



## Full wwPDB EM Validation Report ⓘ

Nov 16, 2022 – 08:11 PM JST

PDB ID : 7VYI  
EMDB ID : EMD-32206  
Title : Membrane arm of deactive state CI from Rotenone dataset  
Authors : Gu, J.K.; Yang, M.J.  
Deposited on : 2021-11-14  
Resolution : 3.10 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.dev43  
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) : 2.31.2

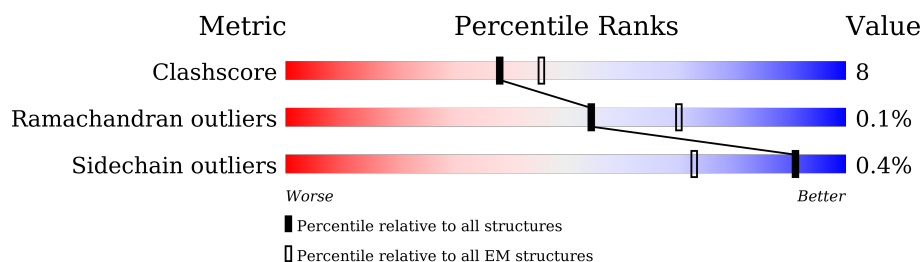
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 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.



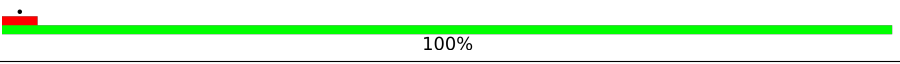

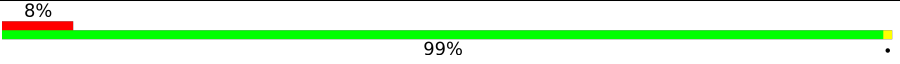
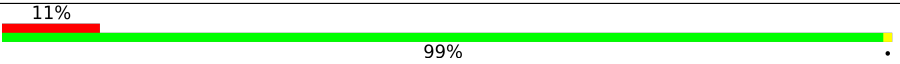
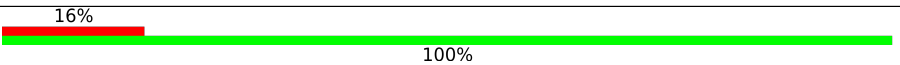
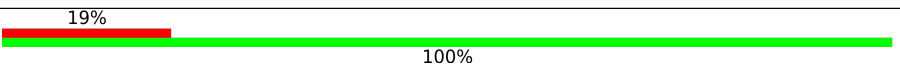
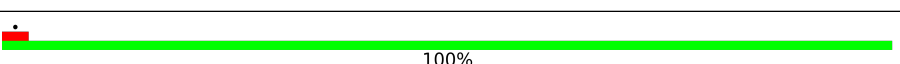
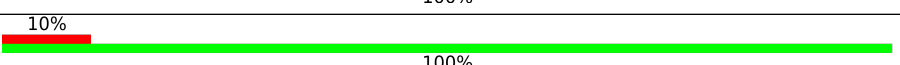
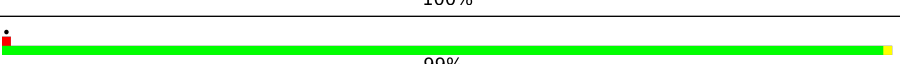
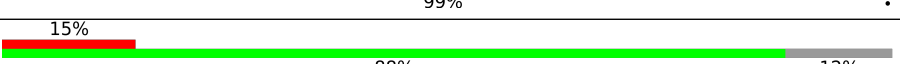
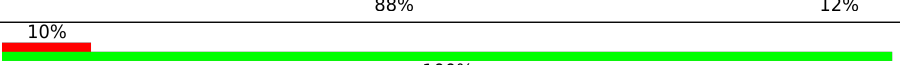
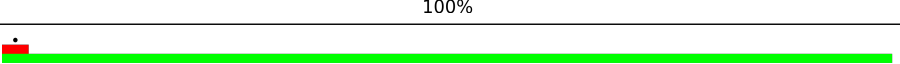
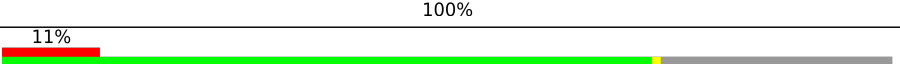
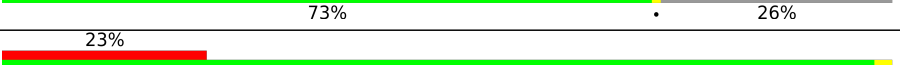
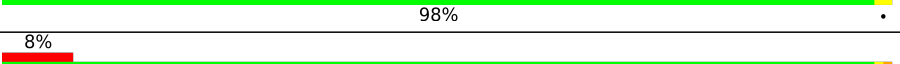
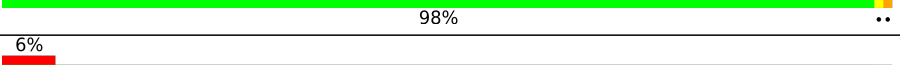
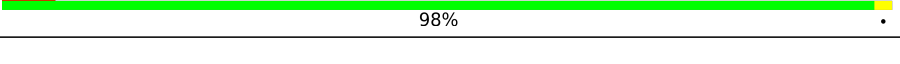
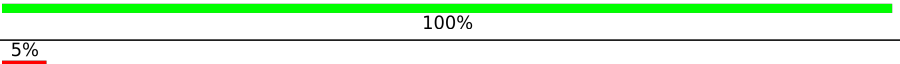
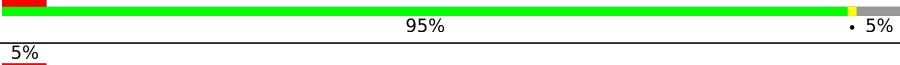
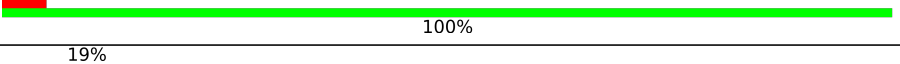
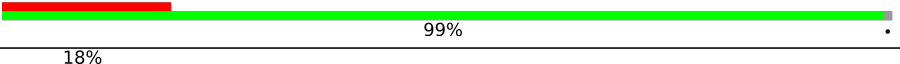
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	Q	40	
2	S	70	
3	U	83	
4	V	140	
5	W	113	
6	X	88	
7	Y	70	
8	Z	84	

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Mol	Chain	Length	Quality of chain
9	a	140	
10	b	126	
11	c	156	
12	d	175	
13	e	107	
14	f	42	
15	g	121	
16	h	105	
17	i	347	
18	j	113	
19	k	98	
20	l	603	
21	m	175	
22	n	56	
23	o	128	
24	p	178	
25	r	459	
26	s	318	
27	u	171	
28	v	125	
29	w	320	

## 2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 38620 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 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Q	40	Total	C	N	O	S	0	0
			333	217	56	59	1		

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S	70	Total	C	N	O	S	0	0
			567	364	104	94	5		

- Molecule 3 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	U	83	Total	C	N	O	S	0	0
			643	417	110	115	1		

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	V	140	Total	C	N	O	S	0	0
			1021	651	174	190	6		

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	113	Total	C	N	O	S	0	0
			949	614	160	167	8		

- Molecule 6 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	88	Total	C	N	O	S	0	0
			693	445	102	141	5		

- Molecule 7 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Y	70	Total	C	N	O	S	0	0
			600	393	98	108	1		

- Molecule 8 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Z	84	Total	C	N	O	S	0	0
			674	437	116	120	1		

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	140	Total	C	N	O	S	0	0
			1161	760	199	199	3		

- Molecule 10 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	103	Total	C	N	O	S	0	0
			879	573	158	147	1		

- Molecule 11 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	156	Total	C	N	O	S	0	0
			1303	846	212	238	7		

- Molecule 12 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	175	Total	C	N	O	S	0	0
			1461	916	265	272	8		

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	e	107	Total	C	N	O	S	0	0
			890	568	145	173	4		

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	f	42	Total	C	N	O	0	0
			342	225	58	59		

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	121	Total	C	N	O	S	0	0
			1000	650	173	171	6		

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	105	Total	C	N	O	S	0	0
			867	550	161	150	6		

- Molecule 17 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	i	347	Total	C	N	O	S	0	0
			2710	1782	420	462	46		

- Molecule 18 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	j	99	Total	C	N	O	S	0	0
			800	545	118	132	5		

- Molecule 19 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	k	98	Total	C	N	O	S	0	0
			748	493	113	128	14		

- Molecule 20 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	l	603	Total	C	N	O	S	0	0
			4785	3173	741	820	51		

- Molecule 21 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	m	129	Total	C	N	O	S	0	0
			951	637	138	168	8		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	n	56	Total	C	N	O	S	0	0
			456	295	83	77	1		

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	o	128	Total	C	N	O	S	0	0
			1062	691	182	189			

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	178	Total	C	N	O	S	0	0
			1530	980	279	263	8		

- Molecule 25 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	459	Total	C	N	O	S	0	0
			3631	2412	572	609	38		

- Molecule 26 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	303	Total	C	N	O	S	0	0
			2394	1607	369	397	21		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	u	171	Total	C	N	O	S	0	0
			1398	887	250	251	10		

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	v	124	Total	C	N	O	S	0	0
			992	622	180	181	9		

