



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 01:10 AM UTC

PDB ID : 9LQW / pdb_00009lqw
EMDB ID : EMD-63307
Title : Cryo-EM structure of the JN241-9-bound state 1b of APLNR homodimer
Authors : Ji, S.; Wang, W.; Yang, Y.; Shen, Q.; Zhang, Y.
Deposited on : 2025-01-28
Resolution : 2.70 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

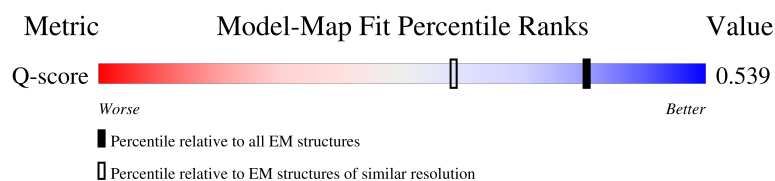
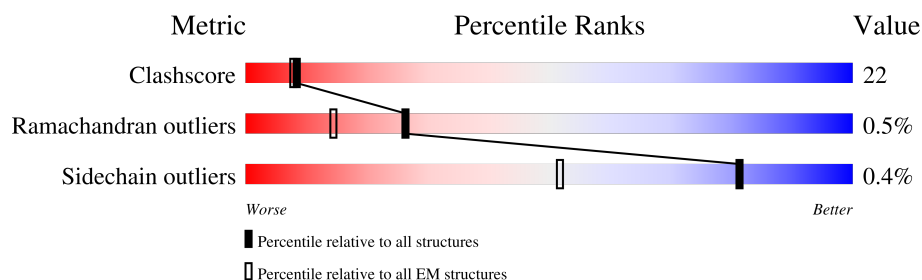
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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	10327 (2.20 - 3.20)

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	380	
1	B	380	
2	C	130	
2	D	130	

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
4	CLR	A	407	-	-	X	-
4	CLR	A	408	-	-	X	-
4	CLR	B	403	-	-	X	-
4	CLR	B	404	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6770 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.

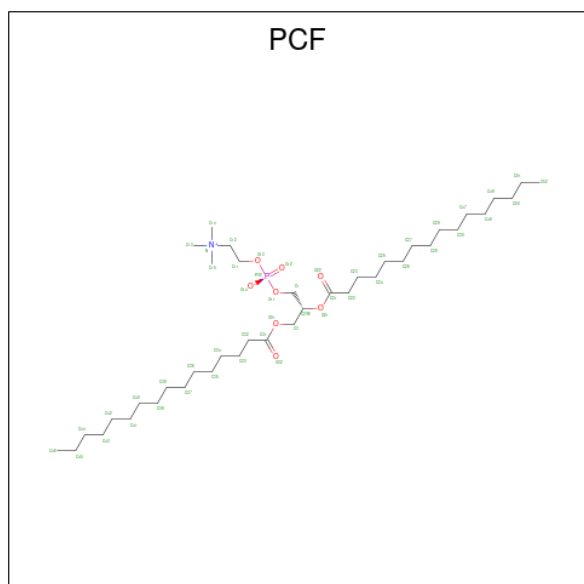
- Molecule 1 is a protein called Apelin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	271	Total	C	N	O	S	0	0
			2157	1442	332	362	21		
1	B	271	Total	C	N	O	S	0	0
			2157	1442	332	362	21		

- Molecule 2 is a protein called JN241-9.

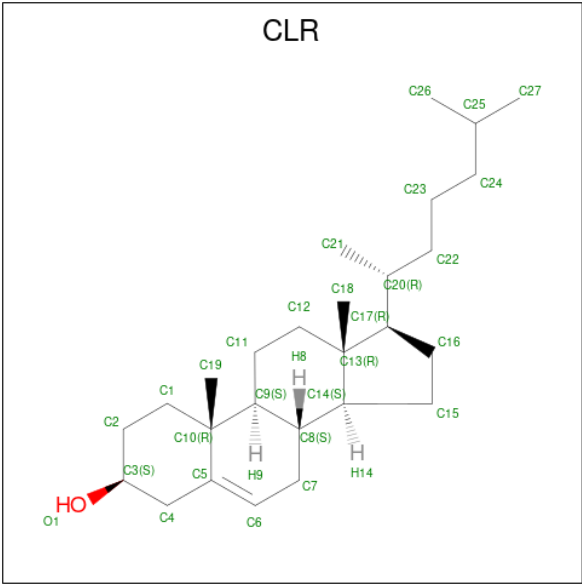
Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	129	Total	C	N	O	S	0	0
			954	585	167	193	9		
2	D	129	Total	C	N	O	S	0	0
			954	585	167	193	9		

- Molecule 3 is 1,2-DIACYL-SN-GLYCERO-3-PHOSHOCHOLINE (CCD ID: PCF) (formula: $C_{40}H_{80}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			50	40	1	8	1	
3	B	1	Total	C	N	O	P	0
			50	40	1	8	1	

- Molecule 4 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



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

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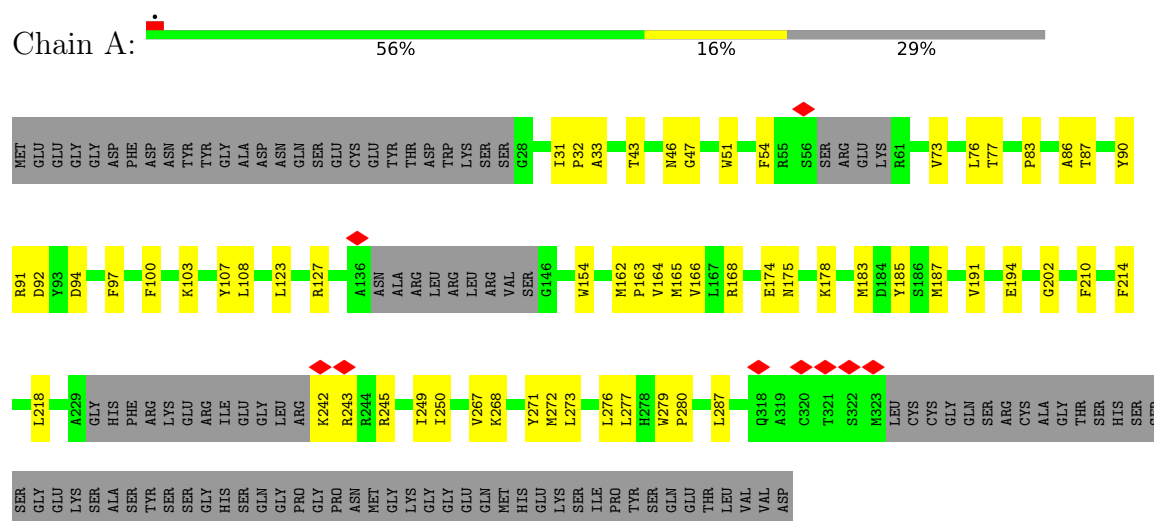
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Mol	Chain	Residues	Atoms			AltConf
4	B	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	

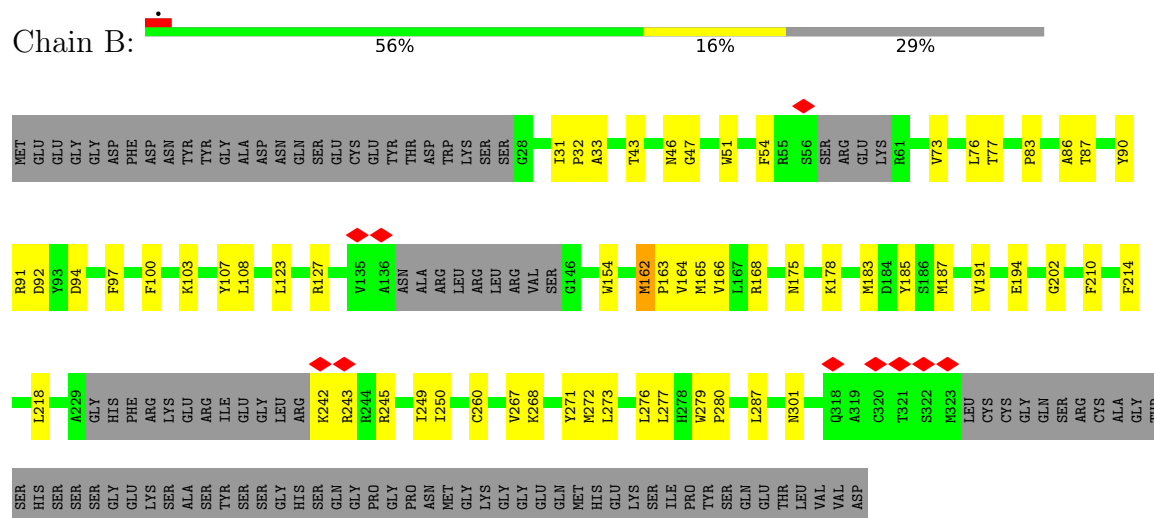
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

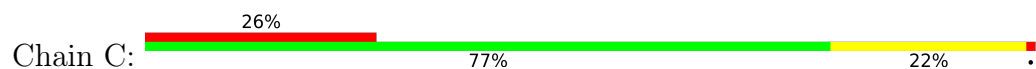
• Molecule 1: Apelin receptor

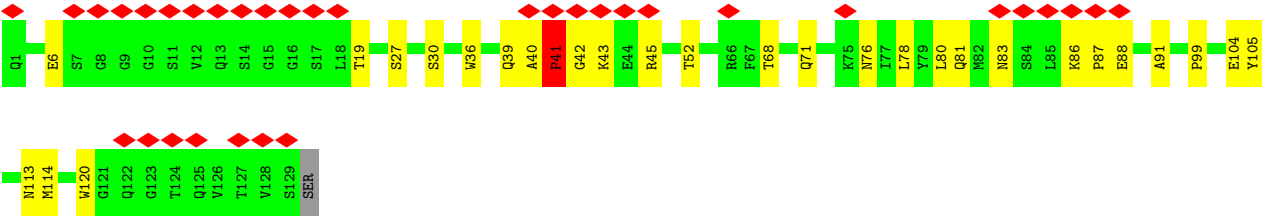


• Molecule 1: Apelin receptor

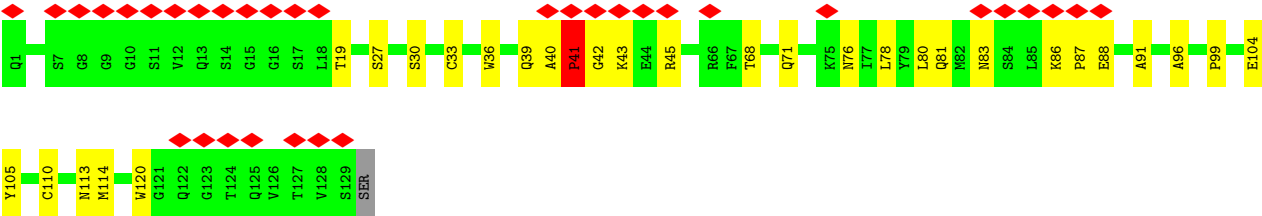
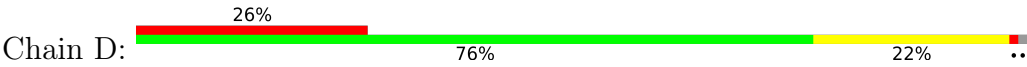


• Molecule 2: JN241-9





• Molecule 2: JN241-9



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	101362	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.109	Depositor
Minimum map value	-0.091	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	208.32, 208.32, 208.32	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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: CLR, PCF

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	0.17	0/2219	0.44	0/3032
1	B	0.17	0/2219	0.44	0/3032
2	C	0.29	1/972 (0.1%)	0.47	1/1311 (0.1%)
2	D	0.29	1/972 (0.1%)	0.47	1/1311 (0.1%)
All	All	0.21	2/6382 (0.0%)	0.45	2/8686 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	41	PRO	N-CD	6.71	1.57	1.47
2	D	41	PRO	N-CD	6.68	1.57	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	42	GLY	N-CA-C	-5.23	108.60	114.40
2	C	42	GLY	N-CA-C	-5.18	108.65	114.40

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	2157	0	2177	69	0
1	B	2157	0	2177	71	0
2	C	954	0	898	26	0
2	D	954	0	898	24	0
3	A	50	0	80	17	0
3	B	50	0	80	18	0
4	A	224	0	368	101	0
4	B	224	0	368	103	0
All	All	6770	0	7046	297	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 22.

