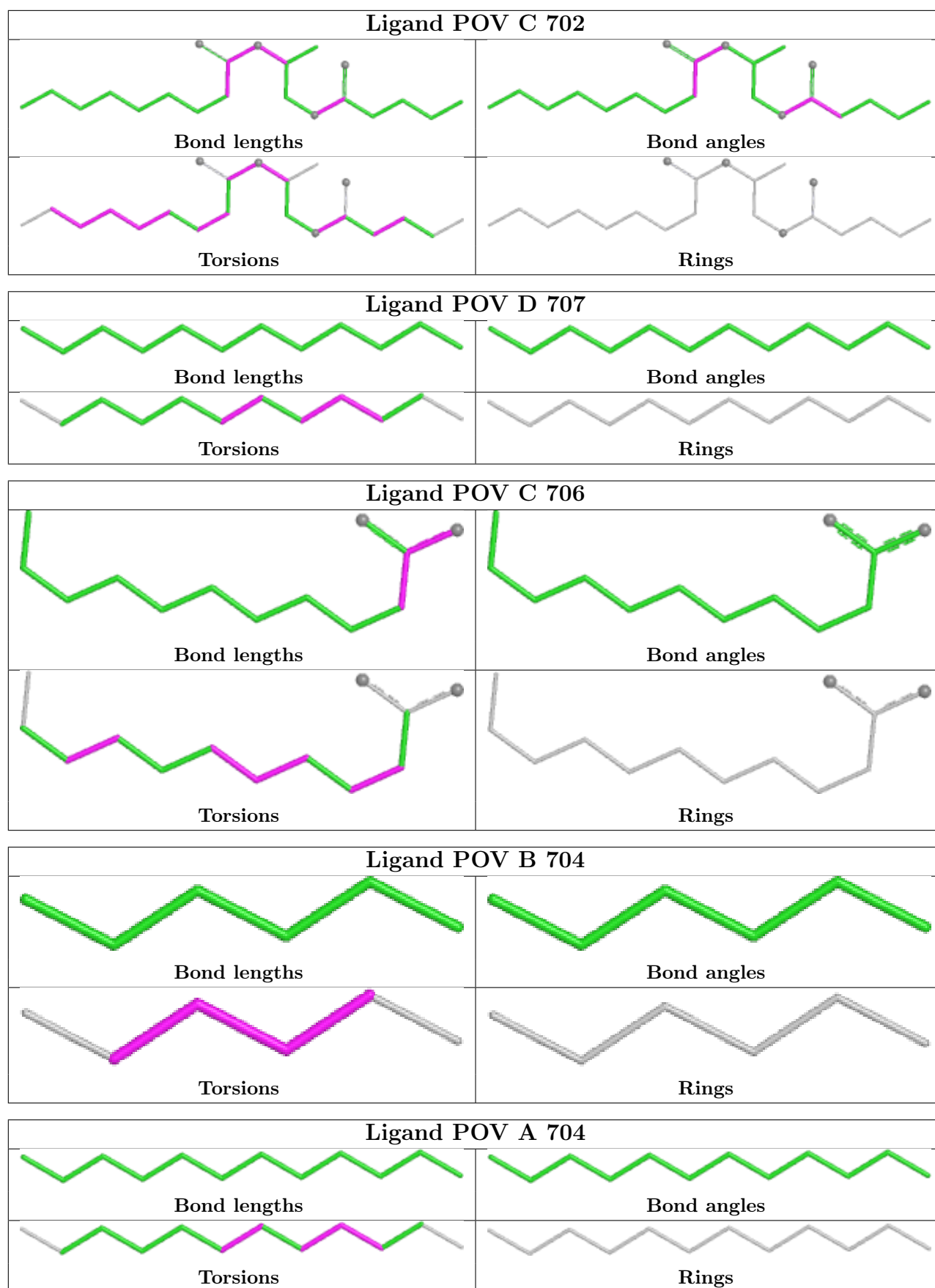
5 monomers are involved in 9 short contacts:

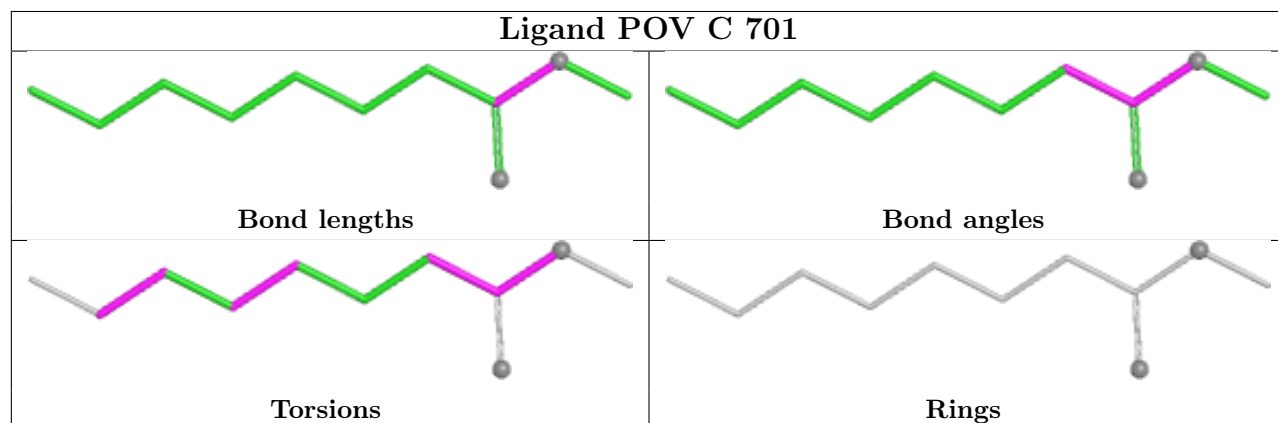
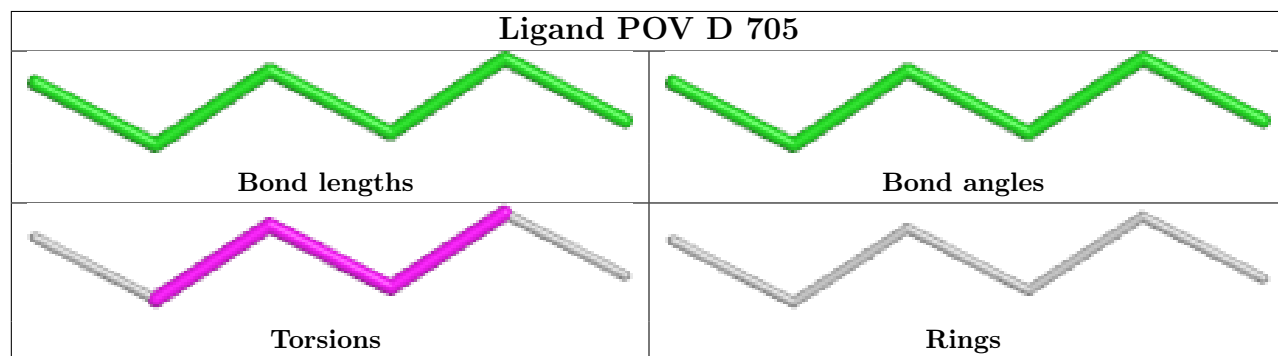
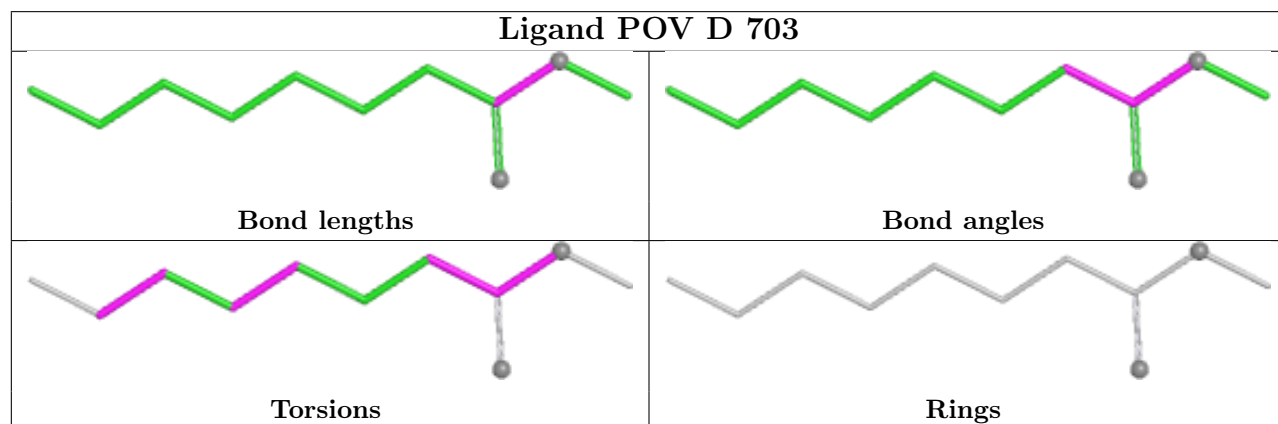
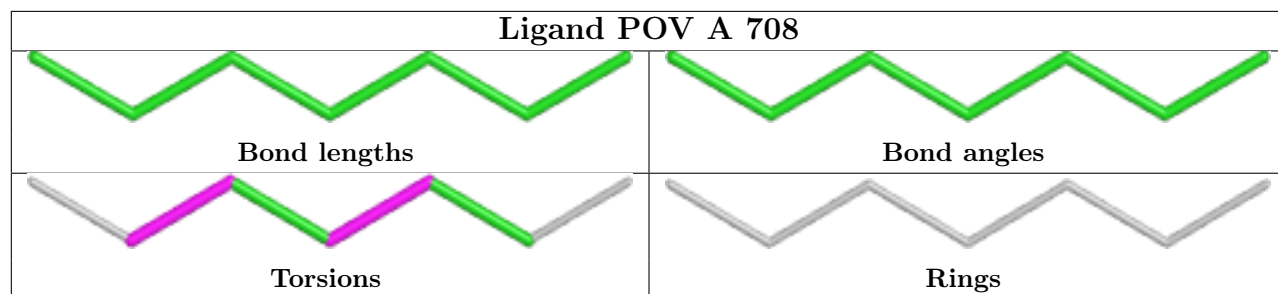
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	708	POV	2	0
2	A	708	POV	2	0
2	D	702	POV	2	0
2	A	707	POV	1	0
2	B	702	POV	2	0