There is a discrepancy between the modelled and reference sequences:

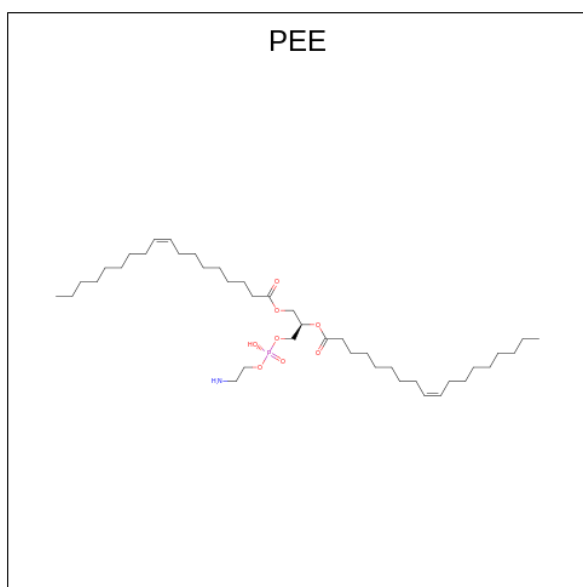
Chain	Residue	Modelled	Actual	Comment	Reference
v	1	MYR	-	acetylation	UNP F1SCH1

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	w	320	Total	C	N	O	S	0	0
			2563	1634	431	488	10		

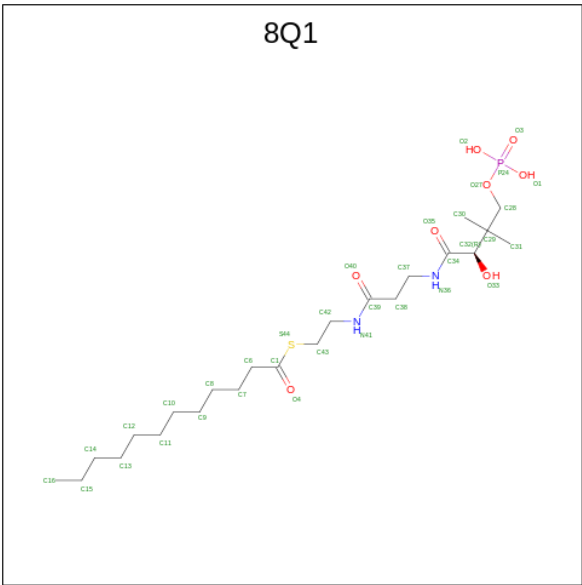
- Molecule 30 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (three-letter code: PEE) (formula:  $C_{41}H_{78}NO_8P$ ) (labeled as "Ligand of Interest" by depositor).





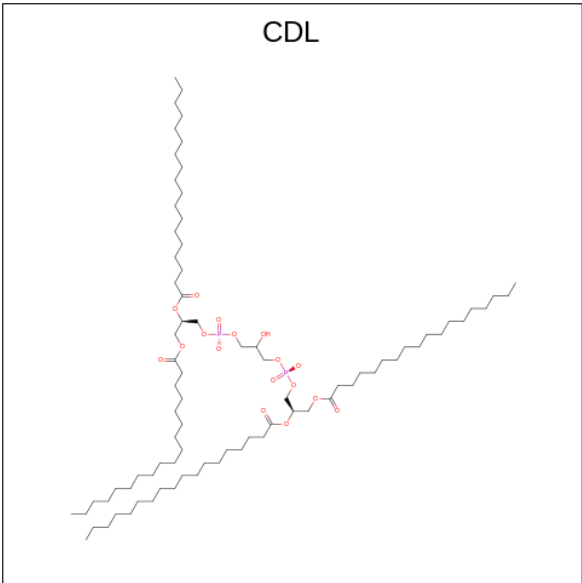
Mol	Chain	Residues	Atoms					AltConf
30	U	1	Total	C	N	O	P	0
			102	82	2	16	2	
30	U	1	Total	C	N	O	P	0
			102	82	2	16	2	
30	b	1	Total	C	N	O	P	0
			46	36	1	8	1	
30	i	1	Total	C	N	O	P	0
			47	37	1	8	1	
30	l	1	Total	C	N	O	P	0
			46	36	1	8	1	
30	m	1	Total	C	N	O	P	0
			41	31	1	8	1	
30	r	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 31 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (three-letter code: 8Q1) (formula: C<sub>23</sub>H<sub>45</sub>N<sub>2</sub>O<sub>8</sub>PS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf	
31	X	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

- Molecule 32 is CARDIOLIPIN (three-letter code: CDL) (formula:  $C_{81}H_{156}O_{17}P_2$ ) (labeled as "Ligand of Interest" by depositor).



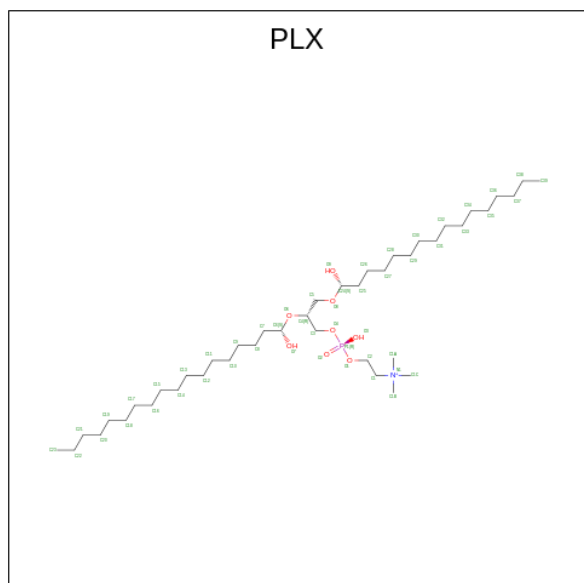
Mol	Chain	Residues	Atoms				AltConf
32	a	1	Total	C	O	P	0
			91	72	17	2	
32	g	1	Total	C	O	P	0
			78	59	17	2	

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Mol	Chain	Residues	Atoms				AltConf
32	i	1	Total	C	O	P	0
			66	47	17	2	
32	l	1	Total	C	O	P	0
			100	81	17	2	
32	r	1	Total	C	O	P	0
			199	161	34	4	
32	r	1	Total	C	O	P	0
			199	161	34	4	

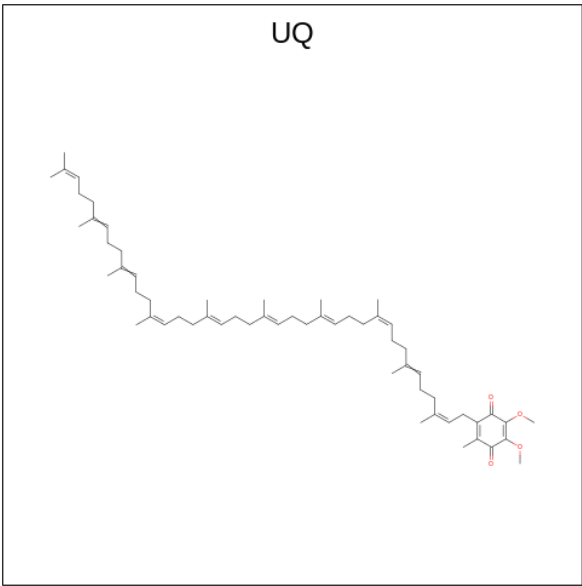
- Molecule 33 is (9R,11S)-9-({[(1S)-1-HYDROXYHEXADECYL]OXY}METHYL)-2,2-DIMETHYL-5,7,10-TRIOXA-2LAMBDA 5 -AZA-6LAMBDA 5 -PHOSPHAOCTACOSANE-6,6,11-TRIOL (three-letter code: PLX) (formula: C<sub>42</sub>H<sub>89</sub>NO<sub>8</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
33	a	1	Total	C	N	O	P
			52	42	1	8	1
33	g	1	Total	C	N	O	P
			52	42	1	8	1
33	j	1	Total	C	N	O	P
			52	42	1	8	1
33	r	1	Total	C	N	O	P
			104	84	2	16	2
33	r	1	Total	C	N	O	P
			104	84	2	16	2

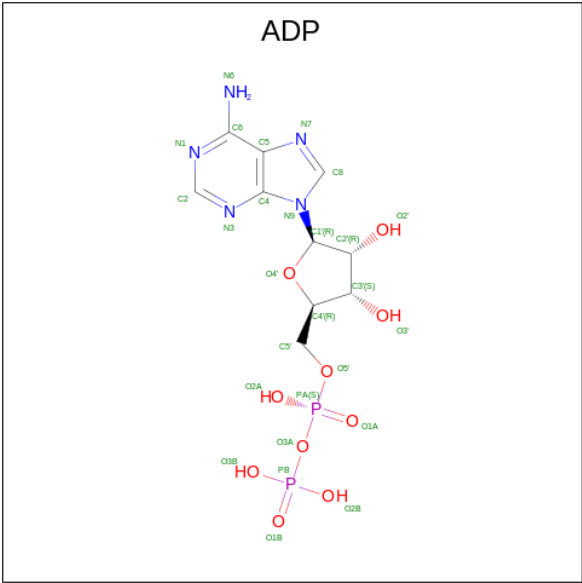
- Molecule 34 is Coenzyme Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-isomer (three-letter code: UQ)

(formula: C<sub>59</sub>H<sub>90</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
34	s	1	Total	C	O	0
			28	24	4	

- Molecule 35 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).