All (297) 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)
2:D:40:ALA:CB	2:D:41:PRO:HD3	1.81	1.09
2:C:40:ALA:CB	2:C:41:PRO:HD3	1.81	1.05
2:C:40:ALA:HB3	2:C:41:PRO:HD3	1.39	1.03
2:D:40:ALA:HB3	2:D:41:PRO:HD3	1.39	1.00
4:B:404:CLR:H183	4:B:408:CLR:H14	1.46	0.97
2:C:40:ALA:HB3	2:C:41:PRO:CD	1.96	0.94
2:D:40:ALA:HB3	2:D:41:PRO:CD	1.96	0.94
4:A:402:CLR:H122	4:B:403:CLR:H72	1.48	0.93
4:A:404:CLR:H14	4:A:408:CLR:H183	1.47	0.92
4:A:407:CLR:H72	4:B:405:CLR:H122	1.48	0.92
1:A:154:TRP:HB3	4:A:404:CLR:H151	1.54	0.90
1:B:154:TRP:HB3	4:B:408:CLR:H151	1.54	0.88
1:B:108:LEU:HD21	4:B:404:CLR:H273	1.61	0.82
2:C:40:ALA:CB	2:C:41:PRO:CD	2.54	0.82
1:A:108:LEU:HD21	4:A:408:CLR:H273	1.60	0.81
1:A:164:VAL:HA	1:A:183:MET:HE1	1.62	0.81
4:A:407:CLR:H181	4:B:404:CLR:H212	1.63	0.81
1:B:164:VAL:HA	1:B:183:MET:HE1	1.62	0.81
2:D:40:ALA:CB	2:D:41:PRO:CD	2.54	0.81
4:A:408:CLR:H212	4:B:403:CLR:H181	1.63	0.80
4:A:407:CLR:H6	4:B:405:CLR:H12	1.64	0.79
1:B:33:ALA:HA	3:B:401:PCF:H491	1.65	0.78
4:A:402:CLR:H12	4:B:403:CLR:H6	1.64	0.78
1:A:33:ALA:HA	3:A:401:PCF:H491	1.68	0.75
1:B:94:ASP:HB2	1:B:178:LYS:HG2	1.68	0.75
1:B:73:VAL:HG11	4:B:404:CLR:H71	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:VAL:CG1	4:A:408:CLR:H151	2.18	0.74
1:A:73:VAL:HG11	4:A:408:CLR:H71	1.69	0.74
1:A:94:ASP:HB2	1:A:178:LYS:HG2	1.68	0.73
1:A:73:VAL:HG11	4:A:408:CLR:H151	1.69	0.73
1:B:73:VAL:CG1	4:B:404:CLR:H151	2.19	0.73
1:B:73:VAL:HG11	4:B:404:CLR:H151	1.70	0.72
4:A:404:CLR:H71	4:A:408:CLR:H182	1.72	0.72
4:B:404:CLR:H182	4:B:408:CLR:H71	1.71	0.71
4:A:402:CLR:H71	4:B:409:CLR:H122	1.73	0.70
1:B:277:LEU:HB3	1:B:279:TRP:NE1	2.07	0.70
4:A:406:CLR:H122	4:B:405:CLR:H71	1.74	0.70
1:A:277:LEU:HB3	1:A:279:TRP:NE1	2.07	0.70
1:B:154:TRP:HB2	4:B:408:CLR:H72	1.74	0.70
1:A:107:TYR:HE2	4:A:408:CLR:H262	1.57	0.69
2:C:40:ALA:HB1	2:C:41:PRO:HD3	1.74	0.69
4:A:409:CLR:H241	4:B:403:CLR:H261	1.73	0.69
4:A:407:CLR:H261	4:B:406:CLR:H241	1.74	0.69
1:A:154:TRP:HB2	4:A:404:CLR:H72	1.74	0.68
2:D:40:ALA:HB1	2:D:41:PRO:HD3	1.73	0.68
1:B:107:TYR:HE2	4:B:404:CLR:H262	1.58	0.68
1:A:166:VAL:HG22	4:A:403:CLR:H152	1.75	0.68
4:A:405:CLR:H242	4:A:407:CLR:H213	1.77	0.67
4:A:406:CLR:H242	4:A:407:CLR:H161	1.77	0.67
4:B:402:CLR:H242	4:B:403:CLR:H213	1.77	0.66
1:B:166:VAL:HG22	4:B:407:CLR:H152	1.76	0.66
2:C:71:GLN:HG3	2:C:78:LEU:HD12	1.76	0.66
4:B:403:CLR:H161	4:B:409:CLR:H242	1.77	0.66
2:C:27:SER:O	2:C:76:ASN:ND2	2.29	0.66
2:D:71:GLN:HG3	2:D:78:LEU:HD12	1.76	0.66
4:B:404:CLR:C26	4:B:408:CLR:H242	2.26	0.66
4:A:405:CLR:H121	4:A:406:CLR:H152	1.79	0.65
2:D:27:SER:O	2:D:76:ASN:ND2	2.29	0.65
4:B:402:CLR:H121	4:B:409:CLR:H152	1.79	0.64
4:B:404:CLR:H263	4:B:408:CLR:H242	1.78	0.64
4:A:404:CLR:H242	4:A:408:CLR:H263	1.80	0.64
4:B:403:CLR:H71	4:B:409:CLR:H151	1.80	0.63
4:A:404:CLR:H242	4:A:408:CLR:C26	2.27	0.63
4:A:406:CLR:H151	4:A:407:CLR:H71	1.81	0.62
1:B:166:VAL:HG22	4:B:407:CLR:H181	1.82	0.61
2:D:86:LYS:HD3	2:D:88:GLU:H	1.65	0.61
4:A:409:CLR:H161	3:B:401:PCF:H421	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:407:CLR:H191	4:B:404:CLR:H112	1.83	0.60
3:A:401:PCF:H421	4:B:406:CLR:H161	1.83	0.60
4:A:407:CLR:H193	4:B:408:CLR:H12	1.84	0.60
1:A:51:TRP:NE1	4:A:405:CLR:H22	2.15	0.60
2:C:86:LYS:HD3	2:C:88:GLU:H	1.65	0.60
1:A:166:VAL:HG22	4:A:403:CLR:H181	1.82	0.60
1:B:51:TRP:NE1	4:B:402:CLR:H22	2.15	0.60
4:A:405:CLR:H12	4:A:407:CLR:H21	1.84	0.60
1:A:191:VAL:HG23	2:C:99:PRO:HD3	1.84	0.59
1:B:86:ALA:HB1	3:B:401:PCF:H291	1.82	0.59
2:C:36:TRP:CD1	2:C:80:LEU:HD13	2.37	0.59
4:B:402:CLR:H12	4:B:403:CLR:H21	1.84	0.59
4:A:407:CLR:H6	4:B:405:CLR:H9	1.84	0.59
4:A:404:CLR:H12	4:B:403:CLR:H193	1.84	0.59
4:A:408:CLR:H112	4:B:403:CLR:H191	1.84	0.59
1:A:86:ALA:HB1	3:A:401:PCF:H291	1.84	0.59
1:B:191:VAL:HG23	2:D:99:PRO:HD3	1.84	0.59
2:D:36:TRP:CD1	2:D:80:LEU:HD13	2.37	0.59
1:A:162:MET:SD	4:A:403:CLR:H222	2.43	0.58
1:A:51:TRP:CD1	4:A:405:CLR:H22	2.38	0.58
1:B:103:LYS:NZ	4:B:407:CLR:H193	2.18	0.58
1:B:162:MET:SD	4:B:407:CLR:H222	2.44	0.58
4:A:402:CLR:H9	4:B:403:CLR:H6	1.84	0.58
4:B:404:CLR:H11	4:B:408:CLR:H3	1.86	0.57
1:B:51:TRP:CD1	4:B:402:CLR:H22	2.38	0.57
1:A:103:LYS:NZ	4:A:403:CLR:H193	2.19	0.57
1:A:123:LEU:HB3	1:A:250:ILE:HD13	1.86	0.57
1:B:87:THR:HA	3:B:401:PCF:H262	1.85	0.57
4:A:404:CLR:H71	4:A:408:CLR:C18	2.35	0.57
2:D:40:ALA:HB2	2:D:91:ALA:HB2	1.87	0.57
1:A:91:ARG:NH2	1:A:94:ASP:OD2	2.29	0.56
1:B:47:GLY:HA3	4:B:402:CLR:H183	1.88	0.56
1:B:123:LEU:HB3	1:B:250:ILE:HD13	1.86	0.56
4:B:404:CLR:C18	4:B:408:CLR:H71	2.35	0.56
1:A:202:GLY:HA3	1:A:272:MET:HE3	1.88	0.56
4:A:404:CLR:H3	4:A:408:CLR:H11	1.87	0.56
2:C:40:ALA:HB2	2:C:91:ALA:HB2	1.87	0.56
1:A:87:THR:HA	3:A:401:PCF:H262	1.87	0.56
3:A:401:PCF:H351	1:B:100:PHE:HD1	1.71	0.56
2:C:86:LYS:HG2	2:C:87:PRO:HD2	1.88	0.55
1:B:202:GLY:HA3	1:B:272:MET:HE3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:86:LYS:HG2	2:D:87:PRO:HD2	1.88	0.55
4:B:404:CLR:H263	4:B:408:CLR:H221	1.89	0.54
1:B:103:LYS:HZ2	4:B:407:CLR:H193	1.72	0.54
1:A:47:GLY:HA3	4:A:405:CLR:H183	1.89	0.54
1:A:73:VAL:O	1:A:77:THR:HG23	2.08	0.54
1:B:91:ARG:NH2	1:B:94:ASP:OD2	2.29	0.54
1:A:100:PHE:HD1	3:B:401:PCF:H351	1.71	0.53
1:B:108:LEU:HD21	4:B:404:CLR:C27	2.36	0.53
1:A:154:TRP:CB	4:A:404:CLR:H72	2.38	0.53
1:A:277:LEU:HB3	1:A:279:TRP:CD1	2.44	0.53
1:B:214:PHE:O	1:B:218:LEU:HG	2.09	0.53
1:B:277:LEU:HB3	1:B:279:TRP:CD1	2.43	0.53
4:A:404:CLR:H221	4:A:408:CLR:H263	1.89	0.53
1:B:73:VAL:O	1:B:77:THR:HG23	2.08	0.53
1:A:210:PHE:O	1:A:214:PHE:HB2	2.09	0.53
1:B:210:PHE:O	1:B:214:PHE:HB2	2.09	0.53
1:A:108:LEU:HD21	4:A:408:CLR:C27	2.36	0.53
2:D:114:MET:SD	2:D:114:MET:N	2.82	0.53
1:B:162:MET:HE1	4:B:408:CLR:H25	1.91	0.52
1:B:154:TRP:CB	4:B:408:CLR:H72	2.38	0.52
1:A:43:THR:HG22	4:A:405:CLR:H232	1.92	0.52
1:B:43:THR:HG22	4:B:402:CLR:H232	1.91	0.52
1:A:162:MET:HE1	4:A:404:CLR:H25	1.91	0.52
2:C:114:MET:SD	2:C:114:MET:N	2.82	0.52
1:A:46:ASN:HB2	1:A:76:LEU:HD13	1.92	0.52
1:B:268:LYS:O	1:B:272:MET:HG2	2.10	0.52
1:A:214:PHE:O	1:A:218:LEU:HG	2.09	0.52
4:A:405:CLR:H12	4:A:407:CLR:C2	2.40	0.52
4:A:403:CLR:H112	3:B:401:PCF:H332	1.92	0.51
4:B:402:CLR:H12	4:B:403:CLR:C2	2.40	0.51
4:A:402:CLR:H12	4:B:403:CLR:H41	1.93	0.51
4:A:409:CLR:H12	3:B:401:PCF:H352	1.93	0.51
4:B:403:CLR:H71	4:B:409:CLR:C15	2.41	0.51
1:A:268:LYS:O	1:A:272:MET:HG2	2.11	0.50
3:A:401:PCF:H332	4:B:407:CLR:H112	1.92	0.50
1:B:46:ASN:HB2	1:B:76:LEU:HD13	1.92	0.50
4:A:406:CLR:C15	4:A:407:CLR:H71	2.41	0.50
1:B:73:VAL:HG12	4:B:404:CLR:H151	1.93	0.50
1:A:100:PHE:CD1	3:B:401:PCF:H351	2.47	0.50
4:A:407:CLR:H41	4:B:405:CLR:H12	1.93	0.50
3:B:401:PCF:H12	3:B:401:PCF:H112	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:404:CLR:H193	4:B:408:CLR:C6	2.41	0.50
4:A:408:CLR:C21	4:B:403:CLR:H181	2.38	0.50
1:B:54:PHE:HE2	4:B:405:CLR:H192	1.77	0.50
1:B:243:ARG:HD2	1:B:245:ARG:HE	1.77	0.50
1:A:54:PHE:HE2	4:A:402:CLR:H192	1.77	0.50
3:A:401:PCF:H351	1:B:100:PHE:CD1	2.47	0.49
4:A:404:CLR:C6	4:A:408:CLR:H193	2.42	0.49
4:A:405:CLR:C24	4:A:407:CLR:H213	2.42	0.49
3:A:401:PCF:H21	4:B:406:CLR:O1	2.13	0.49
1:A:243:ARG:HD2	1:A:245:ARG:HE	1.77	0.49
1:A:127:ARG:HA	1:A:127:ARG:NE	2.27	0.49
4:A:409:CLR:O1	3:B:401:PCF:H21	2.13	0.49
1:B:185:TYR:HB2	1:B:194:GLU:HG2	1.94	0.49
4:B:406:CLR:H262	4:B:406:CLR:H231	1.58	0.49
1:A:73:VAL:HG12	4:A:408:CLR:H151	1.92	0.49
3:A:401:PCF:H112	3:A:401:PCF:H12	1.94	0.49
3:A:401:PCF:H352	4:B:406:CLR:H12	1.95	0.49
1:A:185:TYR:HB2	1:A:194:GLU:HG2	1.94	0.48
1:B:43:THR:CG2	4:B:402:CLR:H232	2.43	0.48
4:A:407:CLR:H181	4:B:404:CLR:C21	2.38	0.48
1:A:242:LYS:HB3	1:A:242:LYS:HE2	1.64	0.48
4:B:402:CLR:C24	4:B:403:CLR:H213	2.42	0.48
2:D:83:ASN:OD1	2:D:83:ASN:N	2.46	0.48
1:A:154:TRP:CH2	4:A:408:CLR:H152	2.48	0.48
1:B:242:LYS:HE2	1:B:242:LYS:HB3	1.63	0.48
1:A:92:ASP:O	1:A:178:LYS:HE3	2.14	0.47
1:B:127:ARG:NE	1:B:127:ARG:HA	2.27	0.47
2:D:41:PRO:C	2:D:43:LYS:N	2.71	0.47
1:B:165:MET:HG2	4:B:407:CLR:H183	1.96	0.47
4:B:406:CLR:H212	4:B:406:CLR:H183	1.97	0.47
1:A:83:PRO:HB3	4:B:406:CLR:H181	1.97	0.47
1:A:43:THR:CG2	4:A:405:CLR:H232	2.45	0.47
1:A:165:MET:HG2	4:A:403:CLR:H183	1.96	0.47
1:B:154:TRP:CH2	4:B:404:CLR:H152	2.49	0.47
2:C:41:PRO:C	2:C:43:LYS:N	2.71	0.47
4:A:407:CLR:H263	4:A:407:CLR:H232	1.62	0.47
1:B:92:ASP:O	1:B:178:LYS:HE3	2.15	0.47
1:B:273:LEU:HD23	1:B:276:LEU:HD23	1.97	0.47
3:B:401:PCF:H422	4:B:403:CLR:H25	1.97	0.46
1:A:97:PHE:CE1	4:B:406:CLR:H6	2.51	0.46
4:A:407:CLR:C19	4:B:404:CLR:H112	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:409:CLR:H6	1:B:97:PHE:CE1	2.51	0.46
1:A:273:LEU:HD23	1:A:276:LEU:HD23	1.98	0.46
4:A:409:CLR:H181	1:B:83:PRO:HB3	1.96	0.46
2:C:83:ASN:OD1	2:C:83:ASN:N	2.46	0.46
4:B:404:CLR:H221	4:B:404:CLR:H25	1.63	0.46
4:B:403:CLR:H71	4:B:409:CLR:H161	1.98	0.46
1:A:168:ARG:HD2	1:A:183:MET:SD	2.56	0.46
3:B:401:PCF:H133	3:B:401:PCF:H111	1.67	0.46
4:A:408:CLR:H112	4:B:403:CLR:C19	2.45	0.45
4:A:409:CLR:H183	4:A:409:CLR:H212	1.97	0.45
4:A:409:CLR:H262	4:A:409:CLR:H231	1.58	0.45
4:B:403:CLR:H222	4:B:409:CLR:H263	1.98	0.45
4:B:404:CLR:H183	4:B:408:CLR:C14	2.32	0.45
2:D:41:PRO:C	2:D:43:LYS:H	2.23	0.45
2:C:19:THR:OG1	2:C:81:GLN:OE1	2.35	0.45
4:A:403:CLR:H121	3:B:401:PCF:H362	1.99	0.45
2:C:41:PRO:C	2:C:43:LYS:H	2.23	0.45
3:A:401:PCF:H422	4:A:407:CLR:H25	1.97	0.45
4:B:404:CLR:H193	4:B:408:CLR:H41	1.99	0.45
4:A:404:CLR:C14	4:A:408:CLR:H183	2.33	0.45
4:A:406:CLR:H161	4:A:407:CLR:H71	1.99	0.45
1:A:175:ASN:HB2	2:C:113:ASN:OD1	2.17	0.45
4:A:405:CLR:H262	4:A:407:CLR:H272	1.98	0.45
2:C:40:ALA:HB3	2:C:41:PRO:HD2	1.93	0.45
1:A:166:VAL:HA	4:A:403:CLR:H182	2.00	0.44
4:A:406:CLR:H122	4:B:405:CLR:C7	2.45	0.44
1:B:187:MET:SD	1:B:187:MET:N	2.89	0.44
3:A:401:PCF:H111	3:A:401:PCF:H133	1.67	0.44
3:A:401:PCF:H362	4:B:407:CLR:H121	1.98	0.44
1:B:168:ARG:HD2	1:B:183:MET:SD	2.56	0.44
1:B:175:ASN:HB2	2:D:113:ASN:OD1	2.17	0.44
4:B:402:CLR:H262	4:B:403:CLR:H272	1.98	0.44
4:B:404:CLR:C21	4:B:408:CLR:H17	2.47	0.44
4:B:408:CLR:H211	4:B:408:CLR:H241	2.00	0.44
4:A:402:CLR:C7	4:B:409:CLR:H122	2.45	0.44
1:B:166:VAL:HA	4:B:407:CLR:H182	1.99	0.44
2:D:19:THR:OG1	2:D:81:GLN:OE1	2.35	0.44
4:A:404:CLR:H17	4:A:408:CLR:C21	2.47	0.44
1:A:187:MET:SD	1:A:187:MET:N	2.89	0.44
1:A:271:TYR:CZ	2:C:30:SER:HB2	2.53	0.44
1:B:90:TYR:CD2	3:B:401:PCF:H251	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:408:CLR:H212	4:B:403:CLR:C18	2.43	0.43
4:A:409:CLR:H3	3:B:401:PCF:H322	2.00	0.43
1:B:271:TYR:CZ	2:D:30:SER:HB2	2.53	0.43
4:B:404:CLR:H183	4:B:404:CLR:H20	1.89	0.43
4:B:406:CLR:H182	4:B:406:CLR:H8	1.77	0.43
4:A:404:CLR:H211	4:A:404:CLR:H241	2.00	0.43
4:A:404:CLR:H41	4:A:408:CLR:H193	1.99	0.43
4:A:406:CLR:H263	4:A:407:CLR:H222	1.99	0.43
1:A:245:ARG:O	1:A:249:ILE:HG13	2.19	0.43
4:A:407:CLR:H261	4:B:406:CLR:C24	2.47	0.43
1:B:86:ALA:C	3:B:401:PCF:H282	2.44	0.43
1:B:243:ARG:HD2	1:B:245:ARG:HH21	1.84	0.43
1:B:245:ARG:O	1:B:249:ILE:HG13	2.19	0.43
1:A:154:TRP:CZ2	4:A:408:CLR:H152	2.53	0.42
4:A:409:CLR:C24	4:B:403:CLR:H261	2.46	0.42
3:A:401:PCF:H421	3:A:401:PCF:H451	1.79	0.42
4:A:403:CLR:H221	4:A:403:CLR:H162	1.19	0.42
2:C:45:ARG:HD3	2:C:120:TRP:CH2	2.54	0.42
2:D:45:ARG:HD3	2:D:120:TRP:CH2	2.54	0.42
1:B:154:TRP:CZ2	4:B:404:CLR:H152	2.54	0.42
2:D:33:CYS:HB2	2:D:110:CYS:HB3	1.92	0.42
2:D:39:GLN:CG	2:D:45:ARG:HA	2.50	0.42
2:C:68:THR:HB	2:C:81:GLN:HB3	2.02	0.42
1:A:279:TRP:HB3	1:A:280:PRO:HD2	2.02	0.41
2:C:39:GLN:CG	2:C:45:ARG:HA	2.50	0.41
2:D:68:THR:HB	2:D:81:GLN:HB3	2.02	0.41
1:A:243:ARG:HD2	1:A:245:ARG:HH21	1.84	0.41
3:A:401:PCF:H322	4:B:406:CLR:H3	2.02	0.41
4:A:404:CLR:H3	4:B:403:CLR:H192	2.01	0.41
4:A:407:CLR:H231	4:B:404:CLR:H211	2.01	0.41
1:A:86:ALA:C	3:A:401:PCF:H282	2.45	0.41
4:A:407:CLR:H192	4:B:408:CLR:H3	2.01	0.41
1:A:162:MET:N	1:A:163:PRO:HD2	2.36	0.41
1:B:166:VAL:CG2	4:B:407:CLR:H181	2.48	0.41
4:B:403:CLR:H272	4:B:403:CLR:H221	2.01	0.41
1:A:90:TYR:CD2	3:A:401:PCF:H251	2.55	0.41
4:A:403:CLR:H232	4:A:403:CLR:H263	1.87	0.41
4:A:407:CLR:H272	4:A:407:CLR:H221	2.01	0.41
1:B:31:ILE:HB	1:B:32:PRO:HD3	2.02	0.41
1:B:32:PRO:HB3	3:B:401:PCF:H292	2.03	0.41
1:B:267:VAL:HG13	1:B:287:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:VAL:CG2	4:A:403:CLR:H181	2.48	0.41
4:A:409:CLR:H6	1:B:97:PHE:CZ	2.56	0.41
1:B:54:PHE:CE2	4:B:405:CLR:H192	2.56	0.41
4:B:403:CLR:H263	4:B:403:CLR:H232	1.62	0.41
1:A:103:LYS:HZ2	4:A:403:CLR:H193	1.83	0.40
1:A:174:GLU:OE1	2:C:52:THR:HB	2.21	0.40
4:A:408:CLR:H211	4:B:403:CLR:H231	2.03	0.40
2:C:6:GLU:H	2:C:6:GLU:CD	2.29	0.40
1:B:73:VAL:HG11	4:B:404:CLR:C7	2.45	0.40
1:A:31:ILE:HB	1:A:32:PRO:HD3	2.02	0.40
1:A:267:VAL:HG13	1:A:287:LEU:HD22	2.03	0.40
1:B:279:TRP:HB3	1:B:280:PRO:HD2	2.02	0.40
4:B:404:CLR:H121	4:B:408:CLR:H9	2.03	0.40
1:A:54:PHE:CE2	4:A:402:CLR:H192	2.56	0.40
4:A:406:CLR:H151	4:A:407:CLR:C7	2.50	0.40
1:B:33:ALA:HA	3:B:401:PCF:C49	2.43	0.40
1:B:260:CYS:CB	1:B:301:ASN:HB2	2.51	0.40
1:A:73:VAL:HG11	4:A:408:CLR:C7	2.45	0.40
1:A:97:PHE:CZ	4:B:406:CLR:H6	2.56	0.40
4:A:404:CLR:H9	4:A:408:CLR:H121	2.03	0.40
2:C:39:GLN:HG2	2:C:45:ARG:HA	2.04	0.40
1:B:162:MET:N	1:B:163:PRO:HD2	2.36	0.40
4:B:407:CLR:H221	4:B:407:CLR:H162	1.19	0.40
4:B:404:CLR:H211	4:B:408:CLR:H213	2.01	0.40
2:D:96:ALA:HB2	2:D:120:TRP:CZ3	2.57	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	263/380 (69%)	258 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	263/380 (69%)	258 (98%)	5 (2%)	0	100	100
2	C	127/130 (98%)	121 (95%)	4 (3%)	2 (2%)	7	20
2	D	127/130 (98%)	121 (95%)	4 (3%)	2 (2%)	7	20
All	All	780/1020 (76%)	758 (97%)	18 (2%)	4 (0%)	26	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	104	GLU
2	D	104	GLU
2	C	41	PRO
2	D	41	PRO

