



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:54 AM UTC

PDB ID : 8X5F / pdb_00008x5f
EMDB ID : EMD-38068
Title : human XPR1 in complex with InsP6
Authors : Jiang, D.H.; Yan, R.
Deposited on : 2023-11-17
Resolution : 2.96 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

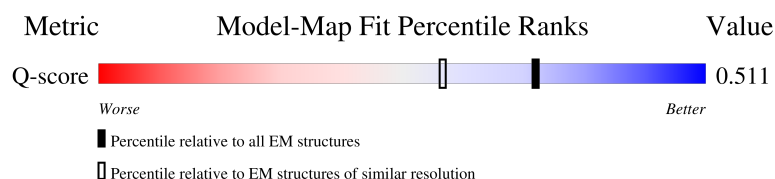
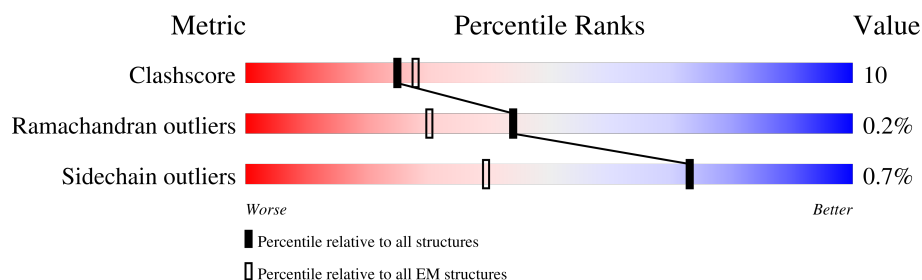
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 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	13155 (2.46 - 3.46)

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	696	14% 77% 11% 11%
1	B	696	14% 75% 13% 11%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	A	701	-	X	-	-
2	PO4	A	702	-	X	-	-
2	PO4	A	703	-	-	X	-
2	PO4	A	704	-	X	-	-
2	PO4	B	1102	-	X	-	-
2	PO4	B	1103	-	X	-	-
2	PO4	B	1104	-	X	X	-
2	PO4	B	1105	-	X	X	-

2 Entry composition [i](#)

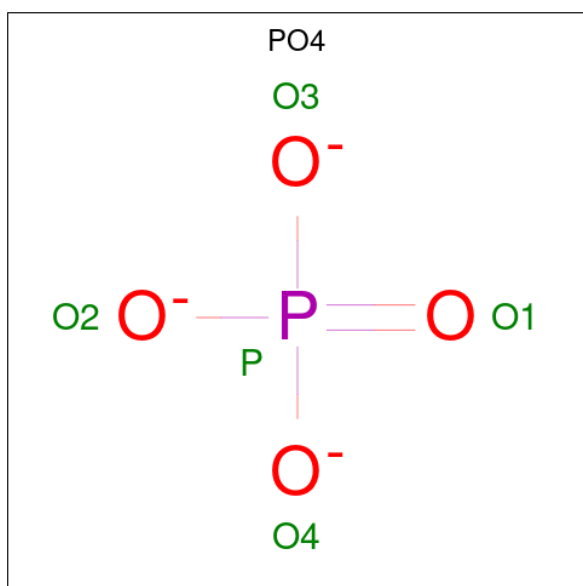
There are 6 unique types of molecules in this entry. The entry contains 10855 atoms, of which 12 are hydrogens and 0 are deuteriums.

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 Solute carrier family 53 member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	616	Total	C	N	O	S	0	0
			5024	3315	833	856	20		
1	B	616	Total	C	N	O	S	0	0
			5020	3312	832	856	20		

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



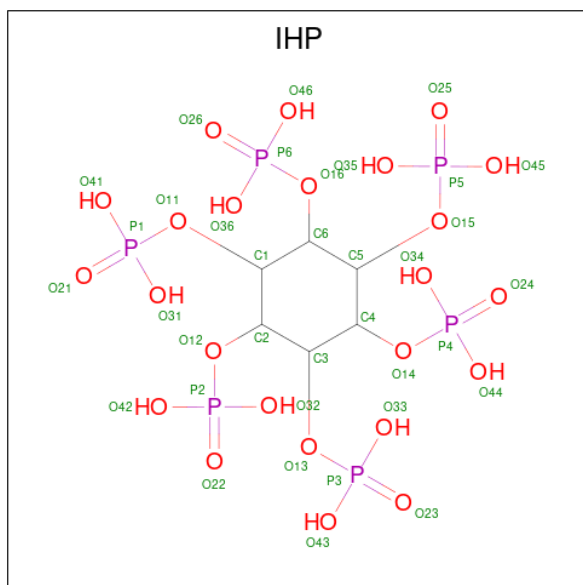
Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total	O	P	0
			5	4	1	
2	A	1	Total	O	P	0
			5	4	1	
2	A	1	Total	O	P	0
			5	4	1	
2	A	1	Total	O	P	0
			5	4	1	
2	B	1	Total	O	P	0
			5	4	1	

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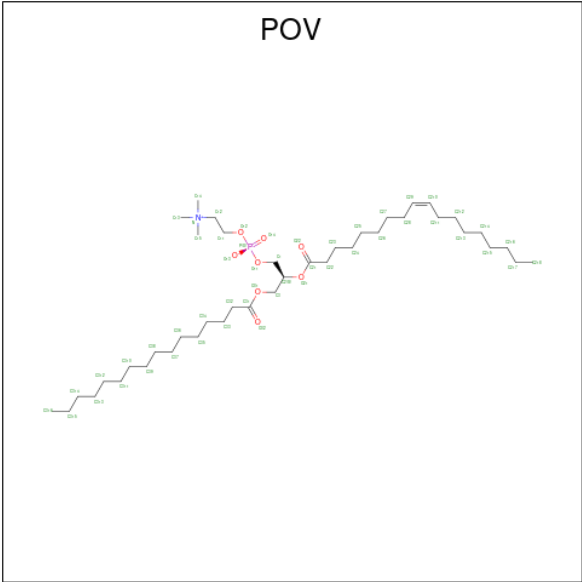
Mol	Chain	Residues	Atoms			AltConf
2	B	1	Total	O	P	0
			5	4	1	
2	B	1	Total	O	P	0
			5	4	1	
2	B	1	Total	O	P	0
			5	4	1	

- Molecule 3 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	O	P	0
			42	6	6	24	6	
3	B	1	Total	C	H	O	P	0
			42	6	6	24	6	

- Molecule 4 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (CCD ID: POV) (formula: $C_{42}H_{82}NO_8P$) (labeled as "Ligand of Interest" by depositor).



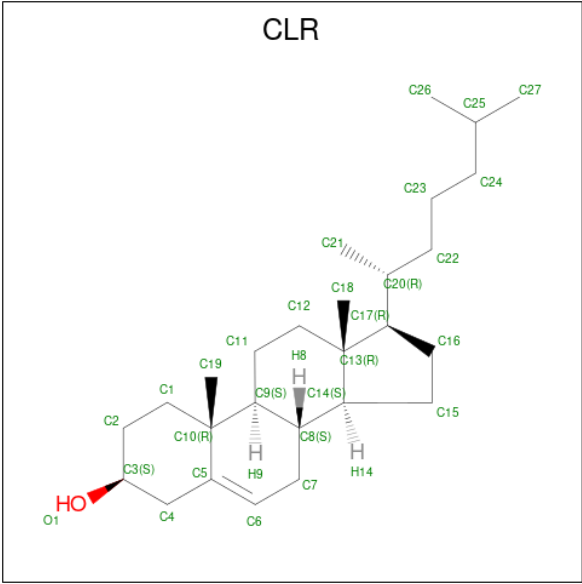
Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	O			0
			17	14	3			
4	A	1	Total	C	O			0
			18	16	2			
4	A	1	Total	C	O			0
			16	14	2			
4	A	1	Total	C	O			0
			16	14	2			
4	A	1	Total	C	O			0
			16	14	2			
4	A	1	Total	C	O			0
			14	12	2			
4	A	1	Total	C	O			0
			16	14	2			
4	A	1	Total	C	O			0
			16	14	2			
4	A	1	Total	C	O			0
			16	14	2			
4	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
4	A	1	Total	C	N	O	P	0
			29	19	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	O	P	0	
			39	30	8	1		
4	B	1	Total	C	O	P	0	
			39	30	8	1		
4	B	1	Total	C	O		0	
			18	16	2			
4	B	1	Total	C	O		0	
			17	14	3			
4	B	1	Total	C	O		0	
			18	16	2			
4	B	1	Total	C	O		0	
			16	14	2			
4	B	1	Total	C	O		0	
			16	14	2			
4	B	1	Total	C	O		0	
			16	14	2			
4	B	1	Total	C	O		0	
			16	14	2			
4	B	1	Total	C	O		0	
			16	14	2			
4	B	1	Total	C	O		0	
			16	14	2			
4	B	1	Total	C	O		0	
			11	9	2			
4	B	1	Total	C	O		0	
			16	14	2			
4	B	1	Total	C	O		0	
			16	14	2			
4	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
4	B	1	Total	C	N	O	P	0
			29	19	1	8	1	

- Molecule 5 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			AltConf
5	A	1	Total	C	O	0
			28	27	1	
5	B	1	Total	C	O	0
			28	27	1	

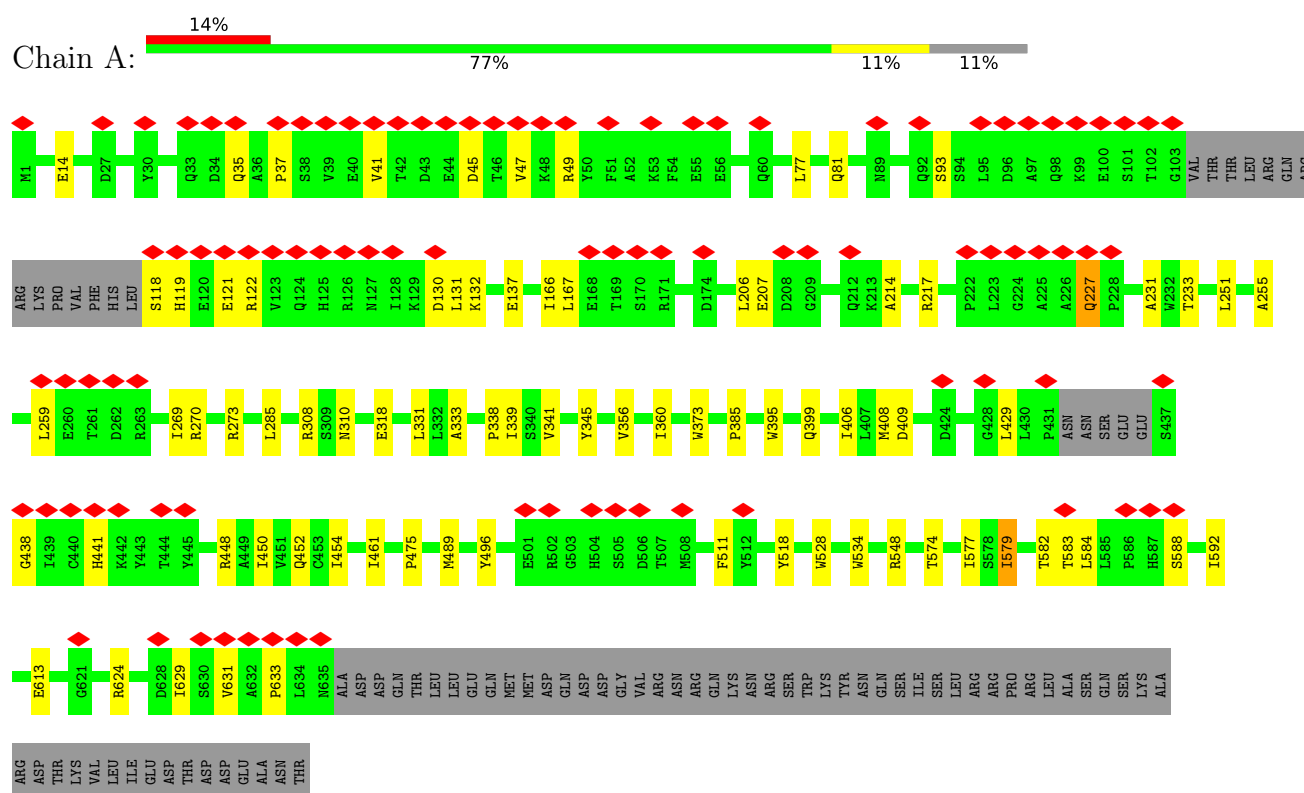
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		AltConf
6	A	2	Total	O	0
			2	2	
6	B	2	Total	O	0
			2	2	

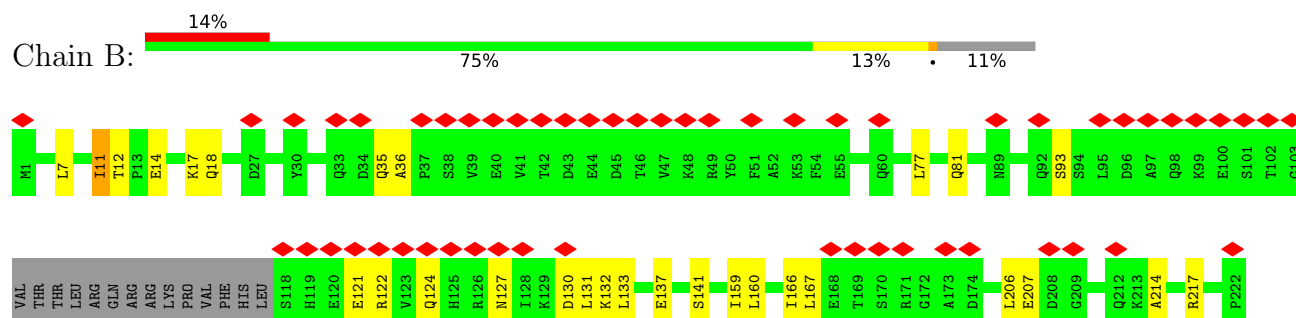
3 Residue-property plots [i](#)

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: Solute carrier family 53 member 1



• Molecule 1: Solute carrier family 53 member 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT	Depositor
Number of particles used	30798, 30798, 30798, 30798, 30798, 30798, 30798, 30798, 30798	Depositor
Resolution determination method	FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.00, 60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k), GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.449	Depositor
Minimum map value	-1.973	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.084	Depositor
Recommended contour level	0.475	Depositor
Map size (Å)	272.0, 272.0, 272.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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: PO4, POV, IHP, CLR

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	0.27	0/5168	0.47	1/7014 (0.0%)
1	B	0.29	0/5164	0.55	6/7010 (0.1%)
All	All	0.28	0/10332	0.51	7/14024 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	93	SER	N-CA-C	6.28	118.12	111.28
1	B	93	SER	N-CA-C	6.27	118.11	111.28
1	B	420	GLU	N-CA-C	5.98	117.79	111.28
1	B	12	THR	CA-C-N	5.63	126.88	119.84
1	B	12	THR	C-N-CA	5.63	126.88	119.84
1	B	581	SER	N-CA-C	5.24	117.47	109.62
1	B	580	THR	N-CA-C	5.14	116.88	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	5024	0	4941	73	0
1	B	5020	0	4930	102	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	20	0	0	4	0
2	B	20	0	0	8	0
3	A	36	6	6	0	0
3	B	36	6	6	0	0
4	A	315	0	452	41	0
4	B	312	0	446	42	0
5	A	28	0	46	1	0
5	B	28	0	46	1	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
All	All	10843	12	10873	227	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 10.