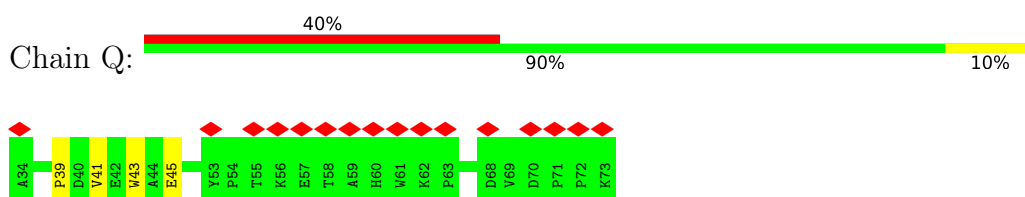


Mol	Chain	Residues	Atoms					AltConf
35	w	1	Total	C	N	O	P	0
			27	10	5	10	2	

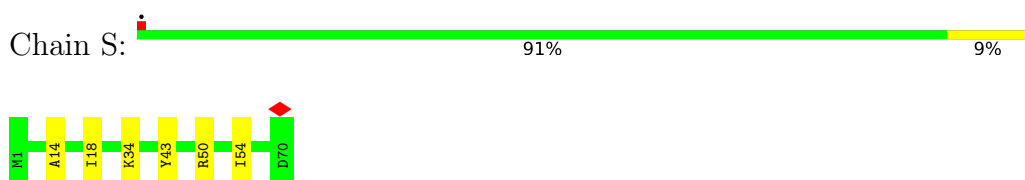
### 3 Residue-property plots [i](#)

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

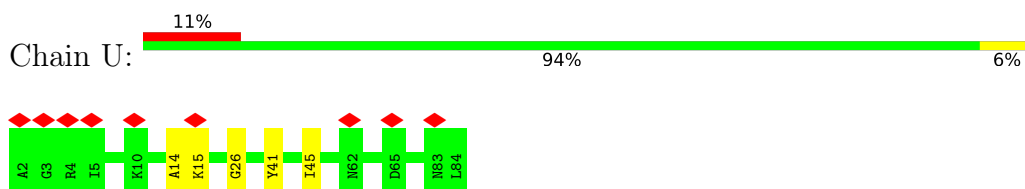
- Molecule 1: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial



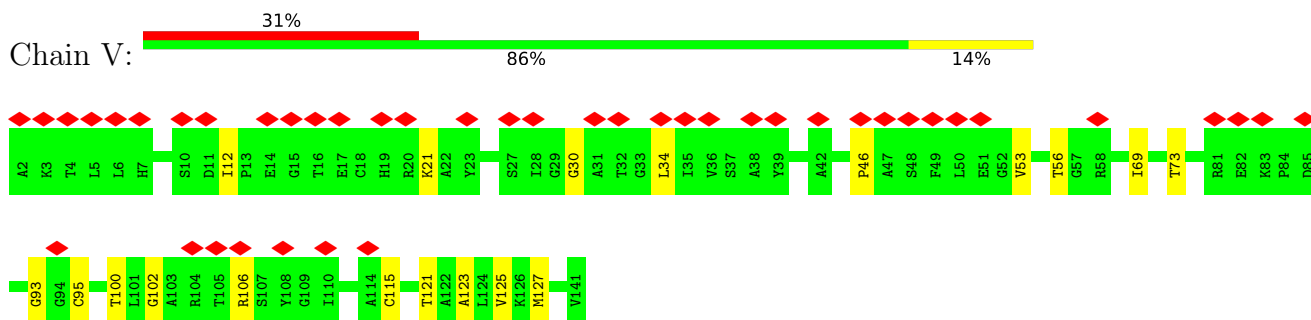
- Molecule 2: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



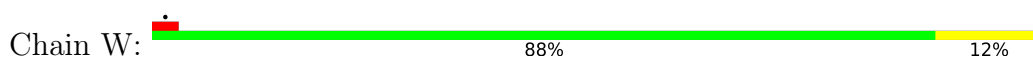
- Molecule 3: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

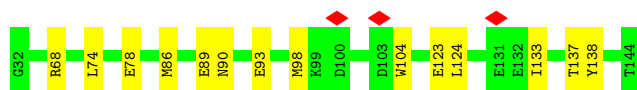


- Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

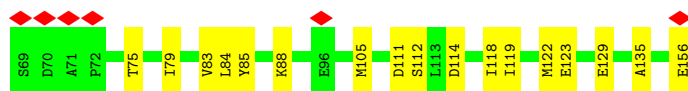
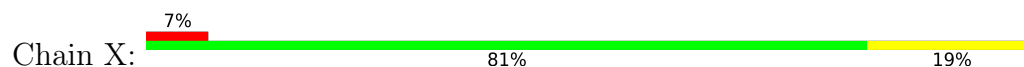


- Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13

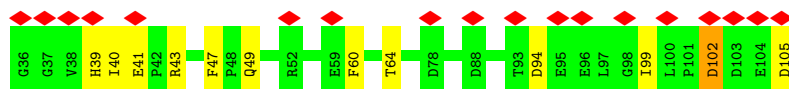
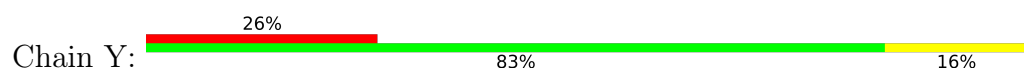




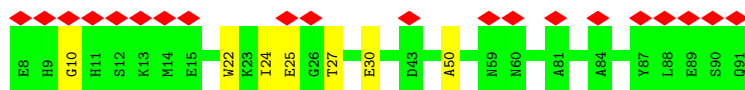
- Molecule 6: Acyl carrier protein, mitochondrial



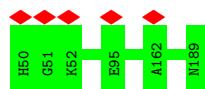
- Molecule 7: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



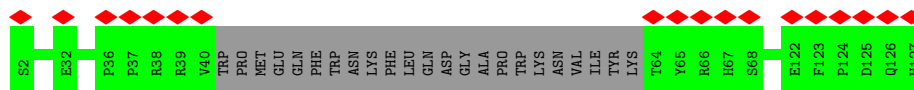
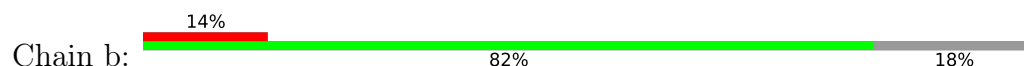
- Molecule 8: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3



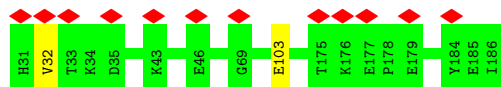
- Molecule 9: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



- Molecule 10: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6

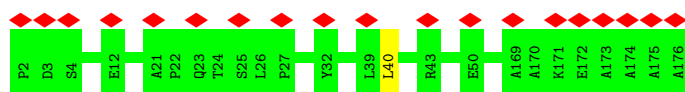


- Molecule 11: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial



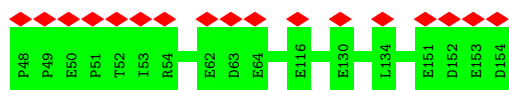
- Molecule 12: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10

Chain d:  11% 99%



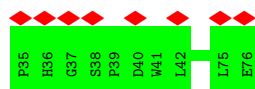
- Molecule 13: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial

Chain e:  16% 100%



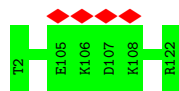
- Molecule 14: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

Chain f:  19% 100%



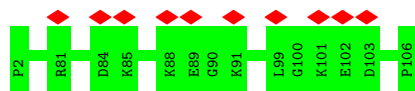
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 subunit C2

Chain g:  0% 100%



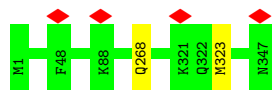
- Molecule 16: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

Chain h:  10% 100%




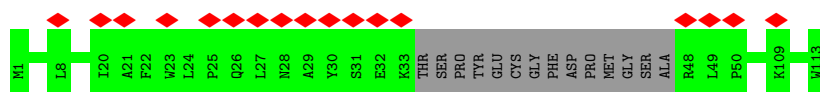
- Molecule 17: NADH-ubiquinone oxidoreductase chain 2

Chain i:  0% 99%

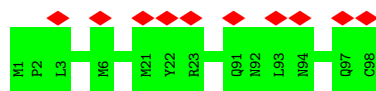


- Molecule 18: NADH-ubiquinone oxidoreductase chain 3

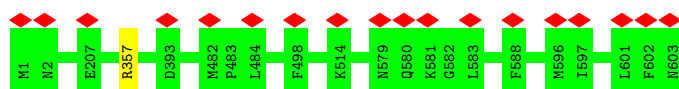
Chain j:  15% 88% 12%



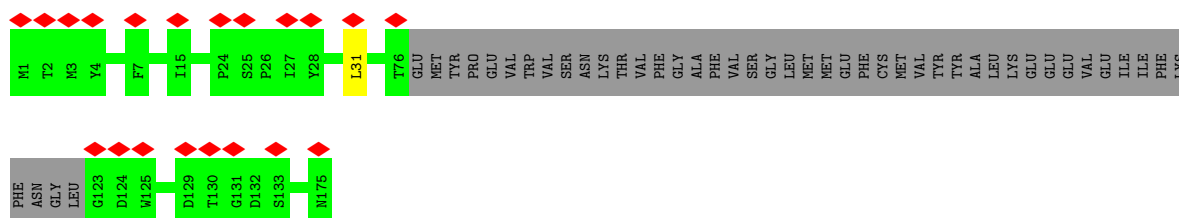
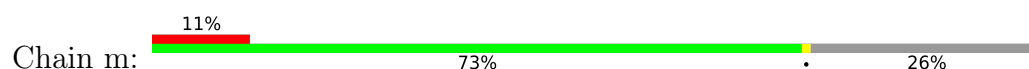
- Molecule 19: NADH-ubiquinone oxidoreductase chain 4L