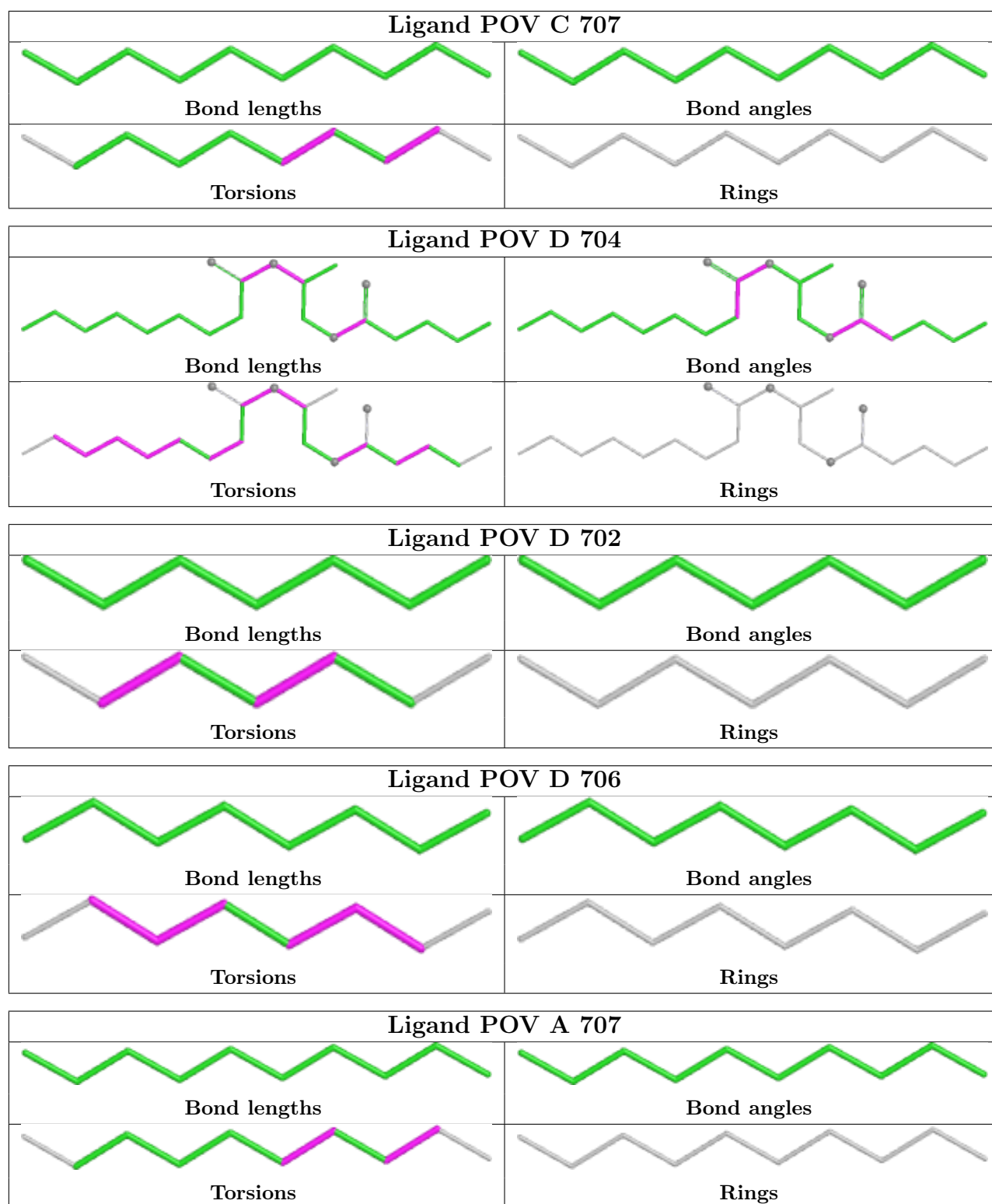
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

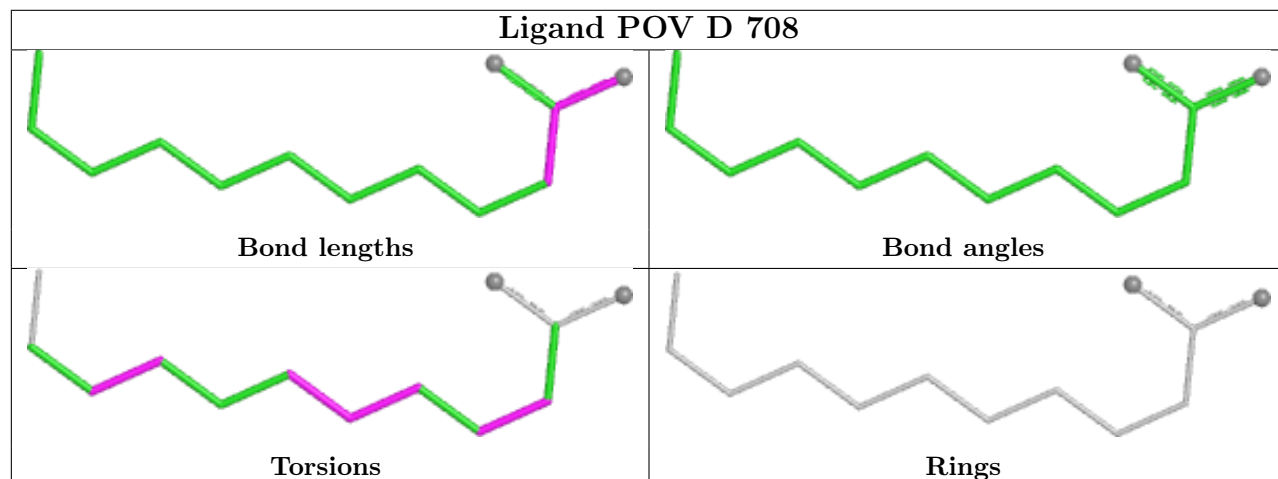
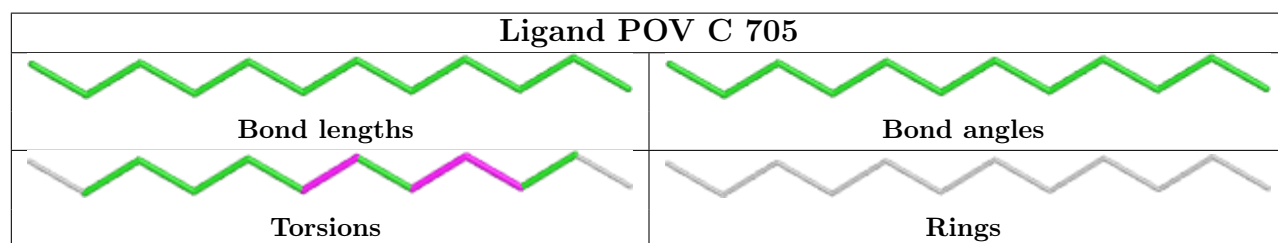
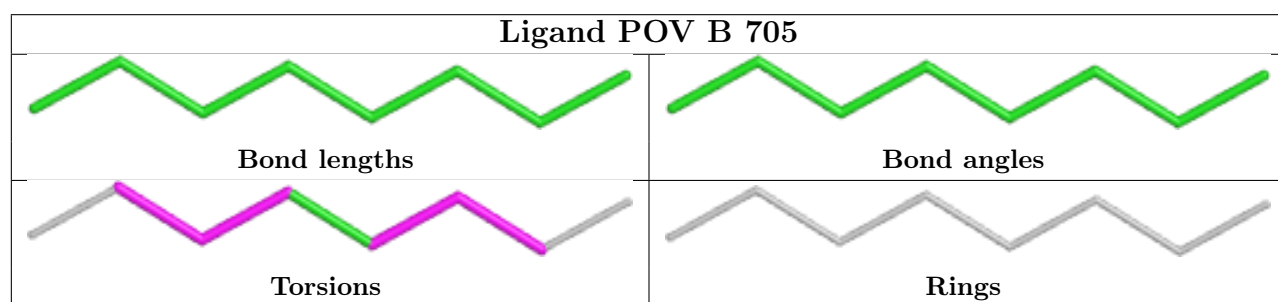
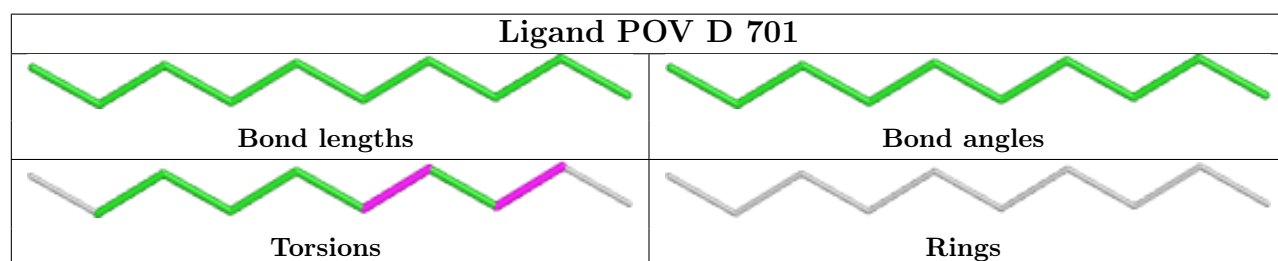
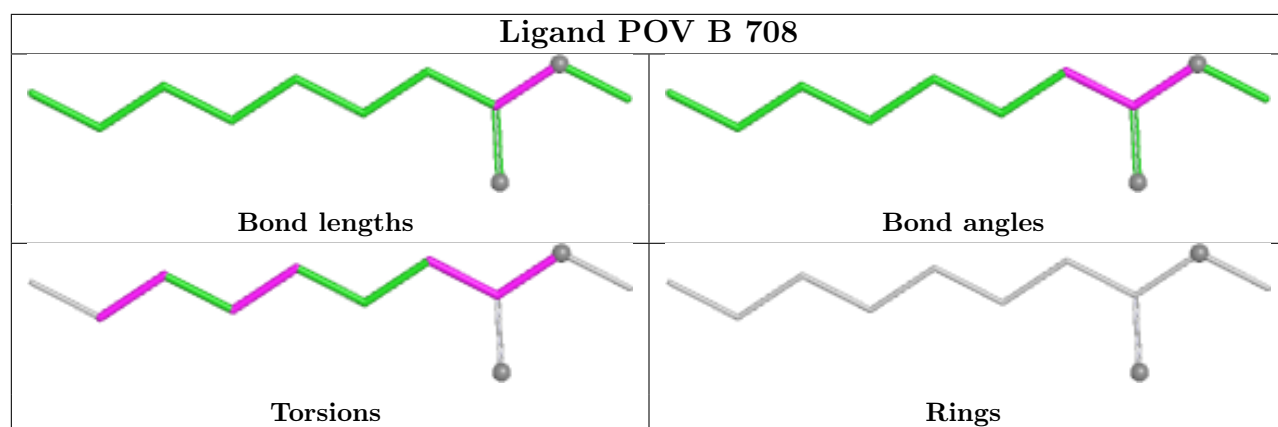
equivalents in the CSD to analyse the geometry.

