



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 11:51 AM UTC

PDB ID : 7RQZ / pdb_00007rqz
EMDB ID : EMD-24641
Title : Cryo-EM structure of the full-length TRPV1 with RTx at 48 degrees Celsius, in an open state, class alpha
Authors : Kwon, D.H.; Suo, Y.; Lee, S.-Y.
Deposited on : 2021-08-08
Resolution : 3.32 Å(reported)
Based on initial model : 7LP9

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

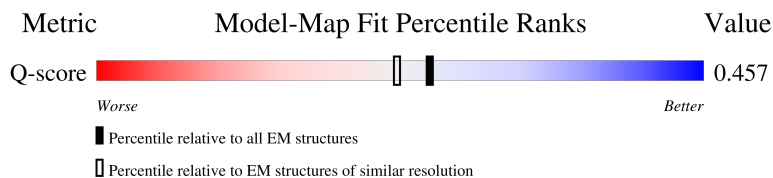
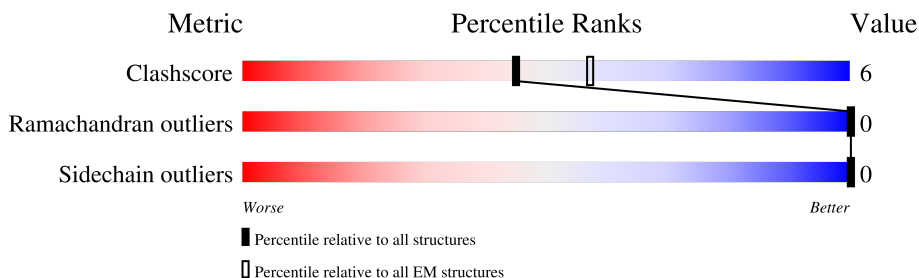
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.32 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	14518 (2.82 - 3.82)

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	868	26% 52% 9% 39%
1	B	868	26% 52% 9% 39%
1	C	868	26% 52% 9% 39%
1	D	868	26% 52% 9% 39%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 33596 atoms, of which 16464 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 Transient receptor potential cation channel subfamily V member 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	532	Total	C	H	N	O	S	0	0
			8007	2698	3902	654	731	22		
1	C	532	Total	C	H	N	O	S	0	0
			8007	2698	3902	654	731	22		
1	B	532	Total	C	H	N	O	S	0	0
			8007	2698	3902	654	731	22		
1	D	532	Total	C	H	N	O	S	0	0
			8007	2698	3902	654	731	22		

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	839	GLU	-	expression tag	UNP O35433
A	840	ASN	-	expression tag	UNP O35433
A	841	SER	-	expression tag	UNP O35433
A	842	LEU	-	expression tag	UNP O35433
A	843	GLU	-	expression tag	UNP O35433
A	844	VAL	-	expression tag	UNP O35433
A	845	LEU	-	expression tag	UNP O35433
A	846	PHE	-	expression tag	UNP O35433
A	847	GLN	-	expression tag	UNP O35433
A	848	GLY	-	expression tag	UNP O35433
A	849	PRO	-	expression tag	UNP O35433
A	850	ASP	-	expression tag	UNP O35433
A	851	TYR	-	expression tag	UNP O35433
A	852	LYS	-	expression tag	UNP O35433
A	853	ASP	-	expression tag	UNP O35433
A	854	ASP	-	expression tag	UNP O35433
A	855	ASP	-	expression tag	UNP O35433
A	856	ASP	-	expression tag	UNP O35433
A	857	LYS	-	expression tag	UNP O35433
A	858	ALA	-	expression tag	UNP O35433
A	859	HIS	-	expression tag	UNP O35433

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Chain	Residue	Modelled	Actual	Comment	Reference
A	860	HIS	-	expression tag	UNP O35433
A	861	HIS	-	expression tag	UNP O35433
A	862	HIS	-	expression tag	UNP O35433
A	863	HIS	-	expression tag	UNP O35433
A	864	HIS	-	expression tag	UNP O35433
A	865	HIS	-	expression tag	UNP O35433
A	866	HIS	-	expression tag	UNP O35433
A	867	HIS	-	expression tag	UNP O35433
A	868	HIS	-	expression tag	UNP O35433
C	839	GLU	-	expression tag	UNP O35433
C	840	ASN	-	expression tag	UNP O35433
C	841	SER	-	expression tag	UNP O35433
C	842	LEU	-	expression tag	UNP O35433
C	843	GLU	-	expression tag	UNP O35433
C	844	VAL	-	expression tag	UNP O35433
C	845	LEU	-	expression tag	UNP O35433
C	846	PHE	-	expression tag	UNP O35433
C	847	GLN	-	expression tag	UNP O35433
C	848	GLY	-	expression tag	UNP O35433
C	849	PRO	-	expression tag	UNP O35433
C	850	ASP	-	expression tag	UNP O35433
C	851	TYR	-	expression tag	UNP O35433
C	852	LYS	-	expression tag	UNP O35433
C	853	ASP	-	expression tag	UNP O35433
C	854	ASP	-	expression tag	UNP O35433
C	855	ASP	-	expression tag	UNP O35433
C	856	ASP	-	expression tag	UNP O35433
C	857	LYS	-	expression tag	UNP O35433
C	858	ALA	-	expression tag	UNP O35433
C	859	HIS	-	expression tag	UNP O35433
C	860	HIS	-	expression tag	UNP O35433
C	861	HIS	-	expression tag	UNP O35433
C	862	HIS	-	expression tag	UNP O35433
C	863	HIS	-	expression tag	UNP O35433
C	864	HIS	-	expression tag	UNP O35433
C	865	HIS	-	expression tag	UNP O35433
C	866	HIS	-	expression tag	UNP O35433
C	867	HIS	-	expression tag	UNP O35433
C	868	HIS	-	expression tag	UNP O35433
B	839	GLU	-	expression tag	UNP O35433
B	840	ASN	-	expression tag	UNP O35433
B	841	SER	-	expression tag	UNP O35433

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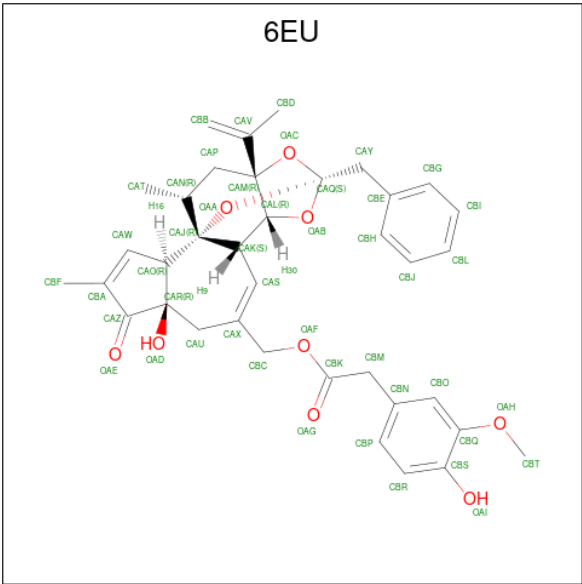
Chain	Residue	Modelled	Actual	Comment	Reference
B	842	LEU	-	expression tag	UNP O35433
B	843	GLU	-	expression tag	UNP O35433
B	844	VAL	-	expression tag	UNP O35433
B	845	LEU	-	expression tag	UNP O35433
B	846	PHE	-	expression tag	UNP O35433
B	847	GLN	-	expression tag	UNP O35433
B	848	GLY	-	expression tag	UNP O35433
B	849	PRO	-	expression tag	UNP O35433
B	850	ASP	-	expression tag	UNP O35433
B	851	TYR	-	expression tag	UNP O35433
B	852	LYS	-	expression tag	UNP O35433
B	853	ASP	-	expression tag	UNP O35433
B	854	ASP	-	expression tag	UNP O35433
B	855	ASP	-	expression tag	UNP O35433
B	856	ASP	-	expression tag	UNP O35433
B	857	LYS	-	expression tag	UNP O35433
B	858	ALA	-	expression tag	UNP O35433
B	859	HIS	-	expression tag	UNP O35433
B	860	HIS	-	expression tag	UNP O35433
B	861	HIS	-	expression tag	UNP O35433
B	862	HIS	-	expression tag	UNP O35433
B	863	HIS	-	expression tag	UNP O35433
B	864	HIS	-	expression tag	UNP O35433
B	865	HIS	-	expression tag	UNP O35433
B	866	HIS	-	expression tag	UNP O35433
B	867	HIS	-	expression tag	UNP O35433
B	868	HIS	-	expression tag	UNP O35433
D	839	GLU	-	expression tag	UNP O35433
D	840	ASN	-	expression tag	UNP O35433
D	841	SER	-	expression tag	UNP O35433
D	842	LEU	-	expression tag	UNP O35433
D	843	GLU	-	expression tag	UNP O35433
D	844	VAL	-	expression tag	UNP O35433
D	845	LEU	-	expression tag	UNP O35433
D	846	PHE	-	expression tag	UNP O35433
D	847	GLN	-	expression tag	UNP O35433
D	848	GLY	-	expression tag	UNP O35433
D	849	PRO	-	expression tag	UNP O35433
D	850	ASP	-	expression tag	UNP O35433
D	851	TYR	-	expression tag	UNP O35433
D	852	LYS	-	expression tag	UNP O35433
D	853	ASP	-	expression tag	UNP O35433

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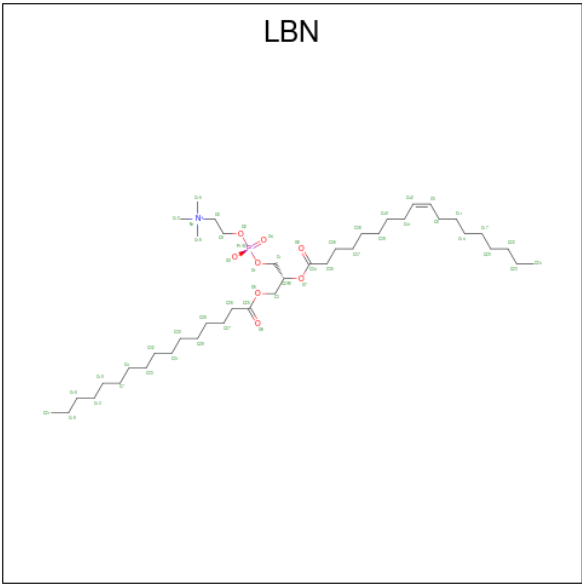
Chain	Residue	Modelled	Actual	Comment	Reference
D	854	ASP	-	expression tag	UNP O35433
D	855	ASP	-	expression tag	UNP O35433
D	856	ASP	-	expression tag	UNP O35433
D	857	LYS	-	expression tag	UNP O35433
D	858	ALA	-	expression tag	UNP O35433
D	859	HIS	-	expression tag	UNP O35433
D	860	HIS	-	expression tag	UNP O35433
D	861	HIS	-	expression tag	UNP O35433
D	862	HIS	-	expression tag	UNP O35433
D	863	HIS	-	expression tag	UNP O35433
D	864	HIS	-	expression tag	UNP O35433
D	865	HIS	-	expression tag	UNP O35433
D	866	HIS	-	expression tag	UNP O35433
D	867	HIS	-	expression tag	UNP O35433
D	868	HIS	-	expression tag	UNP O35433

- Molecule 2 is resiniferatoxin (CCD ID: 6EU) (formula: C₃₇H₄₀O₉).



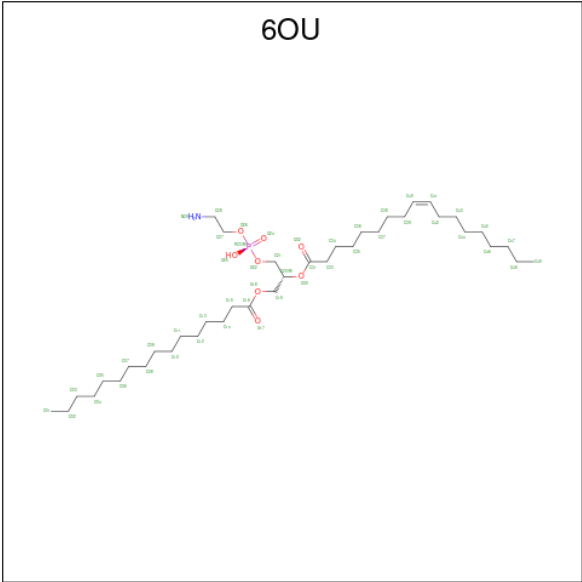
Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	H	O	0
			86	37	40	9	
2	C	1	Total	C	H	O	0
			86	37	40	9	
2	B	1	Total	C	H	O	0
			86	37	40	9	
2	D	1	Total	C	H	O	0
			86	37	40	9	

- Molecule 3 is 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (CCD ID: LBN) (formula: C₄₂H₈₂NO₈P).