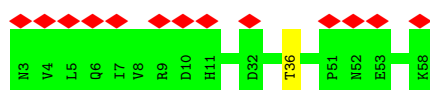
- Molecule 20: NADH-ubiquinone oxidoreductase chain 5



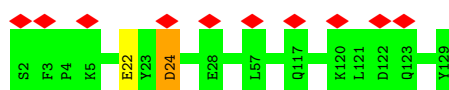
- Molecule 21: NADH-ubiquinone oxidoreductase chain 6



- Molecule 22: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1



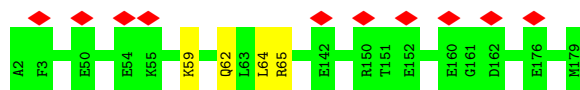
- Molecule 23: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4



- Molecule 24: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

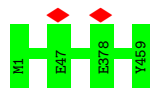






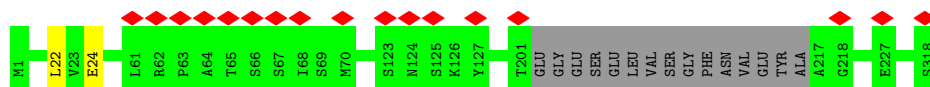
- Molecule 25: NADH-ubiquinone oxidoreductase chain 4

Chain r: 100%



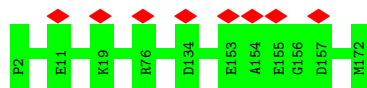
- Molecule 26: NADH-ubiquinone oxidoreductase chain 1

Chain s: 5% 95% 5%



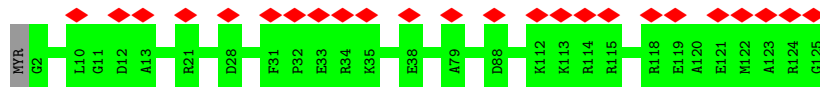
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

Chain u: 5% 100%



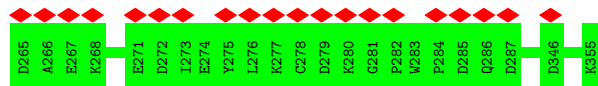
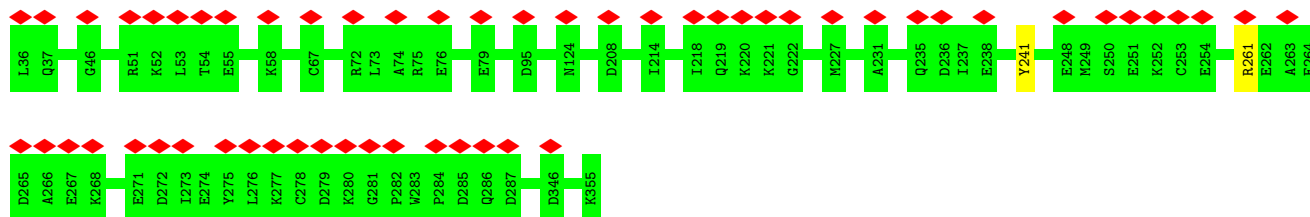
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Chain v: 19% 99%



- Molecule 29: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

Chain w: 18% 99%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63623	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.141	Depositor
Minimum map value	-0.085	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0288	Depositor
Map size (Å)	333.002, 333.002, 333.002	wwPDB
Map dimensions	310, 310, 310	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0742, 1.0742, 1.0742	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEE, CDL, 8Q1, PLX, ADP, UQ

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	Q	0.24	0/350	0.40	0/483
2	S	0.25	0/582	0.48	0/783
3	U	0.25	0/664	0.43	0/912
4	V	0.25	0/1042	0.48	0/1411
5	W	0.25	0/973	0.48	0/1312
6	X	0.25	0/705	0.42	0/956
7	Y	0.25	0/626	0.49	1/857 (0.1%)
8	Z	0.25	0/695	0.44	0/939
9	a	0.26	0/1195	0.48	0/1618
10	b	0.25	0/906	0.51	0/1232
11	c	0.26	0/1359	0.48	0/1861
12	d	0.24	0/1494	0.50	1/2015 (0.0%)
13	e	0.24	0/916	0.46	0/1246
14	f	0.23	0/350	0.41	0/473
15	g	0.26	0/1031	0.46	0/1394
16	h	0.24	0/889	0.47	0/1190
17	i	0.24	0/2773	0.42	0/3768
18	j	0.25	0/819	0.46	0/1117
19	k	0.25	0/759	0.42	0/1029
20	l	0.25	0/4914	0.44	0/6683
21	m	0.26	0/973	0.49	1/1320 (0.1%)
22	n	0.23	0/468	0.45	0/633
23	o	0.25	0/1092	0.51	0/1481
24	p	0.26	0/1586	0.49	0/2150
25	r	0.25	0/3723	0.43	0/5078
26	s	0.25	0/2464	0.44	0/3369
27	u	0.24	0/1436	0.47	0/1938
28	v	0.25	0/1016	0.52	0/1370
29	w	0.25	0/2623	0.47	0/3557
All	All	0.25	0/38423	0.46	3/52175 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	Y	102	ASP	CB-CG-OD1	5.32	123.09	118.30
12	d	40	LEU	CA-CB-CG	5.30	127.48	115.30
21	m	31	LEU	CA-CB-CG	5.04	126.90	115.30

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	Q	333	0	301	2	0
2	S	567	0	565	4	0
3	U	643	0	642	3	0
4	V	1021	0	1027	9	0
5	W	949	0	935	8	0
6	X	693	0	664	15	0
7	Y	600	0	539	8	0
8	Z	674	0	643	5	0
9	a	1161	0	1170	0	0
10	b	879	0	899	0	0
11	c	1303	0	1183	0	0
12	d	1461	0	1429	0	0
13	e	890	0	837	0	0
14	f	342	0	341	0	0
15	g	1000	0	994	0	0
16	h	867	0	871	0	0
17	i	2710	0	2874	0	0
18	j	800	0	855	0	0
19	k	748	0	799	0	0
20	l	4785	0	4933	0	0
21	m	951	0	962	0	0
22	n	456	0	433	0	0
23	o	1062	0	1072	0	0
24	p	1530	0	1466	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	r	3631	0	3839	0	0
26	s	2394	0	2508	0	0
27	u	1398	0	1378	0	0
28	v	992	0	908	0	0
29	w	2563	0	2501	0	0
30	U	102	0	164	2	0
30	b	46	0	69	0	0
30	i	47	0	71	0	0
30	l	46	0	69	0	0
30	m	41	0	59	0	0
30	r	51	0	82	0	0
31	X	35	0	0	3	0
32	a	91	0	132	0	0
32	g	78	0	103	0	0
32	i	66	0	76	0	0
32	l	100	0	156	0	0
32	r	199	0	307	0	0
33	a	52	0	88	0	0
33	g	52	0	88	0	0
33	j	52	0	88	0	0
33	r	104	0	176	0	0
34	s	28	0	31	0	0
35	w	27	0	11	0	0
All	All	38620	0	39338	54	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 8.