All (227) 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:14:GLU:HG2	1:B:624:ARG:O	1.44	1.14
1:A:338:PRO:HG3	4:A:707:POV:H25	1.32	1.11
4:A:720:POV:H22	4:A:720:POV:H26	1.39	1.04
1:A:285:LEU:HD21	4:A:719:POV:H33A	1.41	1.03
1:B:7:LEU:O	1:B:11:ILE:HG12	1.60	1.01
4:A:714:POV:H32	4:A:716:POV:H35	1.44	0.99
1:B:497:SER:OG	1:B:582:THR:HG23	1.65	0.96
1:B:489:MET:HE1	1:B:577:ILE:HD11	1.47	0.96
1:A:489:MET:HE1	1:A:577:ILE:HD11	1.47	0.94
1:B:338:PRO:HG3	4:B:1109:POV:H25	1.49	0.92
1:A:338:PRO:CG	4:A:707:POV:H25	1.99	0.92
1:B:338:PRO:CG	4:B:1109:POV:H25	2.02	0.90
4:A:714:POV:H34A	4:A:716:POV:H37	1.53	0.89
4:B:1113:POV:H32A	4:B:1114:POV:H34A	1.56	0.87
4:A:714:POV:C32	4:A:716:POV:H35	2.03	0.87
1:A:270:ARG:HD3	2:A:703:PO4:O4	1.77	0.83
1:A:285:LEU:HD21	4:A:719:POV:C33	2.07	0.83
4:A:714:POV:C34	4:A:716:POV:H37	2.08	0.83
4:A:719:POV:O13	4:A:719:POV:H13B	1.81	0.80
4:B:1120:POV:H13B	4:B:1120:POV:O13	1.82	0.80
1:B:518:TYR:CD1	1:B:574:THR:CG2	2.65	0.79
1:A:227:GLN:N	1:A:227:GLN:OE1	2.15	0.78
1:A:489:MET:HE1	1:A:577:ILE:CD1	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:231:ALA:HB3	4:B:1101:POV:O12	1.85	0.76
1:B:7:LEU:O	1:B:11:ILE:CG1	2.34	0.75
1:B:489:MET:HE1	1:B:577:ILE:CD1	2.15	0.75
1:A:119:HIS:O	1:A:122:ARG:HG2	1.86	0.75
1:B:518:TYR:CD1	1:B:574:THR:HG21	2.22	0.75
1:B:141:SER:HB3	1:B:626:VAL:HG21	1.70	0.73
1:B:430:LEU:HD12	1:B:430:LEU:O	1.87	0.73
1:A:137:GLU:HG3	1:A:629:ILE:HD13	1.71	0.73
1:A:130:ASP:HB2	1:A:631:VAL:HG23	1.71	0.71
1:A:518:TYR:CD1	1:A:574:THR:CG2	2.73	0.71
1:B:394:PHE:CD1	2:B:1104:PO4:O3	2.44	0.71
1:B:448:ARG:HG3	1:B:448:ARG:HH11	1.56	0.70
4:A:720:POV:H22	4:A:720:POV:C26	2.17	0.70
1:B:518:TYR:HD1	1:B:574:THR:CG2	2.02	0.70
1:A:333:ALA:HB2	4:A:707:POV:H28	1.73	0.69
1:B:310:ASN:HA	4:B:1120:POV:O14	1.92	0.69
4:B:1120:POV:H13B	4:B:1120:POV:P	2.31	0.69
4:A:719:POV:H13B	4:A:719:POV:P	2.32	0.69
1:B:518:TYR:CD1	1:B:574:THR:HG22	2.26	0.69
1:A:489:MET:SD	1:A:574:THR:HG23	2.32	0.68
1:A:518:TYR:HD1	1:A:574:THR:CG2	2.07	0.68
1:A:518:TYR:CD1	1:A:574:THR:HG22	2.29	0.67
1:B:270:ARG:HD3	2:B:1105:PO4:O3	1.95	0.67
1:A:233:THR:HG23	1:A:318:GLU:OE2	1.96	0.66
1:A:408:MET:HE3	1:A:452:GLN:OE1	1.97	0.65
1:B:255:ALA:HA	1:B:259:LEU:HD23	1.77	0.65
1:A:118:SER:OG	1:A:121:GLU:HG2	1.96	0.65
1:A:255:ALA:HA	1:A:259:LEU:HD23	1.78	0.65
1:B:408:MET:HE3	1:B:452:GLN:OE1	1.97	0.65
1:B:217:ARG:O	1:B:308:ARG:NH1	2.30	0.64
4:B:1120:POV:C35	4:B:1120:POV:H39A	2.27	0.64
1:A:217:ARG:O	1:A:308:ARG:NH1	2.30	0.64
4:A:720:POV:H25A	4:A:720:POV:C21	2.27	0.64
1:B:121:GLU:HA	1:B:121:GLU:OE1	1.97	0.64
1:B:14:GLU:N	1:B:14:GLU:OE1	2.31	0.63
1:A:373:TRP:HB2	4:A:719:POV:H15	1.79	0.63
1:B:373:TRP:CD1	4:B:1120:POV:C15	2.81	0.63
4:B:1110:POV:H33	4:B:1116:POV:O31	1.98	0.63
1:A:373:TRP:CD1	4:A:719:POV:C15	2.81	0.63
1:B:447:VAL:HG12	1:B:447:VAL:O	1.99	0.62
1:B:497:SER:OG	1:B:582:THR:CG2	2.45	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:518:TYR:CD1	1:A:574:THR:HG21	2.35	0.62
1:B:338:PRO:HG3	4:B:1109:POV:C25	2.28	0.62
1:A:14:GLU:HG2	1:A:624:ARG:O	1.99	0.62
1:B:133:LEU:HD23	1:B:629:ILE:HG12	1.80	0.61
1:B:412:TYR:HE1	1:B:441:HIS:HB3	1.64	0.61
1:A:582:THR:HG22	1:A:582:THR:O	2.01	0.61
4:A:719:POV:O12	4:A:719:POV:H15A	2.01	0.61
4:A:719:POV:H13B	4:A:719:POV:O12	2.01	0.60
1:B:127:ASN:N	1:B:127:ASN:HD22	1.98	0.60
1:B:420:GLU:OE2	1:B:440:CYS:HB3	2.00	0.60
1:B:233:THR:HG23	1:B:318:GLU:OE2	2.00	0.60
1:A:310:ASN:HA	4:A:719:POV:O14	2.02	0.60
4:B:1121:POV:O22	4:B:1121:POV:H25A	2.00	0.60
1:B:416:PHE:HD1	1:B:420:GLU:OE1	1.84	0.60
4:B:1120:POV:H13B	4:B:1120:POV:O12	2.01	0.60
4:B:1120:POV:O12	4:B:1120:POV:H15A	2.01	0.60
1:B:582:THR:HG23	1:B:582:THR:O	2.01	0.59
1:B:270:ARG:HB3	2:B:1105:PO4:O3	2.03	0.59
1:A:518:TYR:HD1	1:A:574:THR:HG22	1.65	0.58
1:B:489:MET:SD	1:B:574:THR:HG23	2.42	0.58
1:B:626:VAL:O	1:B:626:VAL:HG23	2.03	0.58
1:B:412:TYR:CE1	1:B:441:HIS:HB3	2.38	0.58
1:A:137:GLU:HG3	1:A:629:ILE:CD1	2.32	0.58
1:A:273:ARG:NH2	2:A:703:PO4:O2	2.36	0.58
1:B:278:LEU:HD21	4:B:1120:POV:H21B	1.85	0.58
1:A:269:ILE:HG12	4:A:714:POV:H38A	1.85	0.57
4:B:1120:POV:H39A	4:B:1120:POV:H35	1.87	0.57
1:B:518:TYR:HD1	1:B:574:THR:HG22	1.62	0.57
1:A:130:ASP:CB	1:A:631:VAL:HG23	2.35	0.56
1:B:137:GLU:HG3	1:B:629:ILE:HD13	1.85	0.56
1:A:270:ARG:HD3	2:A:703:PO4:P	2.44	0.56
1:B:448:ARG:HG3	1:B:448:ARG:NH1	2.19	0.56
1:B:459:ARG:HH22	2:B:1104:PO4:P	2.29	0.56
1:A:475:PRO:HB2	1:A:528:TRP:HH2	1.70	0.56
1:B:373:TRP:CD1	4:B:1120:POV:H15	2.41	0.55
1:A:588:SER:O	1:A:592:ILE:HG12	2.07	0.55
4:B:1101:POV:H26	4:B:1101:POV:H34A	1.89	0.55
1:B:334:CYS:SG	1:B:429:LEU:HD23	2.47	0.55
4:B:1120:POV:C35	4:B:1120:POV:C39	2.86	0.54
1:B:130:ASP:HB3	1:B:631:VAL:HA	1.90	0.54
4:A:719:POV:H22	4:A:719:POV:H35	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:714:POV:H34	4:A:716:POV:H37	1.87	0.54
4:A:720:POV:C33	4:A:720:POV:C28	2.86	0.54
1:B:497:SER:OG	1:B:582:THR:O	2.26	0.53
4:A:714:POV:H32A	4:A:716:POV:H35	1.88	0.53
4:A:719:POV:O22	4:A:719:POV:H24	2.08	0.53
1:A:629:ILE:N	1:A:629:ILE:HD12	2.24	0.53
4:A:710:POV:C310	4:A:710:POV:C314	2.85	0.53
1:B:373:TRP:HB2	4:B:1120:POV:H15	1.91	0.52
4:A:720:POV:H26	4:A:720:POV:C22	2.26	0.52
1:B:518:TYR:CE1	1:B:574:THR:CG2	2.92	0.52
1:A:35:GLN:O	1:A:35:GLN:HG2	2.09	0.52
1:A:35:GLN:O	1:A:37:PRO:HD3	2.10	0.52
1:B:35:GLN:O	1:B:36:ALA:C	2.52	0.52
1:A:47:VAL:HG12	1:A:47:VAL:O	2.10	0.51
1:B:333:ALA:HB2	4:B:1109:POV:H28	1.93	0.51
4:A:721:POV:H210	1:B:241:CYS:HB2	1.92	0.51
1:B:573:TRP:CH2	2:B:1102:PO4:O4	2.64	0.50
1:A:231:ALA:HB3	4:A:721:POV:O12	2.12	0.50
1:B:270:ARG:CD	2:B:1105:PO4:O3	2.59	0.50
1:A:130:ASP:HB3	1:A:631:VAL:HA	1.93	0.50
1:B:133:LEU:CD2	1:B:629:ILE:HG12	2.41	0.50
1:A:373:TRP:CD1	4:A:719:POV:H15B	2.46	0.49
1:A:438:GLY:HA2	1:A:441:HIS:CD2	2.48	0.49
1:B:440:CYS:SG	1:B:441:HIS:N	2.84	0.49
1:B:370:SER:HB3	4:B:1120:POV:H23A	1.93	0.49
1:B:534:TRP:O	1:B:548:ARG:NH1	2.46	0.49
1:A:534:TRP:O	1:A:548:ARG:NH1	2.46	0.49
4:A:714:POV:H34	4:A:716:POV:C37	2.42	0.49
1:B:518:TYR:CE1	1:B:574:THR:HG22	2.48	0.48
4:A:706:POV:C32	4:A:706:POV:C2	2.86	0.48
1:B:475:PRO:HB2	1:B:528:TRP:HH2	1.77	0.48
1:B:131:LEU:CD2	1:B:631:VAL:HG21	2.43	0.48
1:A:489:MET:HE1	1:A:577:ILE:CG1	2.44	0.48
4:B:1120:POV:C39	4:B:1120:POV:H35A	2.39	0.48
1:A:132:LYS:HG2	1:A:206:LEU:HD13	1.96	0.48
1:B:270:ARG:HD3	2:B:1105:PO4:P	2.54	0.48
1:B:408:MET:HE1	1:B:448:ARG:O	2.14	0.48
1:B:132:LYS:HG2	1:B:206:LEU:HD13	1.96	0.47
5:A:709:CLR:H121	5:A:709:CLR:H212	1.95	0.47
1:A:408:MET:HE1	1:A:448:ARG:O	2.14	0.47
1:B:489:MET:HE1	1:B:577:ILE:CG1	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1111:CLR:H121	5:B:1111:CLR:H212	1.95	0.47
4:B:1112:POV:O32	4:B:1112:POV:H34A	2.15	0.47
1:B:127:ASN:N	1:B:127:ASN:ND2	2.60	0.47
1:A:131:LEU:HG	1:A:631:VAL:HG21	1.95	0.47
1:A:395:TRP:O	1:A:399:GLN:HG2	2.15	0.46
1:B:285:LEU:HD21	4:B:1120:POV:H34A	1.98	0.46
1:B:395:TRP:O	1:B:399:GLN:HG2	2.15	0.46
4:B:1113:POV:C36	4:B:1114:POV:H37	2.45	0.46
4:A:721:POV:H34A	4:A:721:POV:H26A	1.97	0.46
1:A:385:PRO:HG3	1:A:461:ILE:HG21	1.97	0.46
1:B:344:THR:HG23	1:B:429:LEU:CB	2.46	0.46
1:B:374:LEU:HD22	4:B:1120:POV:C24	2.46	0.46
1:B:318:GLU:HG2	4:B:1121:POV:H22A	1.98	0.46
1:B:450:ILE:O	1:B:454:ILE:HG13	2.16	0.46
1:A:450:ILE:O	1:A:454:ILE:HG13	2.16	0.46
1:B:207:GLU:HG3	1:B:214:ALA:HB2	1.98	0.46
1:B:7:LEU:HG	1:B:11:ILE:HD11	1.97	0.46
1:B:374:LEU:HD22	4:B:1120:POV:H24A	1.97	0.46
1:B:442:LYS:C	1:B:444:THR:H	2.24	0.46
4:B:1113:POV:H34A	4:B:1114:POV:H37	1.97	0.45
1:A:207:GLU:HG3	1:A:214:ALA:HB2	1.98	0.45
1:A:489:MET:HE2	1:A:489:MET:HB3	1.86	0.45
1:A:518:TYR:CE1	1:A:574:THR:HG22	2.51	0.45
1:B:273:ARG:HH22	2:B:1105:PO4:P	2.38	0.45
1:B:385:PRO:HG3	1:B:461:ILE:HG21	1.97	0.45
4:B:1118:POV:H34	4:B:1118:POV:H37A	1.30	0.45
1:B:344:THR:HG23	1:B:429:LEU:HB2	1.97	0.45
1:B:373:TRP:CG	4:B:1120:POV:H15	2.52	0.45
1:B:441:HIS:O	1:B:441:HIS:CG	2.69	0.45
1:A:118:SER:OG	1:A:121:GLU:CG	2.63	0.45
1:B:524:TYR:CD1	4:B:1115:POV:H38	2.52	0.45
1:B:339:ILE:HG22	1:B:341:VAL:H	1.81	0.45
4:A:712:POV:H37A	4:A:712:POV:H34	1.29	0.44
1:A:339:ILE:HG22	1:A:341:VAL:H	1.81	0.44
1:B:441:HIS:O	1:B:441:HIS:CD2	2.70	0.44
1:A:579:ILE:HA	1:A:583:THR:OG1	2.18	0.44
4:A:720:POV:H25A	4:A:720:POV:O22	2.16	0.44
4:A:719:POV:H310	4:A:719:POV:H37	1.66	0.44
1:A:406:ILE:HG23	4:A:719:POV:H21J	2.00	0.43
4:B:1113:POV:H32A	4:B:1114:POV:C34	2.38	0.43
1:A:45:ASP:O	1:A:49:ARG:CB	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ARG:HH22	2:A:703:PO4:P	2.41	0.43
1:A:583:THR:OG1	1:A:584:LEU:N	2.51	0.43
4:A:712:POV:H31B	4:A:712:POV:H38	1.84	0.43
1:B:420:GLU:CD	1:B:440:CYS:HB3	2.44	0.43
4:B:1109:POV:H211	4:B:1109:POV:H28A	1.63	0.43
4:B:1120:POV:H24A	4:B:1120:POV:H27	1.46	0.43
1:A:345:TYR:HB3	1:A:429:LEU:HB2	2.01	0.43
1:B:548:ARG:HH21	1:B:613:GLU:CD	2.27	0.43
4:B:1113:POV:H34A	4:B:1114:POV:C37	2.48	0.42
1:B:251:LEU:HD21	1:B:331:LEU:HD23	2.02	0.42
1:B:166:ILE:HG22	1:B:167:LEU:HD12	2.02	0.42
1:A:285:LEU:HD21	4:A:719:POV:H33	1.98	0.42
1:A:496:TYR:CE2	1:A:511:PHE:HB2	2.55	0.42
4:B:1121:POV:H13B	4:B:1121:POV:H11A	1.68	0.42
1:A:77:LEU:O	1:A:81:GLN:HG2	2.20	0.42
1:A:273:ARG:HB3	1:A:409:ASP:OD2	2.20	0.42
1:A:518:TYR:CE1	1:A:574:THR:CG2	3.03	0.42
4:A:706:POV:H1A	4:A:720:POV:H1A	2.01	0.42
1:A:548:ARG:HH21	1:A:613:GLU:CD	2.27	0.41
4:A:712:POV:C314	4:A:712:POV:H31A	2.50	0.41
1:B:496:TYR:CE2	1:B:511:PHE:HB2	2.55	0.41
1:B:77:LEU:O	1:B:81:GLN:HG2	2.20	0.41
1:B:338:PRO:HG2	4:B:1109:POV:H25	1.91	0.41
1:B:489:MET:HE2	1:B:489:MET:HB3	1.86	0.41
1:A:251:LEU:HD21	1:A:331:LEU:HD23	2.01	0.41
1:B:17:LYS:HA	1:B:17:LYS:HD3	1.75	0.41
1:B:122:ARG:C	1:B:124:GLN:H	2.28	0.41
4:B:1112:POV:H33	4:B:1112:POV:H36A	1.88	0.41
1:A:496:TYR:HE2	1:A:511:PHE:HB2	1.86	0.41
1:A:166:ILE:HG22	1:A:167:LEU:HD12	2.02	0.41
1:A:356:VAL:O	1:A:360:ILE:HG12	2.21	0.41
1:B:273:ARG:HB3	1:B:409:ASP:OD2	2.20	0.41
1:B:160:LEU:HA	1:B:160:LEU:HD23	1.88	0.41
1:B:518:TYR:HD1	1:B:574:THR:HG21	1.72	0.40
1:B:18:GLN:OE1	1:B:18:GLN:HA	2.21	0.40
1:B:159:ILE:HD12	1:B:159:ILE:HA	1.96	0.40
4:B:1120:POV:H35A	4:B:1120:POV:H38	1.71	0.40
1:B:333:ALA:HB2	4:B:1109:POV:C28	2.49	0.40
1:A:35:GLN:O	1:A:35:GLN:CG	2.70	0.40
1:B:496:TYR:HE2	1:B:511:PHE:HB2	1.86	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	A	610/696 (88%)	590 (97%)	18 (3%)	2 (0%)	36	59
1	B	610/696 (88%)	582 (95%)	28 (5%)	0	100	100
All	All	1220/1392 (88%)	1172 (96%)	46 (4%)	2 (0%)	44	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	633	PRO
1	A	41	VAL

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	520/621 (84%)	518 (100%)	2 (0%)	84	92
1	B	519/621 (84%)	514 (99%)	5 (1%)	68	82
All	All	1039/1242 (84%)	1032 (99%)	7 (1%)	73	87

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	227	GLN
1	A	579	ILE
1	B	11	ILE
1	B	579	ILE

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Mol	Chain	Res	Type
1	B	580	THR
1	B	626	VAL
1	B	629	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	92	GLN
1	A	124	GLN
1	A	387	HIS
1	B	21	GLN
1	B	92	GLN
1	B	387	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

42 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	POV	A	714	-	15,15,51	1.16	1 (6%)	15,15,59	0.99	0
4	POV	B	1101	-	38,38,51	1.05	2 (5%)	41,43,59	1.24	4 (9%)
4	POV	A	707	-	17,17,51	1.09	1 (5%)	17,17,59	0.99	1 (5%)
4	POV	B	1121	-	28,28,51	1.25	2 (7%)	34,36,59	1.23	4 (11%)
5	CLR	B	1111	-	31,31,31	1.08	2 (6%)	48,48,48	1.47	10 (20%)
2	PO4	A	701	-	4,4,4	3.07	4 (100%)	6,6,6	0.46	0
4	POV	A	711	-	15,15,51	1.78	2 (13%)	15,15,59	1.20	2 (13%)
5	CLR	A	709	-	31,31,31	1.07	2 (6%)	48,48,48	1.46	10 (20%)
4	POV	B	1115	-	15,15,51	1.18	1 (6%)	15,15,59	1.07	1 (6%)
2	PO4	B	1103	-	4,4,4	3.06	4 (100%)	6,6,6	0.46	0
4	POV	A	717	-	15,15,51	1.79	2 (13%)	15,15,59	1.05	0
4	POV	B	1110	-	15,15,51	1.78	2 (13%)	15,15,59	1.16	1 (6%)
4	POV	B	1119	-	15,15,51	0.89	1 (6%)	15,15,59	1.18	2 (13%)
2	PO4	B	1105	-	4,4,4	3.06	4 (100%)	6,6,6	0.46	0
4	POV	A	712	-	15,15,51	0.90	1 (6%)	15,15,59	1.09	0
4	POV	A	715	-	15,15,51	0.89	1 (6%)	15,15,59	1.18	0
4	POV	A	718	-	17,17,51	1.22	2 (11%)	17,17,59	1.33	4 (23%)
4	POV	A	710	-	15,15,51	0.88	1 (6%)	15,15,59	1.21	0
4	POV	B	1114	-	15,15,51	1.18	1 (6%)	15,15,59	0.98	1 (6%)
2	PO4	A	703	-	4,4,4	2.00	3 (75%)	6,6,6	0.71	0
2	PO4	A	704	-	4,4,4	3.05	4 (100%)	6,6,6	0.47	0
4	POV	B	1109	-	17,17,51	1.09	1 (5%)	17,17,59	1.01	2 (11%)
4	POV	B	1116	-	15,15,51	0.91	1 (6%)	15,15,59	1.04	0
4	POV	A	720	-	28,28,51	1.25	2 (7%)	34,36,59	1.31	6 (17%)
4	POV	B	1107	-	17,17,51	1.22	2 (11%)	17,17,59	1.34	4 (23%)
2	PO4	B	1102	-	4,4,4	3.07	4 (100%)	6,6,6	0.46	0
4	POV	A	713	-	13,13,51	1.91	2 (15%)	13,13,59	1.19	0
2	PO4	B	1104	-	4,4,4	3.05	4 (100%)	6,6,6	0.46	0
4	POV	B	1112	-	15,15,51	1.76	2 (13%)	15,15,59	1.23	2 (13%)
4	POV	A	706	-	16,16,51	0.87	1 (6%)	16,16,59	1.28	2 (12%)
4	POV	B	1120	-	51,51,51	0.94	2 (3%)	57,59,59	1.07	3 (5%)
4	POV	B	1118	-	15,15,51	0.91	1 (6%)	15,15,59	1.09	0
4	POV	B	1117	-	10,10,51	1.08	1 (10%)	10,10,59	1.19	0
4	POV	A	719	-	51,51,51	0.95	2 (3%)	57,59,59	1.09	3 (5%)
2	PO4	A	702	-	4,4,4	3.06	4 (100%)	6,6,6	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	POV	A	721	-	38,38,51	1.05	2 (5%)	41,43,59	1.29	4 (9%)
4	POV	B	1113	-	15,15,51	1.16	1 (6%)	15,15,59	1.07	1 (6%)
3	IHP	B	1106	-	36,36,36	1.53	6 (16%)	60,60,60	1.03	1 (1%)
4	POV	A	716	-	15,15,51	1.18	1 (6%)	15,15,59	1.02	1 (6%)
4	POV	A	708	-	15,15,51	1.75	2 (13%)	15,15,59	1.15	0
3	IHP	A	705	-	36,36,36	1.53	6 (16%)	60,60,60	1.03	1 (1%)
4	POV	B	1108	-	16,16,51	0.88	1 (6%)	16,16,59	1.30	1 (6%)

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	POV	A	714	-	-	8/13/13/55	-
4	POV	B	1101	-	-	13/40/40/55	-
4	POV	A	707	-	-	6/15/15/55	-
4	POV	B	1121	-	-	9/32/32/55	-
5	CLR	B	1111	-	-	2/10/68/68	0/4/4/4
4	POV	A	711	-	-	8/13/13/55	-
5	CLR	A	709	-	-	2/10/68/68	0/4/4/4
4	POV	B	1115	-	-	5/13/13/55	-
4	POV	A	717	-	-	5/13/13/55	-
4	POV	B	1110	-	-	7/13/13/55	-
4	POV	B	1119	-	-	7/13/13/55	-
4	POV	A	712	-	-	7/13/13/55	-
4	POV	A	715	-	-	8/13/13/55	-
4	POV	A	718	-	-	7/15/15/55	-
4	POV	A	710	-	-	8/13/13/55	-
4	POV	B	1114	-	-	4/13/13/55	-
4	POV	B	1109	-	-	6/15/15/55	-
4	POV	B	1116	-	-	11/13/13/55	-
4	POV	A	720	-	-	11/32/32/55	-
4	POV	B	1107	-	-	5/15/15/55	-
4	POV	A	713	-	-	6/11/11/55	-
4	POV	B	1112	-	-	6/13/13/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	POV	A	706	-	-	11/15/15/55	-
4	POV	B	1120	-	-	23/55/55/55	-
4	POV	B	1118	-	-	7/13/13/55	-
4	POV	B	1117	-	-	7/8/8/55	-
4	POV	A	719	-	-	20/55/55/55	-
4	POV	A	721	-	-	14/40/40/55	-
4	POV	B	1113	-	-	5/13/13/55	-
3	IHP	B	1106	-	-	5/30/54/54	0/1/1/1
4	POV	A	716	-	-	3/13/13/55	-
4	POV	A	708	-	-	8/13/13/55	-
3	IHP	A	705	-	-	5/30/54/54	0/1/1/1
4	POV	B	1108	-	-	11/15/15/55	-

