



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 02:40 AM UTC

PDB ID : 8C1Q / pdb_00008c1q
EMDB ID : EMD-16380
Title : Resting state homomeric GluA1 AMPA receptor in complex with TARP gamma 3
Authors : Zhang, D.; Ivica, J.; Krieger, J.M.; Ho, H.; Yamashita, K.; Cais, O.; Greger, I.
Deposited on : 2022-12-21
Resolution : 2.82 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:

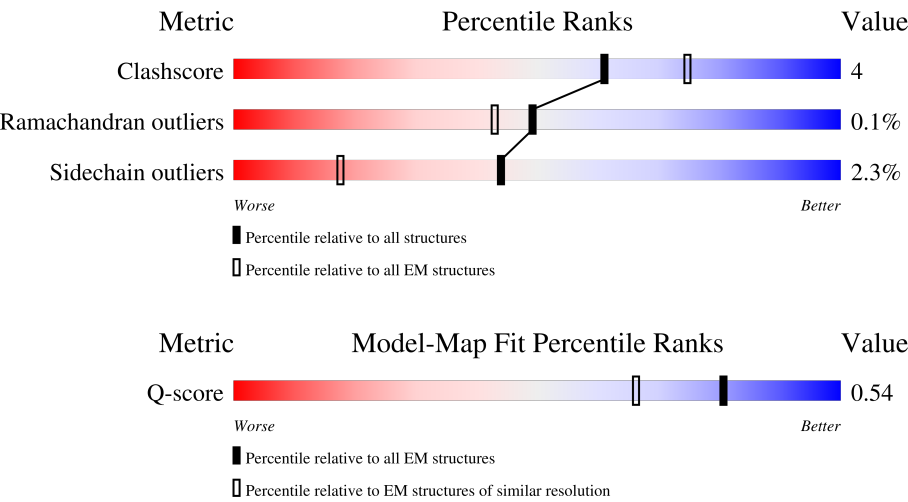
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 2.82 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	11795 (2.32 - 3.32)

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	915	39%5%56%
1	B	915	16% 38%5%56%
1	C	915	18% 37%7%56%
1	D	915	39%.56%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	314	9% 50% 5% 44%
2	F	314	10% 52% 44%
2	G	314	14% 49% 6% 44%
2	H	314	8% 52% 44%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 18462 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 Glutamate receptor 1 flip isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	405	Total	C	N	O	S	4	0
			3179	2064	515	580	20		
1	B	400	Total	C	N	O	S	5	0
			3012	1971	480	542	19		
1	C	406	Total	C	N	O	S	4	0
			3116	2025	500	573	18		
1	D	400	Total	C	N	O	S	5	0
			3152	2050	508	574	20		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	ASP	-	insertion	UNP P19490
A	-5	TYR	-	insertion	UNP P19490
A	-4	LYS	-	insertion	UNP P19490
A	-3	ASP	-	insertion	UNP P19490
A	-2	ASP	-	insertion	UNP P19490
A	-1	ASP	-	insertion	UNP P19490
A	0	ASP	-	insertion	UNP P19490
A	1	LYS	-	insertion	UNP P19490
B	-6	ASP	-	insertion	UNP P19490
B	-5	TYR	-	insertion	UNP P19490
B	-4	LYS	-	insertion	UNP P19490
B	-3	ASP	-	insertion	UNP P19490
B	-2	ASP	-	insertion	UNP P19490
B	-1	ASP	-	insertion	UNP P19490
B	0	ASP	-	insertion	UNP P19490
B	1	LYS	-	insertion	UNP P19490
C	-6	ASP	-	insertion	UNP P19490
C	-5	TYR	-	insertion	UNP P19490
C	-4	LYS	-	insertion	UNP P19490
C	-3	ASP	-	insertion	UNP P19490
C	-2	ASP	-	insertion	UNP P19490
C	-1	ASP	-	insertion	UNP P19490

Continued on next page...

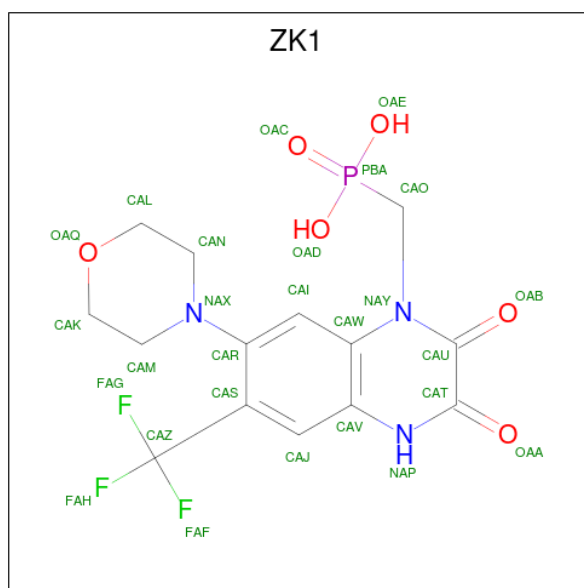
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	ASP	-	insertion	UNP P19490
C	1	LYS	-	insertion	UNP P19490
D	-6	ASP	-	insertion	UNP P19490
D	-5	TYR	-	insertion	UNP P19490
D	-4	LYS	-	insertion	UNP P19490
D	-3	ASP	-	insertion	UNP P19490
D	-2	ASP	-	insertion	UNP P19490
D	-1	ASP	-	insertion	UNP P19490
D	0	ASP	-	insertion	UNP P19490
D	1	LYS	-	insertion	UNP P19490

- Molecule 2 is a protein called Voltage-dependent calcium channel gamma-3 subunit.

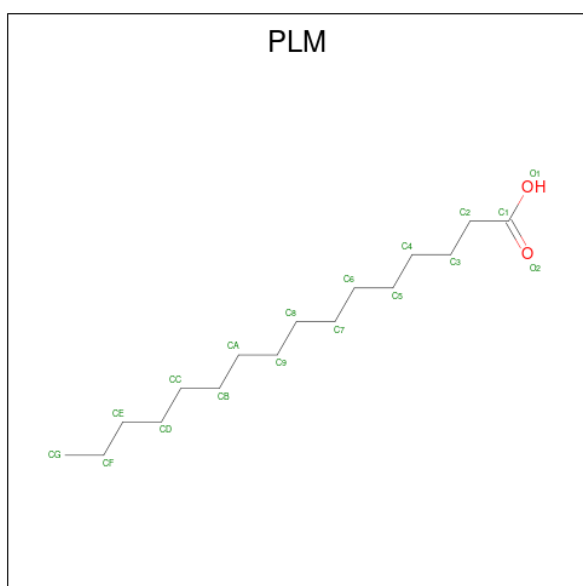
Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	176	Total	C	N	O	S	0	0
			1367	894	229	236	8		
2	F	176	Total	C	N	O	S	0	0
			1367	894	229	236	8		
2	G	176	Total	C	N	O	S	0	0
			1367	894	229	236	8		
2	H	176	Total	C	N	O	S	0	0
			1367	894	229	236	8		

- Molecule 3 is {[7-morpholin-4-yl-2,3-dioxo-6-(trifluoromethyl)-3,4-dihydroquinoxalin-1(2H)-yl]methyl}phosphonic acid (CCD ID: ZK1) (formula: C₁₄H₁₅F₃N₃O₆P).



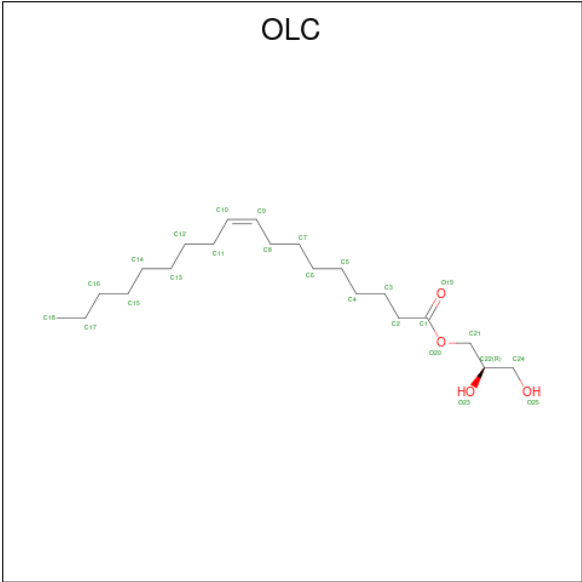
Mol	Chain	Residues	Atoms						AltConf
3	A	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	
3	B	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	
3	C	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	
3	D	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	

- Molecule 4 is PALMITIC ACID (CCD ID: PLM) (formula: $C_{16}H_{32}O_2$).



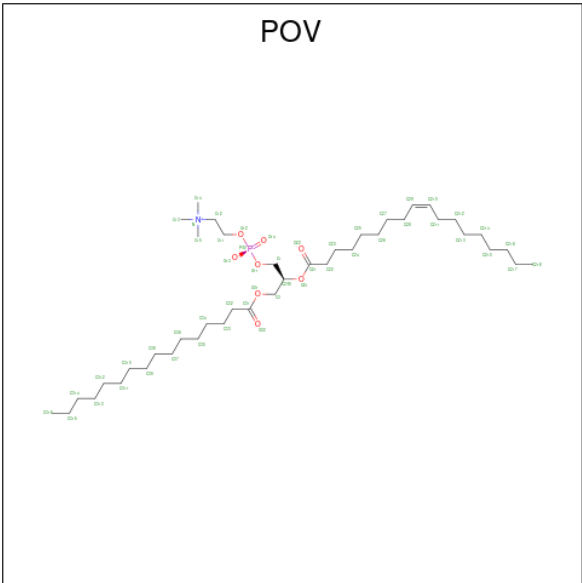
Mol	Chain	Residues	Atoms			AltConf
4	A	1	Total	C	O	0
			18	16	2	
4	B	1	Total	C	O	0
			18	16	2	
4	C	1	Total	C	O	0
			18	16	2	
4	D	1	Total	C	O	0
			18	16	2	

- Molecule 5 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: OLC) (formula: $C_{21}H_{40}O_4$).



Mol	Chain	Residues	Atoms			AltConf
5	A	1	Total	C	O	0
			25	21	4	
5	B	1	Total	C	O	0
			25	21	4	
5	C	1	Total	C	O	0
			25	21	4	
5	D	1	Total	C	O	0
			25	21	4	

- Molecule 6 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylamm onio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P).



Mol	Chain	Residues	Atoms					AltConf
6	E	1	Total	C	N	O	P	0
			37	27	1	8	1	
6	F	1	Total	C	N	O	P	0
			39	29	1	8	1	
6	F	1	Total	C	N	O	P	0
			39	29	1	8	1	
6	G	1	Total	C	N	O	P	0
			37	27	1	8	1	
6	H	1	Total	C	N	O	P	0
			39	29	1	8	1	
6	H	1	Total	C	N	O	P	0
			39	29	1	8	1	

- Molecule 7 is water.

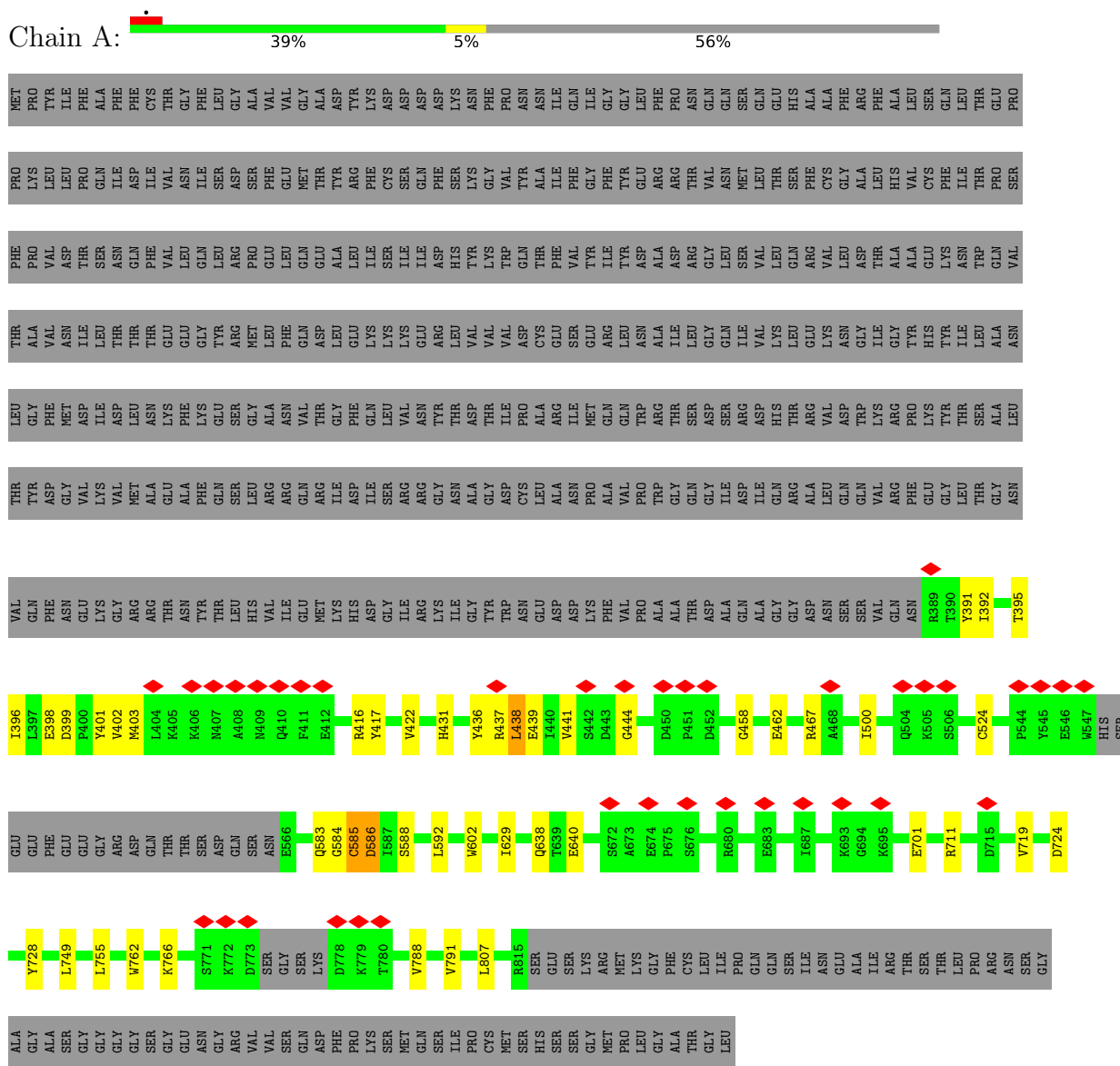
Mol	Chain	Residues	Atoms		AltConf
7	A	6	Total	O	0
			6	6	
7	B	5	Total	O	0
			5	5	
7	C	5	Total	O	0
			5	5	
7	D	6	Total	O	0
			6	6	
7	F	1	Total	O	0
			1	1	
7	G	1	Total	O	0
			1	1	
7	H	1	Total	O	0
			1	1	

3 Residue-property plots

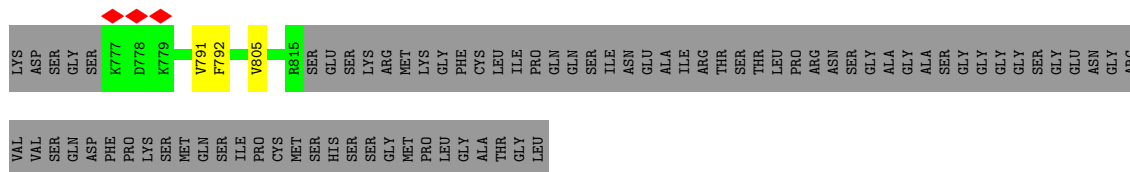
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Glutamate receptor 1 flip isoform

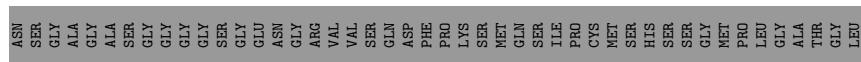
Chain A:



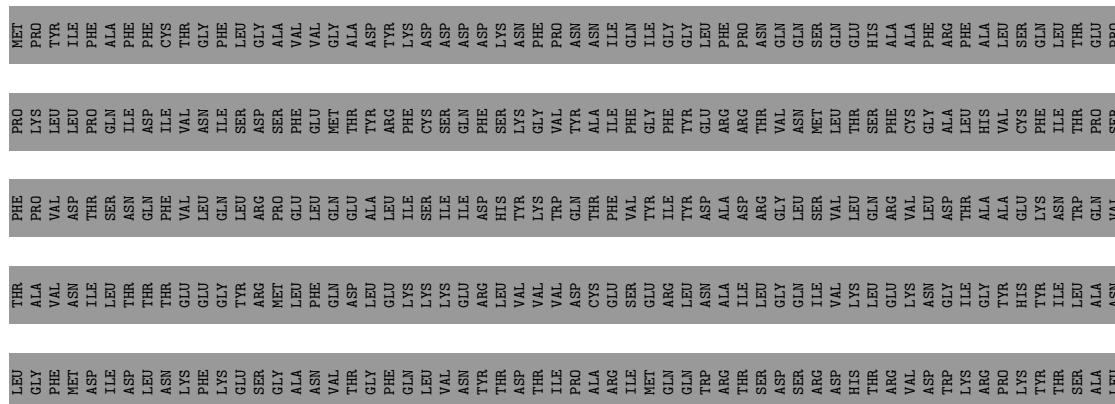
- Molecule 1: Glutamate receptor 1 flip isoform