All (54) 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)
6:X:112:SER:CB	31:X:201:8Q1:O1	1.65	1.40
6:X:85:TYR:HH	8:Z:22:TRP:HE1	1.06	1.00
6:X:123:GLU:HG2	6:X:129:GLU:HA	1.47	0.95
6:X:111:ASP:OD1	6:X:112:SER:N	2.21	0.74
4:V:69:ILE:HG13	4:V:100:THR:HG21	1.83	0.60
6:X:114:ASP:O	6:X:118:ILE:HG13	2.01	0.59
7:Y:39:HIS:NE2	7:Y:41:GLU:OE2	2.35	0.59
4:V:53:VAL:HA	4:V:56:THR:HG22	1.83	0.59
7:Y:40:ILE:HG23	7:Y:49:GLN:HB2	1.86	0.58
6:X:83:VAL:HG22	6:X:122:MET:HE1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:12:ILE:HB	4:V:21:LYS:HD3	1.88	0.56
8:Z:24:ILE:O	8:Z:27:THR:OG1	2.22	0.56
2:S:50:ARG:O	2:S:54:ILE:HG12	2.06	0.56
7:Y:94:ASP:HB3	7:Y:99:ILE:HB	1.90	0.54
8:Z:22:TRP:HB3	8:Z:50:ALA:HB3	1.89	0.54
5:W:89:GLU:O	5:W:93:GLU:HG2	2.08	0.54
7:Y:43:ARG:NH1	7:Y:47:PHE:O	2.42	0.53
4:V:30:GLY:O	4:V:34:LEU:HG	2.09	0.52
5:W:137:THR:HG23	5:W:138:TYR:CD2	2.45	0.52
4:V:123:ALA:O	4:V:127:MET:HG3	2.11	0.51
3:U:26:GLY:HA3	30:U:101:PEE:H37	1.93	0.51
5:W:74:LEU:O	5:W:78:GLU:HG3	2.12	0.50
6:X:83:VAL:HG13	6:X:122:MET:HE1	1.94	0.49
5:W:86:MET:SD	5:W:124:LEU:HB3	2.52	0.49
4:V:121:THR:O	4:V:125:VAL:HG23	2.13	0.49
6:X:118:ILE:O	6:X:122:MET:HG2	2.12	0.49
5:W:90:ASN:ND2	5:W:123:GLU:O	2.45	0.49
4:V:102:GLY:O	4:V:106:ARG:N	2.46	0.49
7:Y:105:ASP:N	7:Y:105:ASP:OD1	2.47	0.48
2:S:43:TYR:CZ	5:W:68:ARG:HG3	2.48	0.48
6:X:105:MET:SD	6:X:105:MET:N	2.87	0.47
7:Y:60:PHE:O	7:Y:64:THR:HG23	2.13	0.47
6:X:79:ILE:O	6:X:83:VAL:HG23	2.15	0.46
31:X:201:8Q1:O27	31:X:201:8Q1:O33	2.31	0.46
4:V:73:THR:OG1	4:V:93:GLY:HA2	2.15	0.46
5:W:98:MET:HG3	5:W:104:TRP:CD1	2.50	0.46
6:X:75:THR:OG1	6:X:156:GLU:O	2.30	0.46
6:X:111:ASP:HB3	6:X:114:ASP:OD1	2.16	0.46
31:X:201:8Q1:O40	31:X:201:8Q1:N36	2.49	0.46
7:Y:102:ASP:OD1	7:Y:102:ASP:O	2.35	0.45
2:S:14:ALA:O	2:S:18:ILE:HG12	2.17	0.44
6:X:83:VAL:HG22	6:X:122:MET:CE	2.47	0.44
30:U:102:PEE:H16	30:U:102:PEE:H21	1.74	0.44
7:Y:39:HIS:HE1	8:Z:10:GLY:HA2	1.83	0.43
6:X:119:ILE:HG21	6:X:135:ALA:HB1	2.01	0.43
8:Z:25:GLU:HA	8:Z:30:GLU:OE1	2.18	0.43
5:W:133:ILE:O	5:W:137:THR:HG22	2.19	0.43
3:U:14:ALA:O	3:U:15:LYS:HG2	2.20	0.42
1:Q:39:PRO:HB3	1:Q:43:TRP:CD1	2.54	0.42
1:Q:41:VAL:O	1:Q:45:GLU:HG2	2.21	0.41
6:X:84:LEU:HB3	6:X:88:LYS:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:95:CYS:HA	4:V:115:CYS:HA	2.03	0.41
2:S:34:LYS:HE3	2:S:34:LYS:HB2	1.92	0.41
3:U:41:TYR:O	3:U:45:ILE:HG13	2.22	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	Q	38/40 (95%)	36 (95%)	2 (5%)	0	100	100
2	S	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
3	U	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
4	V	138/140 (99%)	131 (95%)	6 (4%)	1 (1%)	22	57
5	W	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
6	X	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
7	Y	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
8	Z	82/84 (98%)	79 (96%)	3 (4%)	0	100	100
9	a	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
10	b	99/126 (79%)	98 (99%)	1 (1%)	0	100	100
11	c	154/156 (99%)	146 (95%)	8 (5%)	0	100	100
12	d	173/175 (99%)	169 (98%)	4 (2%)	0	100	100
13	e	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
14	f	40/42 (95%)	39 (98%)	1 (2%)	0	100	100
15	g	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
16	h	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
17	i	345/347 (99%)	331 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	j	95/113 (84%)	89 (94%)	6 (6%)	0	100	100
19	k	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
20	l	601/603 (100%)	577 (96%)	24 (4%)	0	100	100
21	m	125/175 (71%)	114 (91%)	11 (9%)	0	100	100
22	n	54/56 (96%)	52 (96%)	1 (2%)	1 (2%)	8	33
23	o	126/128 (98%)	119 (94%)	6 (5%)	1 (1%)	19	54
24	p	176/178 (99%)	169 (96%)	7 (4%)	0	100	100
25	r	457/459 (100%)	445 (97%)	12 (3%)	0	100	100
26	s	299/318 (94%)	291 (97%)	8 (3%)	0	100	100
27	u	169/171 (99%)	163 (96%)	6 (4%)	0	100	100
28	v	122/125 (98%)	114 (93%)	8 (7%)	0	100	100
29	w	318/320 (99%)	304 (96%)	14 (4%)	0	100	100
All	All	4586/4751 (96%)	4406 (96%)	177 (4%)	3 (0%)	54	83

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	n	36	THR
23	o	24	ASP
4	V	46	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Q	34/34 (100%)	34 (100%)	0	100	100
2	S	58/58 (100%)	58 (100%)	0	100	100
3	U	69/69 (100%)	69 (100%)	0	100	100
4	V	101/101 (100%)	101 (100%)	0	100	100
5	W	99/99 (100%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	X	76/81 (94%)	76 (100%)	0	100	100
7	Y	63/63 (100%)	63 (100%)	0	100	100
8	Z	65/65 (100%)	65 (100%)	0	100	100
9	a	121/122 (99%)	121 (100%)	0	100	100
10	b	98/119 (82%)	98 (100%)	0	100	100
11	c	137/141 (97%)	135 (98%)	2 (2%)	65	85
12	d	155/155 (100%)	155 (100%)	0	100	100
13	e	99/99 (100%)	99 (100%)	0	100	100
14	f	35/38 (92%)	35 (100%)	0	100	100
15	g	108/108 (100%)	108 (100%)	0	100	100
16	h	93/93 (100%)	93 (100%)	0	100	100
17	i	311/311 (100%)	309 (99%)	2 (1%)	86	94
18	j	88/99 (89%)	88 (100%)	0	100	100
19	k	85/85 (100%)	85 (100%)	0	100	100
20	l	537/537 (100%)	536 (100%)	1 (0%)	93	97
21	m	99/141 (70%)	99 (100%)	0	100	100
22	n	46/53 (87%)	46 (100%)	0	100	100
23	o	113/113 (100%)	111 (98%)	2 (2%)	59	82
24	p	158/159 (99%)	154 (98%)	4 (2%)	47	75
25	r	410/410 (100%)	410 (100%)	0	100	100
26	s	263/275 (96%)	261 (99%)	2 (1%)	81	92
27	u	153/153 (100%)	153 (100%)	0	100	100
28	v	97/111 (87%)	97 (100%)	0	100	100
29	w	277/283 (98%)	275 (99%)	2 (1%)	84	93
All	All	4048/4175 (97%)	4033 (100%)	15 (0%)	91	96

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	c	32	VAL
11	c	103	GLU
17	i	268	GLN
17	i	323	MET
20	l	357	ARG

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Mol	Chain	Res	Type
23	o	22	GLU
23	o	24	ASP
24	p	59	LYS
24	p	62	GLN
24	p	64	LEU
24	p	65	ARG
26	s	22	LEU
26	s	24	GLU
29	w	241	TYR
29	w	261	ARG

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

Mol	Chain	Res	Type
20	l	320	ASN
22	n	11	HIS
22	n	14	HIS
23	o	79	ASN
24	p	12	HIS
24	p	33	HIS
25	r	26	ASN

### 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 [i](#)

21 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$
33	PLX	r	503	-	51,51,51	1.15	4 (7%)	55,59,59	0.60	1 (1%)
34	UQ	s	401	-	28,28,63	3.29	7 (25%)	34,37,79	2.67	10 (29%)
30	PEE	m	201	-	40,40,50	1.15	5 (12%)	43,45,55	0.98	2 (4%)
32	CDL	a	201	-	90,90,99	1.13	8 (8%)	96,102,111	0.92	4 (4%)
32	CDL	i	401	-	65,65,99	1.28	8 (12%)	71,77,111	1.02	4 (5%)
33	PLX	a	202	-	51,51,51	1.15	4 (7%)	55,59,59	0.59	1 (1%)
30	PEE	U	101	-	50,50,50	1.16	6 (12%)	53,55,55	0.95	2 (3%)
31	8Q1	X	201	-	31,34,34	1.70	6 (19%)	40,43,43	1.56	6 (15%)
33	PLX	r	502	-	51,51,51	1.14	4 (7%)	55,59,59	0.61	1 (1%)
30	PEE	l	702	-	45,45,50	1.22	6 (13%)	48,50,55	1.01	2 (4%)
35	ADP	w	401	-	24,29,29	3.11	6 (25%)	29,45,45	1.41	4 (13%)
32	CDL	g	202	-	77,77,99	1.20	8 (10%)	83,89,111	0.95	4 (4%)
32	CDL	r	505	-	99,99,99	1.09	9 (9%)	105,111,111	0.85	4 (3%)
33	PLX	g	201	-	51,51,51	1.14	3 (5%)	55,59,59	0.61	1 (1%)
32	CDL	l	701	-	99,99,99	1.09	8 (8%)	105,111,111	0.84	4 (3%)
33	PLX	j	201	-	51,51,51	1.15	4 (7%)	55,59,59	0.58	1 (1%)
30	PEE	r	501	-	50,50,50	1.16	6 (12%)	53,55,55	0.96	2 (3%)
30	PEE	U	102	-	50,50,50	1.16	6 (12%)	53,55,55	0.97	2 (3%)
30	PEE	i	402	-	46,46,50	1.21	6 (13%)	49,51,55	0.99	2 (4%)
32	CDL	r	504	-	98,98,99	1.09	8 (8%)	104,110,111	0.88	4 (3%)
30	PEE	b	201	-	45,45,50	1.22	6 (13%)	48,50,55	0.99	2 (4%)