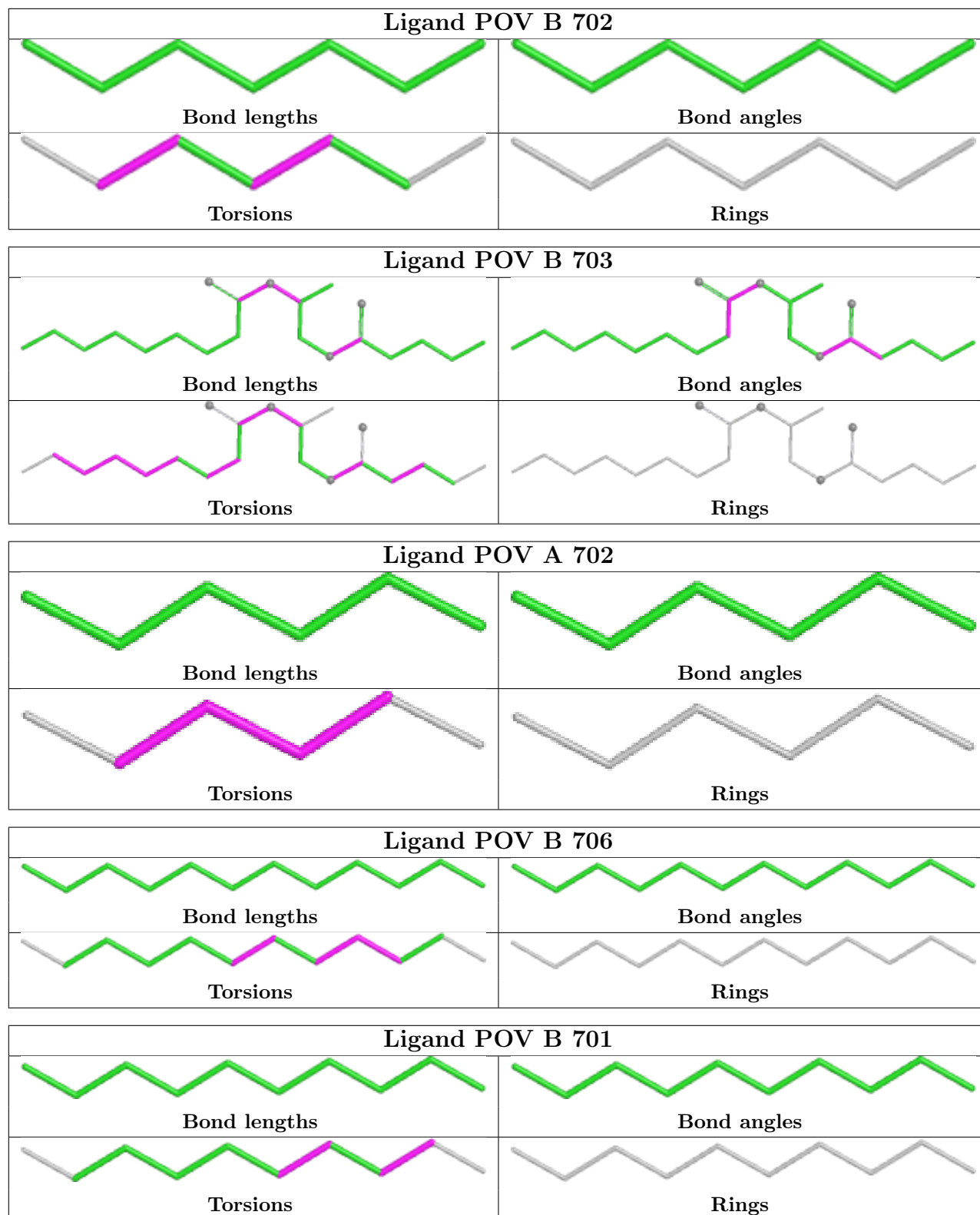


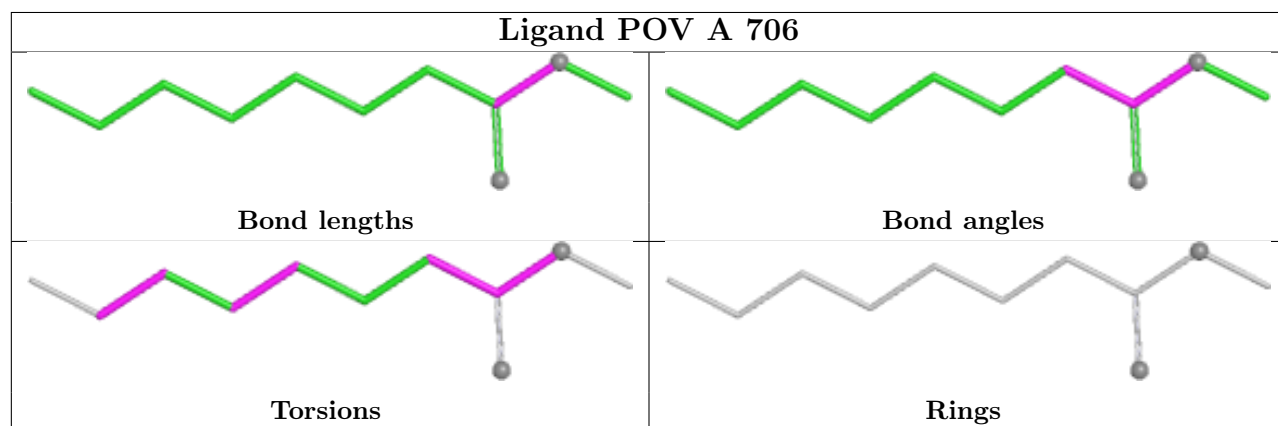
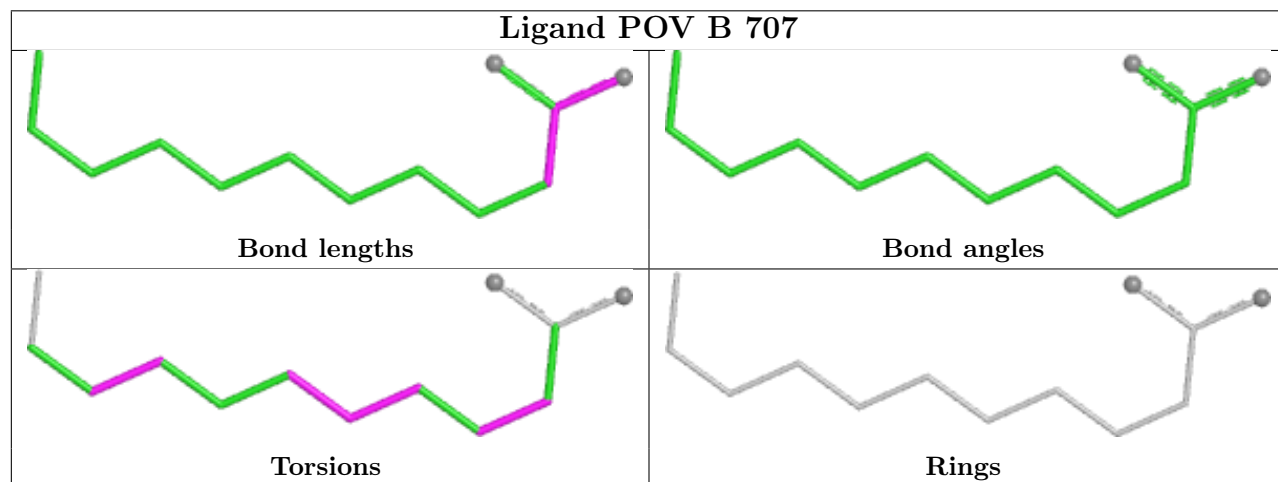
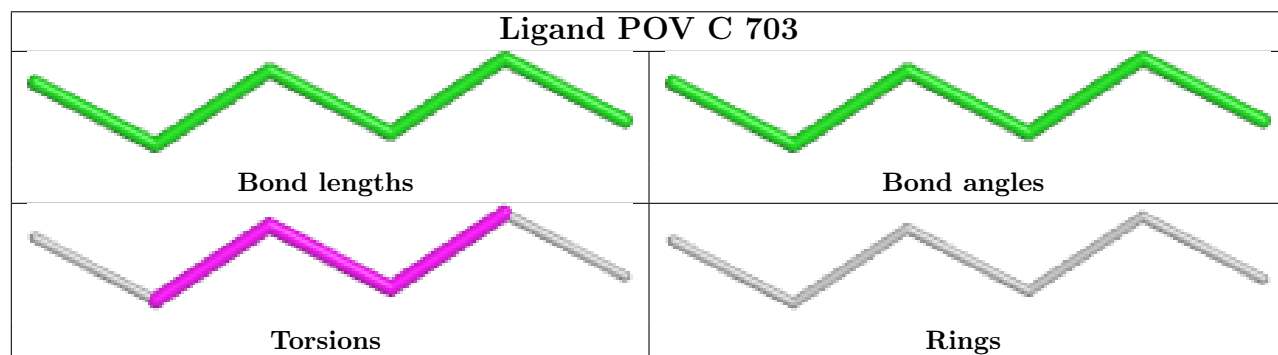
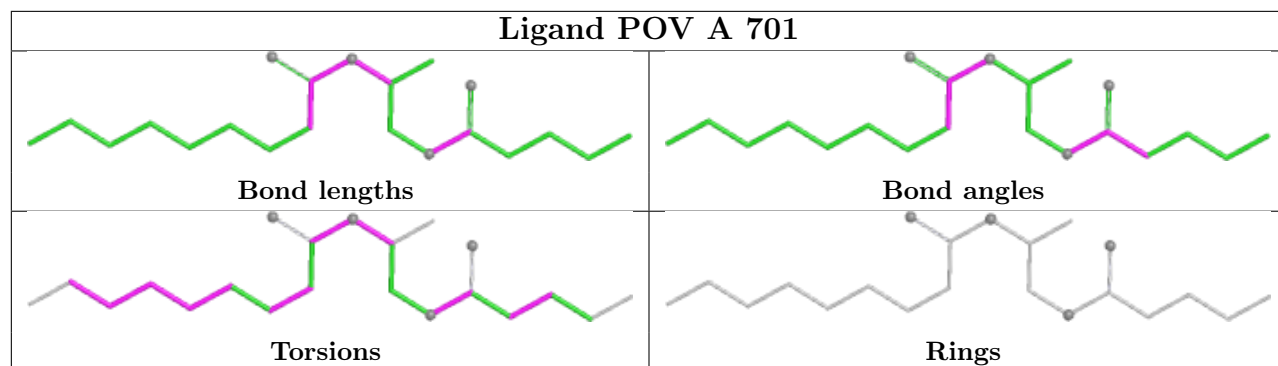












5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

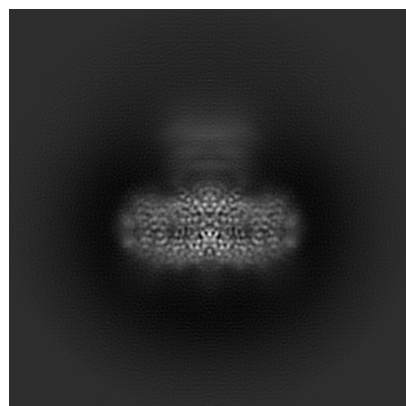
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41193. These allow visual inspection of the internal detail of the map and identification of artifacts.