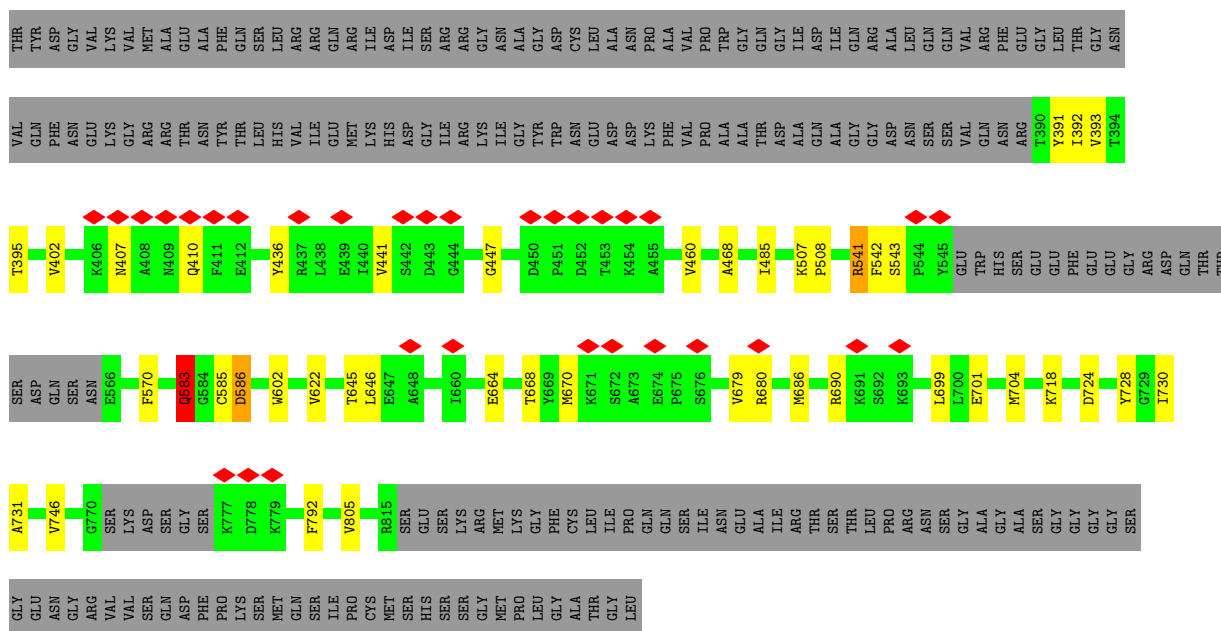


PRO	LYS	LEU	PRO	GLN	ILE	ASP	THR	VAL	ASN	GLY	ILE	SER	ASP	GLY	ALA	VAL	GLU	THR	MET	THR	TYR	ASP	ALA	LYS	CYS	SER	GLN	VAL	THR	PRO	PER						
MET	PRO	TYR	ILE	PHE	ALA	PHE	PHE	CYS	THR	GLY	LEU	PHE	GLY	GLY	ALA	VAL	GLU	THR	ASN	ASP	ASP	LYS	LYS	ASN	PHE	PRO	ASN	GLN	GLN	SER	GLN	GLU	GLY	THR	THR	GLU	PRO

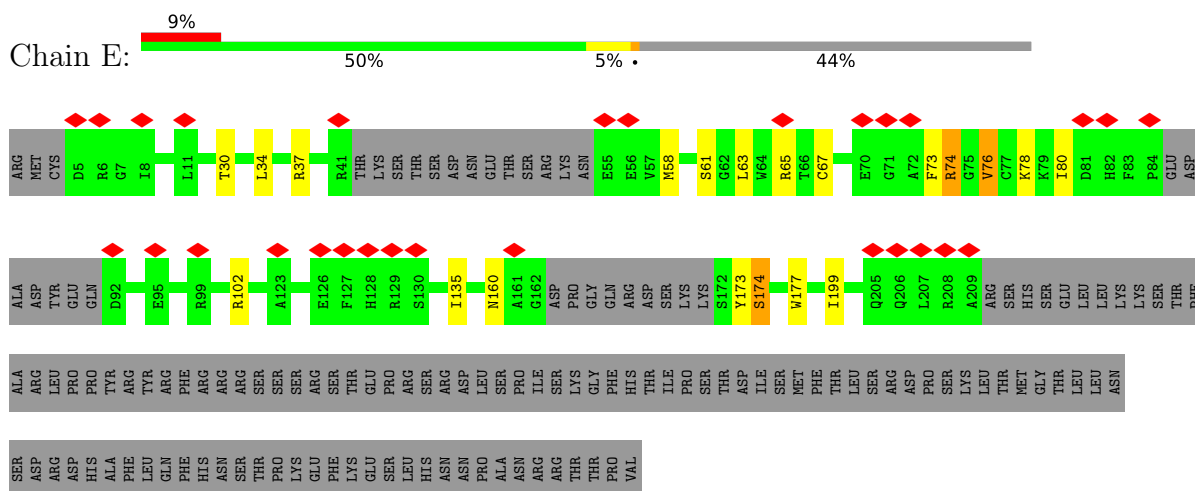


Chain D:

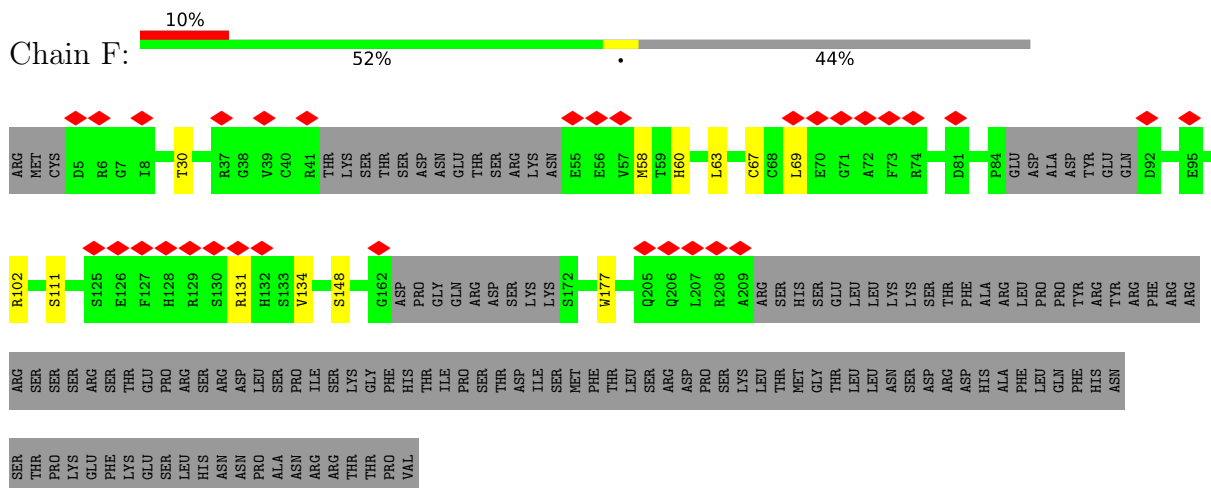




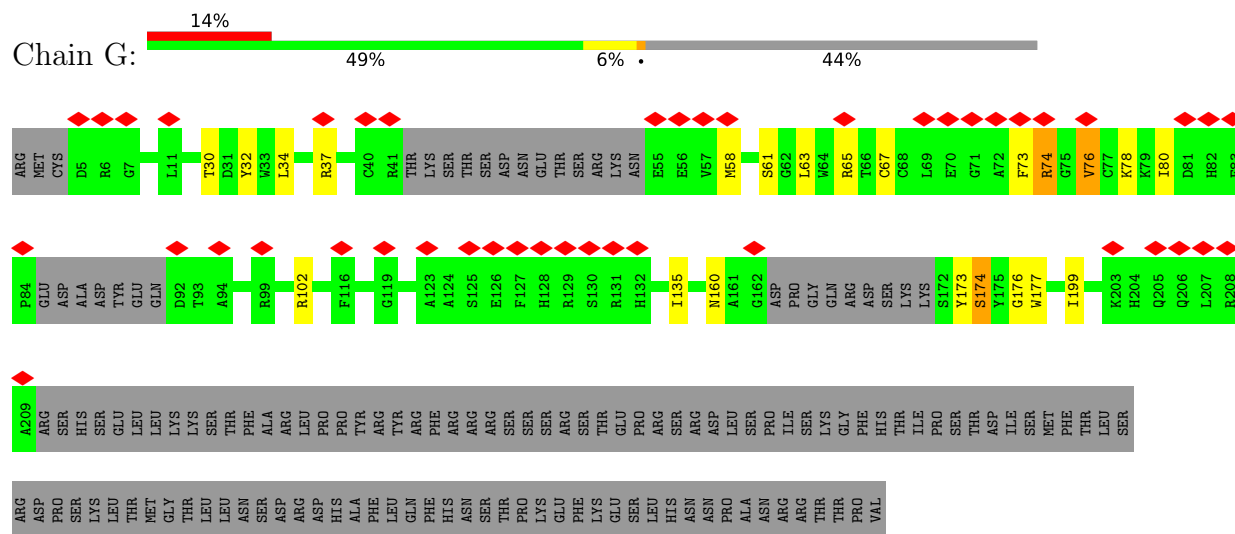
- Molecule 2: Voltage-dependent calcium channel gamma-3 subunit



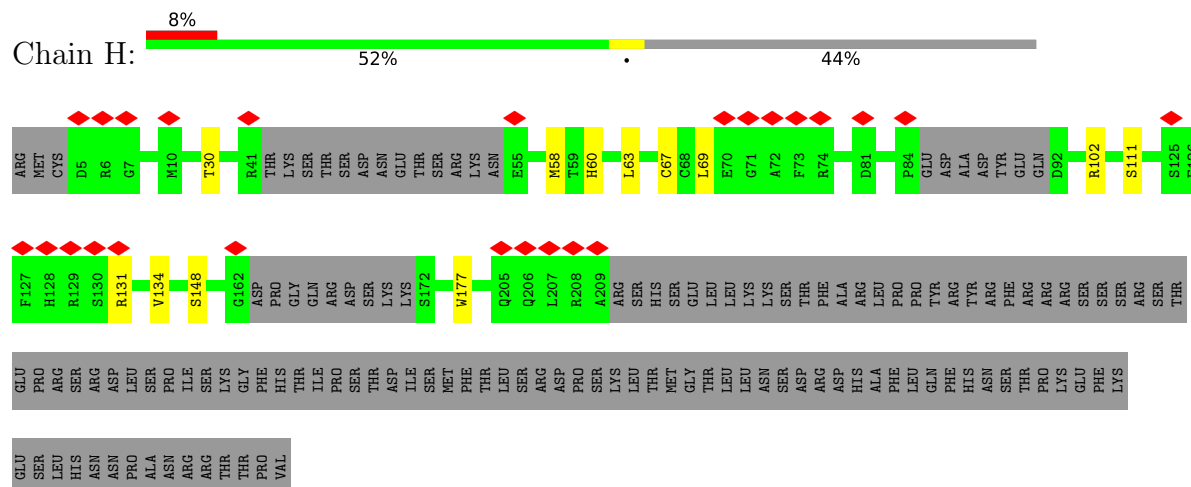
- Molecule 2: Voltage-dependent calcium channel gamma-3 subunit



Chain G:



Chain H:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	252544	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.088	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	241.68, 241.68, 241.68	wwPDB
Map dimensions	228, 228, 228	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZK1, PLM, POV, OLC

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	0.66	0/3249	0.93	1/4389 (0.0%)
1	B	0.66	1/3083 (0.0%)	0.95	6/4185 (0.1%)
1	C	0.65	0/3186	0.92	0/4321
1	D	0.66	0/3225	0.94	2/4355 (0.0%)
2	E	0.59	0/1399	0.88	0/1891
2	F	0.58	0/1399	0.85	0/1891
2	G	0.56	0/1399	0.87	0/1891
2	H	0.58	0/1399	0.85	0/1891
All	All	0.63	1/18339 (0.0%)	0.91	9/24814 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	D	0	4
2	E	0	1
2	G	0	1
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	616	LEU	C-O	-6.92	1.15	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	583	GLN	N-CA-C	-7.02	99.18	109.63
1	B	684	GLU	CB-CA-C	6.54	121.97	110.85
1	B	724	ASP	CA-CB-CG	6.03	118.62	112.60
1	D	570	PHE	CA-CB-CG	6.00	119.80	113.80
1	A	724	ASP	CA-CB-CG	5.50	118.10	112.60
1	D	583	GLN	N-CA-C	-5.35	98.83	110.22
1	B	791	VAL	N-CA-CB	5.11	118.24	110.58
1	B	486	ASP	CA-CB-CG	5.10	117.70	112.60
1	B	570	PHE	CA-CB-CG	5.02	118.82	113.80

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	416	ARG	Sidechain
1	B	541	ARG	Sidechain
1	D	541	ARG	Sidechain
1	D	583	GLN	Mainchain
1	D	680	ARG	Sidechain
2	E	65	ARG	Sidechain
2	G	65	ARG	Sidechain

5.2 Too-close contacts

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	3179	0	3176	28	0
1	B	3012	0	2910	31	0
1	C	3116	0	3034	46	0
1	D	3152	0	3161	30	0
2	E	1367	0	1355	11	0
2	F	1367	0	1355	7	0
2	G	1367	0	1355	13	0
2	H	1367	0	1355	8	0
3	A	27	0	13	0	0
3	B	27	0	13	0	0
3	C	27	0	13	1	0
3	D	27	0	13	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	18	0	31	0	0
4	B	18	0	31	0	0
4	C	18	0	31	0	0
4	D	18	0	31	0	0
5	A	25	0	40	0	0
5	B	25	0	40	0	0
5	C	25	0	40	0	0
5	D	25	0	40	0	0
6	E	37	0	46	0	0
6	F	78	0	100	0	0
6	G	37	0	46	0	0
6	H	78	0	100	0	0
7	A	6	0	0	0	0
7	B	5	0	0	0	0
7	C	5	0	0	0	0
7	D	6	0	0	0	0
7	F	1	0	0	0	0
7	G	1	0	0	0	0
7	H	1	0	0	0	0
All	All	18462	0	18329	161	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 4.

