



## Full wwPDB EM Validation Report ⓘ

Oct 21, 2023 – 01:06 PM EDT

PDB ID : 8SSA  
EMDB ID : EMD-40749  
Title : Structure of AMPA receptor GluA2 complex with auxiliary subunits TARP gamma-5 and cornichon-2 bound to glutamate and channel blocker spermidine (desensitized state)  
Authors : Gangwar, S.P.; Yen, L.Y.; Yelshanskaya, M.V.; Sobolevsky, A.I.  
Deposited on : 2023-05-08  
Resolution : 3.88 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

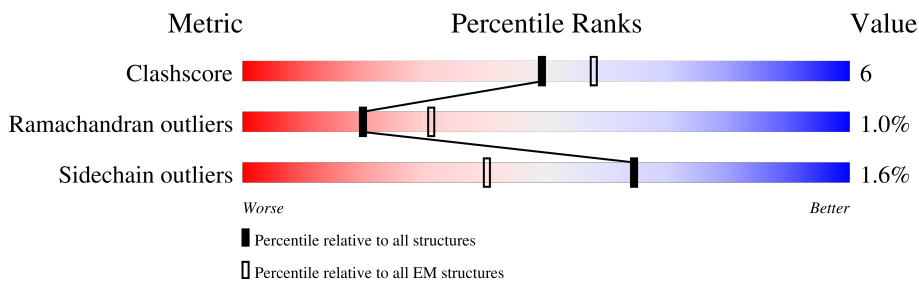
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.88 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1026	
1	B	1026	
1	C	1026	
1	D	1026	
2	E	160	
2	F	160	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 30888 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 2, Voltage-dependent calcium channel gamma-5 subunit chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	986	7759	5006	1272	1440	41	0	0
1	B	792	6238	4001	1036	1171	30	0	0
1	C	986	7759	5006	1272	1440	41	0	0
1	D	792	6238	4001	1036	1171	30	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	GLU	ASN	conflict	UNP P19491
A	382	LEU	VAL	conflict	UNP P19491
A	?	-	LEU	deletion	UNP P19491
A	?	-	THR	deletion	UNP P19491
A	?	-	GLU	deletion	UNP P19491
A	?	-	LEU	deletion	UNP P19491
A	?	-	PRO	deletion	UNP P19491
A	?	-	SER	deletion	UNP P19491
A	384	GLU	GLY	conflict	UNP P19491
A	385	ASP	ASN	conflict	UNP P19491
A	392	GLN	ASN	conflict	UNP P19491
A	754	SER	ASN	conflict	UNP P19491
A	758	VAL	LEU	conflict	UNP P19491
A	827	GLY	-	linker	UNP P19491
A	828	THR	-	linker	UNP P19491
A	829	GLY	-	linker	UNP P19491
A	830	SER	-	linker	UNP P19491
A	831	ALA	-	linker	UNP P19491
B	241	GLU	ASN	conflict	UNP P19491
B	382	LEU	VAL	conflict	UNP P19491
B	?	-	LEU	deletion	UNP P19491

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	THR	deletion	UNP P19491
B	?	-	GLU	deletion	UNP P19491
B	?	-	LEU	deletion	UNP P19491
B	?	-	PRO	deletion	UNP P19491
B	?	-	SER	deletion	UNP P19491
B	384	GLU	GLY	conflict	UNP P19491
B	385	ASP	ASN	conflict	UNP P19491
B	392	GLN	ASN	conflict	UNP P19491
B	754	SER	ASN	conflict	UNP P19491
B	758	VAL	LEU	conflict	UNP P19491
B	827	GLY	-	linker	UNP P19491
B	828	THR	-	linker	UNP P19491
B	829	GLY	-	linker	UNP P19491
B	830	SER	-	linker	UNP P19491
B	831	ALA	-	linker	UNP P19491
C	241	GLU	ASN	conflict	UNP P19491
C	382	LEU	VAL	conflict	UNP P19491
C	?	-	LEU	deletion	UNP P19491
C	?	-	THR	deletion	UNP P19491
C	?	-	GLU	deletion	UNP P19491
C	?	-	LEU	deletion	UNP P19491
C	?	-	PRO	deletion	UNP P19491
C	?	-	SER	deletion	UNP P19491
C	384	GLU	GLY	conflict	UNP P19491
C	385	ASP	ASN	conflict	UNP P19491
C	392	GLN	ASN	conflict	UNP P19491
C	754	SER	ASN	conflict	UNP P19491
C	758	VAL	LEU	conflict	UNP P19491
C	827	GLY	-	linker	UNP P19491
C	828	THR	-	linker	UNP P19491
C	829	GLY	-	linker	UNP P19491
C	830	SER	-	linker	UNP P19491
C	831	ALA	-	linker	UNP P19491
D	241	GLU	ASN	conflict	UNP P19491
D	382	LEU	VAL	conflict	UNP P19491
D	?	-	LEU	deletion	UNP P19491
D	?	-	THR	deletion	UNP P19491
D	?	-	GLU	deletion	UNP P19491
D	?	-	LEU	deletion	UNP P19491
D	?	-	PRO	deletion	UNP P19491
D	?	-	SER	deletion	UNP P19491
D	384	GLU	GLY	conflict	UNP P19491

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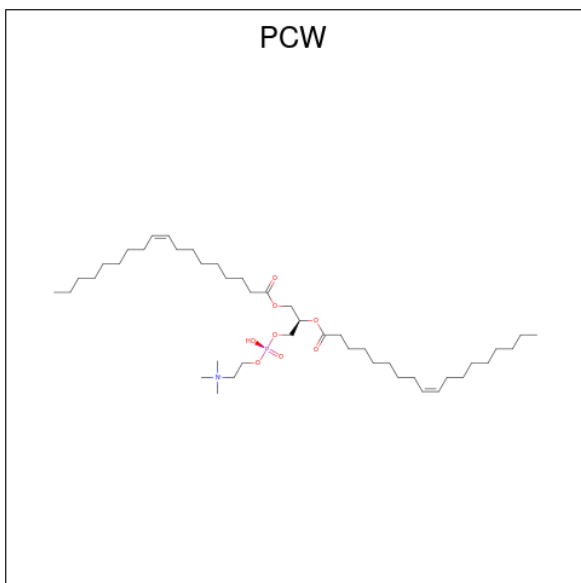
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Chain	Residue	Modelled	Actual	Comment	Reference
D	385	ASP	ASN	conflict	UNP P19491
D	392	GLN	ASN	conflict	UNP P19491
D	754	SER	ASN	conflict	UNP P19491
D	758	VAL	LEU	conflict	UNP P19491
D	827	GLY	-	linker	UNP P19491
D	828	THR	-	linker	UNP P19491
D	829	GLY	-	linker	UNP P19491
D	830	SER	-	linker	UNP P19491
D	831	ALA	-	linker	UNP P19491

- Molecule 2 is a protein called Protein cornichon homolog 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	140	1166	787	175	191	13	0	0
2	F	140	1166	787	175	191	13	0	0

- Molecule 3 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PCW) (formula:  $C_{44}H_{85}NO_8P$ ).



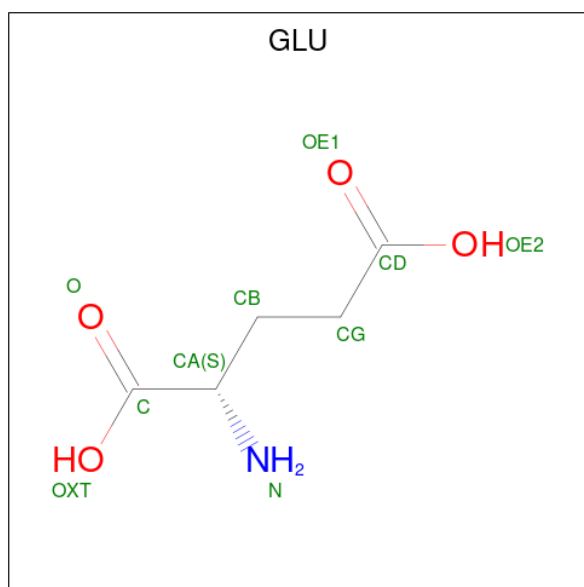
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	A	1	51	41	1	8	1	0
3	A	1	43	33	1	8	1	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	A	1	Total 39	C 29	N 1	O 8	P 1	0
3	A	1	Total 41	C 31	N 1	O 8	P 1	0
3	B	1	Total 43	C 33	N 1	O 8	P 1	0
3	B	1	Total 39	C 29	N 1	O 8	P 1	0
3	C	1	Total 51	C 41	N 1	O 8	P 1	0
3	C	1	Total 43	C 33	N 1	O 8	P 1	0
3	C	1	Total 39	C 29	N 1	O 8	P 1	0
3	C	1	Total 41	C 31	N 1	O 8	P 1	0
3	D	1	Total 43	C 33	N 1	O 8	P 1	0
3	D	1	Total 39	C 29	N 1	O 8	P 1	0

- Molecule 4 is GLUTAMIC ACID (three-letter code: GLU) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



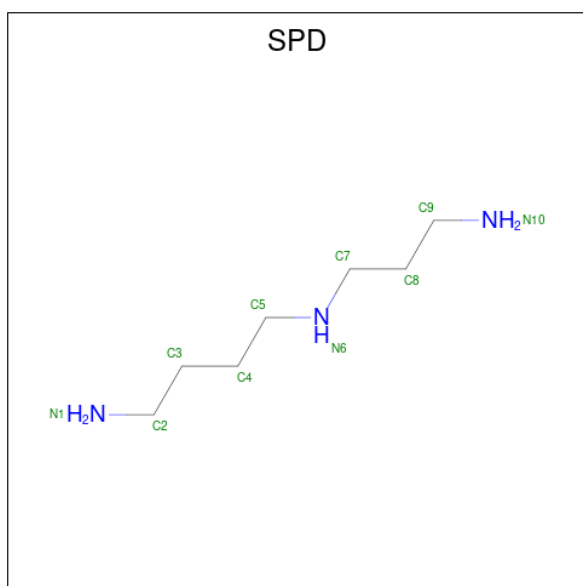
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	A	1	Total 10	C 5	N 1	O 4	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	B	1	Total 10	C 5	N 1	O 4	0
4	C	1	Total 10	C 5	N 1	O 4	0
4	D	1	Total 10	C 5	N 1	O 4	0

- Molecule 5 is SPERMIDINE (three-letter code: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).

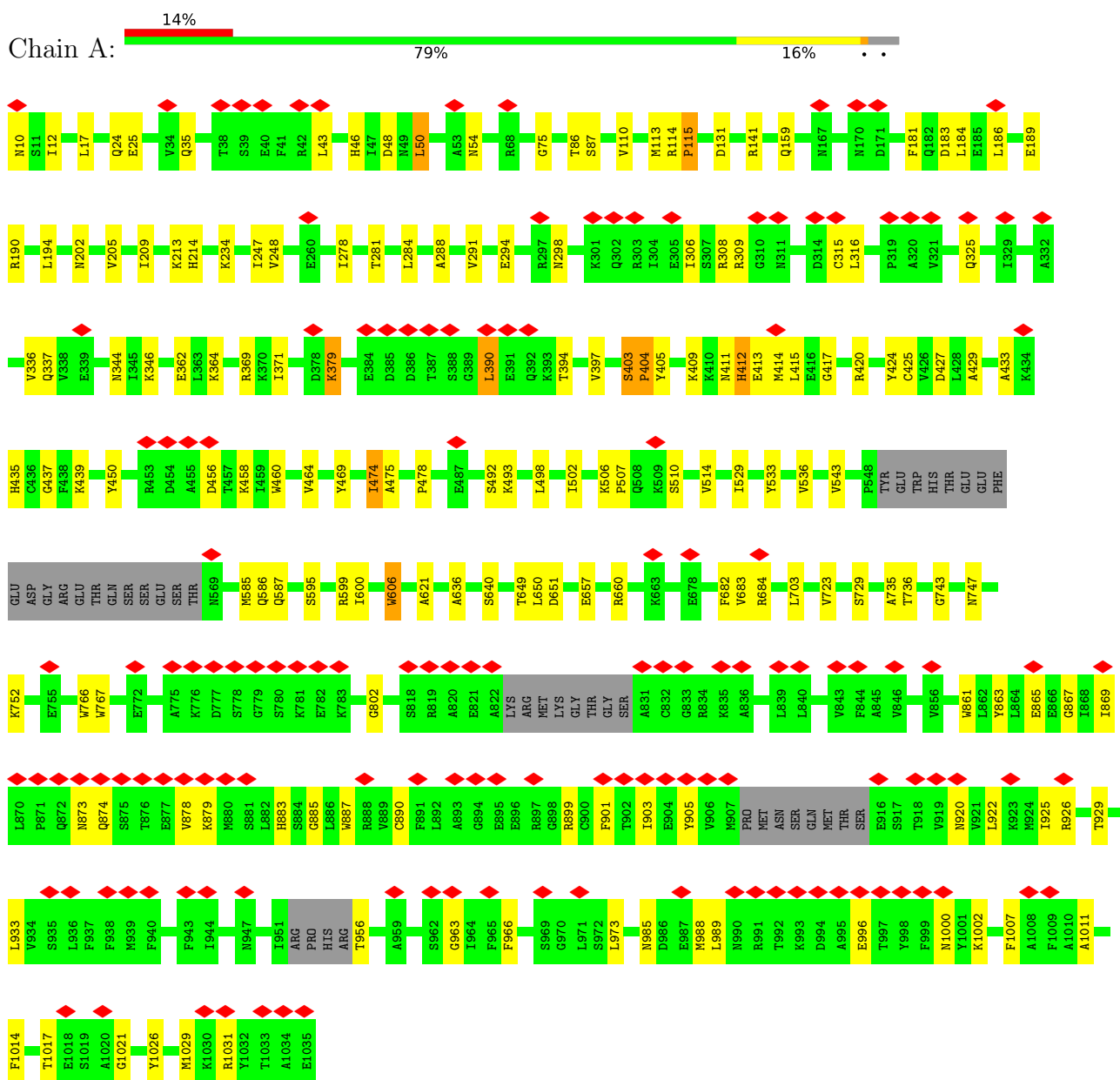


Mol	Chain	Residues	Atoms			AltConf
			Total	C	N	
5	D	1	Total 10	C 7	N 3	0

### 3 Residue-property plots

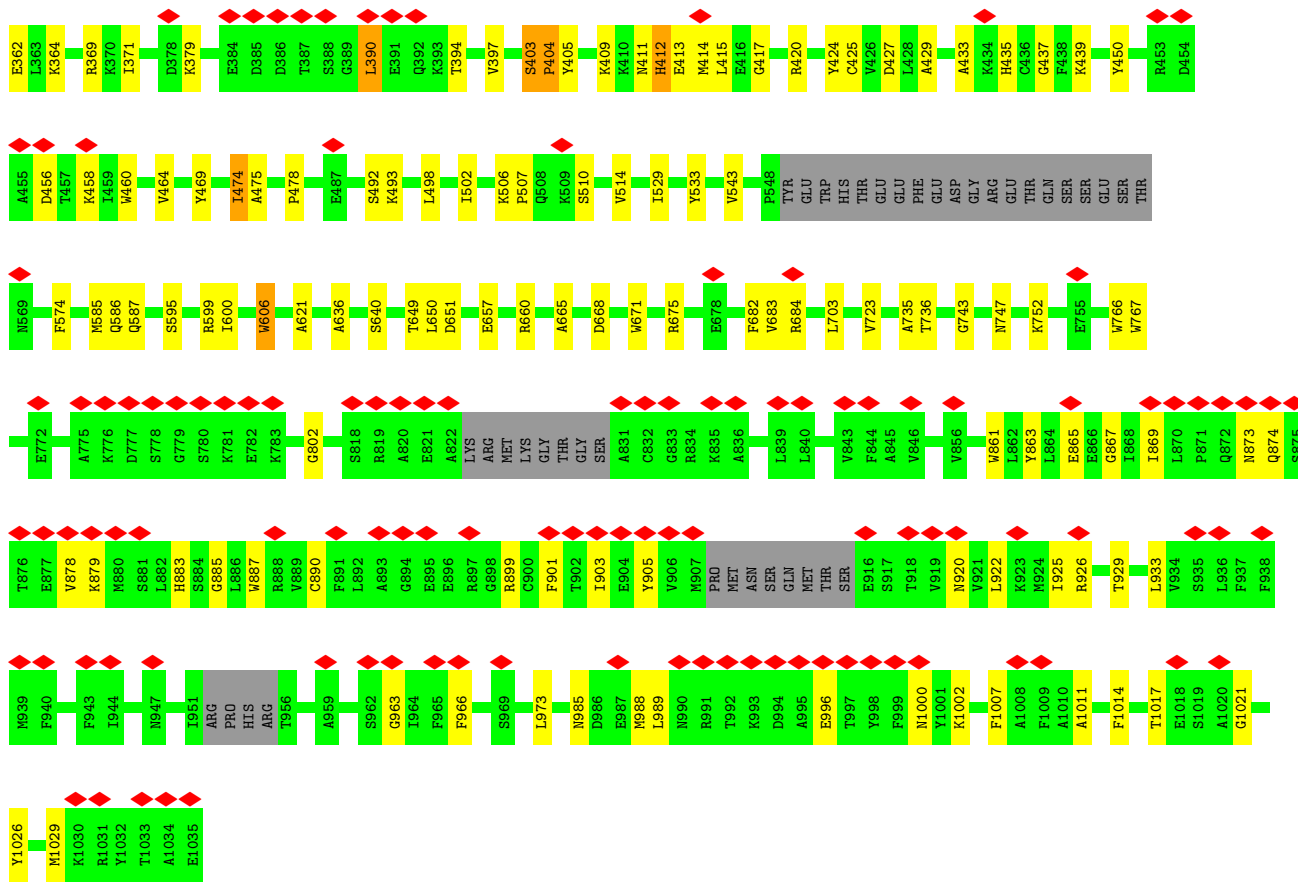
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Glutamate receptor 2, Voltage-dependent calcium channel gamma-5 subunit chimera

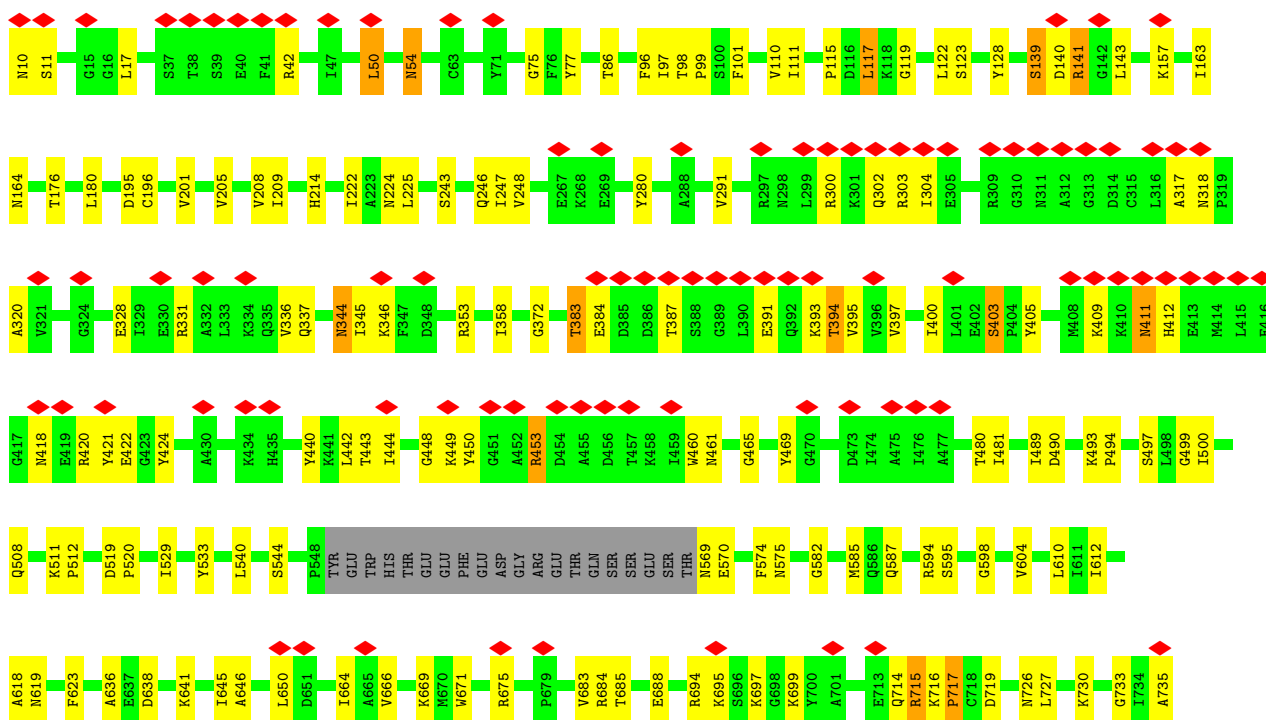


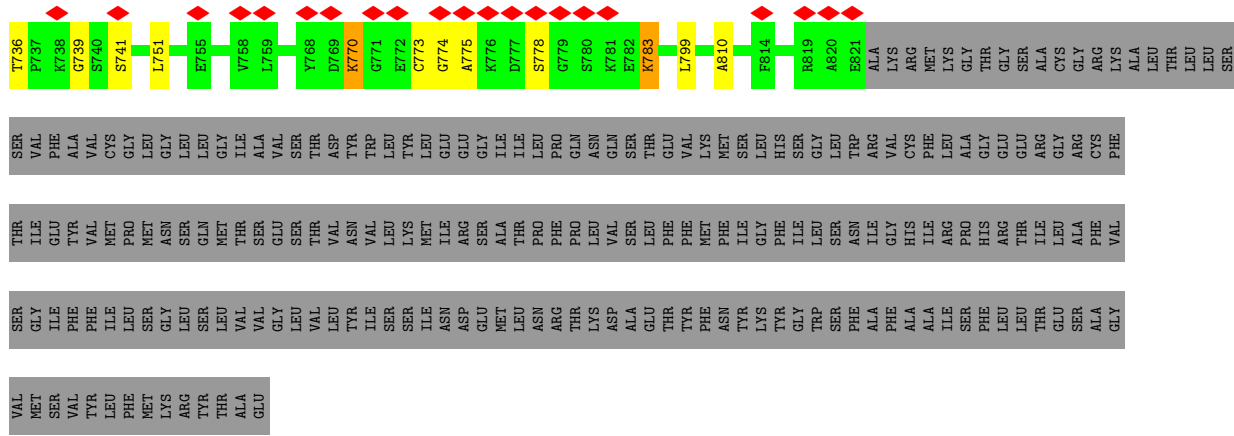




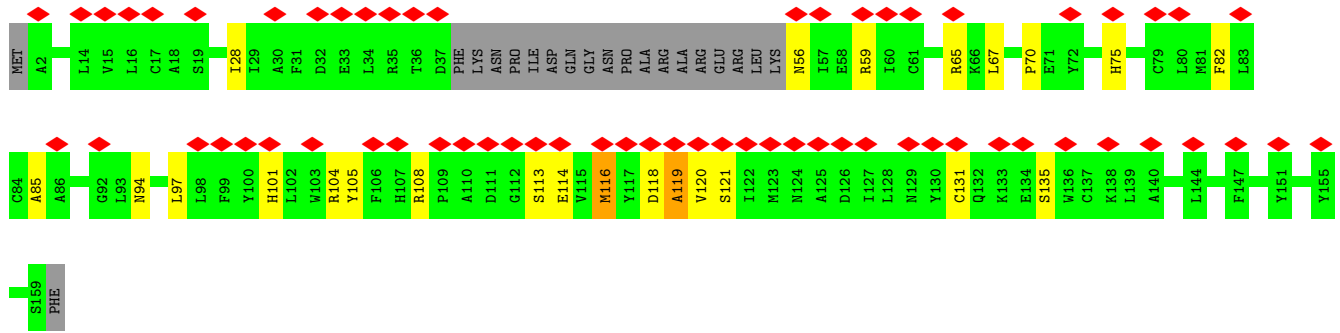
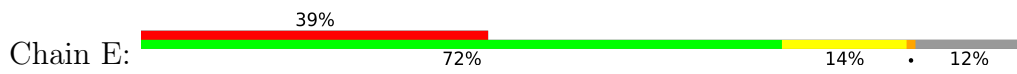