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	236/327 (72%)	236 (100%)	0	100	100
1	B	236/327 (72%)	235 (100%)	1 (0%)	84	93
2	C	100/104 (96%)	99 (99%)	1 (1%)	68	86
2	D	100/104 (96%)	99 (99%)	1 (1%)	68	86
All	All	672/862 (78%)	669 (100%)	3 (0%)	81	93

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	105	TYR
1	B	162	MET
2	D	105	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	ASN
1	A	265	HIS
1	B	112	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

18 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PCF	B	401	-	49,49,49	1.35	5 (10%)	55,57,57	1.21	4 (7%)
4	CLR	A	403	-	31,31,31	1.16	2 (6%)	48,48,48	1.52	12 (25%)
4	CLR	A	404	-	31,31,31	1.12	1 (3%)	48,48,48	1.48	9 (18%)
4	CLR	B	409	-	31,31,31	1.13	1 (3%)	48,48,48	1.47	9 (18%)
4	CLR	A	402	-	31,31,31	1.10	2 (6%)	48,48,48	1.44	7 (14%)
4	CLR	A	408	-	31,31,31	1.10	1 (3%)	48,48,48	1.62	13 (27%)
3	PCF	A	401	-	49,49,49	1.34	5 (10%)	55,57,57	1.21	4 (7%)
4	CLR	A	406	-	31,31,31	1.13	1 (3%)	48,48,48	1.47	9 (18%)
4	CLR	B	405	-	31,31,31	1.10	2 (6%)	48,48,48	1.44	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CLR	B	406	-	31,31,31	1.10	1 (3%)	48,48,48	1.87	14 (29%)
4	CLR	A	409	-	31,31,31	1.09	1 (3%)	48,48,48	1.87	14 (29%)
4	CLR	B	404	-	31,31,31	1.10	1 (3%)	48,48,48	1.62	14 (29%)
4	CLR	A	407	-	31,31,31	1.14	1 (3%)	48,48,48	1.60	10 (20%)
4	CLR	B	408	-	31,31,31	1.12	1 (3%)	48,48,48	1.48	9 (18%)
4	CLR	A	405	-	31,31,31	1.13	1 (3%)	48,48,48	1.57	9 (18%)
4	CLR	B	407	-	31,31,31	1.16	3 (9%)	48,48,48	1.51	12 (25%)
4	CLR	B	403	-	31,31,31	1.14	1 (3%)	48,48,48	1.61	10 (20%)
4	CLR	B	402	-	31,31,31	1.14	1 (3%)	48,48,48	1.57	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PCF	B	401	-	-	23/53/53/53	-
4	CLR	A	403	-	-	6/10/68/68	0/4/4/4
4	CLR	A	404	-	-	1/10/68/68	0/4/4/4
4	CLR	B	409	-	-	2/10/68/68	0/4/4/4
4	CLR	A	402	-	-	5/10/68/68	0/4/4/4
4	CLR	A	408	-	-	7/10/68/68	0/4/4/4
3	PCF	A	401	-	-	23/53/53/53	-
4	CLR	A	406	-	-	2/10/68/68	0/4/4/4
4	CLR	B	405	-	-	5/10/68/68	0/4/4/4
4	CLR	B	406	-	-	5/10/68/68	0/4/4/4
4	CLR	A	409	-	-	5/10/68/68	0/4/4/4
4	CLR	B	404	-	-	7/10/68/68	0/4/4/4
4	CLR	A	407	-	-	6/10/68/68	0/4/4/4
4	CLR	B	408	-	-	1/10/68/68	0/4/4/4
4	CLR	A	405	-	-	6/10/68/68	0/4/4/4
4	CLR	B	407	-	-	6/10/68/68	0/4/4/4
4	CLR	B	403	-	-	6/10/68/68	0/4/4/4
4	CLR	B	402	-	-	6/10/68/68	0/4/4/4

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	PCF	O21-C21	3.43	1.44	1.34
3	A	401	PCF	O21-C21	3.41	1.43	1.34
4	B	407	CLR	C16-C17	3.11	1.60	1.54
3	B	401	PCF	O31-C31	3.08	1.42	1.33
4	B	404	CLR	C16-C17	3.08	1.60	1.54
4	A	403	CLR	C16-C17	3.07	1.60	1.54
4	B	408	CLR	C16-C17	3.06	1.60	1.54
4	A	408	CLR	C16-C17	3.06	1.60	1.54
3	A	401	PCF	O31-C31	3.06	1.42	1.33
4	A	404	CLR	C16-C17	3.05	1.60	1.54
4	B	409	CLR	C16-C17	3.00	1.60	1.54
4	A	406	CLR	C16-C17	2.98	1.60	1.54
4	A	407	CLR	C16-C17	2.97	1.60	1.54
4	B	406	CLR	C16-C17	2.97	1.60	1.54
4	B	403	CLR	C16-C17	2.97	1.60	1.54
4	A	409	CLR	C16-C17	2.94	1.60	1.54
4	B	402	CLR	C16-C17	2.94	1.60	1.54
4	A	405	CLR	C16-C17	2.93	1.60	1.54
4	B	405	CLR	C16-C17	2.80	1.60	1.54
4	A	402	CLR	C16-C17	2.78	1.60	1.54
3	A	401	PCF	C22-C21	2.72	1.58	1.50
3	B	401	PCF	C22-C21	2.69	1.58	1.50
3	B	401	PCF	P-O11	2.29	1.68	1.59
3	A	401	PCF	P-O11	2.28	1.68	1.59
3	B	401	PCF	P-O13	2.17	1.67	1.59
3	A	401	PCF	P-O13	2.16	1.67	1.59
4	B	407	CLR	C7-C8	2.04	1.56	1.53
4	B	407	CLR	C7-C6	2.03	1.54	1.50
4	A	403	CLR	C7-C6	2.01	1.54	1.50
4	A	402	CLR	C16-C15	2.01	1.59	1.54
4	B	405	CLR	C16-C15	2.01	1.59	1.54

All (176) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	409	CLR	C15-C14-C13	4.61	109.26	103.84
4	B	406	CLR	C15-C14-C13	4.58	109.23	103.84
3	B	401	PCF	O21-C21-C22	4.03	120.19	111.48
3	A	401	PCF	O21-C21-C22	4.02	120.17	111.48
4	A	409	CLR	C22-C20-C17	-3.97	102.10	110.33
4	B	406	CLR	C22-C20-C17	-3.97	102.10	110.33
4	B	406	CLR	C13-C14-C8	-3.82	108.99	114.41
4	A	409	CLR	C13-C14-C8	-3.80	109.01	114.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	403	CLR	C13-C17-C20	-3.79	113.65	119.50
4	A	407	CLR	C13-C17-C20	-3.76	113.68	119.50
4	A	405	CLR	C22-C20-C17	-3.50	103.08	110.33
4	B	402	CLR	C22-C20-C17	-3.48	103.11	110.33
4	A	408	CLR	C18-C13-C12	3.46	115.70	110.61
4	B	404	CLR	C18-C13-C12	3.44	115.67	110.61
4	B	409	CLR	C22-C20-C17	-3.32	103.44	110.33
4	A	406	CLR	C22-C20-C17	-3.31	103.46	110.33
4	A	404	CLR	C22-C20-C17	-3.27	103.56	110.33
4	B	408	CLR	C22-C20-C17	-3.26	103.57	110.33
4	A	409	CLR	C12-C13-C14	-3.16	102.52	107.25
4	B	406	CLR	C12-C13-C14	-3.15	102.53	107.25
4	A	407	CLR	C15-C14-C13	3.14	107.53	103.84
4	B	403	CLR	C15-C14-C13	3.14	107.53	103.84
4	A	403	CLR	C22-C20-C17	-3.07	103.97	110.33
4	B	407	CLR	C22-C20-C17	-3.06	104.00	110.33
4	A	409	CLR	C21-C20-C17	3.05	117.46	112.88
4	B	406	CLR	C21-C20-C17	3.04	117.44	112.88
4	B	405	CLR	C18-C13-C12	3.03	115.07	110.61
4	A	402	CLR	C18-C13-C12	3.01	115.04	110.61
3	B	401	PCF	O31-C31-C32	2.95	120.82	111.83
3	A	401	PCF	O31-C31-C32	2.94	120.81	111.83
4	A	405	CLR	C21-C20-C17	2.93	117.28	112.88
4	B	402	CLR	C21-C20-C17	2.91	117.25	112.88
4	B	406	CLR	C16-C17-C20	-2.90	107.79	112.18
4	B	402	CLR	C1-C2-C3	2.89	114.31	110.48
4	B	402	CLR	C19-C10-C9	-2.88	108.43	111.66
4	A	409	CLR	C16-C17-C20	-2.87	107.83	112.18
4	A	405	CLR	C19-C10-C9	-2.85	108.47	111.66
4	A	408	CLR	C13-C17-C20	-2.84	115.10	119.50
4	B	404	CLR	C13-C17-C20	-2.84	115.11	119.50
4	A	404	CLR	C7-C8-C14	-2.84	106.92	110.93
4	A	405	CLR	C1-C2-C3	2.84	114.24	110.48
4	A	409	CLR	C7-C8-C9	2.80	112.96	109.72
4	B	408	CLR	C7-C8-C14	-2.80	106.97	110.93
4	B	406	CLR	C7-C8-C9	2.77	112.92	109.72
4	B	406	CLR	C18-C13-C12	2.77	114.69	110.61
4	A	409	CLR	C18-C13-C12	2.76	114.67	110.61
4	A	404	CLR	C2-C3-C4	-2.76	106.42	110.29
4	B	408	CLR	C2-C3-C4	-2.74	106.43	110.29
4	B	404	CLR	C22-C20-C17	-2.74	104.65	110.33
4	A	408	CLR	C22-C20-C17	-2.74	104.66	110.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	406	CLR	C7-C8-C14	-2.73	107.06	110.93
4	A	409	CLR	C7-C8-C14	-2.72	107.08	110.93
4	A	403	CLR	C11-C12-C13	-2.68	108.22	112.74
4	A	408	CLR	C24-C23-C22	-2.66	101.36	113.28
4	B	402	CLR	C16-C17-C20	-2.66	108.16	112.18
4	B	407	CLR	C11-C12-C13	-2.65	108.26	112.74
4	B	404	CLR	C24-C23-C22	-2.65	101.40	113.28
4	A	404	CLR	C18-C13-C12	2.63	114.48	110.61
4	A	405	CLR	C16-C17-C20	-2.63	108.20	112.18
4	B	408	CLR	C18-C13-C12	2.63	114.48	110.61
4	B	402	CLR	C7-C8-C14	-2.61	107.23	110.93
4	A	402	CLR	C13-C17-C20	-2.60	115.49	119.50
4	B	405	CLR	C13-C17-C20	-2.59	115.50	119.50
4	A	405	CLR	C7-C8-C14	-2.58	107.28	110.93
4	A	406	CLR	C7-C8-C14	-2.57	107.30	110.93
4	B	409	CLR	C7-C8-C14	-2.57	107.30	110.93
4	B	403	CLR	C12-C13-C14	-2.56	103.41	107.25
4	A	403	CLR	C1-C2-C3	2.56	113.87	110.48
4	A	407	CLR	C12-C13-C14	-2.54	103.44	107.25
4	B	404	CLR	C2-C3-C4	-2.52	106.74	110.29
4	A	403	CLR	C4-C5-C10	-2.52	113.20	116.42
4	A	408	CLR	C2-C3-C4	-2.51	106.75	110.29
4	B	407	CLR	C4-C5-C10	-2.51	113.20	116.42
4	A	406	CLR	C18-C13-C12	2.50	114.29	110.61
4	B	403	CLR	C18-C13-C12	2.50	114.29	110.61
4	B	409	CLR	C18-C13-C12	2.49	114.28	110.61
4	B	407	CLR	C1-C2-C3	2.49	113.78	110.48
4	A	407	CLR	C18-C13-C12	2.49	114.27	110.61
3	A	401	PCF	O14-P-O12	-2.44	101.08	112.44
4	B	407	CLR	C15-C14-C13	2.44	106.71	103.84
4	B	404	CLR	C21-C20-C22	-2.43	106.58	110.34
3	B	401	PCF	O14-P-O12	-2.43	101.15	112.44
4	A	405	CLR	C18-C13-C12	2.43	114.18	110.61
4	A	408	CLR	C21-C20-C22	-2.42	106.60	110.34
4	B	402	CLR	C18-C13-C12	2.40	114.15	110.61
4	A	403	CLR	C15-C14-C13	2.40	106.66	103.84
4	A	405	CLR	C15-C14-C13	2.38	106.64	103.84
4	B	403	CLR	C11-C12-C13	-2.38	108.72	112.74
3	B	401	PCF	C11-C12-N	-2.38	108.18	115.82
4	B	402	CLR	C15-C14-C13	2.38	106.64	103.84
3	A	401	PCF	C11-C12-N	-2.38	108.19	115.82
4	B	403	CLR	C13-C14-C8	-2.38	111.04	114.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	409	CLR	C16-C17-C20	-2.37	108.59	112.18
4	A	407	CLR	C13-C14-C8	-2.37	111.05	114.41
4	B	405	CLR	C19-C10-C9	-2.37	109.00	111.66
4	A	407	CLR	C11-C12-C13	-2.36	108.75	112.74
4	B	403	CLR	C3-C4-C5	2.36	115.81	112.05
4	B	404	CLR	C14-C8-C9	-2.36	106.01	109.09
4	A	406	CLR	C16-C17-C20	-2.35	108.62	112.18
4	A	408	CLR	C7-C8-C14	-2.35	107.60	110.93
4	A	407	CLR	C3-C4-C5	2.35	115.79	112.05
4	A	408	CLR	C14-C8-C9	-2.34	106.03	109.09
4	B	404	CLR	C7-C8-C14	-2.33	107.63	110.93
4	A	402	CLR	C19-C10-C9	-2.33	109.04	111.66
4	B	403	CLR	C19-C10-C9	-2.31	109.07	111.66
4	B	406	CLR	C2-C3-C4	-2.31	107.05	110.29
4	A	406	CLR	C21-C20-C17	2.31	116.34	112.88
4	A	402	CLR	C7-C8-C14	-2.30	107.67	110.93
4	A	409	CLR	C2-C3-C4	-2.30	107.05	110.29
4	B	405	CLR	C7-C8-C14	-2.30	107.68	110.93
4	B	404	CLR	C7-C8-C9	2.30	112.38	109.72
4	A	407	CLR	C19-C10-C9	-2.29	109.09	111.66
4	B	409	CLR	C21-C20-C17	2.28	116.31	112.88
4	A	408	CLR	C7-C8-C9	2.28	112.36	109.72
4	B	408	CLR	C9-C10-C5	-2.26	106.35	109.65
4	B	408	CLR	C1-C10-C5	2.25	112.63	108.74
4	A	404	CLR	C1-C10-C5	2.25	112.61	108.74
4	A	404	CLR	C9-C10-C5	-2.22	106.40	109.65
4	A	403	CLR	C3-C4-C5	2.22	115.59	112.05
4	B	403	CLR	C10-C9-C8	-2.21	109.48	112.71
4	B	406	CLR	C9-C10-C5	-2.21	106.41	109.65
4	A	409	CLR	C9-C10-C5	-2.21	106.42	109.65
4	A	407	CLR	C10-C9-C8	-2.21	109.49	112.71
4	B	408	CLR	C19-C10-C9	-2.20	109.19	111.66
4	A	404	CLR	C19-C10-C9	-2.20	109.19	111.66
4	B	407	CLR	C7-C8-C14	-2.20	107.82	110.93
4	A	408	CLR	C16-C17-C20	-2.20	108.85	112.18
4	B	404	CLR	C16-C17-C20	-2.19	108.86	112.18
4	B	407	CLR	C3-C4-C5	2.19	115.54	112.05
4	A	403	CLR	C7-C8-C14	-2.19	107.83	110.93
4	B	404	CLR	C1-C10-C9	-2.19	105.84	108.74
4	A	408	CLR	C1-C10-C9	-2.19	105.84	108.74
4	A	404	CLR	C17-C13-C14	-2.17	97.60	100.10
4	A	406	CLR	C24-C23-C22	-2.16	103.58	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	409	CLR	C24-C23-C22	-2.16	103.59	113.28
4	A	405	CLR	C11-C12-C13	-2.16	109.10	112.74
4	B	407	CLR	C21-C20-C22	-2.16	107.00	110.34
4	A	403	CLR	C21-C20-C22	-2.15	107.02	110.34
4	B	408	CLR	C17-C13-C14	-2.14	97.64	100.10
4	A	402	CLR	C22-C20-C17	-2.13	105.92	110.33
4	A	406	CLR	C17-C13-C14	-2.13	97.66	100.10
4	B	409	CLR	C17-C13-C14	-2.13	97.66	100.10
4	B	405	CLR	C22-C20-C17	-2.12	105.93	110.33
4	B	402	CLR	C11-C12-C13	-2.12	109.17	112.74
4	A	409	CLR	C24-C23-C22	-2.11	103.80	113.28
4	B	406	CLR	C24-C23-C22	-2.11	103.81	113.28
4	B	407	CLR	C24-C23-C22	-2.11	103.81	113.28
4	A	403	CLR	C24-C23-C22	-2.11	103.81	113.28
4	A	404	CLR	C16-C17-C20	-2.10	109.00	112.18
4	A	402	CLR	C15-C14-C13	2.09	106.30	103.84
4	B	404	CLR	C7-C6-C5	-2.09	121.49	125.02
4	A	406	CLR	C19-C10-C9	-2.09	109.31	111.66
4	B	403	CLR	C22-C20-C17	-2.09	106.00	110.33
4	A	408	CLR	C16-C15-C14	-2.09	101.06	105.14
4	B	404	CLR	C16-C15-C14	-2.09	101.06	105.14
4	B	407	CLR	C21-C20-C17	2.08	116.01	112.88
4	B	408	CLR	C16-C17-C20	-2.08	109.03	112.18
4	A	408	CLR	C7-C6-C5	-2.08	121.51	125.02
4	A	403	CLR	C21-C20-C17	2.08	116.00	112.88
4	B	405	CLR	C15-C14-C13	2.08	106.28	103.84
4	A	406	CLR	C11-C12-C13	-2.07	109.24	112.74
4	B	406	CLR	C21-C20-C22	-2.07	107.13	110.34
4	B	409	CLR	C11-C12-C13	-2.06	109.26	112.74
4	B	409	CLR	C19-C10-C9	-2.06	109.34	111.66
4	A	409	CLR	C21-C20-C22	-2.05	107.16	110.34
4	A	407	CLR	C22-C20-C17	-2.05	106.08	110.33
4	A	402	CLR	C3-C4-C5	2.04	115.31	112.05
4	B	405	CLR	C3-C4-C5	2.04	115.31	112.05
4	A	409	CLR	O1-C3-C2	2.03	115.48	110.17
4	B	406	CLR	O1-C3-C2	2.03	115.48	110.17
4	A	403	CLR	C16-C17-C20	-2.03	109.11	112.18
4	B	407	CLR	C16-C17-C20	-2.03	109.11	112.18
4	A	403	CLR	C12-C13-C14	-2.01	104.24	107.25
4	B	407	CLR	C12-C13-C14	-2.01	104.24	107.25
4	B	404	CLR	C1-C10-C5	2.01	112.20	108.74
4	B	405	CLR	C10-C5-C6	2.01	125.86	122.93