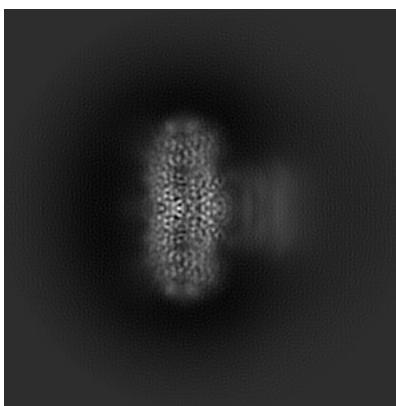
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

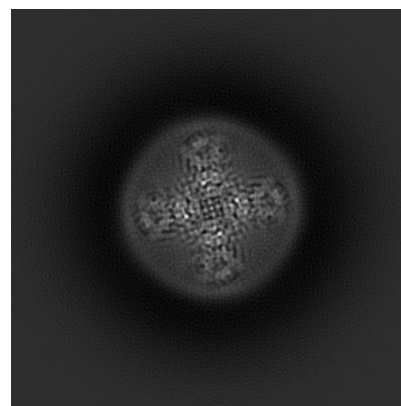
6.1.1 Primary map



X

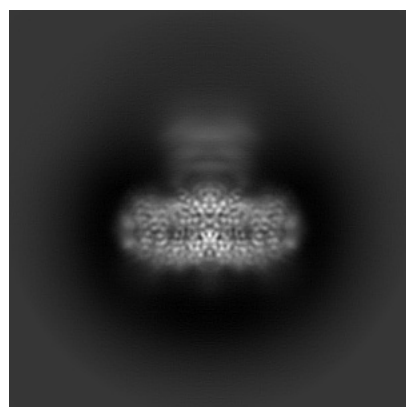


Y

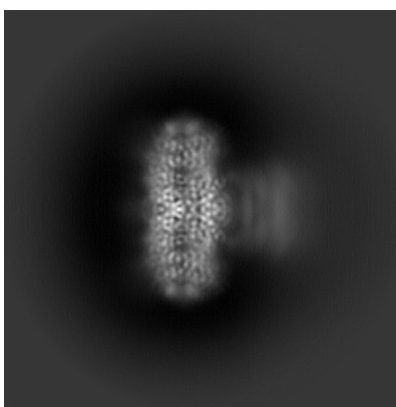


Z

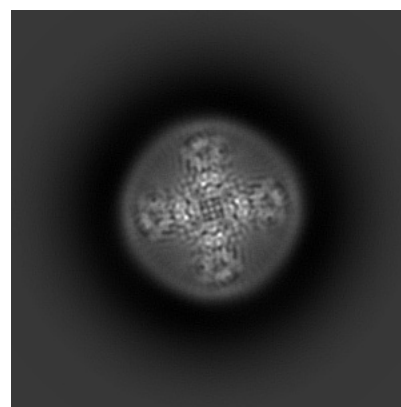
6.1.2 Raw map



X



Y

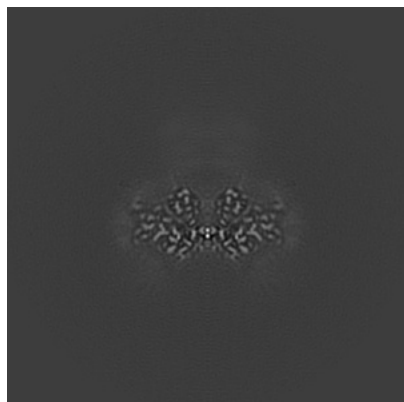


Z

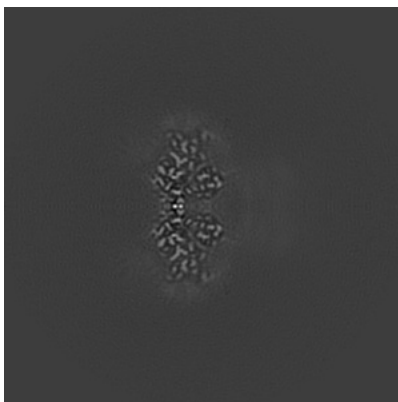
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