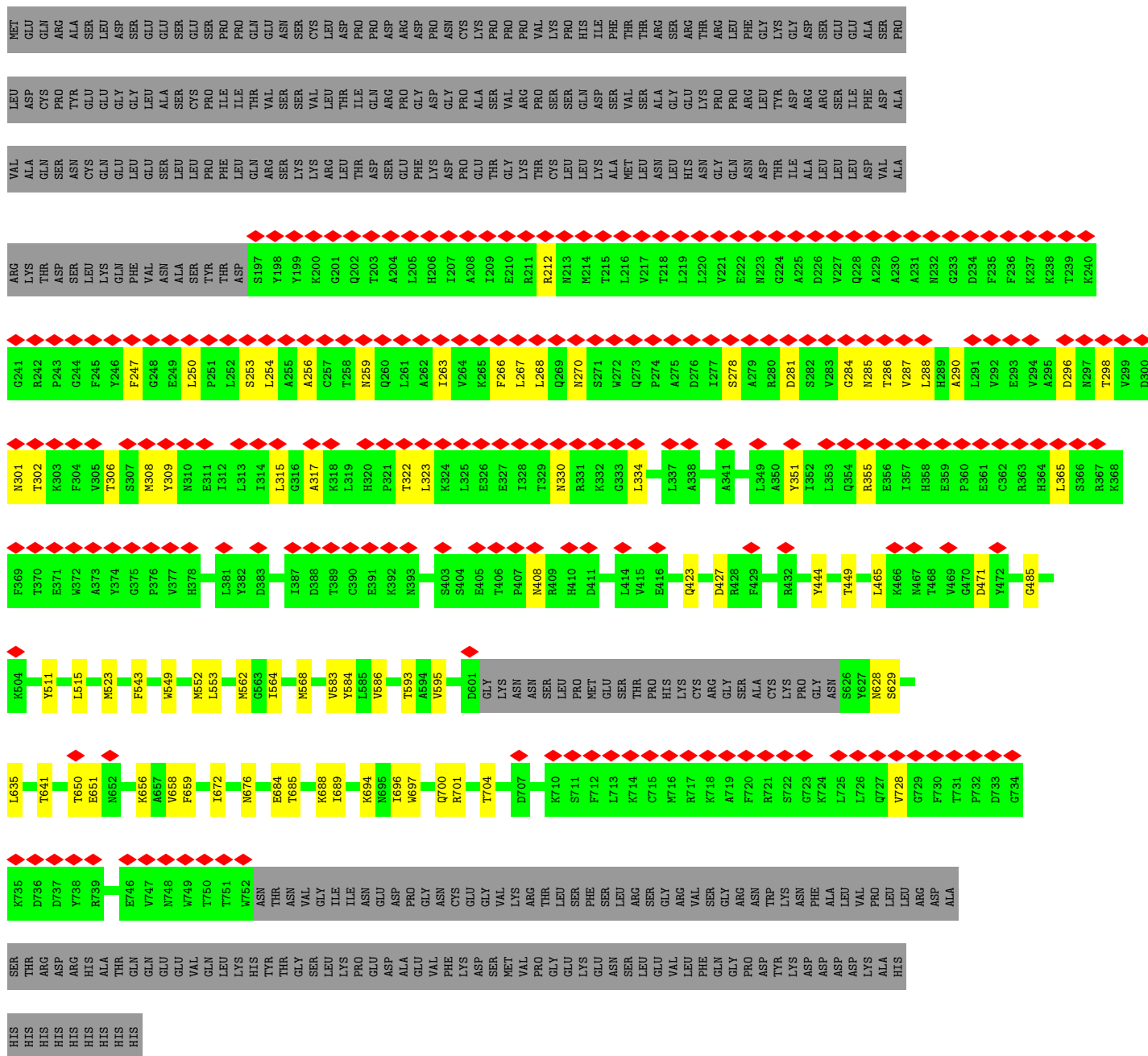
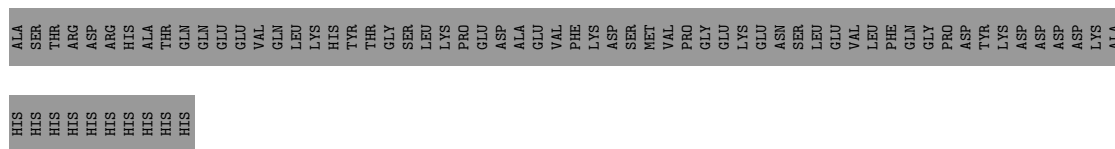


Mol	Chain	Residues	Atoms						AltConf
3	A	1	Total	C	H	N	O	P	0
			76	23	43	1	8	1	
3	A	1	Total	C	H	N	O	P	0
			101	32	59	1	8	1	
3	C	1	Total	C	H	N	O	P	0
			76	23	43	1	8	1	
3	C	1	Total	C	H	N	O	P	0
			101	32	59	1	8	1	
3	B	1	Total	C	H	N	O	P	0
			76	23	43	1	8	1	
3	B	1	Total	C	H	N	O	P	0
			101	32	59	1	8	1	
3	D	1	Total	C	H	N	O	P	0
			101	32	59	1	8	1	
3	D	1	Total	C	H	N	O	P	0
			76	23	43	1	8	1	

- Molecule 4 is [(2 {R})-1-[2-azanylethoxy(oxidanyl)phosphoryl]oxy-3-hexadecanoyloxy-prop an-2-yl] ({Z})-octadec-9-enoate (CCD ID: 6OU) (formula: C₃₉H₇₆NO₈P).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	H	O	P	0
			71	23	39	8	1	
4	A	1	Total	C	H	O		0
			58	21	33	4		
4	C	1	Total	C	H	O	P	0
			71	23	39	8	1	
4	C	1	Total	C	H	O		0
			58	21	33	4		
4	B	1	Total	C	H	O	P	0
			71	23	39	8	1	
4	B	1	Total	C	H	O		0
			58	21	33	4		
4	D	1	Total	C	H	O	P	0
			71	23	39	8	1	
4	D	1	Total	C	H	O		0
			58	21	33	4		



HIS HIS HIS HIS	ALA	THR	GLN	GLU	GLU	VAL	GLN	LEU	LYS	HIS	THR	ASN	THR	ASN	VAL	GLY	ILE	ILE	ASN	PRO	GLU	ASP	ASP	ALA	GLU	VAL	PHE	GLY	LYS	ASP	VAL	GLY	LEU	ASN	TRP	LYS	ASN	PHE	ALA	ASP	ASP	ASP	LYS	ALA	HIS	HIS	HIS	HIS												
	E746	V747	N748	N749	T750	T751	N752	ASN	THR	ASN	THR	ASN	VAL	GLY	ILE	ILE	ASN	GLU	GLU	ASP	PRO	GLY	GLY	LYS	LEU	ASN	ARG	GLY	VAL	LEU	GLY	ASN	ARG	TRP	LYS	ASN	PHE	ALA	LEU	VAL	PRO	LYS	ALA	HIS	HIS	HIS	HIS													
	N628	S629	L635	T641	T650	E651	N652	K656	A657	V658	F659	E684	K688	K694	N695	I696	W697	Q700	R701	D707	K710	S711	F712	L713	K714	C715	M716	R717	K718	A719	F720	R721	S722	K724	L725	L726	Q727	V728	G729	F730	T731	P732	D733	K735	D736	D737	Y738	R739												
	K504	S505	L506	S510	Y511	L515	M523	F543	M549	M552	L553	M562	G563	L564	M568	V583	Y584	L585	V586	T593	A594	V595	D601	GLY	LYS	ASN	ASN	SER	LEU	PRO	THR	LYS	HIS	LYS	CYS	ARG	GLY	SER	ALA	ALA	CYS	LYS	PRO	GLY	ASN	S626	V627													
ARG LYS THR ASP SER LEU LYS GLN PHE VAL ASN ALA SER TYR THR ASP	S197	Y198	Y199	K200	G201	Q202	T203	A204	L205	H206	I207	A208	I209	E210	R211	R212	N213	M214	T215	L216	V217	T218	L219	L220	V221	E222	N223	G224	A225	D226	V227	Q228	A229	A230	A231	N232	G233	D234	F235	F236	K237	K238	T239	K240																
	G241	R242	P243	G244	F245	Y246	F247	G248	E249	L250	P251	L252	S253	L254	A255	A256	C257	T258	N259	Q260	L261	A262	I263	V264	K265	F266	L267	L268	Q269	N270	S271	W272	Q273	P274	A275	D276	I277	S278	A279	R280	D281	S282	V283	G284	N285	T286	V287	L288	H289	A290	L291	V292	E293	V294	A295	D296	N297	T298	V299	D300
	N301	T302	K303	F304	V305	T306	S307	M308	Y309	N310	E311	I312	L313	I314	L315	G316	A317	K318	L319	H320	P321	T322	L323	K324	L325	E326	E327	I328	T329	N330	R331	K332	G333	L334	L337	A338	A341	L349	A350	Y351	I352	L353	Q354	R355	E356	I357	H358	E359	P360	E361	C362	R363	H364	L365	S366	R367	K368			
	F369	T370	E371	V372	A373	V374	G375	P376	V377	H378	L381	Y382	D383	I387	D388	T389	C390	E391	K392	N393	S403	S404	E405	T406	P407	N408	R409	H410	D411	L414	V415	E416	Q423	D427	R428	F429	R432	Y444	T449	L465	K466	N467	N469	G470	D471	Y472	G485													

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18341	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 ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.233	Depositor
Minimum map value	-0.160	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0353	Depositor
Map size (Å)	276.224, 276.224, 276.224	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.079, 1.079, 1.079	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: 6OU, 6EU, LBN

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	0.19	0/4203	0.29	0/5719
1	B	0.19	0/4203	0.29	0/5719
1	C	0.19	0/4203	0.29	0/5719
1	D	0.19	0/4203	0.29	0/5719
All	All	0.19	0/16812	0.29	0/22876

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4105	3902	3959	57	0
1	B	4105	3902	3959	56	0
1	C	4105	3902	3959	59	0
1	D	4105	3902	3959	57	0
2	A	46	40	0	1	0
2	B	46	40	0	1	0
2	C	46	40	0	1	0
2	D	46	40	0	1	0
3	A	75	102	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	75	102	0	0	0
3	C	75	102	0	0	0
3	D	75	102	0	0	0
4	A	57	72	0	1	0
4	B	57	72	0	1	0
4	C	57	72	0	1	0
4	D	57	72	0	1	0
All	All	17132	16464	15836	209	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.

The worst 5 of 209 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:C:423:GLN:NE2	1:C:427:ASP:OD2	2.07	0.87
1:B:423:GLN:NE2	1:B:427:ASP:OD2	2.07	0.87
1:A:423:GLN:NE2	1:A:427:ASP:OD2	2.07	0.87
1:D:423:GLN:NE2	1:D:427:ASP:OD2	2.07	0.86
1:A:449:THR:HG23	1:C:593:THR:HG21	1.61	0.83

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	528/868 (61%)	503 (95%)	25 (5%)	0	100	100
1	B	528/868 (61%)	503 (95%)	25 (5%)	0	100	100
1	C	528/868 (61%)	503 (95%)	25 (5%)	0	100	100
1	D	528/868 (61%)	502 (95%)	26 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2112/3472 (61%)	2011 (95%)	101 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	415/770 (54%)	415 (100%)	0	100	100
1	B	415/770 (54%)	415 (100%)	0	100	100
1	C	415/770 (54%)	415 (100%)	0	100	100
1	D	415/770 (54%)	415 (100%)	0	100	100
All	All	1660/3080 (54%)	1660 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	410	HIS
1	B	687	ASN
1	D	687	ASN
1	D	364	HIS
1	C	364	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

20 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	LBN	D	903	-	32,32,51	1.31	2 (6%)	38,40,59	0.97	1 (2%)
4	6OU	A	904	-	24,24,48	1.28	2 (8%)	26,26,53	0.84	1 (3%)
4	6OU	A	903	-	31,31,48	1.73	4 (12%)	34,36,53	0.93	2 (5%)
4	6OU	D	904	-	31,31,48	1.73	4 (12%)	34,36,53	0.93	2 (5%)
2	6EU	A	901	-	45,52,52	4.49	16 (35%)	44,83,83	2.03	9 (20%)
2	6EU	D	902	-	45,52,52	4.48	16 (35%)	44,83,83	2.03	9 (20%)
4	6OU	D	905	-	24,24,48	1.28	2 (8%)	26,26,53	0.84	1 (3%)
4	6OU	B	903	-	31,31,48	1.73	4 (12%)	34,36,53	0.93	2 (5%)
4	6OU	C	904	-	24,24,48	1.28	1 (4%)	26,26,53	0.85	1 (3%)
2	6EU	C	901	-	45,52,52	4.49	16 (35%)	44,83,83	2.03	9 (20%)
3	LBN	C	905	-	41,41,51	1.36	5 (12%)	47,49,59	0.91	2 (4%)
3	LBN	C	902	-	32,32,51	1.31	2 (6%)	38,40,59	0.97	1 (2%)
4	6OU	C	903	-	31,31,48	1.73	4 (12%)	34,36,53	0.93	2 (5%)
3	LBN	B	905	-	41,41,51	1.36	4 (9%)	47,49,59	0.91	2 (4%)
2	6EU	B	901	-	45,52,52	4.49	16 (35%)	44,83,83	2.02	9 (20%)
3	LBN	A	905	-	41,41,51	1.36	4 (9%)	47,49,59	0.91	2 (4%)
3	LBN	D	901	-	41,41,51	1.36	4 (9%)	47,49,59	0.91	2 (4%)
3	LBN	A	902	-	32,32,51	1.32	2 (6%)	38,40,59	0.97	1 (2%)
4	6OU	B	904	-	24,24,48	1.28	1 (4%)	26,26,53	0.85	1 (3%)
3	LBN	B	902	-	32,32,51	1.31	2 (6%)	38,40,59	0.97	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LBN	D	903	-	-	15/36/36/55	-
4	6OU	A	904	-	-	9/25/25/52	-
4	6OU	A	903	-	-	16/33/33/52	-
4	6OU	D	904	-	-	16/33/33/52	-
2	6EU	A	901	-	-	2/20/101/101	0/8/7/7
2	6EU	D	902	-	-	2/20/101/101	0/8/7/7
4	6OU	D	905	-	-	9/25/25/52	-
4	6OU	B	903	-	-	16/33/33/52	-
4	6OU	C	904	-	-	9/25/25/52	-
2	6EU	C	901	-	-	2/20/101/101	0/8/7/7
3	LBN	C	905	-	-	21/45/45/55	-
3	LBN	C	902	-	-	15/36/36/55	-
4	6OU	C	903	-	-	16/33/33/52	-
3	LBN	B	905	-	-	21/45/45/55	-
2	6EU	B	901	-	-	2/20/101/101	0/8/7/7
3	LBN	A	905	-	-	21/45/45/55	-
3	LBN	D	901	-	-	21/45/45/55	-
3	LBN	A	902	-	-	15/36/36/55	-
4	6OU	B	904	-	-	9/25/25/52	-
3	LBN	B	902	-	-	15/36/36/55	-

The worst 5 of 111 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	6EU	CAS-CAX	17.93	1.61	1.33
2	A	901	6EU	CAS-CAX	17.92	1.61	1.33
2	C	901	6EU	CAS-CAX	17.92	1.61	1.33
2	D	902	6EU	CAS-CAX	17.87	1.61	1.33
2	D	902	6EU	OAB-CAL	-10.84	1.27	1.43

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	6EU	CBD-CAV-CAM	-8.01	97.22	116.79
2	A	901	6EU	CBD-CAV-CAM	-8.00	97.23	116.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	902	6EU	CBD-CAV-CAM	-8.00	97.23	116.79
2	C	901	6EU	CBD-CAV-CAM	-8.00	97.25	116.79
2	D	902	6EU	OAF-CBK-CBM	5.41	119.66	111.21

There are no chirality outliers.