All (161) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:THR:HG21	1:A:402:VAL:HG21	1.56	0.86
1:B:690:ARG:NH1	1:B:715:ASP:OD1	2.18	0.75
1:A:711:ARG:NH2	1:A:766:LYS:O	2.20	0.74
2:E:34:LEU:HD12	2:E:174:SER:O	1.97	0.64
1:C:701:GLU:OE1	3:C:901:ZK1:HAN	1.98	0.63
2:G:34:LEU:HD12	2:G:174:SER:O	1.98	0.63
1:B:698:TYR:CD2	1:B:700:LEU:HD23	2.35	0.61
1:C:654:PHE:O	1:C:658:SER:OG	2.17	0.61
1:C:700:LEU:HD12	1:C:701:GLU:O	2.01	0.61
1:B:700:LEU:HD12	1:B:701:GLU:O	2.02	0.60
1:D:395:THR:CG2	1:D:402:VAL:HG21	2.30	0.60
1:A:749:LEU:HB3	1:A:755:LEU:CD1	2.32	0.60
1:C:447:GLY:CA	1:C:460:VAL:HG22	2.32	0.59
1:C:698:TYR:CD2	1:C:700:LEU:HD23	2.38	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:499:MET:HE3	1:B:700:LEU:HD21	1.84	0.59
2:G:135:ILE:HD13	2:G:199:ILE:HG21	1.85	0.59
1:C:660:ILE:HD11	1:C:663:PHE:CE1	2.37	0.58
1:C:638:GLN:OE1	1:C:640:GLU:N	2.35	0.58
1:C:679:VAL:HG12	1:C:688:ARG:HH12	1.68	0.58
2:E:73:PHE:O	2:E:76:VAL:HB	2.04	0.57
1:B:586[A]:ASP:OD1	1:B:586[A]:ASP:N	2.28	0.57
2:G:73:PHE:O	2:G:76:VAL:HB	2.05	0.57
2:G:30:THR:HG21	2:G:177:TRP:HH2	1.71	0.55
2:E:34:LEU:HD22	2:E:160:ASN:ND2	2.22	0.55
1:D:586[B]:ASP:OD1	1:D:586[B]:ASP:N	2.24	0.55
1:C:398:GLU:HG3	1:C:446:TYR:OH	2.06	0.55
2:E:61:SER:OG	2:E:80:ILE:HD11	2.07	0.54
2:G:34:LEU:HD22	2:G:160:ASN:ND2	2.22	0.54
2:F:30:THR:HG21	2:F:177:TRP:HH2	1.72	0.54
1:A:584[B]:GLY:O	1:A:585[B]:CYS:HB3	2.07	0.54
2:E:30:THR:HG21	2:E:177:TRP:HH2	1.71	0.54
2:E:135:ILE:HD13	2:E:199:ILE:HG21	1.89	0.54
1:D:646:LEU:CD1	1:D:679:VAL:HG23	2.38	0.54
1:C:679:VAL:HG12	1:C:688:ARG:NH1	2.23	0.53
2:H:30:THR:HG21	2:H:177:TRP:HH2	1.74	0.53
1:A:638:GLN:OE1	1:A:640:GLU:N	2.41	0.53
1:D:645:THR:HG23	1:D:670:MET:HE1	1.91	0.53
2:G:61:SER:OG	2:G:80:ILE:HD11	2.09	0.53
1:B:686:MET:O	1:B:689:VAL:HG12	2.10	0.52
1:A:431:HIS:CE1	1:A:749:LEU:HD21	2.45	0.52
1:C:459:MET:HE3	1:C:471:ALA:HB1	1.90	0.52
1:C:456:TRP:CE3	1:C:460:VAL:HG21	2.45	0.52
1:D:701:GLU:OE1	1:D:728:TYR:OH	2.28	0.52
1:A:392:ILE:HD11	1:A:467:ARG:O	2.10	0.51
1:C:447:GLY:HA2	1:C:460:VAL:HG22	1.91	0.51
1:C:586[A]:ASP:OD1	1:C:586[A]:ASP:N	2.42	0.51
1:D:392:ILE:HG23	1:D:468:ALA:HA	1.92	0.51
1:C:447:GLY:HA3	1:C:460:VAL:HG13	1.92	0.50
1:D:586[A]:ASP:OD1	1:D:586[A]:ASP:N	2.22	0.50
1:A:395:THR:CG2	1:A:402:VAL:HG21	2.36	0.50
1:A:586[A]:ASP:OD1	1:A:586[A]:ASP:N	2.39	0.50
1:B:698:TYR:CE2	1:B:700:LEU:HD23	2.46	0.50
1:B:402:VAL:CG2	1:B:421:CYS:SG	3.00	0.49
1:A:583:GLN:HG3	1:D:602:TRP:CG	2.47	0.49
1:C:472:VAL:O	1:C:472:VAL:HG13	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:788:VAL:O	1:C:791:VAL:HG12	2.13	0.49
1:B:740:GLY:O	1:B:744:LEU:HD23	2.11	0.49
1:A:436:TYR:HE2	1:A:438:LEU:HD12	1.78	0.49
1:B:747:LEU:HD11	1:C:477:ILE:HG22	1.93	0.49
1:B:402:VAL:HG23	1:B:421:CYS:SG	2.53	0.49
2:F:30:THR:HG21	2:F:177:TRP:CH2	2.48	0.49
1:C:740:GLY:O	1:C:744:LEU:HD23	2.13	0.48
1:A:586[B]:ASP:OD1	1:A:586[B]:ASP:N	2.45	0.48
1:A:788:VAL:O	1:A:791:VAL:HG12	2.13	0.48
1:C:503:PRO:HD3	1:C:717:MET:SD	2.54	0.48
2:E:37:ARG:HG2	2:E:58:MET:HE2	1.95	0.48
1:C:585[B]:CYS:SG	1:C:586[B]:ASP:N	2.86	0.48
2:H:30:THR:HG21	2:H:177:TRP:CH2	2.49	0.47
1:C:679:VAL:HG11	1:C:685:GLY:HA2	1.97	0.47
1:B:602:TRP:CG	1:C:583:GLN:HG3	2.49	0.47
1:C:431:HIS:CE1	1:C:749:LEU:HD11	2.49	0.47
1:C:479:LEU:O	1:C:483:GLU:OE1	2.33	0.47
1:D:686:MET:SD	1:D:690:ARG:CZ	3.02	0.47
1:D:645:THR:HG22	1:D:699:LEU:HB2	1.96	0.47
1:B:711:ARG:NH2	1:B:766:LYS:O	2.45	0.47
1:B:732:THR:CG2	1:B:736:SER:HB3	2.44	0.47
1:C:496:ILE:HD12	1:C:724:ASP:HB3	1.97	0.47
2:G:34:LEU:HD11	2:G:173:TYR:HB2	1.95	0.47
1:A:395:THR:HG22	1:A:396:ILE:N	2.30	0.47
1:C:807:LEU:C	1:C:807:LEU:HD23	2.40	0.47
1:A:701:GLU:OE1	1:A:728:TYR:OH	2.30	0.46
1:A:807:LEU:HD23	1:A:807:LEU:C	2.39	0.46
1:C:485:ILE:HG23	1:C:732:THR:O	2.15	0.46
1:D:485:ILE:HD12	1:D:731:ALA:HB1	1.97	0.46
1:D:585[B]:CYS:HB2	1:D:586[B]:ASP:OD1	2.14	0.46
2:E:34:LEU:HD11	2:E:173:TYR:HB2	1.96	0.46
1:D:395:THR:HG23	1:D:402:VAL:HG21	1.96	0.46
2:G:37:ARG:HG2	2:G:58:MET:HE2	1.95	0.46
2:E:30:THR:HG21	2:E:177:TRP:CH2	2.50	0.46
1:A:391:TYR:O	1:A:436:TYR:HA	2.14	0.46
2:G:30:THR:HG21	2:G:177:TRP:CH2	2.50	0.46
1:D:585[B]:CYS:HB2	1:D:586[B]:ASP:H	1.47	0.46
1:D:393:VAL:HG23	1:D:436:TYR:HB2	1.98	0.46
1:D:686:MET:SD	1:D:690:ARG:NH1	2.89	0.45
1:C:419:GLY:O	1:C:423:GLU:OE1	2.34	0.45
1:C:586[B]:ASP:N	1:C:586[B]:ASP:OD1	2.48	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:407:ASN:HB2	1:D:410:GLN:HB3	1.99	0.45
1:B:524:CYS:HB3	1:C:792:PHE:CE1	2.52	0.45
1:D:704:MET:HE3	3:D:901:ZK1:HALA	1.99	0.45
1:A:602:TRP:CG	1:B:583:GLN:HG3	2.52	0.45
1:A:402:VAL:HG22	1:A:422:VAL:HG23	1.99	0.45
1:B:492:MET:HE2	1:B:728:TYR:HD2	1.81	0.45
2:H:111:SER:HB2	2:H:148:SER:OG	2.16	0.45
2:G:74:ARG:NH1	2:G:74:ARG:HG3	2.31	0.44
1:B:622:VAL:HG22	1:C:624:ARG:HE	1.82	0.44
1:C:400:PRO:HA	1:C:403:MET:SD	2.57	0.44
1:D:395:THR:O	1:D:441:VAL:HG12	2.17	0.44
2:E:63:LEU:HA	2:E:102:ARG:HH22	1.83	0.44
2:F:131:ARG:O	2:F:134:VAL:HG12	2.18	0.44
1:B:664:GLU:O	1:B:668:THR:HG23	2.18	0.44
1:D:664:GLU:O	1:D:668:THR:HG23	2.18	0.44
1:C:486:ASP:HB3	1:C:739:ARG:CD	2.48	0.44
1:D:646:LEU:HD12	1:D:679:VAL:HG23	1.98	0.44
2:H:60:HIS:CE1	2:H:67:CYS:HB2	2.53	0.43
1:B:743:ASN:O	1:B:747:LEU:HD23	2.18	0.43
1:C:478:THR:O	1:C:482:GLU:HB2	2.18	0.43
2:H:131:ARG:O	2:H:134:VAL:HG12	2.19	0.43
1:A:524:CYS:HB3	1:B:792:PHE:CE1	2.53	0.43
1:D:391:TYR:O	1:D:436:TYR:HA	2.19	0.43
2:H:58:MET:HG3	2:H:69:LEU:HD21	2.00	0.43
1:C:485:ILE:CG2	1:C:732:THR:O	2.66	0.43
2:F:111:SER:HB2	2:F:148:SER:OG	2.18	0.43
1:D:395:THR:HG21	1:D:402:VAL:HG21	1.99	0.43
1:B:690:ARG:NH1	1:B:713:PRO:HD2	2.34	0.43
2:F:58:MET:HG3	2:F:69:LEU:HD21	1.99	0.43
1:B:653:GLU:HA	1:B:656:ARG:HG2	1.99	0.43
1:C:425:ALA:HB2	1:C:472:VAL:HG11	2.01	0.43
1:B:507:LYS:HG3	1:B:508:PRO:HD2	2.01	0.42
1:D:447:GLY:HA3	1:D:460:VAL:HB	2.01	0.42
2:F:60:HIS:CE1	2:F:67:CYS:HB2	2.54	0.42
2:H:63:LEU:HA	2:H:102:ARG:HH22	1.84	0.42
1:A:592:LEU:HD23	1:B:805:VAL:HG11	2.01	0.42
1:C:484:VAL:HG23	1:C:485:ILE:HG13	2.01	0.42
1:A:398:GLU:O	1:A:401:TYR:N	2.50	0.42
2:E:74:ARG:NH1	2:E:74:ARG:HG3	2.31	0.42
2:G:63:LEU:HA	2:G:102:ARG:HH22	1.83	0.42
1:B:485:ILE:HD12	1:B:731:ALA:HB1	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:622:VAL:HG22	1:C:624:ARG:NE	2.34	0.42
1:D:507:LYS:HG3	1:D:508:PRO:HD2	2.02	0.42
1:B:743:ASN:ND2	1:C:482:GLU:OE2	2.52	0.42
1:C:602:TRP:CG	1:D:583:GLN:HG3	2.55	0.42
2:G:135:ILE:HD13	2:G:199:ILE:CG2	2.49	0.42
1:D:646:LEU:HD12	1:D:646:LEU:HA	1.92	0.42
1:C:754:VAL:O	1:C:758:LEU:HD23	2.20	0.42
1:B:456:TRP:CZ3	1:B:460:VAL:HG11	2.56	0.41
1:B:395:THR:HG22	1:B:396:ILE:N	2.34	0.41
1:D:730:ILE:HD12	1:D:746:VAL:CG2	2.50	0.41
1:A:441:VAL:HG13	1:A:444:GLY:HA2	2.03	0.41
1:B:739:ARG:O	1:B:742:VAL:HG22	2.20	0.41
2:G:32:TYR:O	2:G:176:GLY:HA3	2.21	0.41
1:C:524:CYS:HB3	1:D:792:PHE:CE1	2.55	0.41
1:A:403:MET:HE1	1:A:762:TRP:CZ3	2.56	0.41
1:C:428:ILE:HD11	1:C:742:VAL:HG13	2.02	0.41
1:A:585[B]:CYS:SG	1:A:586[B]:ASP:N	2.94	0.41
1:A:403:MET:HE3	1:A:403:MET:HB2	2.00	0.40
1:A:458:GLY:O	1:A:462:GLU:HG2	2.21	0.40
2:H:102:ARG:O	2:H:102:ARG:NH1	2.42	0.40
1:C:393:VAL:HG23	1:C:470:VAL:HG13	2.02	0.40
1:A:500:ILE:CD1	1:A:719:VAL:HG11	2.51	0.40
2:F:63:LEU:HA	2:F:102:ARG:HH22	1.86	0.40
1:C:592:LEU:HD23	1:D:805:VAL:HG11	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	403/915 (44%)	387 (96%)	14 (4%)	2 (0%)	24 53

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	399/915 (44%)	389 (98%)	10 (2%)	0	100	100
1	C	404/915 (44%)	386 (96%)	17 (4%)	1 (0%)	43	71
1	D	399/915 (44%)	387 (97%)	12 (3%)	0	100	100
2	E	168/314 (54%)	163 (97%)	5 (3%)	0	100	100
2	F	168/314 (54%)	165 (98%)	3 (2%)	0	100	100
2	G	168/314 (54%)	163 (97%)	5 (3%)	0	100	100
2	H	168/314 (54%)	166 (99%)	2 (1%)	0	100	100
All	All	2277/4916 (46%)	2206 (97%)	68 (3%)	3 (0%)	49	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	585[A]	CYS
1	A	585[B]	CYS
1	C	447	GLY

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	335/778 (43%)	326 (97%)	9 (3%)	39	72
1	B	296/778 (38%)	285 (96%)	11 (4%)	30	63
1	C	318/778 (41%)	310 (98%)	8 (2%)	42	74
1	D	334/778 (43%)	326 (98%)	8 (2%)	43	75
2	E	142/273 (52%)	137 (96%)	5 (4%)	32	65
2	F	142/273 (52%)	142 (100%)	0	100	100
2	G	142/273 (52%)	137 (96%)	5 (4%)	32	65
2	H	142/273 (52%)	142 (100%)	0	100	100
All	All	1851/4204 (44%)	1805 (98%)	46 (2%)	44	74

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	399	ASP
1	A	417	TYR
1	A	437	ARG
1	A	438	LEU
1	A	439	GLU
1	A	586[A]	ASP
1	A	586[B]	ASP
1	A	588	SER
1	A	629	ILE
1	B	457	ASN
1	B	542	PHE
1	B	543	SER
1	B	586[A]	ASP
1	B	586[B]	ASP
1	B	616	LEU
1	B	622	VAL
1	B	624	ARG
1	B	637	LYS
1	B	684	GLU
1	B	689	VAL
1	C	445	LYS
1	C	502	LYS
1	C	586[A]	ASP
1	C	586[B]	ASP
1	C	588	SER
1	C	629	ILE
1	C	630	GLU
1	C	631	SER
1	D	541	ARG
1	D	542	PHE
1	D	543	SER
1	D	586[A]	ASP
1	D	586[B]	ASP
1	D	622	VAL
1	D	718	LYS
1	D	724	ASP
2	E	67	CYS
2	E	74	ARG
2	E	76	VAL
2	E	78	LYS
2	E	174	SER
2	G	67	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	G	74	ARG
2	G	76	VAL
2	G	78	LYS
2	G	174	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	504	GLN
1	C	582	GLN
1	D	410	GLN
1	D	722	ASN
2	F	9	GLN
2	F	82	HIS
2	H	9	GLN
2	H	82	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](#)

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
4	PLM	A	902	-	17,17,17	0.60	0	17,17,17	0.60	0
4	PLM	B	902	-	17,17,17	0.72	0	17,17,17	0.64	0
5	OLC	A	903	-	24,24,24	0.29	0	25,25,25	0.30	0
5	OLC	C	903	-	24,24,24	0.29	0	25,25,25	0.37	0
6	POV	G	1201	-	36,36,51	0.43	0	42,44,59	0.73	0
6	POV	E	1201	-	36,36,51	0.46	0	42,44,59	0.70	0
6	POV	H	1301	-	38,38,51	0.41	0	44,46,59	0.79	2 (4%)
3	ZK1	B	901	-	29,29,29	1.09	3 (10%)	45,45,45	1.12	5 (11%)
3	ZK1	A	901	-	29,29,29	0.86	1 (3%)	45,45,45	1.15	5 (11%)
4	PLM	D	902	-	17,17,17	0.66	0	17,17,17	0.71	0
6	POV	F	1301	-	38,38,51	0.43	0	44,46,59	0.73	2 (4%)
6	POV	F	1302	-	38,38,51	0.50	0	44,46,59	0.59	0
5	OLC	B	903	-	24,24,24	0.37	0	25,25,25	0.51	0
4	PLM	C	902	-	17,17,17	0.57	0	17,17,17	0.58	0
6	POV	H	1302	-	38,38,51	0.48	0	44,46,59	0.60	0
3	ZK1	C	901	-	29,29,29	1.06	4 (13%)	45,45,45	1.05	2 (4%)
3	ZK1	D	901	-	29,29,29	0.96	3 (10%)	45,45,45	0.93	0
5	OLC	D	903	-	24,24,24	0.37	0	25,25,25	0.54	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PLM	A	902	-	-	9/15/15/15	-
4	PLM	B	902	-	-	8/15/15/15	-
5	OLC	A	903	-	-	7/24/24/24	-
5	OLC	C	903	-	-	6/24/24/24	-
6	POV	G	1201	-	-	11/40/40/55	-
6	POV	E	1201	-	-	12/40/40/55	-
6	POV	H	1301	-	-	19/42/42/55	-
3	ZK1	B	901	-	-	12/13/23/23	0/3/3/3
3	ZK1	A	901	-	-	10/13/23/23	0/3/3/3
4	PLM	D	902	-	-	8/15/15/15	-
6	POV	F	1301	-	-	19/42/42/55	-
6	POV	F	1302	-	-	15/42/42/55	-
5	OLC	B	903	-	-	10/24/24/24	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PLM	C	902	-	-	9/15/15/15	-
6	POV	H	1302	-	-	12/42/42/55	-
3	ZK1	C	901	-	-	13/13/23/23	0/3/3/3
3	ZK1	D	901	-	-	10/13/23/23	0/3/3/3
5	OLC	D	903	-	-	11/24/24/24	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	901	ZK1	CAU-NAY	3.04	1.43	1.38
3	D	901	ZK1	CAU-NAY	2.83	1.43	1.38
3	B	901	ZK1	PBA-OAD	-2.64	1.49	1.55
3	C	901	ZK1	PBA-OAD	-2.53	1.49	1.55
3	C	901	ZK1	PBA-OAE	-2.52	1.49	1.55
3	C	901	ZK1	CAU-NAY	2.40	1.42	1.38
3	B	901	ZK1	PBA-OAE	-2.39	1.49	1.55
3	D	901	ZK1	PBA-OAE	-2.37	1.49	1.55
3	A	901	ZK1	PBA-OAE	-2.27	1.49	1.55
3	C	901	ZK1	CAO-NAY	2.09	1.49	1.46
3	D	901	ZK1	PBA-OAD	-2.05	1.50	1.55

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	901	ZK1	OAA-CAT-CAU	3.51	121.84	119.21
6	H	1301	POV	O21-C2-C1	3.17	119.71	108.34
3	C	901	ZK1	CAI-CAR-NAX	-2.85	118.44	122.59
6	H	1301	POV	C2-O21-C21	2.67	124.19	117.80
3	B	901	ZK1	CAO-NAY-CAW	2.59	123.27	120.12
6	F	1301	POV	O21-C2-C1	2.58	117.58	108.34
3	C	901	ZK1	CAK-CAM-NAX	2.51	114.68	109.93
6	F	1301	POV	C2-O21-C21	2.51	123.80	117.80
3	B	901	ZK1	OAA-CAT-CAU	2.48	121.07	119.21
3	B	901	ZK1	CAI-CAR-NAX	-2.37	119.14	122.59
3	A	901	ZK1	CAI-CAR-CAS	-2.18	118.10	121.00
3	B	901	ZK1	CAW-NAY-CAU	-2.16	120.18	122.84
3	B	901	ZK1	CAL-CAN-NAX	2.16	114.02	109.93
3	A	901	ZK1	CAK-CAM-NAX	2.14	113.98	109.93
3	A	901	ZK1	CAO-NAY-CAW	2.04	122.61	120.12
3	A	901	ZK1	CAI-CAR-NAX	-2.03	119.63	122.59

There are no chirality outliers.

All (201) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	901	ZK1	NAY-CAO-PBA-OAC
3	B	901	ZK1	NAY-CAO-PBA-OAD
3	B	901	ZK1	NAY-CAO-PBA-OAE
3	C	901	ZK1	NAY-CAO-PBA-OAD
3	C	901	ZK1	NAY-CAO-PBA-OAE
3	D	901	ZK1	NAY-CAO-PBA-OAC
3	D	901	ZK1	NAY-CAO-PBA-OAE
5	B	903	OLC	C21-C22-C24-O25
5	D	903	OLC	C21-C22-C24-O25
6	F	1301	POV	C11-O12-P-O11
6	F	1301	POV	C11-O12-P-O13
6	F	1301	POV	C11-O12-P-O14
6	F	1301	POV	O21-C2-C3-O31
6	F	1301	POV	O12-C11-C12-N
6	F	1302	POV	C11-O12-P-O11
6	F	1302	POV	C210-C211-C212-C213
6	H	1301	POV	C11-O12-P-O11
6	H	1301	POV	C11-O12-P-O13
6	H	1301	POV	C11-O12-P-O14
6	H	1301	POV	O21-C2-C3-O31
6	H	1301	POV	C1-C2-O21-C21
6	H	1301	POV	O12-C11-C12-N
6	H	1302	POV	C11-O12-P-O11
6	H	1302	POV	C210-C211-C212-C213
4	D	902	PLM	C1-C2-C3-C4
4	B	902	PLM	C1-C2-C3-C4
6	G	1201	POV	O32-C31-O31-C3
6	E	1201	POV	O32-C31-O31-C3
6	F	1301	POV	C31-C32-C33-C34
5	D	903	OLC	C1-C2-C3-C4
6	H	1301	POV	C31-C32-C33-C34
6	E	1201	POV	C32-C31-O31-C3
6	G	1201	POV	C32-C31-O31-C3
5	B	903	OLC	C1-C2-C3-C4
4	C	902	PLM	CC-CD-CE-CF
6	F	1302	POV	C23-C24-C25-C26
5	A	903	OLC	C3-C4-C5-C6
5	B	903	OLC	C11-C12-C13-C14
5	C	903	OLC	C3-C4-C5-C6
6	H	1302	POV	C23-C24-C25-C26