All (91) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	713	POV	O32-C31	5.66	1.40	1.22
4	A	711	POV	O32-C31	5.66	1.40	1.22
4	A	717	POV	O32-C31	5.63	1.40	1.22
4	B	1110	POV	O32-C31	5.60	1.40	1.22
4	B	1112	POV	O32-C31	5.56	1.40	1.22
4	A	708	POV	O32-C31	5.54	1.40	1.22
2	B	1102	PO4	P-O1	4.71	1.61	1.50
2	A	701	PO4	P-O1	4.70	1.61	1.50
2	B	1105	PO4	P-O1	4.69	1.61	1.50
2	A	704	PO4	P-O1	4.68	1.61	1.50
2	B	1104	PO4	P-O1	4.68	1.61	1.50
2	A	702	PO4	P-O1	4.67	1.61	1.50
2	B	1103	PO4	P-O1	4.67	1.61	1.50
4	B	1114	POV	O31-C31	4.52	1.45	1.30
4	B	1115	POV	O31-C31	4.50	1.45	1.30
4	A	716	POV	O31-C31	4.48	1.45	1.30
4	B	1113	POV	O31-C31	4.46	1.45	1.30
4	A	714	POV	O31-C31	4.44	1.45	1.30
4	B	1109	POV	O21-C21	4.42	1.45	1.30
4	A	707	POV	O21-C21	4.41	1.45	1.30
4	A	719	POV	O31-C31	4.13	1.45	1.33
4	A	719	POV	O21-C21	4.11	1.45	1.34
4	A	721	POV	O21-C21	4.08	1.45	1.34
4	B	1121	POV	O31-C31	4.07	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1101	POV	O21-C21	4.07	1.45	1.34
4	B	1120	POV	O31-C31	4.06	1.45	1.33
4	A	720	POV	O31-C31	4.04	1.45	1.33
4	B	1120	POV	O21-C21	3.98	1.45	1.34
4	B	1101	POV	O31-C31	3.98	1.44	1.33
4	A	721	POV	O31-C31	3.97	1.44	1.33
4	B	1121	POV	O21-C21	3.90	1.45	1.34
4	A	720	POV	O21-C21	3.85	1.45	1.34
4	B	1110	POV	O31-C31	-3.78	1.18	1.30
4	B	1107	POV	C29-C210	3.71	1.52	1.31
4	A	718	POV	C29-C210	3.67	1.52	1.31
4	A	708	POV	O31-C31	-3.67	1.18	1.30
4	A	717	POV	O31-C31	-3.65	1.18	1.30
4	A	711	POV	O31-C31	-3.64	1.18	1.30
4	B	1112	POV	O31-C31	-3.64	1.18	1.30
4	A	713	POV	O31-C31	-3.61	1.18	1.30
3	A	705	IHP	P5-O15	3.53	1.65	1.59
3	B	1106	IHP	P5-O15	3.51	1.65	1.59
3	A	705	IHP	P1-O11	3.47	1.65	1.59
3	B	1106	IHP	P1-O11	3.47	1.65	1.59
3	A	705	IHP	P4-O14	3.19	1.65	1.59
3	B	1106	IHP	P4-O14	3.19	1.65	1.59
3	B	1106	IHP	P2-O12	3.19	1.65	1.59
3	A	705	IHP	P2-O12	3.16	1.65	1.59
4	B	1118	POV	O31-C31	2.97	1.40	1.30
4	A	712	POV	O31-C31	2.95	1.40	1.30
4	B	1119	POV	O31-C31	2.94	1.40	1.30
4	A	718	POV	O21-C21	2.93	1.40	1.30
4	A	715	POV	O31-C31	2.92	1.40	1.30
4	B	1116	POV	O31-C31	2.91	1.40	1.30
4	A	710	POV	O31-C31	2.88	1.40	1.30
4	B	1117	POV	O21-C21	2.88	1.40	1.30
4	B	1107	POV	O21-C21	2.86	1.40	1.30
3	B	1106	IHP	P3-O13	2.76	1.64	1.59
3	A	705	IHP	P3-O13	2.73	1.64	1.59
3	A	705	IHP	P6-O16	2.71	1.64	1.59
3	B	1106	IHP	P6-O16	2.70	1.64	1.59
5	A	709	CLR	C10-C9	-2.42	1.52	1.56
5	B	1111	CLR	C10-C9	-2.38	1.52	1.56
2	A	703	PO4	P-O2	2.37	1.61	1.54
2	A	702	PO4	P-O3	2.36	1.61	1.54
2	B	1103	PO4	P-O3	2.36	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	PO4	P-O3	2.36	1.61	1.54
2	A	704	PO4	P-O2	2.35	1.61	1.54
2	A	703	PO4	P-O3	2.35	1.61	1.54
2	A	701	PO4	P-O2	2.35	1.61	1.54
2	B	1102	PO4	P-O3	2.35	1.61	1.54
2	B	1105	PO4	P-O3	2.34	1.61	1.54
2	B	1104	PO4	P-O3	2.34	1.61	1.54
2	A	702	PO4	P-O2	2.34	1.61	1.54
2	B	1103	PO4	P-O2	2.34	1.61	1.54
2	B	1105	PO4	P-O2	2.33	1.61	1.54
2	A	704	PO4	P-O3	2.33	1.61	1.54
2	B	1104	PO4	P-O2	2.32	1.61	1.54
4	B	1108	POV	O31-C31	2.31	1.40	1.33
2	B	1102	PO4	P-O2	2.31	1.61	1.54
4	A	706	POV	O31-C31	2.24	1.39	1.33
5	A	709	CLR	C13-C14	-2.21	1.50	1.55
5	B	1111	CLR	C13-C14	-2.20	1.50	1.55
2	B	1102	PO4	P-O4	-2.14	1.48	1.54
2	B	1104	PO4	P-O4	-2.13	1.48	1.54
2	A	702	PO4	P-O4	-2.13	1.48	1.54
2	B	1103	PO4	P-O4	-2.13	1.48	1.54
2	B	1105	PO4	P-O4	-2.12	1.48	1.54
2	A	704	PO4	P-O4	-2.12	1.48	1.54
2	A	701	PO4	P-O4	-2.11	1.48	1.54
2	A	703	PO4	P-O4	-2.11	1.48	1.54

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	721	POV	O21-C21-C22	4.26	120.69	111.48
4	A	720	POV	O21-C21-C22	4.23	120.63	111.48
4	A	719	POV	O21-C21-C22	4.09	120.34	111.48
4	B	1121	POV	O21-C21-C22	3.96	120.04	111.48
4	B	1101	POV	O21-C21-C22	3.85	119.80	111.48
3	B	1106	IHP	C6-C5-C4	-3.67	102.38	110.43
3	A	705	IHP	C6-C5-C4	-3.66	102.39	110.43
4	B	1120	POV	O21-C21-C22	3.61	119.30	111.48
5	B	1111	CLR	C13-C17-C20	-3.34	114.35	119.50
5	A	709	CLR	C13-C17-C20	-3.33	114.36	119.50
4	B	1101	POV	O31-C31-C32	3.17	121.51	111.83
4	A	721	POV	O31-C31-C32	3.13	121.38	111.83
4	A	720	POV	O31-C31-C32	3.10	120.56	111.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1121	POV	O31-C31-C32	3.08	120.49	111.15
5	B	1111	CLR	C4-C5-C6	-3.06	116.43	120.57
5	A	709	CLR	C4-C5-C6	-3.02	116.47	120.57
4	A	706	POV	O31-C31-C32	2.87	120.57	111.83
4	B	1120	POV	O31-C31-C32	2.86	120.55	111.83
4	A	719	POV	O31-C31-C32	2.77	120.28	111.83
4	B	1108	POV	O31-C31-C32	2.76	120.25	111.83
5	A	709	CLR	C4-C5-C10	2.75	119.94	116.42
5	B	1111	CLR	C4-C5-C10	2.75	119.94	116.42
5	A	709	CLR	C11-C12-C13	-2.61	108.34	112.74
5	B	1111	CLR	C11-C12-C13	-2.57	108.40	112.74
5	B	1111	CLR	C19-C10-C9	-2.51	108.84	111.66
5	A	709	CLR	C19-C10-C9	-2.48	108.87	111.66
5	A	709	CLR	C7-C8-C14	-2.46	107.45	110.93
4	A	721	POV	O13-P-O14	2.46	120.40	110.83
5	B	1111	CLR	C7-C8-C14	-2.45	107.46	110.93
5	B	1111	CLR	C3-C4-C5	-2.44	108.17	112.05
4	A	720	POV	C2-O21-C21	-2.43	111.97	117.80
4	B	1101	POV	O13-P-O14	2.42	120.28	110.83
5	A	709	CLR	C3-C4-C5	-2.41	108.22	112.05
4	A	720	POV	O21-C21-O22	-2.39	118.11	123.70
5	A	709	CLR	C2-C3-C4	-2.37	106.95	110.29
5	B	1111	CLR	C2-C3-C4	-2.37	106.96	110.29
4	B	1101	POV	O31-C31-O32	-2.30	117.88	123.63
4	A	721	POV	O31-C31-O32	-2.28	117.92	123.63
4	B	1107	POV	C23-C22-C21	-2.26	108.61	114.51
4	B	1110	POV	C33-C32-C31	-2.24	108.67	114.51
5	B	1111	CLR	C19-C10-C5	2.22	111.77	108.38
4	B	1112	POV	C33-C32-C31	-2.20	108.78	114.51
4	A	719	POV	C2-O21-C21	-2.19	112.56	117.80
4	A	707	POV	O21-C21-C22	2.19	120.91	114.00
5	A	709	CLR	C19-C10-C5	2.19	111.72	108.38
4	A	718	POV	C211-C210-C29	-2.17	108.56	124.83
4	A	718	POV	C28-C29-C210	-2.17	108.59	124.83
4	A	720	POV	C11-C12-N	-2.17	108.86	115.82
4	B	1109	POV	O21-C21-C22	2.16	120.83	114.00
4	B	1113	POV	C33-C32-C31	-2.16	108.87	114.51
4	B	1121	POV	C11-C12-N	-2.14	108.94	115.82
4	B	1107	POV	C28-C29-C210	-2.14	108.81	124.83
4	A	711	POV	C33-C32-C31	-2.14	108.94	114.51
4	B	1120	POV	C2-O21-C21	-2.13	112.70	117.80
4	B	1115	POV	C33-C32-C31	-2.12	108.98	114.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1112	POV	O31-C31-C32	2.11	120.68	114.00
4	B	1107	POV	C211-C210-C29	-2.11	109.00	124.83
4	A	720	POV	O31-C31-O32	-2.11	118.35	123.63
4	A	718	POV	C23-C22-C21	-2.08	109.07	114.51
4	A	716	POV	O31-C31-C32	2.08	120.56	114.00
5	A	709	CLR	C8-C7-C6	-2.08	109.89	112.76
4	A	706	POV	C3-C2-C1	-2.07	109.47	113.55
4	B	1121	POV	O31-C31-O32	-2.06	118.47	123.63
4	B	1114	POV	O31-C31-C32	2.04	120.44	114.00
5	B	1111	CLR	C8-C7-C6	-2.03	109.95	112.76
4	B	1107	POV	O21-C21-C22	2.03	120.40	114.00
4	B	1109	POV	C23-C22-C21	-2.02	109.23	114.51
4	A	711	POV	O31-C31-C32	2.01	120.36	114.00
4	A	718	POV	O21-C21-C22	2.01	120.36	114.00
4	B	1119	POV	O31-C31-C32	2.01	120.36	114.00
4	B	1119	POV	C33-C32-C31	-2.01	109.27	114.51

There are no chirality outliers.

All (270) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	706	POV	O11-C1-C2-C3
4	A	719	POV	C1-O11-P-O13
4	A	719	POV	C11-O12-P-O11
4	A	719	POV	C11-O12-P-O13
4	A	719	POV	O12-C11-C12-N
4	A	720	POV	C1-O11-P-O12
4	A	720	POV	C1-O11-P-O13
4	A	720	POV	C1-O11-P-O14
4	B	1108	POV	O11-C1-C2-C3
4	B	1108	POV	O32-C31-O31-C3
4	B	1120	POV	C1-O11-P-O12
4	B	1120	POV	C1-O11-P-O13
4	B	1120	POV	C11-O12-P-O11
4	B	1120	POV	C11-O12-P-O13
4	B	1120	POV	O12-C11-C12-N
4	B	1121	POV	C1-O11-P-O12
4	B	1121	POV	C1-O11-P-O13
4	B	1121	POV	C1-O11-P-O14
4	A	706	POV	O32-C31-O31-C3
4	A	706	POV	C32-C31-O31-C3
4	B	1108	POV	C32-C31-O31-C3

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Mol	Chain	Res	Type	Atoms
4	A	706	POV	C2-C3-O31-C31
4	B	1108	POV	C2-C3-O31-C31
5	A	709	CLR	C21-C20-C22-C23
5	B	1111	CLR	C21-C20-C22-C23
4	A	711	POV	C37-C38-C39-C310
4	A	720	POV	C22-C23-C24-C25
4	B	1108	POV	C1-C2-C3-O31
4	B	1119	POV	C36-C37-C38-C39
4	A	712	POV	C34-C35-C36-C37
4	B	1118	POV	C34-C35-C36-C37
4	B	1107	POV	C211-C210-C29-C28
4	A	719	POV	C31-C32-C33-C34
4	B	1118	POV	C311-C310-C39-C38
4	A	712	POV	C311-C310-C39-C38
4	B	1120	POV	C35-C36-C37-C38
4	B	1120	POV	C33-C34-C35-C36
4	A	721	POV	C31-C32-C33-C34
4	B	1101	POV	C31-C32-C33-C34
4	A	718	POV	C210-C211-C212-C213
4	A	715	POV	C31-C32-C33-C34
4	A	710	POV	C31-C32-C33-C34
4	B	1101	POV	C22-C21-O21-C2
4	A	710	POV	C33-C34-C35-C36
4	A	718	POV	C23-C24-C25-C26
4	A	708	POV	C35-C36-C37-C38
4	A	711	POV	C35-C36-C37-C38
4	A	717	POV	C32-C33-C34-C35
4	A	719	POV	C37-C38-C39-C310
4	A	721	POV	C23-C24-C25-C26
4	A	711	POV	C34-C35-C36-C37
4	A	713	POV	C32-C33-C34-C35
4	A	715	POV	C33-C34-C35-C36
4	A	719	POV	C33-C34-C35-C36
4	B	1108	POV	C32-C33-C34-C35
4	B	1119	POV	C35-C36-C37-C38
4	A	717	POV	C31-C32-C33-C34
4	A	718	POV	C21-C22-C23-C24
4	B	1107	POV	C25-C26-C27-C28
4	B	1110	POV	C37-C38-C39-C310
4	B	1116	POV	C310-C311-C312-C313
4	B	1112	POV	C32-C33-C34-C35
4	B	1119	POV	C33-C34-C35-C36

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Mol	Chain	Res	Type	Atoms
4	B	1117	POV	C23-C24-C25-C26
4	B	1101	POV	O22-C21-O21-C2
4	A	711	POV	C311-C310-C39-C38
4	A	715	POV	C32-C33-C34-C35
4	A	706	POV	C36-C37-C38-C39
4	A	713	POV	C33-C34-C35-C36
4	A	715	POV	C36-C37-C38-C39
4	B	1108	POV	C34-C35-C36-C37
4	A	706	POV	C33-C34-C35-C36
4	A	713	POV	C35-C36-C37-C38
4	A	721	POV	C21-C22-C23-C24
4	A	718	POV	C25-C26-C27-C28
4	B	1117	POV	C22-C23-C24-C25
4	B	1107	POV	C210-C211-C212-C213
4	B	1107	POV	C21-C22-C23-C24
4	A	708	POV	C31-C32-C33-C34
4	B	1113	POV	C34-C35-C36-C37
4	B	1112	POV	C35-C36-C37-C38
4	A	721	POV	C22-C21-O21-C2
4	B	1120	POV	C22-C23-C24-C25
4	A	718	POV	C211-C210-C29-C28
4	B	1116	POV	C33-C34-C35-C36
4	B	1116	POV	C35-C36-C37-C38
4	B	1121	POV	C22-C23-C24-C25
4	B	1101	POV	C21-C22-C23-C24
4	B	1108	POV	C33-C34-C35-C36
4	A	721	POV	O21-C2-C3-O31
4	A	708	POV	C37-C38-C39-C310
4	A	711	POV	C32-C33-C34-C35
4	A	716	POV	C32-C33-C34-C35
4	A	720	POV	C22-C21-O21-C2
4	B	1108	POV	C311-C310-C39-C38
4	A	706	POV	C34-C35-C36-C37
4	A	721	POV	C22-C23-C24-C25
4	B	1110	POV	C31-C32-C33-C34
4	A	721	POV	O22-C21-O21-C2
4	B	1101	POV	C25-C26-C27-C28
4	A	715	POV	C34-C35-C36-C37
4	B	1114	POV	C35-C36-C37-C38
4	A	719	POV	C1-C2-C3-O31
4	B	1101	POV	C1-C2-C3-O31
4	A	710	POV	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
4	A	721	POV	C210-C211-C212-C213
4	B	1120	POV	C210-C211-C212-C213
4	A	710	POV	C39-C310-C311-C312
4	B	1109	POV	C25-C26-C27-C28
4	B	1117	POV	C25-C26-C27-C28
4	A	710	POV	C311-C312-C313-C314
4	A	719	POV	C210-C211-C212-C213
4	A	721	POV	C26-C27-C28-C29
4	B	1109	POV	C26-C27-C28-C29
4	A	712	POV	C33-C34-C35-C36
4	B	1118	POV	C33-C34-C35-C36
4	B	1112	POV	C311-C312-C313-C314
4	A	713	POV	C37-C38-C39-C310
4	A	717	POV	C35-C36-C37-C38
4	B	1101	POV	O21-C2-C3-O31
4	A	707	POV	C25-C26-C27-C28
4	B	1108	POV	C36-C37-C38-C39
4	A	715	POV	C39-C310-C311-C312
4	A	708	POV	C33-C34-C35-C36
4	A	708	POV	C310-C311-C312-C313
4	B	1108	POV	C35-C36-C37-C38
4	B	1120	POV	C36-C37-C38-C39
4	B	1120	POV	C212-C213-C214-C215
4	B	1110	POV	C33-C34-C35-C36
4	B	1116	POV	C32-C33-C34-C35
4	A	710	POV	C310-C311-C312-C313
4	A	720	POV	O11-C1-C2-C3
4	A	706	POV	C37-C38-C39-C310
4	B	1110	POV	C32-C33-C34-C35
4	B	1114	POV	C32-C33-C34-C35
4	B	1118	POV	C310-C311-C312-C313
4	B	1119	POV	C39-C310-C311-C312
4	A	721	POV	C1-C2-C3-O31
4	A	712	POV	C37-C38-C39-C310
4	A	719	POV	C23-C24-C25-C26
4	B	1110	POV	C36-C37-C38-C39
4	B	1118	POV	C37-C38-C39-C310
4	B	1115	POV	C34-C35-C36-C37
4	B	1120	POV	C23-C24-C25-C26
4	B	1107	POV	C23-C24-C25-C26
4	A	710	POV	C36-C37-C38-C39
5	A	709	CLR	C17-C20-C22-C23

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Mol	Chain	Res	Type	Atoms
5	B	1111	CLR	C17-C20-C22-C23
4	A	712	POV	C310-C311-C312-C313
4	B	1101	POV	C213-C214-C215-C216
4	A	711	POV	C33-C34-C35-C36
4	A	721	POV	C24-C25-C26-C27
4	A	720	POV	O22-C21-O21-C2
4	A	716	POV	C35-C36-C37-C38
4	A	710	POV	C34-C35-C36-C37
4	B	1116	POV	C31-C32-C33-C34
4	A	719	POV	O21-C2-C3-O31
4	A	719	POV	C25-C26-C27-C28
4	B	1116	POV	C34-C35-C36-C37
4	B	1112	POV	C37-C38-C39-C310
4	A	719	POV	C24-C25-C26-C27
4	A	716	POV	C33-C34-C35-C36
4	A	720	POV	O12-C11-C12-N
4	B	1121	POV	O12-C11-C12-N
4	B	1120	POV	C311-C310-C39-C38
4	B	1117	POV	C21-C22-C23-C24
4	B	1115	POV	C37-C38-C39-C310
4	A	720	POV	O11-C1-C2-O21
4	B	1113	POV	C36-C37-C38-C39
4	B	1120	POV	C24-C25-C26-C27
4	A	714	POV	C311-C310-C39-C38
4	B	1101	POV	C211-C212-C213-C214
4	A	719	POV	C1-O11-P-O12
4	A	720	POV	C11-O12-P-O14
4	B	1121	POV	C11-O12-P-O14
4	A	721	POV	C25-C26-C27-C28
4	A	708	POV	C34-C35-C36-C37
4	A	715	POV	C35-C36-C37-C38
4	A	718	POV	C26-C27-C28-C29
4	B	1119	POV	C310-C311-C312-C313
4	B	1101	POV	C24-C25-C26-C27
4	B	1116	POV	C311-C312-C313-C314
4	B	1121	POV	C24-C25-C26-C27
4	B	1115	POV	C310-C311-C312-C313
4	B	1117	POV	O21-C21-C22-C23
4	B	1115	POV	C39-C310-C311-C312
4	B	1114	POV	C33-C34-C35-C36
4	B	1116	POV	C311-C310-C39-C38
4	A	714	POV	C34-C35-C36-C37

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Mol	Chain	Res	Type	Atoms
4	A	706	POV	C35-C36-C37-C38
4	A	714	POV	O32-C31-C32-C33
4	B	1120	POV	C1-C2-C3-O31
4	A	715	POV	C311-C310-C39-C38
4	A	719	POV	C35-C36-C37-C38
4	B	1117	POV	C24-C25-C26-C27
4	B	1116	POV	O31-C31-C32-C33
4	B	1117	POV	O22-C21-C22-C23
4	A	714	POV	O31-C31-C32-C33
4	B	1116	POV	O32-C31-C32-C33
4	A	713	POV	O31-C31-C32-C33
4	A	721	POV	C214-C215-C216-C217
4	B	1101	POV	C29-C210-C211-C212
4	A	717	POV	O32-C31-C32-C33
4	A	706	POV	C1-C2-C3-O31
4	A	707	POV	C26-C27-C28-C29
3	A	705	IHP	C1-O11-P1-O21
3	A	705	IHP	C3-O13-P3-O23
3	A	705	IHP	C6-O16-P6-O26
3	B	1106	IHP	C1-O11-P1-O21
3	B	1106	IHP	C3-O13-P3-O23
3	B	1106	IHP	C6-O16-P6-O26
4	A	713	POV	O32-C31-C32-C33
4	B	1119	POV	C32-C33-C34-C35
4	A	717	POV	O31-C31-C32-C33
4	A	712	POV	O32-C31-C32-C33
4	B	1120	POV	O11-C1-C2-O21
4	B	1121	POV	O11-C1-C2-O21
4	A	711	POV	O31-C31-C32-C33
4	B	1118	POV	O32-C31-C32-C33
4	B	1110	POV	C311-C310-C39-C38
4	A	707	POV	C211-C212-C213-C214
4	B	1121	POV	O11-C1-C2-C3
4	A	714	POV	C311-C312-C313-C314
4	A	708	POV	O31-C31-C32-C33
4	B	1114	POV	C34-C35-C36-C37
4	A	711	POV	O32-C31-C32-C33
4	B	1110	POV	C35-C36-C37-C38
4	A	712	POV	O31-C31-C32-C33
4	B	1109	POV	C211-C212-C213-C214
4	A	707	POV	C27-C28-C29-C210
4	A	714	POV	C35-C36-C37-C38