5 of 252 torsion outliers are listed below:

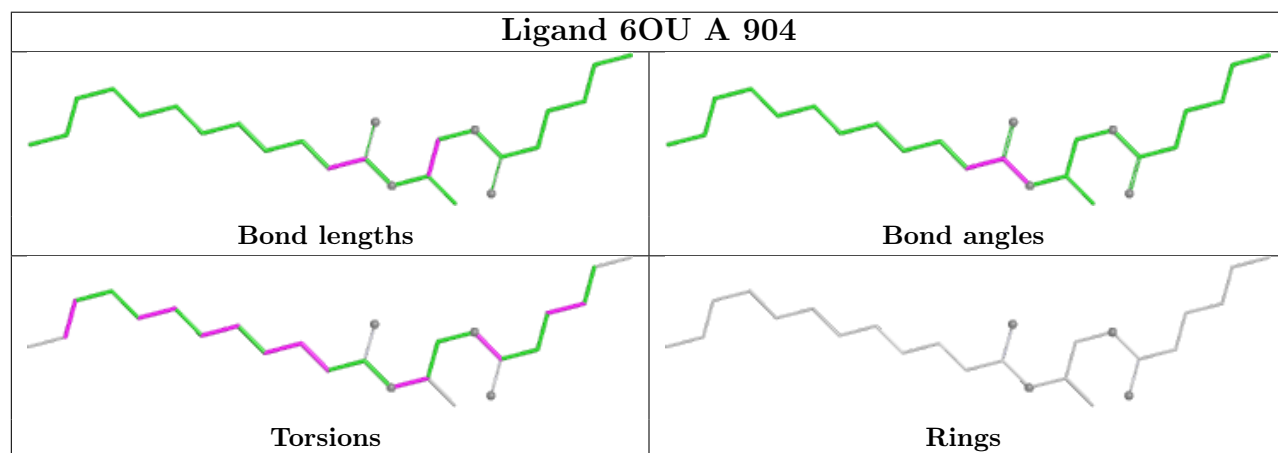
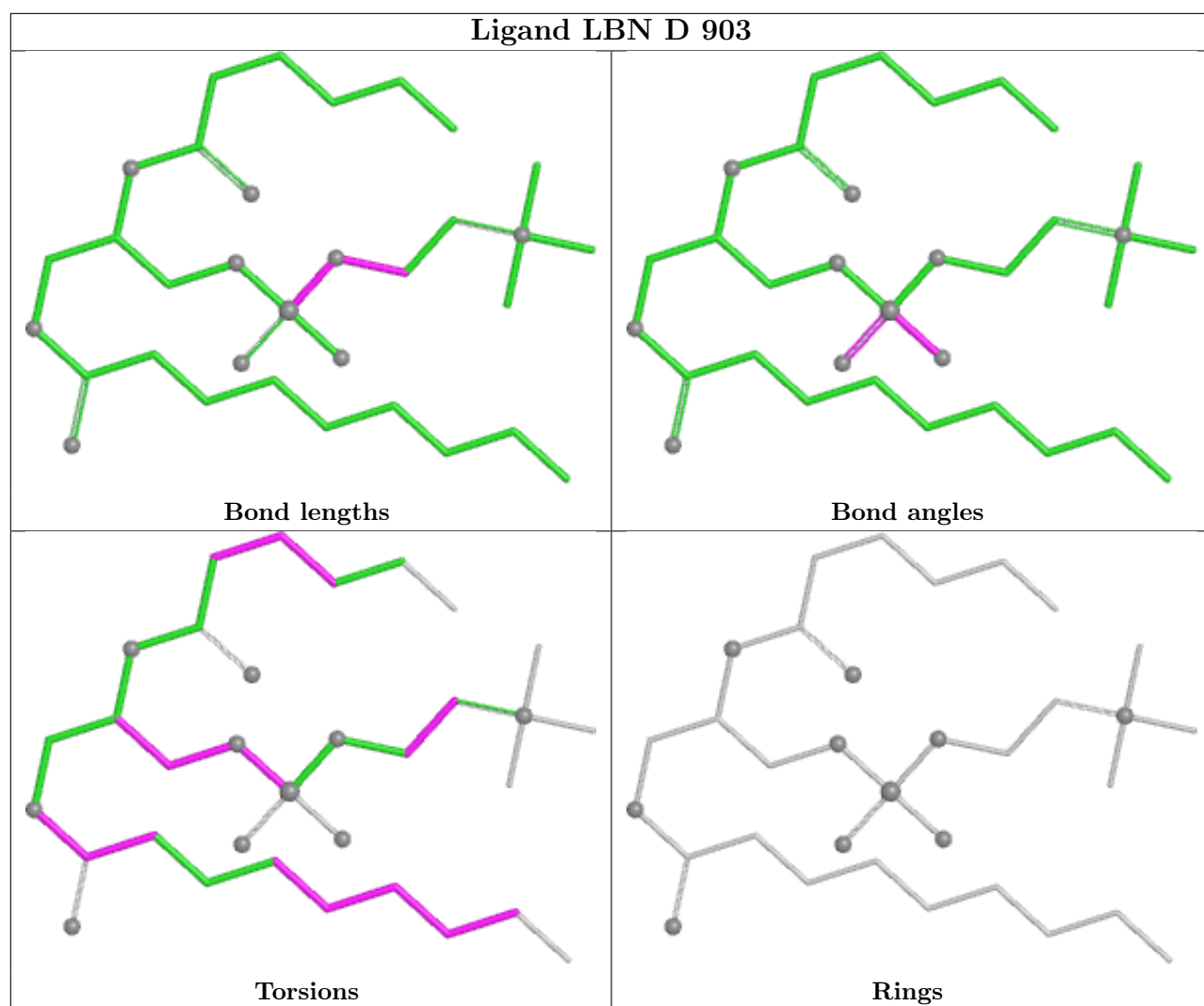
Mol	Chain	Res	Type	Atoms
3	A	902	LBN	N1-C6-C9-O2
3	A	905	LBN	C2-C1-O1-P1
3	A	905	LBN	C1-O1-P1-O2
3	A	905	LBN	C1-O1-P1-O3
3	A	905	LBN	C9-O2-P1-O1

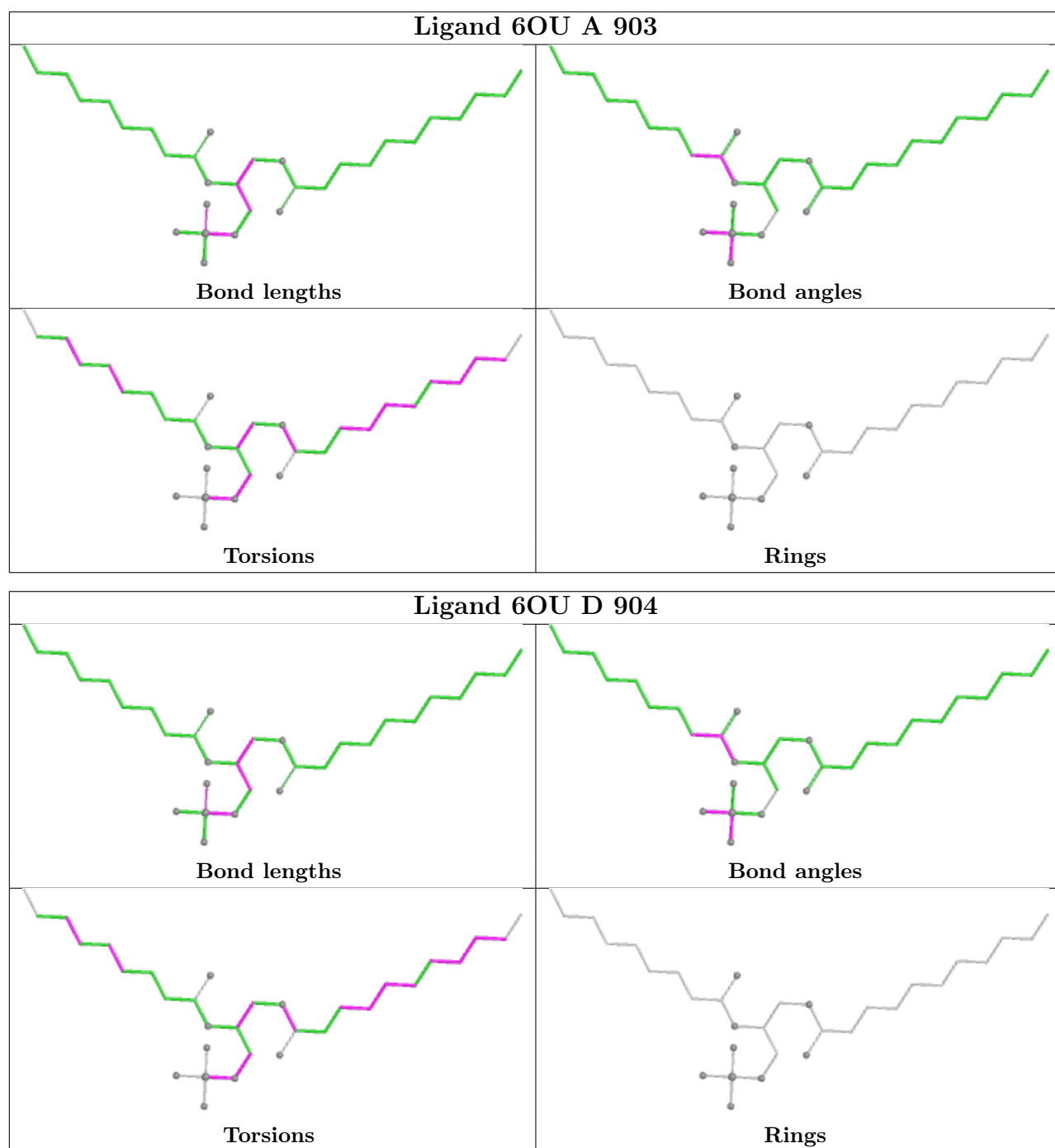
There are no ring outliers.

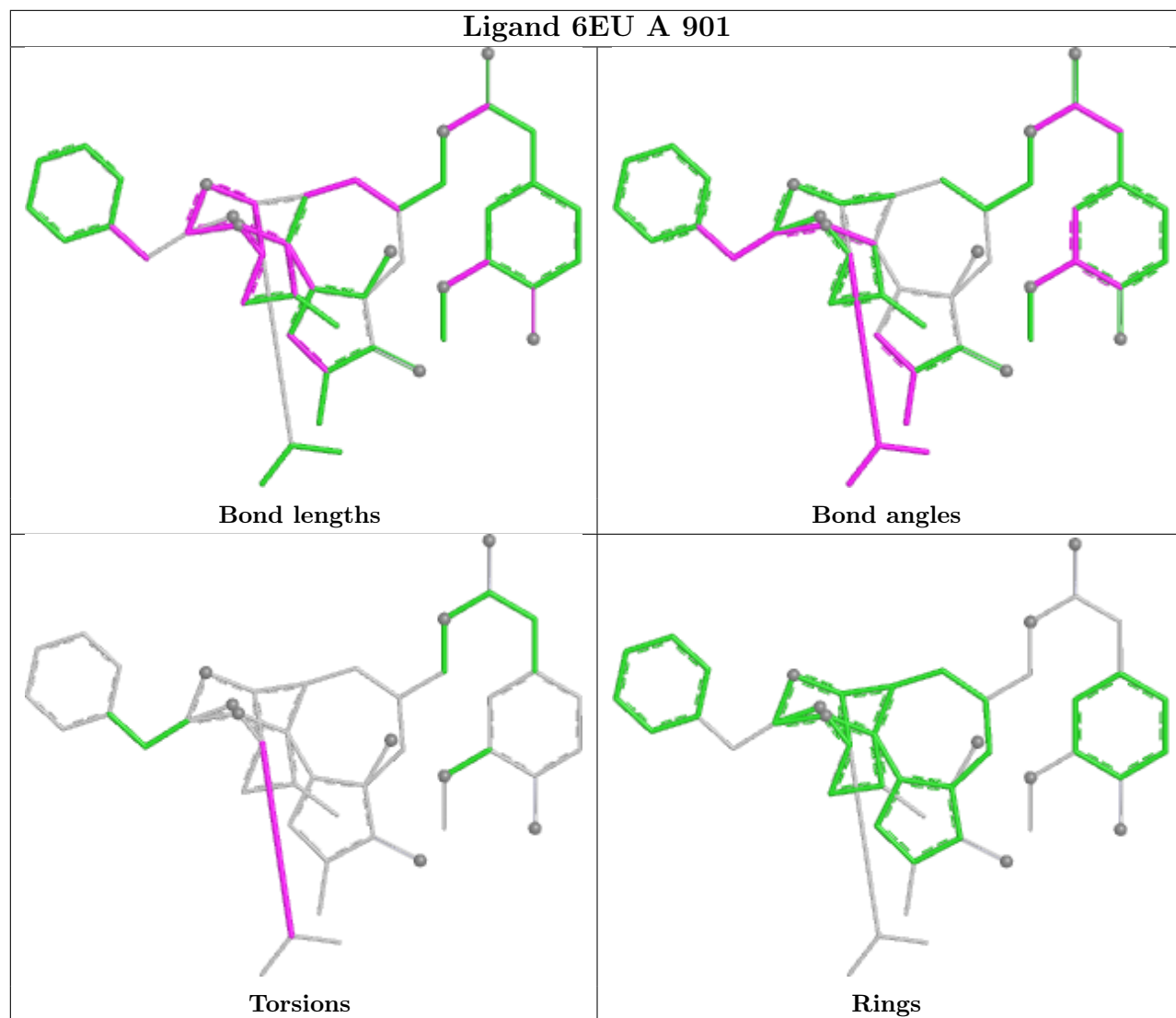
8 monomers are involved in 8 short contacts:

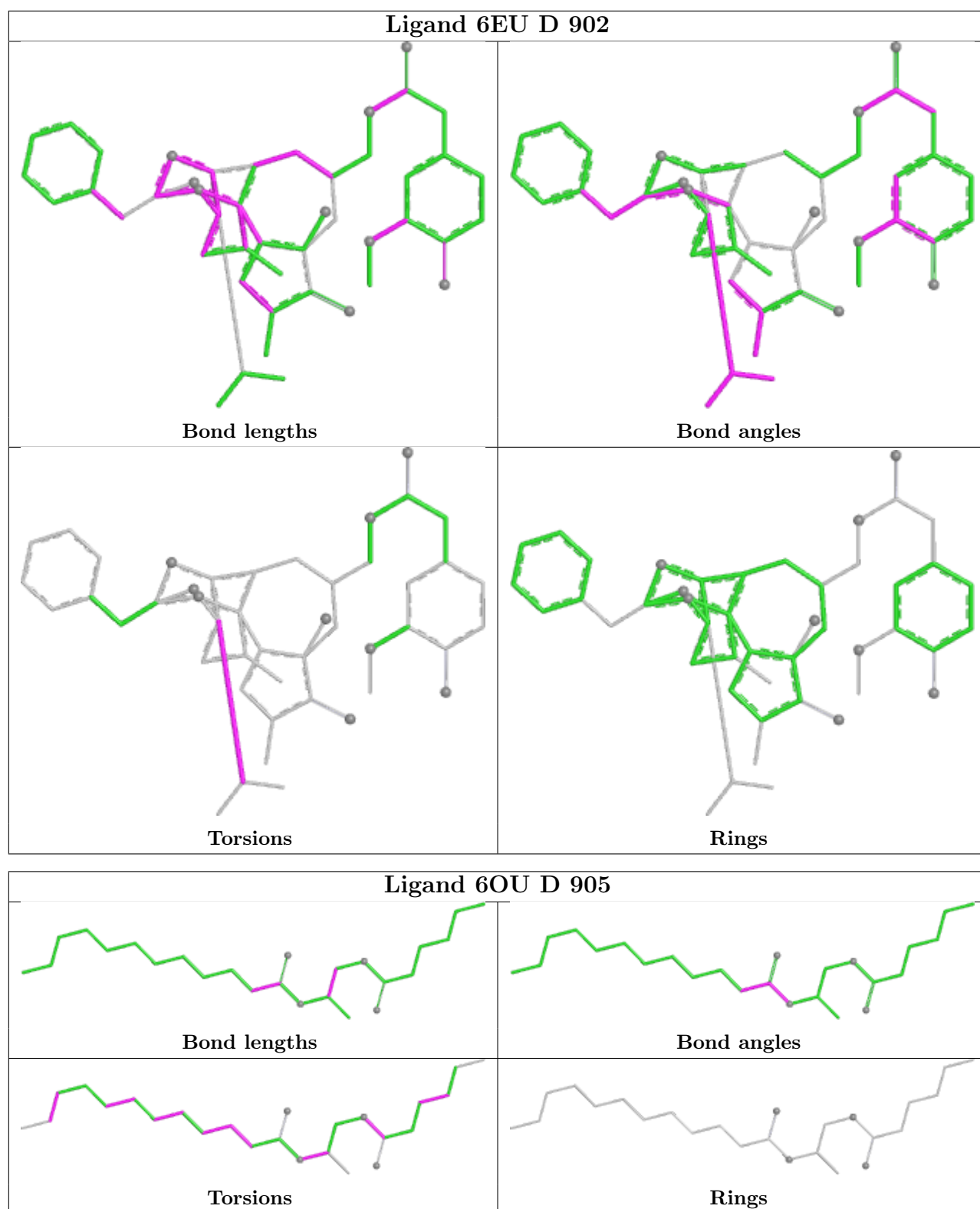
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	903	6OU	1	0
4	D	904	6OU	1	0
2	A	901	6EU	1	0
2	D	902	6EU	1	0
4	B	903	6OU	1	0
2	C	901	6EU	1	0
4	C	903	6OU	1	0
2	B	901	6EU	1	0

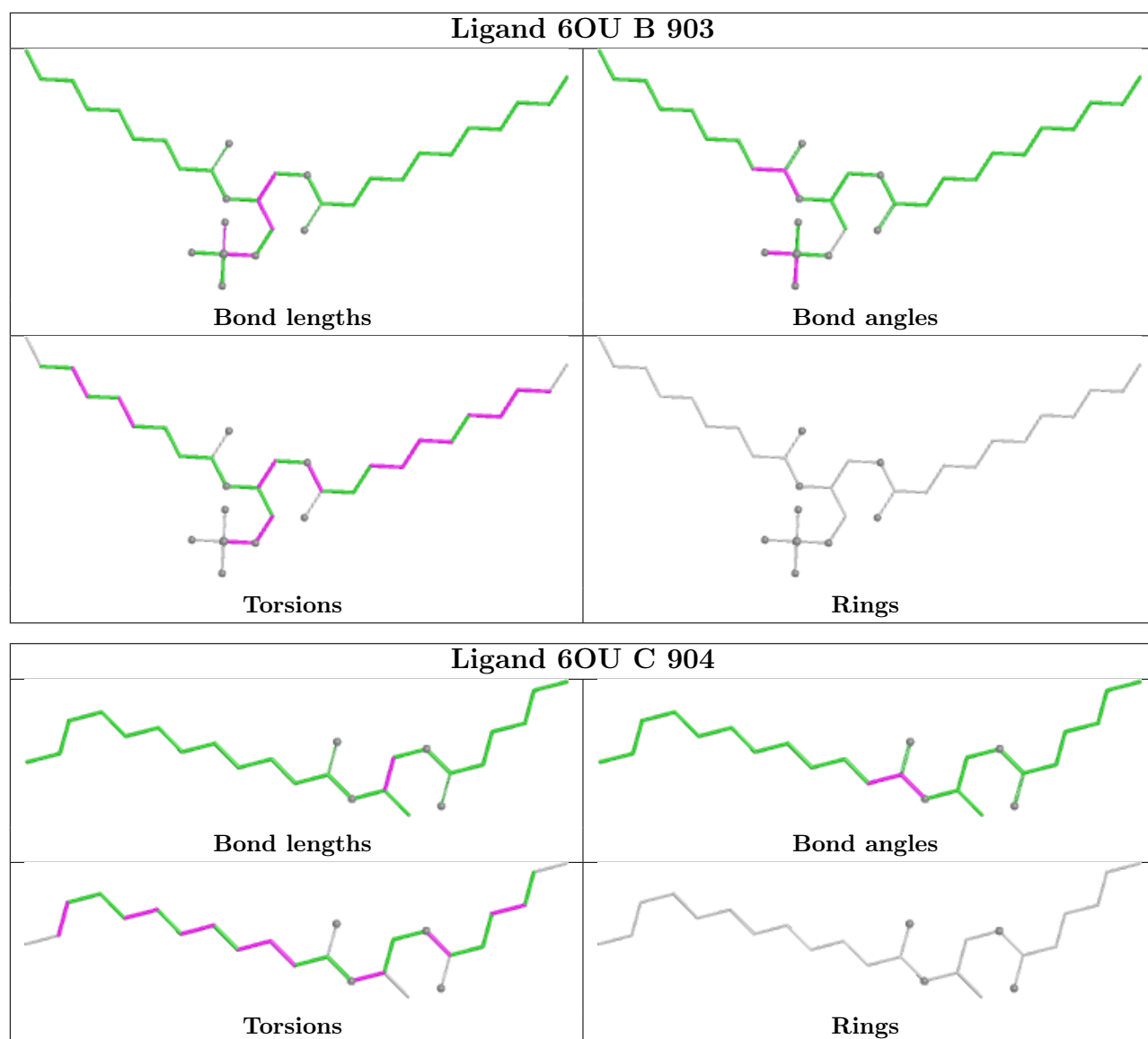
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