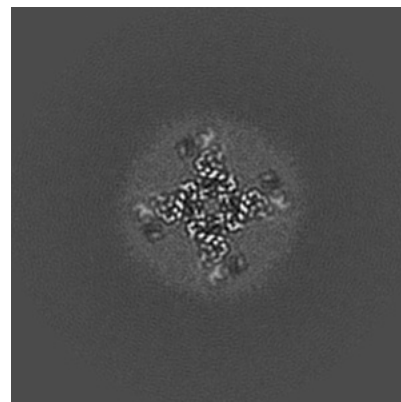
6.2.1 Primary map



X Index: 150

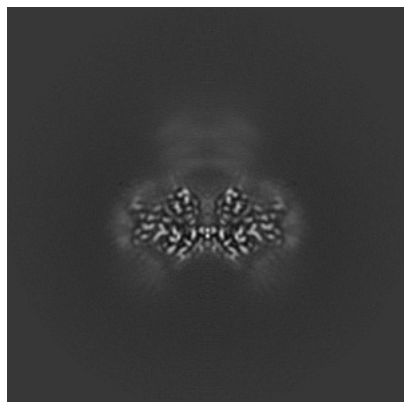


Y Index: 150

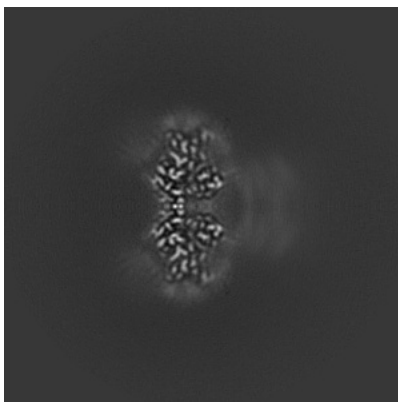


Z Index: 150

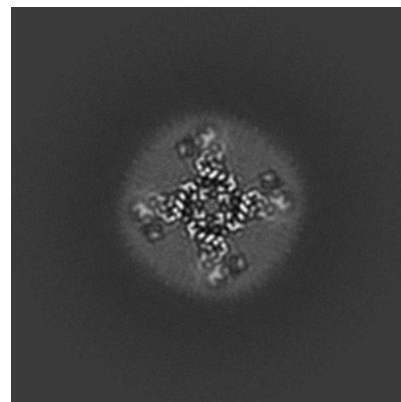
6.2.2 Raw map



X Index: 150



Y Index: 150

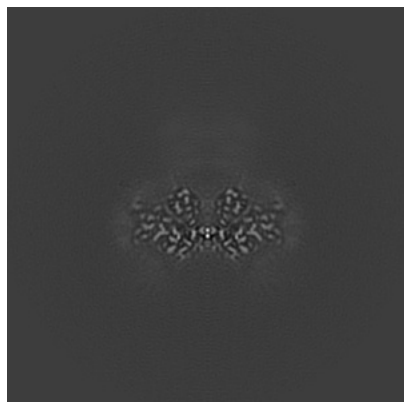


Z Index: 150

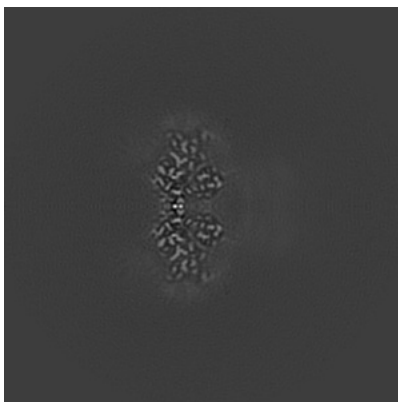
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

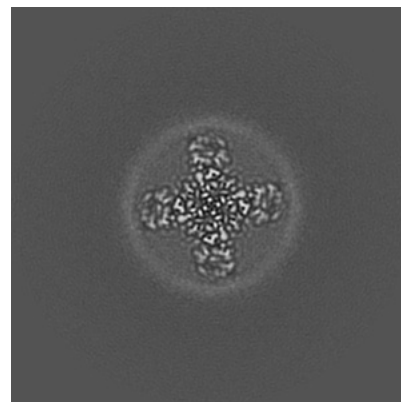
6.3.1 Primary map



X Index: 150

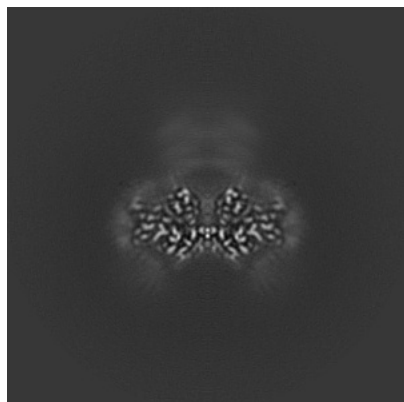


Y Index: 150

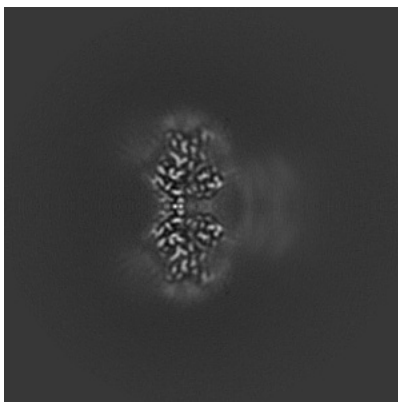


Z Index: 125

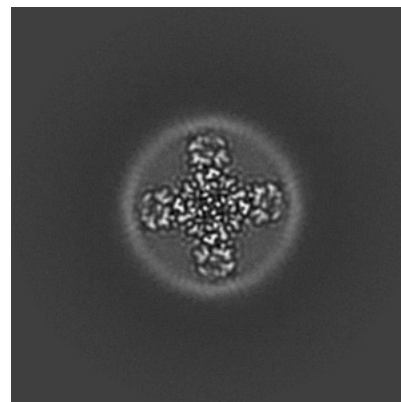
6.3.2 Raw map



X Index: 150



Y Index: 150

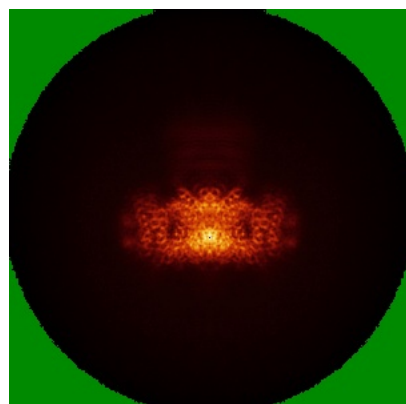


Z Index: 125

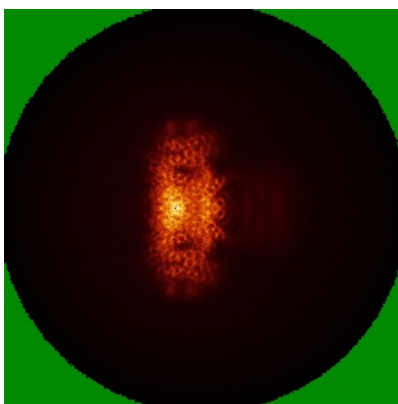
The images above show the largest variance slices of the map in three orthogonal directions.

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

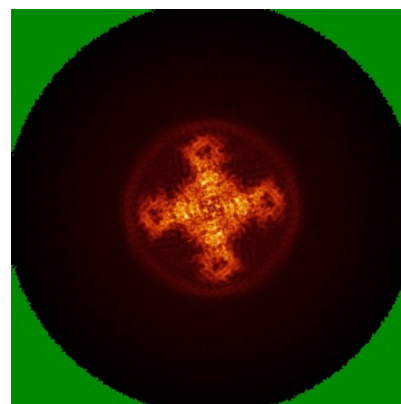
6.4.1 Primary map



X

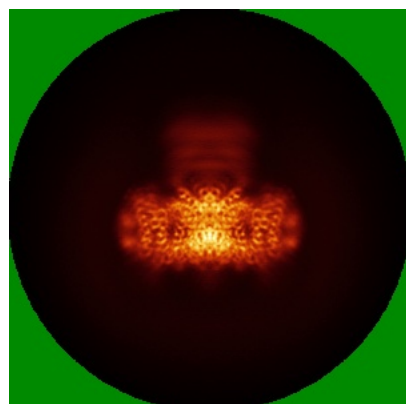


Y

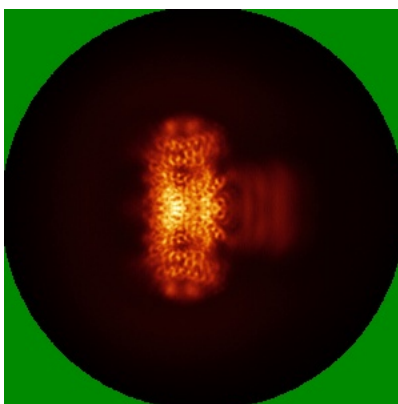


Z

6.4.2 Raw map



X



Y

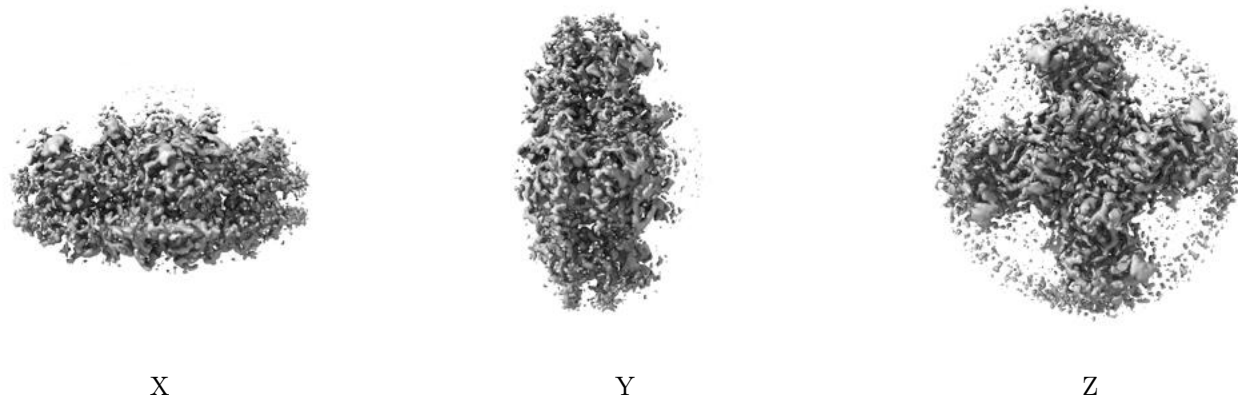


Z

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.