● Molecule 1: Glutamate receptor 2, Voltage-dependent calcium channel gamma-5 subunit chimera

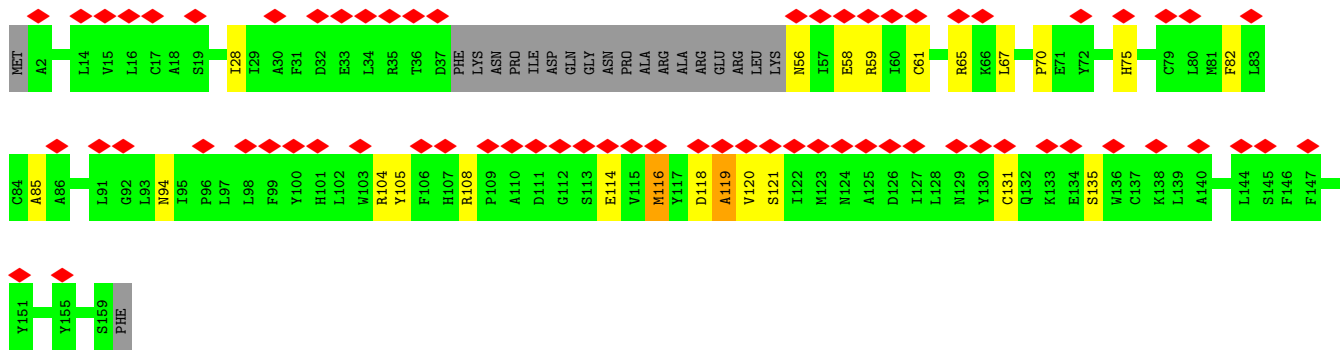
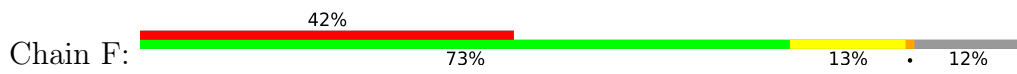




• Molecule 2: Protein cornichon homolog 2



• Molecule 2: Protein cornichon homolog 2



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	58186	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	58	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.816	Depositor
Minimum map value	-0.463	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.095	Depositor
Map size ( $\text{\AA}$ )	345.28, 345.28, 345.28	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.83, 0.83, 0.83	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PCW, SPD

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	0.48	1/7923 (0.0%)	0.65	3/10704 (0.0%)
1	B	0.49	0/6369	0.68	4/8603 (0.0%)
1	C	0.48	1/7923 (0.0%)	0.65	3/10704 (0.0%)
1	D	0.49	0/6369	0.68	4/8603 (0.0%)
2	E	0.36	0/1203	0.65	1/1636 (0.1%)
2	F	0.36	0/1203	0.64	1/1636 (0.1%)
All	All	0.48	2/30990 (0.0%)	0.66	16/41886 (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	9
1	B	0	9
1	C	0	9
1	D	0	9
2	E	0	2
2	F	0	2
All	All	0	40

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	606	TRP	CB-CG	-5.60	1.40	1.50
1	A	606	TRP	CB-CG	-5.52	1.40	1.50

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	117	LEU	CA-CB-CG	6.62	130.53	115.30
1	B	117	LEU	CA-CB-CG	6.61	130.50	115.30
1	C	50	LEU	CA-CB-CG	6.27	129.73	115.30
1	A	50	LEU	CA-CB-CG	6.27	129.72	115.30
1	A	390	LEU	CA-CB-CG	6.00	129.10	115.30
1	C	390	LEU	CA-CB-CG	5.97	129.03	115.30
1	B	383	THR	C-N-CA	5.76	136.10	121.70
1	D	383	THR	C-N-CA	5.76	136.10	121.70
2	E	67	LEU	CA-CB-CG	5.53	128.02	115.30
1	D	650	LEU	CA-CB-CG	5.45	127.84	115.30
1	B	650	LEU	CA-CB-CG	5.44	127.81	115.30
2	F	67	LEU	CA-CB-CG	5.41	127.74	115.30
1	A	498	LEU	CB-CG-CD2	-5.36	101.89	111.00
1	C	498	LEU	CB-CG-CD2	-5.33	101.94	111.00
1	B	50	LEU	CA-CB-CG	5.22	127.30	115.30
1	D	50	LEU	CA-CB-CG	5.20	127.25	115.30

There are no chirality outliers.

All (40) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	403	SER	Peptide
1	A	412	HIS	Peptide
1	A	456	ASP	Peptide
1	A	458	LYS	Peptide
1	A	510	SER	Peptide
1	A	514	VAL	Peptide
1	A	683	VAL	Peptide
1	A	873	ASN	Peptide
1	A	878	VAL	Peptide
1	B	139	SER	Peptide
1	B	393	LYS	Peptide
1	B	394	THR	Peptide
1	B	403	SER	Peptide
1	B	449	LYS	Peptide
1	B	714	GLN	Peptide
1	B	716	LYS	Peptide
1	B	739	GLY	Peptide
1	B	783	LYS	Peptide
1	C	403	SER	Peptide
1	C	412	HIS	Peptide
1	C	456	ASP	Peptide
1	C	458	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	C	510	SER	Peptide
1	C	514	VAL	Peptide
1	C	683	VAL	Peptide
1	C	873	ASN	Peptide
1	C	878	VAL	Peptide
1	D	139	SER	Peptide
1	D	393	LYS	Peptide
1	D	394	THR	Peptide
1	D	403	SER	Peptide
1	D	449	LYS	Peptide
1	D	714	GLN	Peptide
1	D	716	LYS	Peptide
1	D	739	GLY	Peptide
1	D	783	LYS	Peptide
2	E	105	TYR	Peptide
2	E	119	ALA	Peptide
2	F	105	TYR	Peptide
2	F	119	ALA	Peptide

## 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	7759	0	7768	90	0
1	B	6238	0	6228	91	0
1	C	7759	0	7768	88	0
1	D	6238	0	6228	94	0
2	E	1166	0	1152	12	0
2	F	1166	0	1152	11	0
3	A	174	0	234	5	0
3	B	82	0	107	6	0
3	C	174	0	234	2	0
3	D	82	0	107	5	0
4	A	10	0	5	1	0
4	B	10	0	5	1	0
4	C	10	0	5	1	0
4	D	10	0	5	1	0
5	D	10	0	19	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	30888	0	31017	376	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 6.

All (376) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:480:THR:HG1	4:D:1103:GLU:N	1.88	0.71
1:B:128:TYR:HH	1:B:243:SER:HG	1.36	0.70
1:B:480:THR:HG1	4:B:1103:GLU:N	1.88	0.70
1:C:736:THR:HG21	1:C:743:GLY:HA2	1.76	0.67
1:A:736:THR:HG21	1:A:743:GLY:HA2	1.76	0.66
1:B:345:ILE:HG12	1:B:353:ARG:HH12	1.62	0.65
1:B:604:VAL:HG21	1:C:802:GLY:HA3	1.79	0.65
1:D:345:ILE:HG12	1:D:353:ARG:HH12	1.62	0.65
2:E:28:ILE:HG22	2:E:135:SER:HB2	1.78	0.65
1:A:433:ALA:HA	1:A:437:GLY:HA3	1.79	0.65
1:D:715:ARG:HA	1:D:770:LYS:HG3	1.79	0.65
1:B:715:ARG:HA	1:B:770:LYS:HG3	1.79	0.64
2:F:28:ILE:HG22	2:F:135:SER:HB2	1.79	0.64
1:A:87:SER:OG	1:B:54:ASN:ND2	2.31	0.64
1:A:24:GLN:HE21	1:A:278:ILE:HD12	1.64	0.63
1:A:405:TYR:HA	1:A:424:TYR:HB3	1.80	0.63
1:C:405:TYR:HA	1:C:424:TYR:HB3	1.80	0.63
1:C:24:GLN:HE21	1:C:278:ILE:HD12	1.64	0.63
1:C:478:PRO:O	4:C:1104:GLU:N	2.32	0.63
1:D:646:ALA:H	1:D:699:LYS:HB3	1.64	0.62
1:C:433:ALA:HA	1:C:437:GLY:HA3	1.79	0.62
1:A:478:PRO:O	4:A:1104:GLU:N	2.32	0.62
1:B:646:ALA:H	1:B:699:LYS:HB3	1.64	0.62
1:C:574:PHE:HB2	3:C:1103:PCW:H122	1.81	0.61
1:C:12:ILE:HD11	1:C:43:LEU:HG	1.83	0.60
1:B:405:TYR:HA	1:B:424:TYR:HB3	1.83	0.60
1:C:417:GLY:O	1:C:420:ARG:NH1	2.34	0.60
1:D:405:TYR:HA	1:D:424:TYR:HB3	1.84	0.60
1:D:86:THR:HG22	1:D:110:VAL:HG21	1.84	0.60
1:B:86:THR:HG22	1:B:110:VAL:HG21	1.84	0.60
1:A:651:ASP:HB2	1:A:682:PHE:HB3	1.84	0.60
1:D:773:CYS:SG	1:D:774:GLY:N	2.75	0.59
1:A:417:GLY:O	1:A:420:ARG:NH1	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:903:ILE:O	1:C:926:ARG:NH2	2.35	0.59
1:A:12:ILE:HD11	1:A:43:LEU:HG	1.83	0.59
1:C:651:ASP:HB2	1:C:682:PHE:HB3	1.84	0.59
1:A:409:LYS:HG3	1:A:411:ASN:H	1.68	0.58
1:A:308:ARG:O	1:A:309:ARG:NE	2.36	0.58
1:C:308:ARG:O	1:C:309:ARG:NE	2.36	0.58
1:C:600:ILE:HG12	3:D:1101:PCW:H412	1.85	0.58
1:C:409:LYS:HG3	1:C:411:ASN:H	1.68	0.58
1:D:247:ILE:HD11	1:D:280:TYR:HB2	1.85	0.57
1:B:773:CYS:SG	1:B:774:GLY:N	2.75	0.57
1:B:141:ARG:NH2	1:B:195:ASP:OD1	2.36	0.57
1:D:511:LYS:NZ	1:D:512:PRO:O	2.35	0.57
1:D:141:ARG:NH2	1:D:195:ASP:OD1	2.36	0.57
1:B:247:ILE:HD11	1:B:280:TYR:HB2	1.85	0.57
1:A:600:ILE:HG12	3:B:1101:PCW:H412	1.86	0.57
1:C:86:THR:HG22	1:C:110:VAL:HG21	1.86	0.57
1:A:86:THR:HG22	1:A:110:VAL:HG21	1.86	0.56
1:B:500:ILE:HB	1:B:727:LEU:HB2	1.88	0.56
1:C:190:ARG:NE	1:C:469:TYR:OH	2.31	0.56
1:D:500:ILE:HB	1:D:727:LEU:HB2	1.88	0.56
1:D:372:GLY:HA2	1:D:383:THR:H	1.70	0.56
1:A:903:ILE:O	1:A:926:ARG:NH2	2.35	0.56
1:B:372:GLY:HA2	1:B:383:THR:H	1.70	0.56
1:A:183:ASP:HA	1:A:186:LEU:HD13	1.87	0.56
1:C:475:ALA:HB3	1:C:735:ALA:HB3	1.88	0.56
2:E:104:ARG:NH2	2:E:131:CYS:SG	2.79	0.56
1:B:511:LYS:NZ	1:B:512:PRO:O	2.35	0.55
1:C:183:ASP:HA	1:C:186:LEU:HD13	1.87	0.55
1:B:694:ARG:NH1	1:B:719:ASP:OD2	2.39	0.55
1:D:344:ASN:O	1:D:353:ARG:NH2	2.40	0.55
1:D:694:ARG:NH1	1:D:719:ASP:OD2	2.39	0.55
1:C:649:THR:HB	1:C:703:LEU:HB2	1.89	0.55
2:F:104:ARG:NH2	2:F:131:CYS:SG	2.80	0.55
1:A:985:ASN:HA	1:A:988:MET:HB2	1.89	0.54
1:B:344:ASN:O	1:B:353:ARG:NH2	2.40	0.54
1:A:475:ALA:HB3	1:A:735:ALA:HB3	1.88	0.54
1:B:618:ALA:HA	1:C:621:ALA:HB2	1.88	0.54
1:B:595:SER:OG	1:B:598:GLY:N	2.39	0.54
1:A:181:PHE:HB3	1:A:213:LYS:HE3	1.90	0.54
1:C:181:PHE:HB3	1:C:213:LYS:HE3	1.90	0.54
1:A:543:VAL:HG23	1:B:810:ALA:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:649:THR:HB	1:A:703:LEU:HB2	1.89	0.54
1:C:985:ASN:HA	1:C:988:MET:HB2	1.89	0.54
1:D:595:SER:OG	1:D:598:GLY:N	2.39	0.53
1:A:190:ARG:NE	1:A:469:TYR:OH	2.31	0.53
1:C:989:LEU:O	1:D:508:GLN:NE2	2.42	0.53
1:A:364:LYS:HG3	1:A:369:ARG:HE	1.74	0.53
1:D:246:GLN:HE21	1:D:248:VAL:H	1.57	0.53
1:A:802:GLY:HA3	1:D:604:VAL:HG21	1.91	0.53
3:B:1102:PCW:H331	2:E:70:PRO:HA	1.89	0.53
1:D:302:GLN:HG3	1:D:304:ILE:HG12	1.91	0.53
1:A:869:ILE:HG22	1:A:996:GLU:HA	1.91	0.52
1:C:869:ILE:HG22	1:C:996:GLU:HA	1.91	0.52
1:D:403:SER:O	1:D:405:TYR:N	2.42	0.52
1:A:25:GLU:OE2	1:A:281:THR:OG1	2.27	0.52
1:A:867:GLY:HA2	1:A:879:LYS:HB3	1.91	0.52
1:C:364:LYS:HG3	1:C:369:ARG:HE	1.74	0.52
1:D:529:ILE:O	1:D:533:TYR:N	2.42	0.52
1:D:645:ILE:HG22	1:D:699:LYS:HG2	1.92	0.52
1:C:25:GLU:OE2	1:C:281:THR:OG1	2.27	0.52
1:A:989:LEU:O	1:B:508:GLN:NE2	2.43	0.52
1:B:638:ASP:HA	1:B:641:LYS:HB2	1.92	0.52
1:B:671:TRP:O	1:B:675:ARG:N	2.42	0.52
1:D:209:ILE:HA	1:D:214:HIS:HD2	1.75	0.52
1:D:490:ASP:O	1:D:736:THR:OG1	2.24	0.52
1:A:649:THR:OG1	1:A:650:LEU:N	2.43	0.51
1:C:1017:THR:O	1:C:1021:GLY:N	2.43	0.51
1:B:246:GLN:HE21	1:B:248:VAL:H	1.57	0.51
1:B:403:SER:O	1:B:405:TYR:N	2.42	0.51
1:B:302:GLN:HG3	1:B:304:ILE:HG12	1.91	0.51
1:C:867:GLY:HA2	1:C:879:LYS:HB3	1.91	0.51
1:C:294:GLU:OE2	1:C:298:ASN:ND2	2.43	0.51
1:A:1017:THR:O	1:A:1021:GLY:N	2.43	0.51
1:B:529:ILE:O	1:B:533:TYR:N	2.42	0.51
1:A:729:SER:HB3	1:D:497:SER:HB3	1.93	0.51
1:A:973:LEU:HD23	1:A:1014:PHE:HB2	1.92	0.51
1:B:209:ILE:HA	1:B:214:HIS:HD2	1.75	0.51
1:B:645:ILE:HG22	1:B:699:LYS:HG2	1.92	0.51
1:D:638:ASP:HA	1:D:641:LYS:HB2	1.92	0.51
1:A:54:ASN:OD1	1:B:87:SER:OG	2.28	0.51
1:B:397:VAL:O	1:B:443:THR:OG1	2.28	0.51
1:C:87:SER:OG	1:D:54:ASN:ND2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:649:THR:OG1	1:C:650:LEU:N	2.43	0.50
1:A:186:LEU:HD23	1:B:157:LYS:HE3	1.93	0.50
1:D:520:PRO:O	1:D:619:ASN:ND2	2.40	0.50
1:A:294:GLU:OE2	1:A:298:ASN:ND2	2.43	0.50
1:B:775:ALA:HA	1:B:778:SER:HB2	1.94	0.50
2:E:56:ASN:OD1	2:E:59:ARG:NH1	2.45	0.50
2:F:82:PHE:HA	2:F:85:ALA:HB3	1.93	0.50
1:A:202:ASN:HA	1:A:205:VAL:HG12	1.93	0.50
1:C:585:MET:O	1:C:587:GLN:NE2	2.45	0.50
1:C:973:LEU:HD23	1:C:1014:PHE:HB2	1.92	0.50
1:D:77:TYR:HE1	1:D:98:THR:HG21	1.76	0.50
1:B:300:ARG:O	1:B:303:ARG:NH2	2.45	0.50
1:C:425:CYS:O	1:C:429:ALA:N	2.41	0.50
1:D:570:GLU:O	1:D:575:ASN:ND2	2.40	0.50
1:D:671:TRP:O	1:D:675:ARG:N	2.42	0.50
3:D:1102:PCW:H331	2:F:70:PRO:HA	1.94	0.50
1:C:586:GLN:OE1	5:D:1104:SPD:N10	2.43	0.49
1:C:922:LEU:HD23	1:C:925:ILE:HD12	1.94	0.49
1:A:922:LEU:HD23	1:A:925:ILE:HD12	1.94	0.49
1:D:337:GLN:HE22	1:D:346:LYS:HD3	1.78	0.49
1:A:585:MET:O	1:A:587:GLN:NE2	2.45	0.49
1:D:300:ARG:O	1:D:303:ARG:NH2	2.45	0.49
1:B:77:TYR:HE1	1:B:98:THR:HG21	1.76	0.49
1:A:1007:PHE:O	1:A:1011:ALA:N	2.39	0.49
1:C:901:PHE:HE2	1:C:905:TYR:H	1.60	0.48
1:A:585:MET:SD	1:A:585:MET:N	2.87	0.48
1:C:585:MET:SD	1:C:585:MET:N	2.87	0.48
1:D:128:TYR:OH	1:D:243:SER:OG	2.21	0.48
2:F:56:ASN:OD1	2:F:59:ARG:NH1	2.46	0.48
1:A:657:GLU:OE1	1:A:660:ARG:NH2	2.46	0.48
1:A:901:PHE:HE2	1:A:905:TYR:H	1.60	0.48
1:C:202:ASN:HA	1:C:205:VAL:HG12	1.93	0.48
1:D:775:ALA:HA	1:D:778:SER:HB2	1.94	0.48
1:A:425:CYS:O	1:A:429:ALA:N	2.41	0.48
1:B:337:GLN:HE22	1:B:346:LYS:HD3	1.78	0.48
1:B:205:VAL:HA	1:B:208:VAL:HG22	1.96	0.48
1:A:291:VAL:HG13	1:A:336:VAL:HG21	1.96	0.48
1:B:247:ILE:HG22	1:B:358:ILE:HG12	1.96	0.48
1:D:205:VAL:HA	1:D:208:VAL:HG22	1.96	0.48
1:D:480:THR:HG21	1:D:730:LYS:HE2	1.96	0.48
2:E:82:PHE:HA	2:E:85:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:492:SER:OG	1:C:493:LYS:N	2.46	0.48
1:C:113:MET:HG3	1:C:284:LEU:HD22	1.96	0.48
1:C:291:VAL:HG13	1:C:336:VAL:HG21	1.96	0.48
1:B:570:GLU:OE2	1:B:594:ARG:NH2	2.44	0.48
1:B:519:ASP:HB3	1:B:623:PHE:HE2	1.78	0.47
1:C:657:GLU:OE1	1:C:660:ARG:NH2	2.46	0.47
2:F:118:ASP:OD1	2:F:118:ASP:N	2.42	0.47
1:A:492:SER:OG	1:A:493:LYS:N	2.46	0.47
1:A:863:TYR:HB2	1:A:1002:LYS:HB3	1.95	0.47
1:B:588:GLY:HA3	5:D:1104:SPD:H22	1.95	0.47
1:D:397:VAL:O	1:D:443:THR:OG1	2.28	0.47
1:D:666:VAL:HA	1:D:669:LYS:HE2	1.96	0.47
1:A:113:MET:HG3	1:A:284:LEU:HD22	1.96	0.47
1:A:379:LYS:HD2	1:A:379:LYS:HA	1.80	0.47
1:B:480:THR:HG21	1:B:730:LYS:HE2	1.96	0.47
1:B:481:ILE:HD11	1:B:733:GLY:HA3	1.97	0.47
1:B:520:PRO:O	1:B:619:ASN:ND2	2.40	0.47
1:B:570:GLU:O	1:B:575:ASN:ND2	2.40	0.47
1:C:863:TYR:HB2	1:C:1002:LYS:HB3	1.95	0.47
1:D:409:LYS:HE2	1:D:411:ASN:HB2	1.97	0.47
1:A:925:ILE:O	1:A:929:THR:N	2.48	0.47
1:C:306:ILE:HG21	1:C:325:GLN:HG2	1.96	0.47
1:C:362:GLU:HG3	1:C:371:ILE:HG12	1.97	0.47
2:E:97:LEU:O	2:E:101:HIS:N	2.41	0.47
1:B:666:VAL:HA	1:B:669:LYS:HE2	1.96	0.47
1:D:519:ASP:HB3	1:D:623:PHE:HE2	1.78	0.47
1:B:400:ILE:HA	1:B:444:ILE:HG23	1.97	0.47
1:B:409:LYS:HE2	1:B:411:ASN:HB2	1.97	0.47
1:D:328:GLU:OE1	1:D:331:ARG:NH2	2.36	0.47
1:D:421:TYR:HD2	1:D:442:LEU:HB3	1.80	0.47
2:E:108:ARG:HG3	2:E:116:MET:HB2	1.97	0.47
1:A:362:GLU:HG3	1:A:371:ILE:HG12	1.97	0.46
2:F:119:ALA:O	2:F:121:SER:N	2.48	0.46
1:B:421:TYR:HD2	1:B:442:LEU:HB3	1.80	0.46
1:C:403:SER:O	1:C:405:TYR:N	2.47	0.46
3:A:1101:PCW:H83	3:A:1101:PCW:H41	1.79	0.46
1:B:574:PHE:HB2	3:B:1102:PCW:H142	1.96	0.46
1:C:46:HIS:NE2	1:C:48:ASP:OD1	2.49	0.46
2:E:119:ALA:O	2:E:121:SER:N	2.48	0.46
1:D:574:PHE:HB2	3:D:1102:PCW:H142	1.97	0.46
1:A:46:HIS:NE2	1:A:48:ASP:OD1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:LEU:HD23	1:D:157:LYS:HE3	1.97	0.46
1:B:465:GLY:HA2	1:B:469:TYR:HE2	1.80	0.46
1:C:883:HIS:CE1	1:C:890:CYS:HB2	2.51	0.46
1:C:925:ILE:O	1:C:929:THR:N	2.48	0.46
1:A:404:PRO:HG2	1:A:767:TRP:HE1	1.80	0.46
1:B:201:VAL:HG21	1:B:222:ILE:HG23	1.98	0.46
1:B:694:ARG:HH22	1:B:717:PRO:HG2	1.81	0.46
1:C:606:TRP:HB3	1:D:585:MET:HG3	1.97	0.46
1:D:247:ILE:HG22	1:D:358:ILE:HG12	1.96	0.46
1:D:481:ILE:HD11	1:D:733:GLY:HA3	1.96	0.46
1:C:404:PRO:HG2	1:C:767:TRP:HE1	1.81	0.46
1:D:209:ILE:HA	1:D:214:HIS:CD2	2.51	0.46
1:D:400:ILE:HA	1:D:444:ILE:HG23	1.97	0.46
1:D:499:GLY:HA3	1:D:726:ASN:HA	1.98	0.46
1:A:306:ILE:HG21	1:A:325:GLN:HG2	1.96	0.45
1:A:412:HIS:O	1:A:414:MET:N	2.50	0.45
1:B:209:ILE:HA	1:B:214:HIS:CD2	2.51	0.45
1:C:412:HIS:O	1:C:414:MET:N	2.50	0.45
1:A:883:HIS:CE1	1:A:890:CYS:HB2	2.51	0.45
2:F:108:ARG:HG3	2:F:116:MET:HB2	1.98	0.45
1:A:865:GLU:HB2	1:A:1000:ASN:HB2	1.98	0.45
1:C:364:LYS:HE3	1:C:369:ARG:HH11	1.82	0.45
1:C:606:TRP:CD1	1:D:587:GLN:HG3	2.51	0.45
1:D:201:VAL:HG21	1:D:222:ILE:HG23	1.98	0.45
1:D:570:GLU:OE2	1:D:594:ARG:NH2	2.44	0.45
1:A:364:LYS:HE3	1:A:369:ARG:HH11	1.82	0.45
1:C:427:ASP:OD2	1:C:766:TRP:NE1	2.37	0.45
1:D:465:GLY:HA2	1:D:469:TYR:HE2	1.80	0.45
2:E:75:HIS:HE1	2:E:94:ASN:HB2	1.82	0.45
1:A:315:CYS:SG	1:A:316:LEU:N	2.90	0.45
1:B:544:SER:O	1:B:569:ASN:ND2	2.50	0.45
1:D:544:SER:O	1:D:569:ASN:ND2	2.49	0.45
1:D:694:ARG:HH22	1:D:717:PRO:HG2	1.81	0.45
1:D:409:LYS:HD2	1:D:422:GLU:HG2	1.99	0.45
1:A:209:ILE:HD12	1:A:234:LYS:HE2	1.99	0.45
1:A:586:GLN:HG2	1:B:587:GLN:HE22	1.82	0.45
1:C:963:GLY:HA2	1:C:966:PHE:HD2	1.82	0.45
1:B:97:ILE:HA	1:B:111:ILE:HB	1.99	0.45
1:A:209:ILE:HG12	1:A:214:HIS:CG	2.52	0.45
1:B:499:GLY:HA3	1:B:726:ASN:HA	1.98	0.45
1:C:209:ILE:HG12	1:C:214:HIS:CG	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:865:GLU:HB2	1:C:1000:ASN:HB2	1.98	0.45
1:C:315:CYS:SG	1:C:316:LEU:N	2.90	0.44
1:A:427:ASP:OD2	1:A:766:TRP:NE1	2.37	0.44
1:A:636:ALA:O	1:A:640:SER:N	2.51	0.44
1:A:963:GLY:HA2	1:A:966:PHE:HD2	1.82	0.44
1:C:435:HIS:CE1	1:C:752:LYS:HE2	2.53	0.44
1:C:671:TRP:O	1:C:675:ARG:N	2.45	0.44
2:E:118:ASP:N	2:E:118:ASP:OD1	2.41	0.44
2:F:75:HIS:HE1	2:F:94:ASN:HB2	1.82	0.44
1:C:209:ILE:HD12	1:C:234:LYS:HE2	1.99	0.44
1:C:1007:PHE:O	1:C:1011:ALA:N	2.38	0.44
1:B:328:GLU:OE1	1:B:331:ARG:NH2	2.36	0.44
1:B:409:LYS:HD2	1:B:422:GLU:HG2	1.99	0.44
1:B:482:THR:O	1:B:486:GLU:N	2.48	0.44
1:D:119:GLY:O	1:D:123:SER:N	2.51	0.44
1:B:453:ARG:HB3	1:B:460:TRP:CE2	2.53	0.44
1:C:606:TRP:CZ3	1:D:582:GLY:HA2	2.53	0.44
1:B:490:ASP:O	1:B:736:THR:OG1	2.24	0.43
1:B:664:ILE:HG22	1:B:666:VAL:HG12	2.00	0.43
1:B:493:LYS:HD2	1:B:751:LEU:HD21	1.99	0.43
1:C:543:VAL:HG23	1:D:810:ALA:HB2	1.99	0.43
1:D:493:LYS:HD2	1:D:751:LEU:HD21	1.99	0.43
1:B:17:LEU:HB2	1:B:75:GLY:HA3	2.01	0.43
3:B:1102:PCW:H142	3:B:1102:PCW:H172	1.83	0.43
1:C:636:ALA:O	1:C:640:SER:N	2.50	0.43
3:D:1102:PCW:H122	3:D:1102:PCW:H151	1.69	0.43
2:F:65:ARG:HD3	2:F:114:GLU:HB3	1.99	0.43
1:D:96:PHE:O	1:D:111:ILE:N	2.43	0.43
1:D:453:ARG:HB3	1:D:460:TRP:CE2	2.53	0.43
1:A:536:VAL:HG22	1:B:803:LEU:HD21	2.01	0.43
1:C:529:ILE:O	1:C:533:TYR:N	2.52	0.43
1:D:17:LEU:HB2	1:D:75:GLY:HA3	2.01	0.43
1:D:412:HIS:HB2	1:D:420:ARG:HA	2.01	0.43
1:A:435:HIS:CE1	1:A:752:LYS:HE2	2.53	0.43
1:A:861:TRP:HD1	1:A:885:GLY:HA2	1.83	0.43
1:C:861:TRP:HD1	1:C:885:GLY:HA2	1.83	0.43
1:D:97:ILE:HA	1:D:111:ILE:HB	1.99	0.43
1:A:506:LYS:HA	1:A:507:PRO:HD3	1.89	0.43
1:A:194:LEU:HD23	1:A:194:LEU:HA	1.82	0.43
1:A:529:ILE:O	1:A:533:TYR:N	2.52	0.43
1:D:664:ILE:HG22	1:D:666:VAL:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:GLY:O	1:B:123:SER:N	2.51	0.43
1:B:139:SER:O	1:B:141:ARG:N	2.39	0.43
1:C:284:LEU:O	1:C:288:ALA:N	2.52	0.43
1:C:595:SER:O	1:C:599:ARG:N	2.51	0.43
1:A:1026:TYR:HA	1:A:1029:MET:HB2	2.01	0.42
3:B:1102:PCW:H122	3:B:1102:PCW:H151	1.72	0.42
1:C:131:ASP:O	1:C:159:GLN:N	2.50	0.42
1:C:397:VAL:HG12	1:C:474:ILE:HG23	2.01	0.42
1:D:196:CYS:O	1:D:224:ASN:ND2	2.40	0.42
1:D:387:THR:HB	1:D:391:GLU:H	1.84	0.42
1:D:529:ILE:HD11	1:D:612:ILE:HG21	2.01	0.42
1:C:506:LYS:HA	1:C:507:PRO:HD3	1.89	0.42
1:D:489:ILE:HD13	1:D:735:ALA:HB1	2.01	0.42
1:D:685:THR:HG22	1:D:688:GLU:H	1.85	0.42
1:B:291:VAL:HG13	1:B:336:VAL:HG11	2.02	0.42
1:B:489:ILE:HD13	1:B:735:ALA:HB1	2.01	0.42
1:B:529:ILE:HD11	1:B:612:ILE:HG21	2.01	0.42
1:C:17:LEU:HB2	1:C:75:GLY:HA3	2.01	0.42
1:C:394:THR:HA	1:C:439:LYS:HB2	2.01	0.42
1:C:1026:TYR:HA	1:C:1029:MET:HB2	2.01	0.42
1:D:225:LEU:HB2	1:D:280:TYR:CE2	2.55	0.42
1:D:291:VAL:HG13	1:D:336:VAL:HG11	2.02	0.42
1:A:284:LEU:O	1:A:288:ALA:N	2.52	0.42
1:B:247:ILE:HG13	1:B:248:VAL:HG23	2.02	0.42
1:C:247:ILE:HG23	1:C:248:VAL:HG13	2.02	0.42
1:A:247:ILE:HG23	1:A:248:VAL:HG13	2.01	0.42
1:B:387:THR:HB	1:B:391:GLU:H	1.84	0.42
1:A:394:THR:HA	1:A:439:LYS:HB2	2.01	0.42
1:B:101:PHE:CG	1:B:141:ARG:HB2	2.55	0.42
1:D:481:ILE:HD12	1:D:494:PRO:HG3	2.01	0.42
1:A:17:LEU:HB2	1:A:75:GLY:HA3	2.01	0.42
1:A:621:ALA:HB2	1:D:618:ALA:HA	2.01	0.42
1:C:209:ILE:HA	1:C:214:HIS:CD2	2.55	0.42
1:D:101:PHE:CG	1:D:141:ARG:HB2	2.55	0.42
1:D:317:ALA:HB3	1:D:320:ALA:HA	2.02	0.42
1:B:317:ALA:HB3	1:B:320:ALA:HA	2.02	0.42
1:D:119:GLY:HA2	1:D:122:LEU:HB2	2.02	0.42
1:D:247:ILE:HG13	1:D:248:VAL:HG23	2.02	0.42
1:A:956:THR:O	1:A:1031:ARG:NH1	2.53	0.42
3:A:1101:PCW:H122	3:A:1101:PCW:H151	1.84	0.42
1:B:196:CYS:O	1:B:224:ASN:ND2	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:887:TRP:HZ2	1:A:933:LEU:HD11	1.85	0.41
1:B:412:HIS:HB2	1:B:420:ARG:HA	2.01	0.41
2:E:65:ARG:HD3	2:E:114:GLU:HB3	2.02	0.41
1:B:225:LEU:HB2	1:B:280:TYR:CE2	2.55	0.41
1:A:131:ASP:O	1:A:159:GLN:N	2.50	0.41
1:C:24:GLN:NE2	1:C:278:ILE:HD12	2.34	0.41
1:D:143:LEU:HA	1:D:143:LEU:HD12	1.87	0.41
3:A:1105:PCW:H341	3:A:1105:PCW:H371	1.62	0.41
1:B:473:ASP:OD1	1:B:473:ASP:N	2.53	0.41
1:B:481:ILE:HD12	1:B:494:PRO:HG3	2.01	0.41
3:B:1102:PCW:H121	3:B:1102:PCW:H31	1.76	0.41
1:C:665:ALA:HA	1:C:668:ASP:HB2	2.02	0.41
3:C:1105:PCW:H39	3:C:1105:PCW:H362	1.86	0.41
1:D:695:LYS:O	1:D:697:LYS:NZ	2.51	0.41
3:D:1102:PCW:H31	3:D:1102:PCW:H121	1.77	0.41
1:A:337:GLN:HE21	1:A:346:LYS:HE2	1.86	0.41
1:A:397:VAL:HG12	1:A:474:ILE:HG23	2.01	0.41
3:A:1103:PCW:H82	3:A:1103:PCW:H42	1.79	0.41
1:D:610:LEU:HD12	1:D:610:LEU:HA	1.84	0.41
1:D:685:THR:O	1:D:688:GLU:N	2.53	0.41
1:A:403:SER:O	1:A:405:TYR:N	2.47	0.41
1:A:502:ILE:HB	1:A:723:VAL:HB	2.02	0.41
1:A:114:ARG:HA	1:A:115:PRO:HD3	1.95	0.41
1:B:119:GLY:HA2	1:B:122:LEU:HB2	2.02	0.41
1:B:685:THR:O	1:B:688:GLU:N	2.53	0.41
1:C:450:TYR:HE1	1:C:478:PRO:HG2	1.85	0.41
1:D:540:LEU:HD23	1:D:540:LEU:HA	1.84	0.41
1:A:209:ILE:HA	1:A:214:HIS:CD2	2.55	0.41
1:A:364:LYS:HD3	1:A:364:LYS:HA	1.85	0.41
1:A:595:SER:O	1:A:599:ARG:N	2.51	0.41
1:A:606:TRP:HB3	1:B:585:MET:HG3	2.03	0.41
1:B:418:ASN:HB3	1:B:440:TYR:CZ	2.56	0.41
1:B:506:LYS:HD3	1:B:507:PRO:HD2	2.03	0.41
1:C:194:LEU:HA	1:C:194:LEU:HD23	1.82	0.41
1:C:502:ILE:HB	1:C:723:VAL:HB	2.02	0.41
1:C:887:TRP:HZ2	1:C:933:LEU:HD11	1.85	0.41
1:D:98:THR:HA	1:D:99:PRO:HD3	1.81	0.41
1:B:685:THR:HG22	1:B:688:GLU:H	1.85	0.41
1:C:460:TRP:HB3	1:C:464:VAL:HG23	2.02	0.41
1:D:163:ILE:HG21	1:D:180:LEU:HD11	2.03	0.41
1:C:586:GLN:HG2	1:D:587:GLN:HE22	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:11:SER:HA	1:D:42:ARG:H	1.86	0.40
2:F:58:GLU:HA	2:F:61:CYS:HB2	2.03	0.40
1:A:460:TRP:HB3	1:A:464:VAL:HG23	2.02	0.40
1:B:334:LYS:NZ	1:B:349:GLN:O	2.41	0.40
1:B:400:ILE:HD12	1:B:448:GLY:HA3	2.03	0.40
1:D:799:LEU:HD12	1:D:799:LEU:HA	1.89	0.40
1:B:249:ASP:OD2	1:B:370:LYS:NZ	2.45	0.40
1:A:184:LEU:HD22	1:A:189:GLU:HB2	2.04	0.40
1:A:450:TYR:HE1	1:A:478:PRO:HG2	1.85	0.40
3:A:1103:PCW:H351	3:A:1103:PCW:H382	1.93	0.40
1:D:176:THR:O	1:D:180:LEU:N	2.54	0.40
2:E:65:ARG:CZ	2:E:113:SER:HB3	2.52	0.40
1:B:401:LEU:HB3	1:B:444:ILE:HD13	2.03	0.40
1:D:400:ILE:HD12	1:D:448:GLY:HA3	2.03	0.40
1:D:418:ASN:HB3	1:D:440:TYR:CZ	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	976/1026 (95%)	863 (88%)	106 (11%)	7 (1%)	22	60
1	B	788/1026 (77%)	683 (87%)	94 (12%)	11 (1%)	11	46
1	C	976/1026 (95%)	863 (88%)	106 (11%)	7 (1%)	22	60
1	D	788/1026 (77%)	683 (87%)	94 (12%)	11 (1%)	11	46
2	E	136/160 (85%)	119 (88%)	16 (12%)	1 (1%)	22	60
2	F	136/160 (85%)	119 (88%)	16 (12%)	1 (1%)	22	60
All	All	3800/4424 (86%)	3330 (88%)	432 (11%)	38 (1%)	20	52