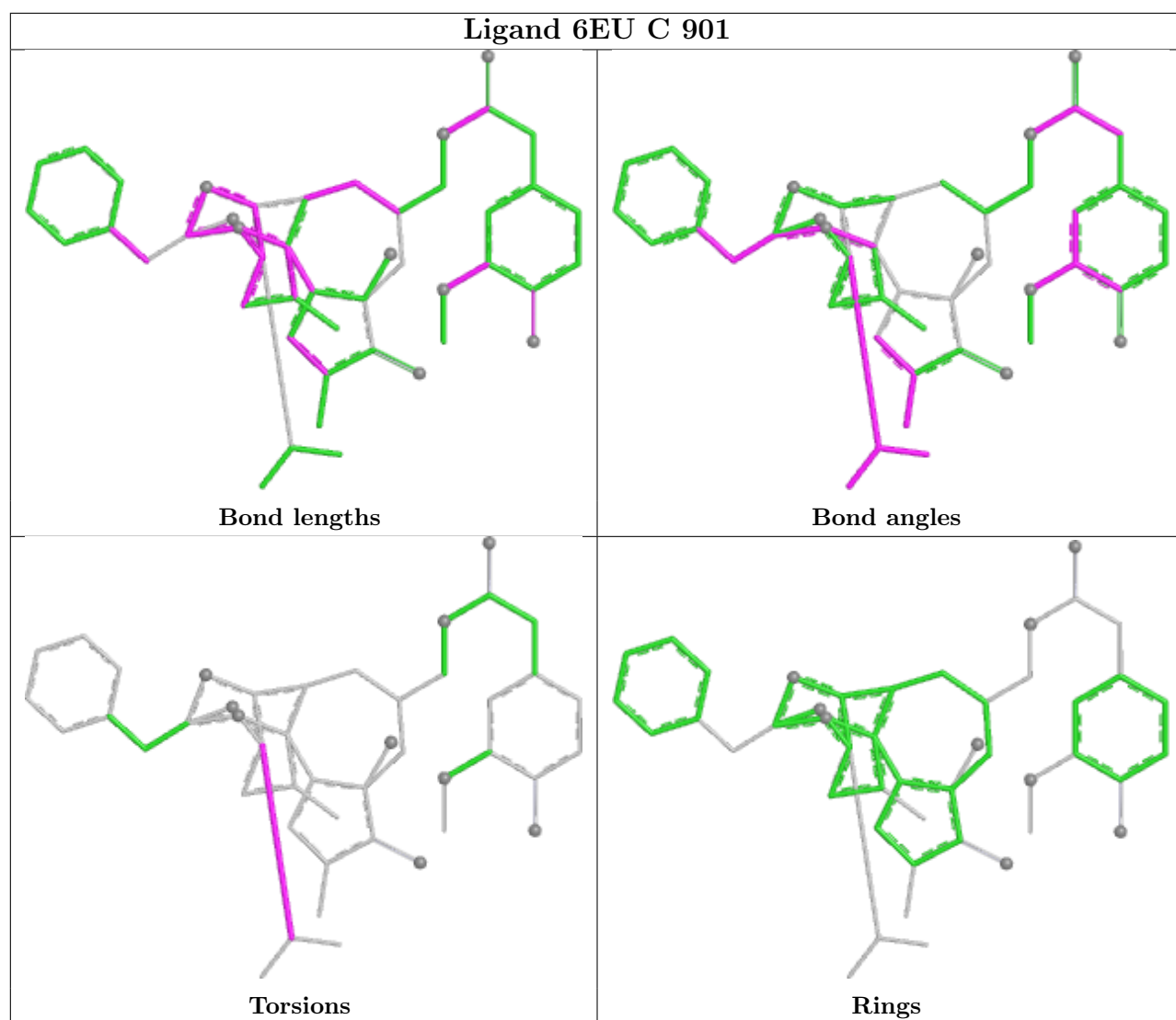


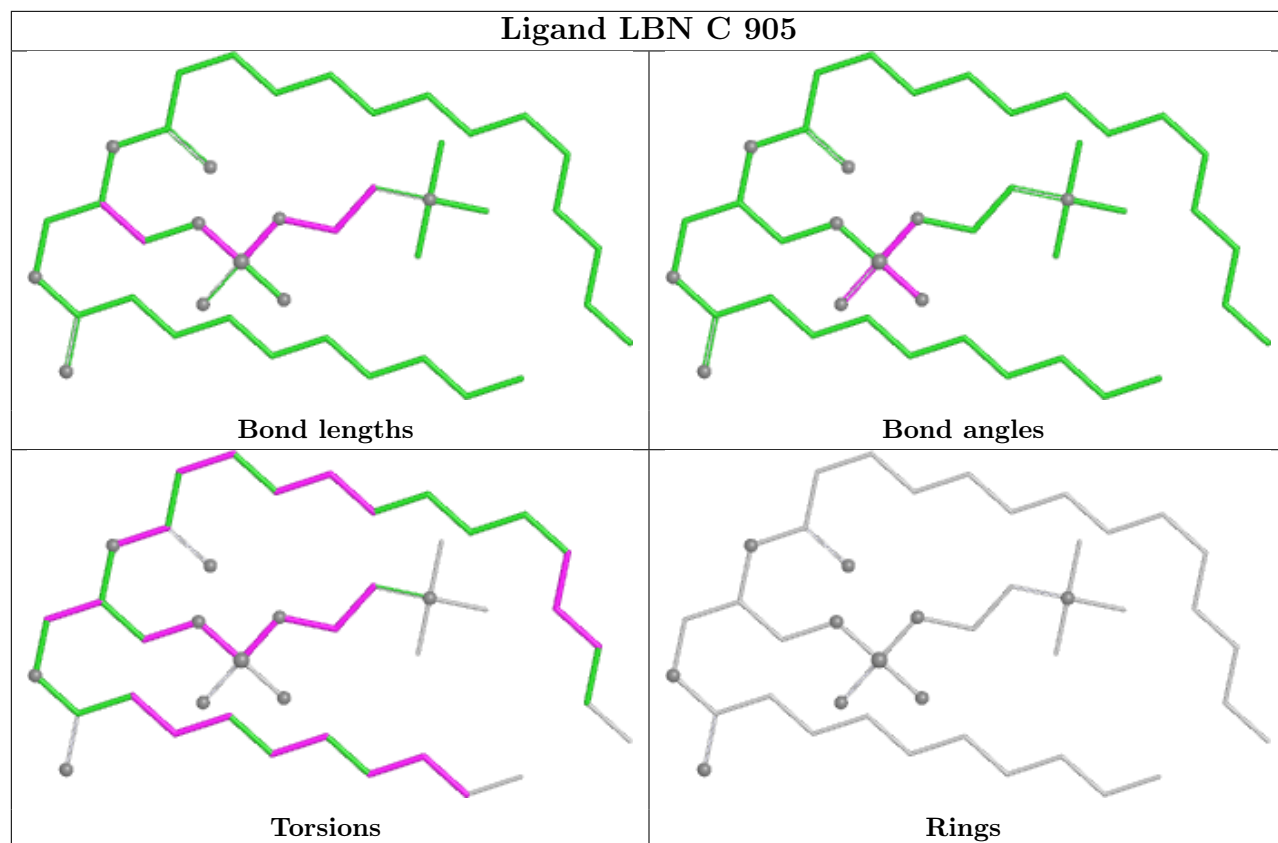


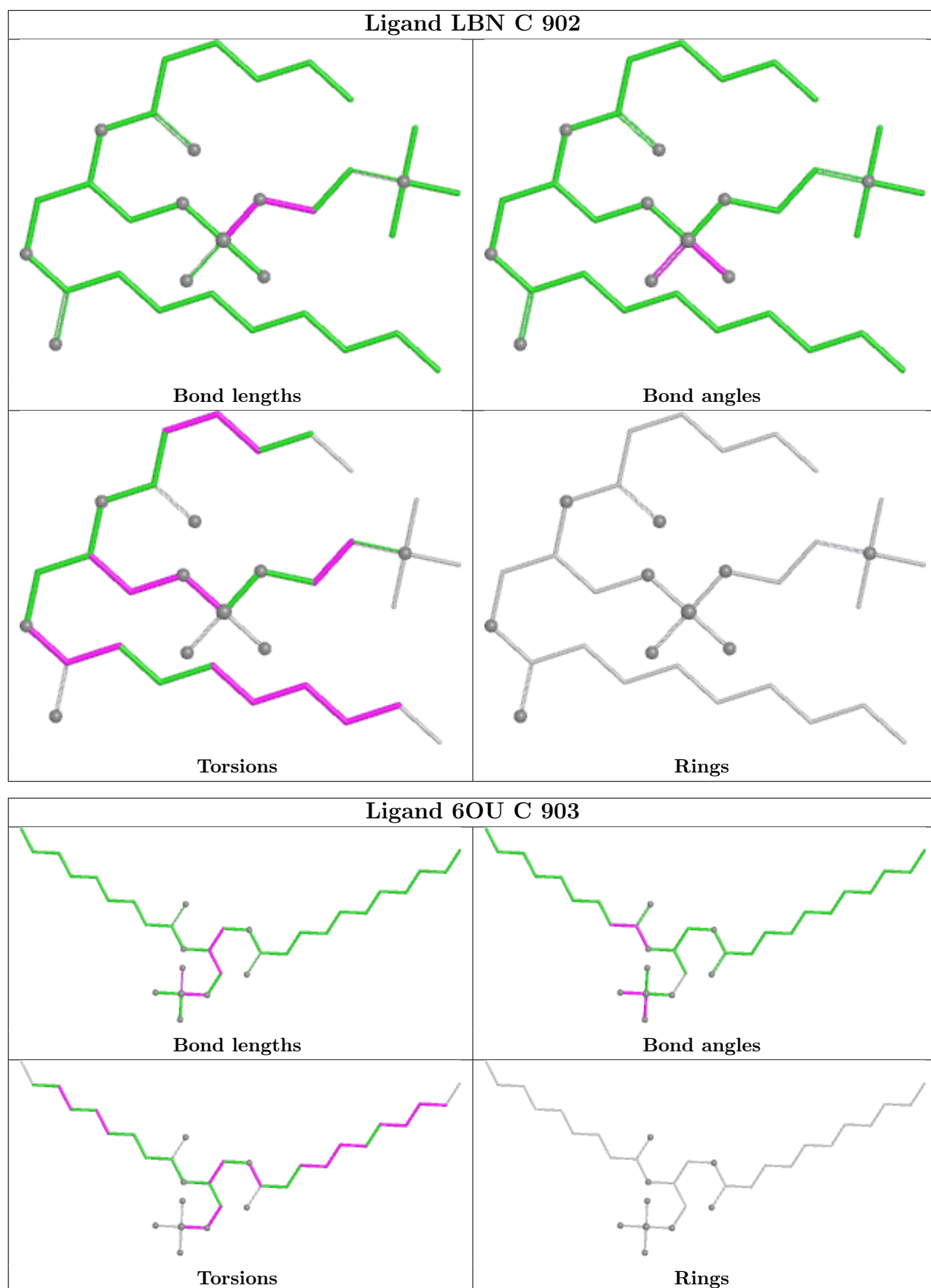


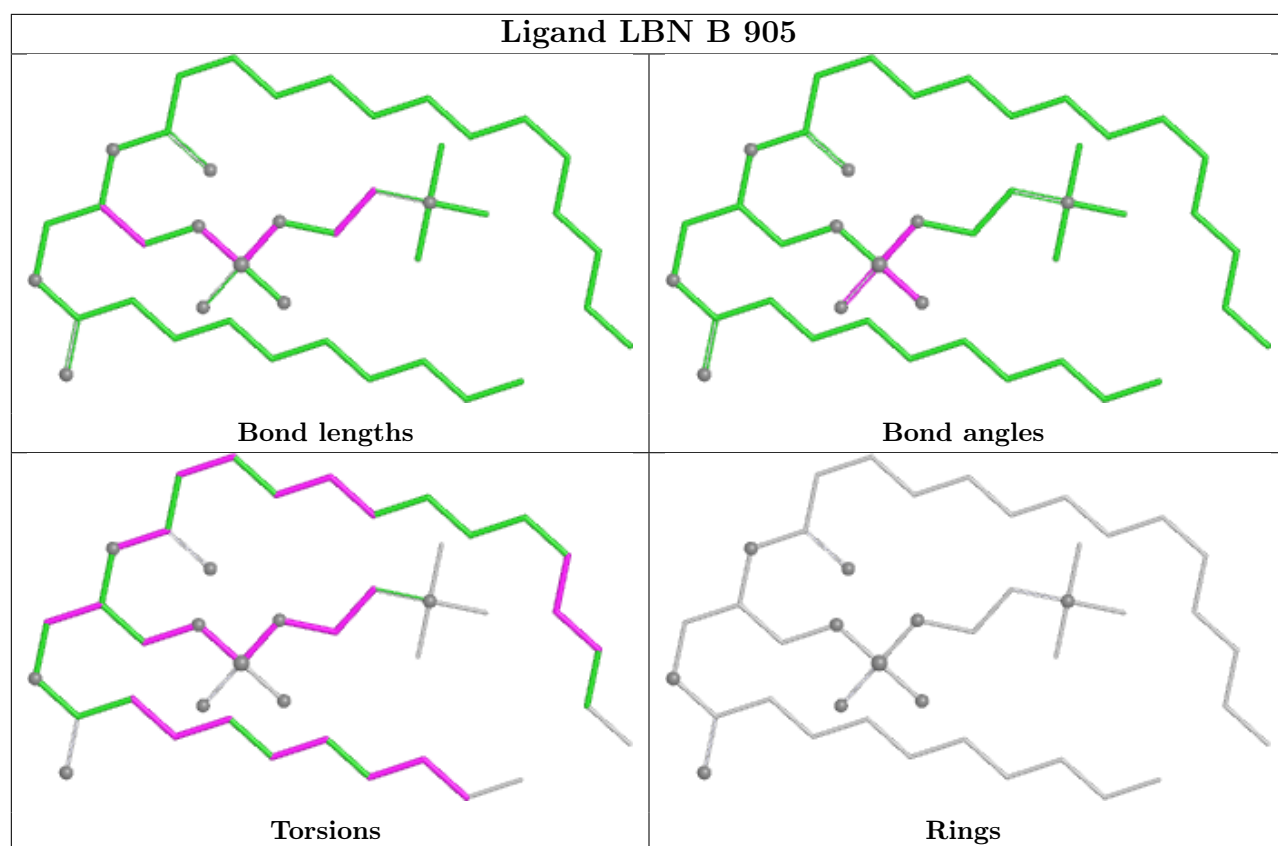


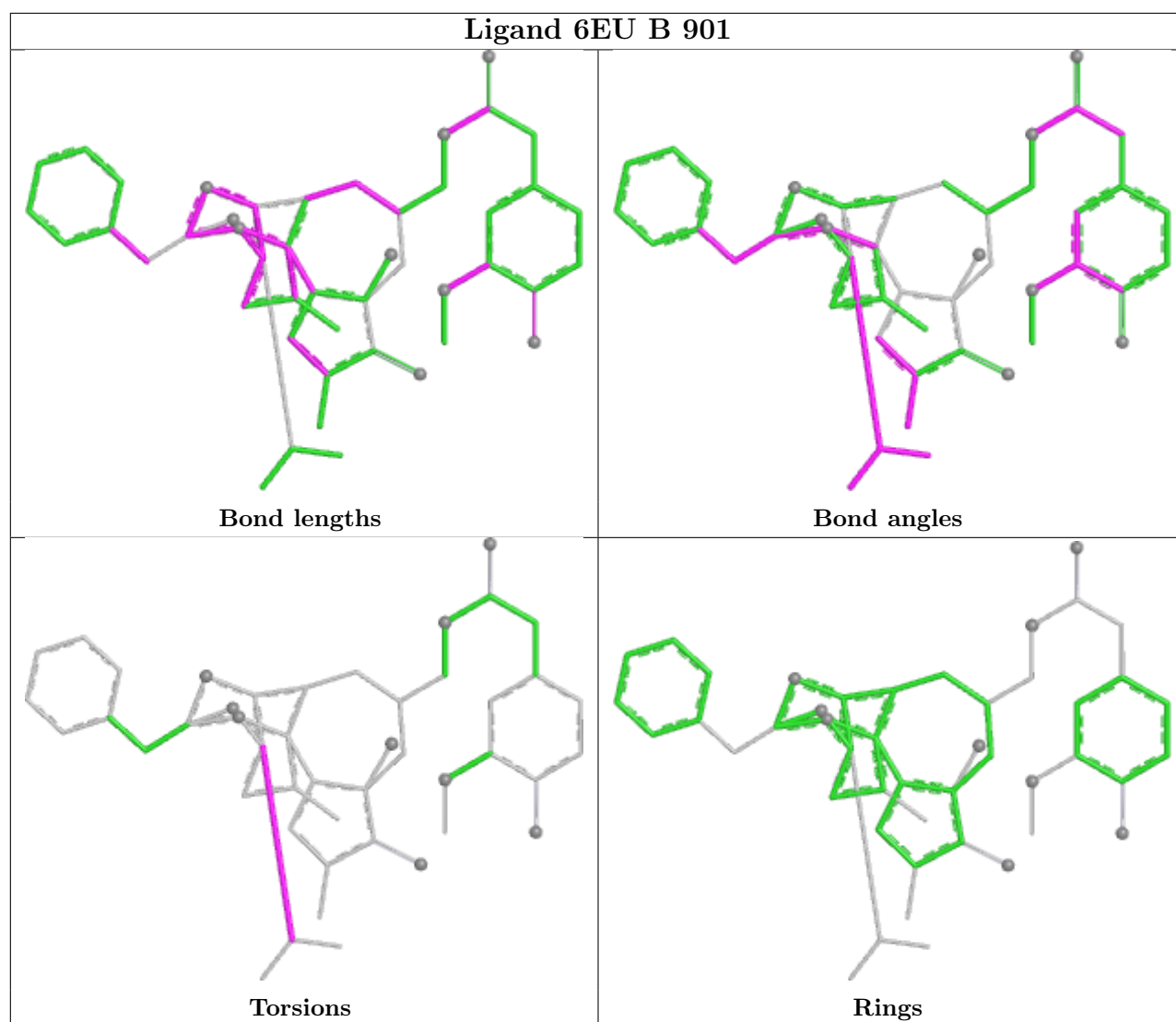


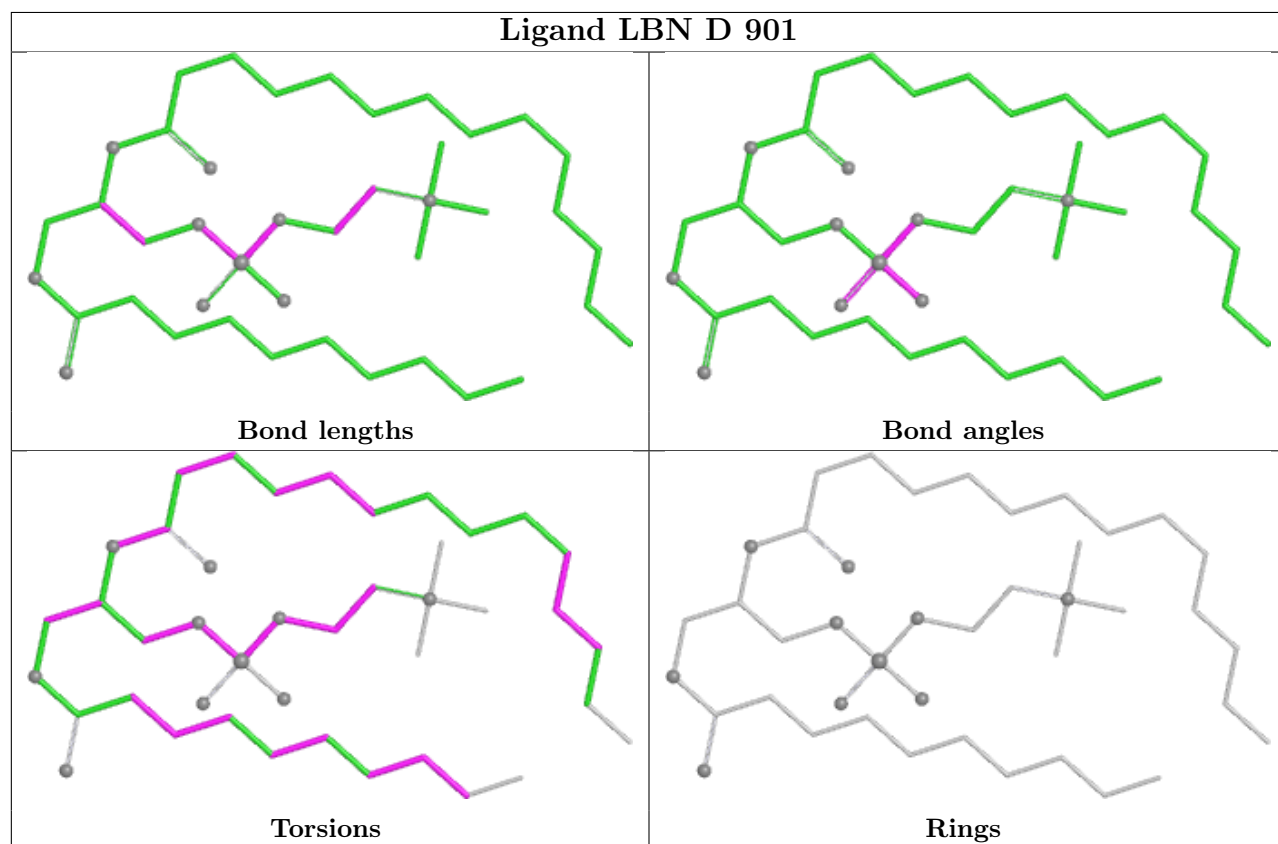
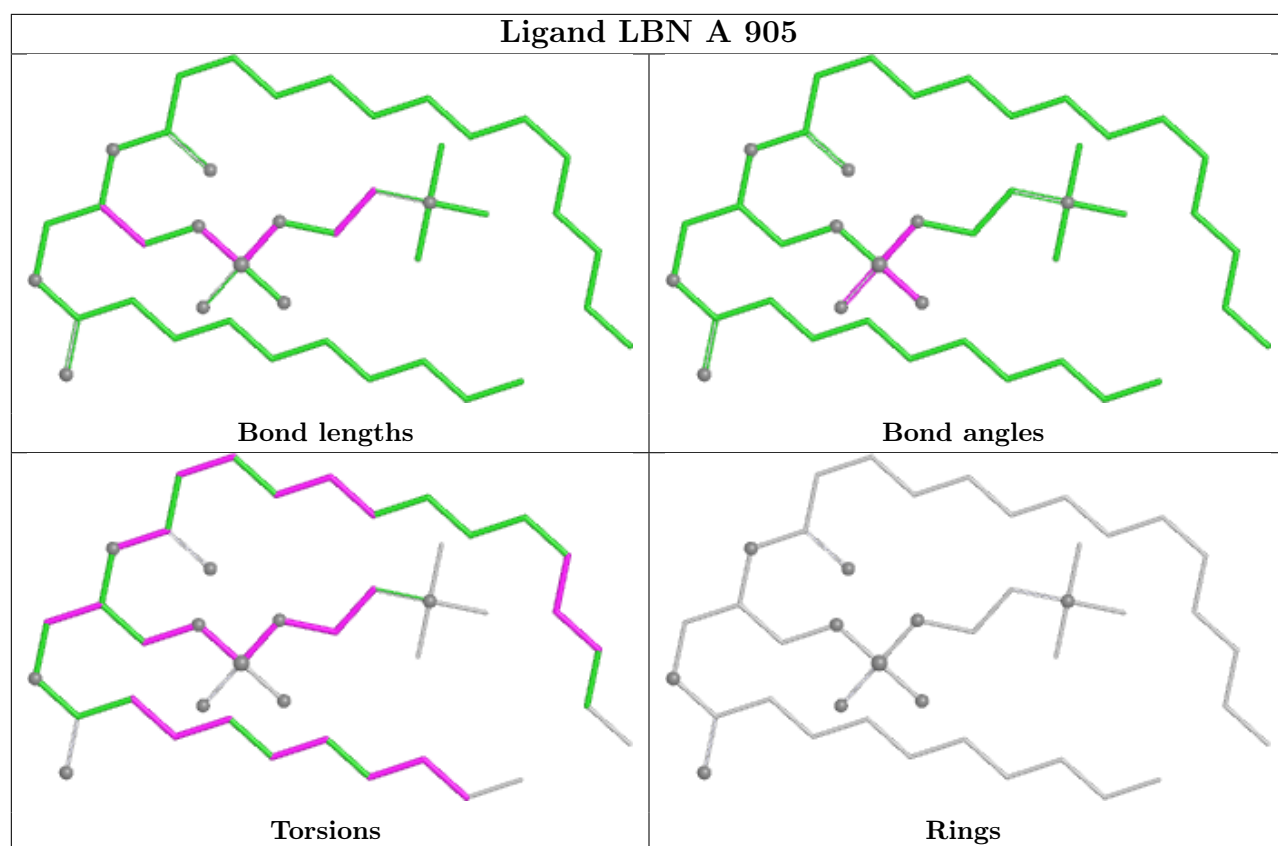


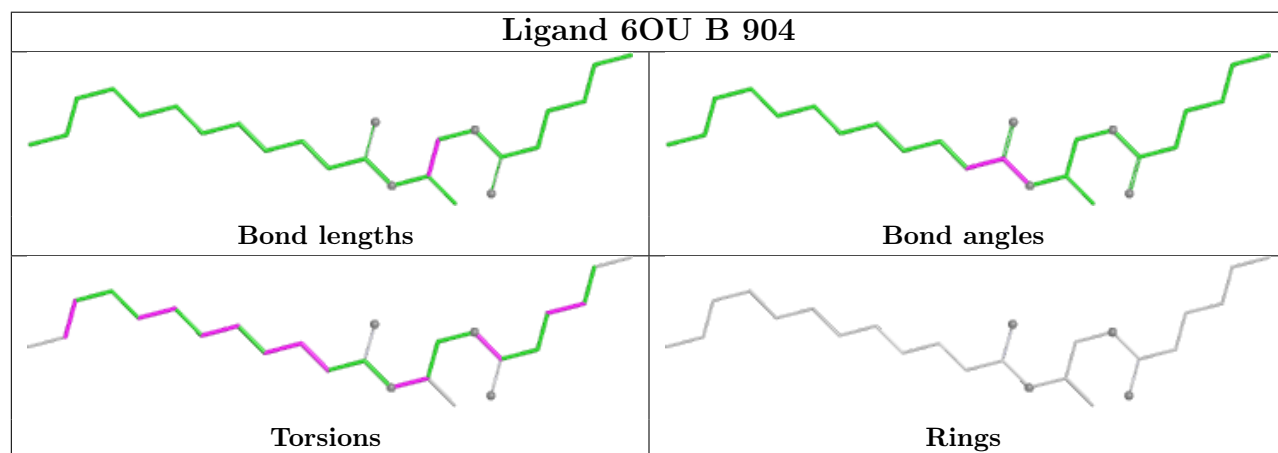