There are no chirality outliers.

All (122) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	PCF	C1-O11-P-O12
3	A	401	PCF	C1-O11-P-O13
3	A	401	PCF	O22-C21-O21-C2
3	B	401	PCF	C1-O11-P-O12
3	B	401	PCF	C1-O11-P-O13
3	B	401	PCF	O22-C21-O21-C2
4	A	403	CLR	C13-C17-C20-C21
4	A	408	CLR	C13-C17-C20-C21
4	B	404	CLR	C13-C17-C20-C21
4	B	407	CLR	C13-C17-C20-C21
4	A	403	CLR	C21-C20-C22-C23
4	B	407	CLR	C21-C20-C22-C23
4	A	403	CLR	C16-C17-C20-C21
4	B	407	CLR	C16-C17-C20-C21
4	A	402	CLR	C13-C17-C20-C21
4	B	405	CLR	C13-C17-C20-C21
3	A	401	PCF	C22-C21-O21-C2
3	B	401	PCF	C22-C21-O21-C2
4	A	408	CLR	C16-C17-C20-C21
4	B	404	CLR	C16-C17-C20-C21
4	A	402	CLR	C13-C17-C20-C22
4	A	403	CLR	C13-C17-C20-C22
4	A	408	CLR	C13-C17-C20-C22
4	B	404	CLR	C13-C17-C20-C22
4	B	405	CLR	C13-C17-C20-C22
4	B	407	CLR	C13-C17-C20-C22
4	A	403	CLR	C16-C17-C20-C22
4	A	405	CLR	C16-C17-C20-C22
4	B	402	CLR	C16-C17-C20-C22
4	B	407	CLR	C16-C17-C20-C22
4	A	406	CLR	C17-C20-C22-C23
4	B	409	CLR	C17-C20-C22-C23
4	A	402	CLR	C21-C20-C22-C23
4	B	405	CLR	C21-C20-C22-C23
4	A	402	CLR	C16-C17-C20-C21
4	B	405	CLR	C16-C17-C20-C21
4	A	406	CLR	C21-C20-C22-C23
4	B	409	CLR	C21-C20-C22-C23
4	A	408	CLR	C16-C17-C20-C22
4	B	404	CLR	C16-C17-C20-C22

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Mol	Chain	Res	Type	Atoms
4	A	403	CLR	C17-C20-C22-C23
4	A	405	CLR	C17-C20-C22-C23
4	B	402	CLR	C17-C20-C22-C23
4	B	407	CLR	C17-C20-C22-C23
4	A	409	CLR	C20-C22-C23-C24
4	B	406	CLR	C20-C22-C23-C24
4	A	408	CLR	C21-C20-C22-C23
4	B	404	CLR	C21-C20-C22-C23
4	A	405	CLR	C21-C20-C22-C23
4	B	402	CLR	C21-C20-C22-C23
4	A	408	CLR	C17-C20-C22-C23
4	B	404	CLR	C17-C20-C22-C23
3	A	401	PCF	C40-C41-C42-C43
3	B	401	PCF	C40-C41-C42-C43
3	A	401	PCF	C38-C39-C40-C41
3	B	401	PCF	C38-C39-C40-C41
3	A	401	PCF	C32-C33-C34-C35
3	B	401	PCF	C32-C33-C34-C35
4	A	409	CLR	C16-C17-C20-C22
4	B	406	CLR	C16-C17-C20-C22
3	A	401	PCF	C33-C34-C35-C36
3	B	401	PCF	C33-C34-C35-C36
4	A	404	CLR	C20-C22-C23-C24
4	B	408	CLR	C20-C22-C23-C24
4	B	403	CLR	C22-C23-C24-C25
4	A	407	CLR	C22-C23-C24-C25
4	A	405	CLR	C16-C17-C20-C21
4	B	402	CLR	C16-C17-C20-C21
4	A	402	CLR	C16-C17-C20-C22
4	B	405	CLR	C16-C17-C20-C22
4	A	409	CLR	C23-C24-C25-C27
4	B	406	CLR	C23-C24-C25-C27
3	A	401	PCF	C2-C1-O11-P
3	B	401	PCF	C2-C1-O11-P
3	A	401	PCF	C1-C2-C3-O31
3	B	401	PCF	C1-C2-C3-O31
3	A	401	PCF	C35-C36-C37-C38
3	B	401	PCF	C35-C36-C37-C38
4	A	409	CLR	C23-C24-C25-C26
4	B	406	CLR	C23-C24-C25-C26
4	A	407	CLR	C13-C17-C20-C21
4	B	403	CLR	C13-C17-C20-C21

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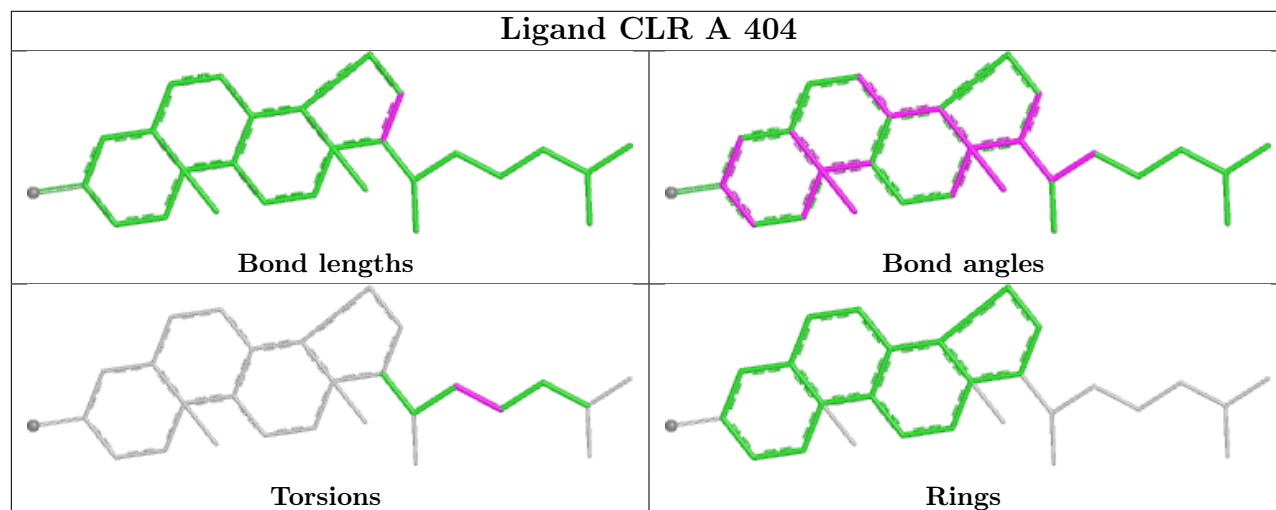
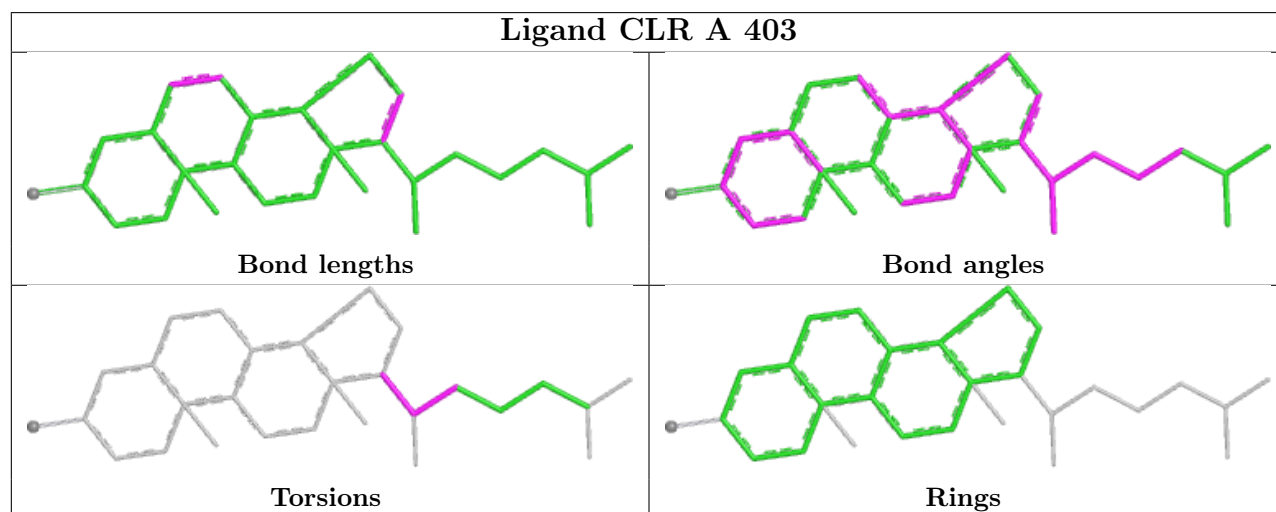
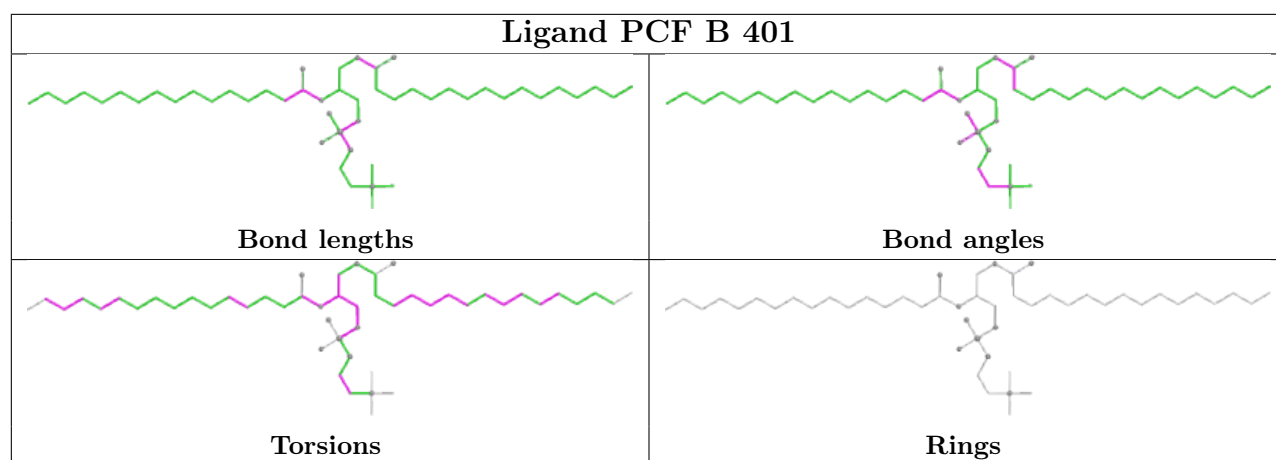
Mol	Chain	Res	Type	Atoms
3	A	401	PCF	O11-C1-C2-C3
3	B	401	PCF	O11-C1-C2-C3
3	A	401	PCF	C1-C2-O21-C21
3	B	401	PCF	C1-C2-O21-C21
3	A	401	PCF	O13-C11-C12-N
3	B	401	PCF	O13-C11-C12-N
3	A	401	PCF	O11-C1-C2-O21
3	B	401	PCF	O11-C1-C2-O21
3	A	401	PCF	O21-C2-C3-O31
3	B	401	PCF	O21-C2-C3-O31
4	A	405	CLR	C13-C17-C20-C22
4	B	402	CLR	C13-C17-C20-C22
3	A	401	PCF	C1-O11-P-O14
3	B	401	PCF	C1-O11-P-O14
4	A	405	CLR	C13-C17-C20-C21
4	B	402	CLR	C13-C17-C20-C21
4	A	408	CLR	C23-C24-C25-C27
4	B	404	CLR	C23-C24-C25-C27
4	A	407	CLR	C21-C20-C22-C23
3	A	401	PCF	C48-C49-C50-C51
3	B	401	PCF	C48-C49-C50-C51
4	B	403	CLR	C21-C20-C22-C23
4	A	407	CLR	C17-C20-C22-C23
3	A	401	PCF	C49-C50-C51-C52
3	B	401	PCF	C49-C50-C51-C52
4	A	409	CLR	C22-C23-C24-C25
4	B	406	CLR	C22-C23-C24-C25
4	B	403	CLR	C17-C20-C22-C23
4	A	407	CLR	C13-C17-C20-C22
4	B	403	CLR	C13-C17-C20-C22
4	A	407	CLR	C16-C17-C20-C21
4	B	403	CLR	C16-C17-C20-C21
3	A	401	PCF	C37-C38-C39-C40
3	B	401	PCF	C37-C38-C39-C40
3	B	401	PCF	C30-C47-C48-C49
3	A	401	PCF	C30-C47-C48-C49
3	B	401	PCF	C23-C24-C25-C26
3	A	401	PCF	C23-C24-C25-C26
3	A	401	PCF	C34-C35-C36-C37
3	B	401	PCF	C34-C35-C36-C37