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	413	GLU
1	A	874	GLN
1	B	384	GLU
1	C	413	GLU
1	C	874	GLN
1	D	384	GLU
1	B	115	PRO
1	B	140	ASP
1	D	115	PRO
1	D	140	ASP
2	E	120	VAL
2	F	120	VAL
1	B	717	PRO
1	D	717	PRO
1	A	379	LYS
1	B	394	THR
1	B	450	TYR
1	B	636	ALA
1	B	715	ARG
1	C	379	LYS
1	D	394	THR
1	D	450	TYR
1	D	636	ALA
1	D	715	ARG
1	A	404	PRO
1	B	139	SER
1	B	395	VAL
1	B	741	SER
1	C	404	PRO
1	D	139	SER
1	D	395	VAL
1	D	741	SER
1	A	115	PRO
1	A	684	ARG
1	C	115	PRO
1	C	684	ARG
1	A	474	ILE
1	C	474	ILE

### 5.3.2 Protein sidechains [i](#)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	840/877 (96%)	830 (99%)	10 (1%)	71	83
1	B	675/877 (77%)	660 (98%)	15 (2%)	52	71
1	C	840/877 (96%)	830 (99%)	10 (1%)	71	83
1	D	675/877 (77%)	660 (98%)	15 (2%)	52	71
2	E	126/143 (88%)	125 (99%)	1 (1%)	81	89
2	F	126/143 (88%)	125 (99%)	1 (1%)	81	89
All	All	3282/3794 (86%)	3230 (98%)	52 (2%)	64	79

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	35	GLN
1	A	50	LEU
1	A	141	ARG
1	A	344	ASN
1	A	390	LEU
1	A	415	LEU
1	A	747	ASN
1	A	899	ARG
1	A	920	ASN
1	B	10	ASN
1	B	50	LEU
1	B	54	ASN
1	B	117	LEU
1	B	141	ARG
1	B	164	ASN
1	B	318	ASN
1	B	344	ASN
1	B	411	ASN
1	B	453	ARG
1	B	461	ASN
1	B	683	VAL
1	B	684	ARG
1	B	770	LYS
1	B	783	LYS
1	C	10	ASN

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Mol	Chain	Res	Type
1	C	35	GLN
1	C	50	LEU
1	C	141	ARG
1	C	344	ASN
1	C	390	LEU
1	C	415	LEU
1	C	747	ASN
1	C	899	ARG
1	C	920	ASN
1	D	10	ASN
1	D	50	LEU
1	D	54	ASN
1	D	117	LEU
1	D	141	ARG
1	D	164	ASN
1	D	318	ASN
1	D	344	ASN
1	D	411	ASN
1	D	453	ARG
1	D	461	ASN
1	D	683	VAL
1	D	684	ARG
1	D	770	LYS
1	D	783	LYS
2	E	116	MET
2	F	116	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	24	GLN
1	A	344	ASN
1	A	747	ASN
1	A	920	ASN
1	B	10	ASN
1	B	35	GLN
1	B	46	HIS
1	B	54	ASN
1	B	164	ASN
1	B	214	HIS
1	B	246	GLN

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Mol	Chain	Res	Type
1	B	318	ASN
1	B	337	GLN
1	B	344	ASN
1	B	392	GLN
1	B	411	ASN
1	B	435	HIS
1	B	461	ASN
1	B	508	GLN
1	B	587	GLN
1	C	10	ASN
1	C	344	ASN
1	C	747	ASN
1	C	920	ASN
1	D	10	ASN
1	D	35	GLN
1	D	46	HIS
1	D	54	ASN
1	D	164	ASN
1	D	214	HIS
1	D	246	GLN
1	D	318	ASN
1	D	337	GLN
1	D	344	ASN
1	D	411	ASN
1	D	435	HIS
1	D	461	ASN
1	D	508	GLN
2	E	75	HIS
2	F	75	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 monosaccharides in this entry.

## 5.6 Ligand geometry

17 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	GLU	D	1103	-	8,9,9	1.02	1 (12%)	10,11,11	1.28	2 (20%)
3	PCW	A	1101	-	50,50,53	1.06	3 (6%)	56,58,61	0.97	2 (3%)
3	PCW	C	1105	-	40,40,53	1.17	3 (7%)	45,48,61	0.98	3 (6%)
3	PCW	A	1105	-	40,40,53	1.16	3 (7%)	45,48,61	0.99	3 (6%)
3	PCW	D	1101	-	42,42,53	1.11	3 (7%)	48,50,61	1.05	4 (8%)
3	PCW	D	1102	-	38,38,53	1.18	2 (5%)	43,46,61	1.10	3 (6%)
4	GLU	B	1103	-	8,9,9	1.02	1 (12%)	10,11,11	1.28	2 (20%)
3	PCW	C	1101	-	50,50,53	1.06	3 (6%)	56,58,61	0.96	2 (3%)
3	PCW	A	1102	-	42,42,53	1.14	3 (7%)	48,50,61	1.05	4 (8%)
3	PCW	C	1103	-	38,38,53	1.15	3 (7%)	44,46,61	1.07	2 (4%)
3	PCW	C	1102	-	42,42,53	1.14	3 (7%)	48,50,61	1.05	4 (8%)
4	GLU	C	1104	-	8,9,9	1.11	1 (12%)	10,11,11	1.51	1 (10%)
3	PCW	B	1101	-	42,42,53	1.11	3 (7%)	48,50,61	1.06	4 (8%)
5	SPD	D	1104	-	9,9,9	0.45	0	8,8,8	0.83	0
3	PCW	A	1103	-	38,38,53	1.16	3 (7%)	44,46,61	1.07	3 (6%)
3	PCW	B	1102	-	38,38,53	1.17	2 (5%)	43,46,61	1.11	3 (6%)
4	GLU	A	1104	-	8,9,9	1.12	1 (12%)	10,11,11	1.49	1 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GLU	D	1103	-	-	1/9/9/9	-
3	PCW	A	1101	-	-	26/54/54/57	-
3	PCW	C	1105	-	-	26/44/44/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PCW	A	1105	-	-	25/44/44/57	-
3	PCW	D	1101	-	-	30/46/46/57	-
3	PCW	D	1102	-	-	24/42/42/57	-
4	GLU	B	1103	-	-	1/9/9/9	-
3	PCW	C	1101	-	-	26/54/54/57	-
3	PCW	A	1102	-	-	27/46/46/57	-
3	PCW	C	1103	-	-	25/42/42/57	-
3	PCW	C	1102	-	-	27/46/46/57	-
4	GLU	C	1104	-	-	0/9/9/9	-
3	PCW	B	1101	-	-	29/46/46/57	-
5	SPD	D	1104	-	-	3/7/7/7	-
3	PCW	A	1103	-	-	23/42/42/57	-
3	PCW	B	1102	-	-	24/42/42/57	-
4	GLU	A	1104	-	-	0/9/9/9	-

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1101	PCW	O2-C31	2.99	1.42	1.34
3	A	1103	PCW	O3-C11	2.98	1.42	1.33
3	A	1101	PCW	O2-C31	2.97	1.42	1.34
3	C	1103	PCW	O3-C11	2.94	1.41	1.33
3	D	1102	PCW	O2-C31	2.94	1.42	1.34
3	D	1102	PCW	O3-C11	2.92	1.41	1.33
3	B	1102	PCW	O3-C11	2.91	1.41	1.33
3	B	1102	PCW	O2-C31	2.90	1.42	1.34
3	A	1101	PCW	O3-C11	2.89	1.41	1.33
3	C	1101	PCW	O3-C11	2.89	1.41	1.33
3	A	1102	PCW	O2-C31	2.86	1.42	1.34
3	B	1101	PCW	O2-C2	-2.84	1.39	1.46
3	D	1101	PCW	O2-C2	-2.83	1.39	1.46
3	C	1102	PCW	O2-C31	2.82	1.42	1.34
3	A	1103	PCW	O2-C31	2.79	1.42	1.34
3	A	1105	PCW	O3-C11	2.76	1.41	1.33
3	A	1105	PCW	O2-C31	2.74	1.42	1.34
3	C	1105	PCW	O3-C11	2.73	1.41	1.33
3	C	1105	PCW	O2-C31	2.71	1.42	1.34
3	C	1103	PCW	O2-C31	2.71	1.42	1.34
3	B	1101	PCW	O3-C11	2.70	1.41	1.33
3	D	1101	PCW	O3-C11	2.67	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1102	PCW	O3-C11	2.62	1.41	1.33
3	A	1102	PCW	O3-C11	2.61	1.41	1.33
3	C	1102	PCW	O2-C2	-2.52	1.40	1.46
3	A	1102	PCW	O2-C2	-2.48	1.40	1.46
3	C	1105	PCW	O2-C2	-2.45	1.40	1.46
3	A	1105	PCW	O2-C2	-2.38	1.40	1.46
3	B	1101	PCW	O2-C31	2.36	1.41	1.34
3	C	1103	PCW	O2-C2	-2.36	1.40	1.46
3	D	1101	PCW	O2-C31	2.35	1.40	1.34
4	A	1104	GLU	OXT-C	-2.31	1.23	1.30
4	C	1104	GLU	OXT-C	-2.30	1.23	1.30
3	A	1103	PCW	O2-C2	-2.27	1.40	1.46
4	B	1103	GLU	OXT-C	-2.07	1.23	1.30
4	D	1103	GLU	OXT-C	-2.07	1.23	1.30
3	A	1101	PCW	O2-C2	-2.03	1.41	1.46
3	C	1101	PCW	O2-C2	-2.03	1.41	1.46

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1102	PCW	O2-C31-C32	4.52	121.25	111.50
3	A	1102	PCW	O2-C31-C32	4.50	121.20	111.50
3	D	1102	PCW	O2-C31-C32	4.44	121.06	111.50
3	B	1102	PCW	O2-C31-C32	4.42	121.03	111.50
3	A	1103	PCW	O2-C31-C32	4.41	121.00	111.50
3	C	1103	PCW	O2-C31-C32	4.36	120.89	111.50
3	A	1101	PCW	O2-C31-C32	4.14	120.42	111.50
3	C	1101	PCW	O2-C31-C32	4.10	120.33	111.50
3	A	1105	PCW	O2-C31-C32	3.84	119.78	111.50
3	C	1105	PCW	O2-C31-C32	3.70	119.48	111.50
4	C	1104	GLU	OXT-C-O	-3.60	115.91	124.09
3	B	1101	PCW	O2-C31-C32	3.57	119.20	111.50
4	A	1104	GLU	OXT-C-O	-3.56	116.01	124.09
3	D	1101	PCW	O2-C31-C32	3.53	119.11	111.50
4	B	1103	GLU	OXT-C-O	-2.87	117.56	124.09
4	D	1103	GLU	OXT-C-O	-2.85	117.61	124.09
3	B	1101	PCW	C6-N-C5	2.80	121.36	109.92
3	D	1101	PCW	C6-N-C5	2.80	121.36	109.92
3	C	1101	PCW	O3-C11-C12	2.75	120.54	111.91
3	A	1101	PCW	O3-C11-C12	2.75	120.52	111.91
3	D	1101	PCW	C2-O2-C31	-2.69	111.17	117.79
3	B	1101	PCW	C2-O2-C31	-2.60	111.39	117.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1103	PCW	O3-C11-C12	2.54	119.88	111.91
3	A	1103	PCW	O3-C11-C12	2.50	119.74	111.91
3	A	1105	PCW	O3-C11-C12	2.44	119.56	111.91
3	C	1105	PCW	O3-C11-C12	2.43	119.52	111.91
3	A	1102	PCW	C6-N-C5	2.28	119.26	109.92
3	D	1101	PCW	O3-C11-C12	2.28	119.06	111.91
3	B	1101	PCW	O3-C11-C12	2.27	119.04	111.91
3	C	1102	PCW	C6-N-C5	2.27	119.20	109.92
3	B	1102	PCW	C2-O2-C31	2.24	123.32	117.79
3	B	1102	PCW	O3-C11-C12	2.24	118.93	111.91
4	D	1103	GLU	OXT-C-CA	2.24	121.01	113.38
4	B	1103	GLU	OXT-C-CA	2.24	121.00	113.38
3	D	1102	PCW	O3-C11-C12	2.23	118.90	111.91
3	D	1102	PCW	C2-O2-C31	2.15	123.09	117.79
3	C	1102	PCW	O3-C11-C12	2.12	118.58	111.91
3	C	1105	PCW	C6-N-C5	2.12	118.58	109.92
3	A	1105	PCW	C6-N-C5	2.10	118.51	109.92
3	A	1103	PCW	C6-N-C5	2.09	118.45	109.92
3	A	1102	PCW	O3-C11-C12	2.08	118.43	111.91
3	C	1102	PCW	O2-C31-O31	-2.07	118.70	123.70
3	A	1102	PCW	O2-C31-O31	-2.05	118.76	123.70

There are no chirality outliers.