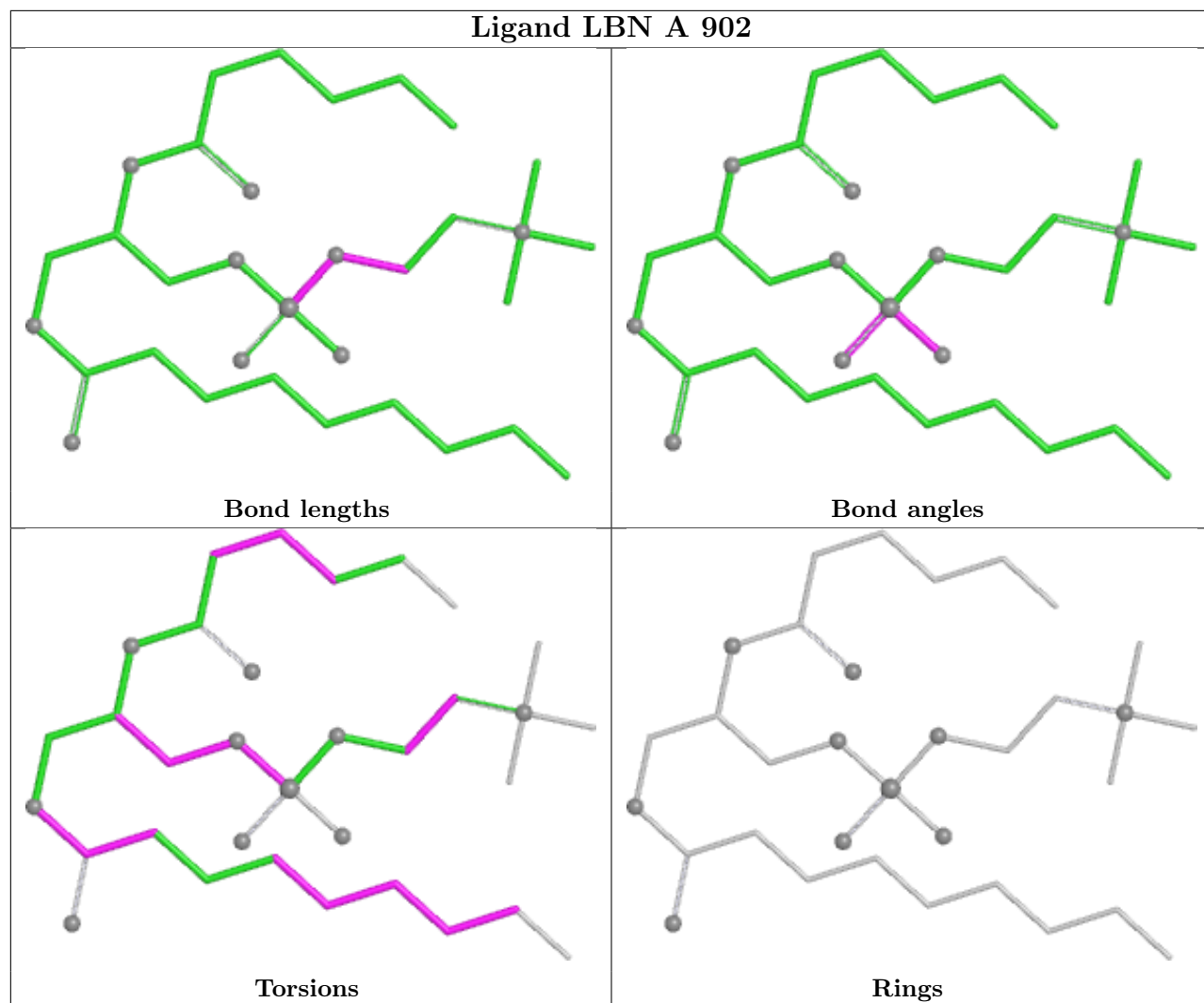


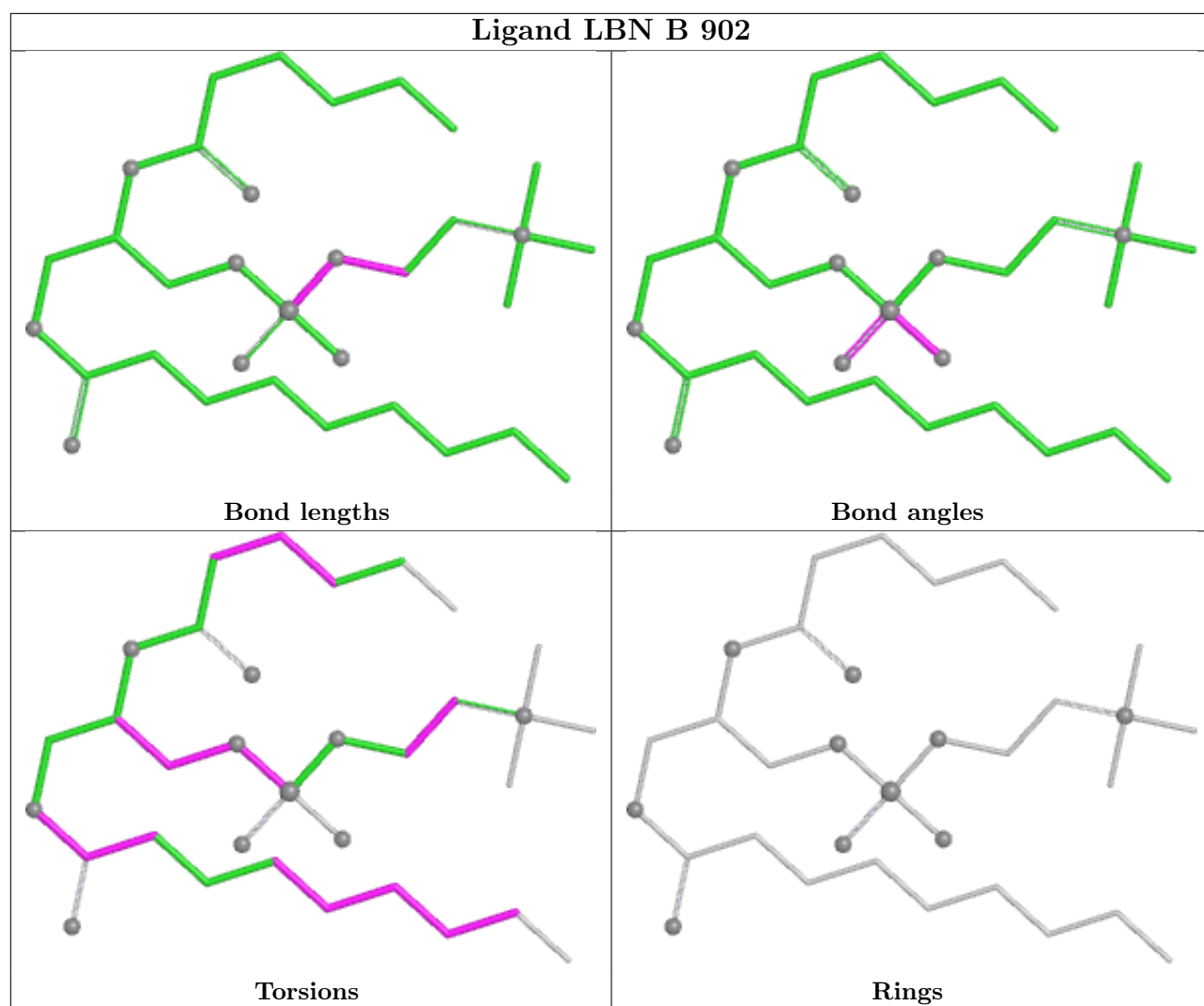












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

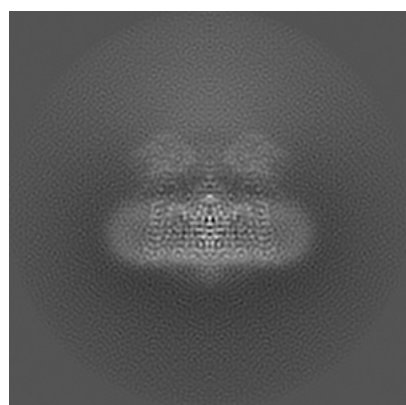
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24641. These allow visual inspection of the internal detail of the map and identification of artifacts.