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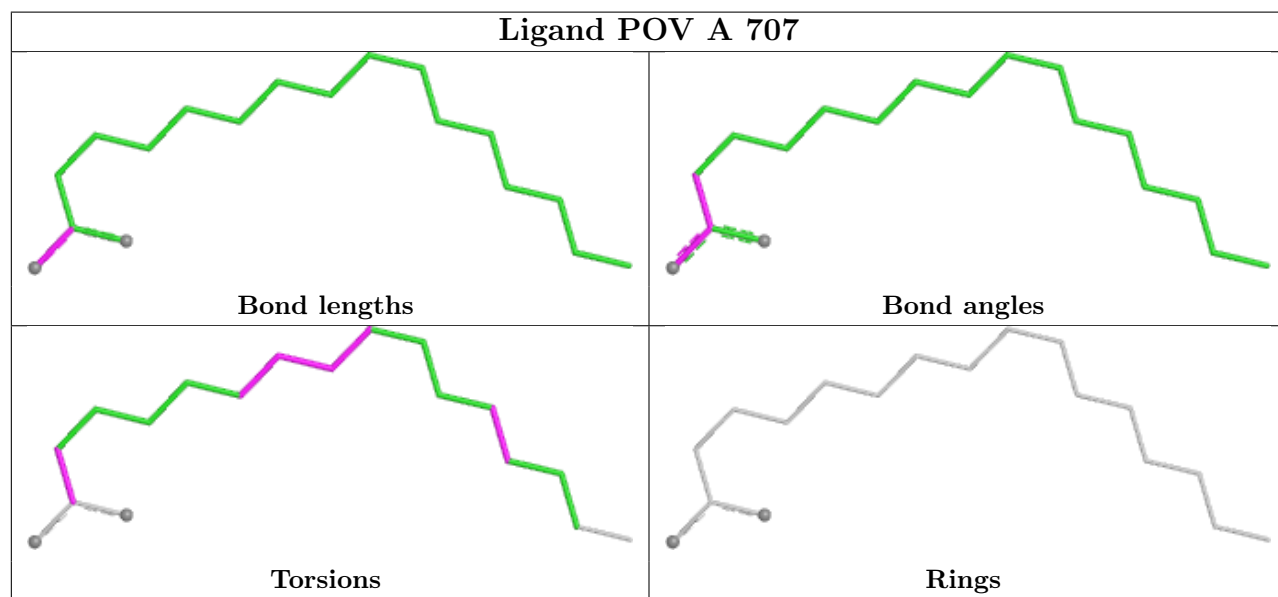
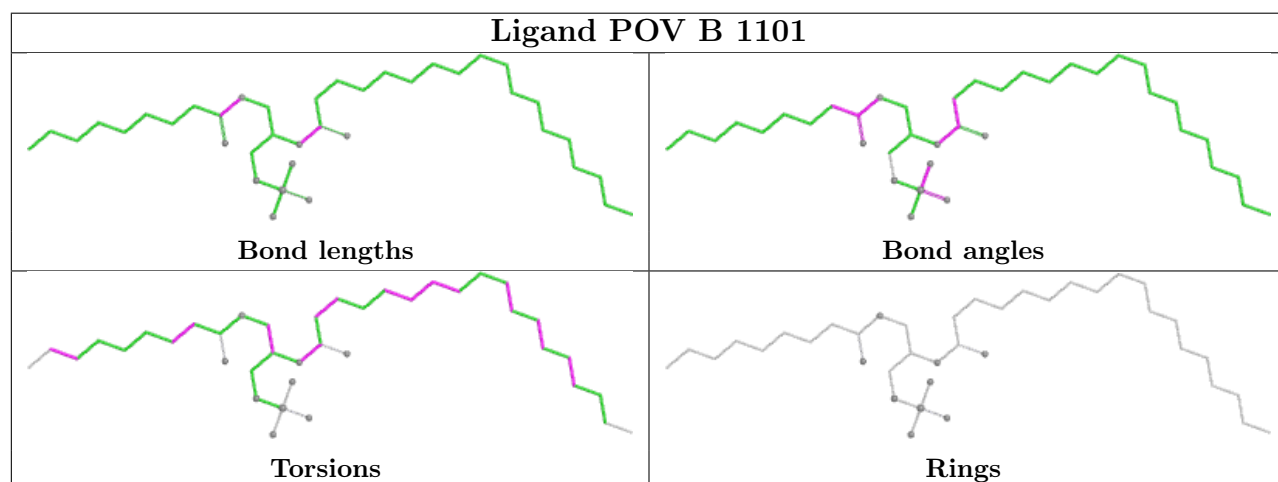
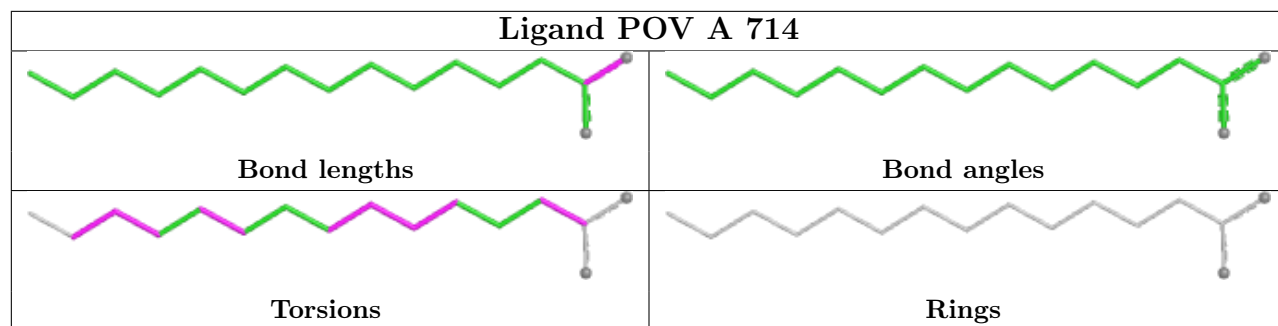
Mol	Chain	Res	Type	Atoms
4	B	1113	POV	C37-C38-C39-C310
4	A	719	POV	C11-C12-N-C13
4	B	1120	POV	C11-C12-N-C13
4	B	1118	POV	O31-C31-C32-C33
4	A	714	POV	C33-C34-C35-C36
4	B	1109	POV	C22-C23-C24-C25
4	A	714	POV	C310-C311-C312-C313
4	B	1113	POV	O32-C31-C32-C33
4	A	718	POV	C29-C210-C211-C212
4	A	719	POV	C213-C214-C215-C216
4	A	708	POV	O32-C31-C32-C33
4	B	1101	POV	C26-C27-C28-C29
3	A	705	IHP	C1-O11-P1-O31
3	A	705	IHP	C1-O11-P1-O41
3	B	1106	IHP	C1-O11-P1-O31
3	B	1106	IHP	C1-O11-P1-O41
4	A	707	POV	O22-C21-C22-C23
4	A	707	POV	O21-C21-C22-C23
4	B	1119	POV	C37-C38-C39-C310
4	B	1112	POV	O31-C31-C32-C33
4	B	1101	POV	C36-C37-C38-C39
4	B	1116	POV	C36-C37-C38-C39
4	B	1109	POV	O22-C21-C22-C23
4	A	720	POV	O31-C31-C32-C33
4	A	719	POV	C27-C28-C29-C210
4	B	1113	POV	O31-C31-C32-C33
4	A	719	POV	C11-C12-N-C14
4	B	1120	POV	C11-C12-N-C14
4	B	1120	POV	C29-C210-C211-C212
4	A	721	POV	O21-C21-C22-C23
4	B	1120	POV	O31-C31-C32-C33
4	B	1120	POV	O21-C2-C3-O31
4	B	1115	POV	O31-C31-C32-C33
4	B	1120	POV	C27-C28-C29-C210
4	B	1112	POV	O32-C31-C32-C33
4	A	706	POV	O31-C31-C32-C33
4	A	719	POV	C29-C210-C211-C212
4	B	1109	POV	O21-C21-C22-C23
4	B	1120	POV	O32-C31-C32-C33

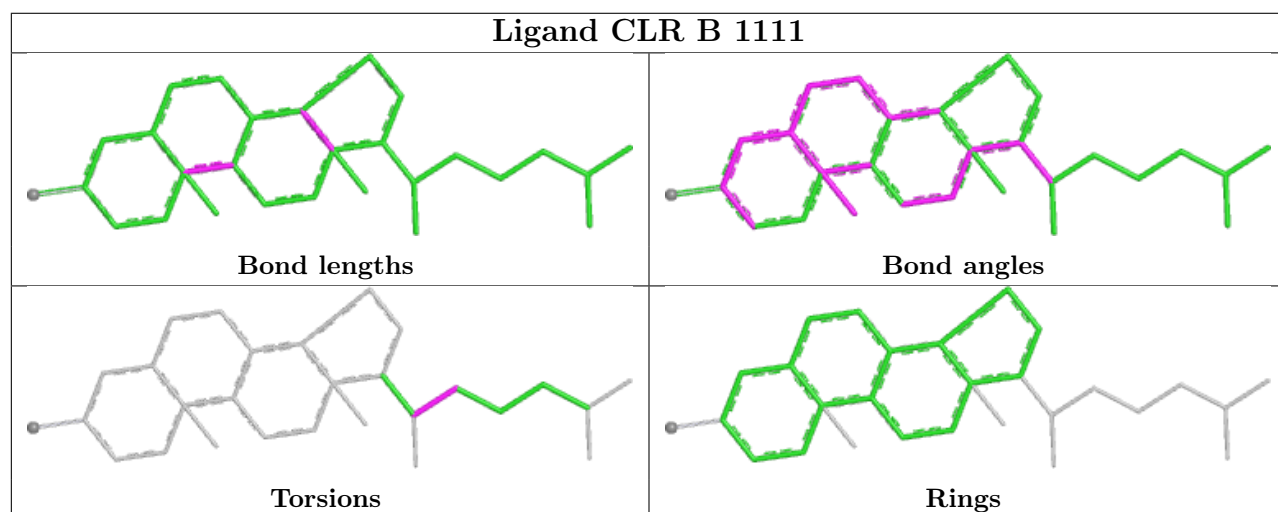
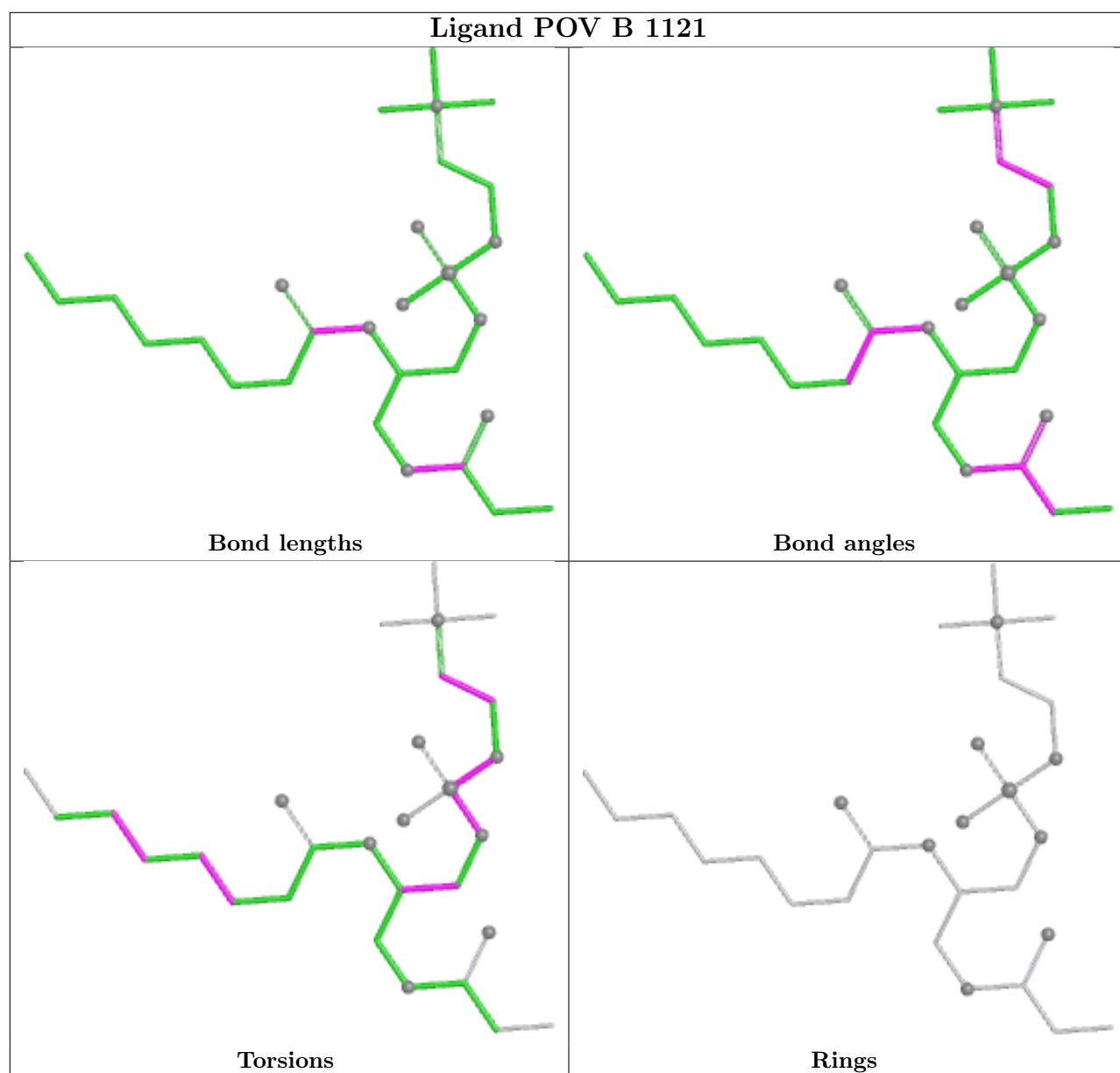
There are no ring outliers.

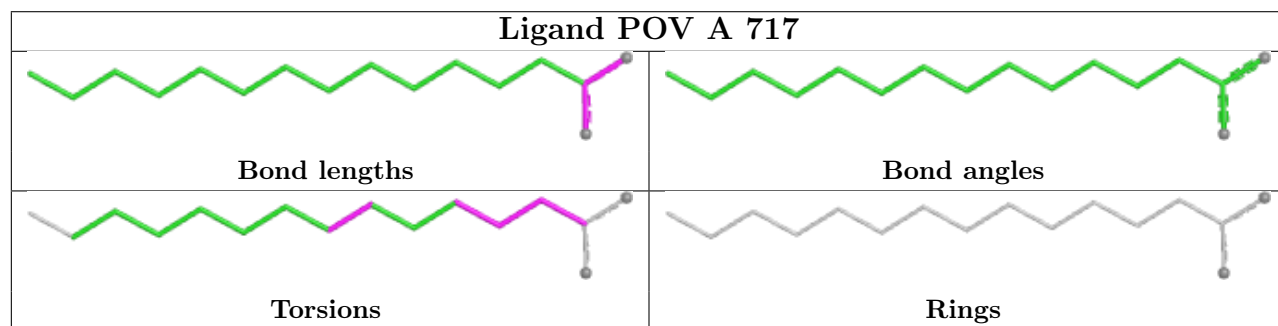
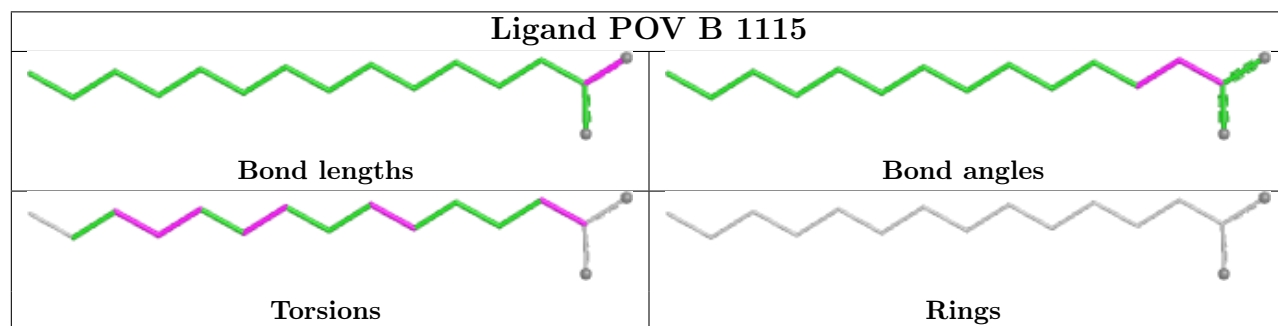
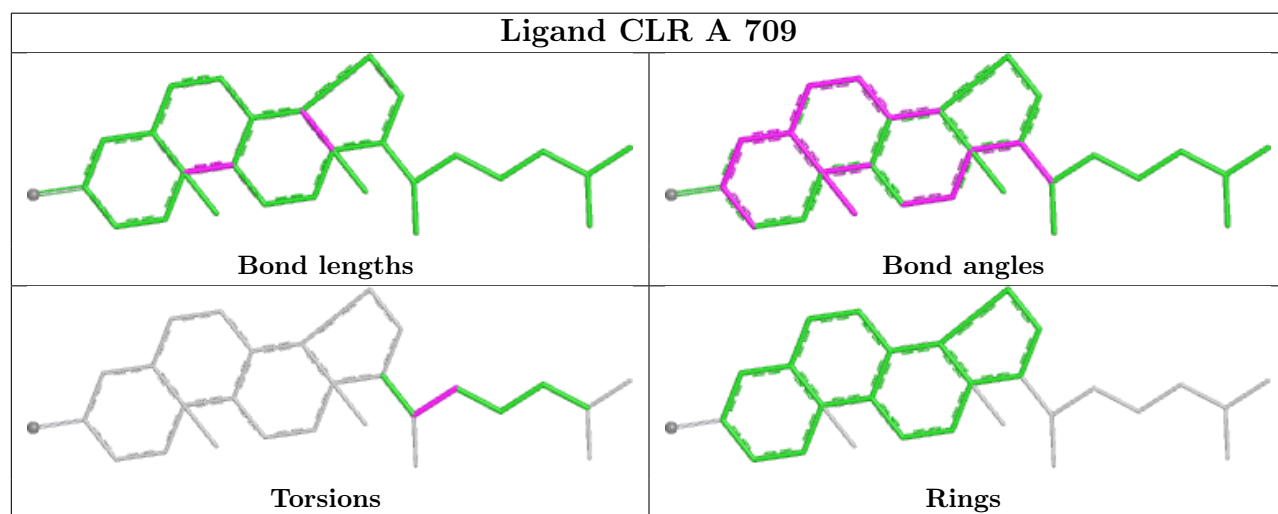
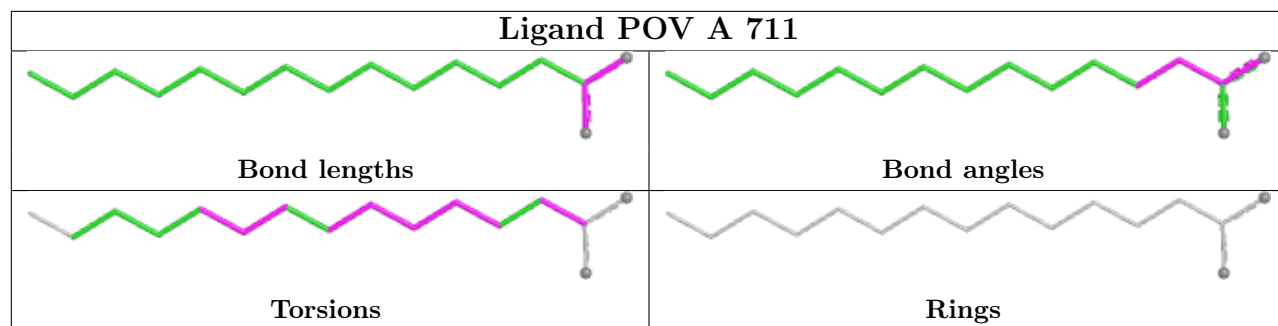
26 monomers are involved in 97 short contacts:

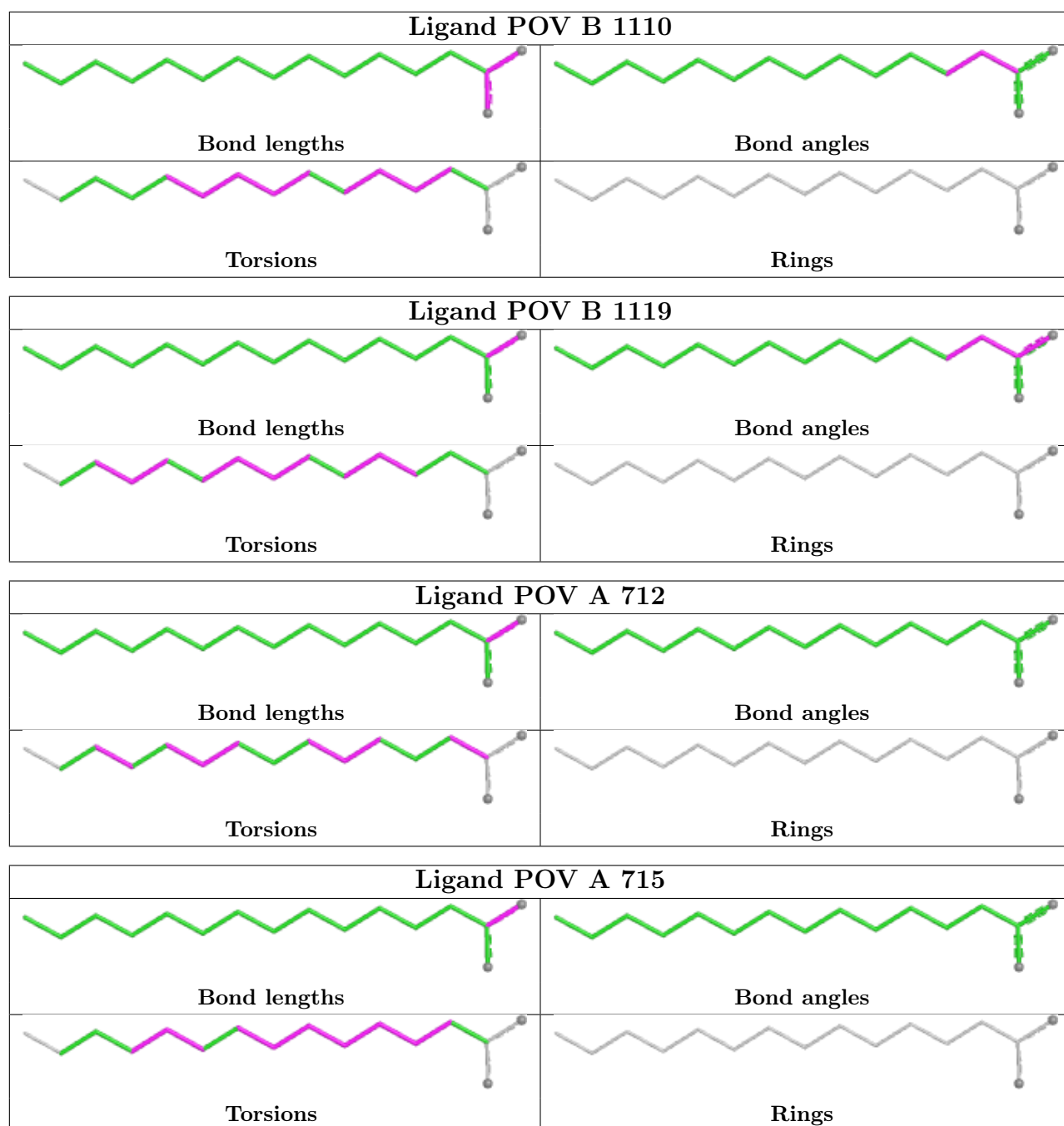
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	714	POV	8	0
4	B	1101	POV	2	0
4	A	707	POV	3	0
4	B	1121	POV	3	0
5	B	1111	CLR	1	0
5	A	709	CLR	1	0
4	B	1115	POV	1	0
4	B	1110	POV	1	0
2	B	1105	PO4	5	0
4	A	712	POV	3	0
4	A	710	POV	1	0
4	B	1114	POV	5	0
2	A	703	PO4	4	0
4	B	1109	POV	7	0
4	B	1116	POV	1	0
4	A	720	POV	7	0
2	B	1102	PO4	1	0
2	B	1104	PO4	2	0
4	B	1112	POV	2	0
4	A	706	POV	2	0
4	B	1120	POV	20	0
4	B	1118	POV	1	0
4	A	719	POV	15	0
4	A	721	POV	3	0
4	B	1113	POV	5	0
4	A	716	POV	7	0

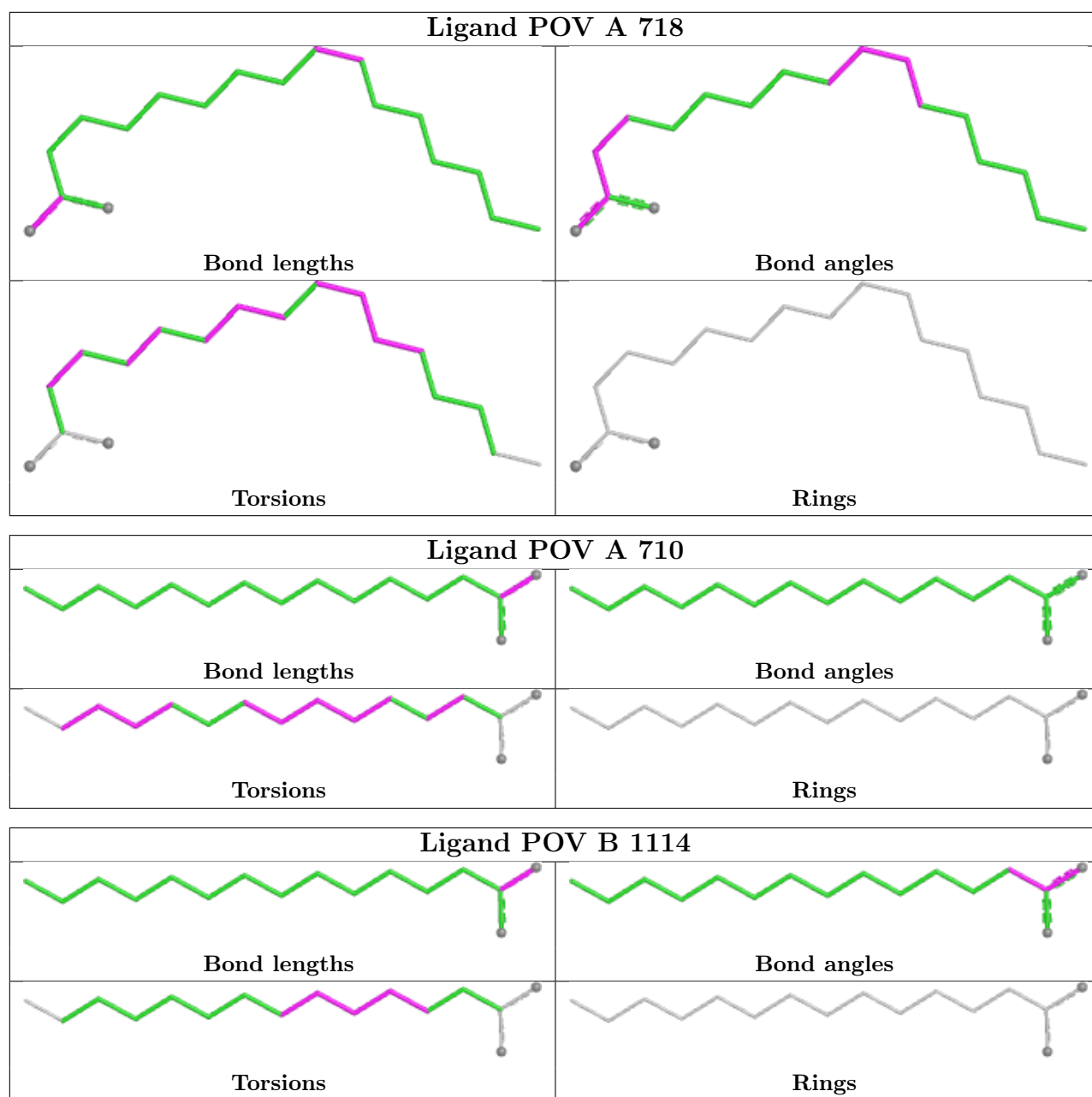
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

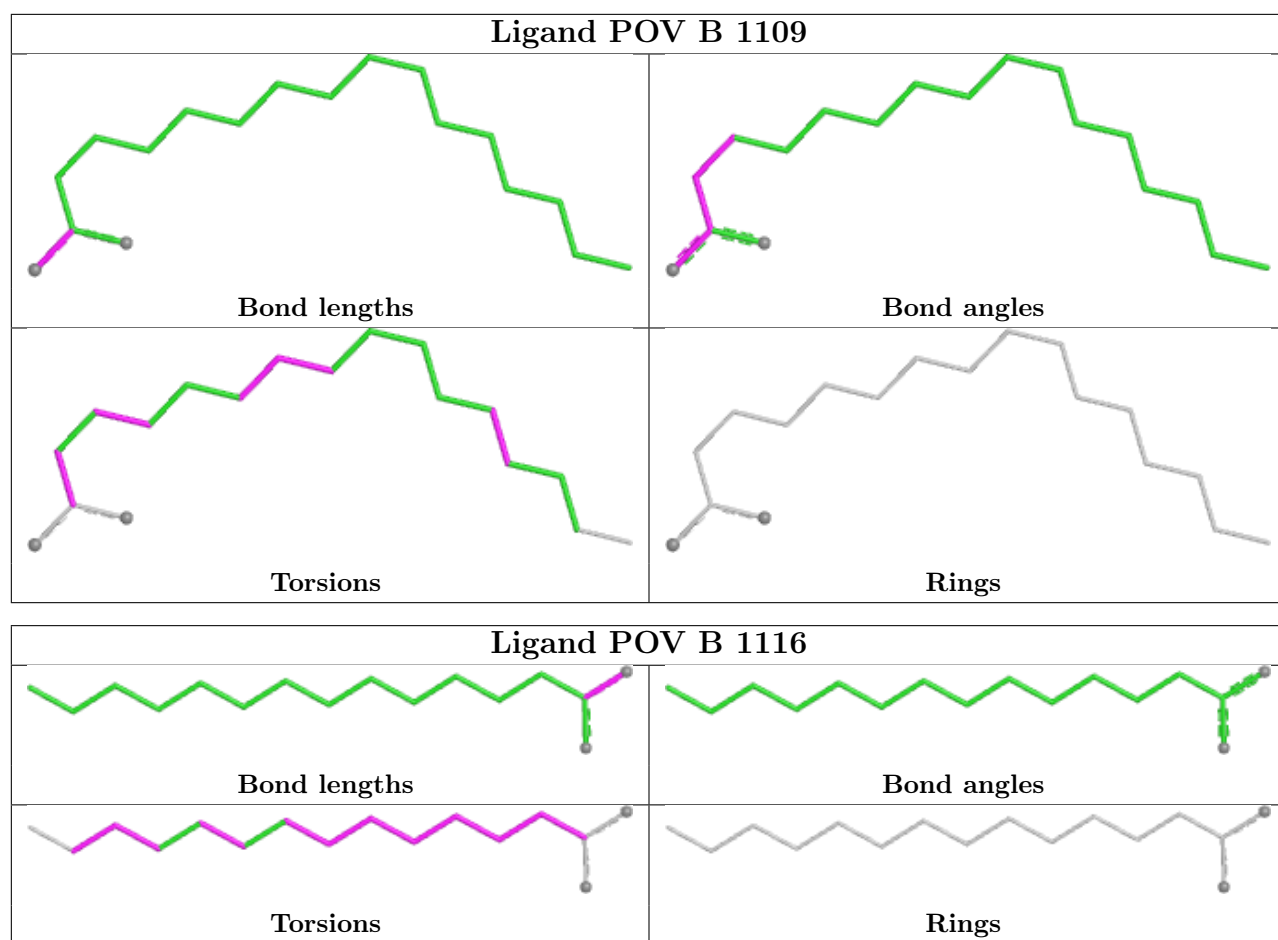


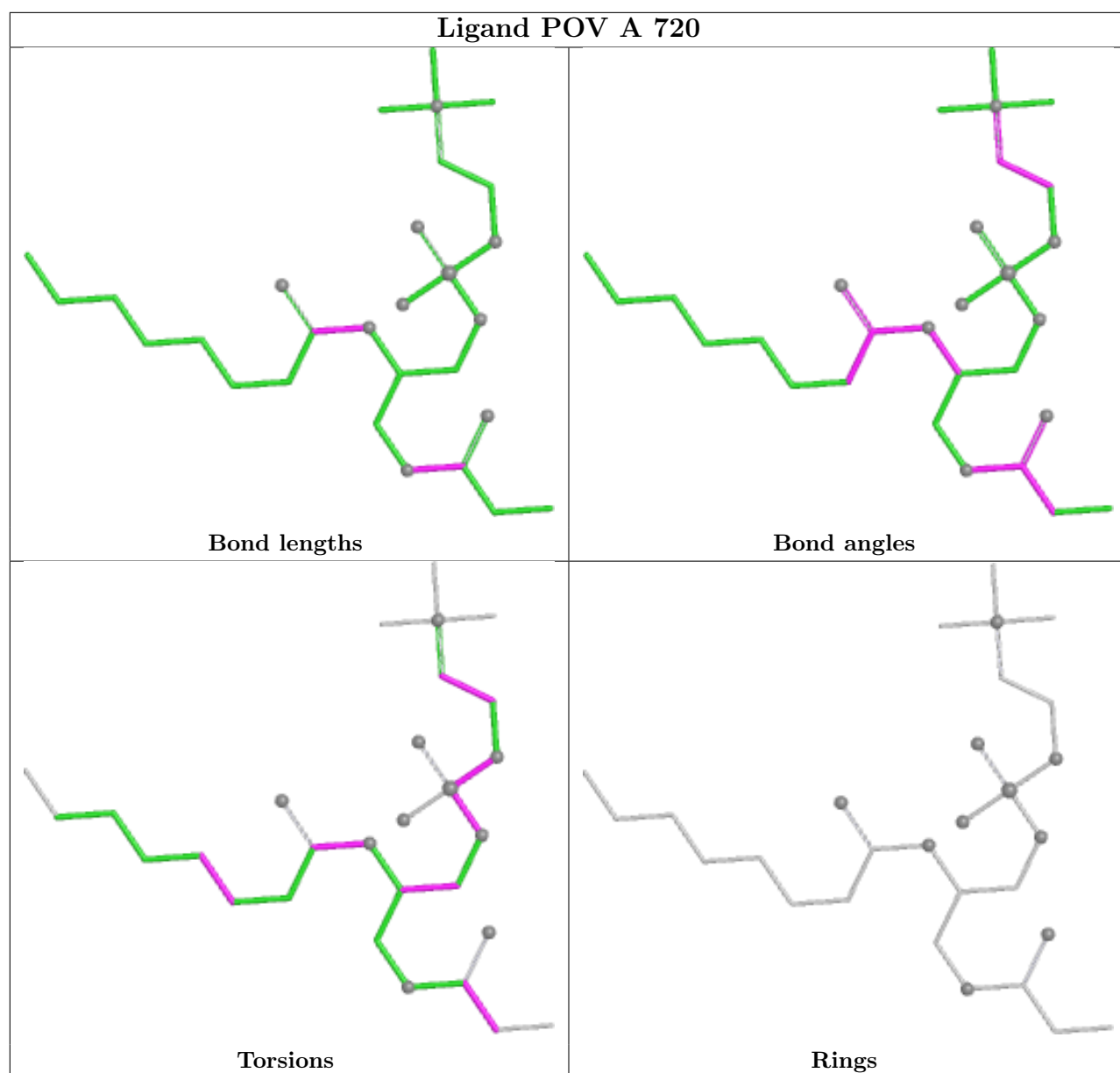


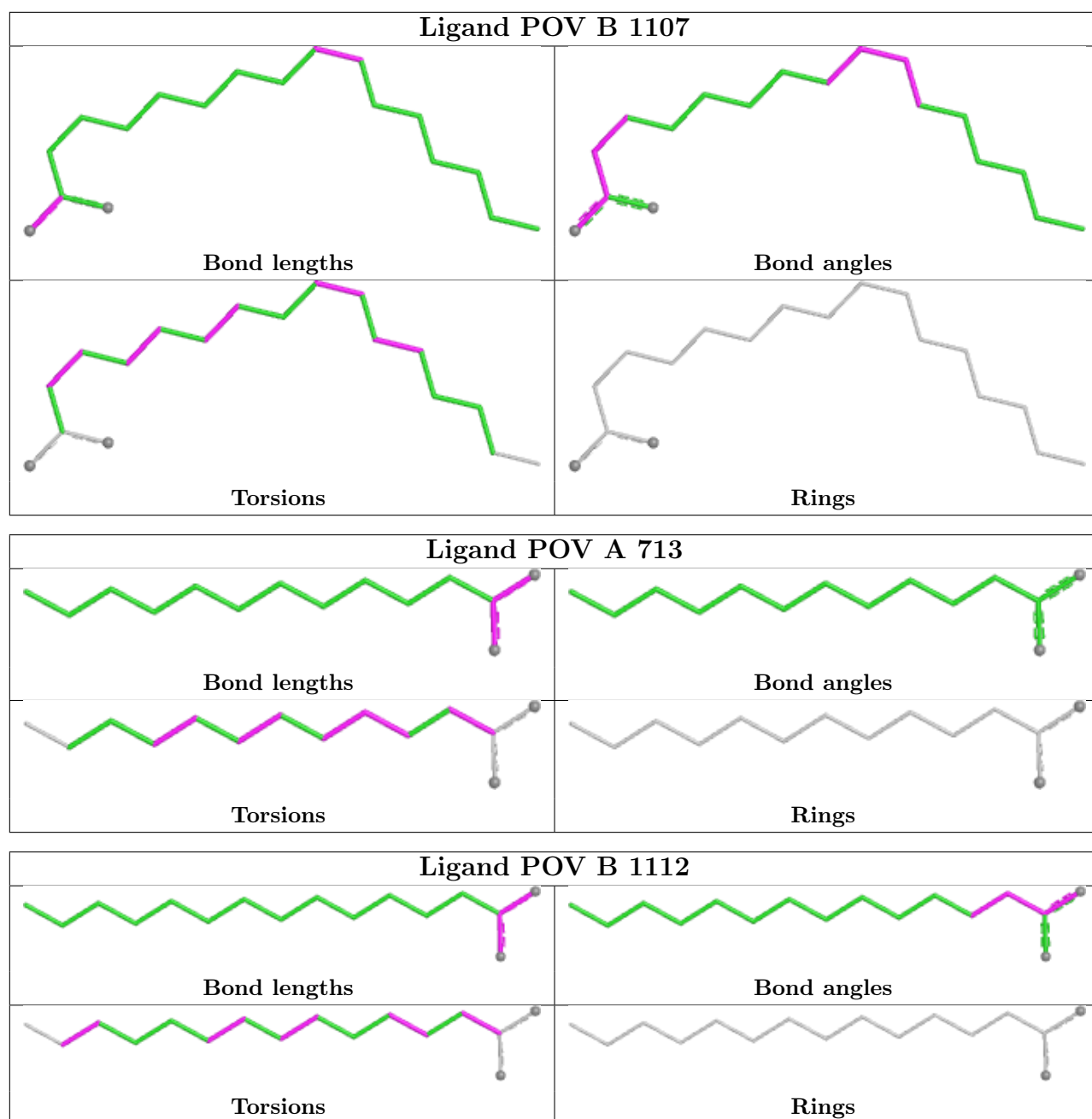


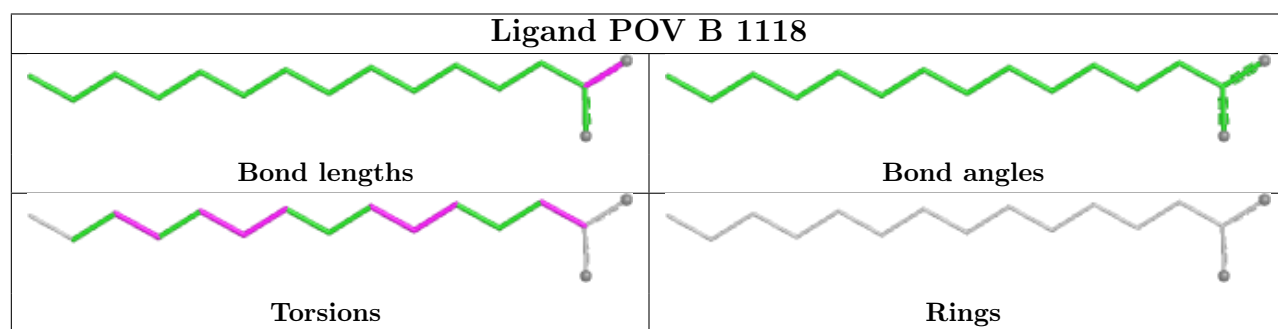
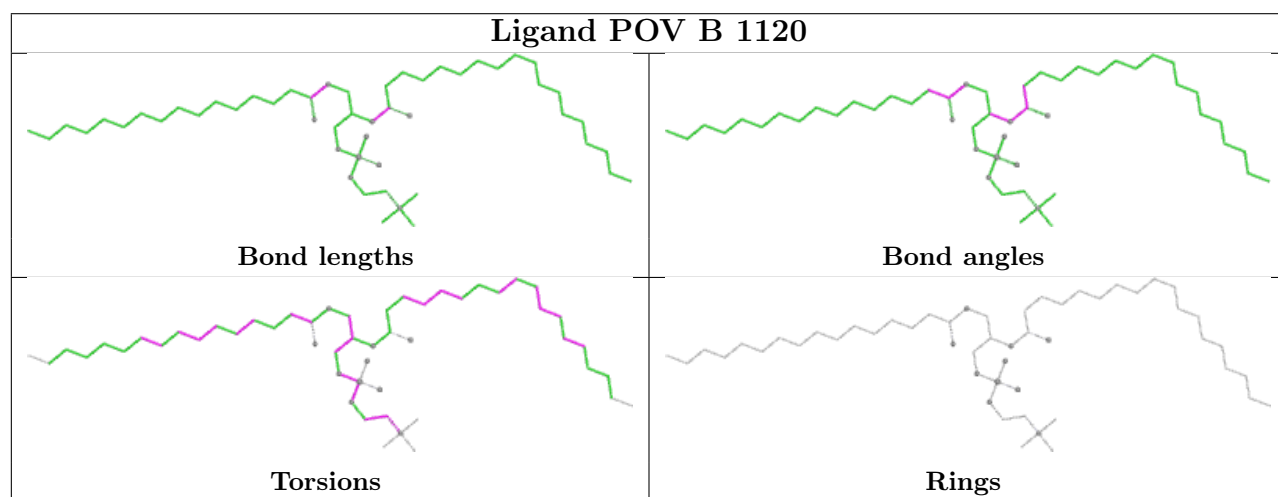
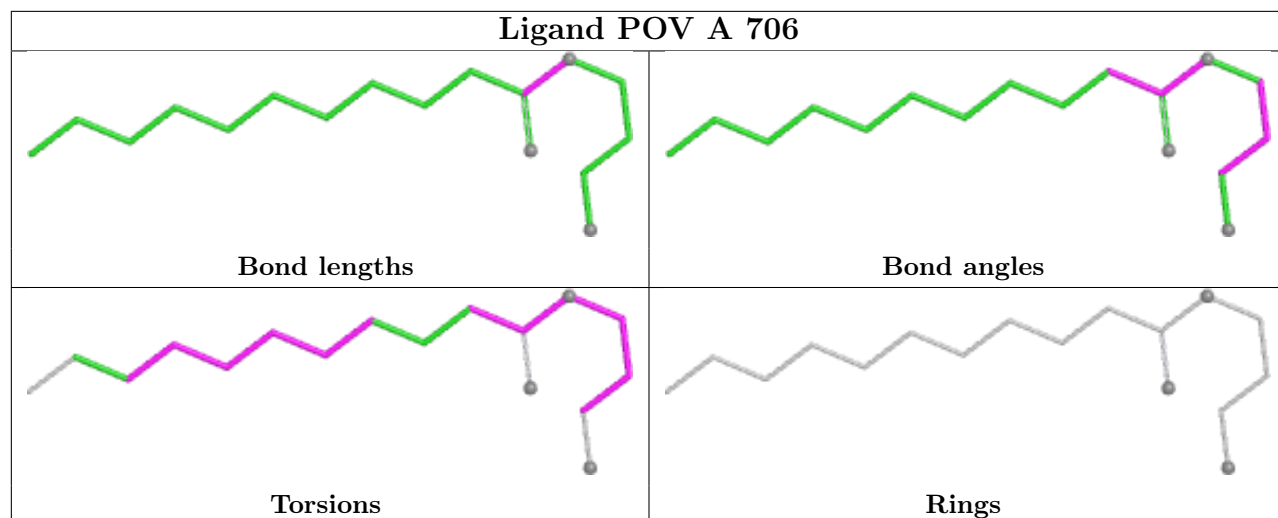