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
33	PLX	r	503	-	-	32/55/55/55	-
34	UQ	s	401	-	-	8/21/45/87	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	PEE	m	201	-	-	17/44/44/54	-
32	CDL	a	201	-	-	51/101/101/110	-
32	CDL	i	401	-	-	37/76/76/110	-
33	PLX	a	202	-	-	28/55/55/55	-
30	PEE	U	101	-	-	28/54/54/54	-
31	8Q1	X	201	-	-	12/41/41/41	-
33	PLX	r	502	-	-	20/55/55/55	-
30	PEE	l	702	-	-	23/49/49/54	-
35	ADP	w	401	-	-	4/12/32/32	0/3/3/3
32	CDL	g	202	-	-	38/88/88/110	-
32	CDL	r	505	-	-	64/110/110/110	-
33	PLX	g	201	-	-	21/55/55/55	-
32	CDL	l	701	-	-	63/110/110/110	-
33	PLX	j	201	-	-	30/55/55/55	-
30	PEE	r	501	-	-	24/54/54/54	-
30	PEE	U	102	-	-	24/54/54/54	-
30	PEE	i	402	-	-	21/50/50/54	-
32	CDL	r	504	-	-	52/109/109/110	-
30	PEE	b	201	-	-	32/49/49/54	-

All (128) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	s	401	UQ	C13-C14	9.33	1.55	1.33
34	s	401	UQ	C8-C9	9.00	1.54	1.33
35	w	401	ADP	C3'-C4'	-8.86	1.30	1.53
34	s	401	UQ	C18-C19	8.24	1.56	1.32
35	w	401	ADP	O4'-C4'	7.74	1.62	1.45
35	w	401	ADP	O4'-C1'	-6.78	1.31	1.41
31	X	201	8Q1	C34-N36	5.43	1.45	1.33
31	X	201	8Q1	C39-N41	5.42	1.45	1.33
35	w	401	ADP	C6-N6	3.88	1.48	1.34
30	m	201	PEE	C18-C19	3.75	1.53	1.31
30	r	501	PEE	C18-C19	3.74	1.53	1.31
30	U	102	PEE	C18-C19	3.73	1.53	1.31
30	l	702	PEE	C18-C19	3.73	1.53	1.31
30	U	101	PEE	C18-C19	3.72	1.53	1.31
30	i	402	PEE	C18-C19	3.72	1.53	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	b	201	PEE	C18-C19	3.71	1.53	1.31
30	b	201	PEE	C39-C38	3.67	1.53	1.31
30	l	702	PEE	C39-C38	3.66	1.53	1.31
30	i	402	PEE	C39-C38	3.66	1.53	1.31
30	U	101	PEE	C39-C38	3.66	1.53	1.31
30	U	102	PEE	C39-C38	3.66	1.53	1.31
30	r	501	PEE	C39-C38	3.65	1.52	1.31
32	i	401	CDL	OA8-CA7	3.47	1.43	1.33
32	l	701	CDL	OA8-CA7	3.46	1.43	1.33
32	g	202	CDL	OA8-CA7	3.45	1.43	1.33
32	r	505	CDL	OA8-CA7	3.44	1.43	1.33
32	r	504	CDL	OA8-CA7	3.42	1.43	1.33
32	a	201	CDL	OA8-CA7	3.42	1.43	1.33
35	w	401	ADP	O2'-C2'	-3.36	1.35	1.43
35	w	401	ADP	O3'-C3'	3.12	1.50	1.43
32	l	701	CDL	OB6-CB5	3.07	1.43	1.34
32	a	201	CDL	OB6-CB5	3.05	1.42	1.34
32	i	401	CDL	OB6-CB5	3.04	1.42	1.34
32	r	505	CDL	OB6-CB5	3.03	1.42	1.34
32	g	202	CDL	OB8-CB7	3.03	1.42	1.33
32	r	504	CDL	OB6-CB5	3.02	1.42	1.34
32	i	401	CDL	OB8-CB7	3.02	1.42	1.33
32	r	504	CDL	OB8-CB7	3.01	1.42	1.33
32	r	505	CDL	OB8-CB7	3.01	1.42	1.33
32	l	701	CDL	OA6-CA5	3.01	1.42	1.34
32	g	202	CDL	OB6-CB5	3.00	1.42	1.34
32	l	701	CDL	OB8-CB7	2.98	1.42	1.33
32	a	201	CDL	OB8-CB7	2.97	1.42	1.33
32	a	201	CDL	OA6-CA5	2.97	1.42	1.34
32	r	505	CDL	OA6-CA5	2.97	1.42	1.34
32	i	401	CDL	OA6-CA5	2.94	1.42	1.34
32	g	202	CDL	OA6-CA5	2.93	1.42	1.34
32	r	504	CDL	OA6-CA5	2.93	1.42	1.34
33	g	201	PLX	O6-C4	-2.72	1.41	1.44
33	a	202	PLX	O6-C4	-2.71	1.41	1.44
33	r	503	PLX	O6-C4	-2.69	1.41	1.44
34	s	401	UQ	C6-C1	2.68	1.54	1.46
33	j	201	PLX	O6-C4	-2.60	1.41	1.44
30	U	102	PEE	O3-C30	2.50	1.40	1.33
30	i	402	PEE	O3-C30	2.47	1.40	1.33
30	l	702	PEE	O3-C30	2.47	1.40	1.33
30	r	501	PEE	O3-C30	2.46	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	U	101	PEE	O3-C30	2.45	1.40	1.33
32	g	202	CDL	OA6-CA4	-2.43	1.40	1.46
30	b	201	PEE	O3-C30	2.43	1.40	1.33
30	m	201	PEE	O3-C30	2.42	1.40	1.33
33	j	201	PLX	C7-C6	2.42	1.55	1.50
30	i	402	PEE	O2-C2	-2.41	1.40	1.46
33	r	502	PLX	C7-C6	2.41	1.55	1.50
30	r	501	PEE	O2-C2	-2.40	1.40	1.46
30	U	101	PEE	O2-C2	-2.39	1.40	1.46
32	r	504	CDL	OA6-CA4	-2.39	1.40	1.46
30	l	702	PEE	O2-C2	-2.39	1.40	1.46
30	b	201	PEE	O2-C2	-2.38	1.40	1.46
30	m	201	PEE	O2-C10	2.38	1.41	1.34
32	r	505	CDL	OA6-CA4	-2.37	1.40	1.46
32	l	701	CDL	OA6-CA4	-2.36	1.40	1.46
30	U	102	PEE	O2-C10	2.35	1.40	1.34
31	X	201	8Q1	C1-S44	2.34	1.81	1.76
32	i	401	CDL	OA6-CA4	-2.34	1.40	1.46
32	a	201	CDL	OA6-CA4	-2.33	1.40	1.46
30	U	102	PEE	O2-C2	-2.33	1.40	1.46
33	r	503	PLX	C7-C6	2.33	1.55	1.50
34	s	401	UQ	C7-C8	2.32	1.54	1.50
31	X	201	8Q1	C6-C1	2.32	1.53	1.50
33	a	202	PLX	C7-C6	2.31	1.55	1.50
33	g	201	PLX	C7-C6	2.30	1.55	1.50
33	r	502	PLX	O6-C4	-2.29	1.41	1.44
30	U	101	PEE	O2-C10	2.29	1.40	1.34
30	l	702	PEE	O2-C10	2.29	1.40	1.34
30	b	201	PEE	O2-C10	2.27	1.40	1.34
30	i	402	PEE	O2-C10	2.27	1.40	1.34
30	m	201	PEE	O2-C2	-2.25	1.41	1.46
32	g	202	CDL	PB2-OB2	2.24	1.68	1.59
30	r	501	PEE	O2-C10	2.24	1.40	1.34
32	i	401	CDL	PB2-OB2	2.24	1.68	1.59
32	l	701	CDL	PB2-OB2	2.23	1.68	1.59
32	r	505	CDL	PB2-OB5	2.21	1.68	1.59
32	r	504	CDL	PB2-OB2	2.21	1.68	1.59
32	i	401	CDL	PB2-OB5	2.20	1.68	1.59
31	X	201	8Q1	O35-C34	-2.20	1.19	1.23
32	a	201	CDL	PB2-OB2	2.19	1.68	1.59
32	r	505	CDL	PB2-OB2	2.19	1.68	1.59
31	X	201	8Q1	O40-C39	-2.18	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	s	401	UQ	O4-C4	-2.17	1.18	1.23
32	l	701	CDL	PB2-OB5	2.17	1.68	1.59
32	g	202	CDL	PB2-OB5	2.17	1.68	1.59
32	r	504	CDL	PB2-OB5	2.17	1.68	1.59
32	a	201	CDL	OB6-CB4	-2.16	1.41	1.46
32	r	505	CDL	OB6-CB4	-2.15	1.41	1.46
32	a	201	CDL	PB2-OB5	2.15	1.68	1.59
32	r	504	CDL	OB6-CB4	-2.15	1.41	1.46
32	g	202	CDL	OB6-CB4	-2.14	1.41	1.46
33	j	201	PLX	P1-O4	2.13	1.67	1.59
33	r	502	PLX	P1-O4	2.12	1.67	1.59
33	g	201	PLX	P1-O4	2.12	1.67	1.59
32	i	401	CDL	OB6-CB4	-2.11	1.41	1.46
33	r	503	PLX	P1-O4	2.11	1.67	1.59
30	b	201	PEE	O3-C3	-2.10	1.40	1.45
33	a	202	PLX	P1-O4	2.10	1.67	1.59
32	l	701	CDL	OB6-CB4	-2.10	1.41	1.46
30	l	702	PEE	O3-C3	-2.09	1.40	1.45
30	U	101	PEE	O3-C3	-2.09	1.40	1.45
30	m	201	PEE	O3-C3	-2.08	1.40	1.45
30	i	402	PEE	O3-C3	-2.07	1.40	1.45
30	r	501	PEE	O3-C3	-2.05	1.40	1.45
34	s	401	UQ	O1-C1	-2.05	1.18	1.23
33	r	502	PLX	P1-O1	2.04	1.67	1.59
33	j	201	PLX	P1-O1	2.04	1.67	1.59
30	U	102	PEE	O3-C3	-2.03	1.40	1.45
33	r	503	PLX	P1-O1	2.03	1.67	1.59
33	a	202	PLX	P1-O1	2.02	1.67	1.59
32	r	505	CDL	C11-CA5	2.00	1.56	1.50