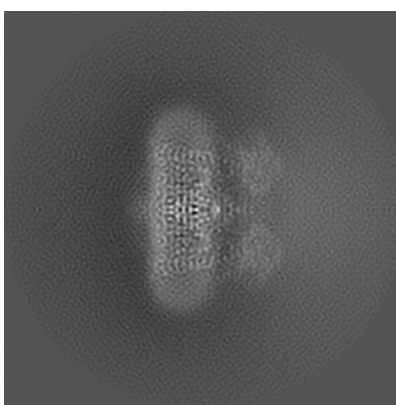
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

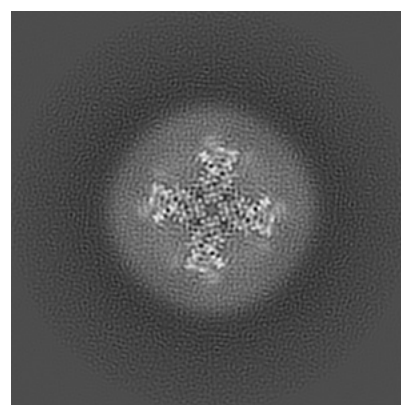
6.1.1 Primary map



X



Y

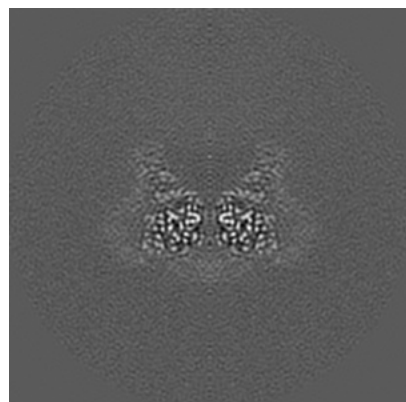


Z

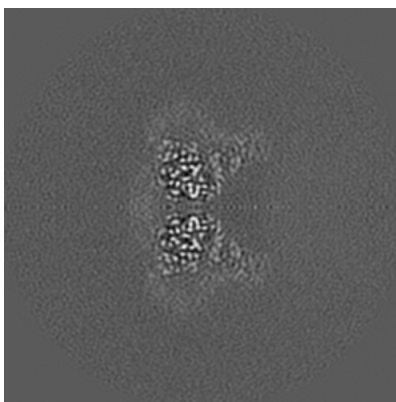
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

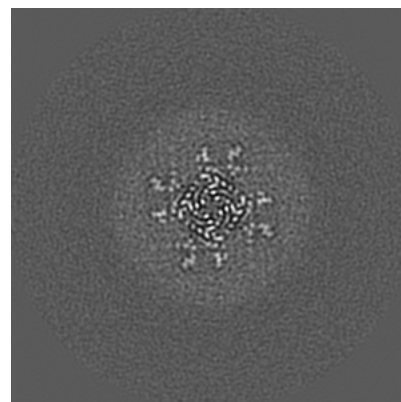
6.2.1 Primary map



X Index: 128



Y Index: 128

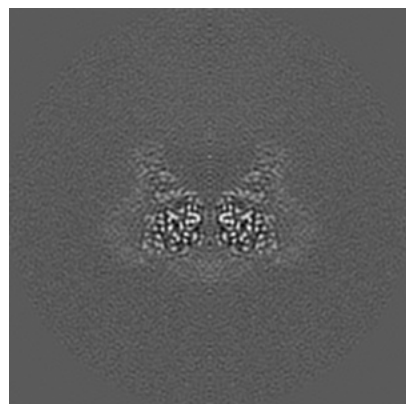


Z Index: 128

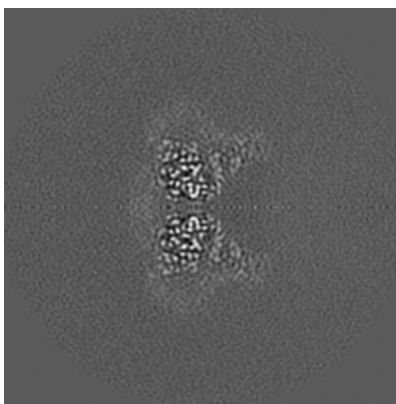
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

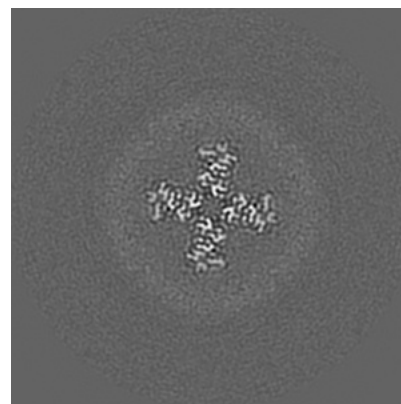
6.3.1 Primary map



X Index: 128



Y Index: 128

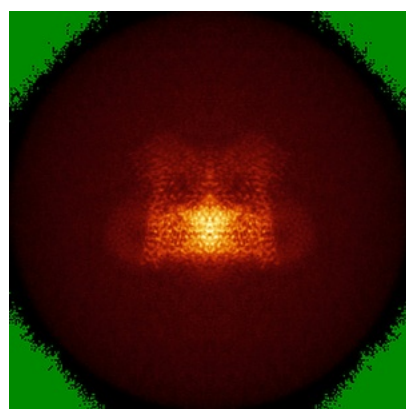


Z Index: 115

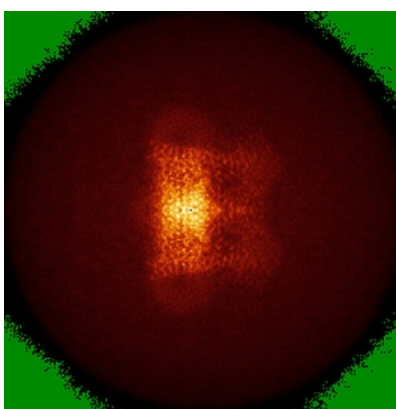
The images above show the largest variance slices of the map in three orthogonal directions.

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

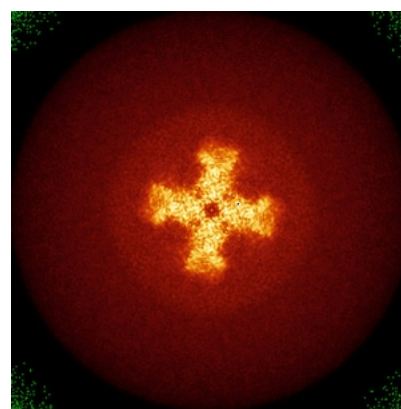
6.4.1 Primary map



X



Y

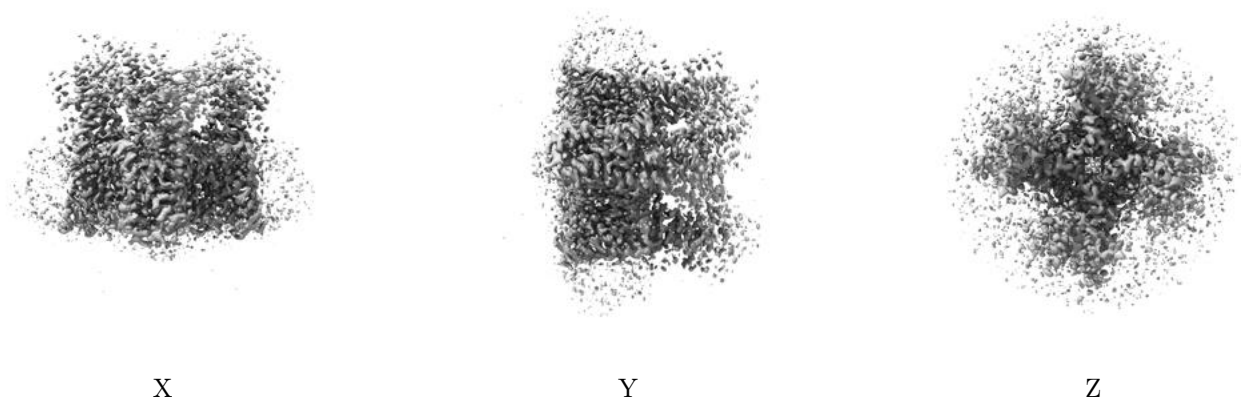


Z

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 0.0353. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

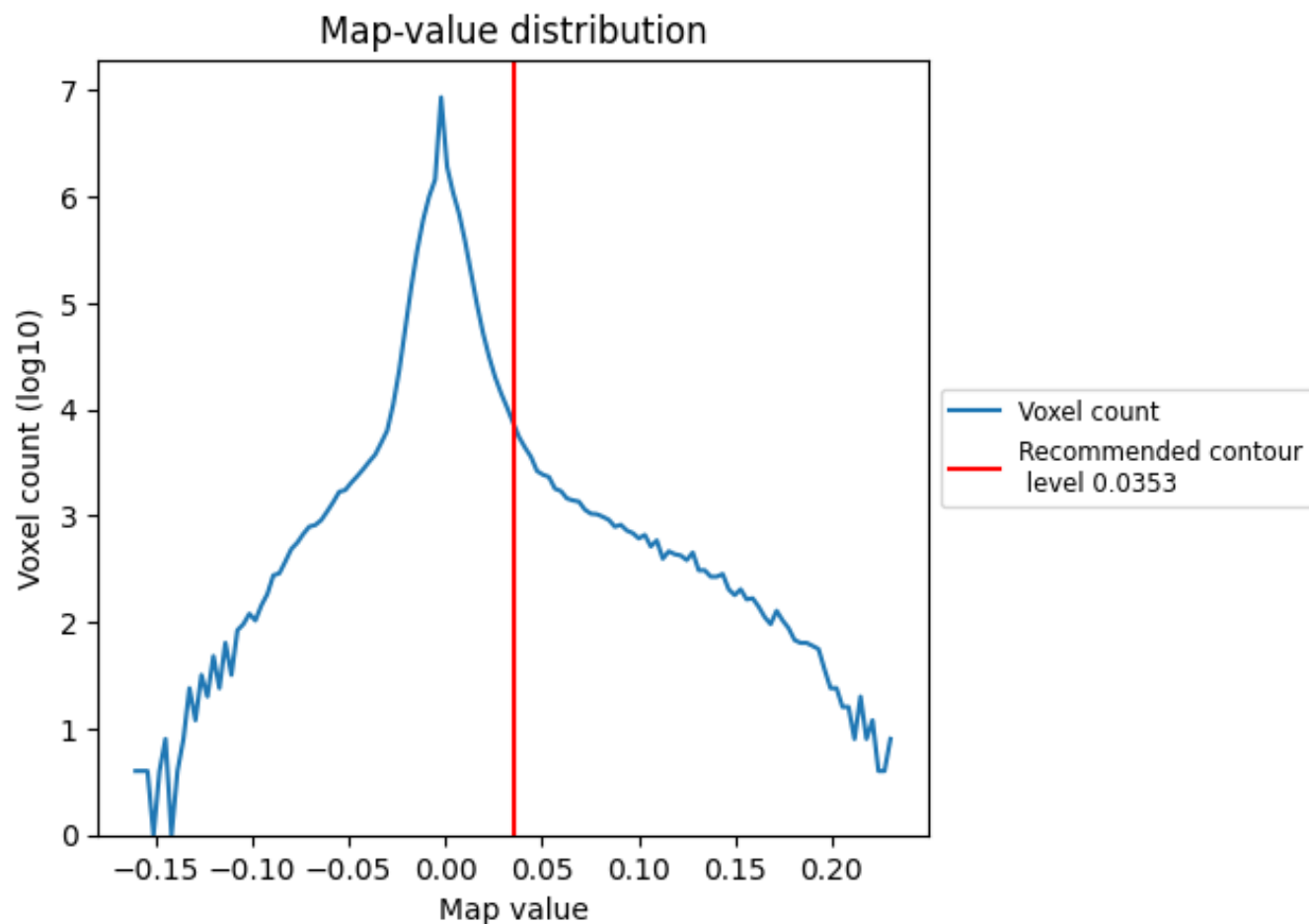
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

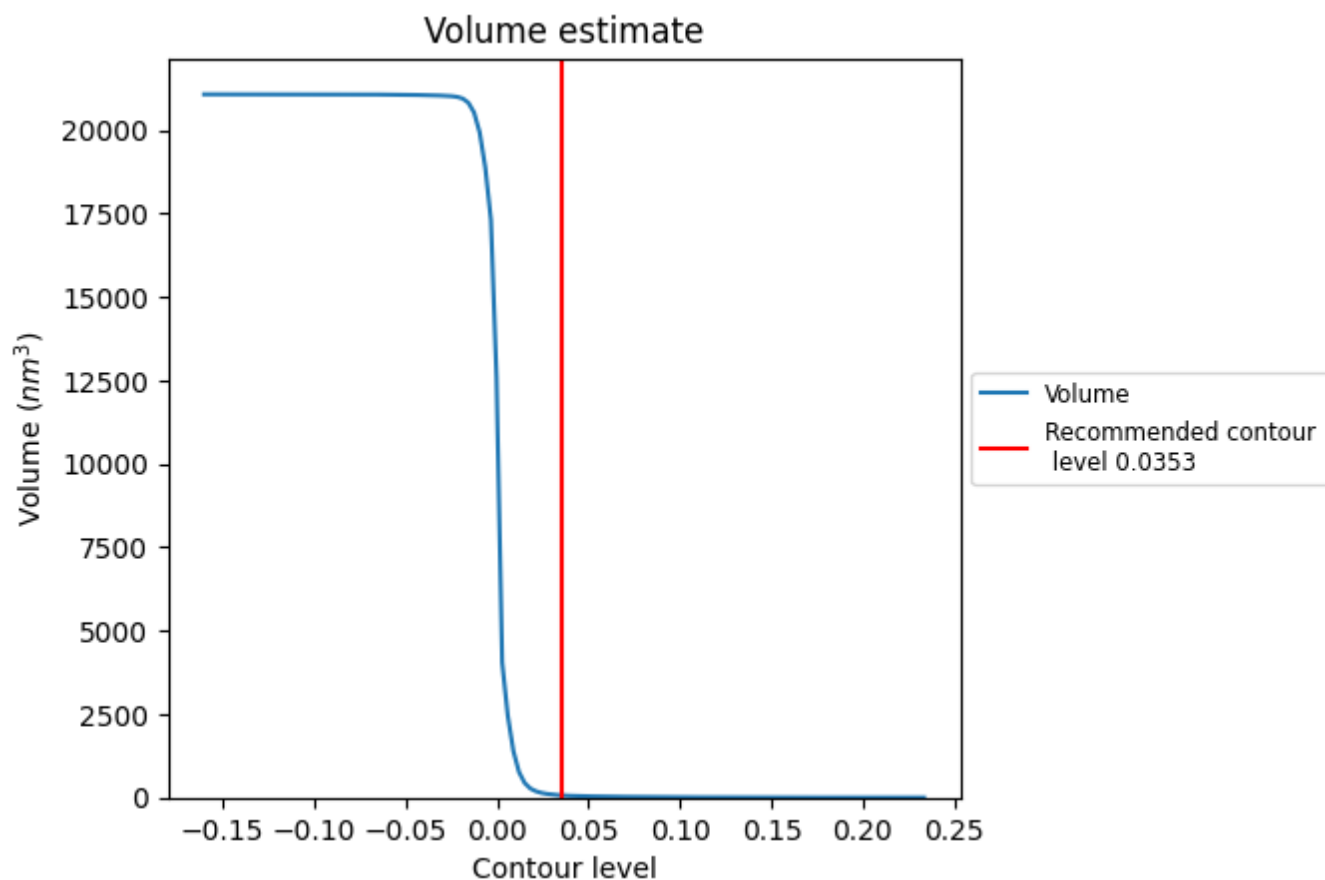
This section contains the results of statistical analysis of the map.