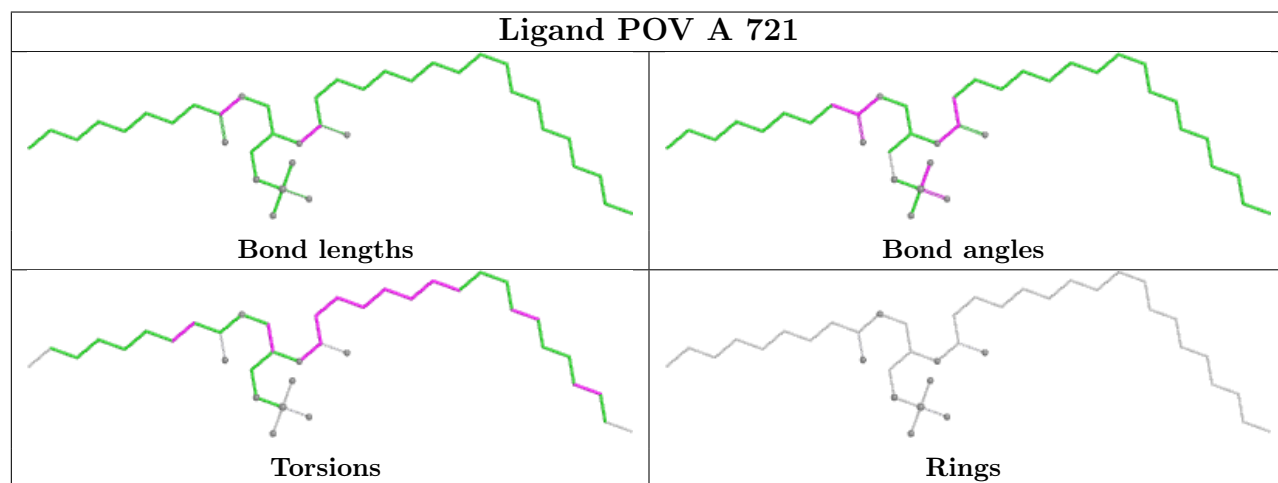
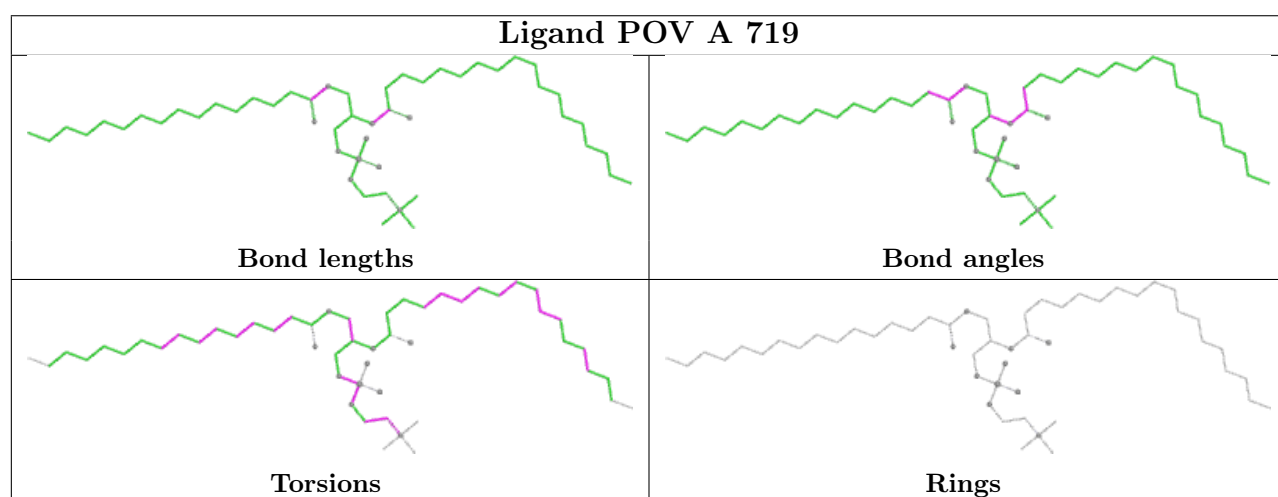
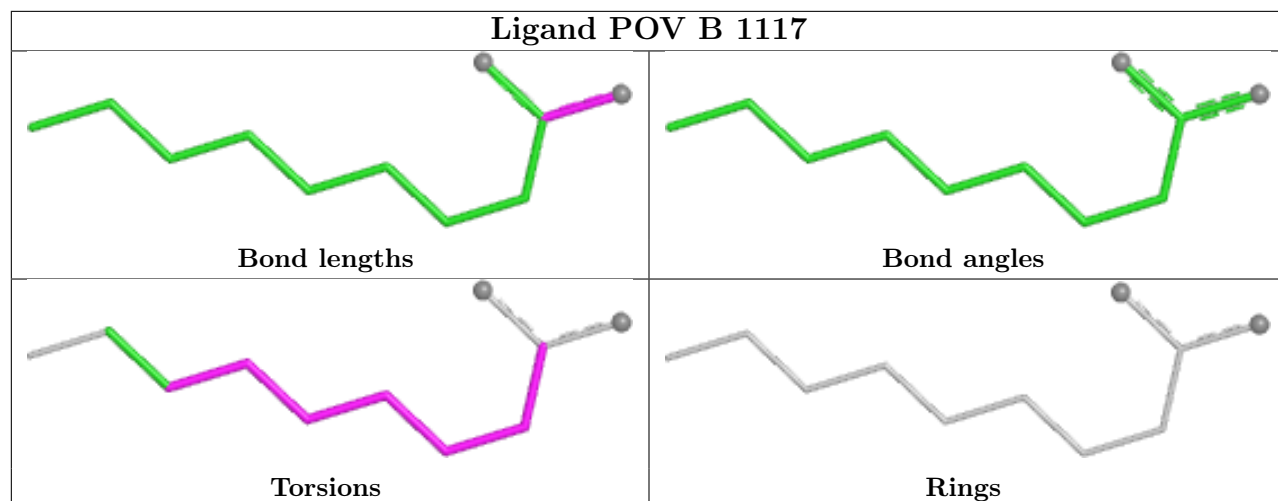


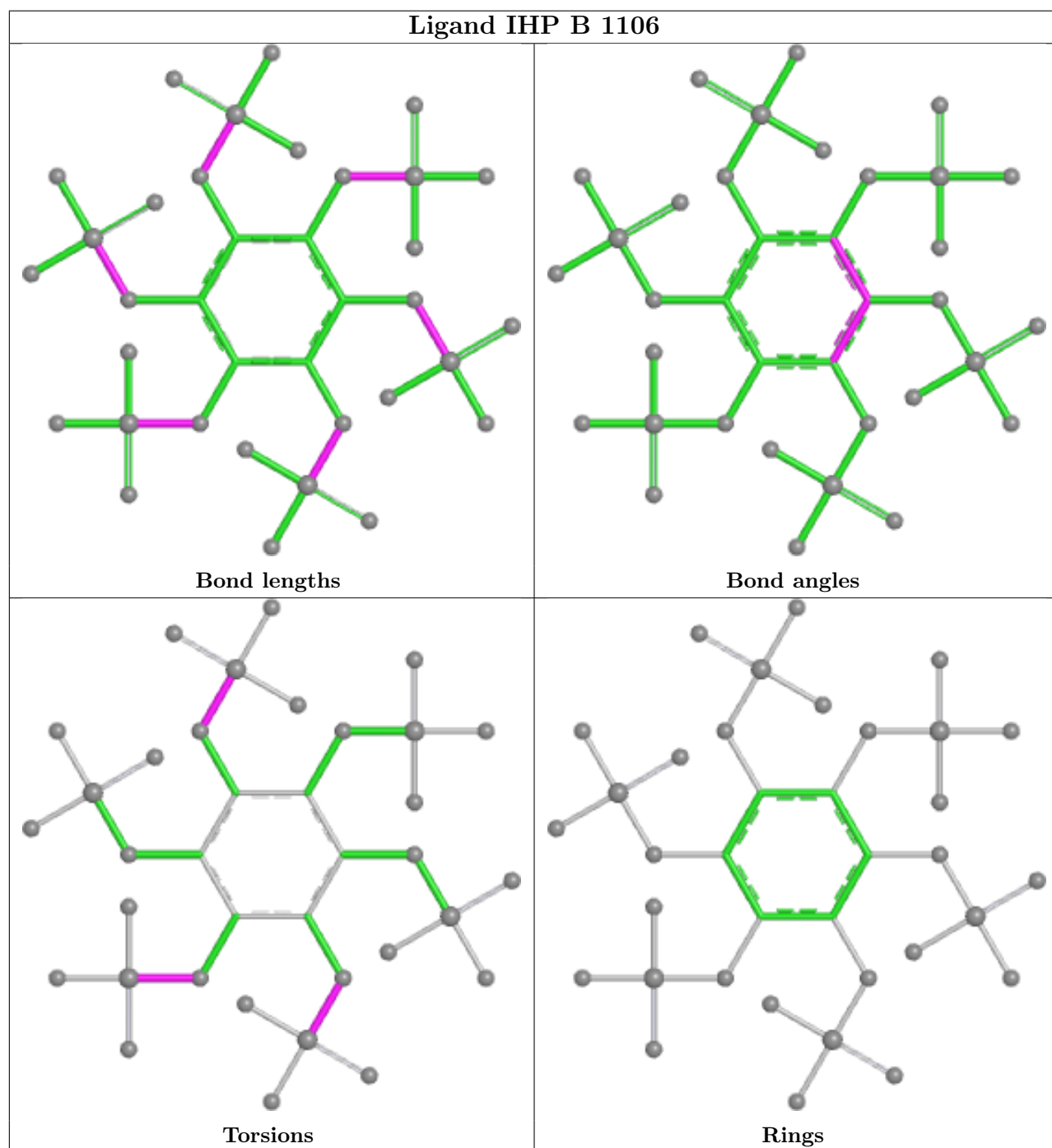
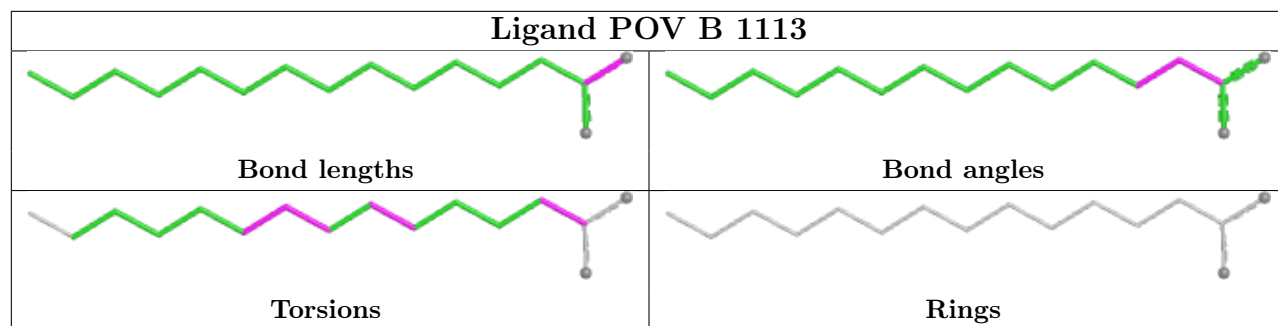


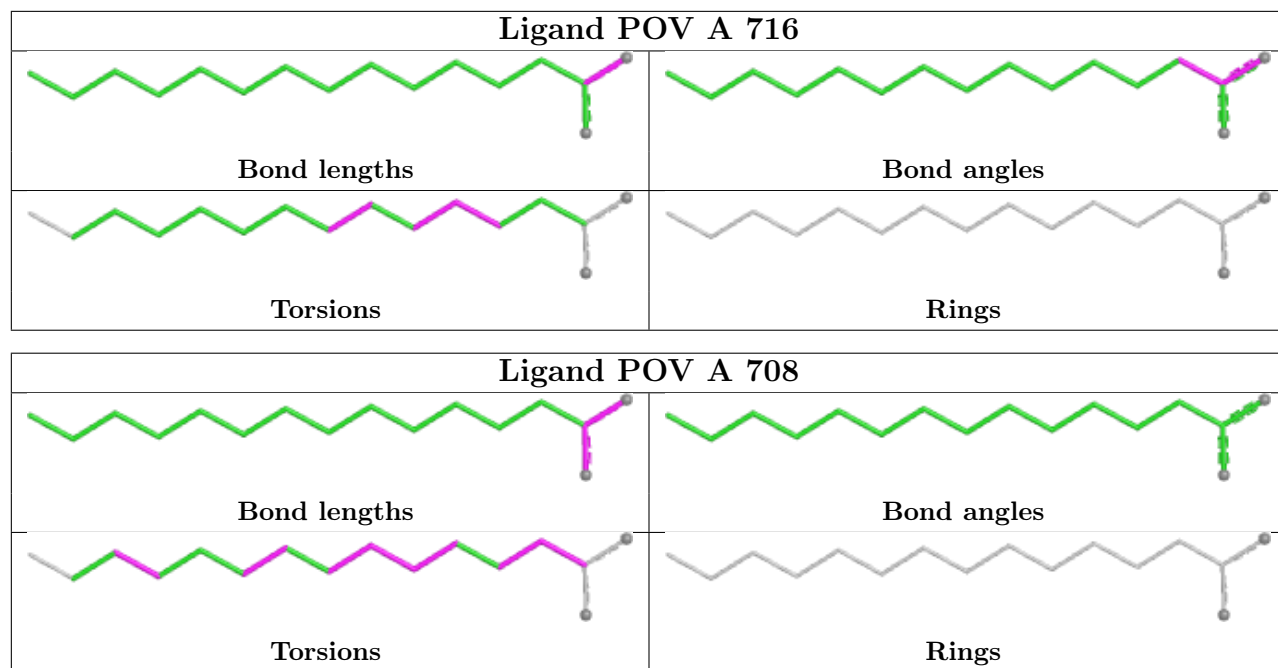




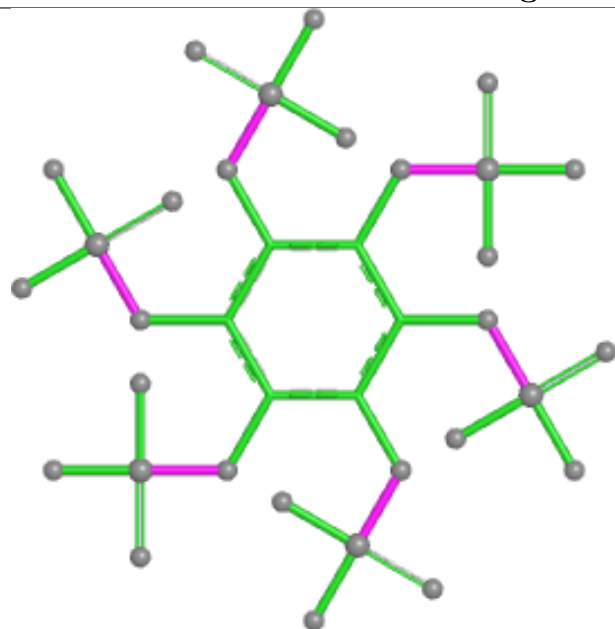




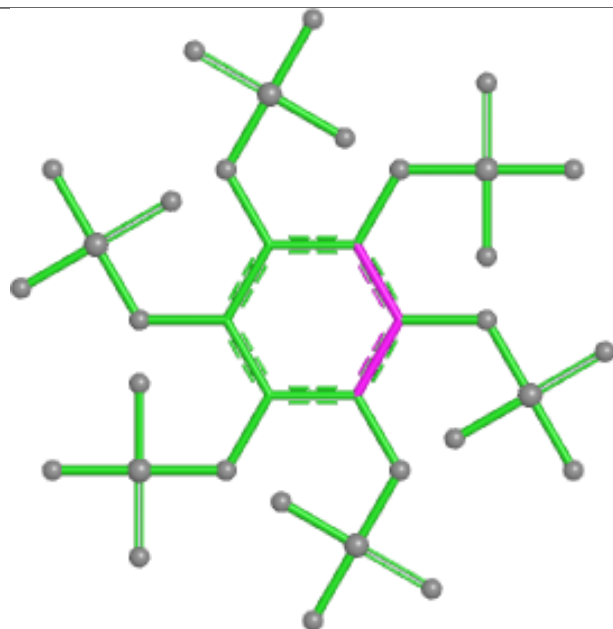




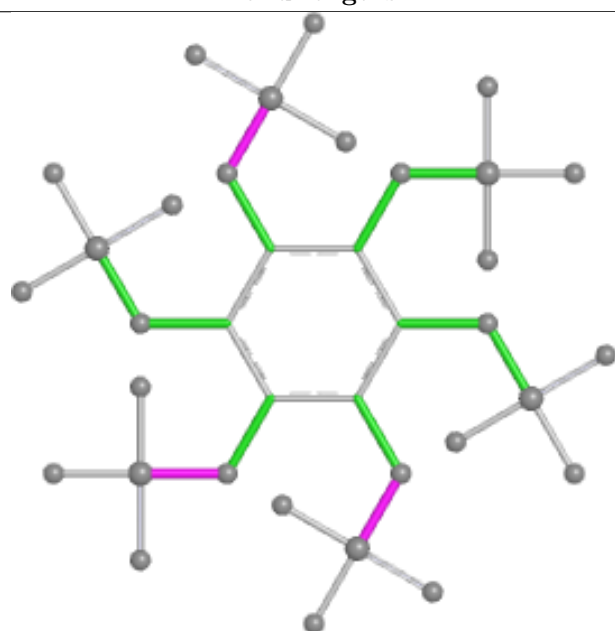
Ligand IHP A 705



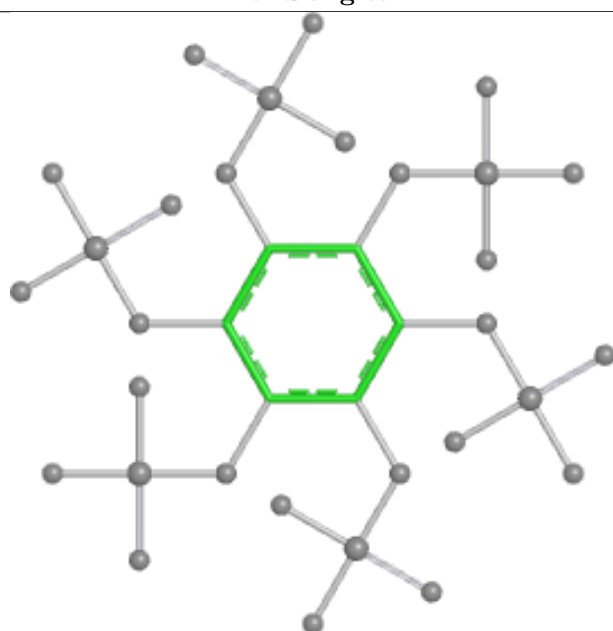
Bond lengths



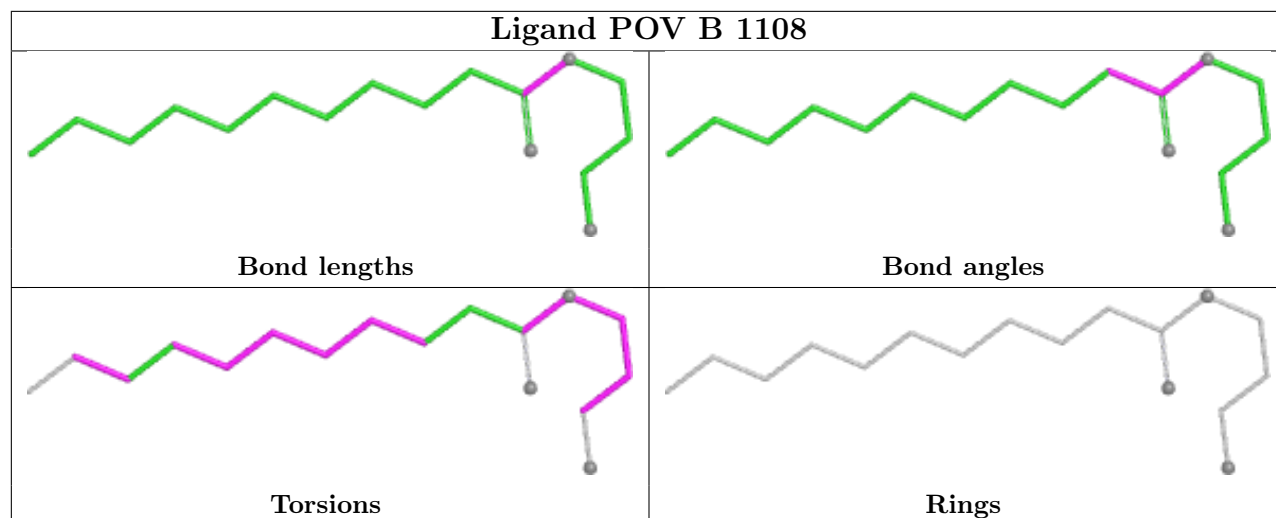
Bond angles



Torsions



Rings



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.