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
5	B	903	OLC	O23-C22-C24-O25
5	D	903	OLC	O23-C22-C24-O25
6	H	1301	POV	C34-C35-C36-C37
4	A	902	PLM	CC-CD-CE-CF
4	B	902	PLM	C3-C4-C5-C6
6	F	1301	POV	C33-C34-C35-C36
4	D	902	PLM	C3-C4-C5-C6
5	B	903	OLC	C12-C13-C14-C15
6	H	1301	POV	C33-C34-C35-C36
5	D	903	OLC	C11-C12-C13-C14
4	D	902	PLM	C4-C5-C6-C7
4	B	902	PLM	C4-C5-C6-C7
6	G	1201	POV	C23-C24-C25-C26
5	A	903	OLC	C14-C15-C16-C17
6	F	1301	POV	C36-C37-C38-C39
6	E	1201	POV	C23-C24-C25-C26
5	A	903	OLC	C10-C11-C12-C13
5	B	903	OLC	C6-C7-C8-C9
6	G	1201	POV	C26-C27-C28-C29
5	B	903	OLC	C5-C6-C7-C8
4	A	902	PLM	CA-CB-CC-CD
6	F	1301	POV	C34-C35-C36-C37
6	F	1302	POV	C25-C26-C27-C28
5	D	903	OLC	C6-C7-C8-C9
6	E	1201	POV	C26-C27-C28-C29
5	D	903	OLC	C5-C6-C7-C8
4	C	902	PLM	CA-CB-CC-CD
5	D	903	OLC	C14-C15-C16-C17
5	D	903	OLC	C12-C13-C14-C15
4	B	902	PLM	C9-CA-CB-CC
6	H	1302	POV	O22-C21-O21-C2
6	F	1301	POV	C1-C2-C3-O31
6	F	1301	POV	C35-C36-C37-C38
5	C	903	OLC	C10-C11-C12-C13
4	D	902	PLM	C9-CA-CB-CC
6	G	1201	POV	C22-C23-C24-C25
6	G	1201	POV	C25-C26-C27-C28
5	D	903	OLC	C2-C3-C4-C5
3	A	901	ZK1	CAI-CAR-NAX-CAM
6	F	1301	POV	C1-C2-O21-C21
6	H	1301	POV	C25-C26-C27-C28
6	F	1301	POV	C26-C27-C28-C29

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
6	H	1301	POV	C26-C27-C28-C29
6	E	1201	POV	C22-C23-C24-C25
5	B	903	OLC	C4-C5-C6-C7
5	C	903	OLC	C14-C15-C16-C17
6	H	1302	POV	C22-C21-O21-C2
6	H	1301	POV	C35-C36-C37-C38
6	F	1302	POV	C24-C25-C26-C27
6	E	1201	POV	C25-C26-C27-C28
3	C	901	ZK1	CAI-CAR-NAX-CAM
6	F	1301	POV	C25-C26-C27-C28
3	C	901	ZK1	CAR-CAS-CAZ-FAF
4	B	902	PLM	CD-CE-CF-CG
4	D	902	PLM	CD-CE-CF-CG
6	H	1302	POV	C24-C25-C26-C27
6	F	1302	POV	C22-C21-O21-C2
3	C	901	ZK1	CAR-CAS-CAZ-FAG
3	C	901	ZK1	CAR-CAS-CAZ-FAH
6	G	1201	POV	C21-C22-C23-C24
5	D	903	OLC	C4-C5-C6-C7
4	A	902	PLM	C5-C6-C7-C8
4	C	902	PLM	C5-C6-C7-C8
6	F	1302	POV	O22-C21-O21-C2
6	H	1302	POV	C25-C26-C27-C28
5	C	903	OLC	C9-C10-C11-C12
3	B	901	ZK1	CAR-CAS-CAZ-FAH
6	H	1301	POV	C1-C2-C3-O31
5	C	903	OLC	C11-C12-C13-C14
5	B	903	OLC	C2-C3-C4-C5
6	E	1201	POV	C21-C22-C23-C24
3	B	901	ZK1	CAR-CAS-CAZ-FAG
6	F	1302	POV	O21-C2-C3-O31
3	B	901	ZK1	CAR-CAS-CAZ-FAF
3	D	901	ZK1	CAI-CAR-NAX-CAN
3	A	901	ZK1	CAI-CAR-NAX-CAN
3	A	901	ZK1	NAY-CAO-PBA-OAD
3	A	901	ZK1	NAY-CAO-PBA-OAE
3	C	901	ZK1	NAY-CAO-PBA-OAC
3	D	901	ZK1	NAY-CAO-PBA-OAD
3	B	901	ZK1	CAI-CAR-NAX-CAM
3	C	901	ZK1	CAI-CAR-NAX-CAN
3	D	901	ZK1	CAR-CAS-CAZ-FAF
5	A	903	OLC	C9-C10-C11-C12

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
6	H	1301	POV	O22-C21-O21-C2
4	A	902	PLM	C2-C3-C4-C5
3	D	901	ZK1	CAI-CAR-NAX-CAM
6	G	1201	POV	O22-C21-O21-C2
6	F	1301	POV	C12-C11-O12-P
6	H	1301	POV	C12-C11-O12-P
6	H	1302	POV	O21-C2-C3-O31
3	A	901	ZK1	CAR-CAS-CAZ-FAH
6	E	1201	POV	O22-C21-O21-C2
3	A	901	ZK1	CAR-CAS-CAZ-FAF
3	D	901	ZK1	CAR-CAS-CAZ-FAH
3	D	901	ZK1	CAR-CAS-CAZ-FAG
4	C	902	PLM	C2-C3-C4-C5
5	B	903	OLC	C14-C15-C16-C17
3	A	901	ZK1	CAR-CAS-CAZ-FAG
3	B	901	ZK1	CAS-CAR-NAX-CAM
3	D	901	ZK1	CAS-CAR-NAX-CAM
3	D	901	ZK1	CAS-CAR-NAX-CAN
4	A	902	PLM	C9-CA-CB-CC
6	F	1302	POV	C11-O12-P-O14
6	H	1302	POV	C11-O12-P-O14
3	B	901	ZK1	CAI-CAR-NAX-CAN
3	A	901	ZK1	CAS-CAR-NAX-CAM
3	C	901	ZK1	CAS-CAR-NAX-CAM
5	C	903	OLC	C6-C7-C8-C9
3	A	901	ZK1	CAS-CAR-NAX-CAN
3	C	901	ZK1	CAS-CAR-NAX-CAN
4	C	902	PLM	C8-C9-CA-CB
5	A	903	OLC	C15-C16-C17-C18
6	F	1301	POV	O22-C21-O21-C2
4	B	902	PLM	O1-C1-C2-C3
6	G	1201	POV	C24-C25-C26-C27
4	D	902	PLM	O2-C1-C2-C3
4	B	902	PLM	O2-C1-C2-C3
6	G	1201	POV	C22-C21-O21-C2
4	C	902	PLM	C9-CA-CB-CC
4	D	902	PLM	O1-C1-C2-C3
6	F	1302	POV	C1-C2-C3-O31
4	C	902	PLM	O1-C1-C2-C3
3	C	901	ZK1	CAJ-CAS-CAZ-FAH
3	A	901	ZK1	NAY-CAO-PBA-OAC
6	H	1301	POV	C24-C25-C26-C27

Continued on next page...

Continued from previous page...

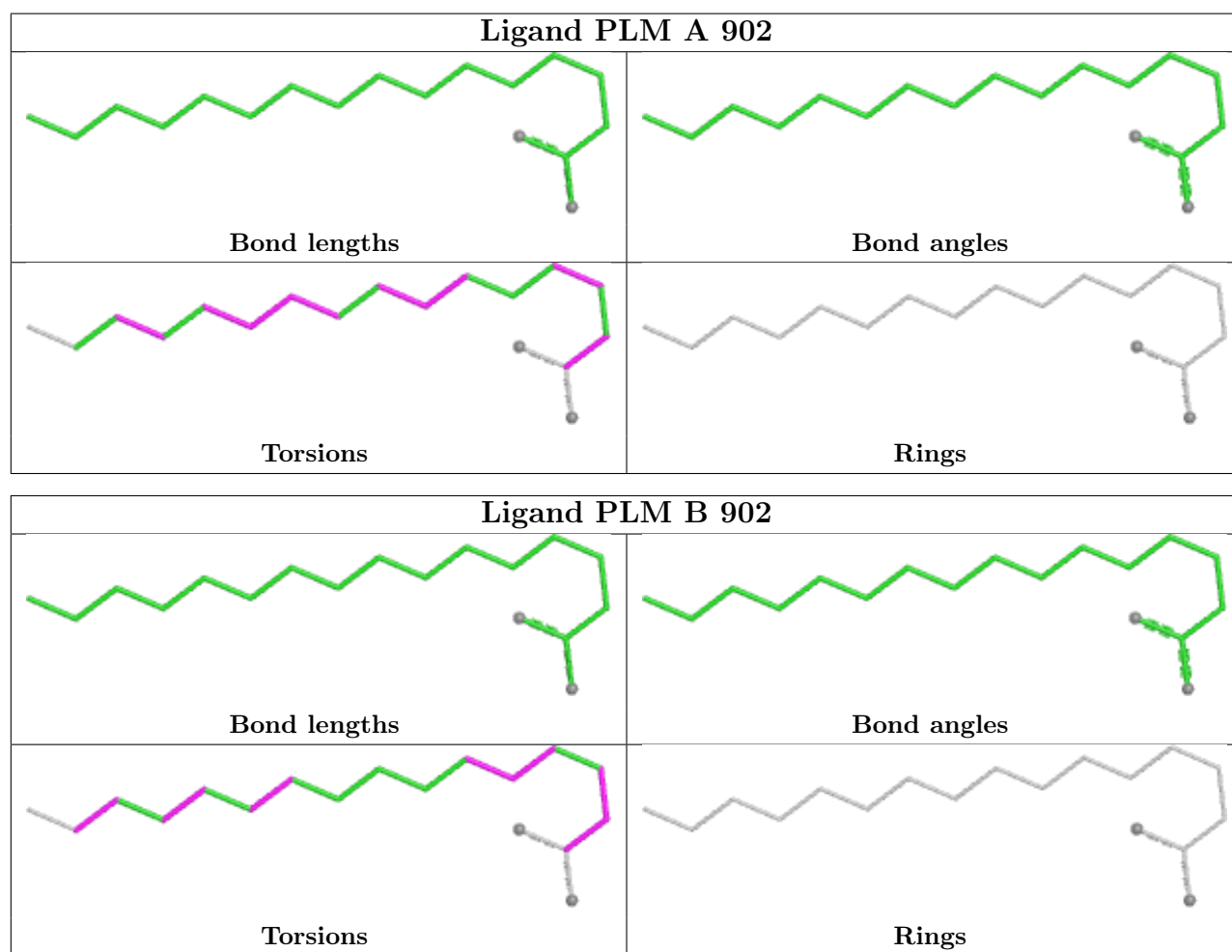
Mol	Chain	Res	Type	Atoms
6	E	1201	POV	C24-C25-C26-C27
4	A	902	PLM	O1-C1-C2-C3
6	F	1302	POV	C27-C28-C29-C210
3	C	901	ZK1	CAJ-CAS-CAZ-FAG
4	A	902	PLM	O2-C1-C2-C3
3	C	901	ZK1	CAJ-CAS-CAZ-FAF
6	F	1302	POV	O31-C31-C32-C33
6	F	1301	POV	C24-C25-C26-C27
4	A	902	PLM	C6-C7-C8-C9
3	B	901	ZK1	CAS-CAR-NAX-CAN
4	C	902	PLM	O2-C1-C2-C3
4	C	902	PLM	C6-C7-C8-C9
6	H	1301	POV	O31-C31-C32-C33
6	E	1201	POV	C29-C210-C211-C212
6	H	1302	POV	C27-C28-C29-C210
6	E	1201	POV	O12-C11-C12-N
6	G	1201	POV	O12-C11-C12-N
6	F	1301	POV	O31-C31-C32-C33
6	H	1302	POV	O31-C31-C32-C33
6	E	1201	POV	C22-C21-O21-C2
4	D	902	PLM	CB-CC-CD-CE
5	A	903	OLC	C11-C12-C13-C14
4	B	902	PLM	CB-CC-CD-CE
6	H	1301	POV	O32-C31-C32-C33
4	A	902	PLM	C8-C9-CA-CB
5	D	903	OLC	C13-C14-C15-C16
6	H	1302	POV	O32-C31-C32-C33
6	F	1302	POV	C32-C33-C34-C35
6	F	1301	POV	O32-C31-C32-C33
6	F	1302	POV	O32-C31-C32-C33
3	B	901	ZK1	CAJ-CAS-CAZ-FAH
6	F	1302	POV	C22-C23-C24-C25
3	B	901	ZK1	CAJ-CAS-CAZ-FAG
6	H	1301	POV	C22-C21-O21-C2
5	A	903	OLC	C6-C7-C8-C9

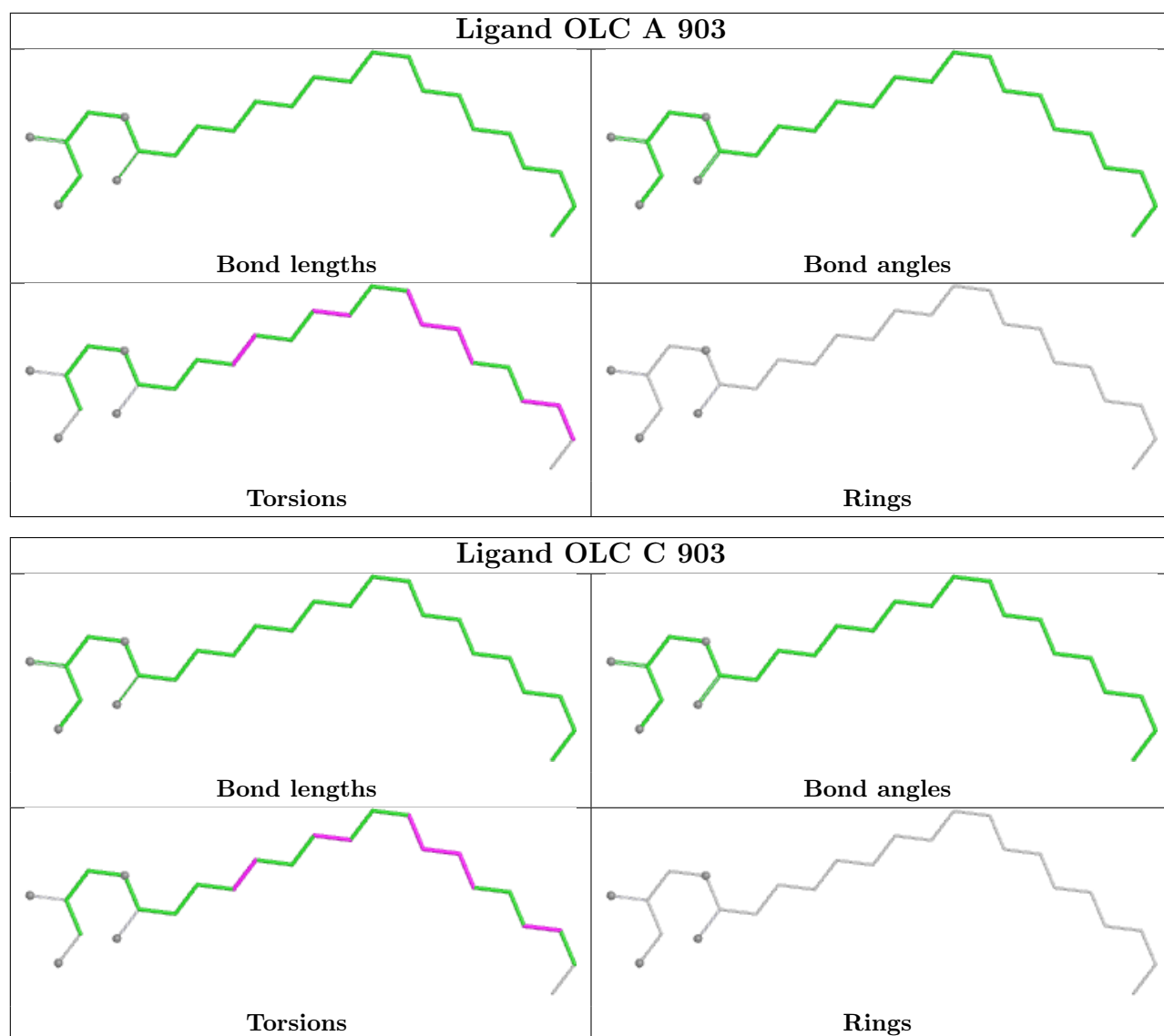
There are no ring outliers.

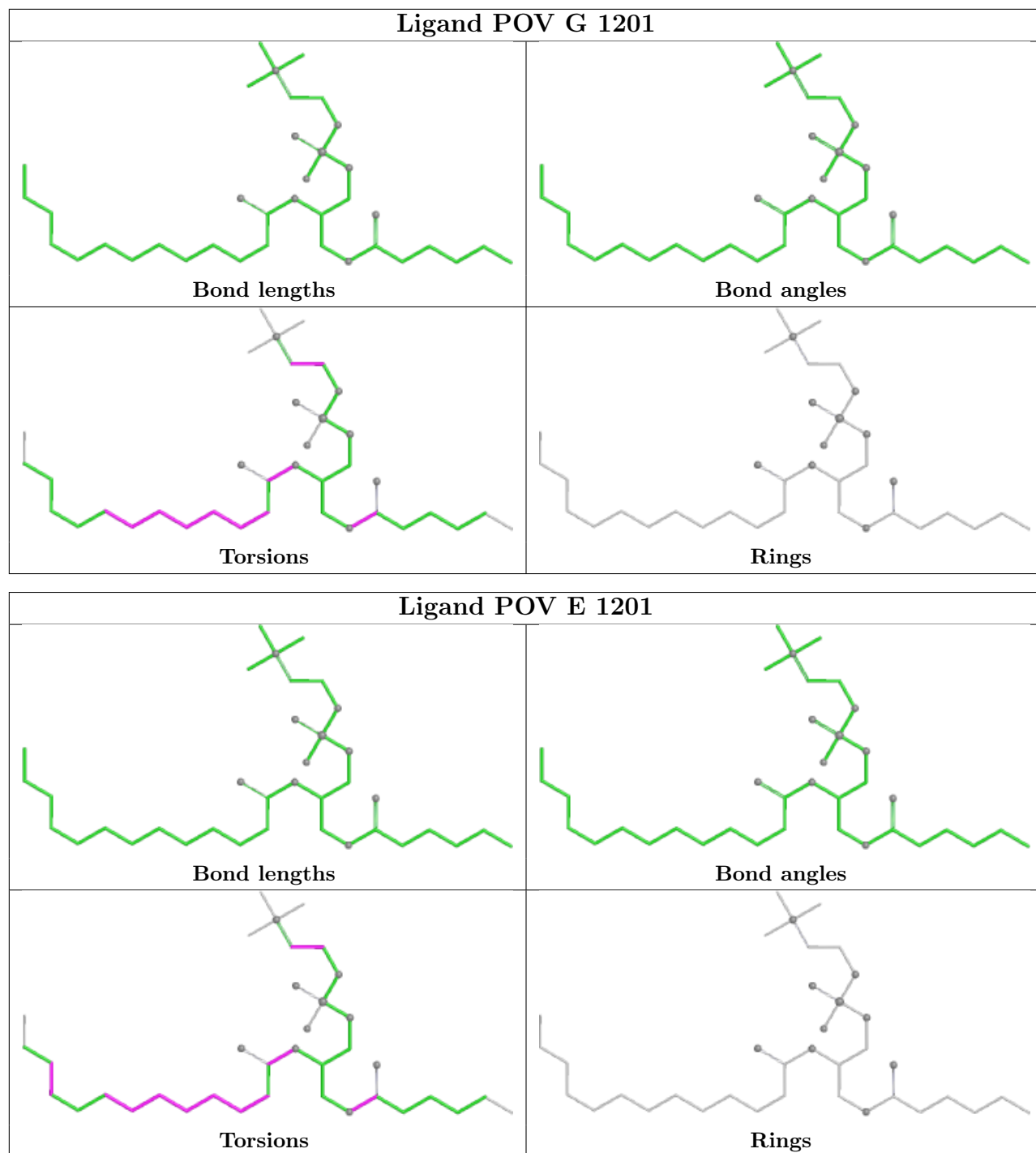
2 monomers are involved in 2 short contacts:

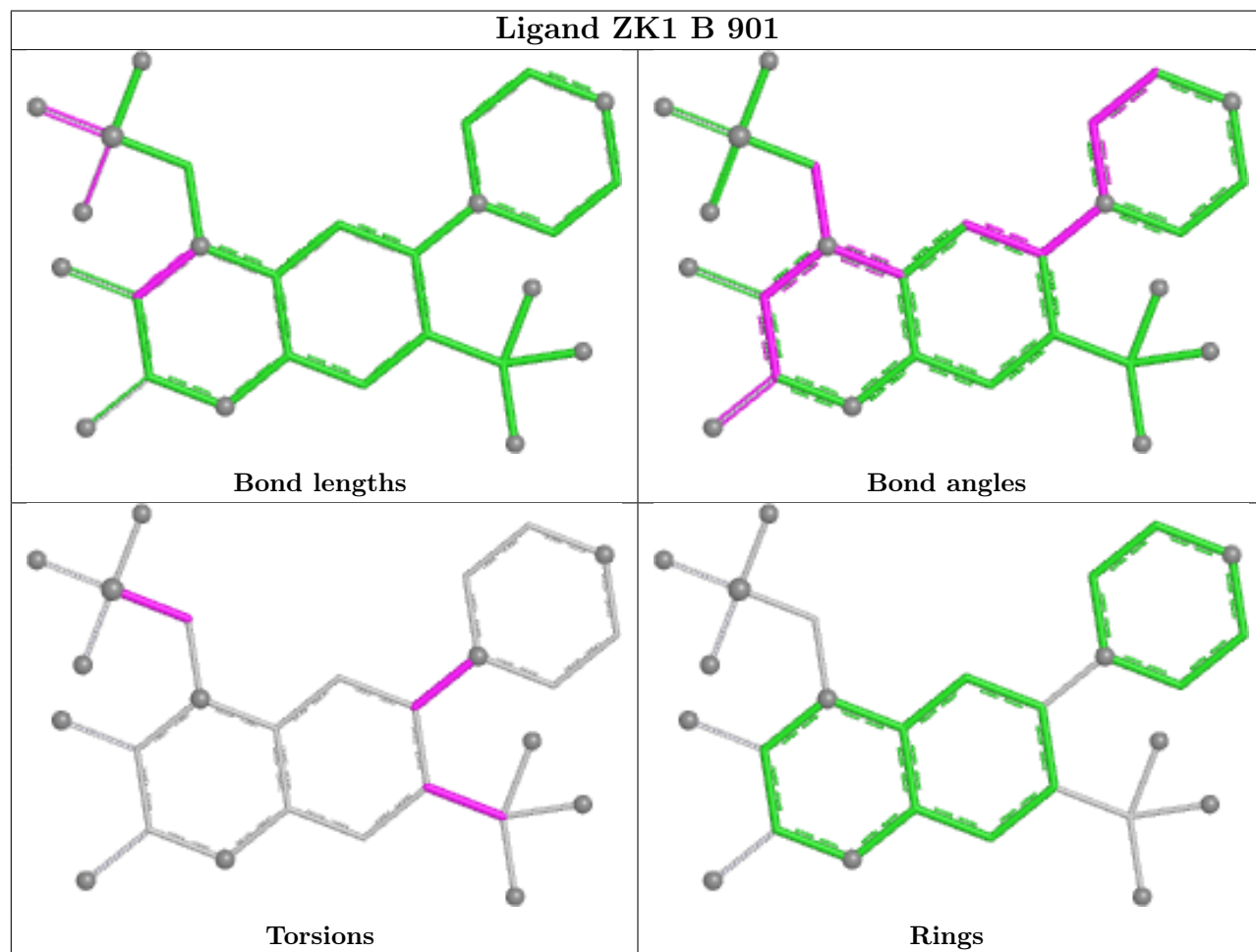
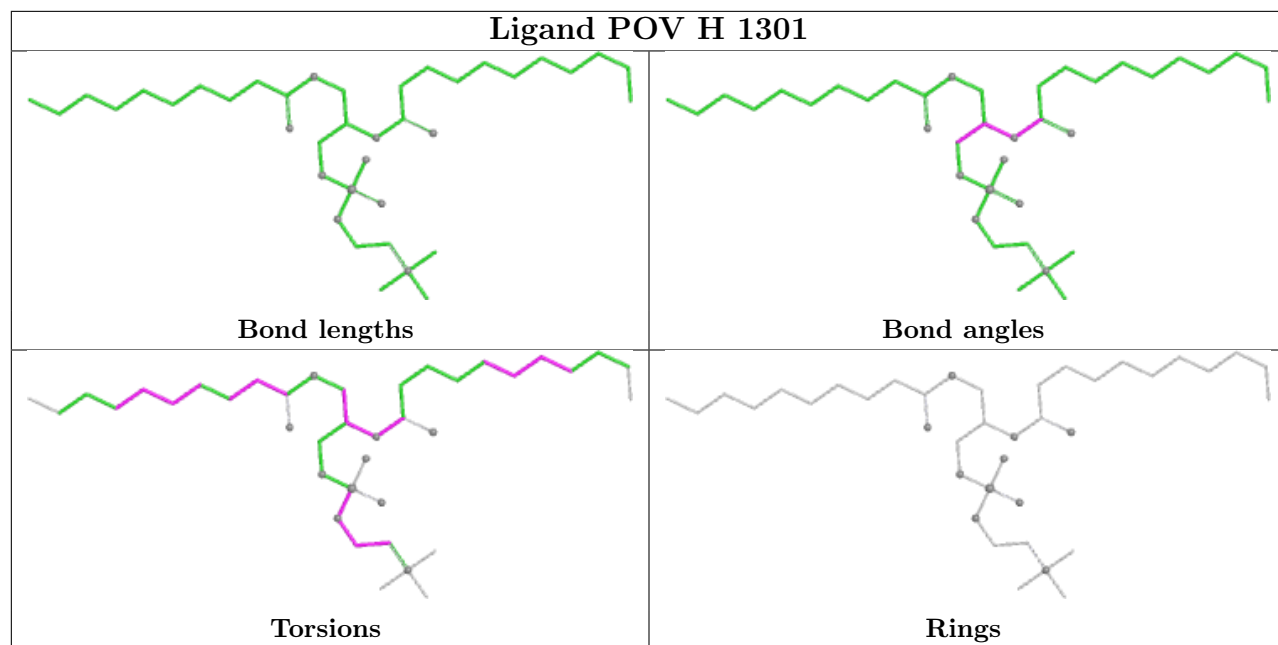
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	901	ZK1	1	0
3	D	901	ZK1	1	0

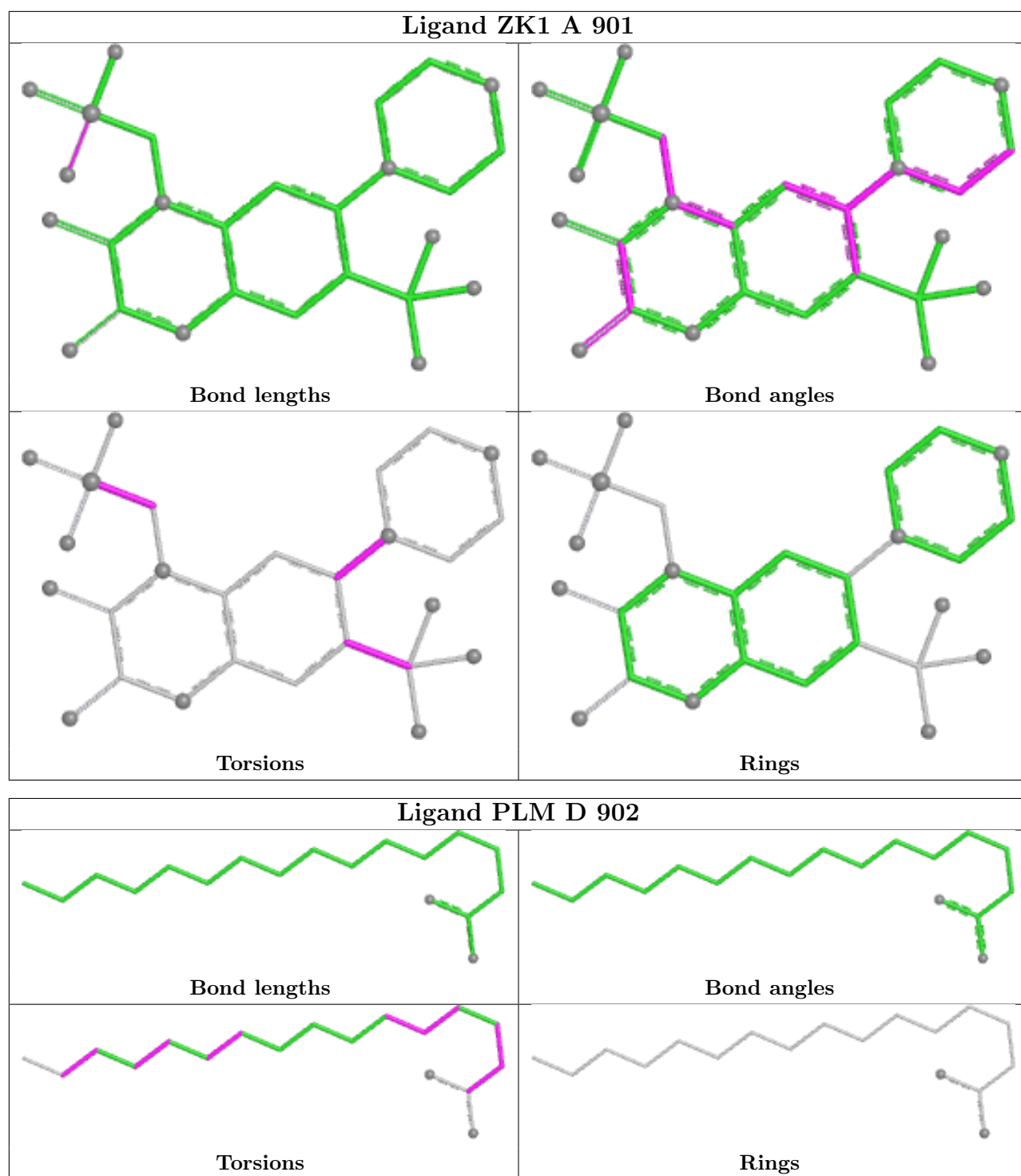
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

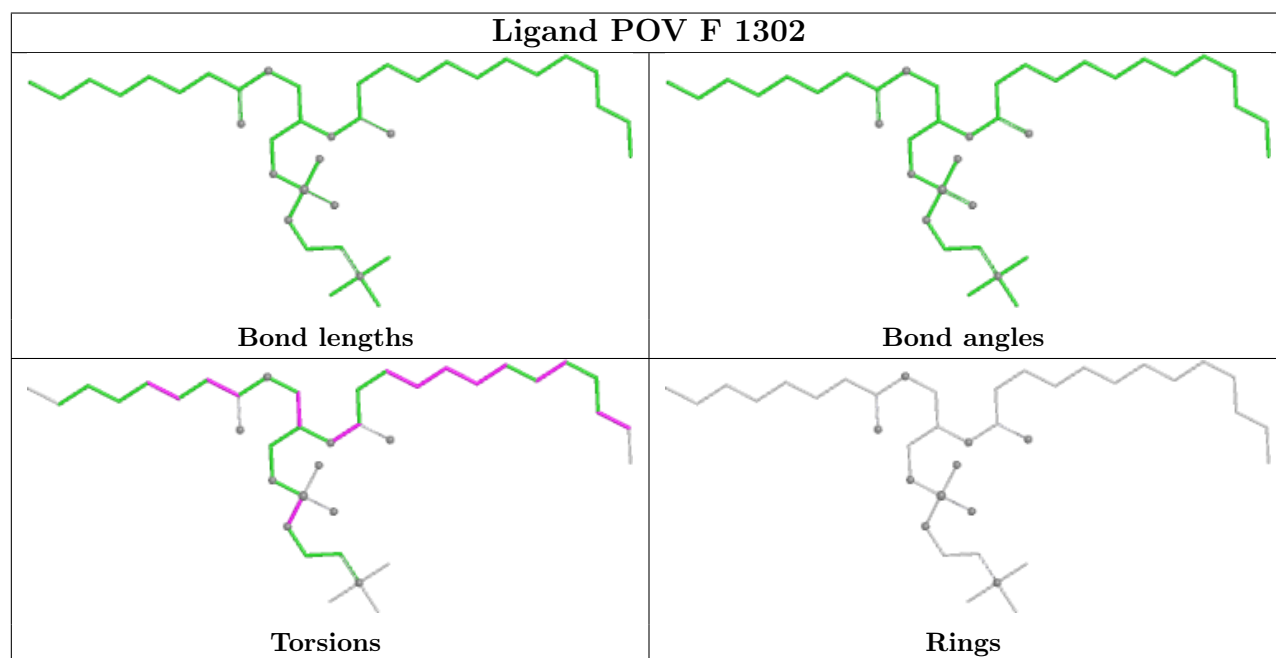
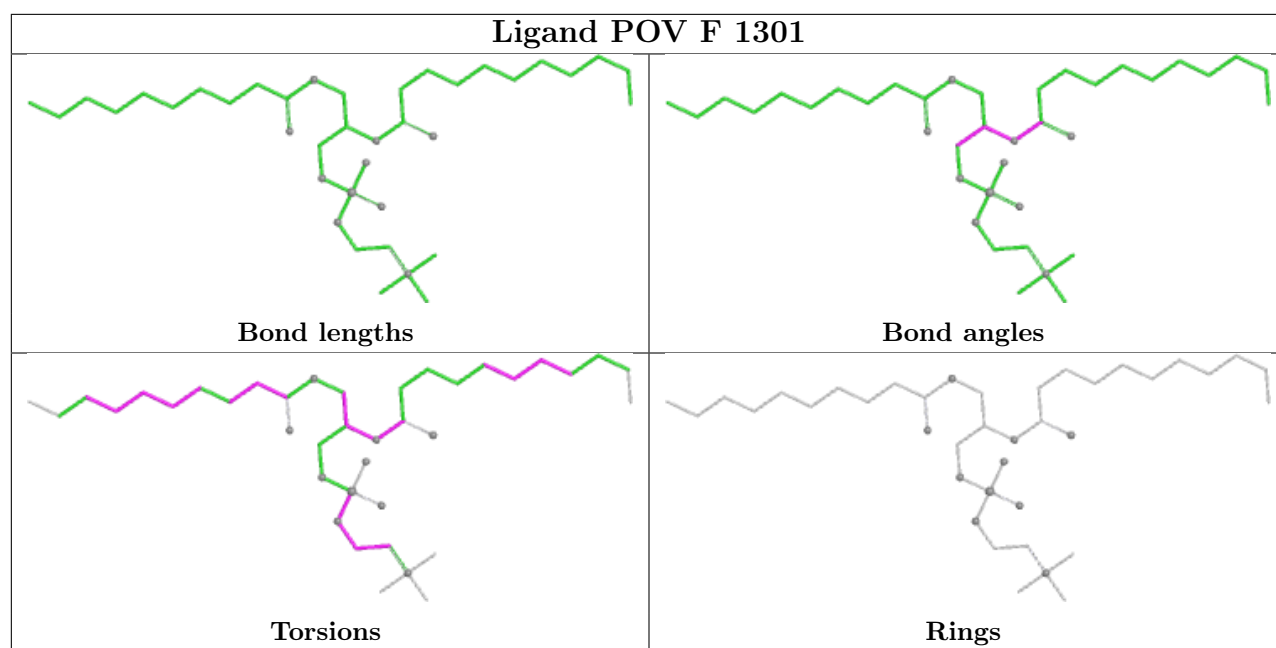