All (317) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1101	PCW	C12-C11-O3-C3
3	A	1101	PCW	O11-C11-O3-C3
3	A	1101	PCW	C32-C31-O2-C2
3	A	1102	PCW	C32-C31-O2-C2
3	A	1102	PCW	O31-C31-O2-C2
3	A	1102	PCW	C4-O4P-P-O2P
3	A	1103	PCW	O4P-C4-C5-N
3	A	1103	PCW	O31-C31-O2-C2
3	A	1103	PCW	C4-O4P-P-O1P
3	A	1103	PCW	C4-O4P-P-O2P
3	A	1105	PCW	O11-C11-O3-C3
3	A	1105	PCW	C1-O3P-P-O2P
3	B	1101	PCW	C32-C31-O2-C2
3	B	1102	PCW	C5-C4-O4P-P
3	B	1102	PCW	C32-C31-O2-C2
3	B	1102	PCW	C4-O4P-P-O1P

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Mol	Chain	Res	Type	Atoms
3	C	1101	PCW	C12-C11-O3-C3
3	C	1101	PCW	C32-C31-O2-C2
3	C	1102	PCW	C32-C31-O2-C2
3	C	1102	PCW	O31-C31-O2-C2
3	C	1102	PCW	C4-O4P-P-O2P
3	C	1102	PCW	C4-O4P-P-O3P
3	C	1103	PCW	O4P-C4-C5-N
3	C	1103	PCW	O31-C31-O2-C2
3	C	1103	PCW	C4-O4P-P-O1P
3	C	1103	PCW	C4-O4P-P-O2P
3	C	1103	PCW	C4-O4P-P-O3P
3	C	1105	PCW	C1-O3P-P-O2P
3	D	1101	PCW	C32-C31-O2-C2
3	D	1102	PCW	C5-C4-O4P-P
3	D	1102	PCW	C32-C31-O2-C2
3	D	1102	PCW	C4-O4P-P-O1P
5	D	1104	SPD	C7-C8-C9-N10
3	B	1102	PCW	O11-C11-O3-C3
3	C	1101	PCW	O11-C11-O3-C3
3	C	1105	PCW	O11-C11-O3-C3
3	D	1102	PCW	O11-C11-O3-C3
3	A	1105	PCW	C12-C11-O3-C3
3	B	1102	PCW	C12-C11-O3-C3
3	C	1105	PCW	C12-C11-O3-C3
3	D	1102	PCW	C12-C11-O3-C3
3	A	1103	PCW	O11-C11-O3-C3
3	C	1103	PCW	O11-C11-O3-C3
3	A	1101	PCW	O31-C31-O2-C2
3	B	1102	PCW	O31-C31-O2-C2
3	C	1101	PCW	O31-C31-O2-C2
3	D	1102	PCW	O31-C31-O2-C2
3	A	1103	PCW	C12-C11-O3-C3
3	C	1103	PCW	C12-C11-O3-C3
3	A	1103	PCW	C32-C31-O2-C2
3	C	1103	PCW	C32-C31-O2-C2
3	B	1101	PCW	O31-C31-O2-C2
3	D	1101	PCW	O31-C31-O2-C2
3	D	1101	PCW	C4-C5-N-C6
3	A	1102	PCW	C12-C11-O3-C3
3	C	1102	PCW	C12-C11-O3-C3
3	C	1101	PCW	C14-C15-C16-C17
3	A	1103	PCW	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
3	C	1101	PCW	C12-C13-C14-C15
3	A	1101	PCW	C12-C13-C14-C15
3	A	1101	PCW	C14-C15-C16-C17
3	A	1103	PCW	C2-C3-O3-C11
3	A	1102	PCW	O11-C11-O3-C3
3	C	1102	PCW	O11-C11-O3-C3
3	A	1105	PCW	C34-C35-C36-C37
3	B	1101	PCW	C4-C5-N-C6
3	B	1101	PCW	C12-C11-O3-C3
3	D	1101	PCW	C12-C11-O3-C3
3	C	1105	PCW	C34-C35-C36-C37
3	C	1101	PCW	C31-C32-C33-C34
3	C	1105	PCW	C11-C12-C13-C14
3	D	1102	PCW	C14-C15-C16-C17
3	A	1101	PCW	C20-C21-C22-C23
3	B	1101	PCW	O11-C11-O3-C3
3	A	1101	PCW	C31-C32-C33-C34
3	A	1105	PCW	C11-C12-C13-C14
3	D	1101	PCW	C11-C12-C13-C14
3	B	1102	PCW	C14-C15-C16-C17
3	D	1102	PCW	C12-C13-C14-C15
3	C	1103	PCW	C2-C3-O3-C11
3	D	1101	PCW	O11-C11-O3-C3
3	A	1105	PCW	C36-C37-C38-C39
3	C	1105	PCW	C36-C37-C38-C39
3	B	1101	PCW	C31-C32-C33-C34
3	A	1102	PCW	C4-O4P-P-O3P
3	A	1103	PCW	C4-O4P-P-O3P
3	A	1105	PCW	C1-O3P-P-O4P
3	B	1102	PCW	C1-O3P-P-O4P
3	B	1102	PCW	C4-O4P-P-O3P
3	C	1103	PCW	C1-O3P-P-O4P
3	C	1105	PCW	C1-O3P-P-O4P
3	C	1105	PCW	C4-O4P-P-O3P
3	D	1102	PCW	C1-O3P-P-O4P
3	D	1102	PCW	C4-O4P-P-O3P
3	B	1102	PCW	C12-C13-C14-C15
3	B	1101	PCW	C4-C5-N-C7
3	B	1101	PCW	C4-C5-N-C8
3	B	1102	PCW	C4-C5-N-C6
3	B	1102	PCW	C4-C5-N-C7
3	B	1102	PCW	C4-C5-N-C8

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Mol	Chain	Res	Type	Atoms
3	D	1101	PCW	C4-C5-N-C7
3	D	1102	PCW	C4-C5-N-C6
3	D	1102	PCW	C4-C5-N-C7
3	C	1101	PCW	C20-C21-C22-C23
3	B	1101	PCW	C15-C16-C17-C18
3	C	1105	PCW	C35-C36-C37-C38
3	D	1101	PCW	C15-C16-C17-C18
3	A	1101	PCW	C23-C24-C25-C26
3	C	1105	PCW	C33-C34-C35-C36
3	A	1102	PCW	C41-C42-C43-C44
3	A	1105	PCW	C33-C34-C35-C36
3	A	1105	PCW	C35-C36-C37-C38
3	A	1105	PCW	O3P-C1-C2-O2
3	C	1105	PCW	O3P-C1-C2-O2
3	B	1101	PCW	C11-C12-C13-C14
3	D	1101	PCW	C31-C32-C33-C34
3	A	1102	PCW	C15-C16-C17-C18
3	C	1102	PCW	C41-C42-C43-C44
3	D	1101	PCW	C13-C14-C15-C16
3	B	1101	PCW	C13-C14-C15-C16
3	A	1101	PCW	C40-C41-C42-C43
3	C	1101	PCW	C40-C41-C42-C43
3	C	1101	PCW	C23-C24-C25-C26
3	C	1102	PCW	C15-C16-C17-C18
3	D	1101	PCW	C4-C5-N-C8
3	D	1102	PCW	C4-C5-N-C8
3	A	1102	PCW	C34-C35-C36-C37
3	B	1101	PCW	C35-C36-C37-C38
3	C	1102	PCW	C34-C35-C36-C37
3	D	1101	PCW	C41-C42-C43-C44
3	D	1102	PCW	C32-C33-C34-C35
3	A	1102	PCW	C12-C13-C14-C15
3	B	1101	PCW	C41-C42-C43-C44
3	C	1102	PCW	C12-C13-C14-C15
3	D	1102	PCW	C11-C12-C13-C14
3	B	1102	PCW	C11-C12-C13-C14
3	B	1101	PCW	C14-C15-C16-C17
3	B	1101	PCW	C32-C33-C34-C35
3	A	1101	PCW	C21-C22-C23-C24
3	A	1105	PCW	C32-C33-C34-C35
3	A	1102	PCW	O3P-C1-C2-O2
3	C	1102	PCW	O3P-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	C	1103	PCW	C4-C5-N-C6
3	A	1101	PCW	C36-C37-C38-C39
3	A	1103	PCW	C36-C37-C38-C39
3	C	1101	PCW	C36-C37-C38-C39
3	D	1101	PCW	C14-C15-C16-C17
3	C	1105	PCW	C32-C33-C34-C35
3	A	1103	PCW	C1-O3P-P-O4P
3	A	1105	PCW	C4-O4P-P-O3P
3	D	1101	PCW	C35-C36-C37-C38
3	C	1102	PCW	C13-C14-C15-C16
3	A	1101	PCW	C16-C17-C18-C19
3	A	1102	PCW	C16-C17-C18-C19
3	C	1101	PCW	C16-C17-C18-C19
3	D	1101	PCW	C32-C33-C34-C35
3	C	1101	PCW	C21-C22-C23-C24
3	C	1102	PCW	C32-C33-C34-C35
3	C	1103	PCW	C35-C36-C37-C38
3	D	1102	PCW	C34-C35-C36-C37
3	B	1102	PCW	C32-C33-C34-C35
3	C	1103	PCW	C33-C34-C35-C36
3	A	1101	PCW	C11-C12-C13-C14
3	C	1101	PCW	C11-C12-C13-C14
3	A	1102	PCW	C32-C33-C34-C35
3	C	1102	PCW	C16-C17-C18-C19
3	C	1103	PCW	C36-C37-C38-C39
3	A	1103	PCW	C33-C34-C35-C36
3	D	1102	PCW	C1-C2-O2-C31
3	A	1102	PCW	C37-C38-C39-C40
3	C	1102	PCW	C37-C38-C39-C40
3	C	1101	PCW	C13-C14-C15-C16
3	B	1101	PCW	O3P-C1-C2-O2
3	A	1102	PCW	C13-C14-C15-C16
3	B	1101	PCW	C39-C40-C41-C42
3	C	1101	PCW	C15-C16-C17-C18
3	C	1102	PCW	C33-C34-C35-C36
3	A	1101	PCW	C13-C14-C15-C16
3	A	1102	PCW	C33-C34-C35-C36
3	C	1103	PCW	C4-C5-N-C7
3	A	1102	PCW	O3P-C1-C2-C3
3	A	1105	PCW	O3P-C1-C2-C3
3	C	1102	PCW	O3P-C1-C2-C3
3	C	1105	PCW	O3P-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
3	A	1101	PCW	C15-C16-C17-C18
3	B	1102	PCW	C34-C35-C36-C37
3	A	1105	PCW	C2-C1-O3P-P
3	C	1105	PCW	C2-C1-O3P-P
3	C	1101	PCW	C41-C42-C43-C44
3	B	1101	PCW	C40-C41-C42-C43
3	A	1101	PCW	C41-C42-C43-C44
3	C	1103	PCW	C39-C40-C41-C42
3	C	1103	PCW	C12-C13-C14-C15
3	A	1101	PCW	C2-C1-O3P-P
3	C	1101	PCW	C2-C1-O3P-P
3	C	1103	PCW	C4-C5-N-C8
5	D	1104	SPD	C2-C3-C4-C5
3	A	1105	PCW	C19-C20-C21-C22
3	C	1105	PCW	C19-C20-C21-C22
3	B	1101	PCW	O3P-C1-C2-C3
3	C	1103	PCW	C3-C2-O2-C31
3	B	1102	PCW	C33-C34-C35-C36
3	A	1101	PCW	C1-C2-C3-O3
3	A	1102	PCW	C1-C2-C3-O3
3	A	1105	PCW	C1-C2-C3-O3
3	B	1101	PCW	C1-C2-C3-O3
3	C	1101	PCW	C1-C2-C3-O3
3	C	1105	PCW	C1-C2-C3-O3
3	D	1101	PCW	C1-C2-C3-O3
3	D	1101	PCW	C39-C40-C41-C42
3	A	1105	PCW	O2-C2-C3-O3
3	B	1101	PCW	O2-C2-C3-O3
3	C	1105	PCW	O2-C2-C3-O3
3	D	1101	PCW	O2-C2-C3-O3
3	D	1101	PCW	C36-C37-C38-C39
3	D	1102	PCW	C36-C37-C38-C39
3	A	1103	PCW	C39-C40-C41-C42
5	D	1104	SPD	C3-C4-C5-N6
3	A	1101	PCW	C4-C5-N-C8
3	A	1103	PCW	C1-O3P-P-O1P
3	A	1103	PCW	C1-O3P-P-O2P
3	A	1105	PCW	C1-O3P-P-O1P
3	A	1105	PCW	C4-O4P-P-O1P
3	B	1102	PCW	C1-O3P-P-O1P
3	B	1102	PCW	C1-O3P-P-O2P
3	C	1103	PCW	C1-O3P-P-O1P

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Mol	Chain	Res	Type	Atoms
3	C	1103	PCW	C1-O3P-P-O2P
3	C	1105	PCW	C1-O3P-P-O1P
3	C	1105	PCW	C4-O4P-P-O1P
3	D	1102	PCW	C1-O3P-P-O1P
3	D	1102	PCW	C1-O3P-P-O2P
3	B	1101	PCW	C42-C43-C44-C45
3	C	1103	PCW	C13-C14-C15-C16
3	D	1101	PCW	C40-C41-C42-C43
3	D	1101	PCW	O3P-C1-C2-O2
3	C	1101	PCW	C4-C5-N-C8
3	B	1101	PCW	O3-C11-C12-C13
3	A	1102	PCW	O4P-C4-C5-N
3	C	1102	PCW	C1-C2-C3-O3
3	C	1102	PCW	O4P-C4-C5-N
3	A	1102	PCW	O2-C2-C3-O3
3	C	1102	PCW	O2-C2-C3-O3
3	D	1102	PCW	C33-C34-C35-C36
3	A	1101	PCW	C34-C35-C36-C37
3	A	1103	PCW	C37-C38-C39-C40
3	C	1101	PCW	C34-C35-C36-C37
3	A	1101	PCW	C1-C2-O2-C31
3	A	1103	PCW	C3-C2-O2-C31
3	B	1102	PCW	C1-C2-O2-C31
3	C	1101	PCW	C1-C2-O2-C31
3	D	1101	PCW	O3P-C1-C2-C3
3	A	1101	PCW	C4-C5-N-C6
3	A	1103	PCW	C13-C14-C15-C16
3	A	1105	PCW	C17-C18-C19-C20
3	A	1102	PCW	C1-O3P-P-O4P
3	C	1102	PCW	C1-O3P-P-O4P
3	C	1105	PCW	C13-C14-C15-C16
3	A	1102	PCW	C39-C40-C41-C42
3	B	1101	PCW	C37-C38-C39-C40
3	C	1105	PCW	C17-C18-C19-C20
3	D	1101	PCW	C37-C38-C39-C40
3	B	1101	PCW	C36-C37-C38-C39
3	C	1103	PCW	C37-C38-C39-C40
3	D	1101	PCW	O3-C11-C12-C13
3	B	1101	PCW	C17-C18-C19-C20
3	A	1103	PCW	C35-C36-C37-C38
3	D	1101	PCW	C12-C13-C14-C15
3	C	1103	PCW	C31-C32-C33-C34

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Mol	Chain	Res	Type	Atoms
3	A	1101	PCW	C4-C5-N-C7
3	C	1101	PCW	C4-C5-N-C7
3	C	1105	PCW	C12-C13-C14-C15
3	A	1105	PCW	C12-C13-C14-C15
3	C	1102	PCW	C39-C40-C41-C42
3	C	1103	PCW	C11-C12-C13-C14
3	C	1105	PCW	C31-C32-C33-C34
3	B	1102	PCW	C39-C40-C41-C42
3	D	1102	PCW	C39-C40-C41-C42
3	D	1101	PCW	C34-C35-C36-C37
3	D	1102	PCW	O3-C11-C12-C13
3	A	1102	PCW	O3-C11-C12-C13
3	C	1101	PCW	C37-C38-C39-C40
3	A	1103	PCW	O3-C11-C12-C13
3	A	1105	PCW	C31-C32-C33-C34
3	C	1101	PCW	C4-C5-N-C6
3	B	1102	PCW	O3-C11-C12-C13
3	C	1102	PCW	O3-C11-C12-C13
3	C	1105	PCW	C37-C38-C39-C40
3	A	1103	PCW	C32-C33-C34-C35
3	B	1101	PCW	O2-C31-C32-C33
3	B	1102	PCW	C36-C37-C38-C39
3	D	1101	PCW	O2-C31-C32-C33
3	A	1101	PCW	C37-C38-C39-C40
3	A	1105	PCW	C37-C38-C39-C40
3	A	1105	PCW	C13-C14-C15-C16
3	A	1103	PCW	O11-C11-C12-C13
3	D	1102	PCW	O11-C11-C12-C13
3	B	1101	PCW	O31-C31-C32-C33
3	B	1102	PCW	O11-C11-C12-C13
3	D	1101	PCW	O31-C31-C32-C33
3	A	1102	PCW	O11-C11-C12-C13
3	C	1102	PCW	O11-C11-C12-C13
3	D	1101	PCW	C42-C43-C44-C45
3	B	1101	PCW	C1-O3P-P-O2P
3	C	1105	PCW	C4-O4P-P-O2P
3	D	1101	PCW	C1-O3P-P-O2P
3	A	1105	PCW	O2-C31-C32-C33
3	C	1105	PCW	O2-C31-C32-C33
3	A	1102	PCW	C5-C4-O4P-P
3	C	1102	PCW	C5-C4-O4P-P
3	A	1102	PCW	O31-C31-C32-C33

*Continued on next page...*



*Continued from previous page...*

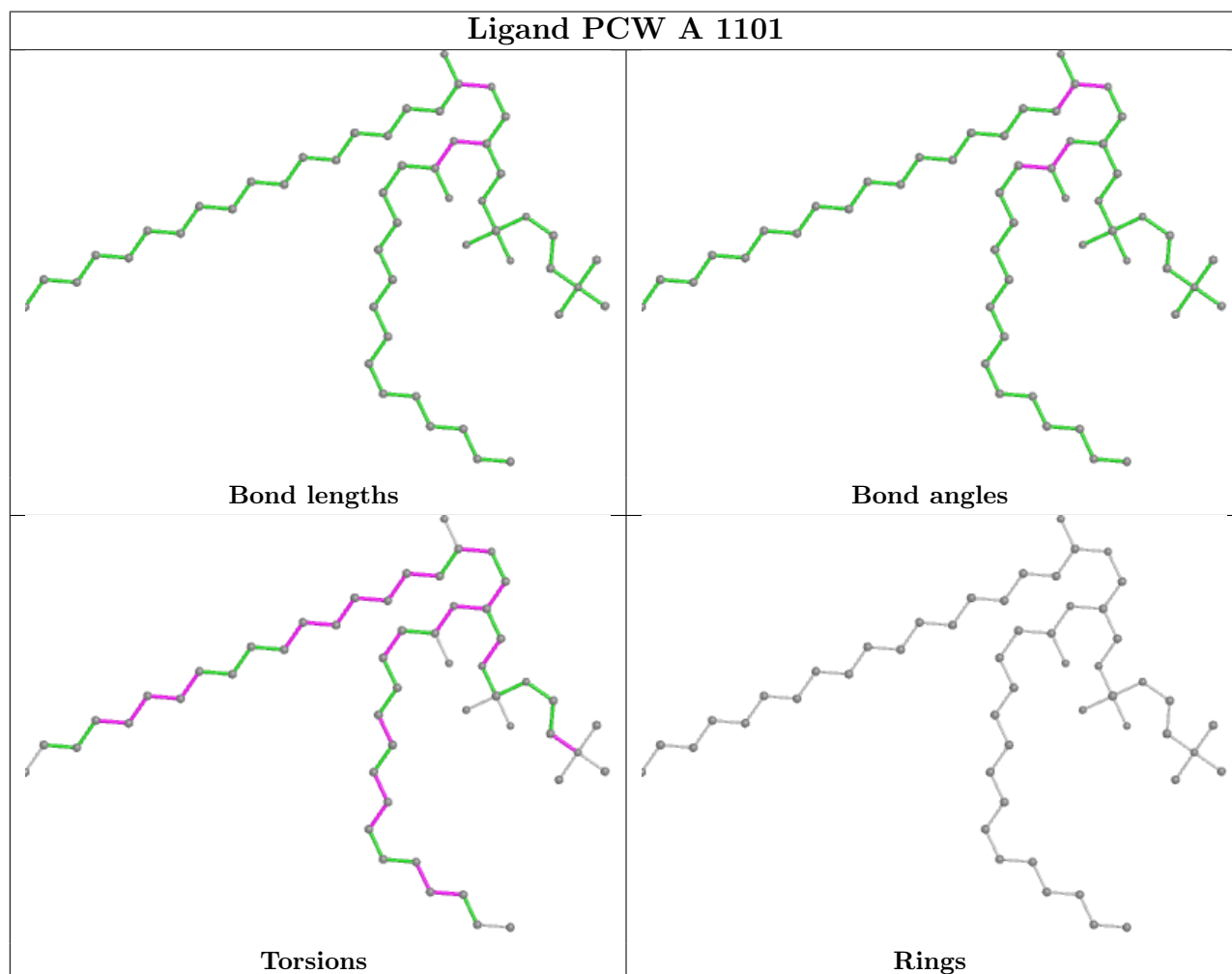
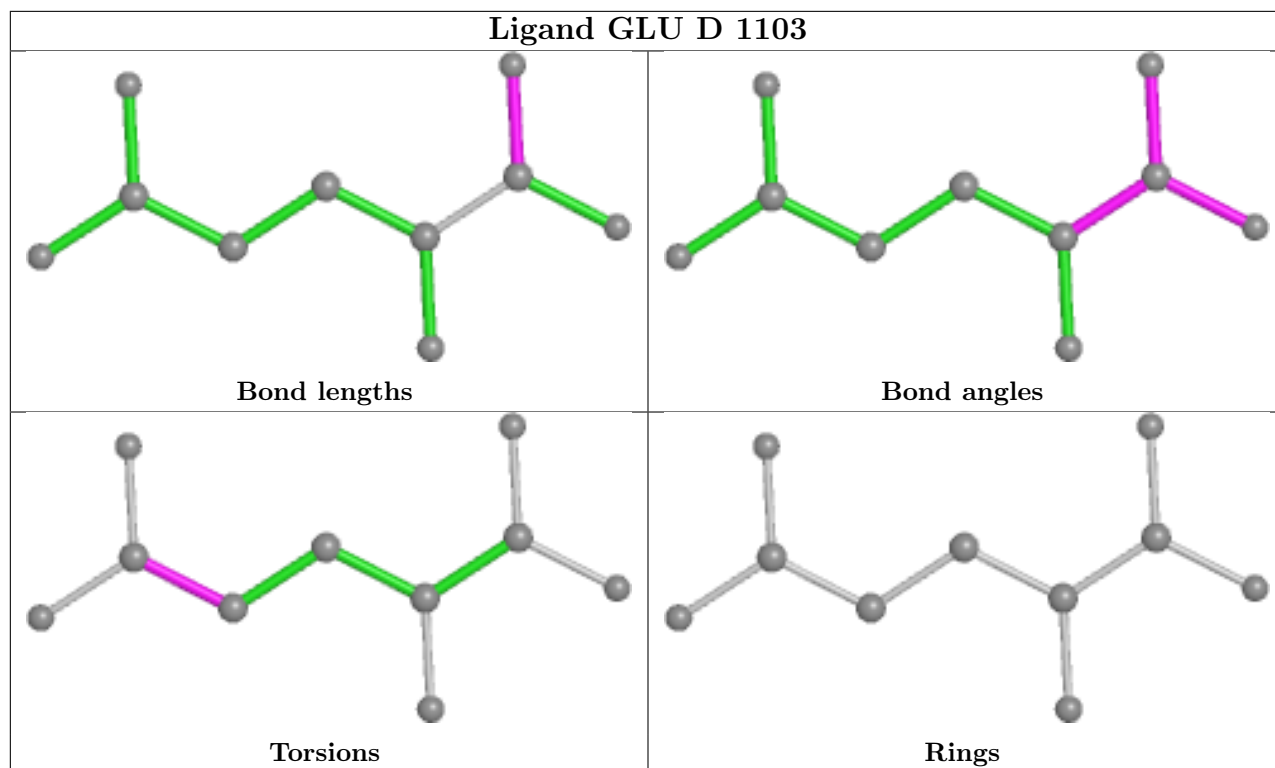
Mol	Chain	Res	Type	Atoms
3	C	1102	PCW	O31-C31-C32-C33
3	A	1102	PCW	O2-C31-C32-C33
3	C	1102	PCW	O2-C31-C32-C33
3	C	1101	PCW	C22-C23-C24-C25
3	A	1101	PCW	C22-C23-C24-C25
4	B	1103	GLU	OE1-CD-CG-CB
4	D	1103	GLU	OE1-CD-CG-CB