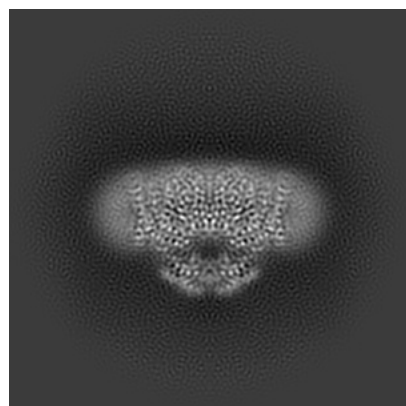
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38068. These allow visual inspection of the internal detail of the map and identification of artifacts.

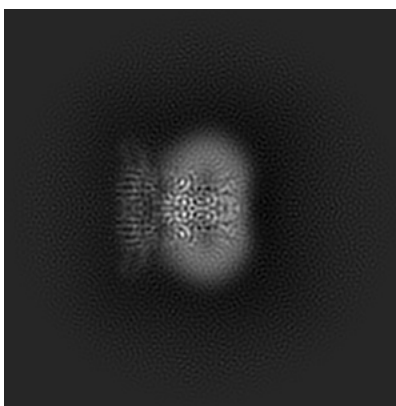
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

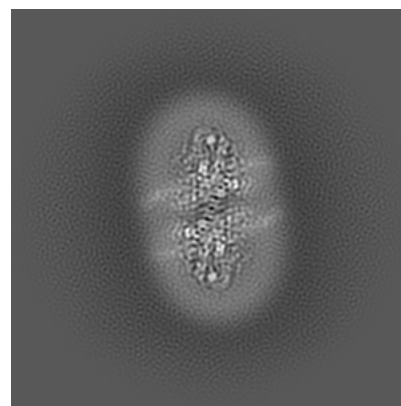
6.1.1 Primary map



X

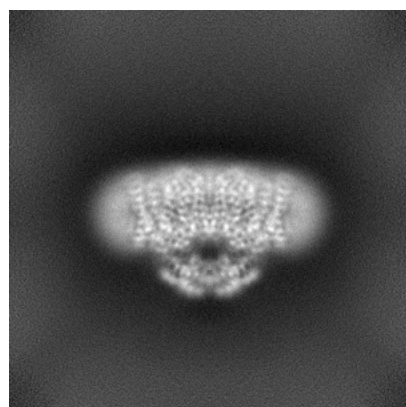


Y

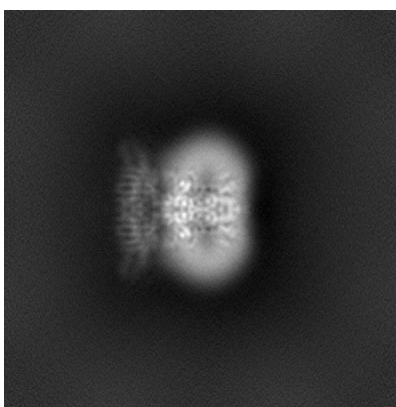


Z

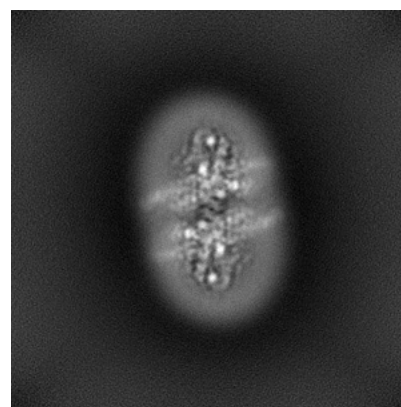
6.1.2 Raw map



X



Y

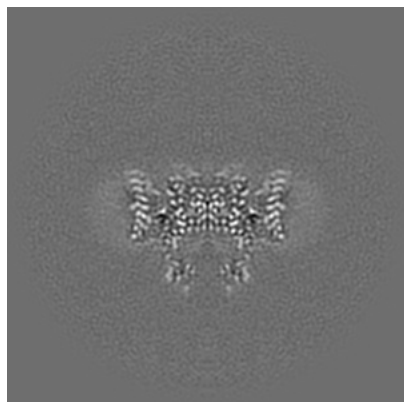


Z

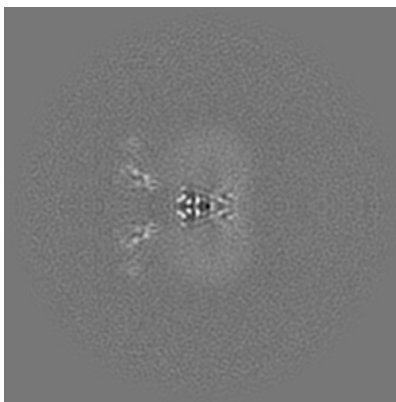
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

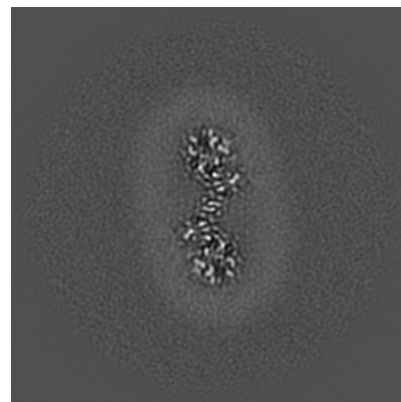
6.2.1 Primary map



X Index: 160

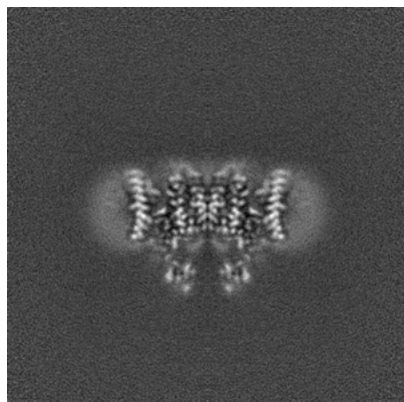


Y Index: 160

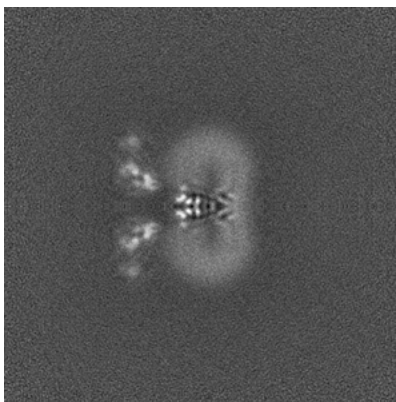


Z Index: 160

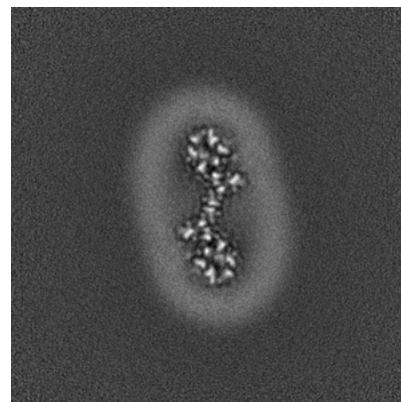
6.2.2 Raw map



X Index: 160



Y Index: 160

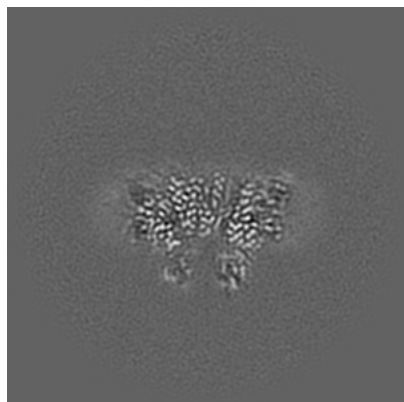


Z Index: 160

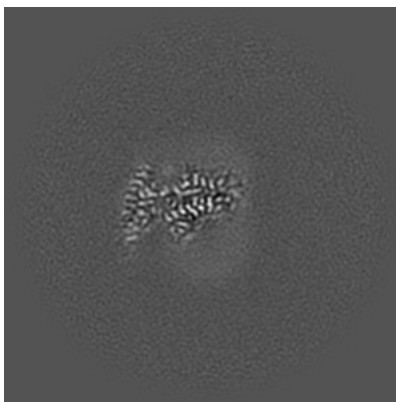
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

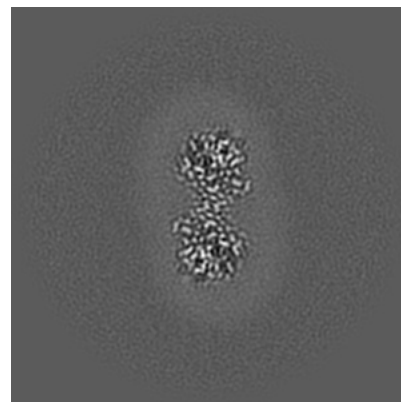
6.3.1 Primary map



X Index: 155

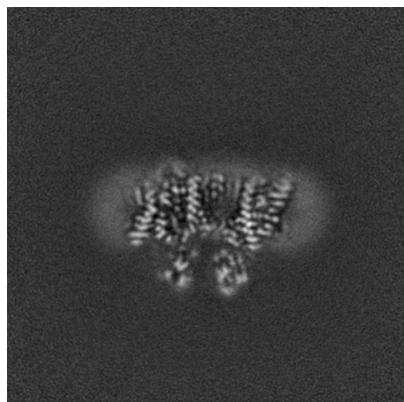


Y Index: 182

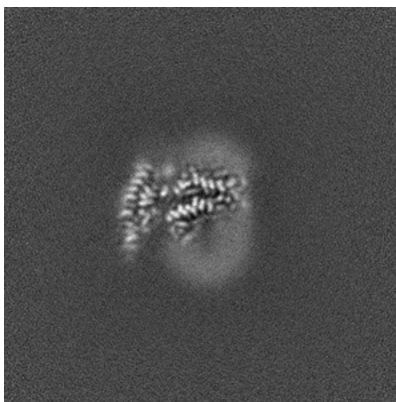


Z Index: 148

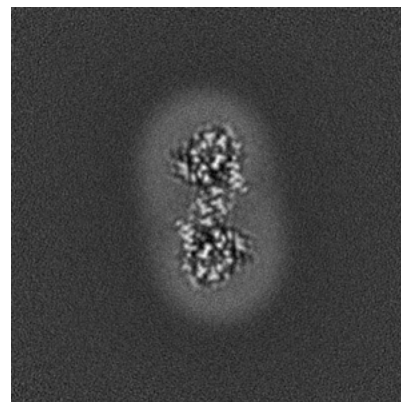
6.3.2 Raw map



X Index: 152



Y Index: 181

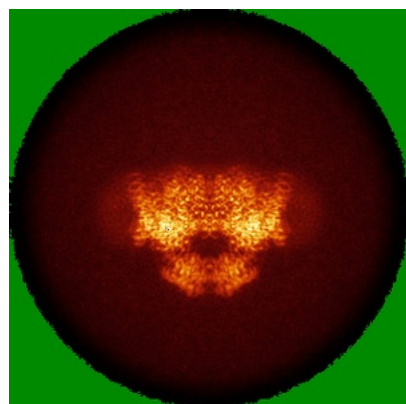


Z Index: 143

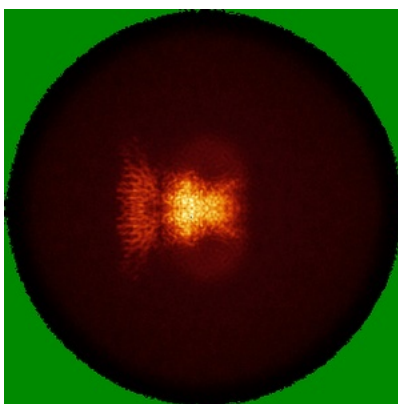
The images above show the largest variance slices of the map in three orthogonal directions.

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

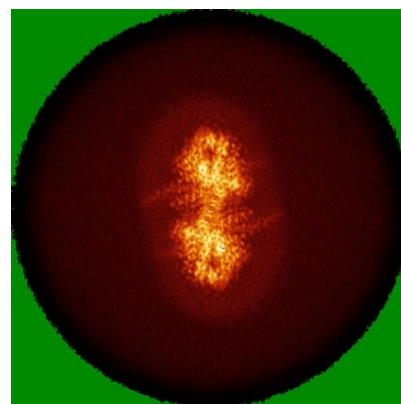
6.4.1 Primary map



X

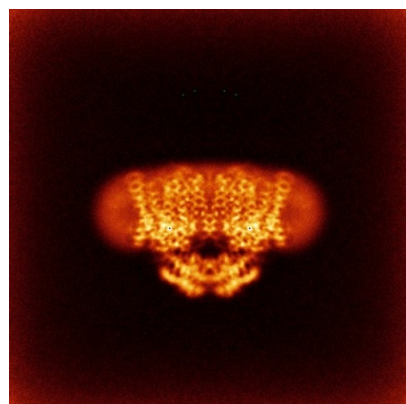


Y

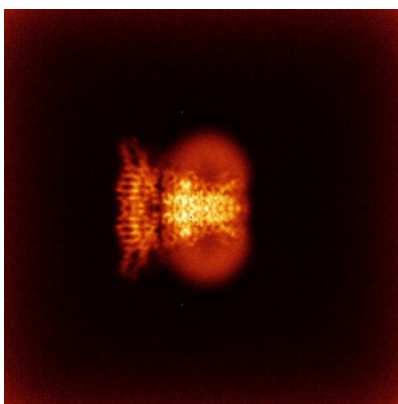


Z

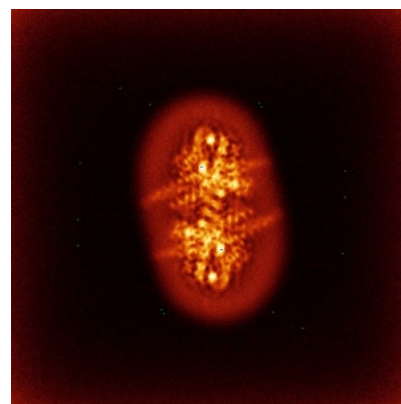
6.4.2 Raw map



X



Y

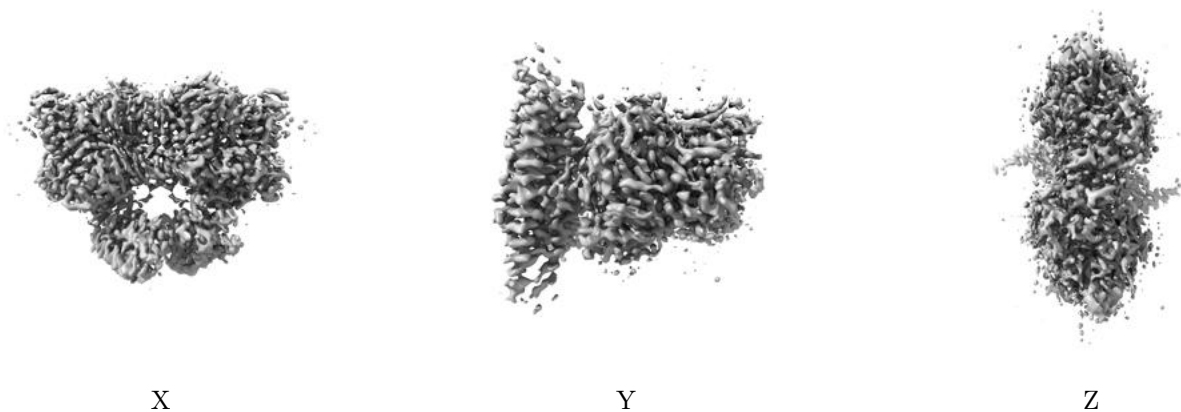


Z

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.

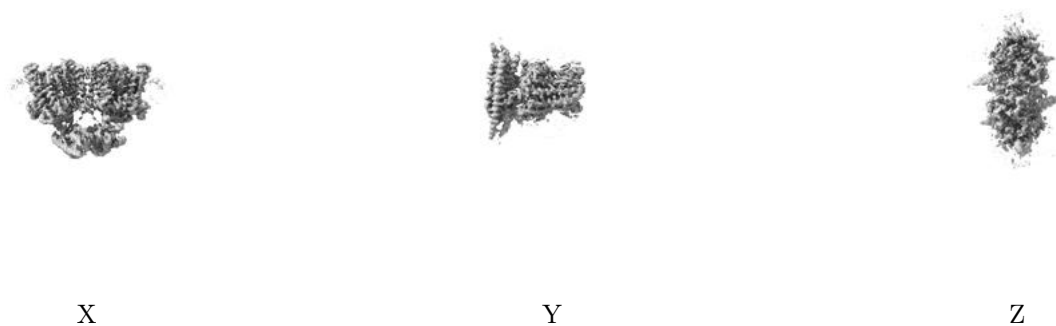
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.475. 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.