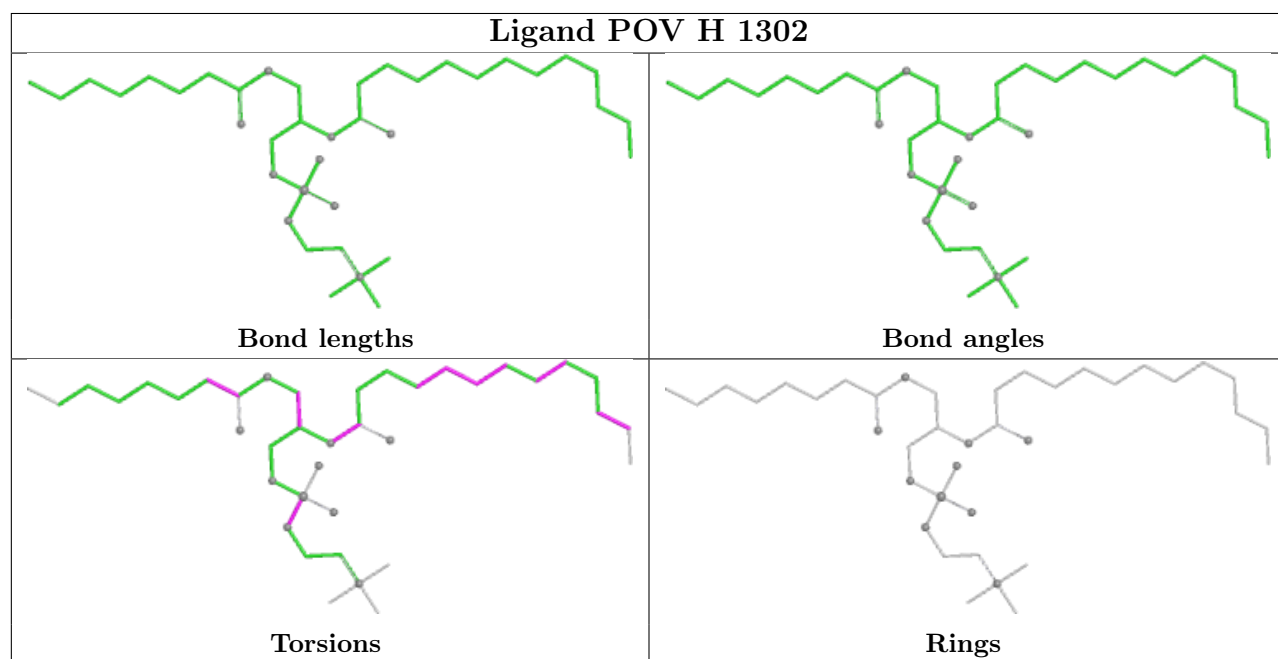
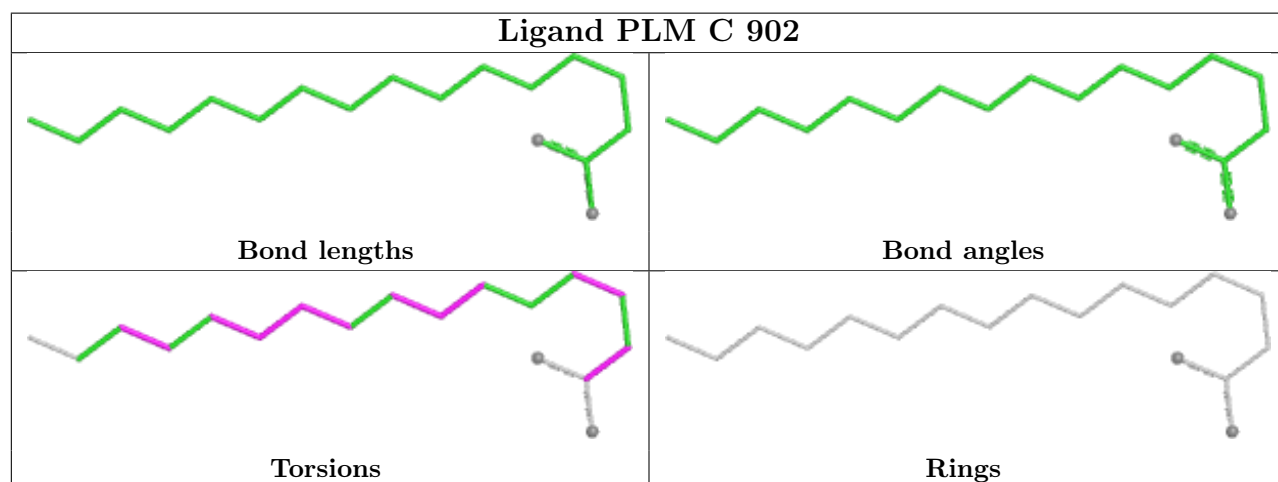
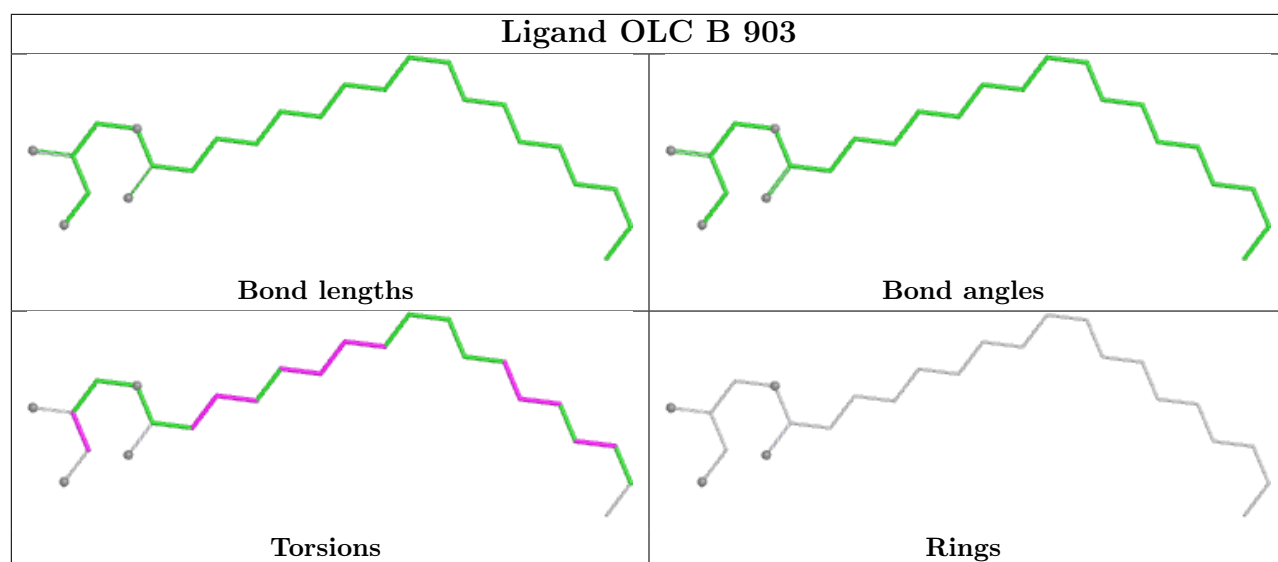


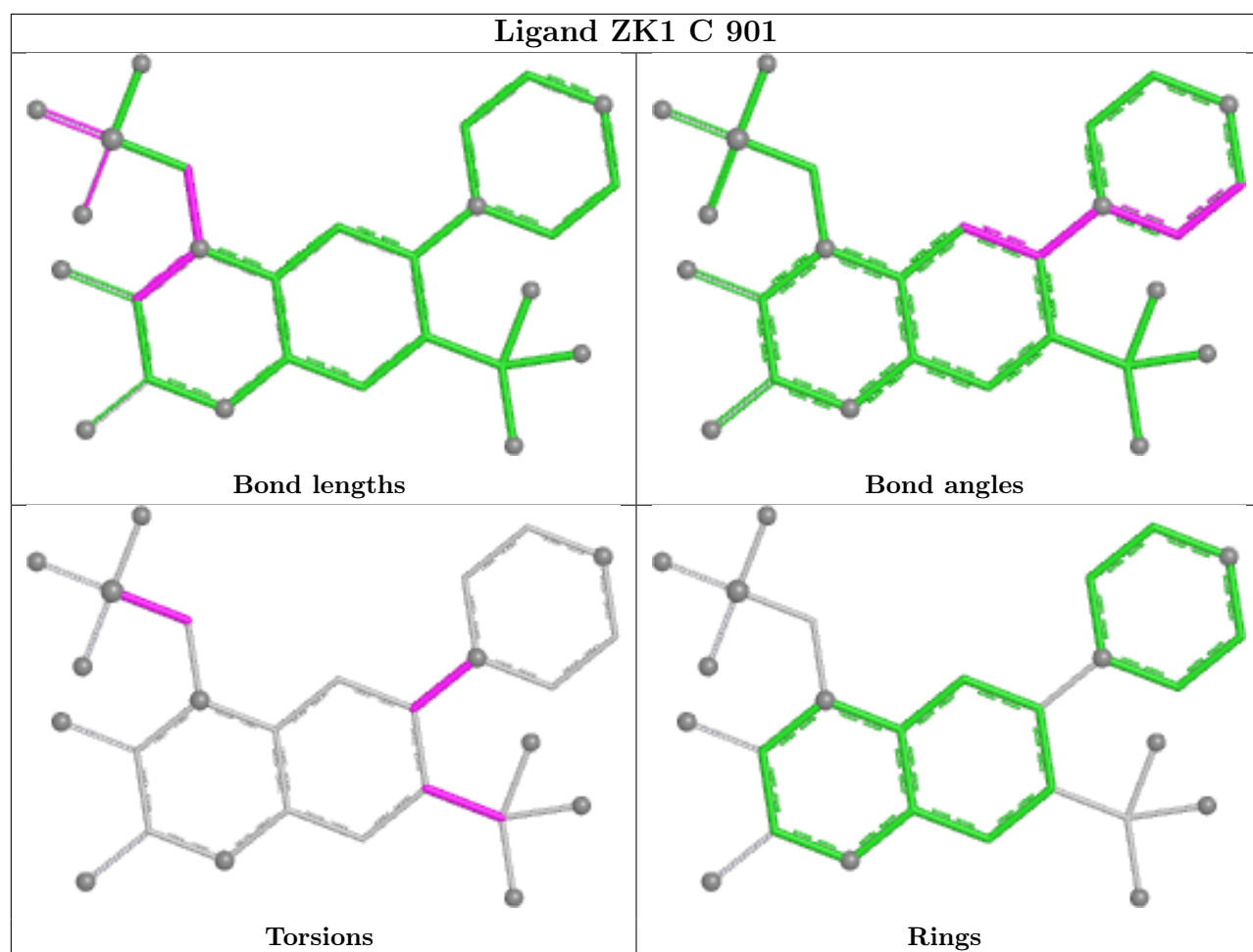


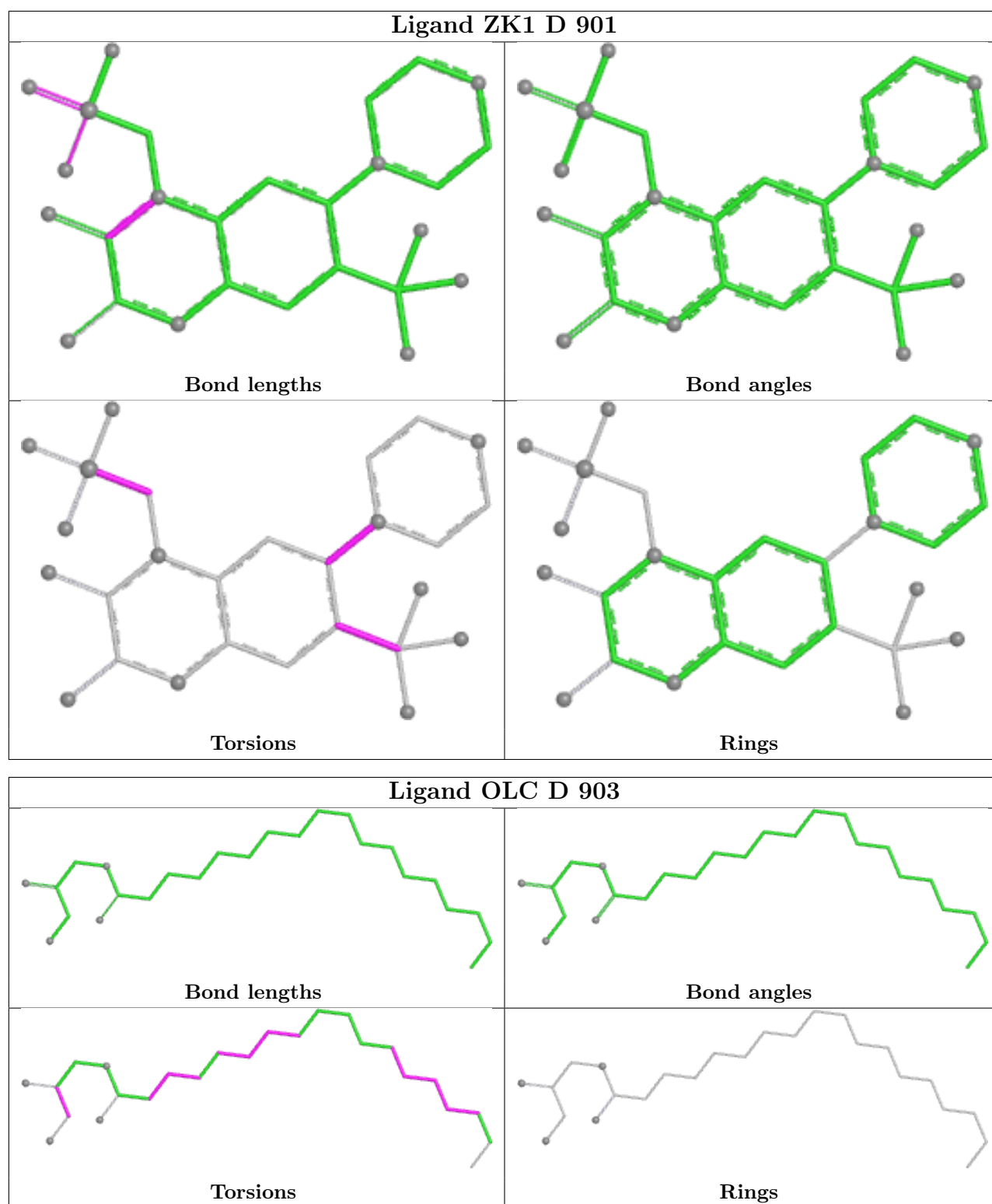












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

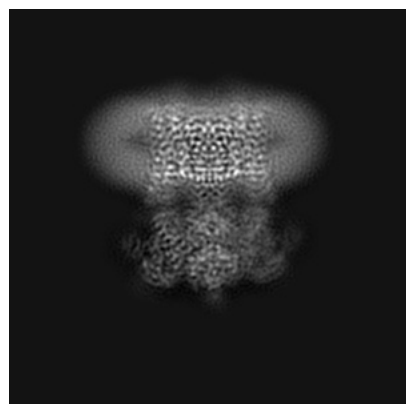
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16380. These allow visual inspection of the internal detail of the map and identification of artifacts.

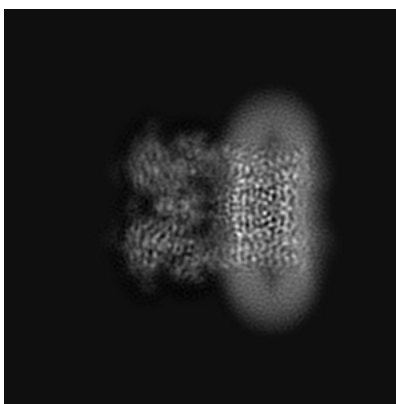
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

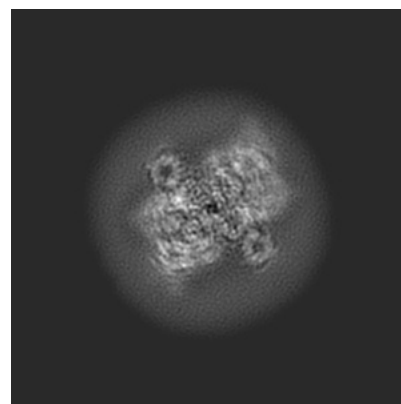
6.1.1 Primary map



X

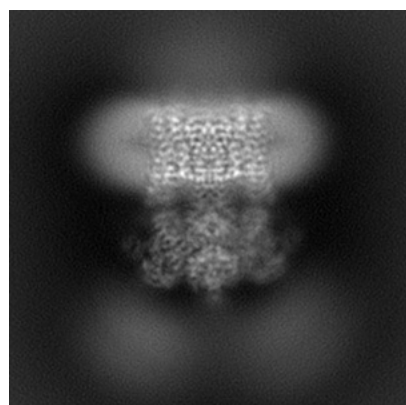


Y

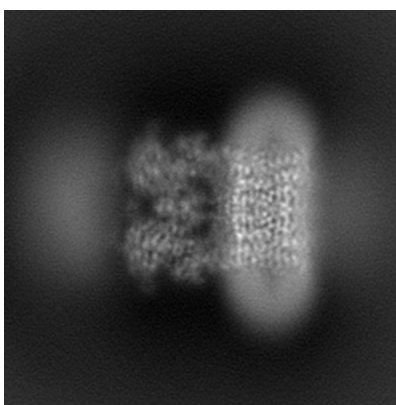


Z

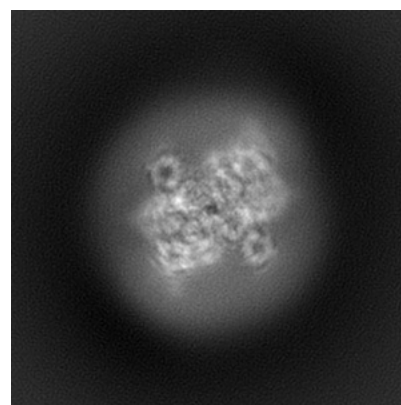
6.1.2 Raw map



X



Y

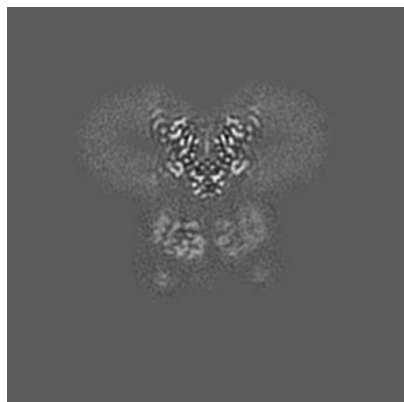


Z

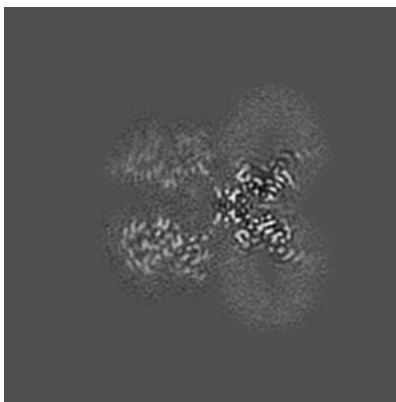
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