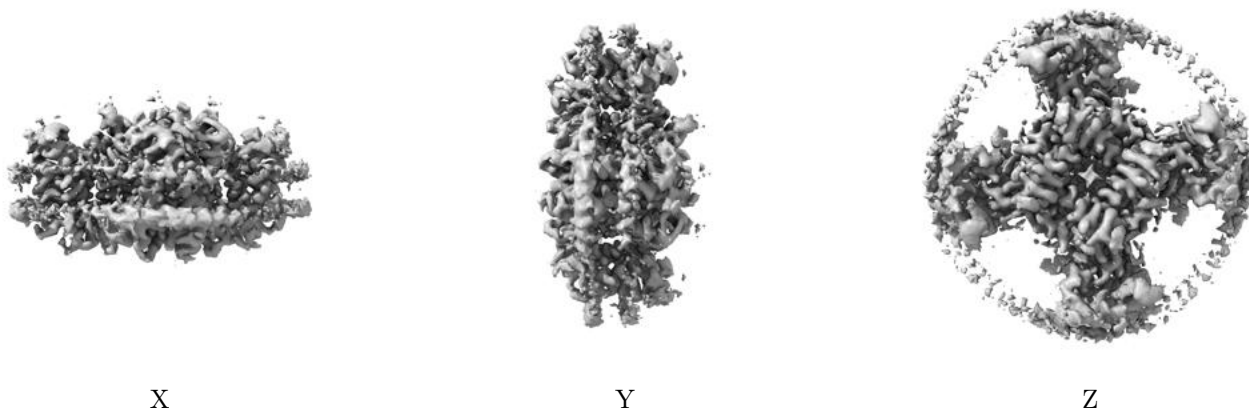
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

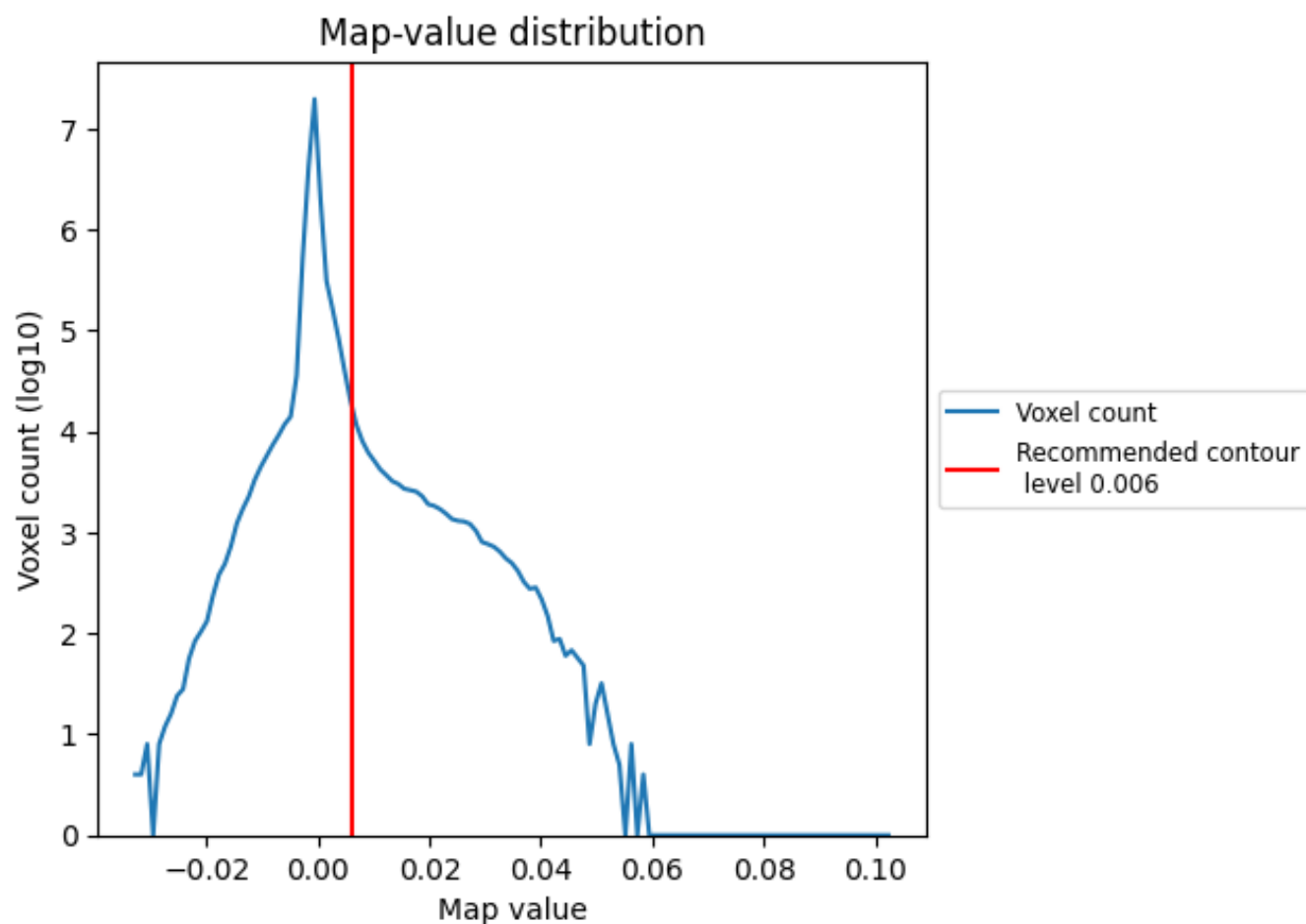
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

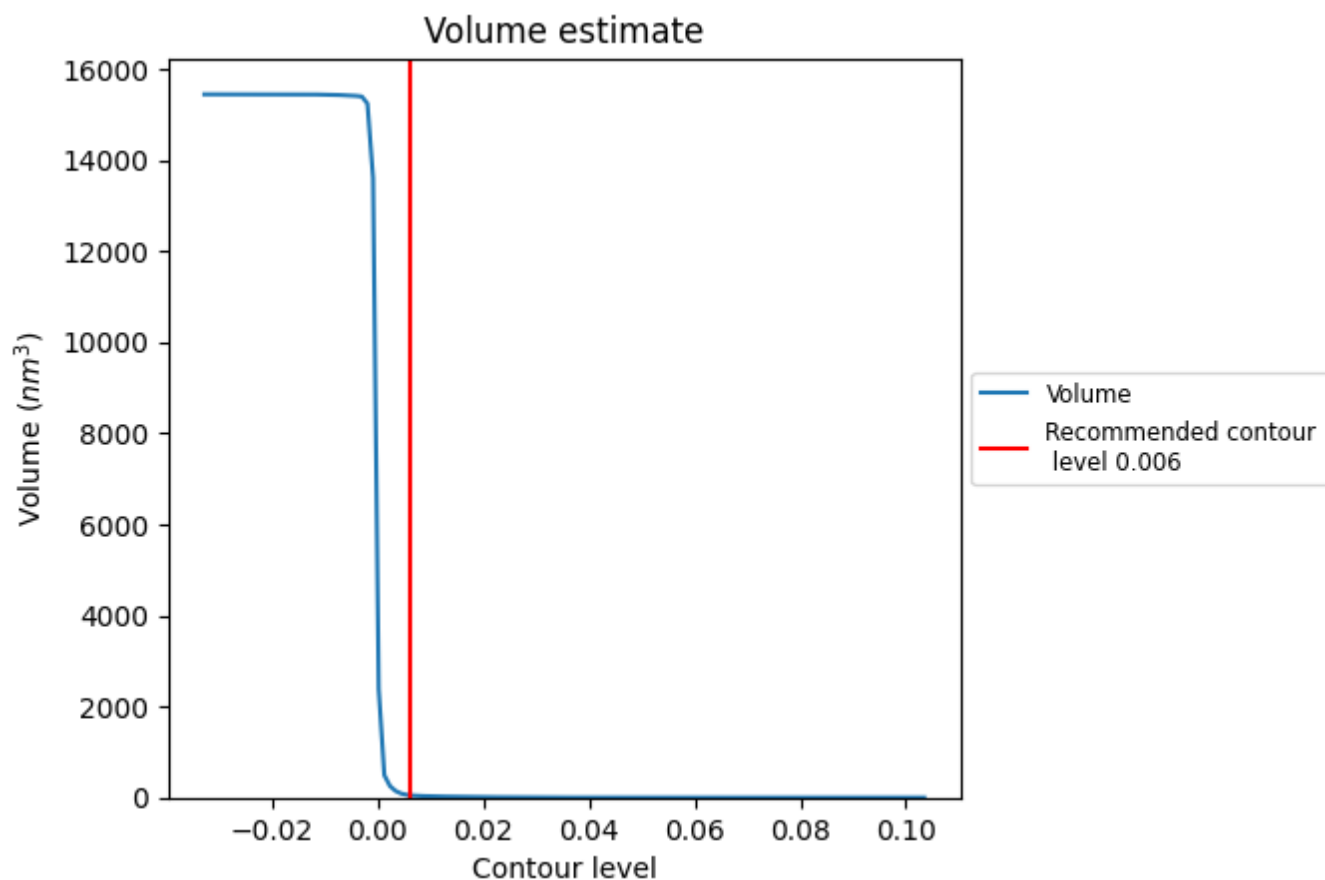
This section contains the results of statistical analysis of the map.