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	s	401	UQ	C7-C8-C9	-8.74	112.25	126.79
31	X	201	8Q1	C6-C1-S44	6.02	120.46	113.46
34	s	401	UQ	C12-C13-C14	-5.99	113.25	127.66
35	w	401	ADP	N3-C2-N1	-4.48	121.67	128.68
34	s	401	UQ	C10-C9-C8	-4.31	112.61	123.68
34	s	401	UQ	C11-C9-C8	-4.27	112.48	121.12
34	s	401	UQ	C15-C14-C13	-4.20	112.89	123.68
32	a	201	CDL	OA6-CA5-C11	4.19	120.53	111.50
30	U	102	PEE	O2-C10-C11	4.15	120.45	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	m	201	PEE	O2-C10-C11	4.09	120.32	111.50
30	l	702	PEE	O2-C10-C11	4.09	120.31	111.50
32	i	401	CDL	OA6-CA5-C11	4.09	120.31	111.50
32	g	202	CDL	OB6-CB5-C51	4.03	120.19	111.50
32	r	504	CDL	OA6-CA5-C11	4.03	120.19	111.50
32	r	505	CDL	OB6-CB5-C51	3.99	120.11	111.50
34	s	401	UQ	C17-C18-C19	-3.99	114.12	127.75
30	b	201	PEE	O2-C10-C11	3.98	120.07	111.50
30	i	402	PEE	O2-C10-C11	3.97	120.06	111.50
32	i	401	CDL	OB6-CB5-C51	3.94	120.00	111.50
30	r	501	PEE	O2-C10-C11	3.94	120.00	111.50
32	r	504	CDL	OB6-CB5-C51	3.94	119.98	111.50
32	l	701	CDL	OB6-CB5-C51	3.93	119.97	111.50
34	s	401	UQ	C16-C14-C13	-3.92	113.18	121.12
32	a	201	CDL	OB6-CB5-C51	3.91	119.92	111.50
32	l	701	CDL	OA6-CA5-C11	3.91	119.92	111.50
30	U	101	PEE	O2-C10-C11	3.87	119.85	111.50
32	r	505	CDL	OA6-CA5-C11	3.87	119.84	111.50
32	g	202	CDL	OA6-CA5-C11	3.85	119.80	111.50
31	X	201	8Q1	O4-C1-C6	-3.53	119.81	123.99
34	s	401	UQ	C21-C19-C18	-3.44	112.69	122.65
34	s	401	UQ	C20-C19-C18	-3.08	113.74	122.65
31	X	201	8Q1	C37-C38-C39	2.78	116.98	112.36
34	s	401	UQ	CM5-C5-C6	-2.68	120.02	124.40
30	U	102	PEE	O3-C30-C31	2.68	120.33	111.91
30	r	501	PEE	O3-C30-C31	2.68	120.31	111.91
30	l	702	PEE	O3-C30-C31	2.67	120.30	111.91
32	g	202	CDL	OB8-CB7-C71	2.66	120.26	111.91
32	r	504	CDL	OB8-CB7-C71	2.64	120.19	111.91
32	a	201	CDL	OB8-CB7-C71	2.62	120.13	111.91
32	a	201	CDL	OA8-CA7-C31	2.61	120.11	111.91
30	U	101	PEE	O3-C30-C31	2.60	120.06	111.91
32	i	401	CDL	OB8-CB7-C71	2.59	120.03	111.91
32	g	202	CDL	OA8-CA7-C31	2.59	120.02	111.91
32	i	401	CDL	OA8-CA7-C31	2.58	120.00	111.91
32	l	701	CDL	OA8-CA7-C31	2.57	119.98	111.91
35	w	401	ADP	PA-O3A-PB	-2.56	124.03	132.83
32	r	504	CDL	OA8-CA7-C31	2.56	119.95	111.91
32	r	505	CDL	OB8-CB7-C71	2.56	119.93	111.91
30	b	201	PEE	O3-C30-C31	2.54	119.88	111.91
30	i	402	PEE	O3-C30-C31	2.53	119.86	111.91
32	l	701	CDL	OB8-CB7-C71	2.51	119.77	111.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	r	505	CDL	OA8-CA7-C31	2.50	119.75	111.91
33	r	503	PLX	C1A-N1-C1	2.50	120.13	109.92
30	m	201	PEE	O3-C30-C31	2.47	119.66	111.91
33	j	201	PLX	C1A-N1-C1	2.42	119.80	109.92
33	r	502	PLX	C1A-N1-C1	2.40	119.75	109.92
33	g	201	PLX	C1A-N1-C1	2.38	119.66	109.92
33	a	202	PLX	C1A-N1-C1	2.35	119.51	109.92
35	w	401	ADP	O4'-C1'-C2'	-2.28	103.59	106.93
31	X	201	8Q1	C38-C39-N41	2.27	120.24	116.42
31	X	201	8Q1	O4-C1-S44	-2.22	119.72	122.61
31	X	201	8Q1	C43-S44-C1	2.17	108.64	101.87
35	w	401	ADP	C4-C5-N7	-2.16	107.15	109.40

There are no chirality outliers.

All (629) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	U	101	PEE	C1-O3P-P-O1P
30	U	101	PEE	C4-O4P-P-O1P
30	b	201	PEE	C1-O3P-P-O2P
30	b	201	PEE	C1-O3P-P-O1P
30	b	201	PEE	C1-O3P-P-O4P
30	b	201	PEE	C4-O4P-P-O2P
30	i	402	PEE	C11-C10-O2-C2
30	l	702	PEE	C11-C10-O2-C2
30	l	702	PEE	O3P-C1-C2-O2
30	l	702	PEE	C4-O4P-P-O3P
30	m	201	PEE	C11-C10-O2-C2
30	m	201	PEE	O4-C10-O2-C2
31	X	201	8Q1	C1-C6-C7-C8
31	X	201	8Q1	C28-C29-C32-C34
31	X	201	8Q1	C28-C29-C32-O33
31	X	201	8Q1	C30-C29-C32-C34
31	X	201	8Q1	C30-C29-C32-O33
31	X	201	8Q1	C31-C29-C32-C34
31	X	201	8Q1	N36-C37-C38-C39
31	X	201	8Q1	C42-C43-S44-C1
32	a	201	CDL	O1-C1-CA2-OA2
32	a	201	CDL	CA2-C1-CB2-OB2
32	a	201	CDL	CA3-OA5-PA1-OA2
32	a	201	CDL	OA5-CA3-CA4-OA6
32	a	201	CDL	CB2-OB2-PB2-OB3