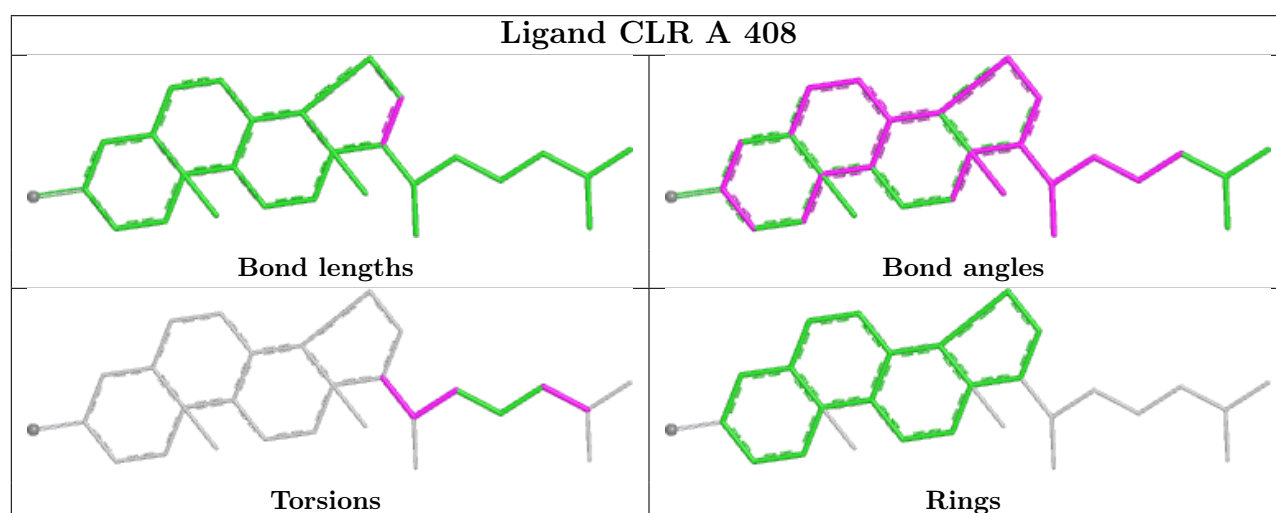
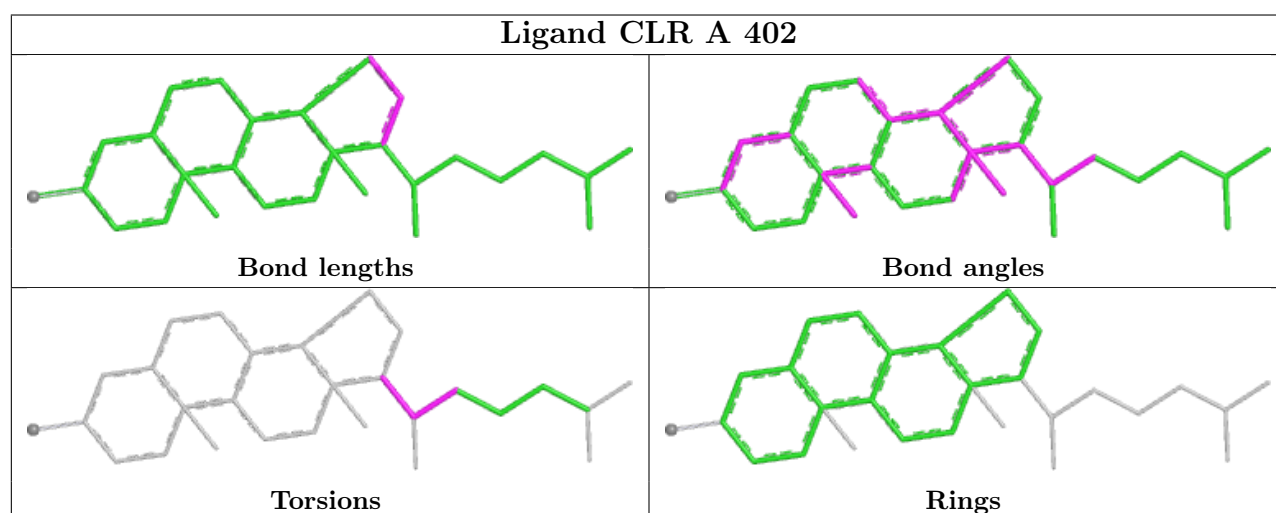
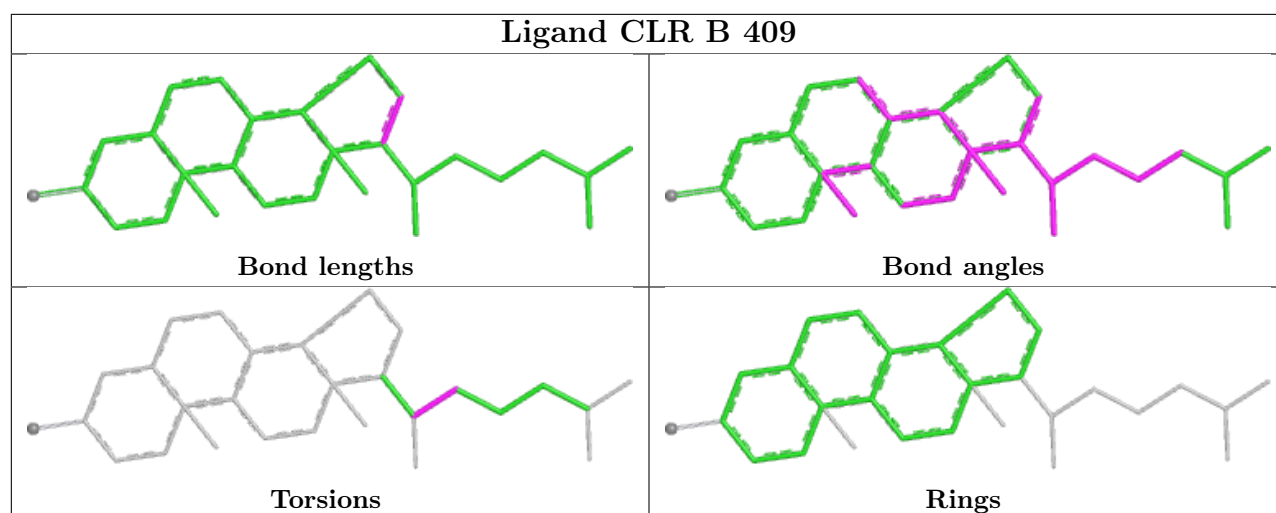
There are no ring outliers.

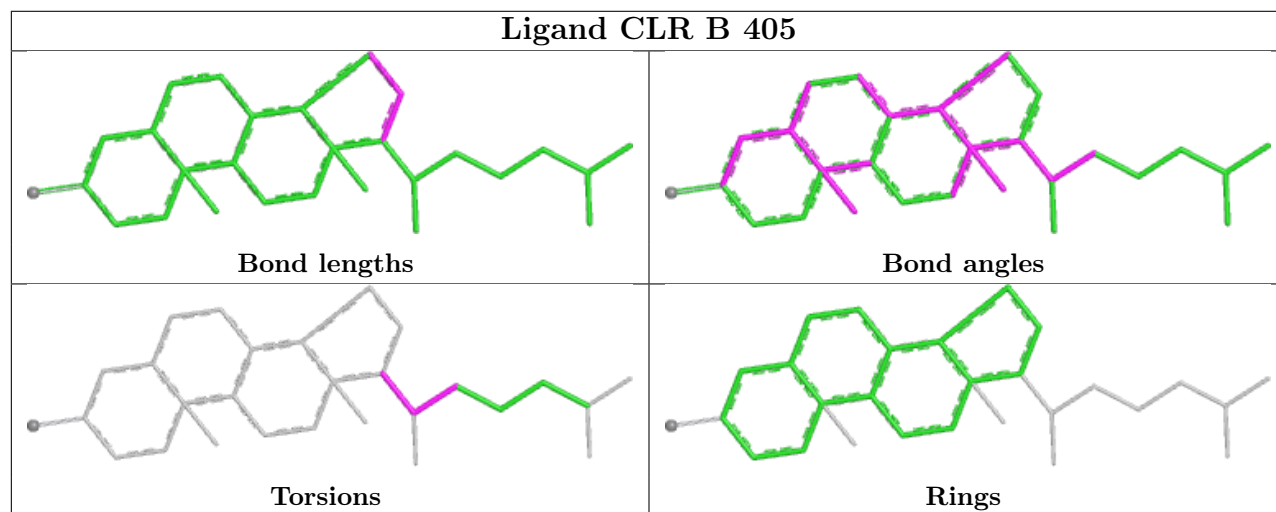
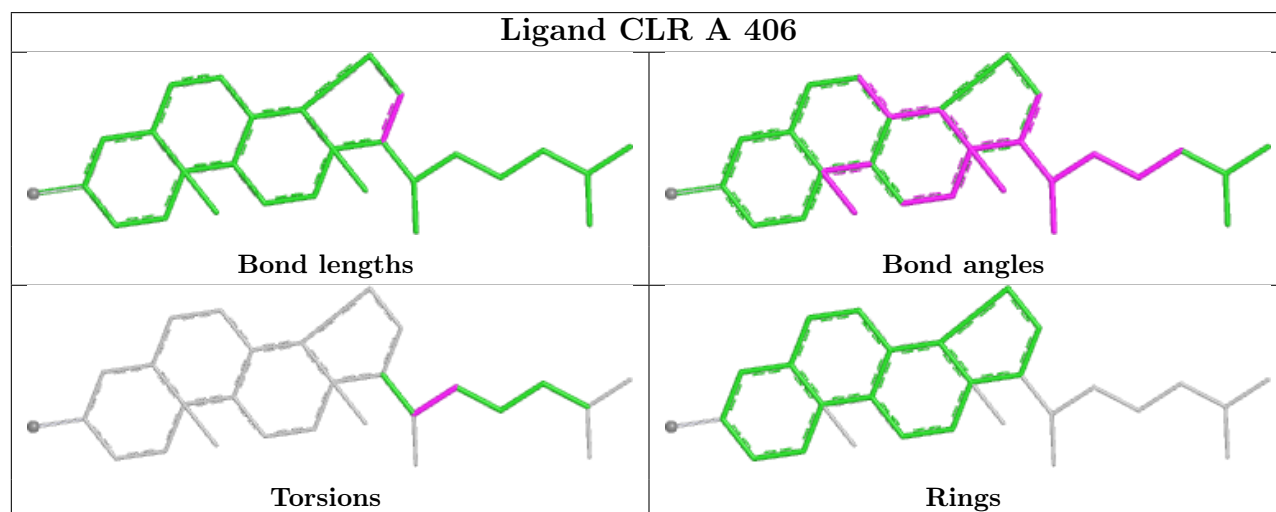
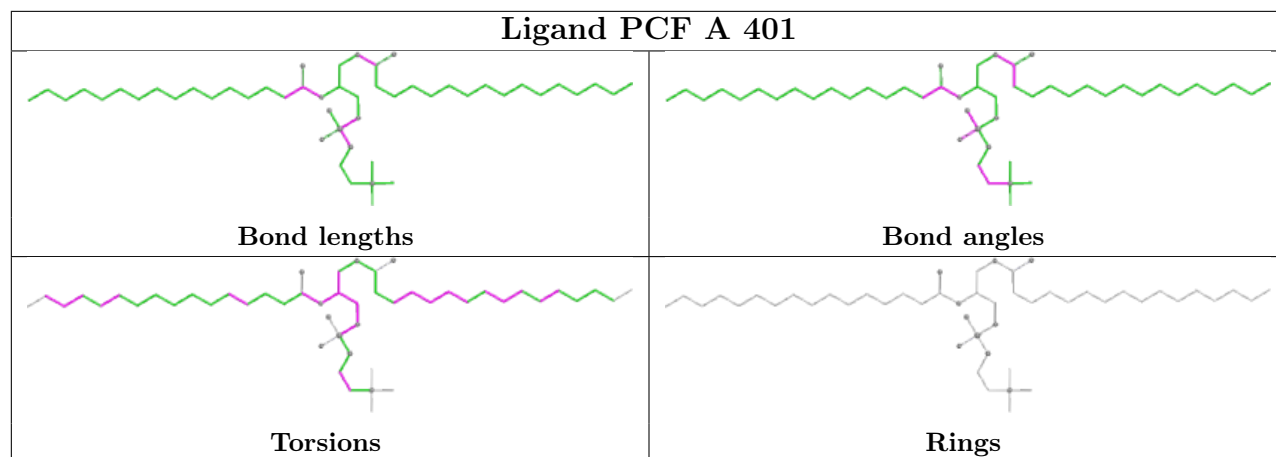
18 monomers are involved in 194 short contacts:

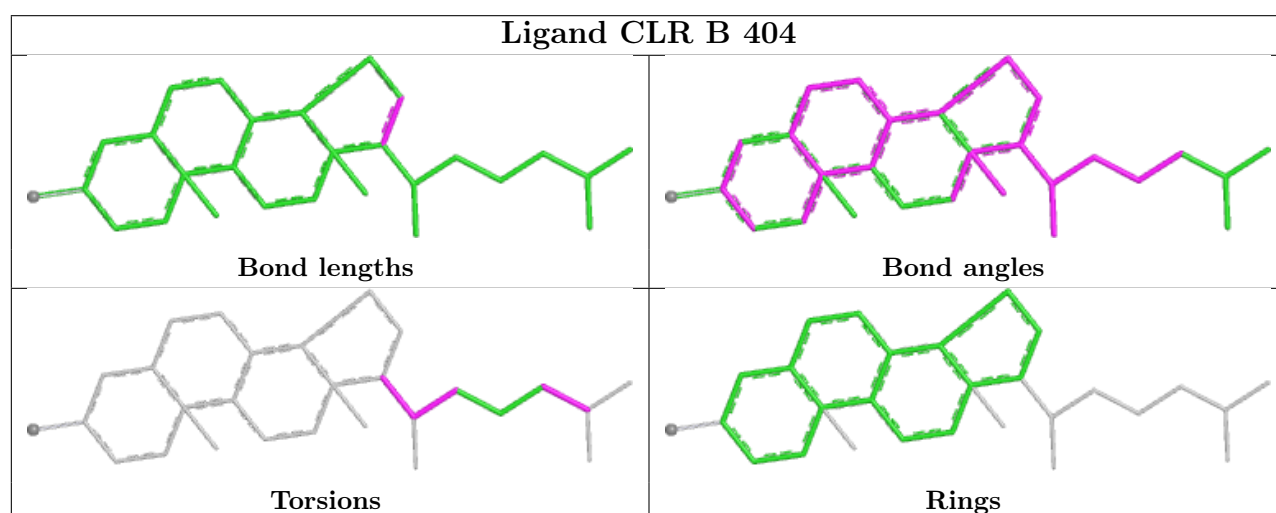
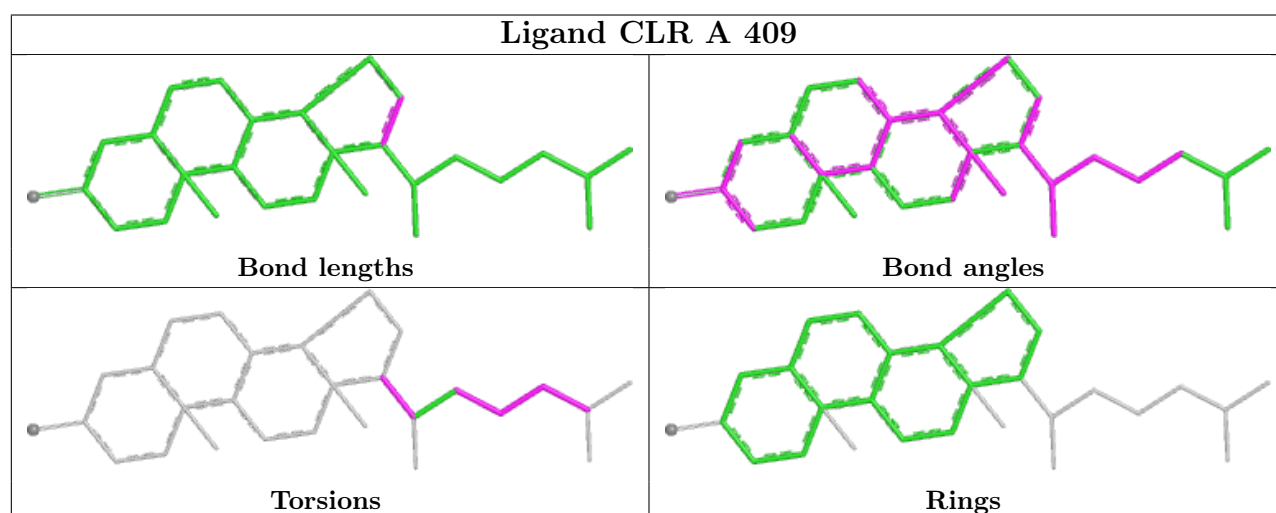
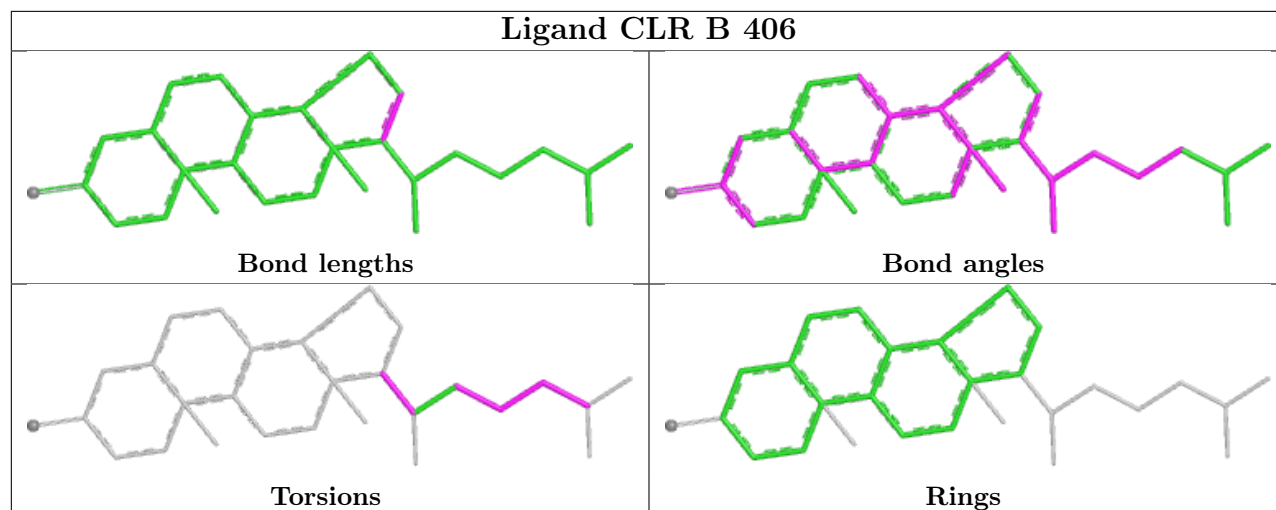
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	PCF	18	0
4	A	403	CLR	12	0
4	A	404	CLR	19	0
4	B	409	CLR	8	0
4	A	402	CLR	8	0
4	A	408	CLR	28	0
3	A	401	PCF	17	0
4	A	406	CLR	9	0
4	B	405	CLR	8	0
4	B	406	CLR	12	0
4	A	409	CLR	11	0
4	B	404	CLR	30	0
4	A	407	CLR	27	0
4	B	408	CLR	20	0
4	A	405	CLR	11	0
4	B	407	CLR	11	0
4	B	403	CLR	27	0
4	B	402	CLR	11	0