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.

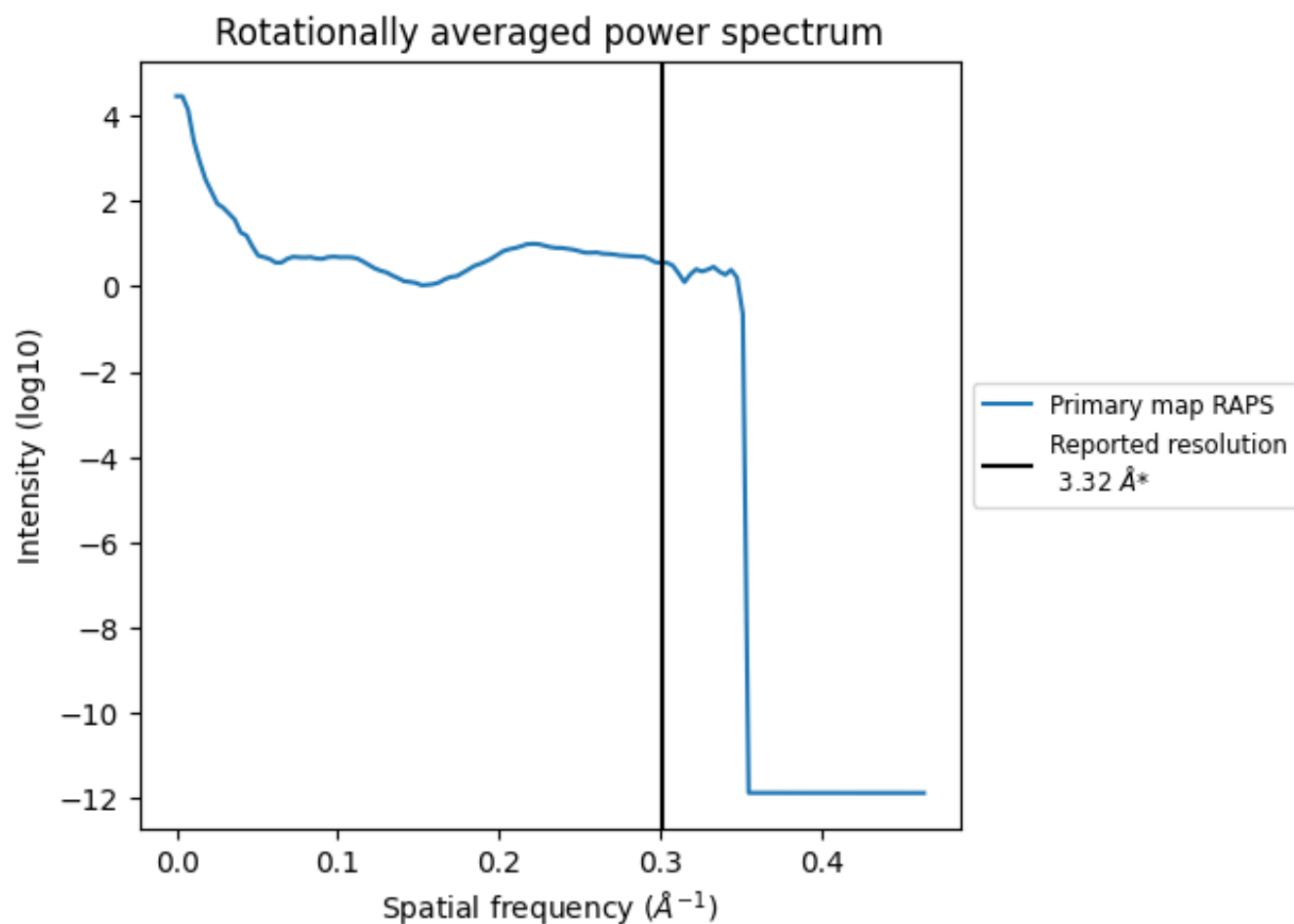
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 66 nm^3 ; this corresponds to an approximate mass of 59 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 0.301 Å⁻¹

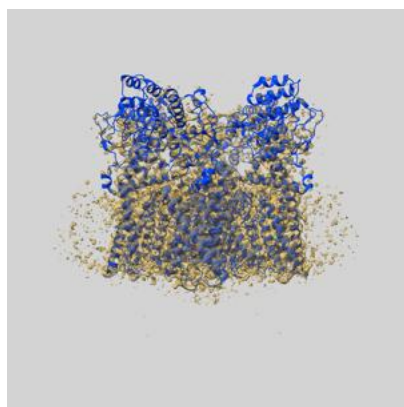
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

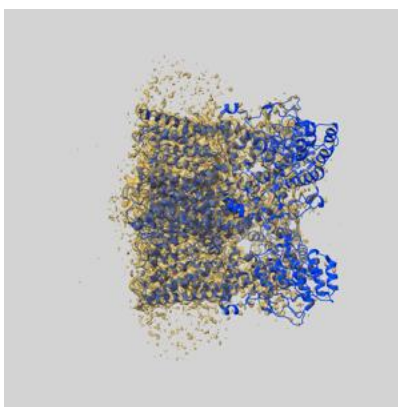
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24641 and PDB model 7RQZ. Per-residue inclusion information can be found in section 3 on page 9.

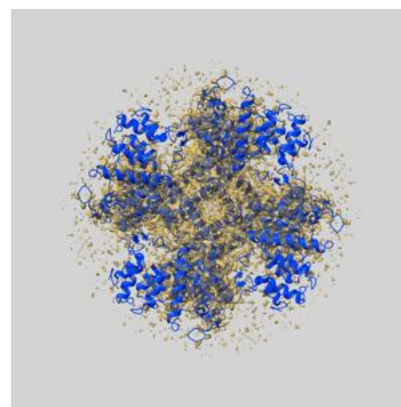
9.1 Map-model overlay [i](#)



X



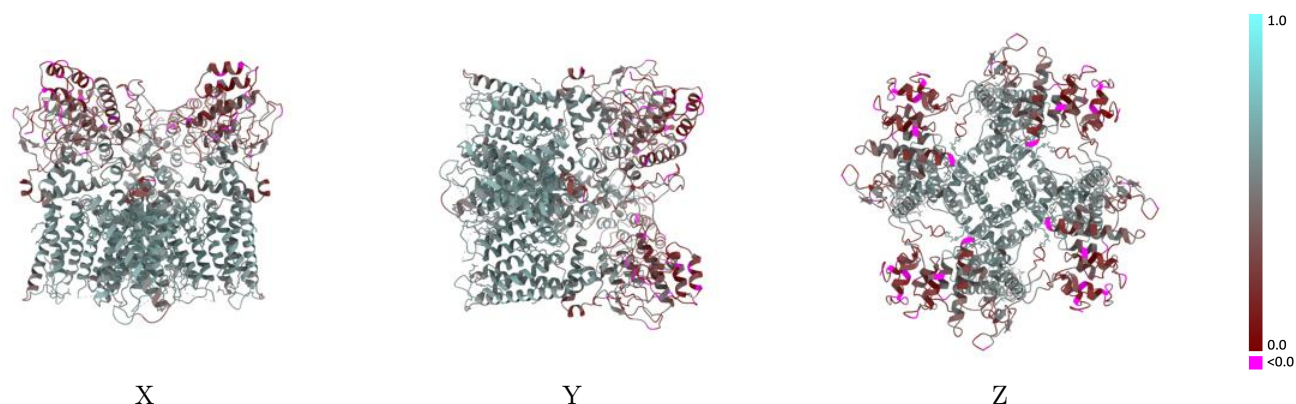
Y



Z

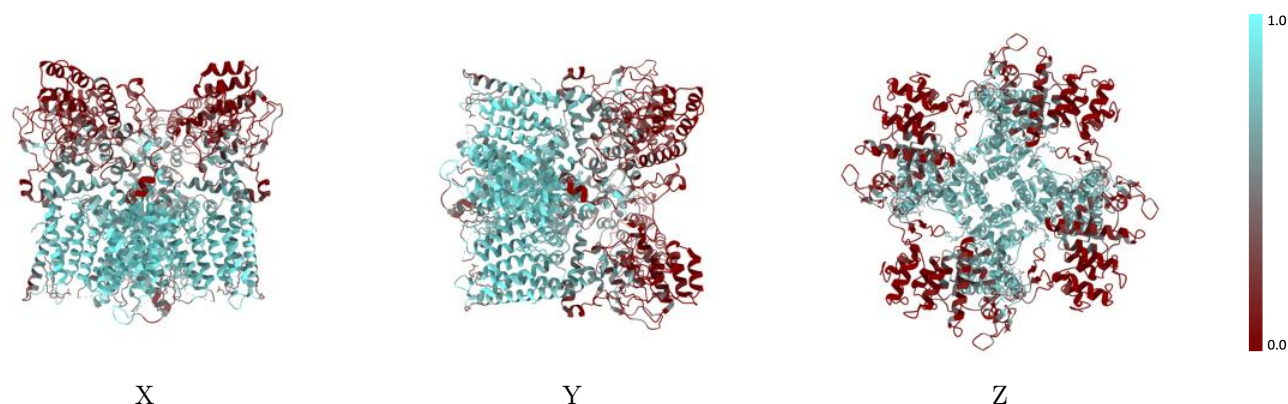
The images above show the 3D surface view of the map at the recommended contour level 0.0353 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



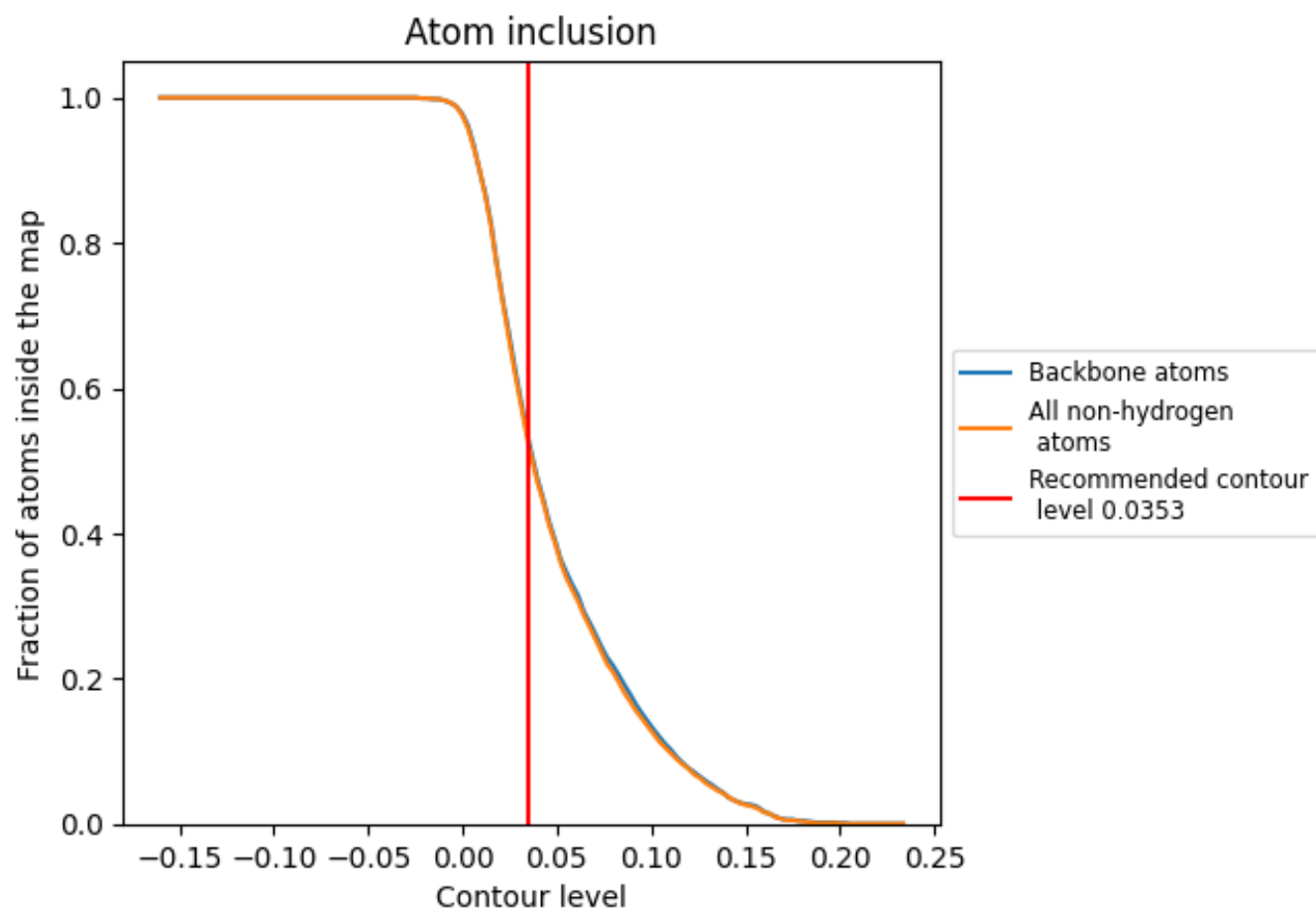
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0353).

9.4 Atom inclusion [i](#)



At the recommended contour level, 52% of all backbone atoms, 52% 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 (0.0353) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5170	0.4570
A	0.5140	0.4570
B	0.5140	0.4570
C	0.5130	0.4570
D	0.5130	0.4570