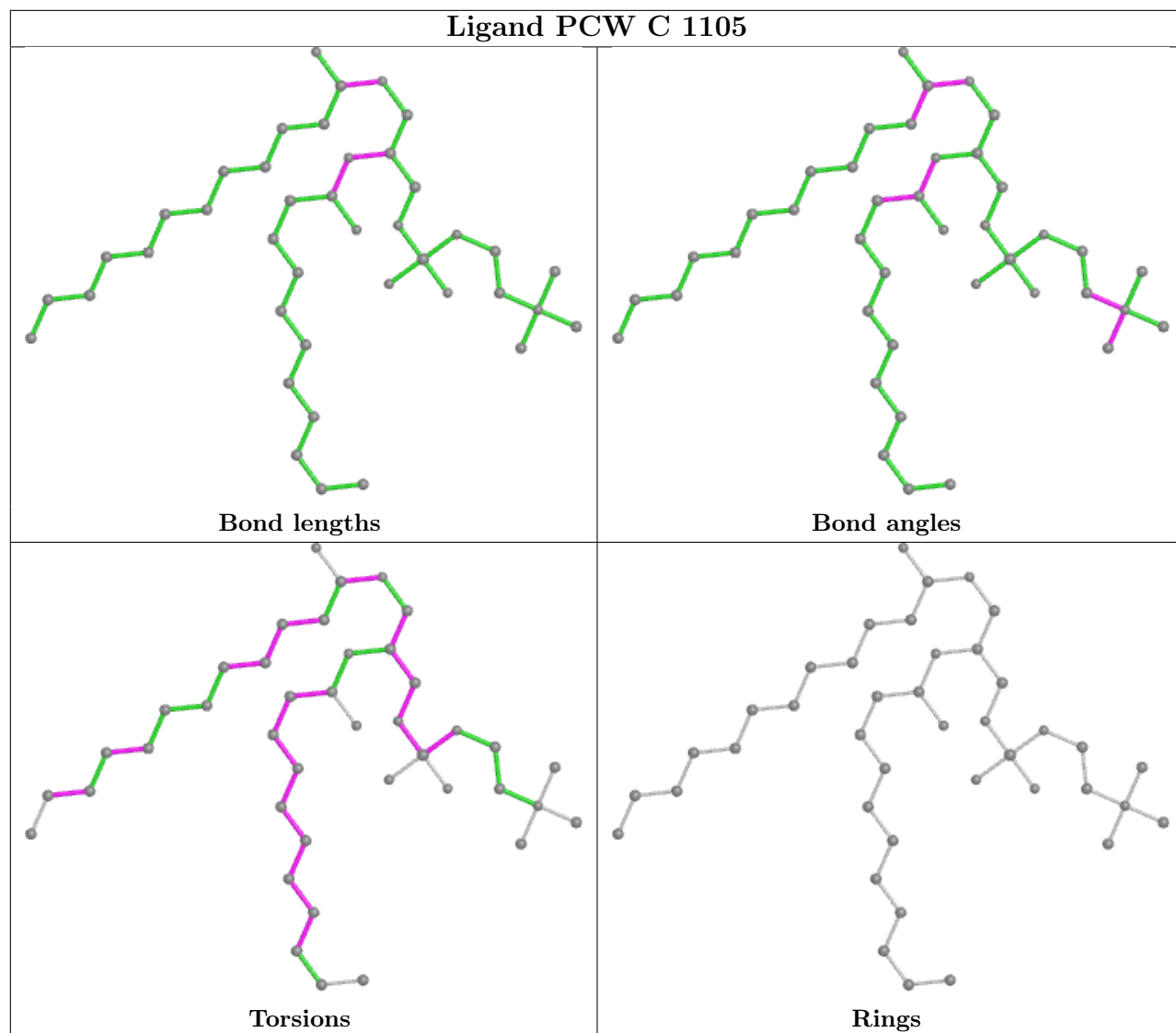
There are no ring outliers.

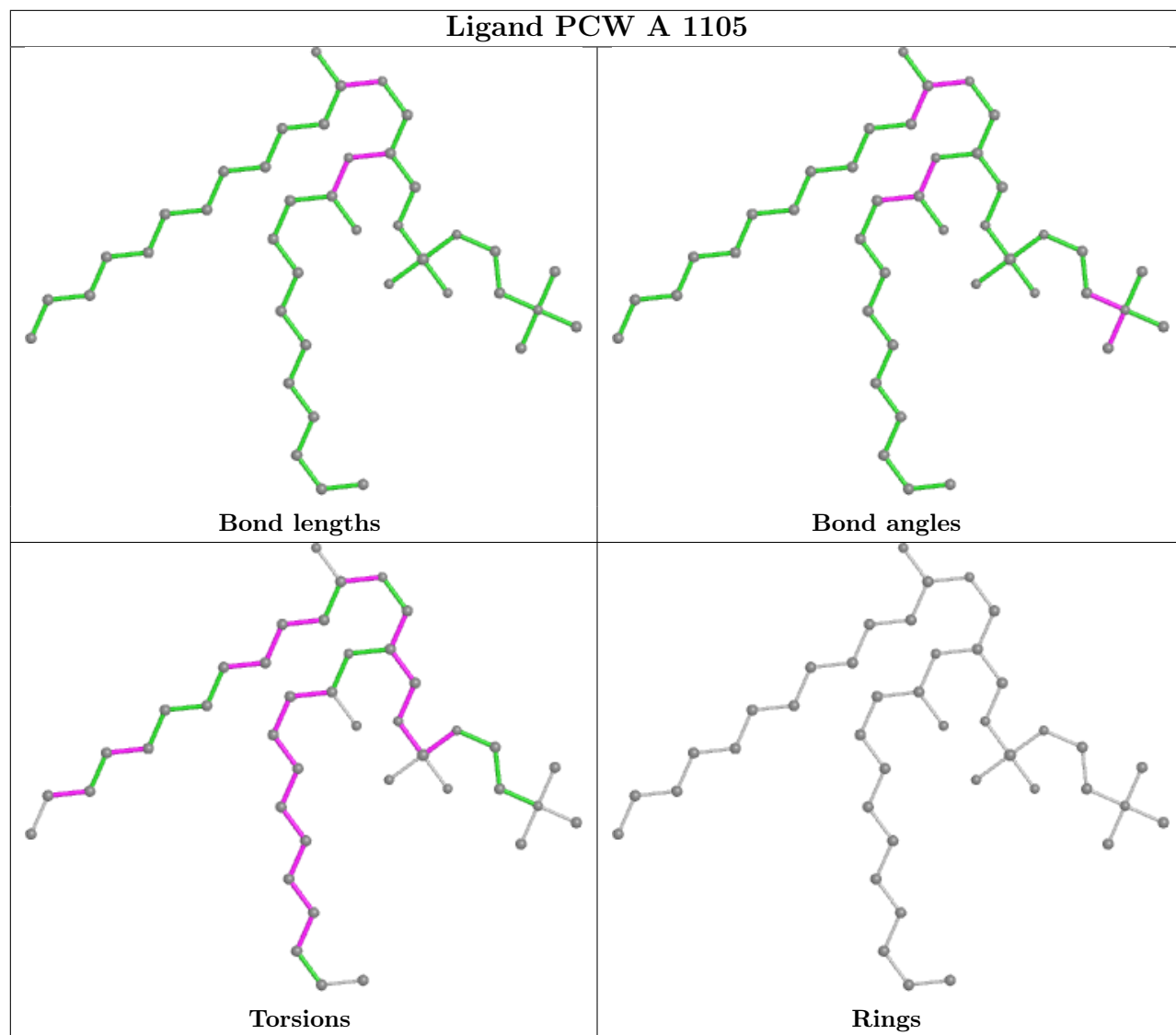
14 monomers are involved in 24 short contacts:

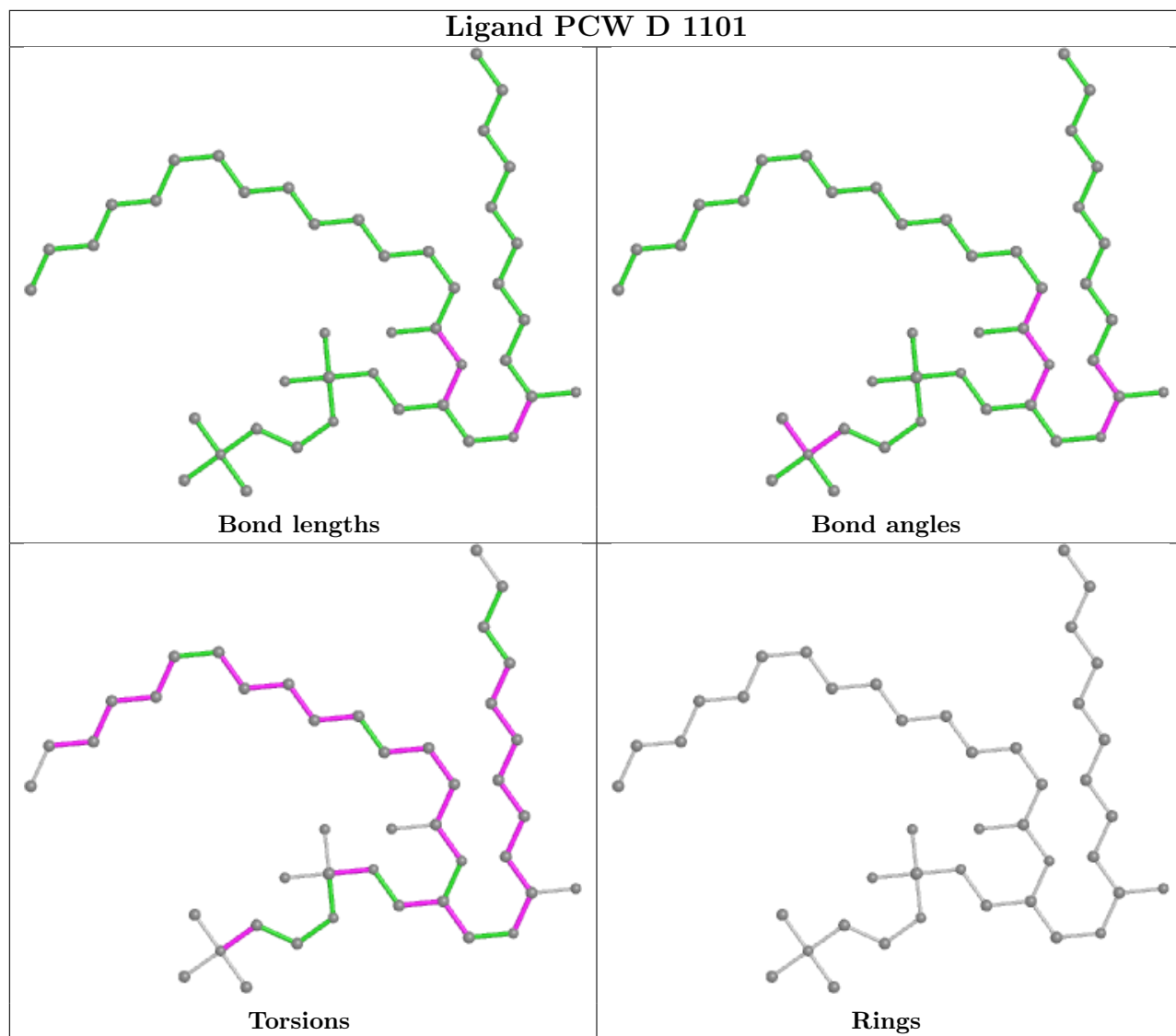
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1103	GLU	1	0
3	A	1101	PCW	2	0
3	C	1105	PCW	1	0
3	A	1105	PCW	1	0
3	D	1101	PCW	1	0
3	D	1102	PCW	4	0
4	B	1103	GLU	1	0
3	C	1103	PCW	1	0
4	C	1104	GLU	1	0
3	B	1101	PCW	1	0
5	D	1104	SPD	2	0
3	A	1103	PCW	2	0
3	B	1102	PCW	5	0
4	A	1104	GLU	1	0

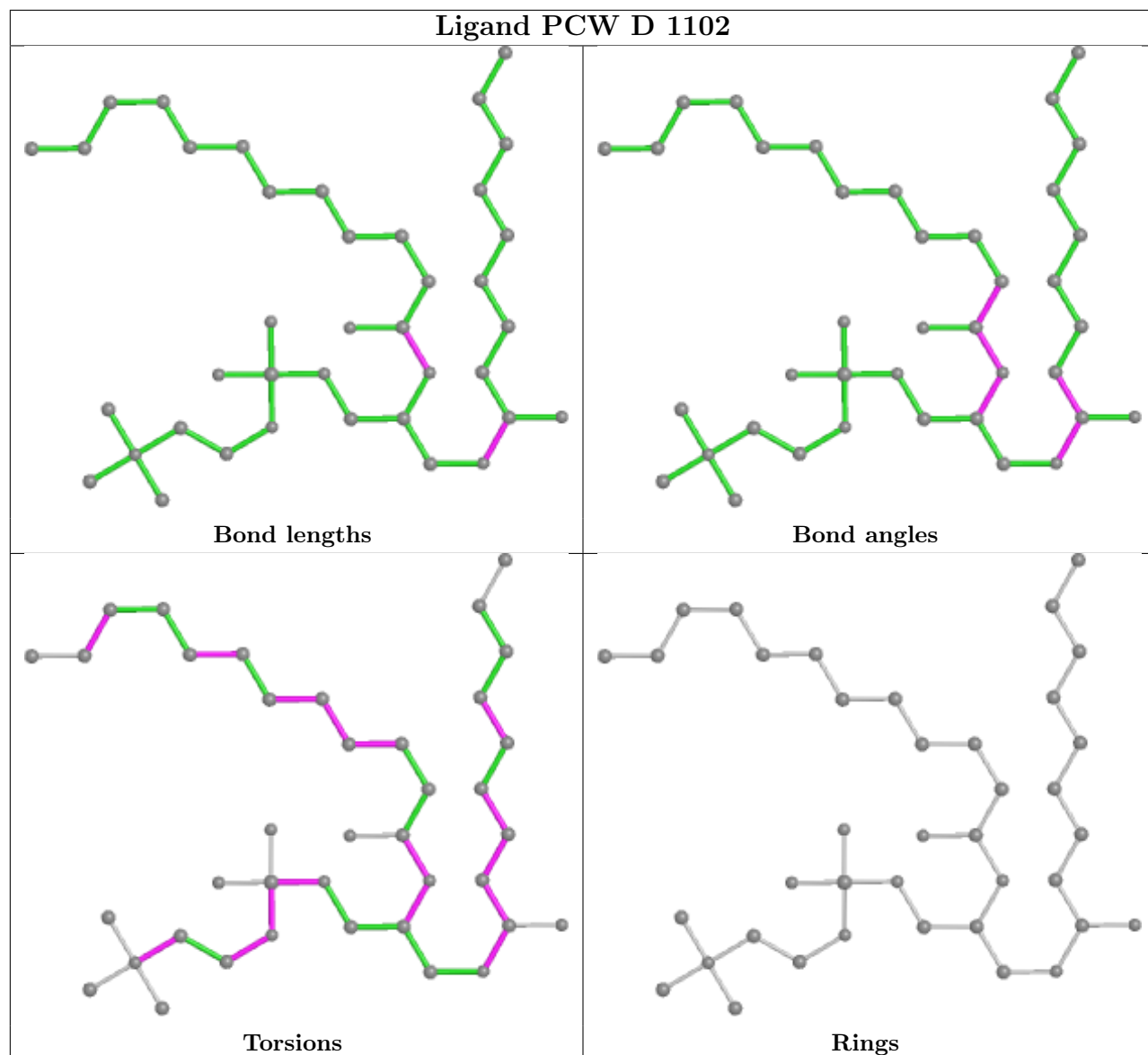
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

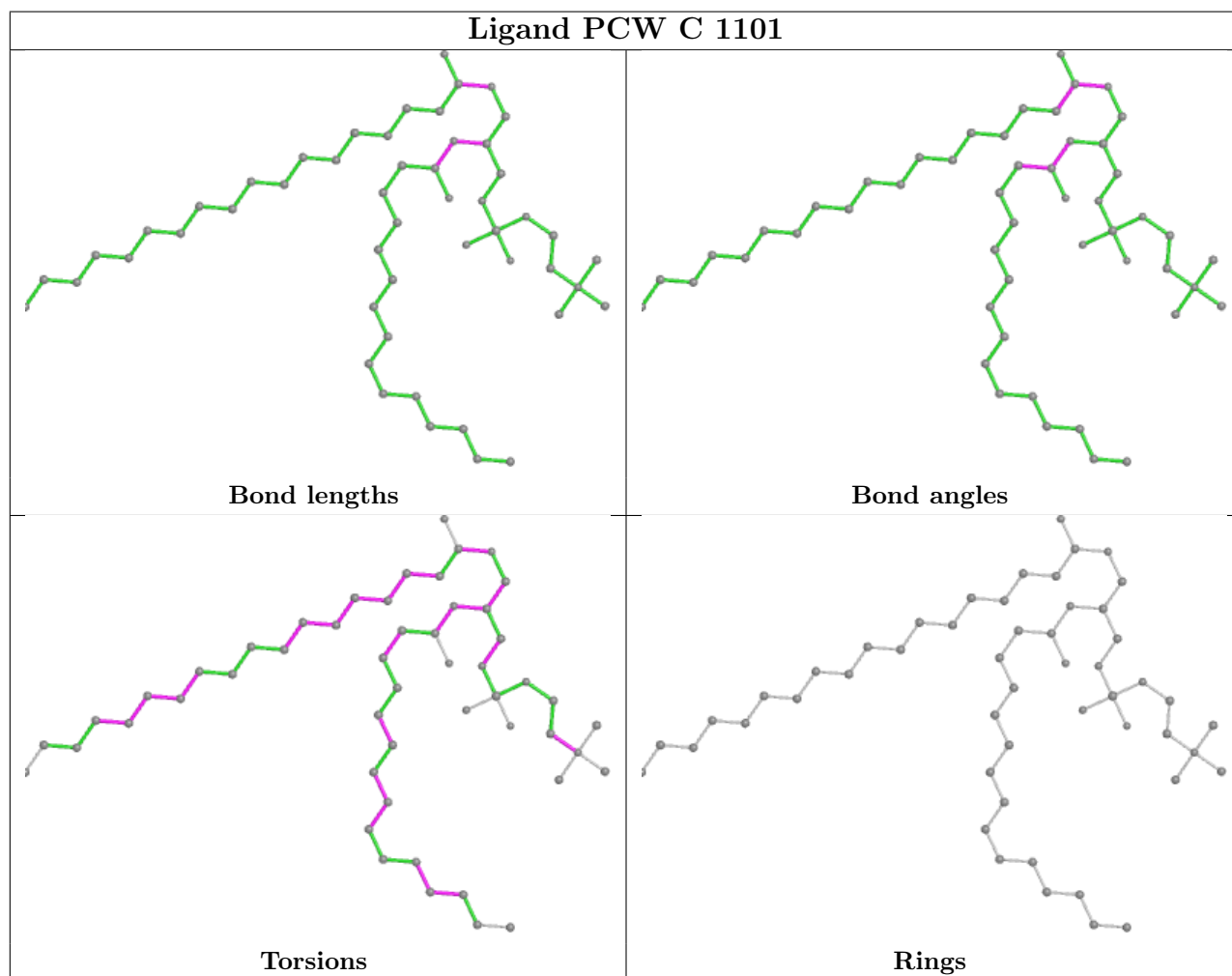
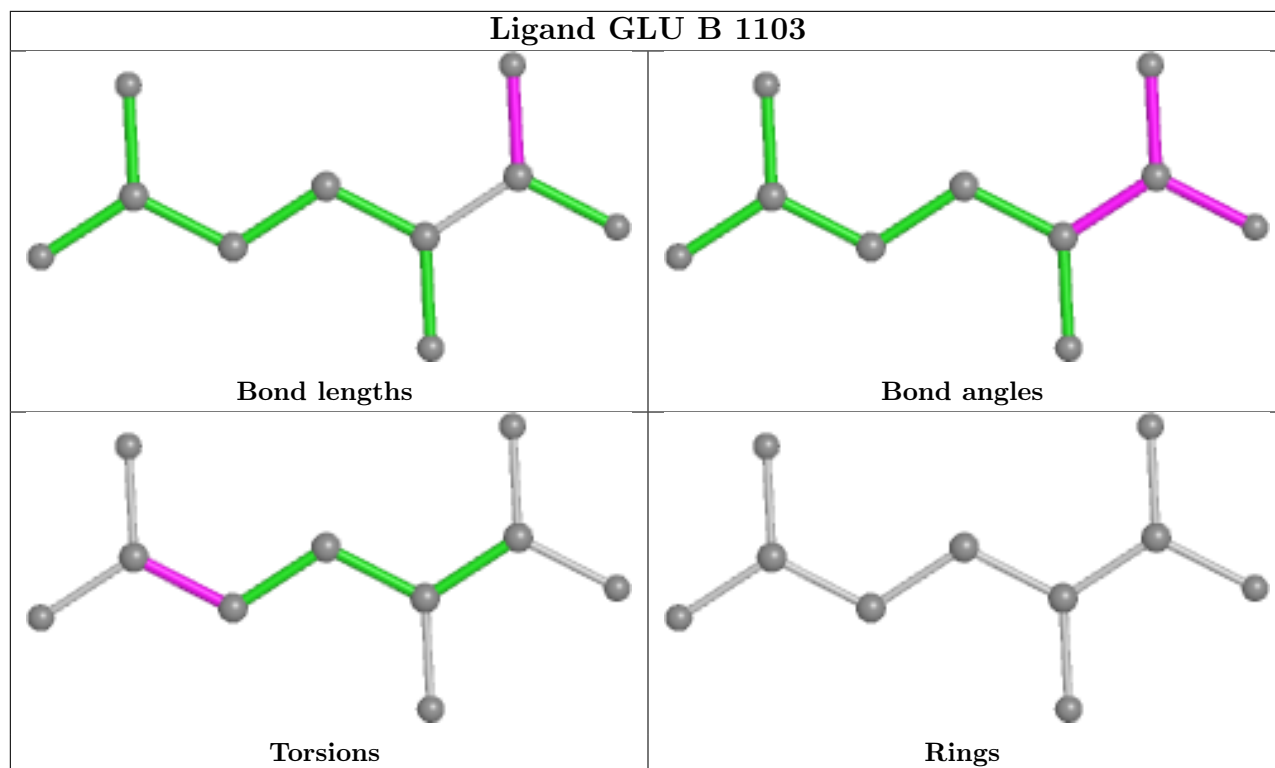