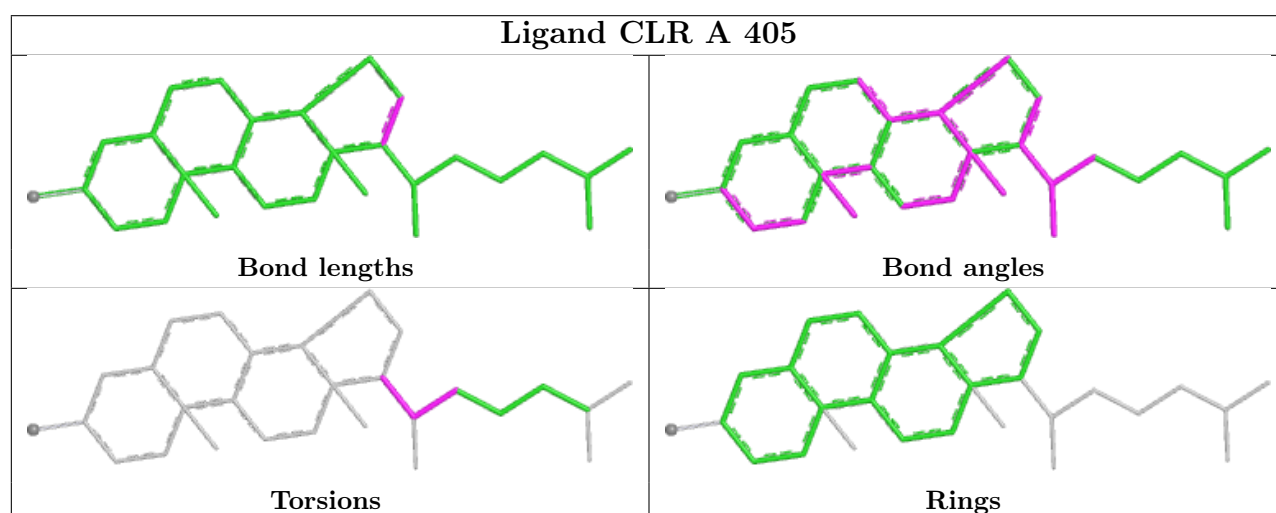
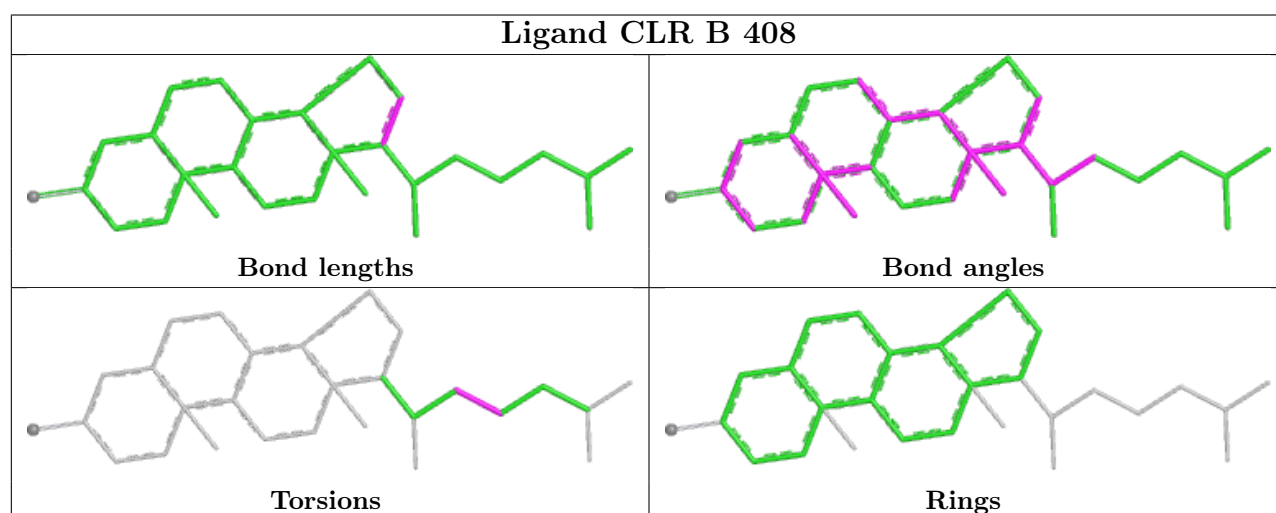
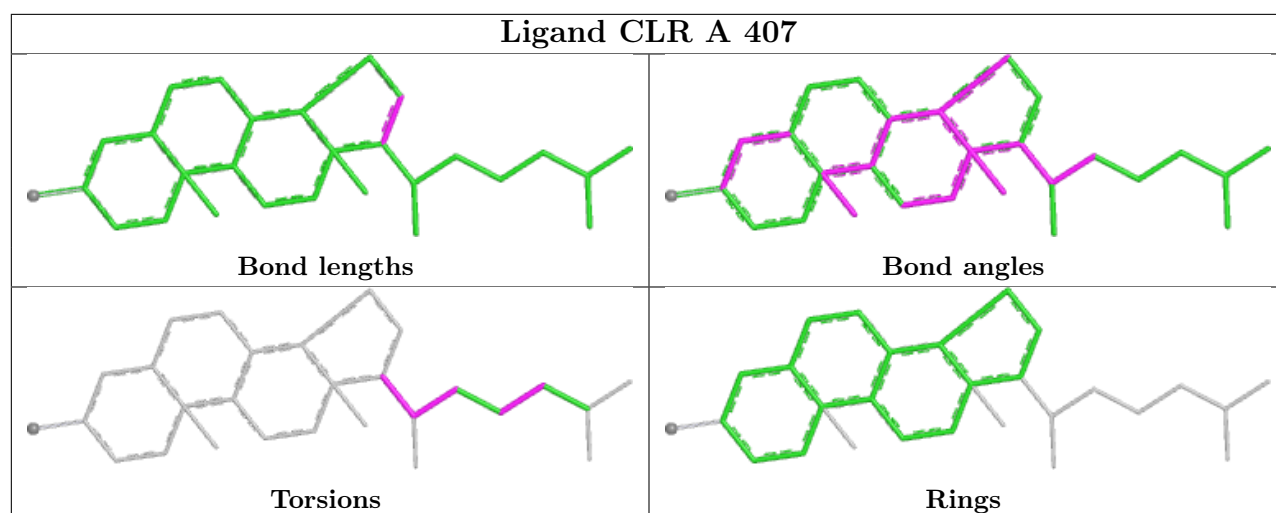
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

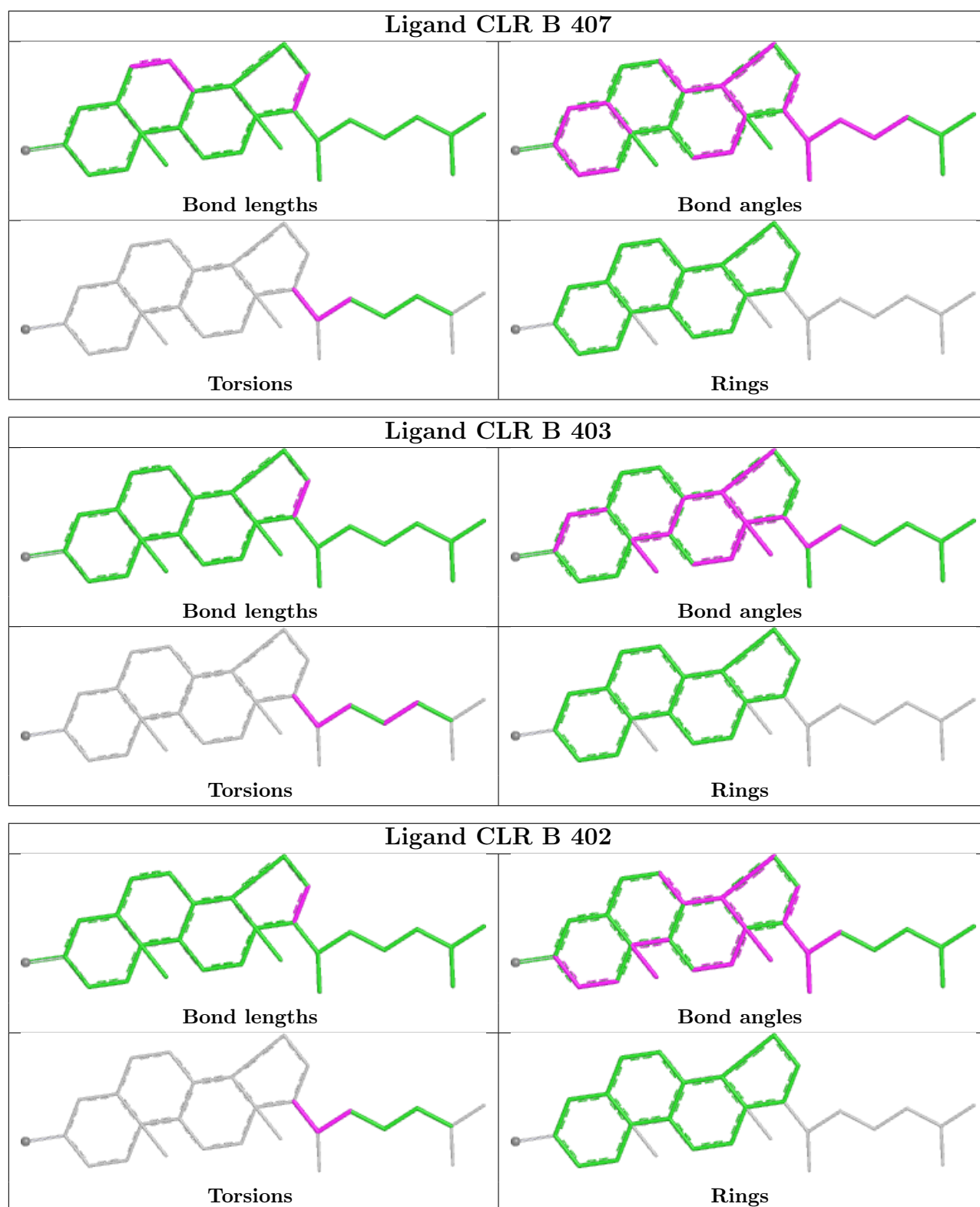












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

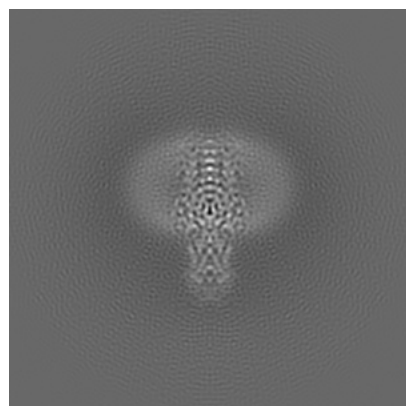
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63307. These allow visual inspection of the internal detail of the map and identification of artifacts.

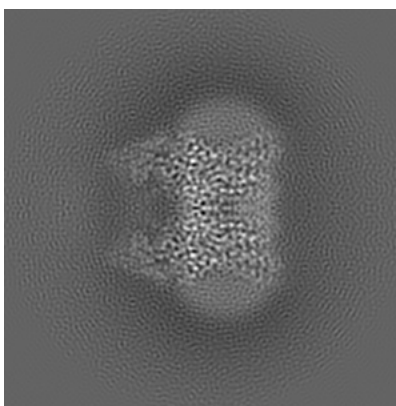
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

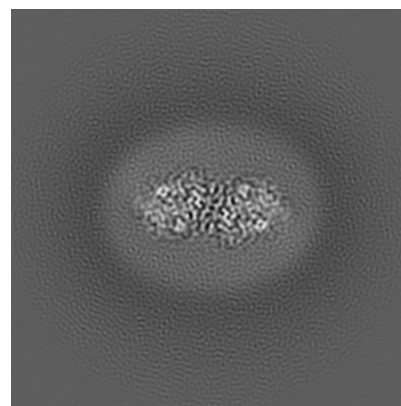
6.1.1 Primary map



X

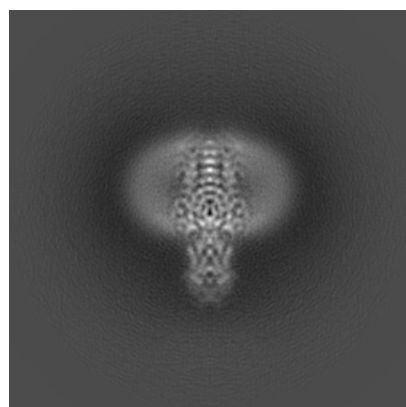


Y

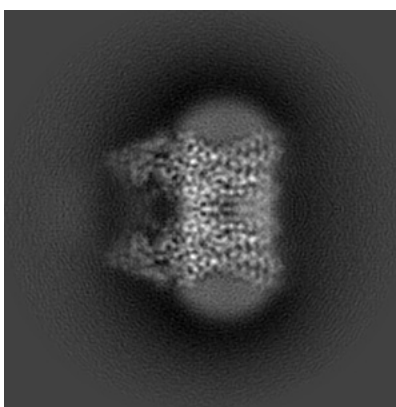


Z

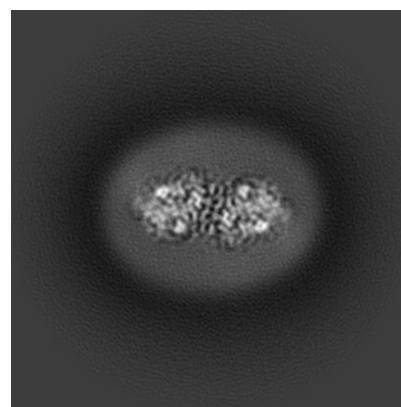
6.1.2 Raw map



X



Y

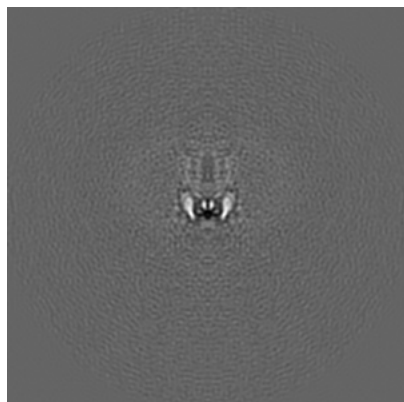


Z

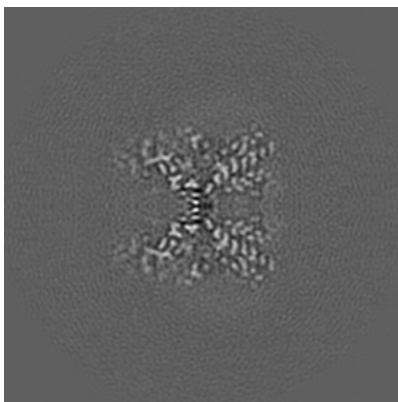
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