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.

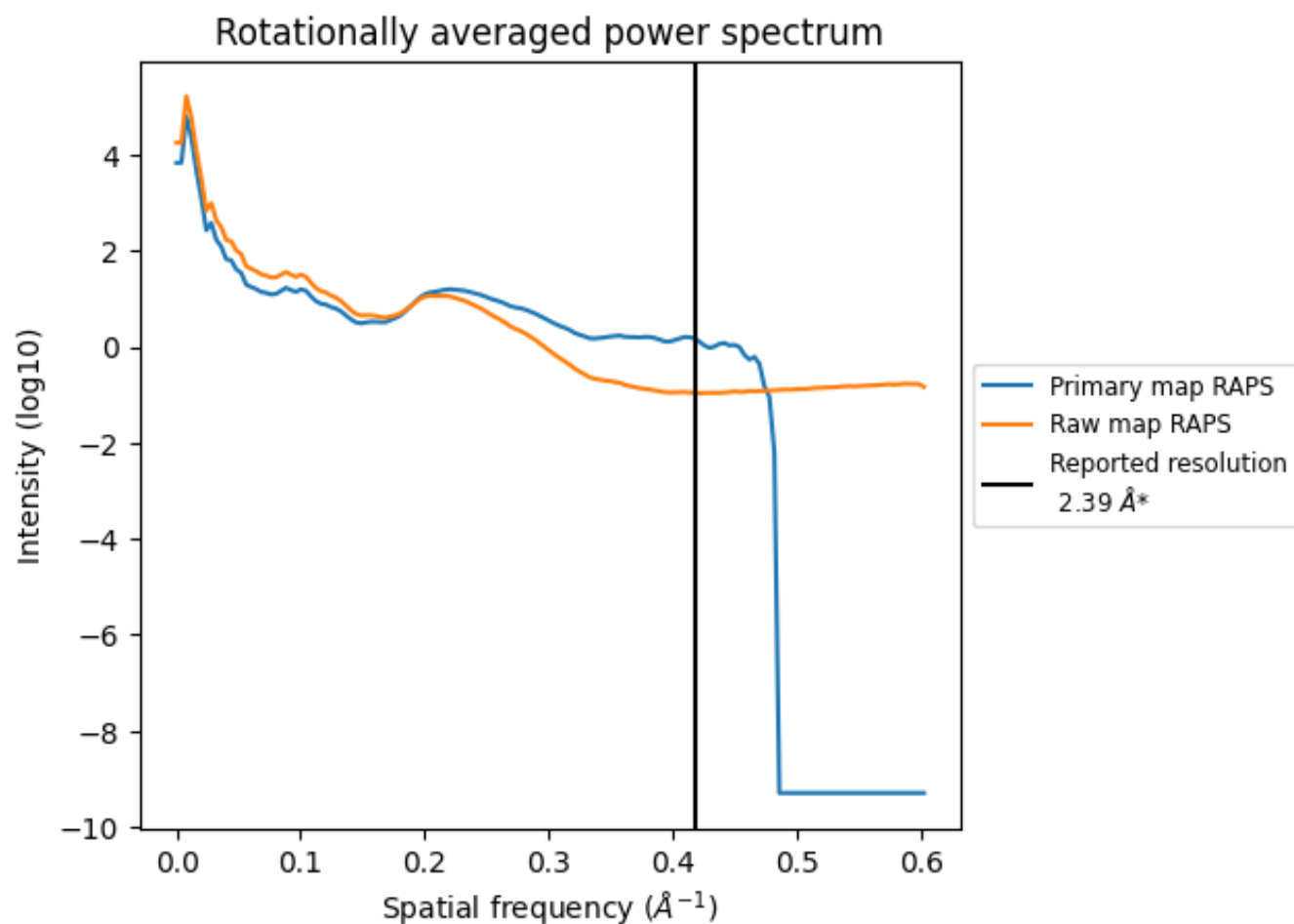
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 53 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 ⓘ

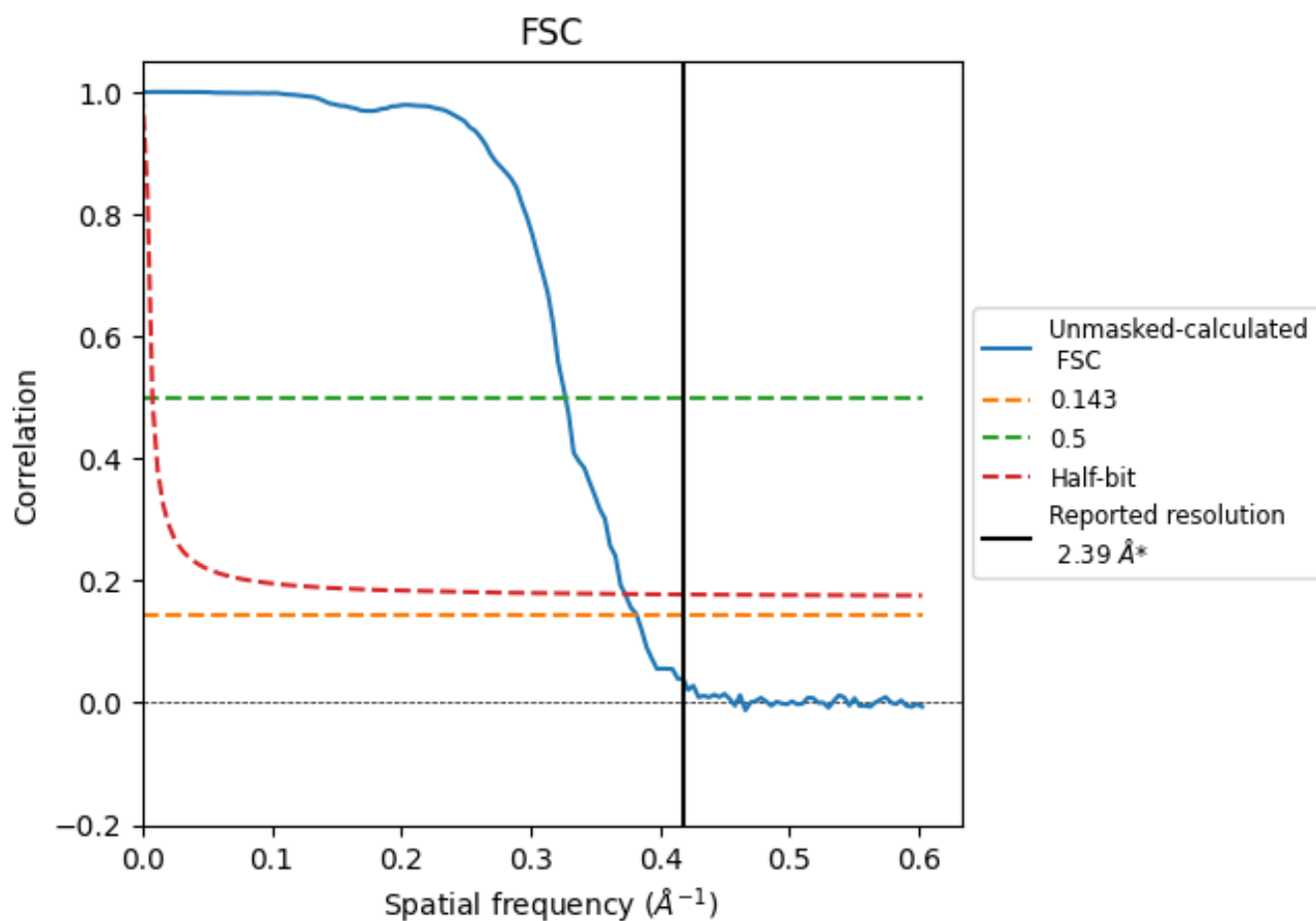


*Reported resolution corresponds to spatial frequency of 0.418 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.418 Å⁻¹