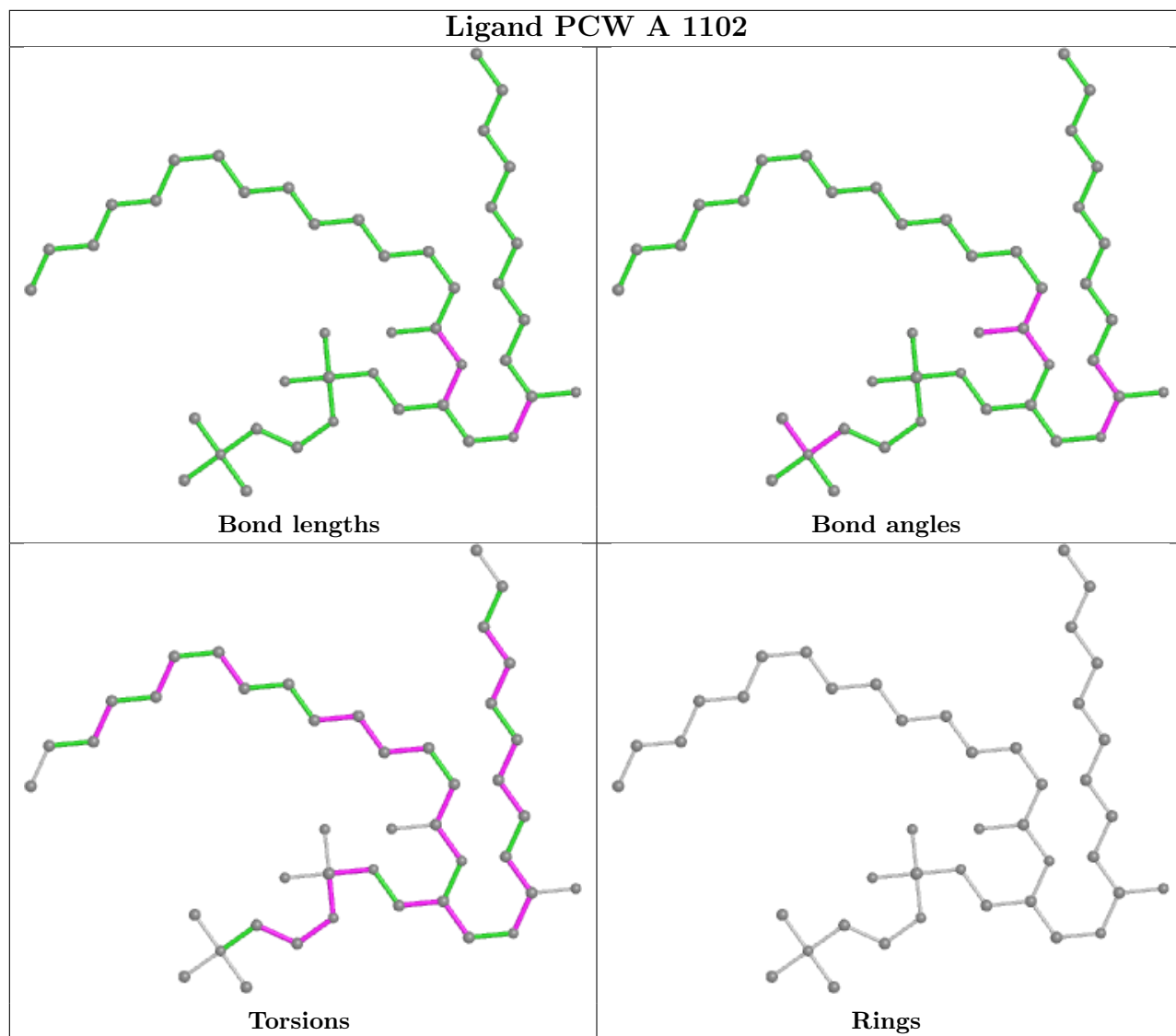




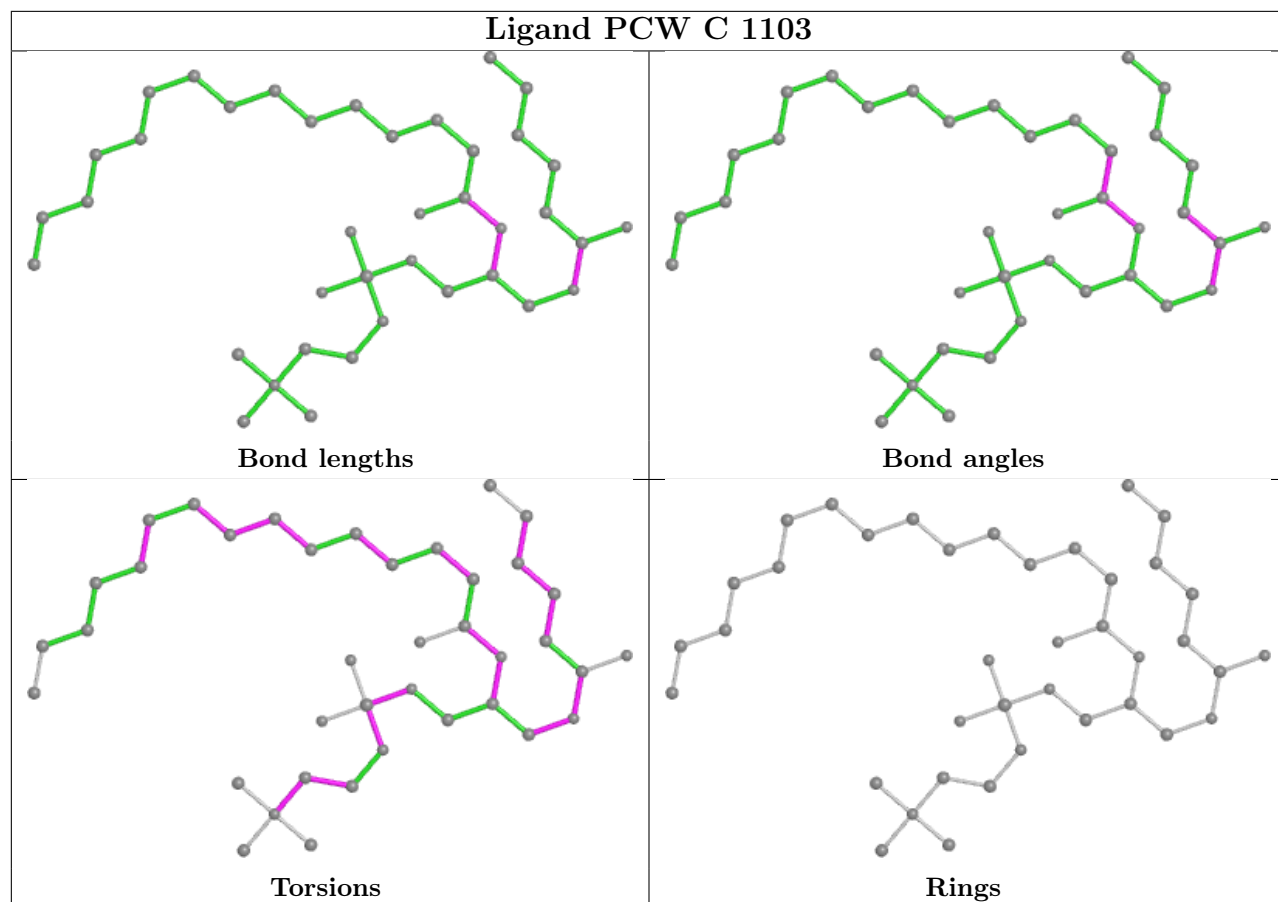


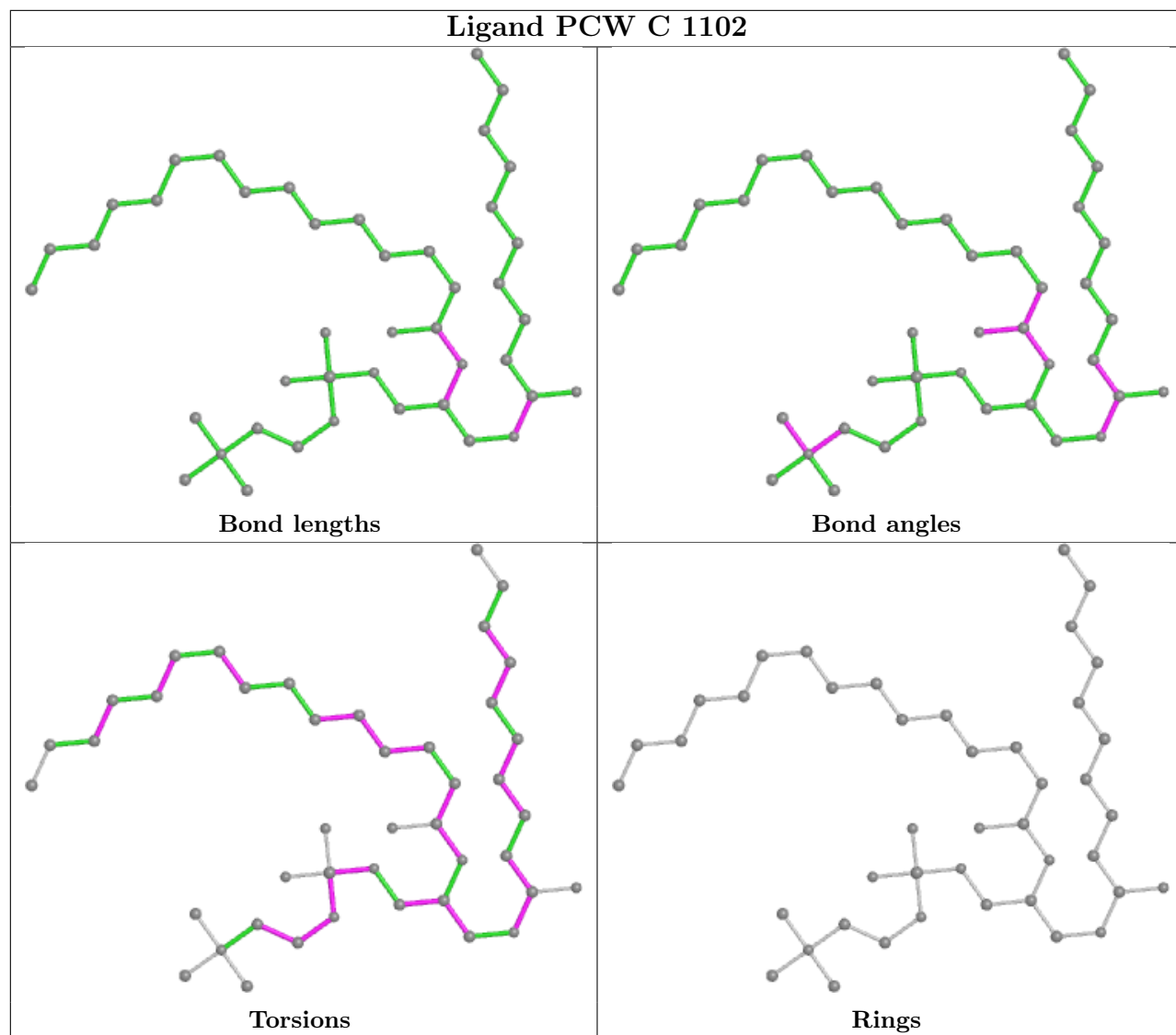


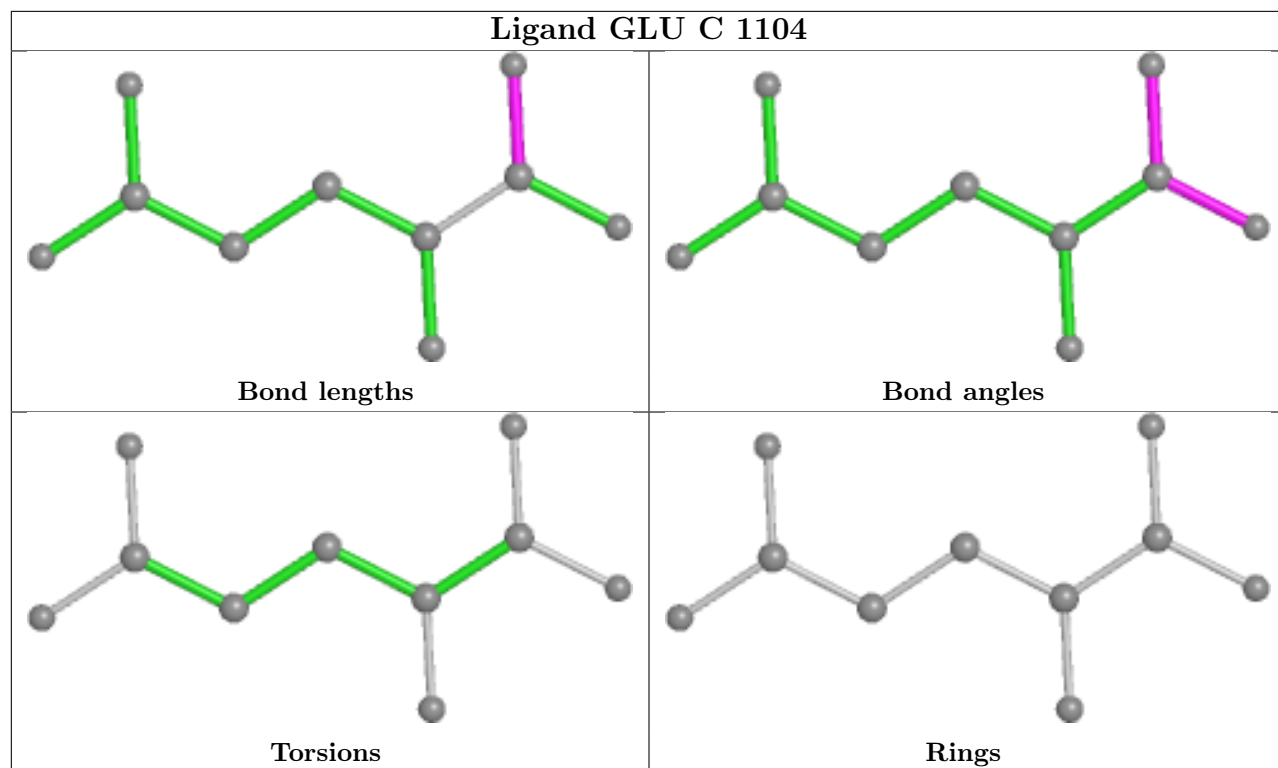


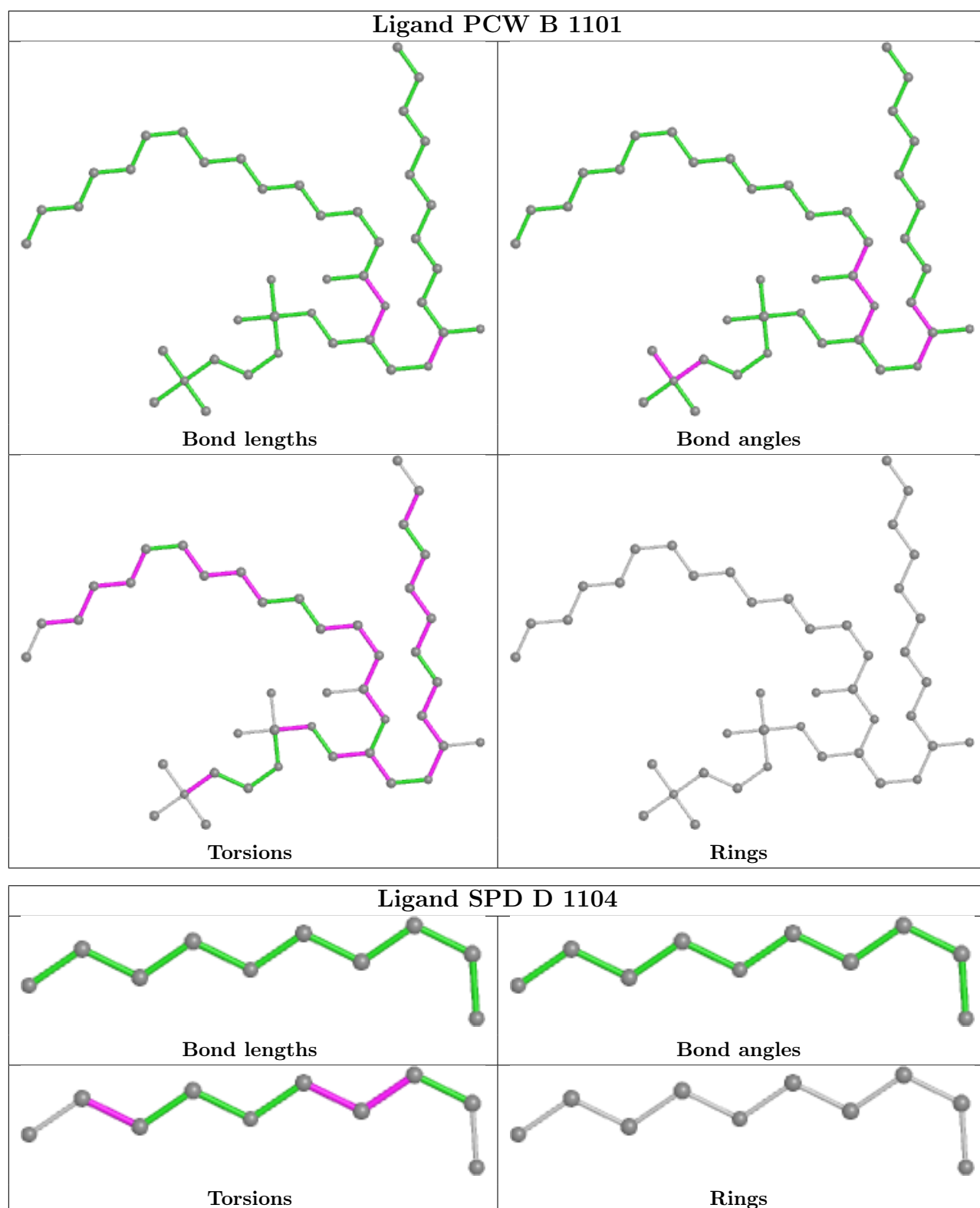


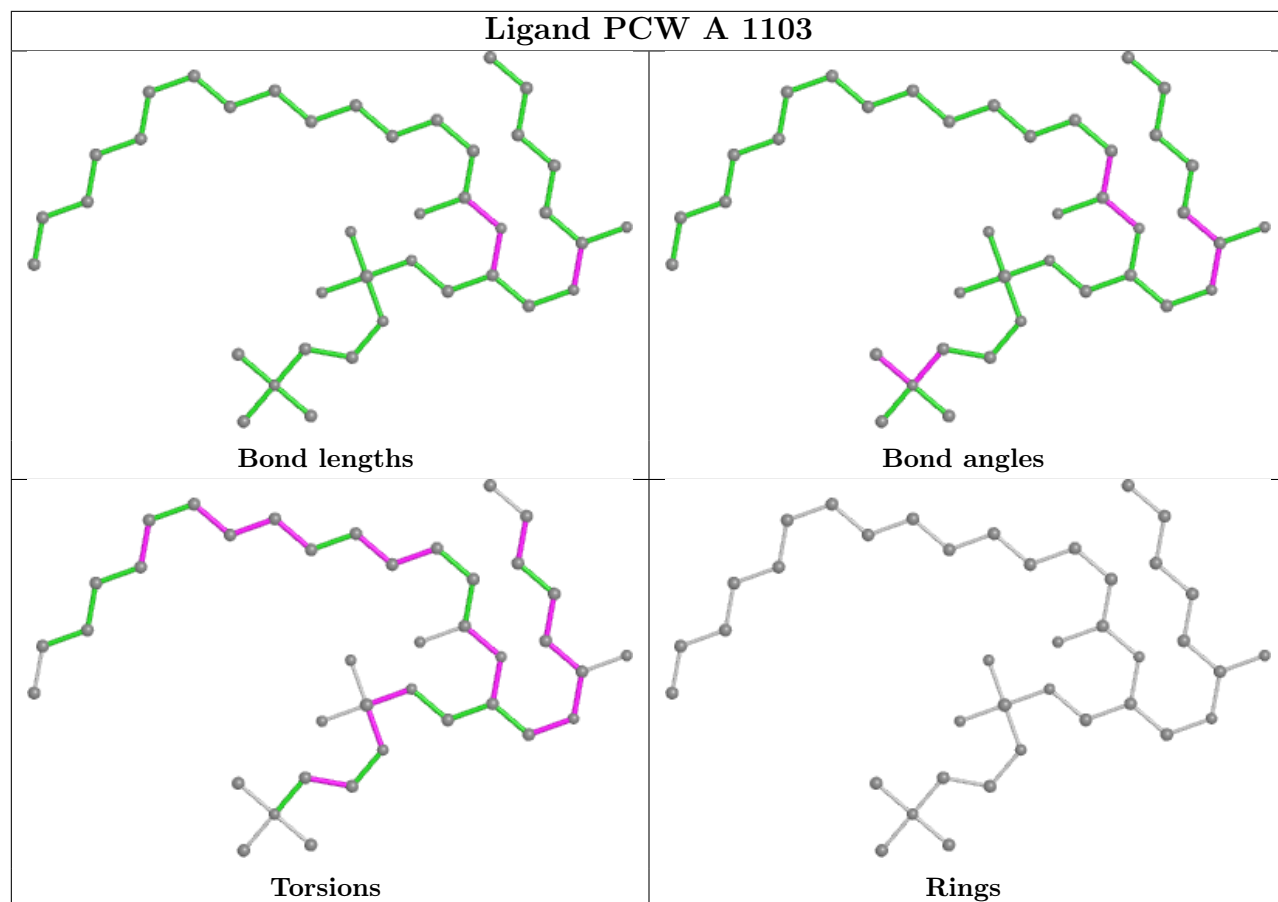


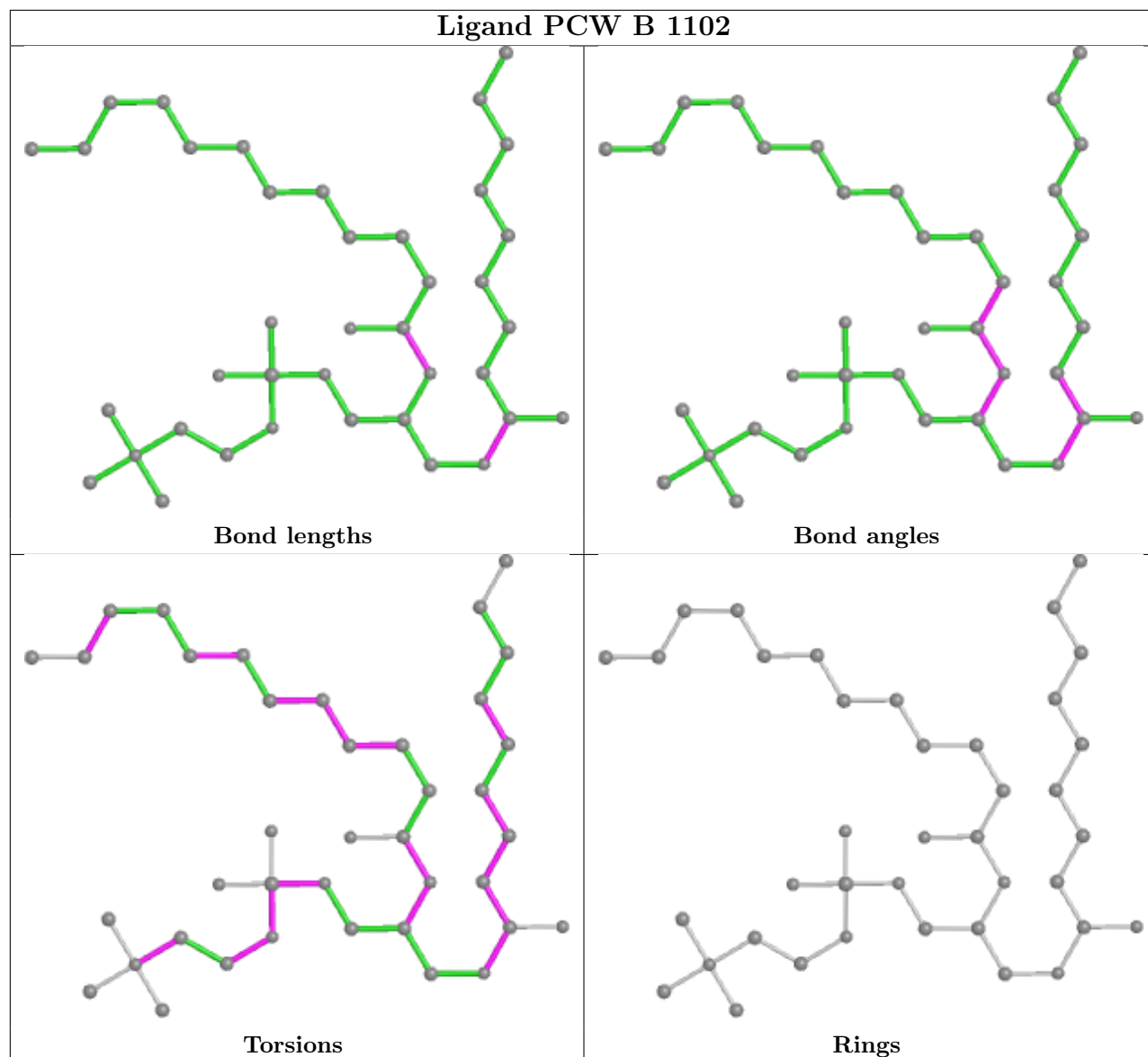


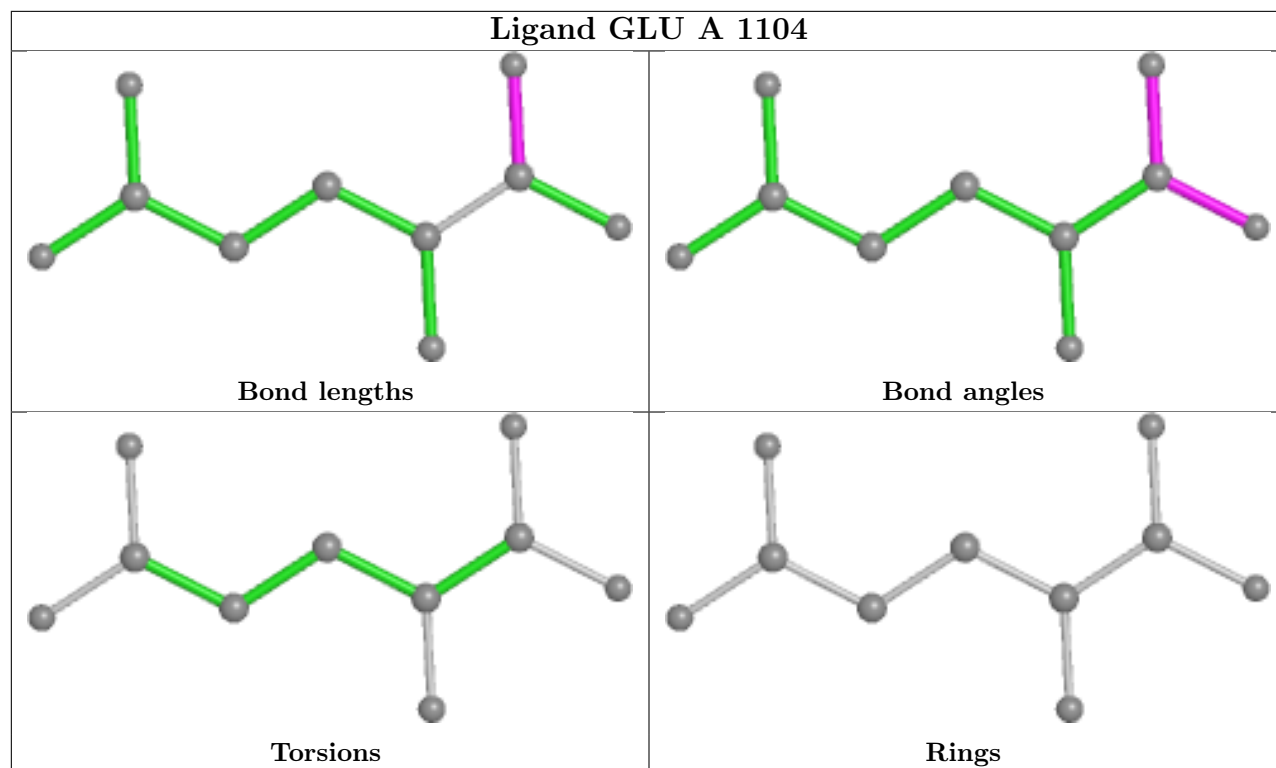












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

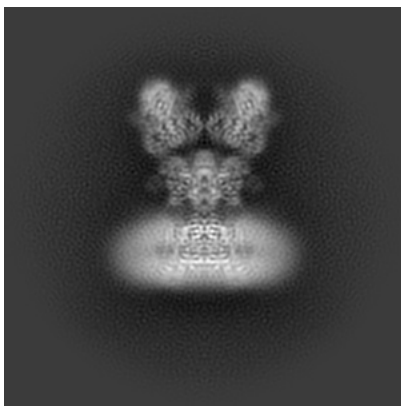
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40749. These allow visual inspection of the internal detail of the map and identification of artifacts.

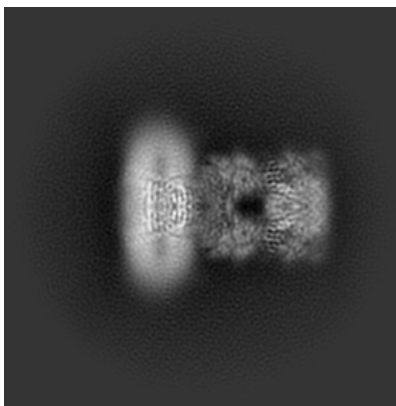
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

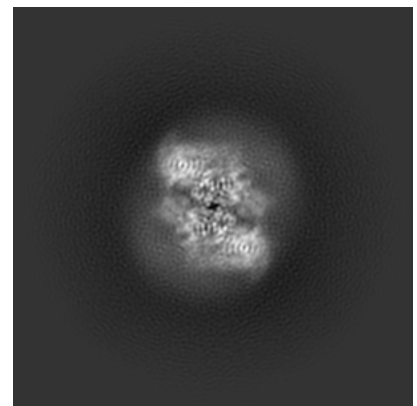
#### 6.1.1 Primary map



X

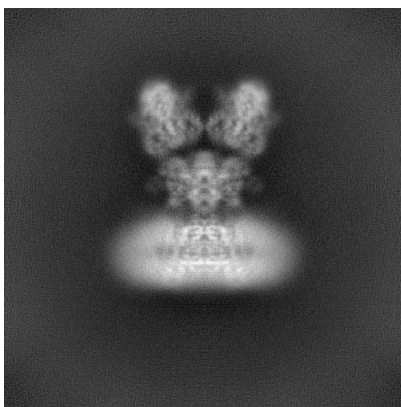


Y

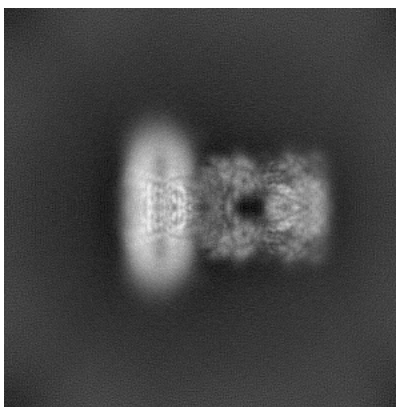


Z

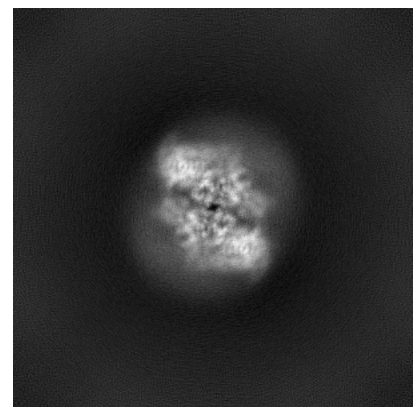
#### 6.1.2 Raw map



X



Y



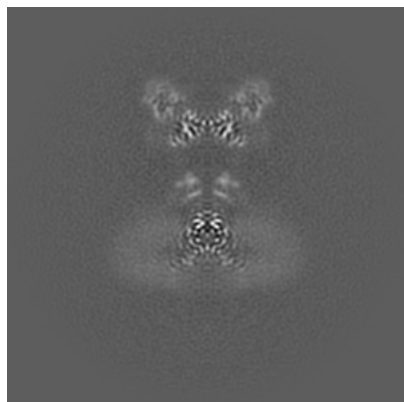
Z

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

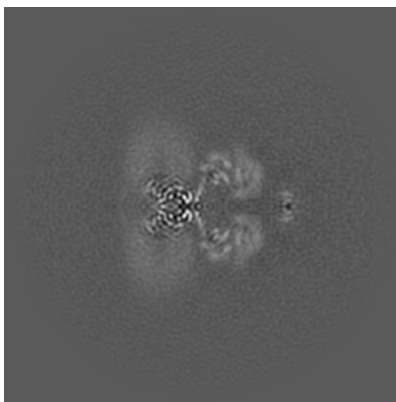


## 6.2 Central slices [i](#)

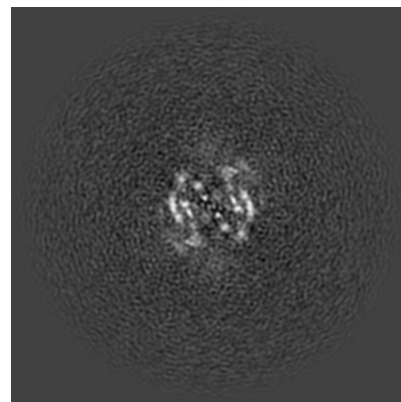
### 6.2.1 Primary map



X Index: 208

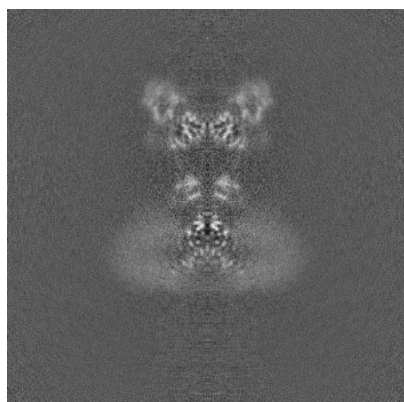


Y Index: 208

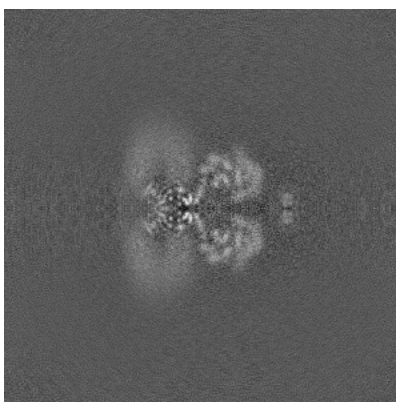


Z Index: 208