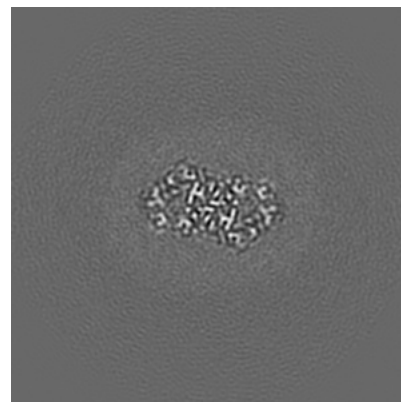
6.2.1 Primary map



X Index: 112

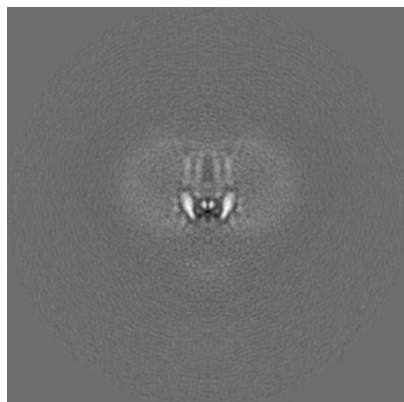


Y Index: 112

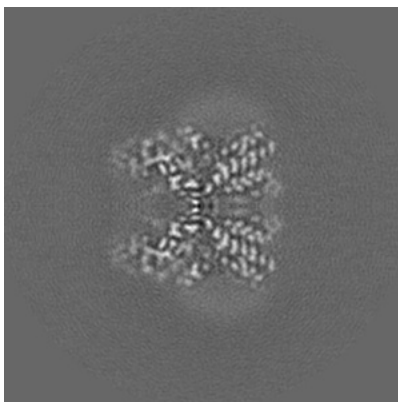


Z Index: 112

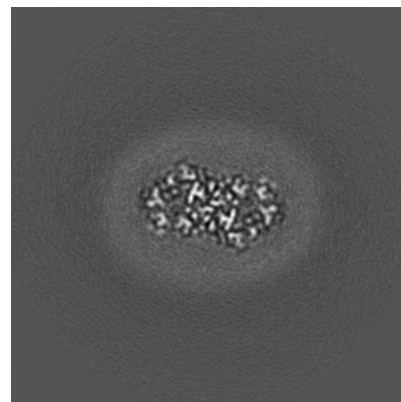
6.2.2 Raw map



X Index: 112



Y Index: 112

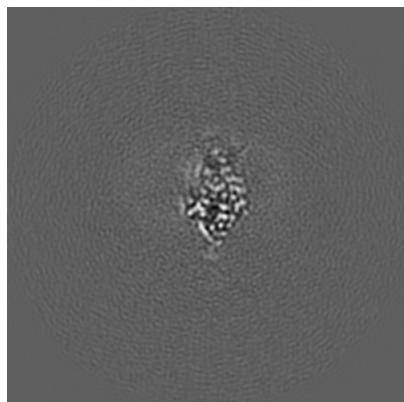


Z Index: 112

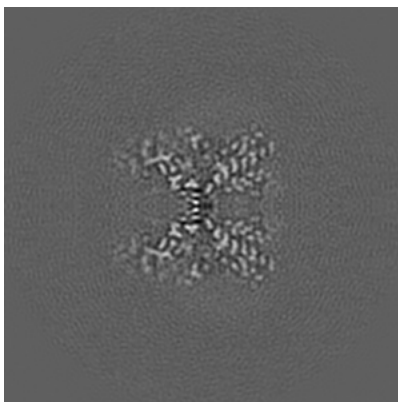
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

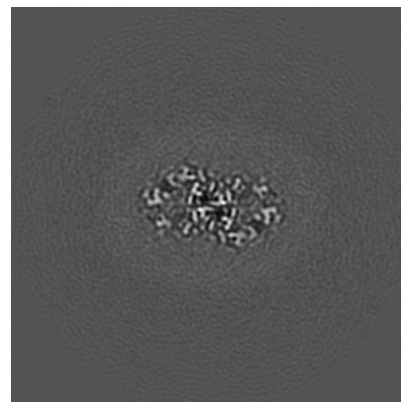
6.3.1 Primary map



X Index: 102

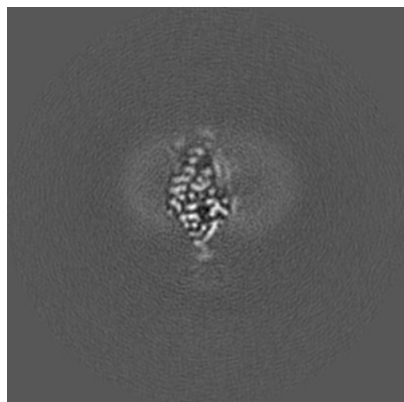


Y Index: 112

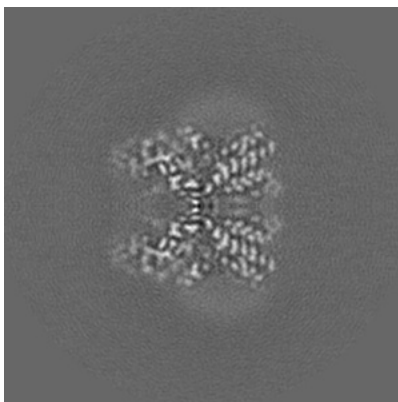


Z Index: 111

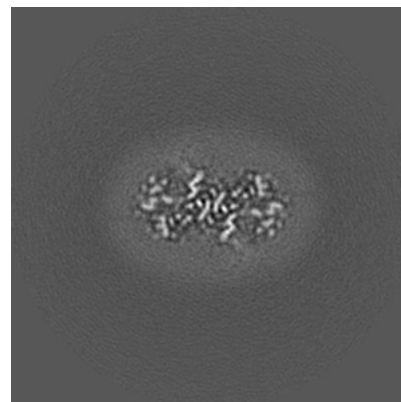
6.3.2 Raw map



X Index: 122



Y Index: 112

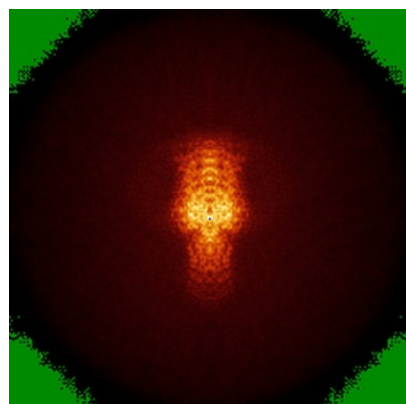


Z Index: 106

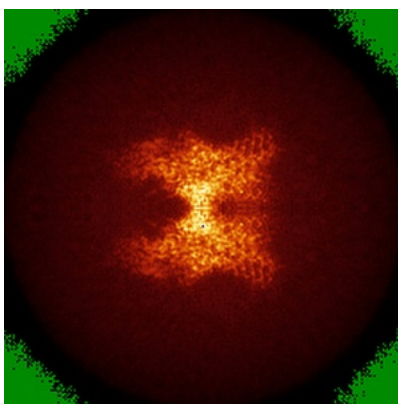
The images above show the largest variance slices of the map in three orthogonal directions.

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

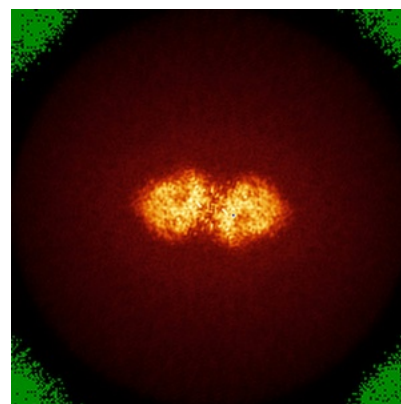
6.4.1 Primary map



X

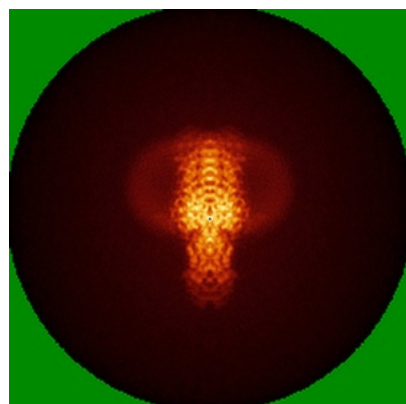


Y

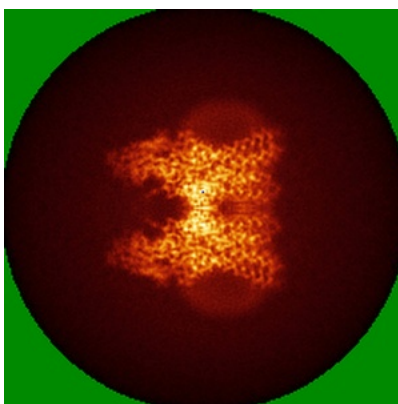


Z

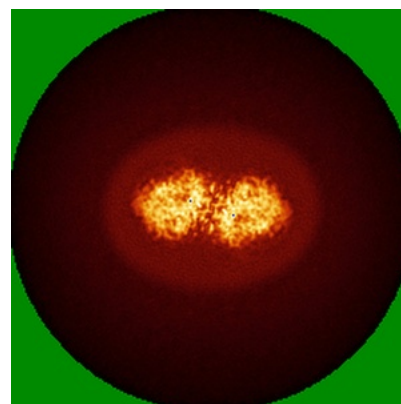
6.4.2 Raw map



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](#)

This section was not generated.

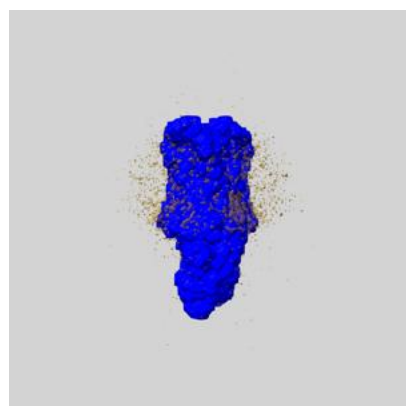
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

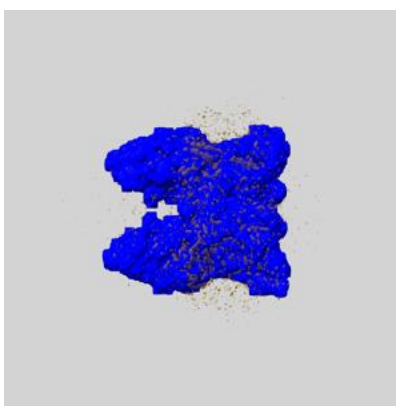
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

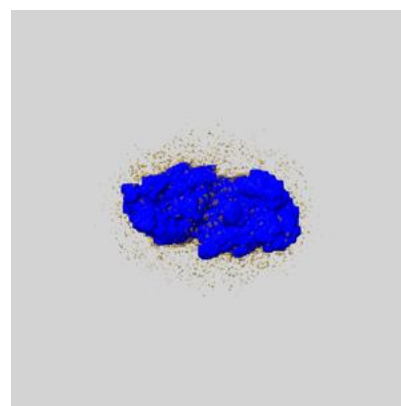
6.6.1 emd_63307_msk_1.map [i](#)



X



Y

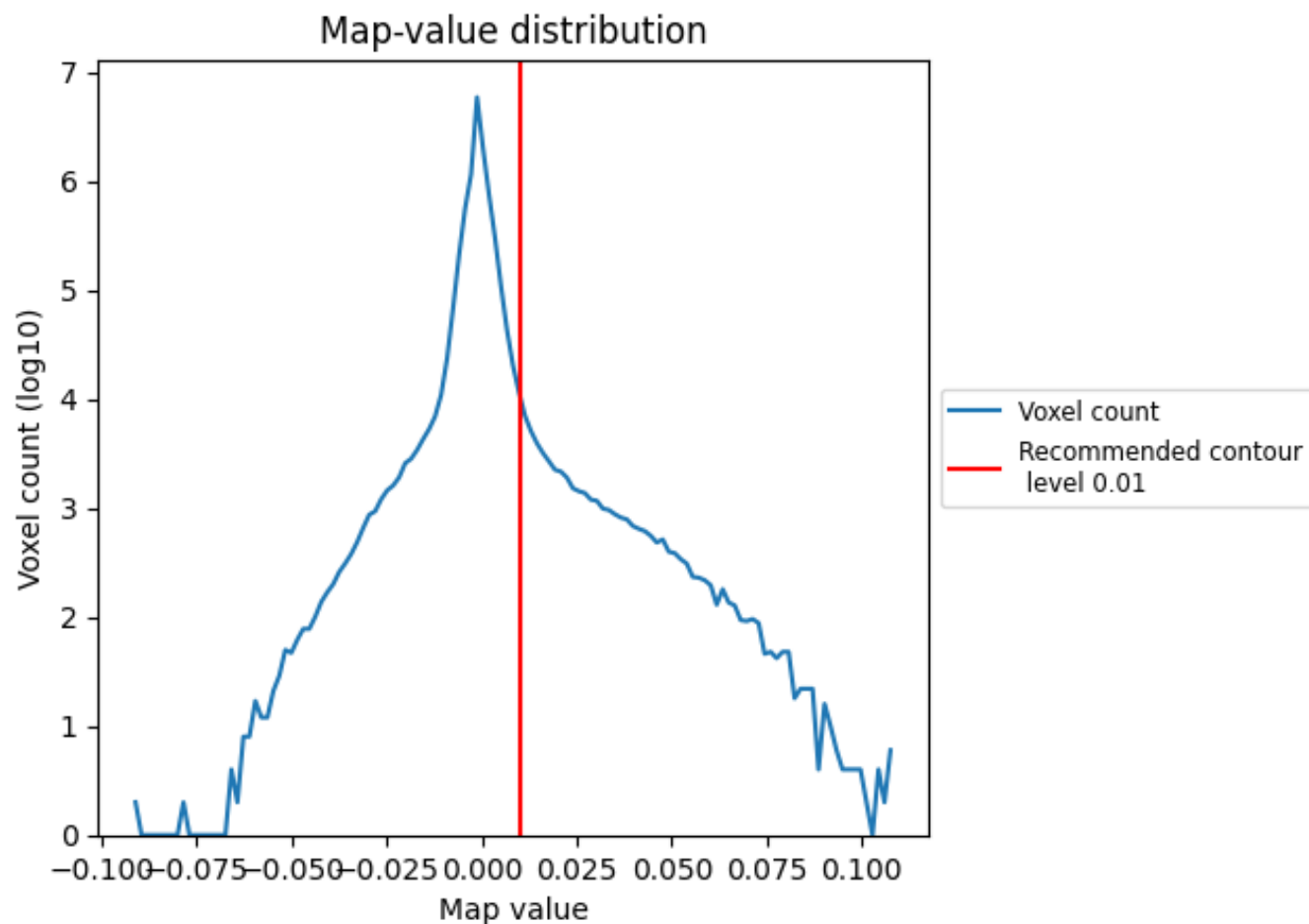


Z

7 Map analysis [i](#)

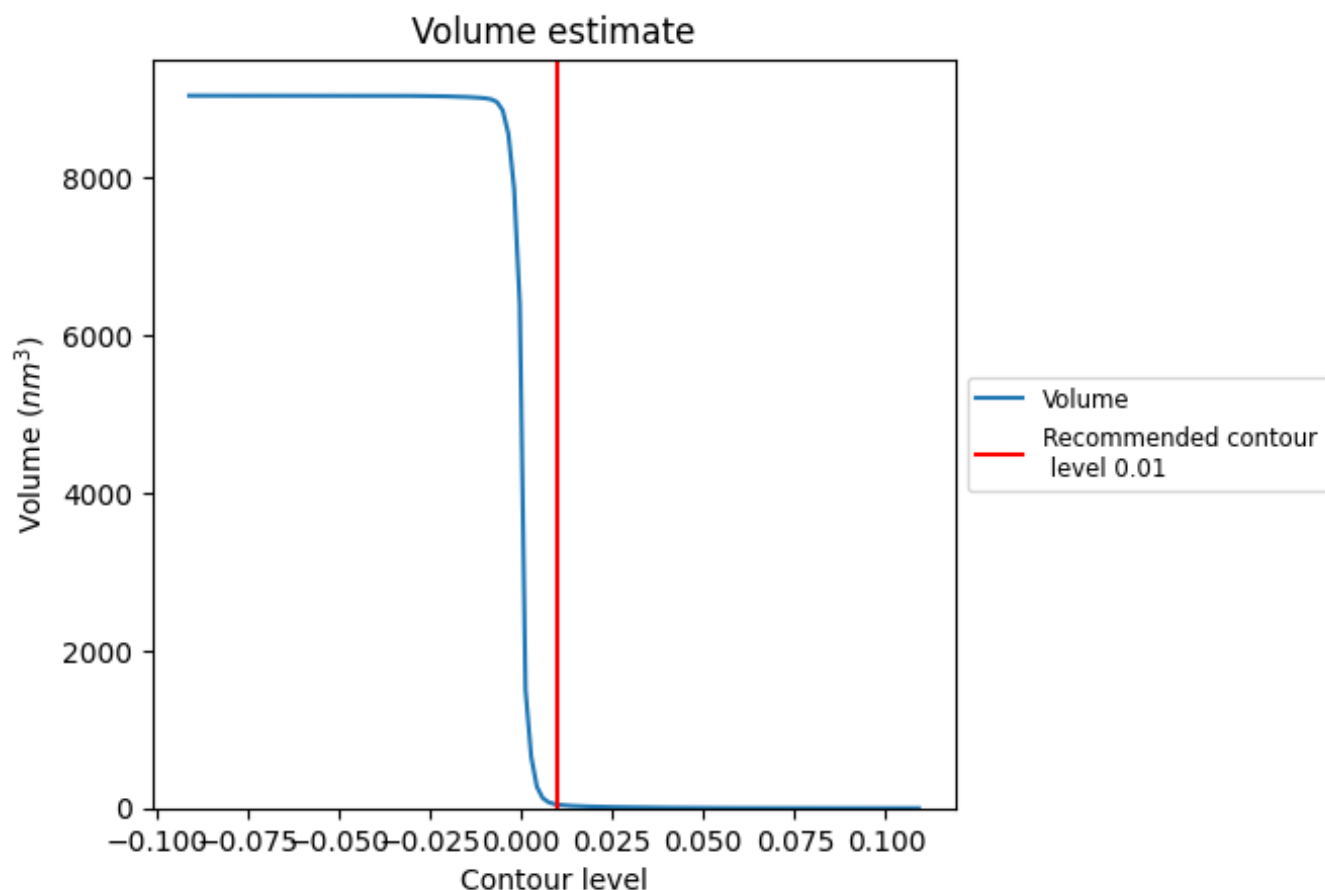
This section contains the results of statistical analysis of the map.