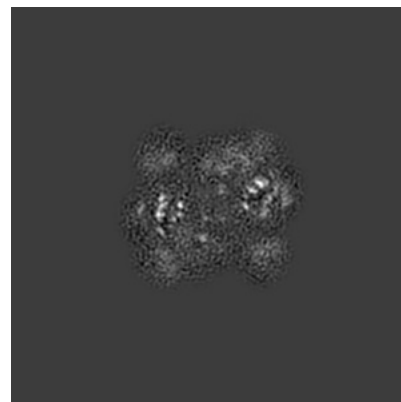
6.2.1 Primary map



X Index: 114

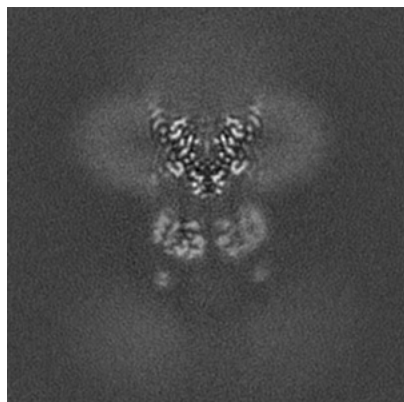


Y Index: 114

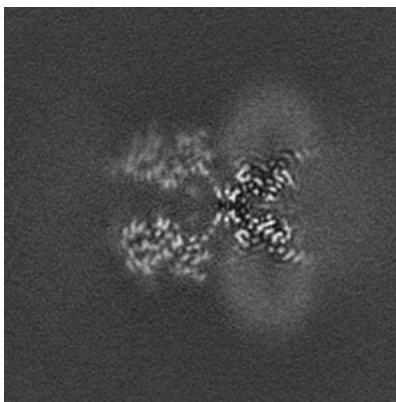


Z Index: 114

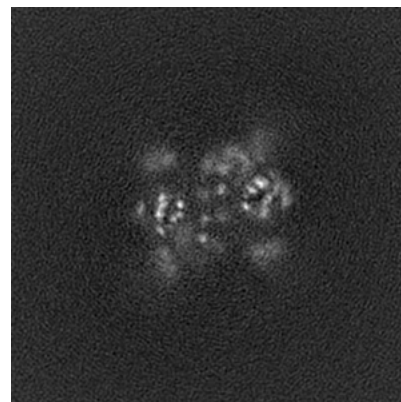
6.2.2 Raw map



X Index: 114



Y Index: 114

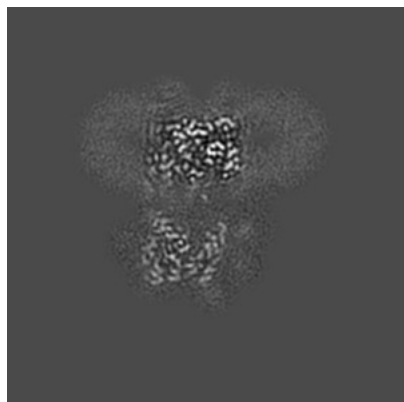


Z Index: 114

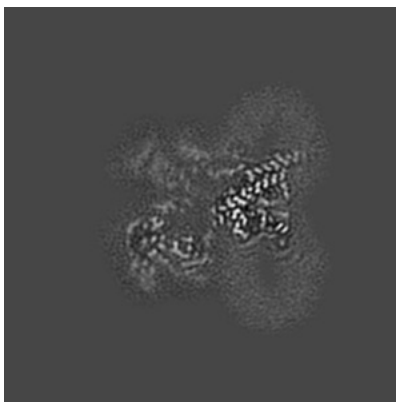
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

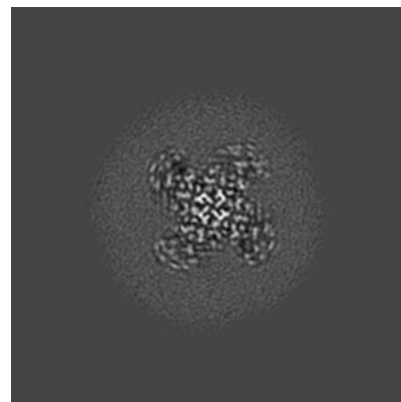
6.3.1 Primary map



X Index: 102

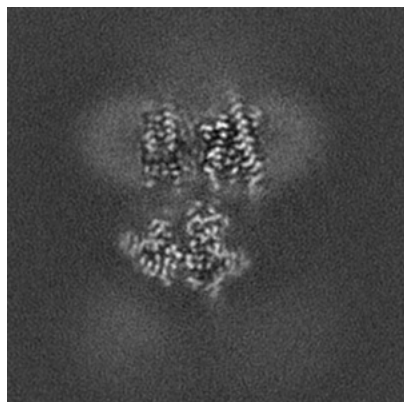


Y Index: 110

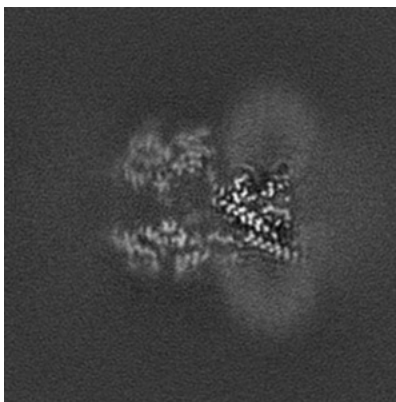


Z Index: 136

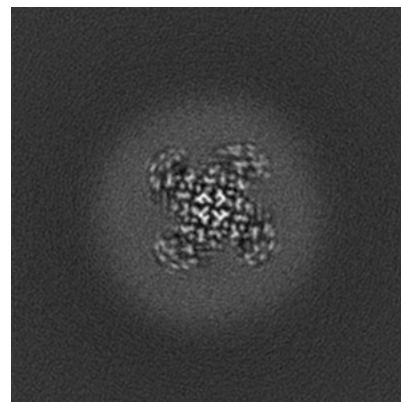
6.3.2 Raw map



X Index: 94



Y Index: 118

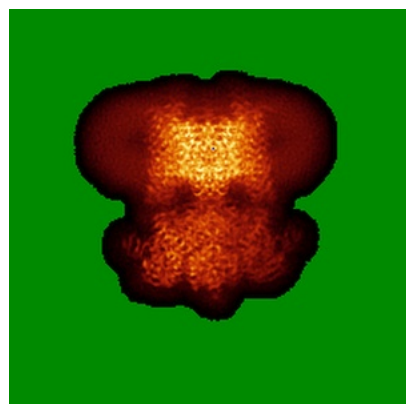


Z Index: 136

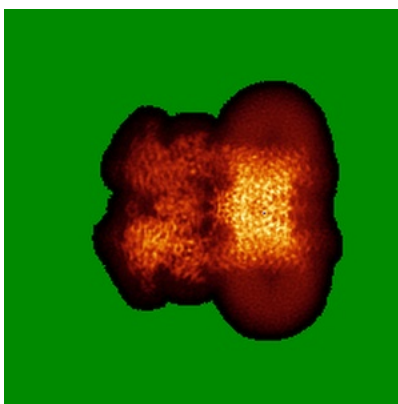
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

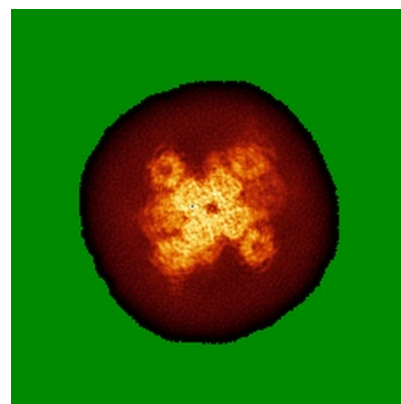
6.4.1 Primary map



X

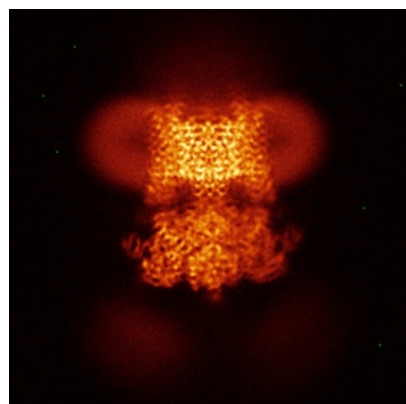


Y

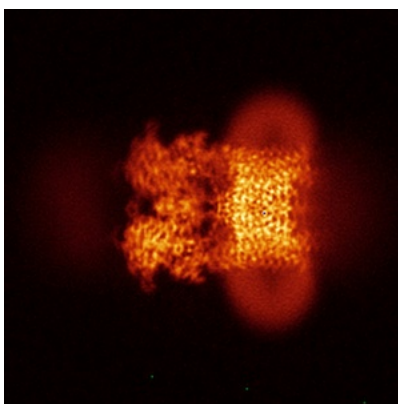


Z

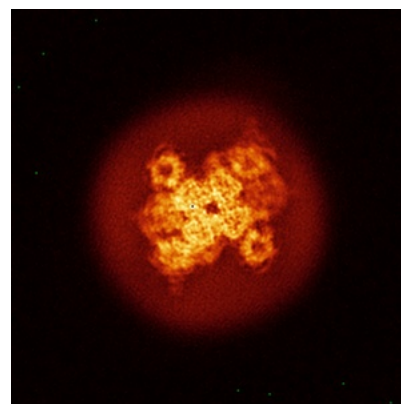
6.4.2 Raw map



X



Y

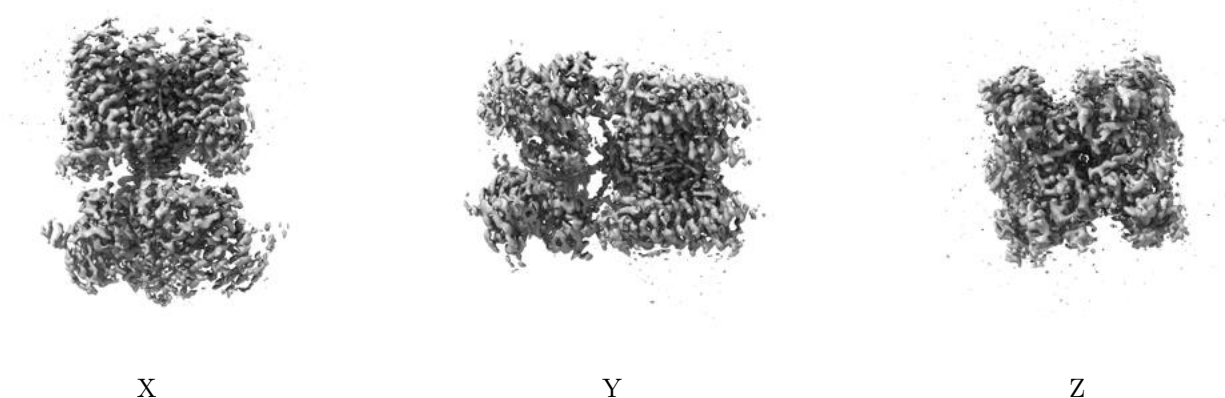


Z

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.

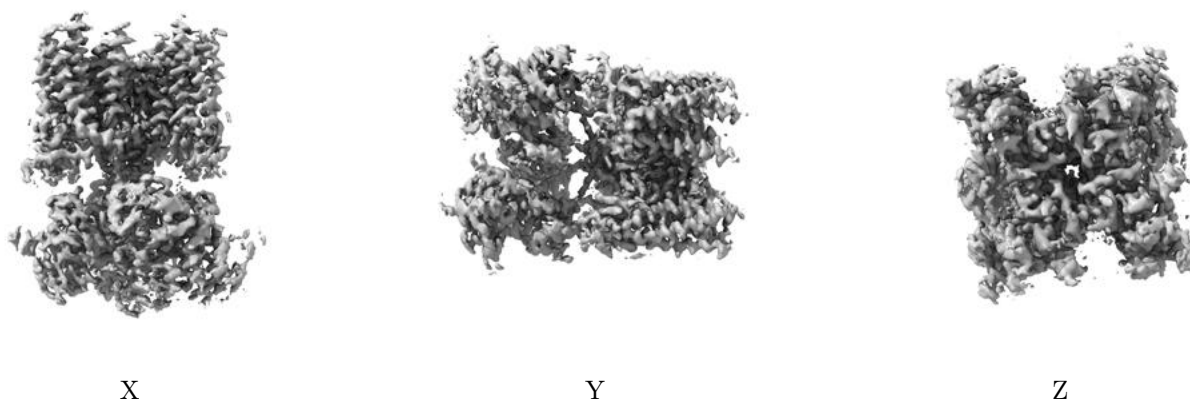
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.014. 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.

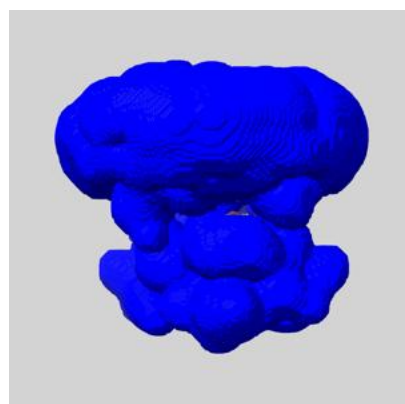
6.6 Mask visualisation [i](#)

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

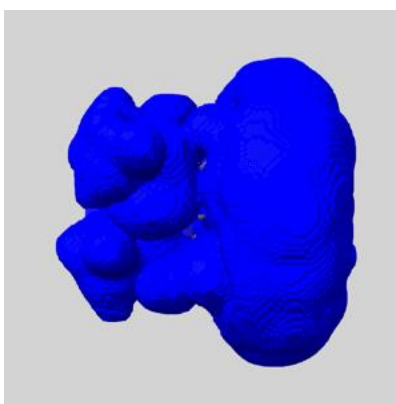
A mask typically either:

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

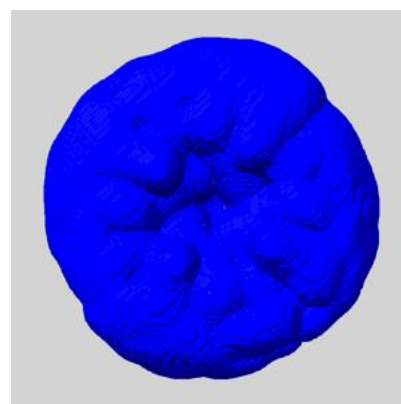
6.6.1 emd_16380_msk_1.map [i](#)



X



Y

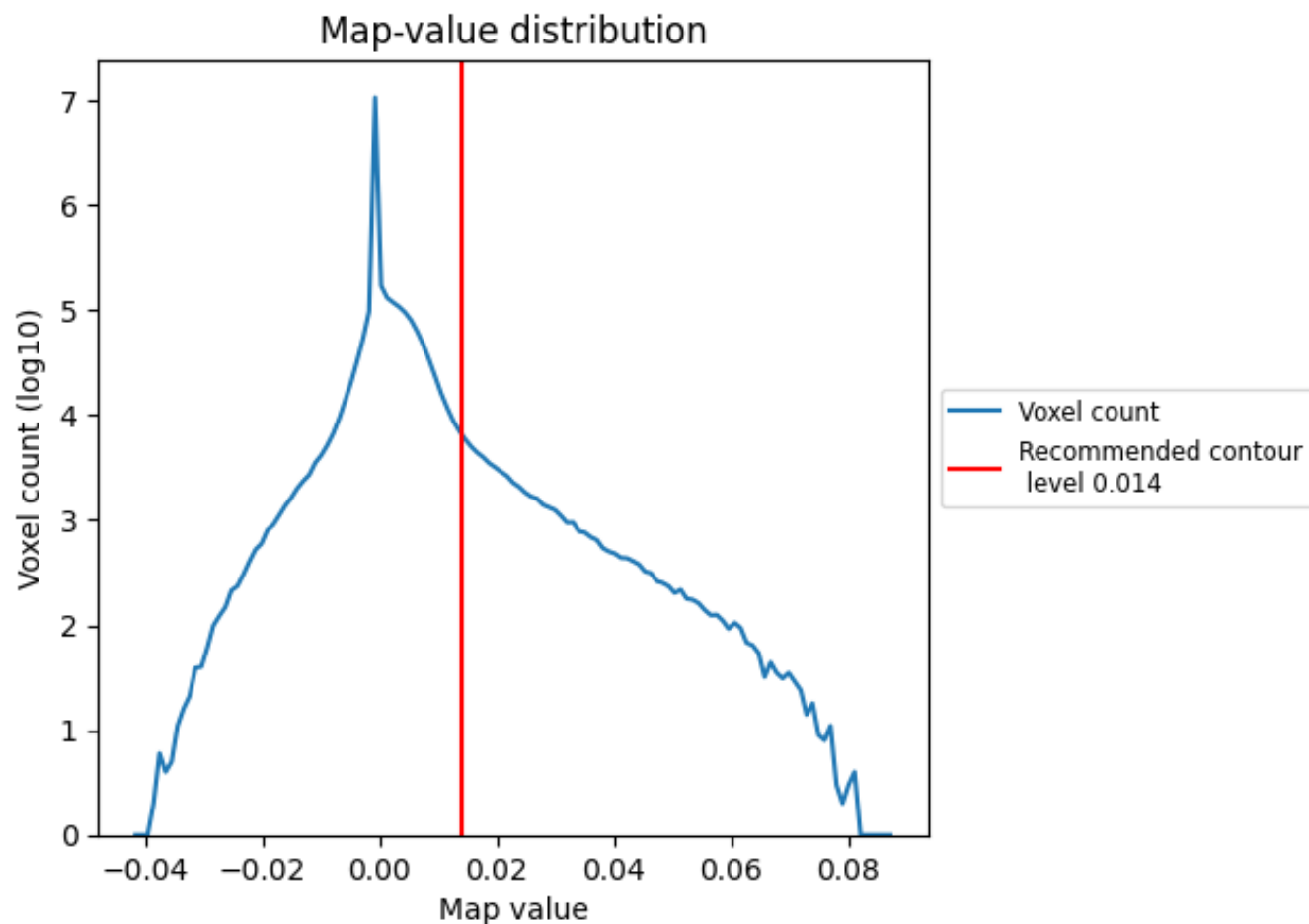


Z

7 Map analysis [i](#)

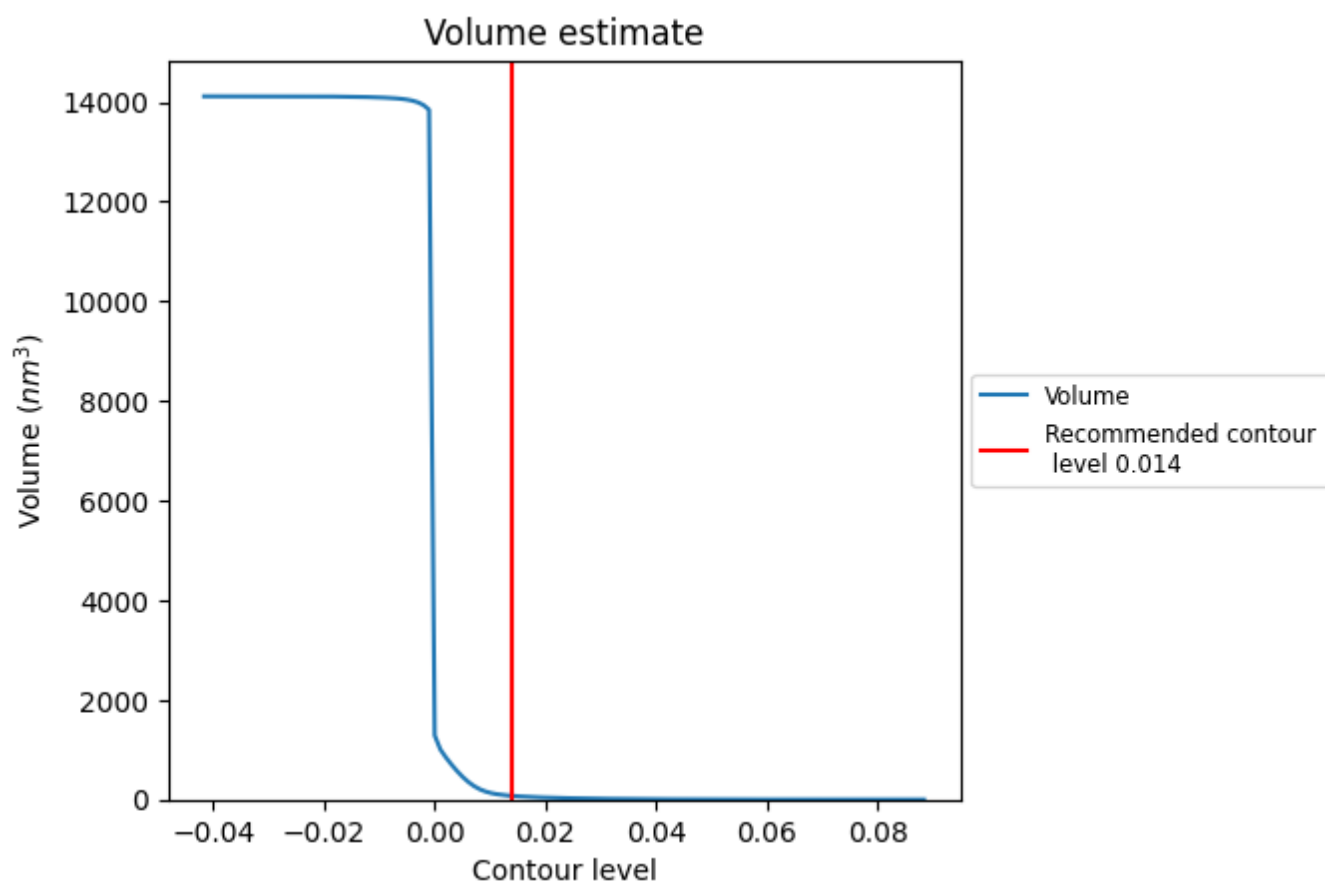
This section contains the results of statistical analysis of the map.