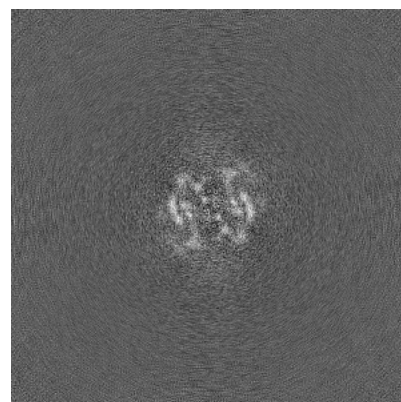
### 6.2.2 Raw map



X Index: 208



Y Index: 208

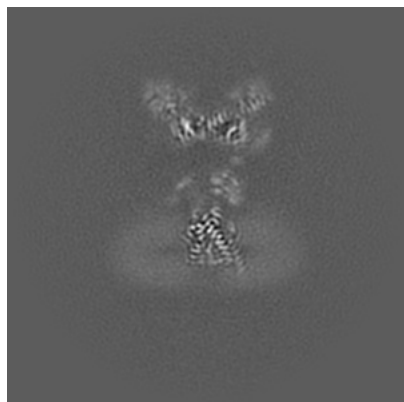


Z Index: 208

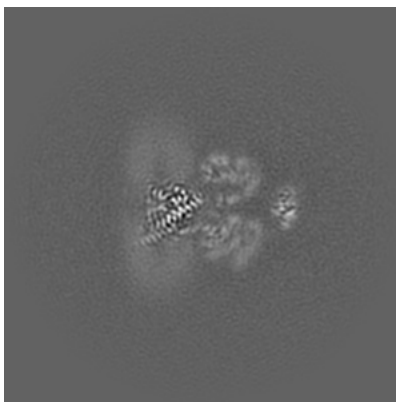
The images above show central slices of the map in three orthogonal directions.

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

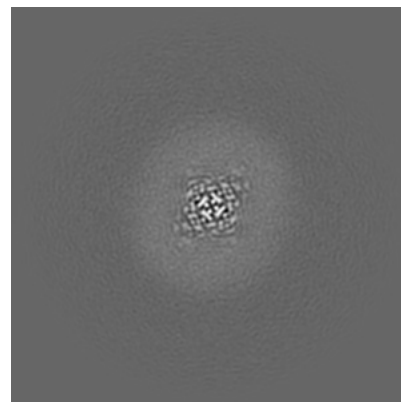
### 6.3.1 Primary map



X Index: 203

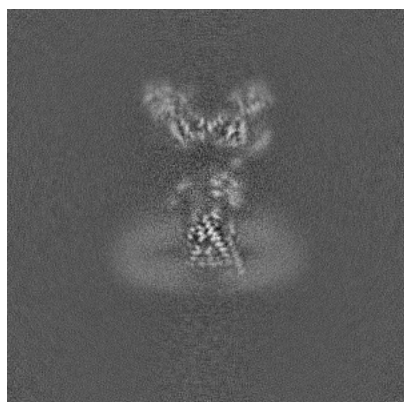


Y Index: 202

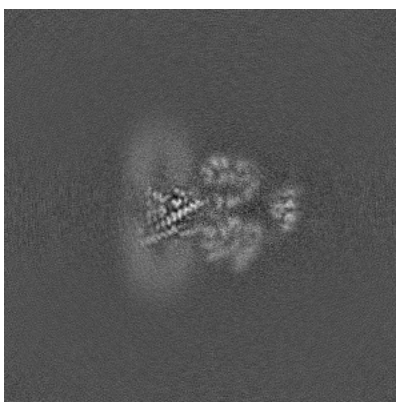


Z Index: 182

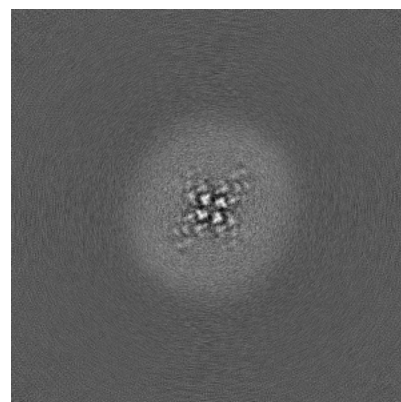
### 6.3.2 Raw map



X Index: 202



Y Index: 201

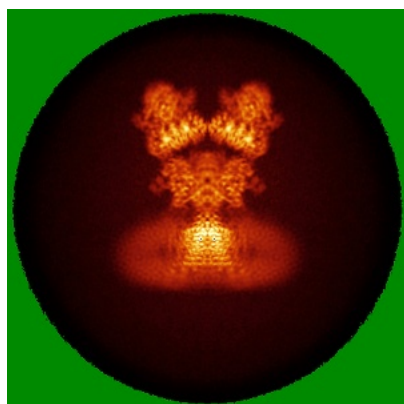


Z Index: 177

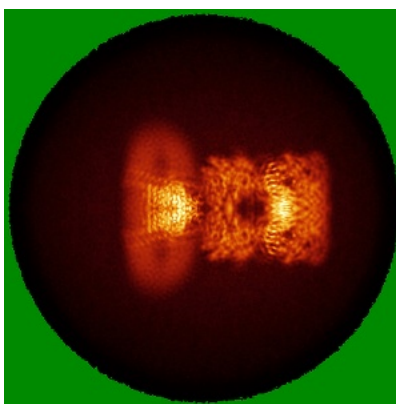
The images above show the largest variance slices of the map in three orthogonal directions.

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

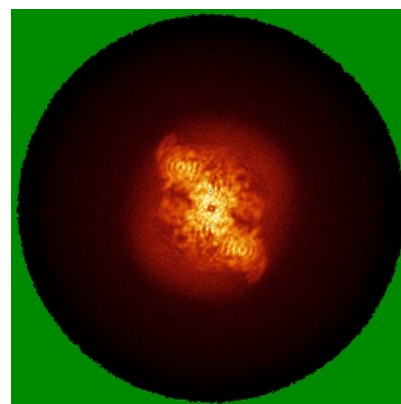
### 6.4.1 Primary map



X

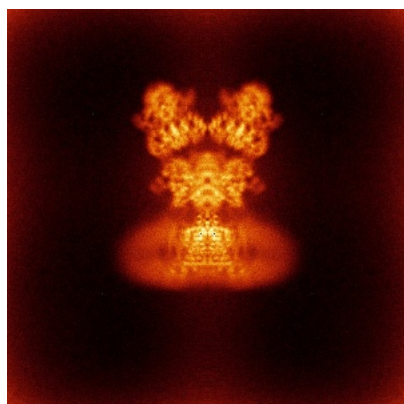


Y

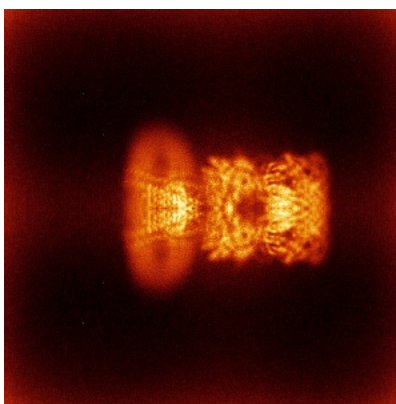


Z

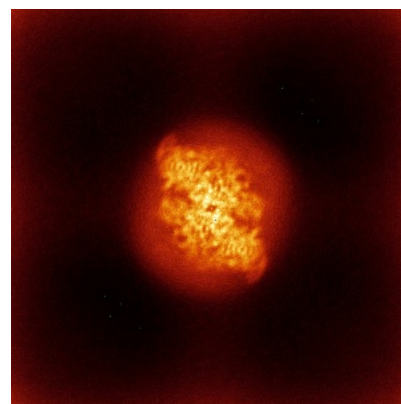
### 6.4.2 Raw map



X



Y

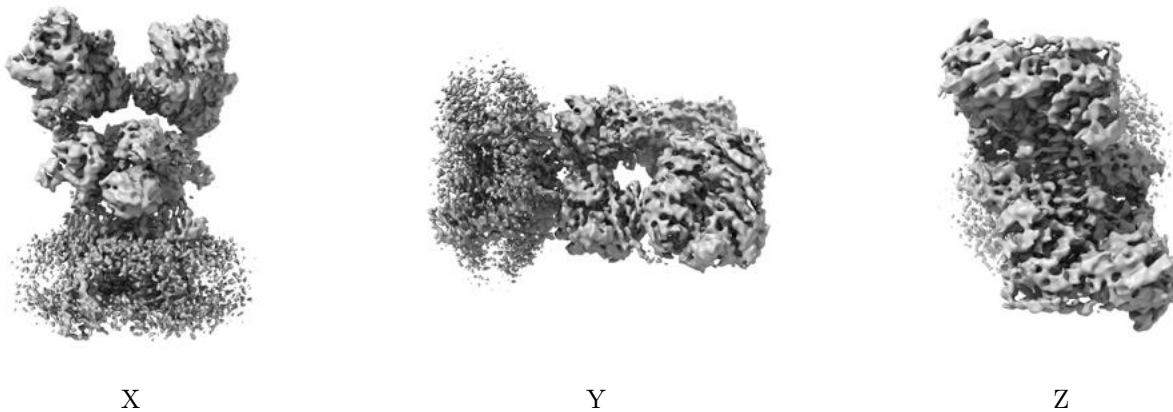


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

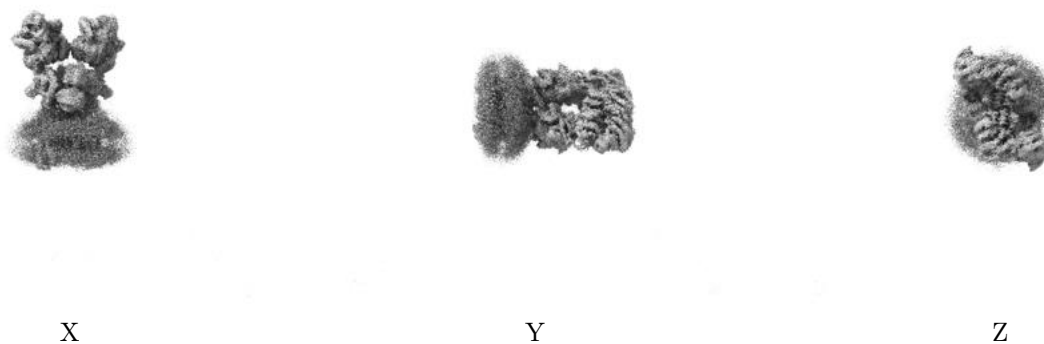
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.095. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