8.2 Resolution estimates [i](#)

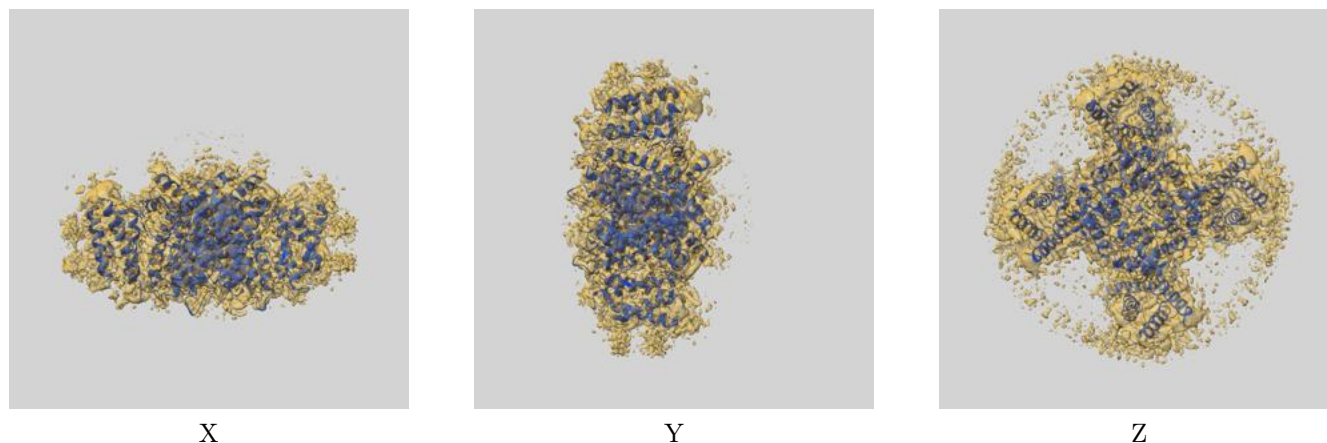
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.39	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.62	3.06	2.68

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

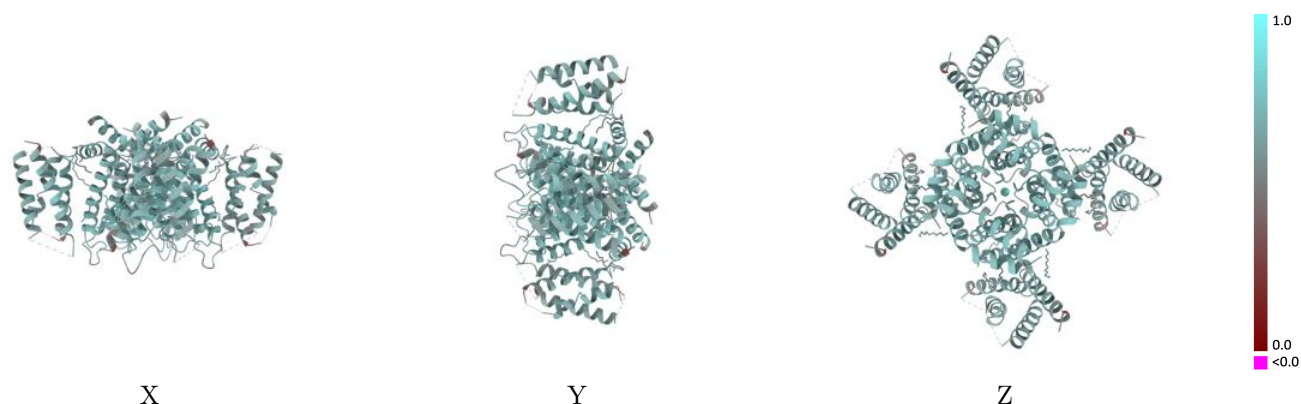
This section contains information regarding the fit between EMDB map EMD-41193 and PDB model 8TEO. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



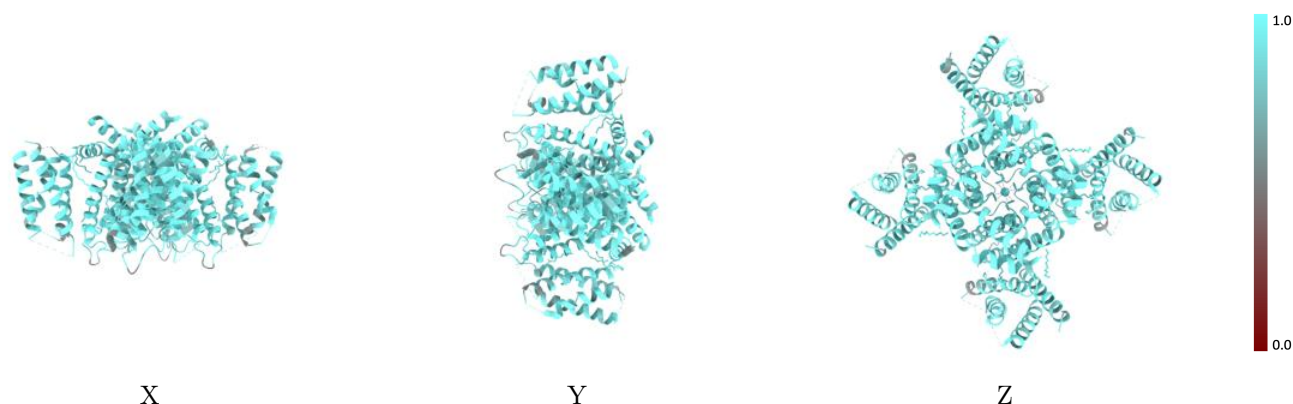
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



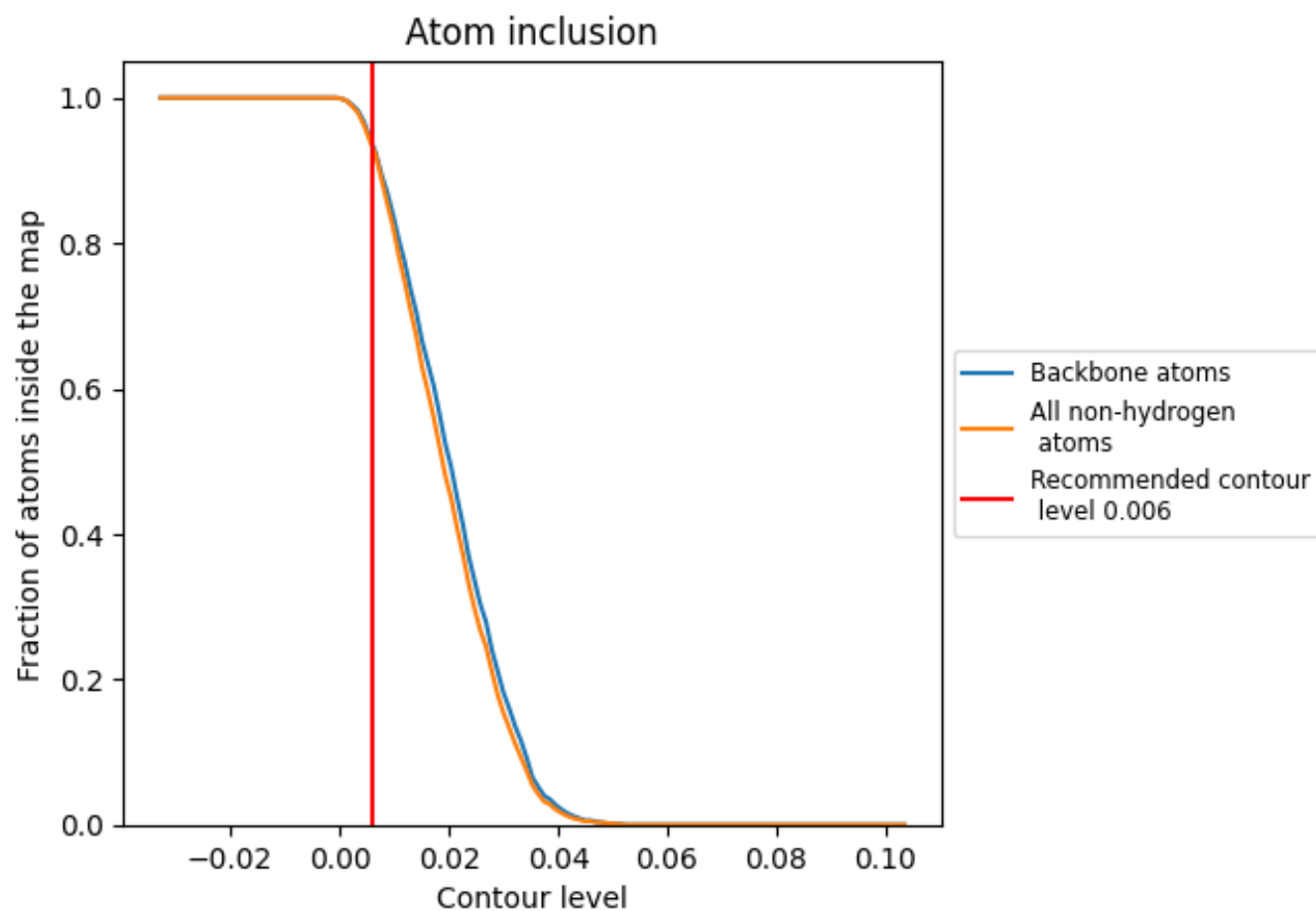
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9330	0.6320
A	0.9360	0.6330
B	0.9370	0.6310
C	0.9370	0.6330
D	0.9360	0.6320