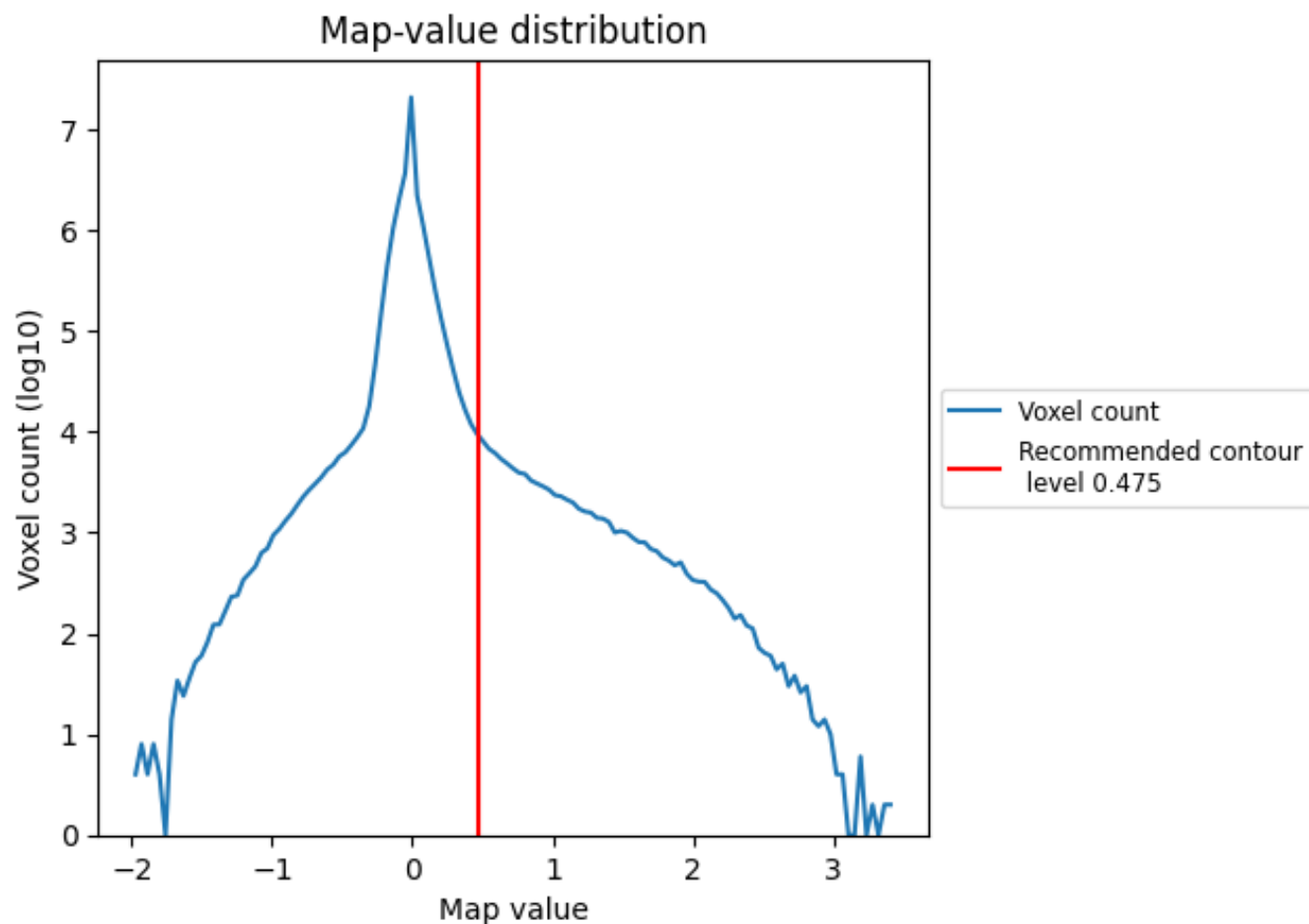
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

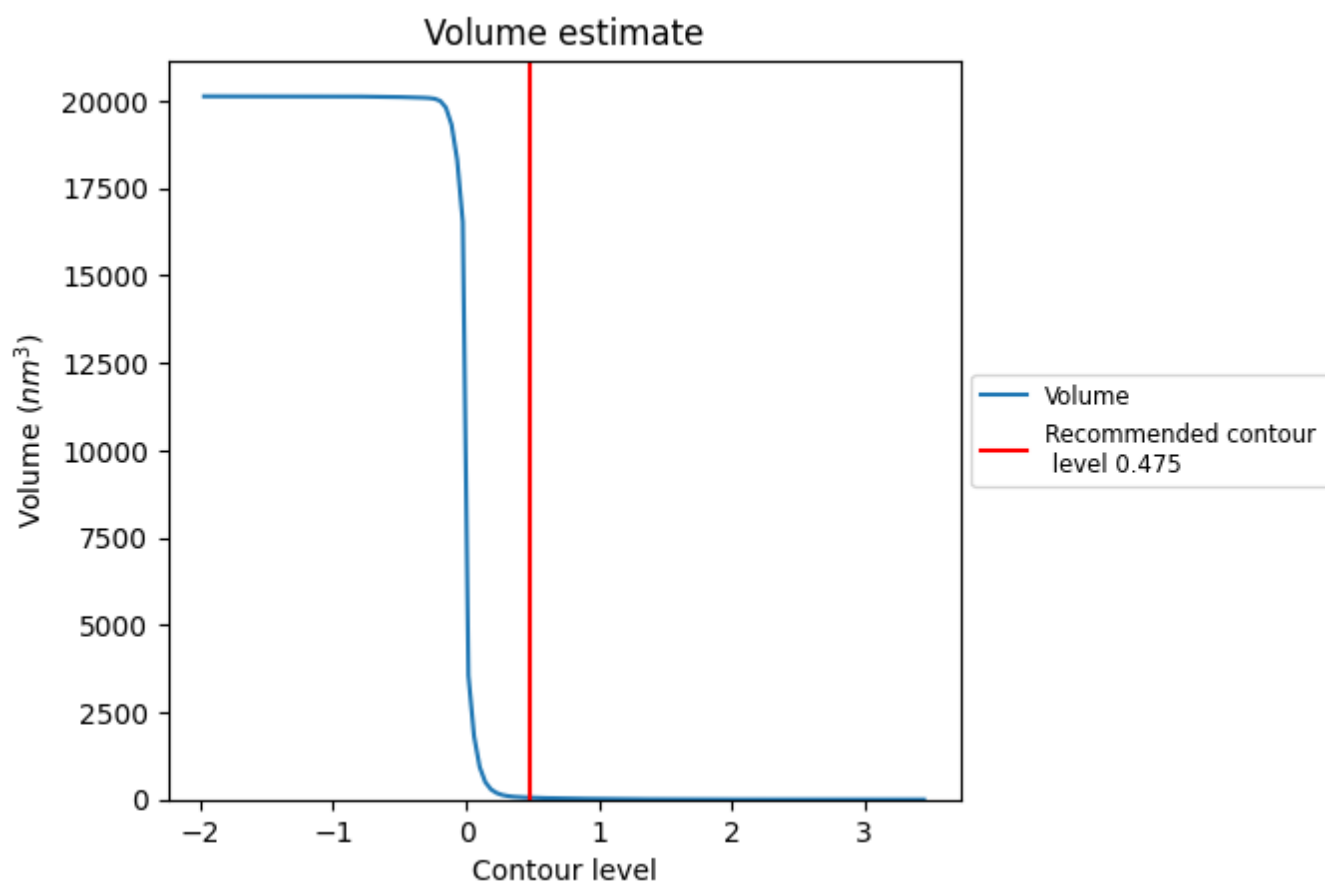
This section contains the results of statistical analysis of the map.

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.

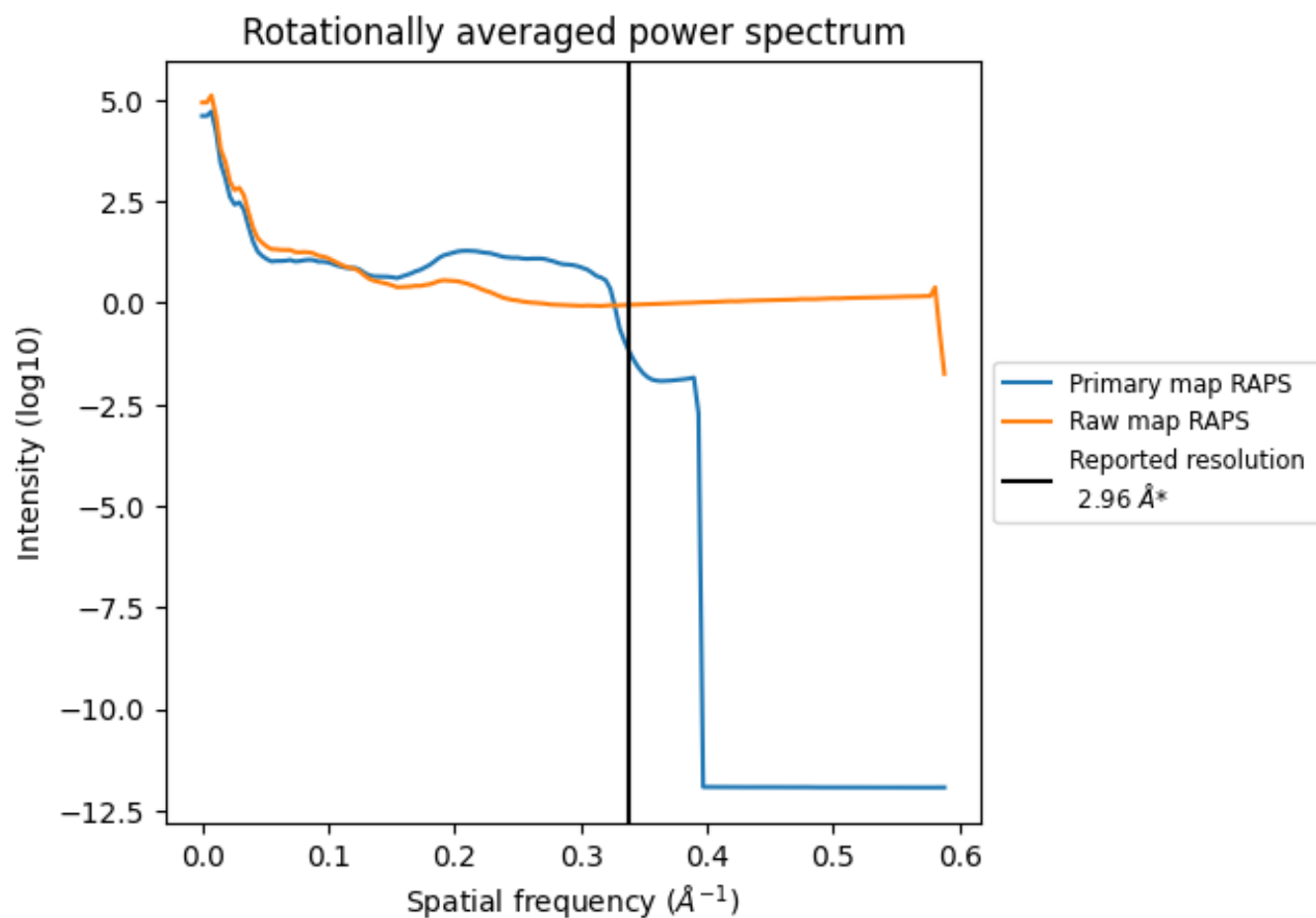
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 56 nm^3 ; this corresponds to an approximate mass of 51 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 ⓘ

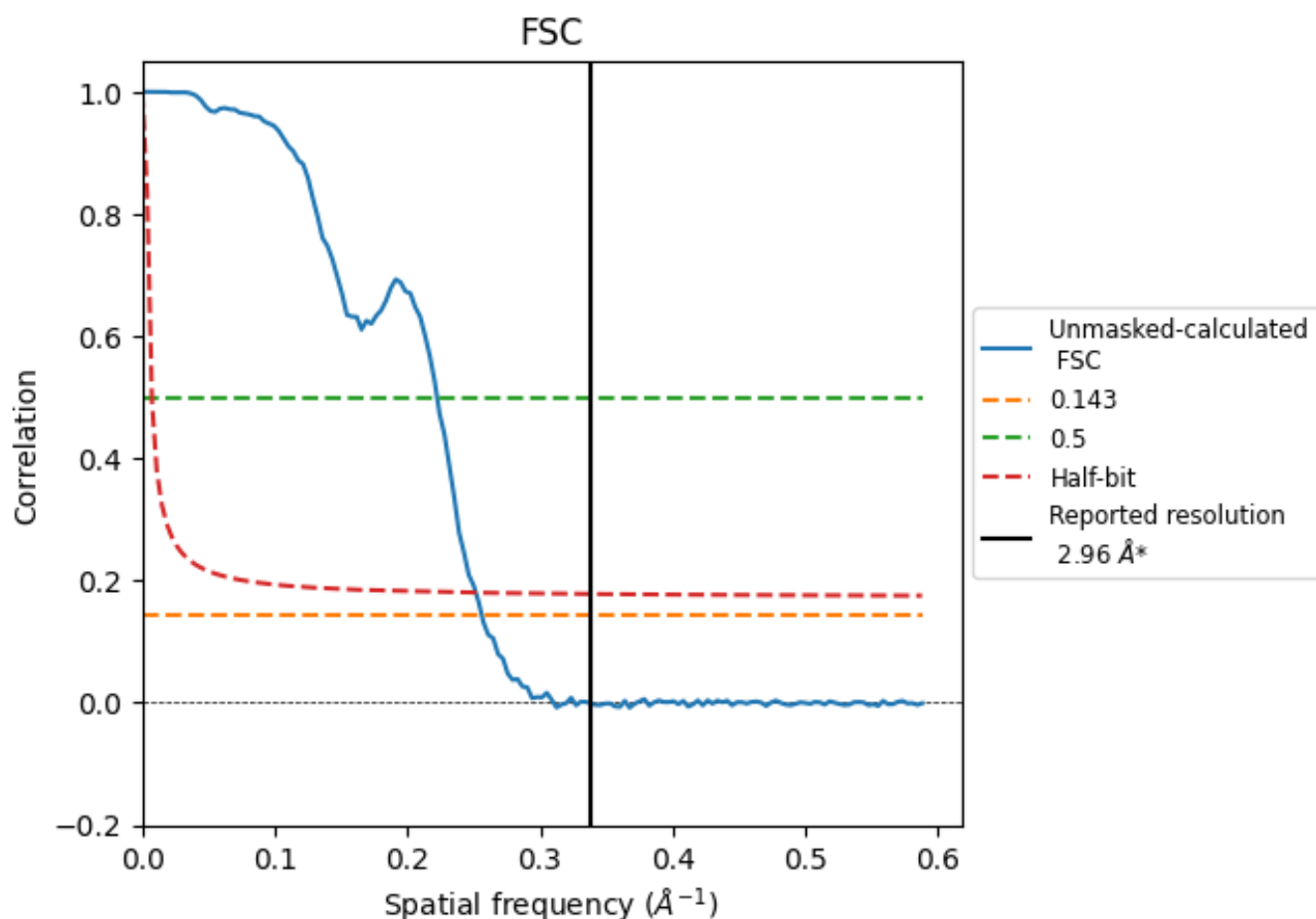


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

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 $0.338 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

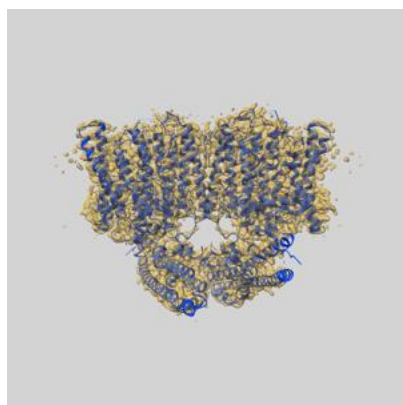
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.90	4.50	3.97

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

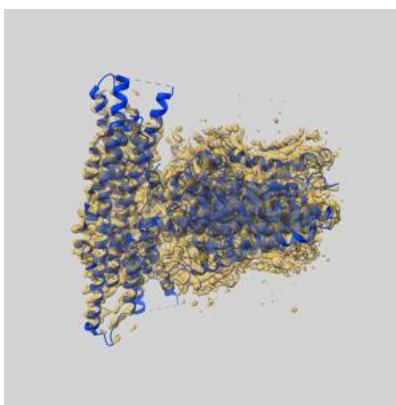
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38068 and PDB model 8X5F. Per-residue inclusion information can be found in section [3](#) on page [9](#).

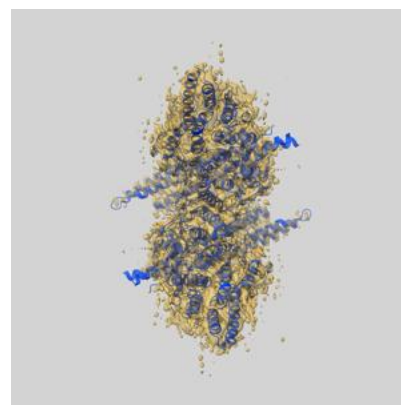
9.1 Map-model overlay [i](#)



X



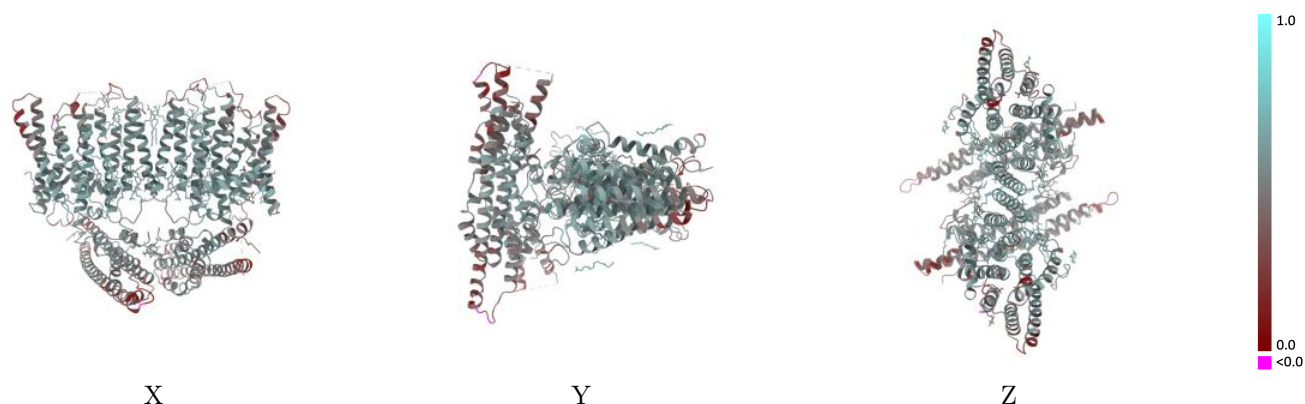
Y



Z

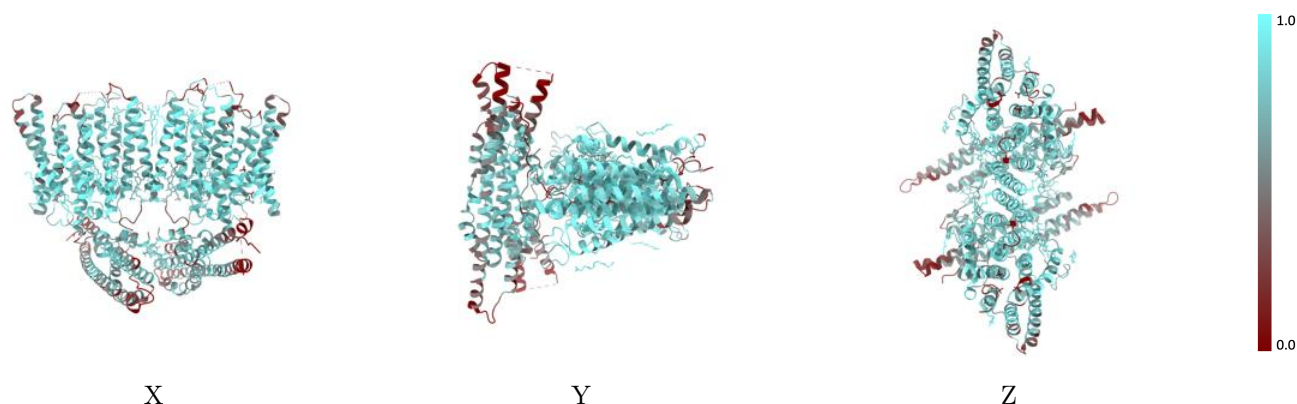
The images above show the 3D surface view of the map at the recommended contour level 0.475 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



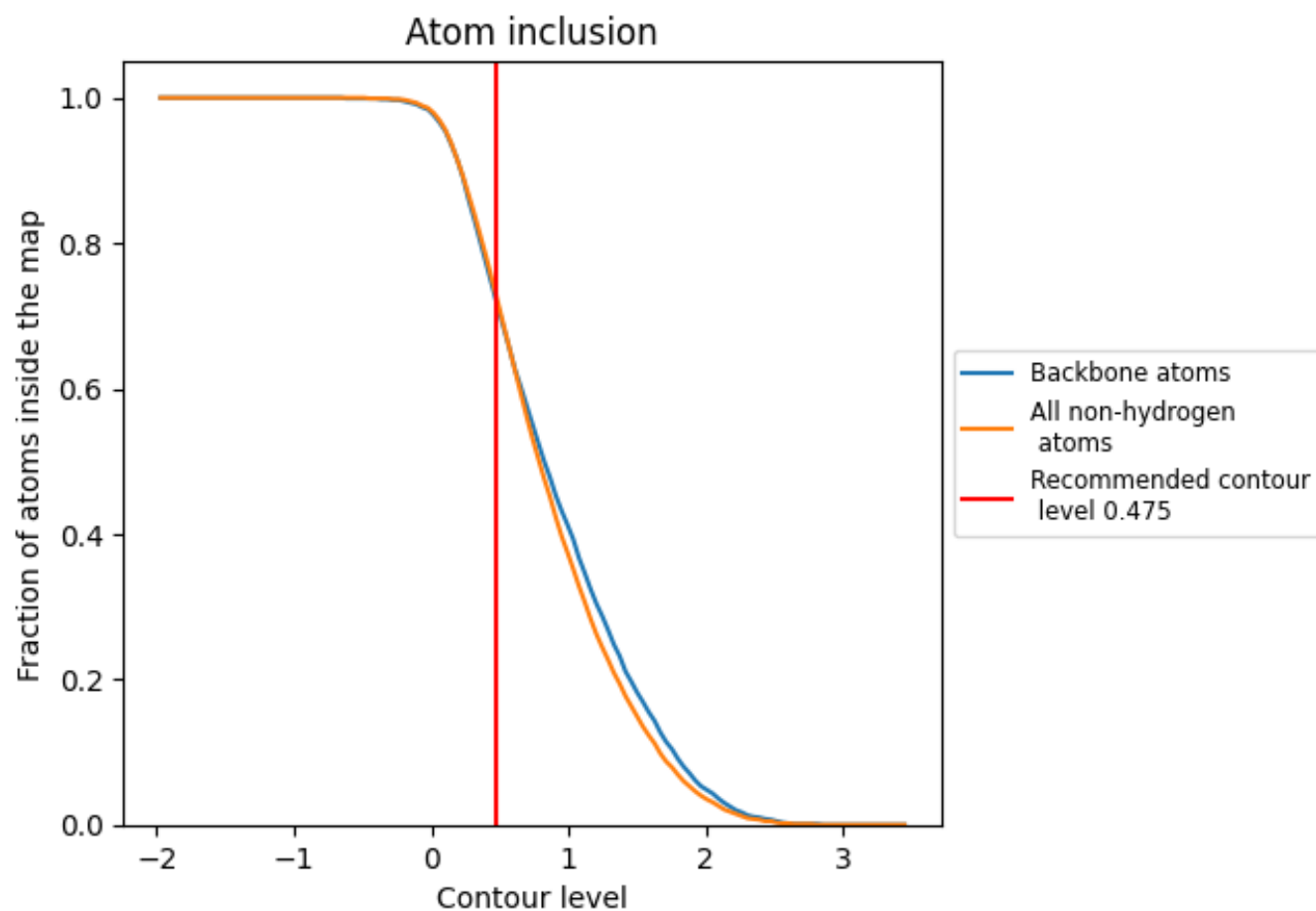
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.475).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 73% 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 (0.475) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7270	0.5110
A	0.7280	0.5090
B	0.7280	0.5130