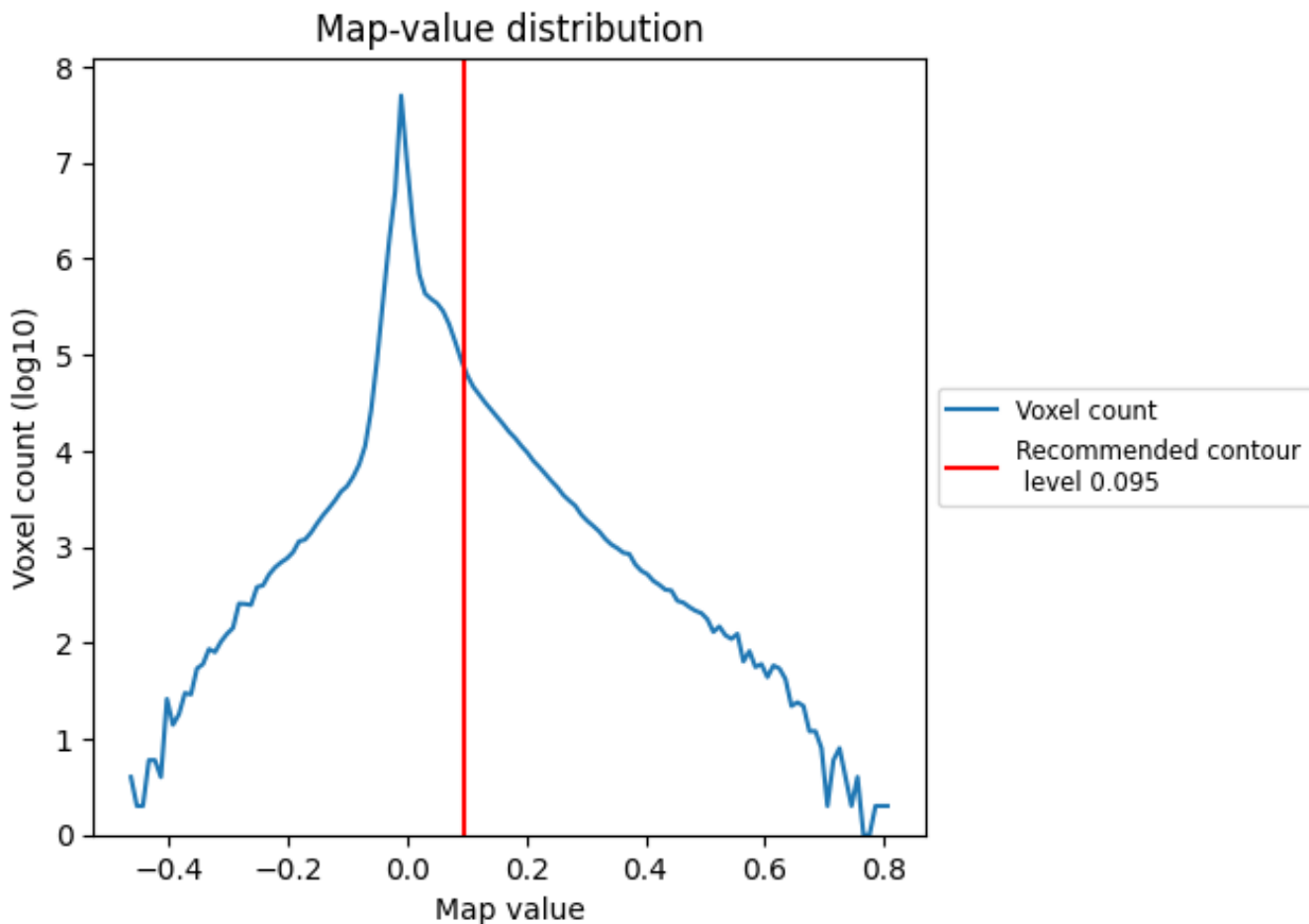
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

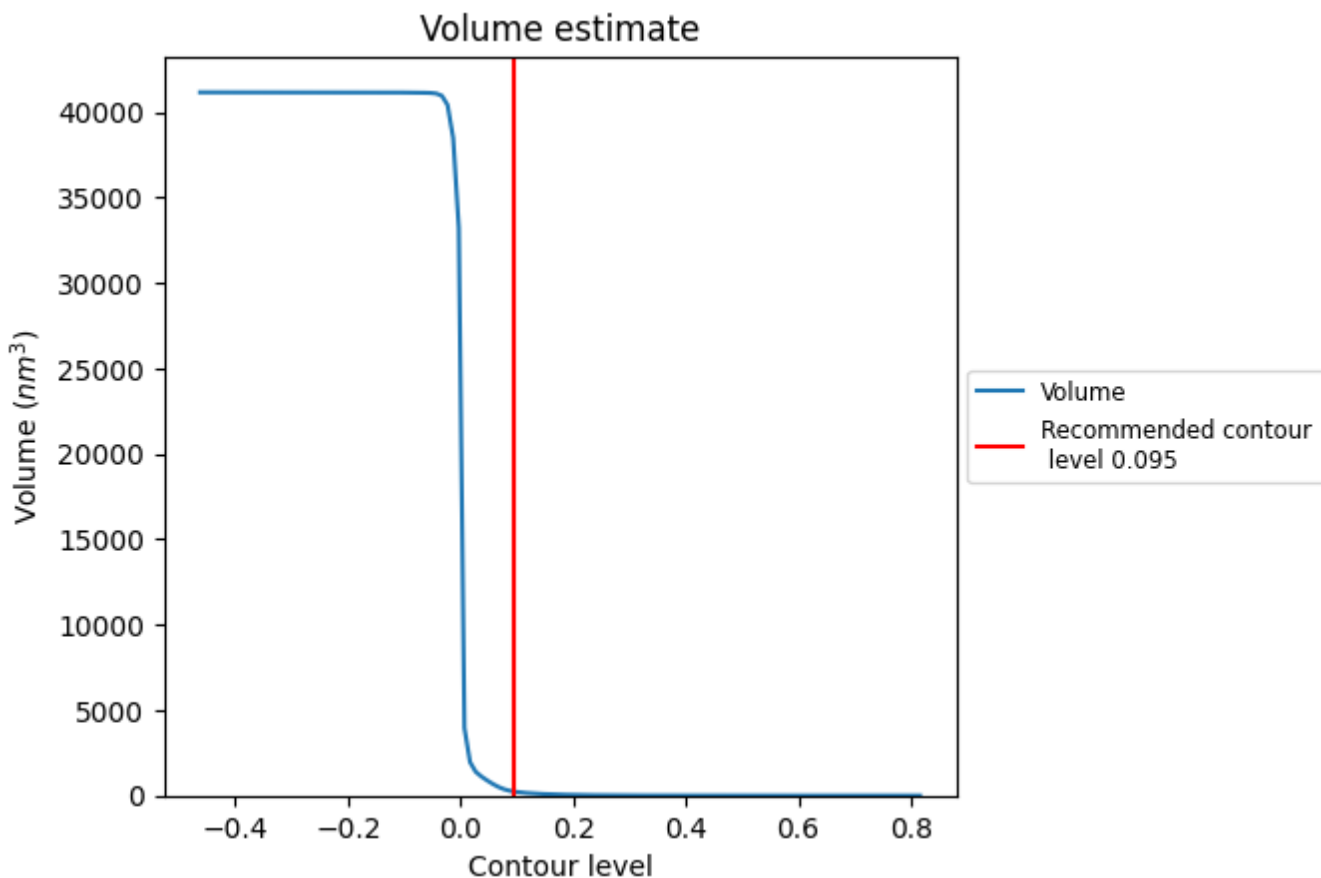
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

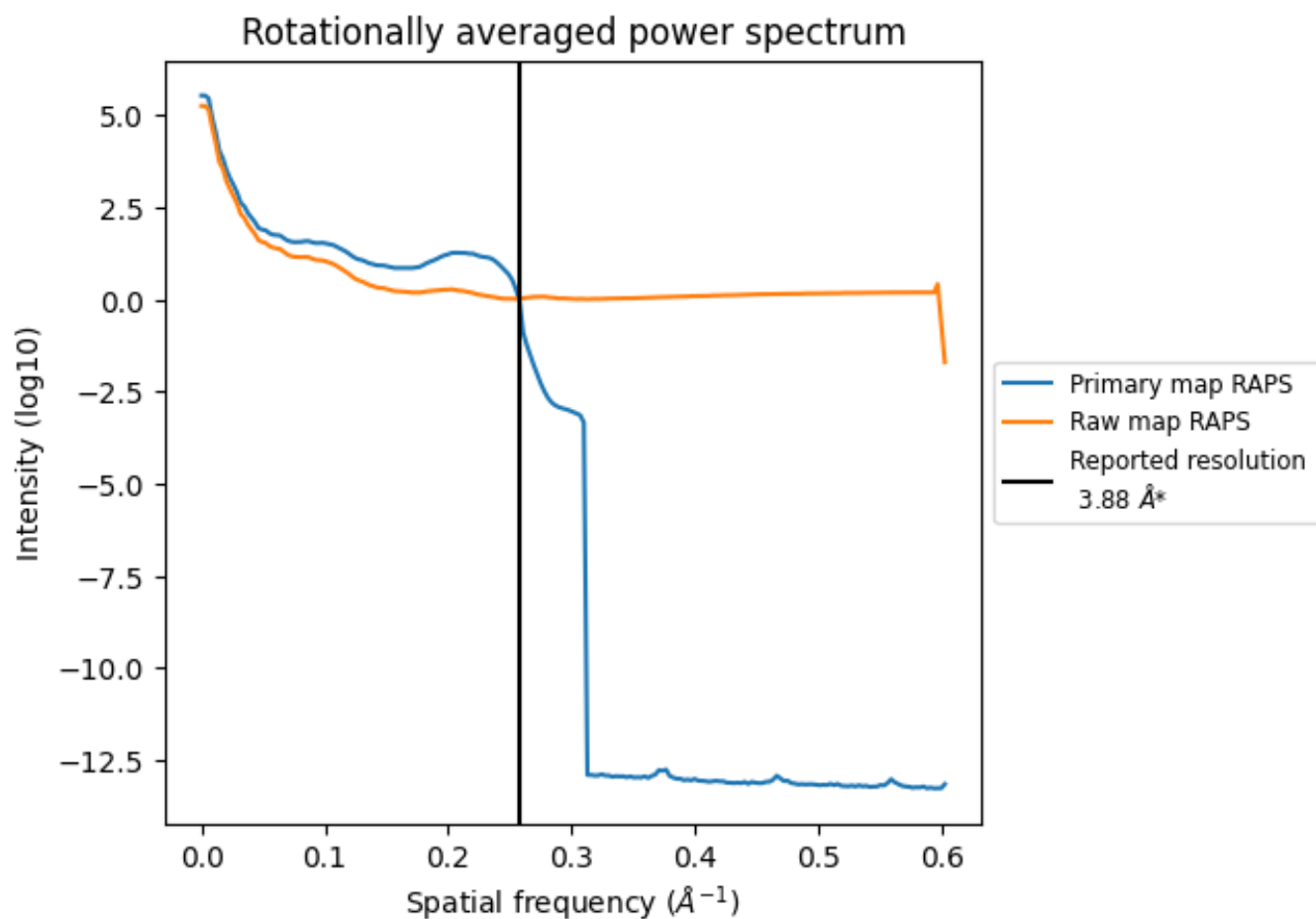
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 232 nm<sup>3</sup>; this corresponds to an approximate mass of 209 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)

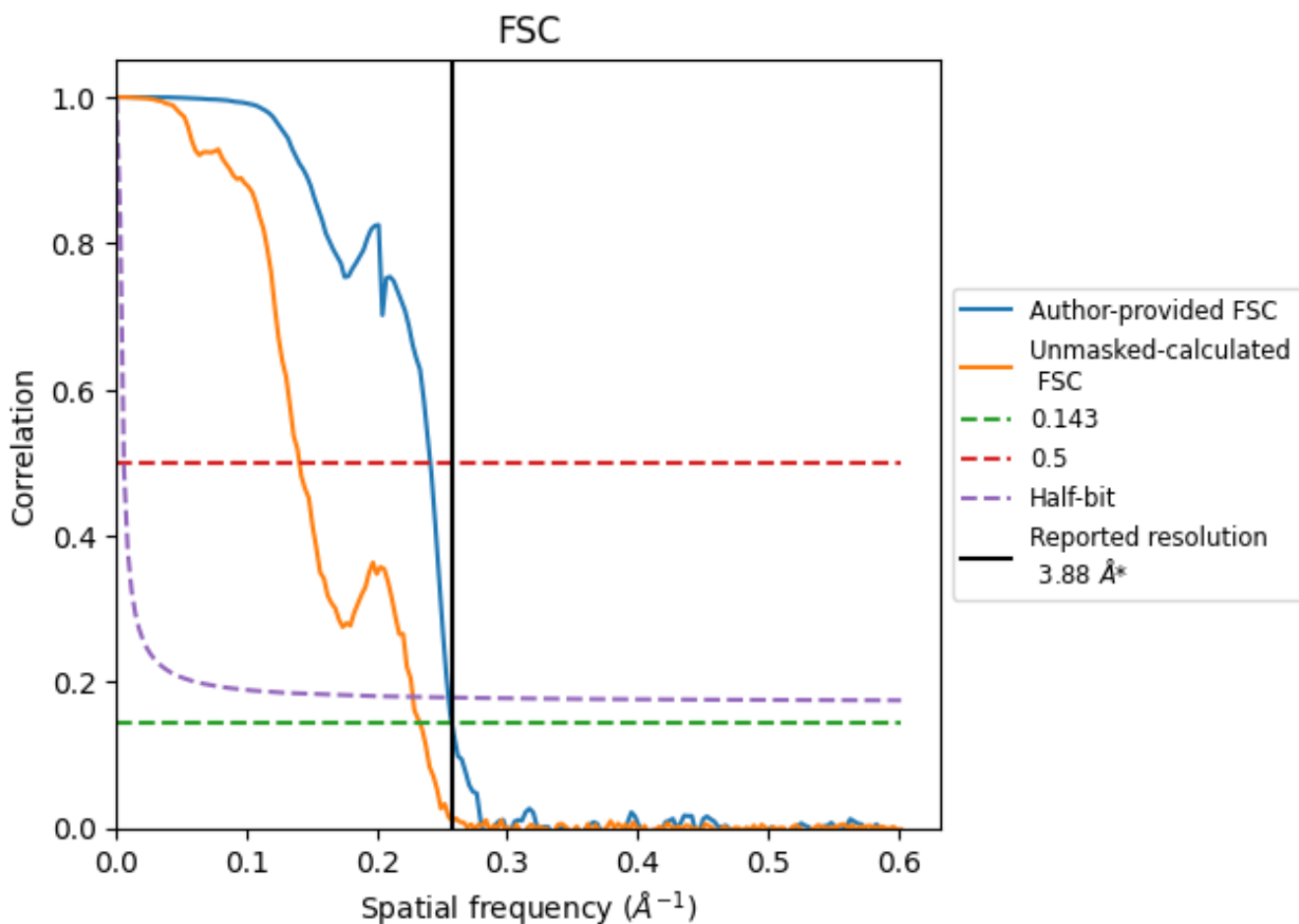


\*Reported resolution corresponds to spatial frequency of 0.258 Å<sup>-1</sup>

## 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 0.258 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

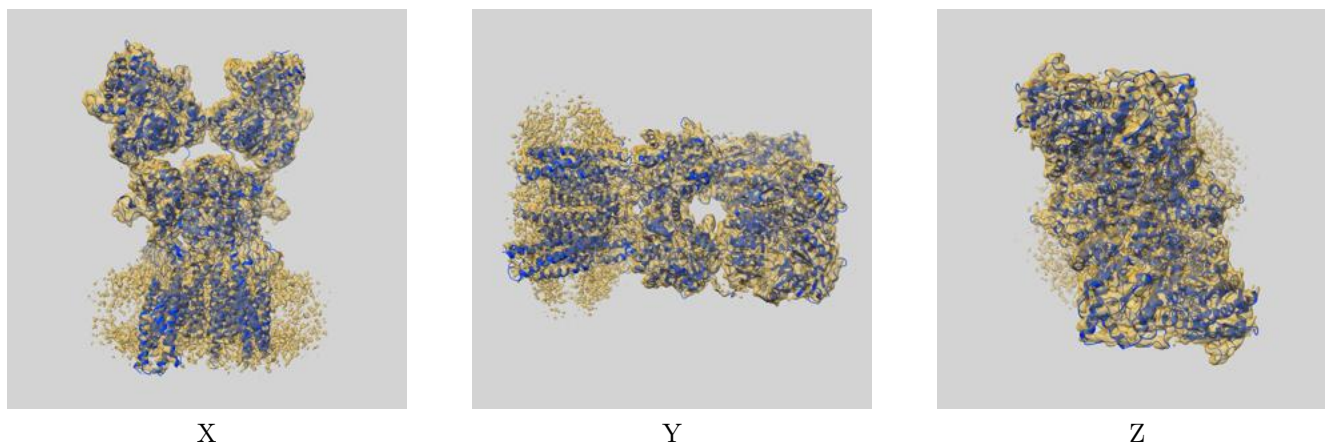
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.88	-	-
Author-provided FSC curve	3.88	4.15	3.92
Unmasked-calculated*	4.29	7.12	4.39

\*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 4.29 differs from the reported value 3.88 by more than 10 %

## 9 Map-model fit [i](#)

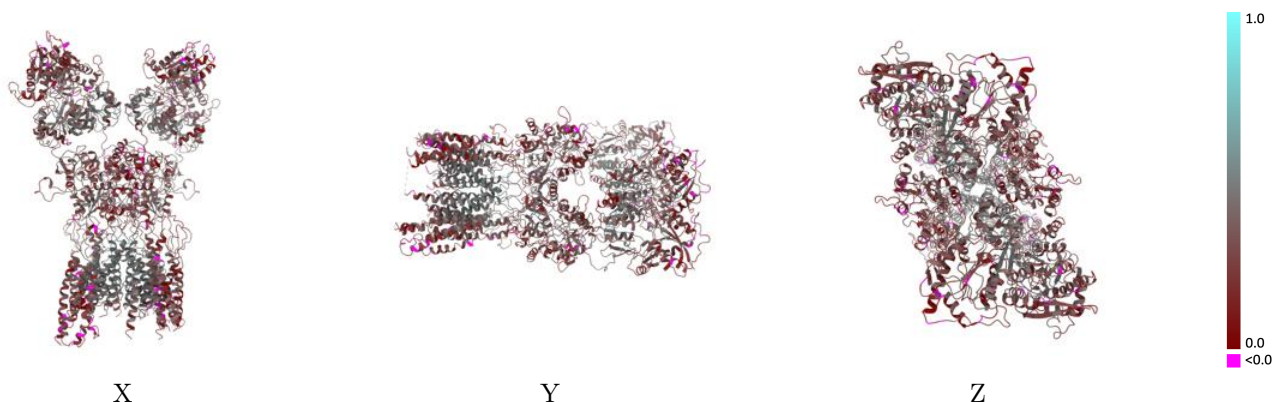
This section contains information regarding the fit between EMDB map EMD-40749 and PDB model 8SSA. Per-residue inclusion information can be found in section 3 on page 8.

### 9.1 Map-model overlay [i](#)



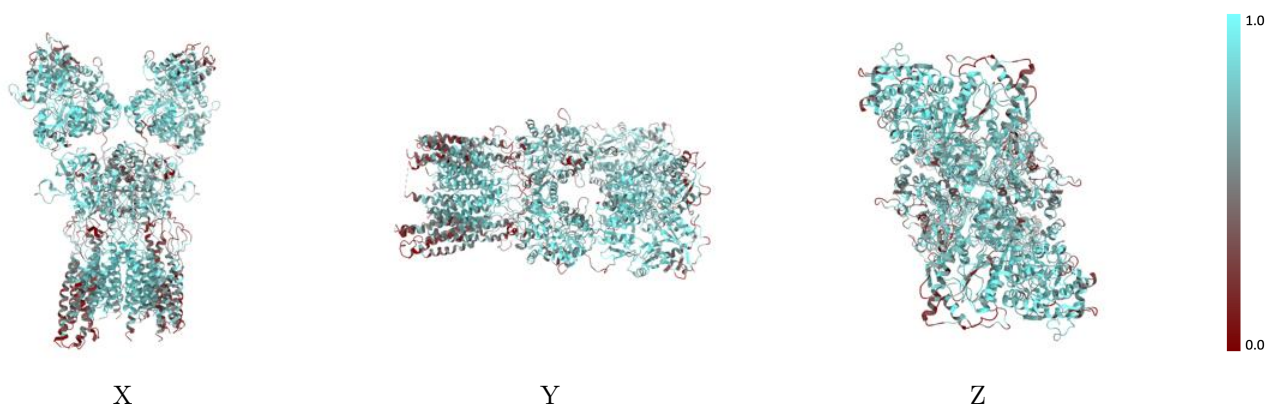
The images above show the 3D surface view of the map at the recommended contour level 0.095 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



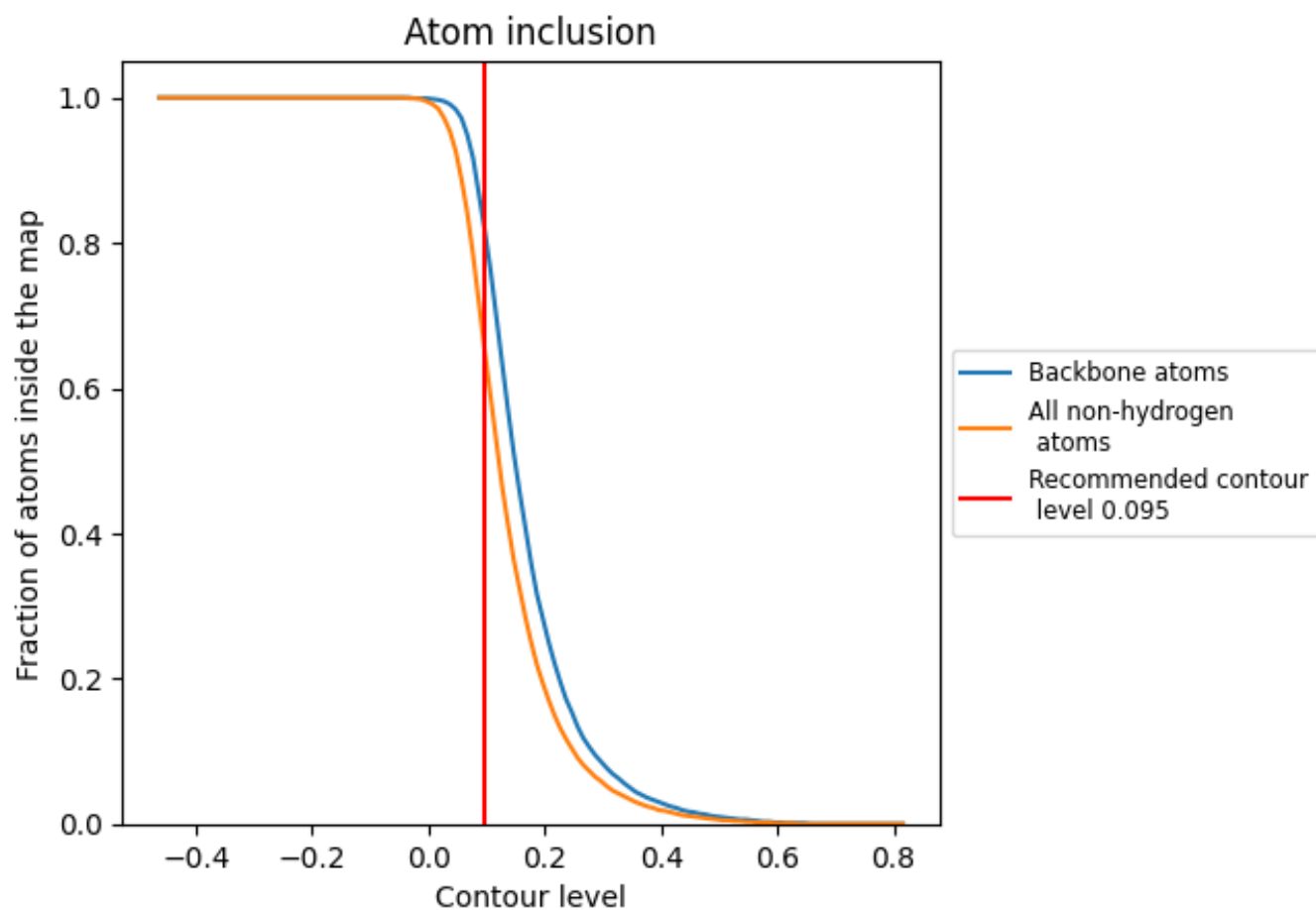
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.095).















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 66% of all non-hydrogen atoms, are inside the map.

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

The table lists the average atom inclusion at the recommended contour level (0.095) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6630	 0.3250
A	 0.6920	 0.3440
B	 0.6680	 0.3090
C	 0.6930	 0.3440
D	 0.6740	 0.3160
E	 0.4200	 0.2610
F	 0.4200	 0.2580