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.

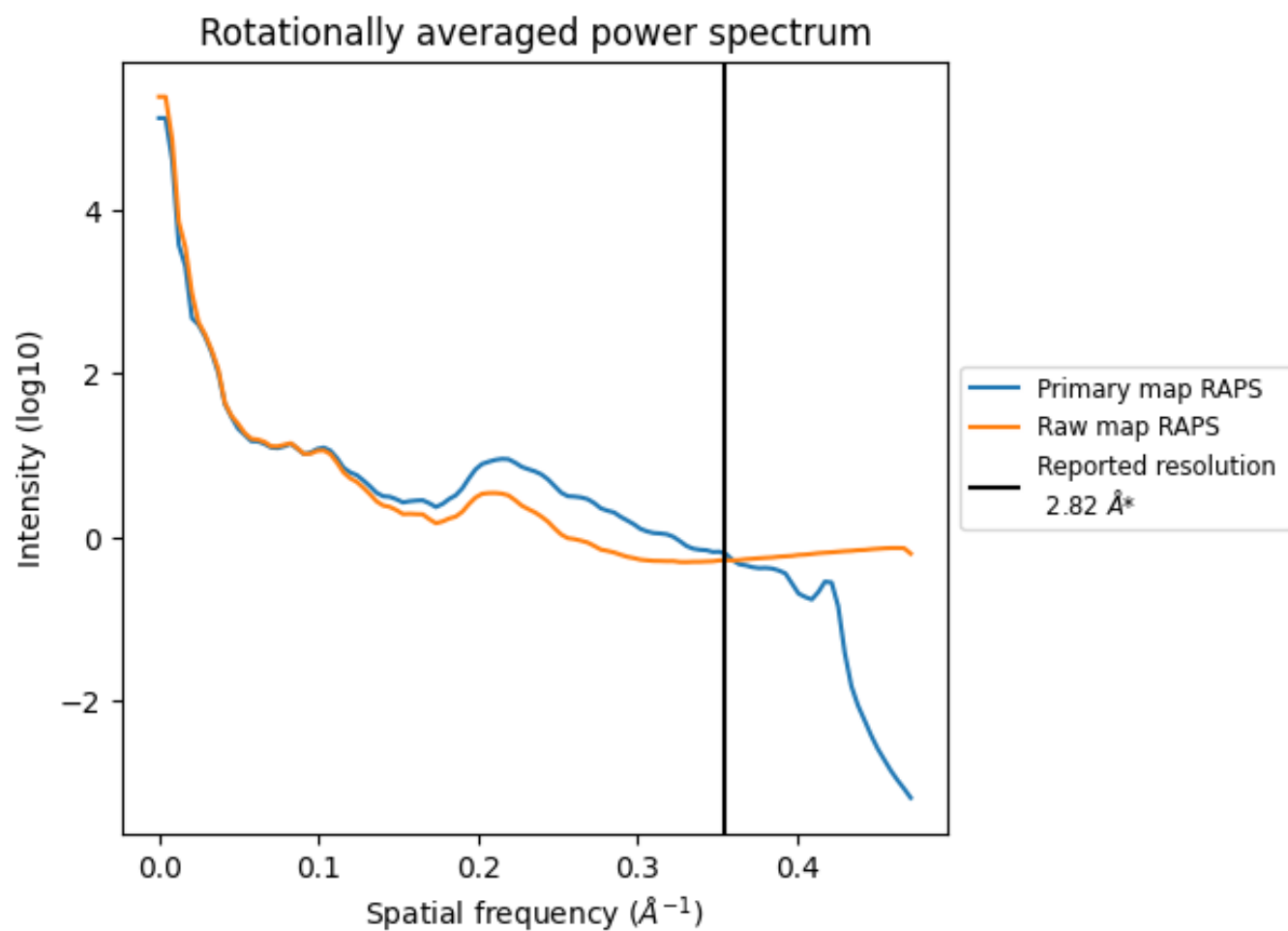
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 74 nm³; this corresponds to an approximate mass of 67 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 ⓘ

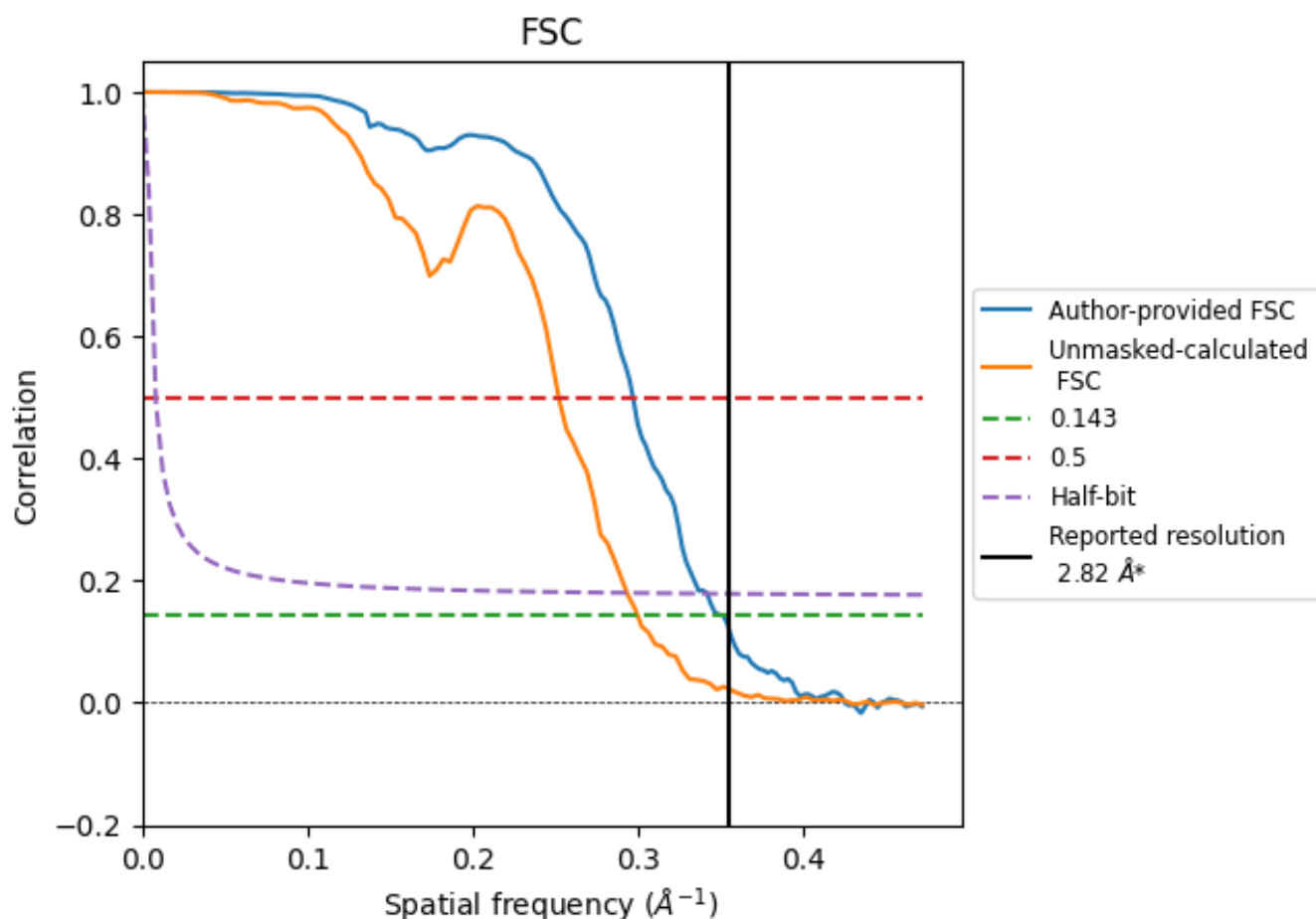


*Reported resolution corresponds to spatial frequency of 0.355 $\text{\AA}^{-1}$

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 $0.355 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

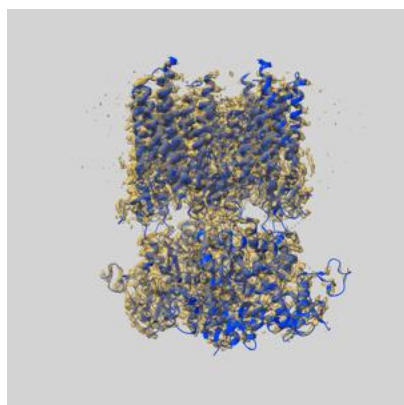
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.82	-	-
Author-provided FSC curve	2.85	3.37	2.92
Unmasked-calculated*	3.34	3.97	3.41

*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 3.34 differs from the reported value 2.82 by more than 10 %

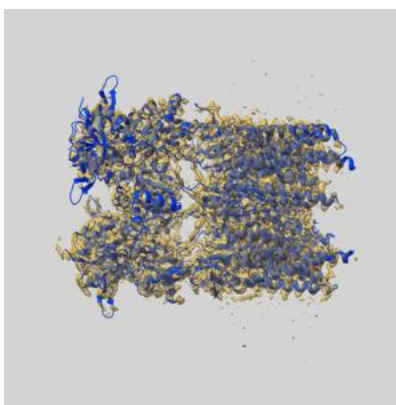
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16380 and PDB model 8C1Q. Per-residue inclusion information can be found in section [3](#) on page [9](#).

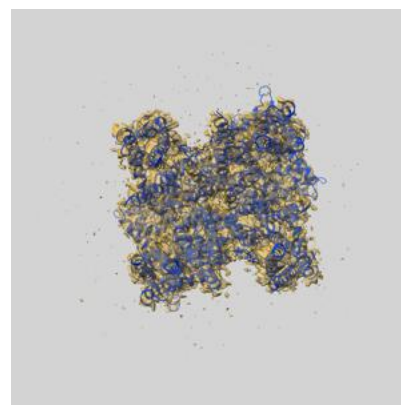
9.1 Map-model overlay [i](#)



X



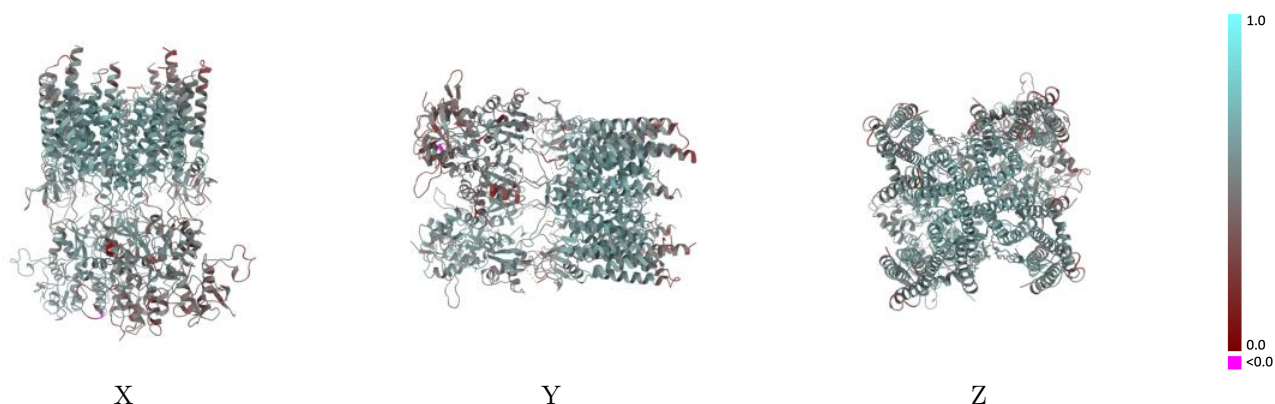
Y



Z

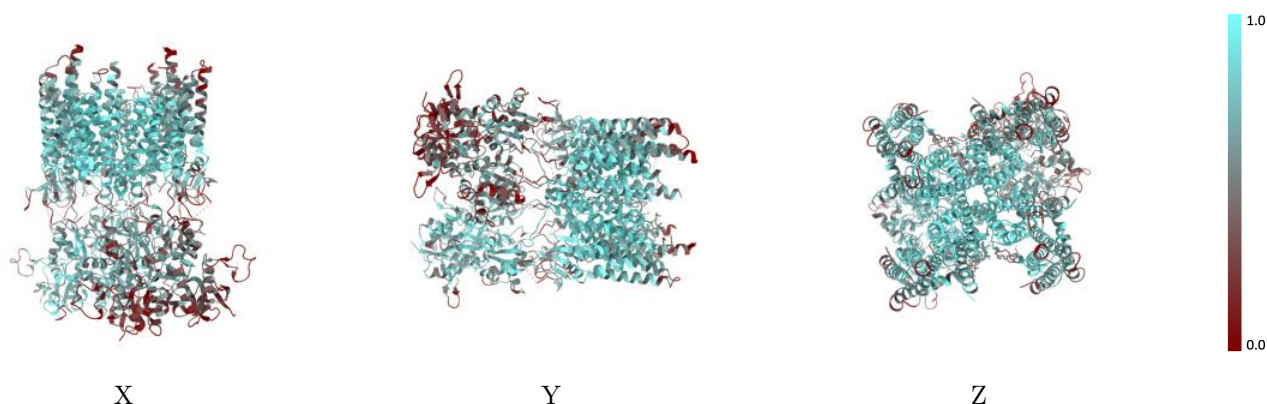
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



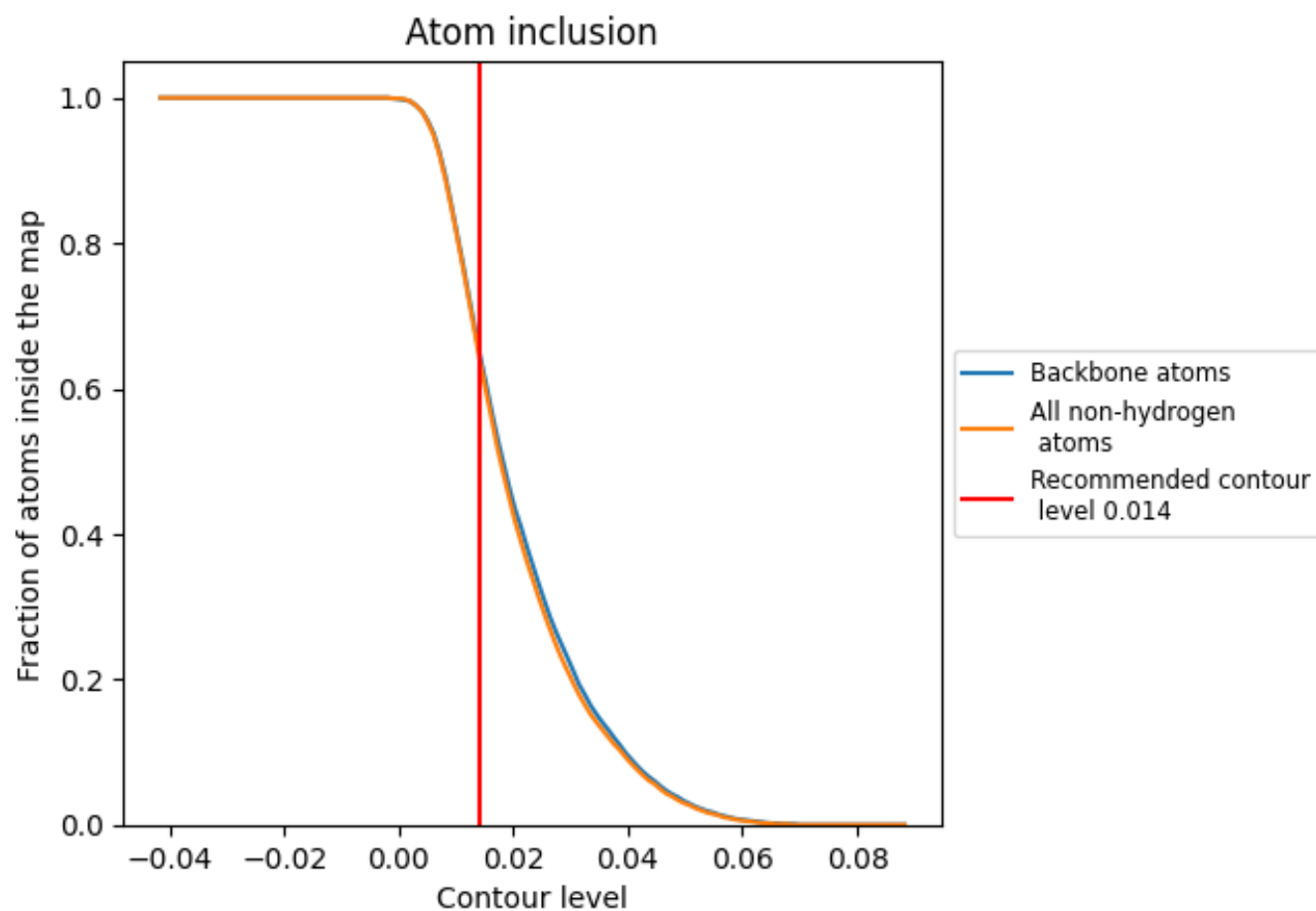
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 65% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6460	0.5400
A	0.7570	0.5810
B	0.5690	0.5140
C	0.5410	0.5060
D	0.7560	0.5750
E	0.6630	0.5440
F	0.6560	0.5480
G	0.5650	0.5010
H	0.6640	0.5210

1.0

0.0

<0.0