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.

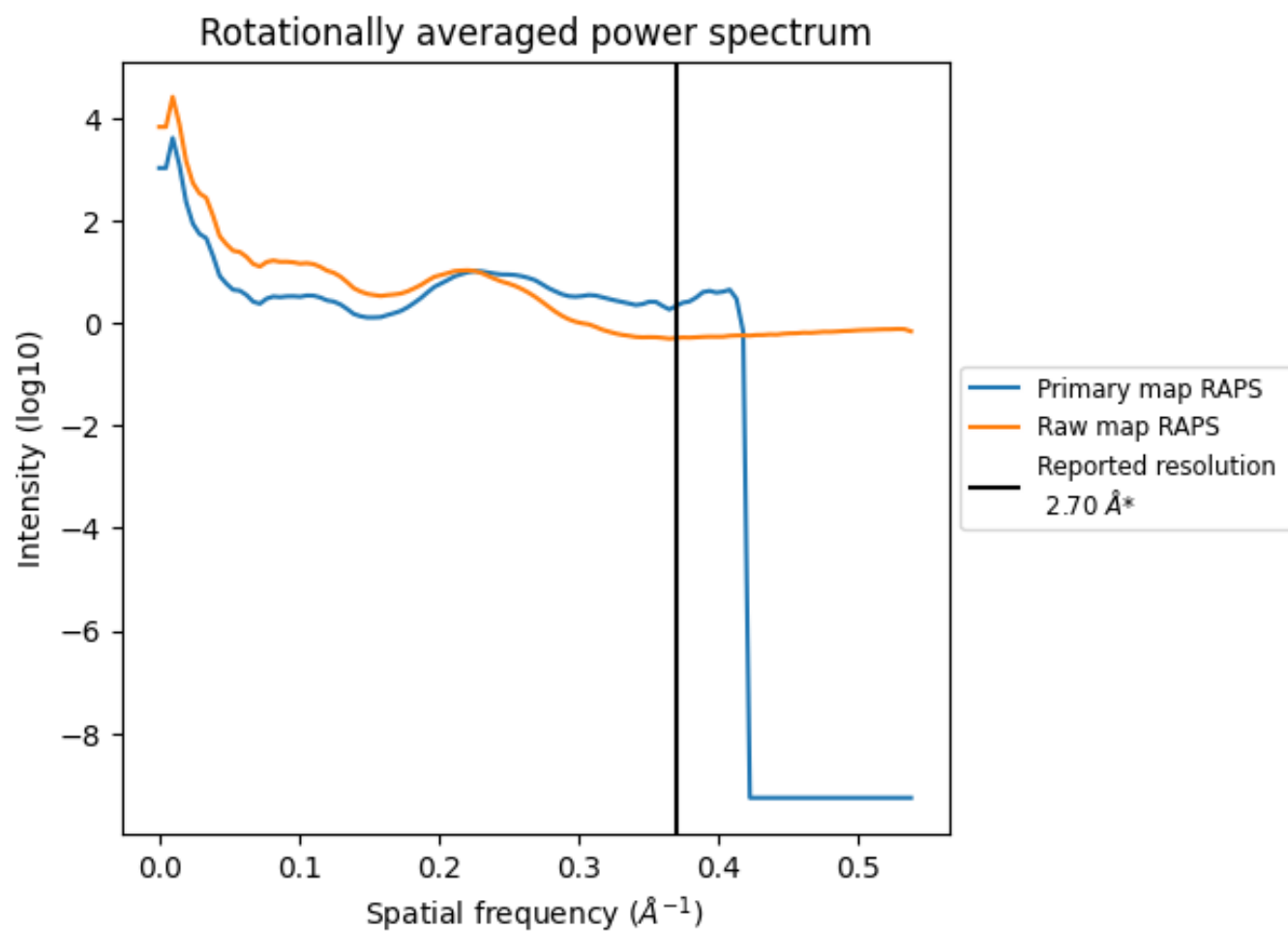
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 46 nm^3 ; this corresponds to an approximate mass of 41 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 ⓘ

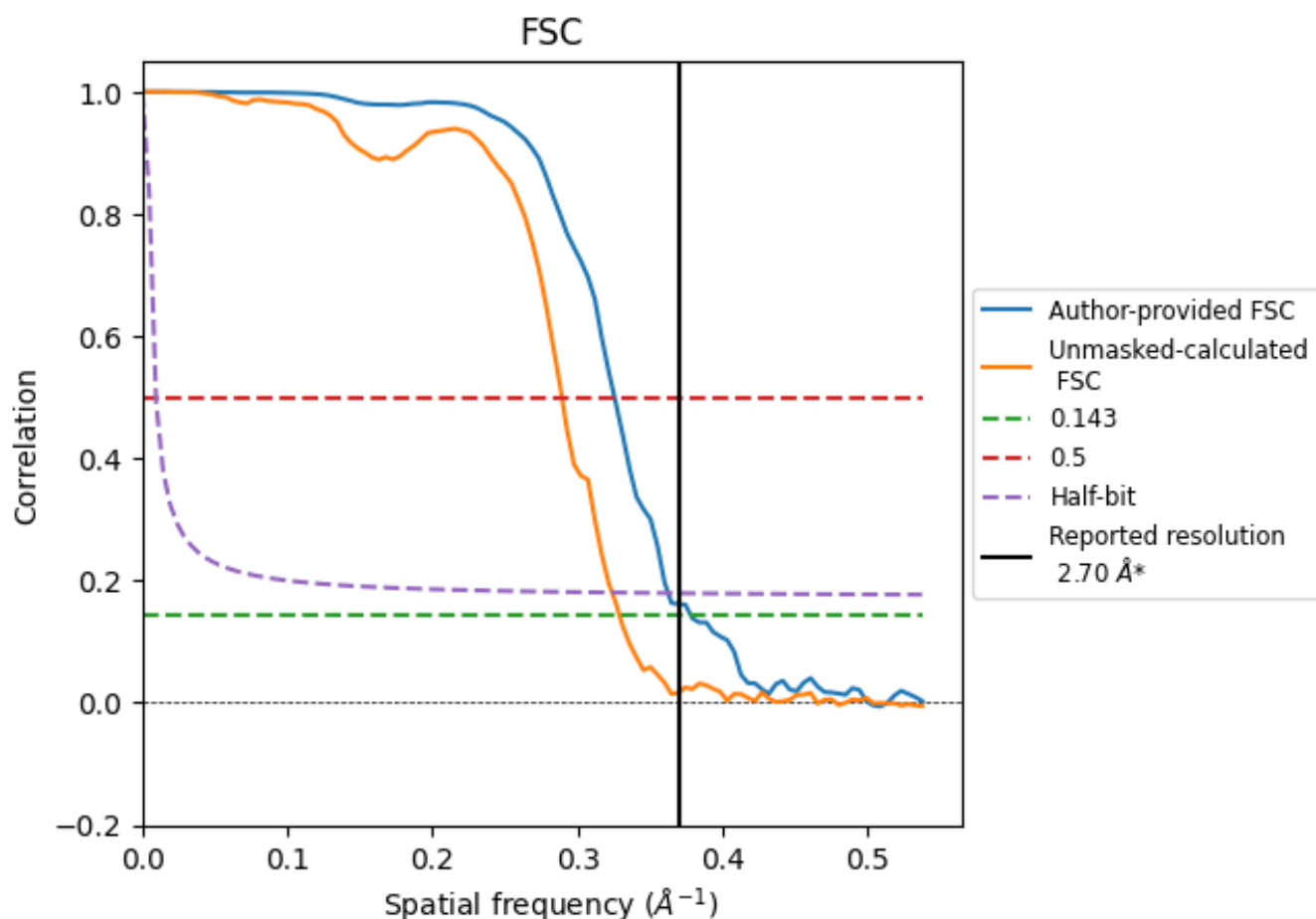


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

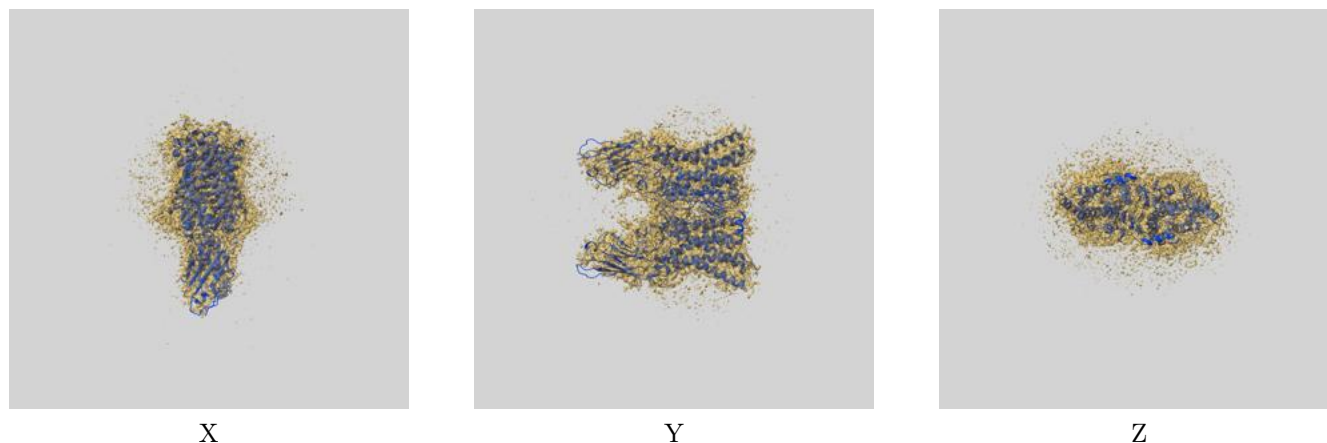
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.64	3.07	2.76
Unmasked-calculated*	3.04	3.46	3.09

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.04 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

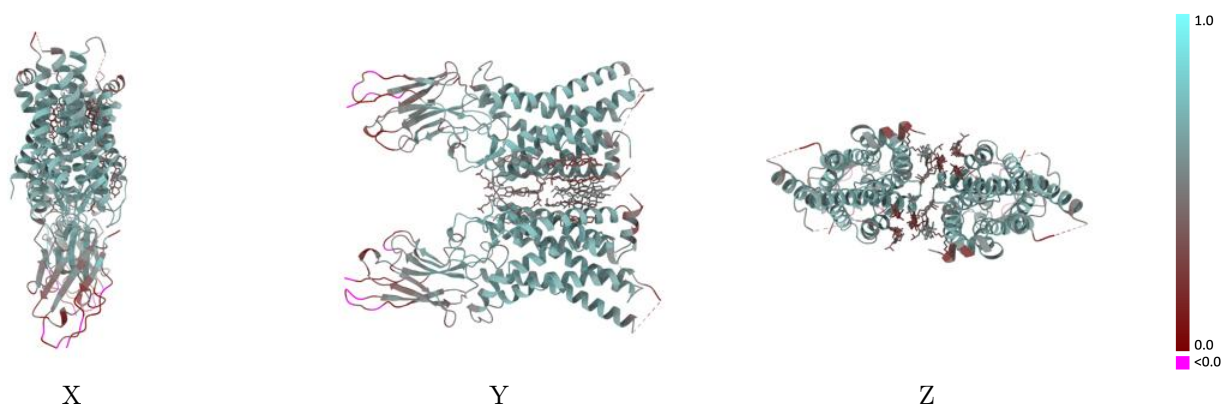
This section contains information regarding the fit between EMDB map EMD-63307 and PDB model 9LQW. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



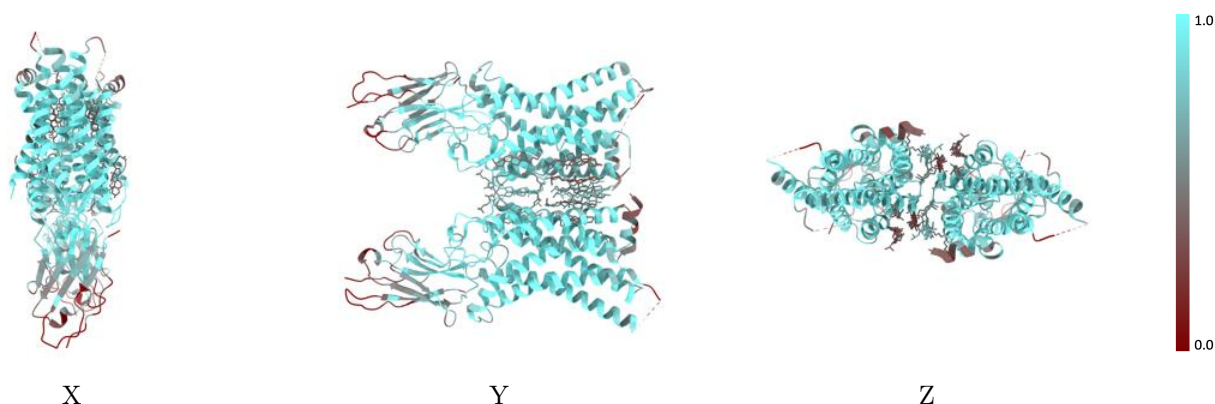
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



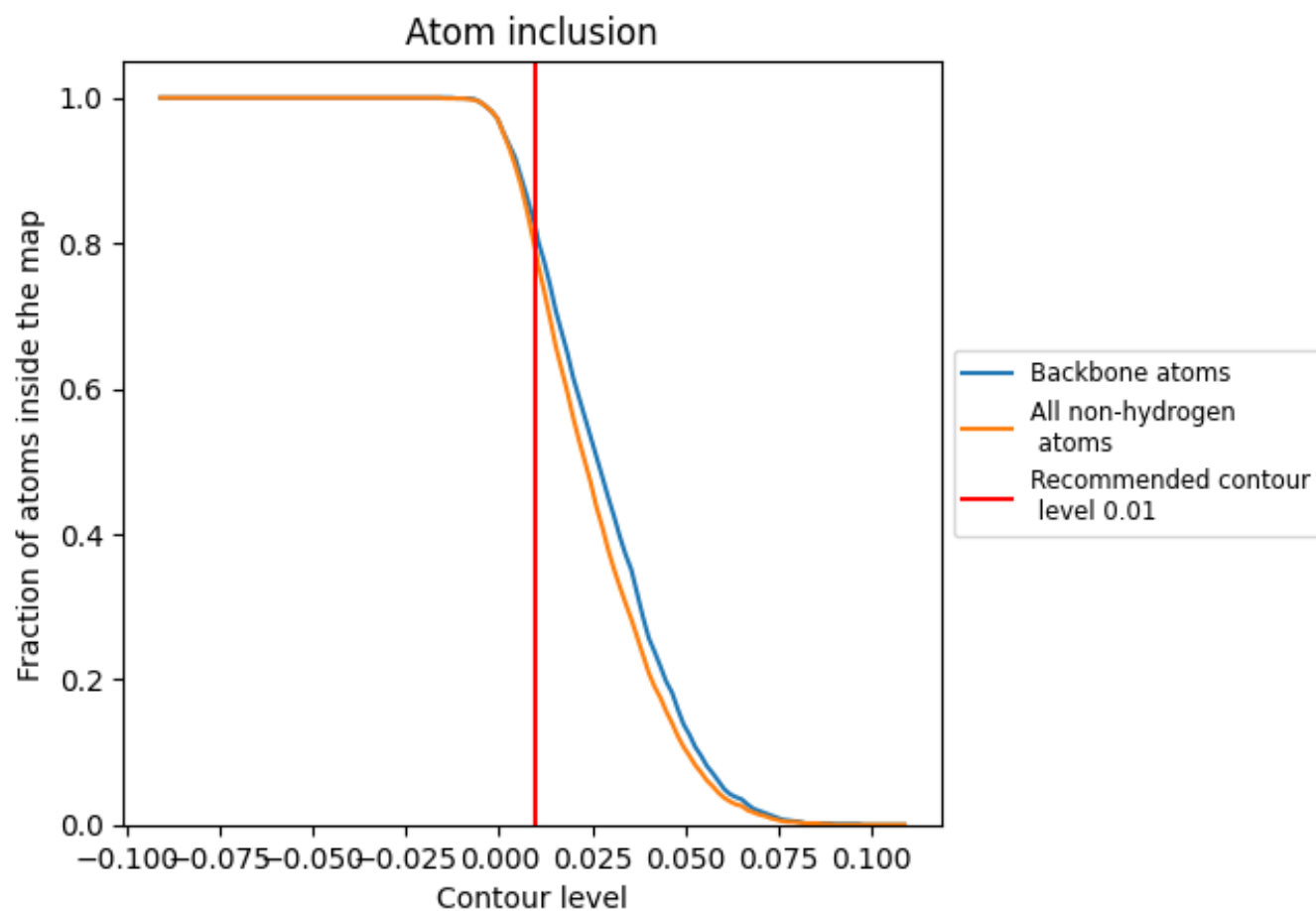
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7850	0.5390
A	0.8570	0.5830
B	0.8540	0.5820
C	0.6040	0.4310
D	0.6070	0.4280