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Mol	Chain	Res	Type	Atoms
32	a	201	CDL	CB2-OB2-PB2-OB4
32	a	201	CDL	CB3-OB5-PB2-OB3
32	a	201	CDL	CB3-OB5-PB2-OB4
32	g	202	CDL	CB2-C1-CA2-OA2
32	g	202	CDL	CA2-C1-CB2-OB2
32	g	202	CDL	CA3-OA5-PA1-OA3
32	g	202	CDL	CA3-OA5-PA1-OA4
32	i	401	CDL	CA2-OA2-PA1-OA5
32	i	401	CDL	CA3-OA5-PA1-OA3
32	i	401	CDL	CB2-OB2-PB2-OB4
32	i	401	CDL	CB3-OB5-PB2-OB3
32	l	701	CDL	CA2-OA2-PA1-OA4
32	l	701	CDL	CA3-OA5-PA1-OA4
32	l	701	CDL	OA6-CA4-CA6-OA8
32	l	701	CDL	CB2-OB2-PB2-OB3
32	l	701	CDL	CB2-OB2-PB2-OB5
32	l	701	CDL	OB6-CB4-CB6-OB8
32	r	504	CDL	O1-C1-CA2-OA2
32	r	504	CDL	CB2-OB2-PB2-OB3
32	r	504	CDL	CB2-OB2-PB2-OB4
32	r	504	CDL	CB3-OB5-PB2-OB3
32	r	505	CDL	CA2-OA2-PA1-OA3
32	r	505	CDL	CA2-OA2-PA1-OA4
32	r	505	CDL	CA2-OA2-PA1-OA5
32	r	505	CDL	CA3-OA5-PA1-OA2
32	r	505	CDL	CA3-OA5-PA1-OA3
32	r	505	CDL	CA3-OA5-PA1-OA4
32	r	505	CDL	CB2-OB2-PB2-OB3
32	r	505	CDL	CB2-OB2-PB2-OB4
32	r	505	CDL	CB2-OB2-PB2-OB5
33	a	202	PLX	O7-C6-O6-C4
33	a	202	PLX	C2-O1-P1-O2
33	a	202	PLX	C25-C24-O8-C5
33	j	201	PLX	O7-C6-C7-C8
33	j	201	PLX	O9-C24-O8-C5
33	r	502	PLX	O7-C6-O6-C4
33	r	502	PLX	C5-C4-O6-C6
33	r	503	PLX	C2-O1-P1-O4
33	r	503	PLX	C2-O1-P1-O2
33	r	503	PLX	C2-O1-P1-O3
33	r	503	PLX	C25-C24-O8-C5
33	r	503	PLX	O9-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
34	s	401	UQ	C7-C8-C9-C10
34	s	401	UQ	C7-C8-C9-C11
34	s	401	UQ	C12-C11-C9-C10
34	s	401	UQ	C12-C13-C14-C16
35	w	401	ADP	C5'-O5'-PA-O3A
32	i	401	CDL	OA9-CA7-OA8-CA6
32	r	504	CDL	OA9-CA7-OA8-CA6
32	i	401	CDL	C31-CA7-OA8-CA6
32	r	504	CDL	C31-CA7-OA8-CA6
30	i	402	PEE	O4-C10-O2-C2
30	l	702	PEE	O4-C10-O2-C2
32	r	505	CDL	C71-CB7-OB8-CB6
34	s	401	UQ	C17-C18-C19-C21
32	l	701	CDL	C59-C60-C61-C62
30	l	702	PEE	C31-C30-O3-C3
30	U	101	PEE	C17-C18-C19-C20
30	U	102	PEE	C37-C38-C39-C40
32	l	701	CDL	OB9-CB7-OB8-CB6
32	l	701	CDL	O1-C1-CA2-OA2
32	r	504	CDL	O1-C1-CB2-OB2
32	r	505	CDL	OB9-CB7-OB8-CB6
30	b	201	PEE	C11-C10-O2-C2
32	r	505	CDL	C51-CB5-OB6-CB4
32	l	701	CDL	C75-C76-C77-C78
33	a	202	PLX	C9-C10-C11-C12
32	l	701	CDL	C35-C36-C37-C38
33	a	202	PLX	C7-C8-C9-C10
33	g	201	PLX	C10-C11-C12-C13
33	r	502	PLX	C9-C10-C11-C12
33	r	503	PLX	C12-C13-C14-C15
32	l	701	CDL	C71-CB7-OB8-CB6
30	l	702	PEE	O5-C30-O3-C3
32	l	701	CDL	C11-C12-C13-C14
32	r	504	CDL	C55-C56-C57-C58
33	j	201	PLX	C28-C29-C30-C31
34	s	401	UQ	C9-C11-C12-C13
32	a	201	CDL	CB2-C1-CA2-OA2
32	r	505	CDL	CB2-C1-CA2-OA2
30	b	201	PEE	O4-C10-O2-C2
30	U	101	PEE	C31-C30-O3-C3
30	b	201	PEE	C31-C30-O3-C3
30	m	201	PEE	C31-C30-O3-C3

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Mol	Chain	Res	Type	Atoms
32	i	401	CDL	C71-CB7-OB8-CB6
32	g	202	CDL	C71-C72-C73-C74
32	g	202	CDL	C75-C76-C77-C78
33	a	202	PLX	O4-C3-C4-O6
33	j	201	PLX	C15-C16-C17-C18
32	a	201	CDL	O1-C1-CB2-OB2
30	b	201	PEE	O5-C30-O3-C3
30	m	201	PEE	O5-C30-O3-C3
30	U	102	PEE	C11-C10-O2-C2
32	g	202	CDL	CB7-C71-C72-C73
30	U	101	PEE	O5-C30-O3-C3
30	U	102	PEE	C30-C31-C32-C33
32	r	504	CDL	CB7-C71-C72-C73
30	r	501	PEE	C10-C11-C12-C13
32	a	201	CDL	CA7-C31-C32-C33
32	i	401	CDL	CB7-C71-C72-C73
33	g	201	PLX	C12-C13-C14-C15
33	r	502	PLX	C30-C31-C32-C33
32	r	505	CDL	OB7-CB5-OB6-CB4
33	j	201	PLX	C2-C1-N1-C1A
33	r	503	PLX	C2-C1-N1-C1A
32	r	505	CDL	CA7-C31-C32-C33
32	r	505	CDL	CB7-C71-C72-C73
30	U	101	PEE	C11-C10-O2-C2
30	l	702	PEE	C23-C24-C25-C26
32	i	401	CDL	OB9-CB7-OB8-CB6
30	i	402	PEE	C10-C11-C12-C13
32	g	202	CDL	O1-C1-CA2-OA2
32	i	401	CDL	O1-C1-CA2-OA2
32	r	505	CDL	O1-C1-CA2-OA2
30	U	102	PEE	O4-C10-O2-C2
30	U	102	PEE	C17-C18-C19-C20
30	i	402	PEE	C17-C18-C19-C20
30	U	101	PEE	C1-O3P-P-O4P
30	r	501	PEE	C1-O3P-P-O4P
32	a	201	CDL	CB2-OB2-PB2-OB5
32	a	201	CDL	CB3-OB5-PB2-OB2
32	g	202	CDL	CA2-OA2-PA1-OA5
32	g	202	CDL	CA3-OA5-PA1-OA2
32	i	401	CDL	CA3-OA5-PA1-OA2
32	i	401	CDL	CB3-OB5-PB2-OB2
32	l	701	CDL	CA2-OA2-PA1-OA5

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Mol	Chain	Res	Type	Atoms
32	l	701	CDL	CA3-OA5-PA1-OA2
32	l	701	CDL	CB3-OB5-PB2-OB2
32	r	504	CDL	CA2-OA2-PA1-OA5
32	r	504	CDL	CB2-OB2-PB2-OB5
32	r	505	CDL	CB3-OB5-PB2-OB2
33	a	202	PLX	C2-O1-P1-O4
32	l	701	CDL	CB5-C51-C52-C53
32	a	201	CDL	C71-CB7-OB8-CB6
30	m	201	PEE	C13-C14-C15-C16
32	i	401	CDL	CB2-C1-CA2-OA2
32	l	701	CDL	CB2-C1-CA2-OA2
32	r	504	CDL	CB2-C1-CA2-OA2
32	r	504	CDL	CA2-C1-CB2-OB2
30	U	101	PEE	O4-C10-O2-C2
33	r	503	PLX	C2-C1-N1-C1C
32	a	201	CDL	C34-C35-C36-C37
30	i	402	PEE	C35-C36-C37-C38
30	r	501	PEE	C11-C10-O2-C2
32	a	201	CDL	C51-CB5-OB6-CB4
30	r	501	PEE	C12-C13-C14-C15
32	a	201	CDL	C11-C12-C13-C14
32	a	201	CDL	C17-C18-C19-C20
32	i	401	CDL	C71-C72-C73-C74
32	r	504	CDL	C58-C59-C60-C61
32	r	504	CDL	C61-C62-C63-C64
32	r	504	CDL	C62-C63-C64-C65
32	r	505	CDL	C56-C57-C58-C59
33	g	201	PLX	C11-C10-C9-C8
33	g	201	PLX	C33-C34-C35-C36
33	j	201	PLX	C27-C28-C29-C30
33	r	503	PLX	C13-C14-C15-C16
30	U	101	PEE	C43-C44-C45-C46
32	a	201	CDL	C33-C34-C35-C36
32	i	401	CDL	C37-C38-C39-C40
32	r	505	CDL	C12-C13-C14-C15
33	a	202	PLX	C26-C27-C28-C29
33	g	201	PLX	C9-C10-C11-C12
33	r	502	PLX	C27-C28-C29-C30
30	r	501	PEE	O4-C10-O2-C2
32	a	201	CDL	OB7-CB5-OB6-CB4
30	l	702	PEE	C31-C32-C33-C34
32	r	504	CDL	C52-C53-C54-C55

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Mol	Chain	Res	Type	Atoms
30	b	201	PEE	C17-C18-C19-C20
30	l	702	PEE	C37-C38-C39-C40
30	r	501	PEE	C17-C18-C19-C20
32	a	201	CDL	C31-C32-C33-C34
32	r	504	CDL	C82-C83-C84-C85
32	r	505	CDL	C71-C72-C73-C74
32	g	202	CDL	O1-C1-CB2-OB2
32	a	201	CDL	C75-C76-C77-C78
32	l	701	CDL	C54-C55-C56-C57
32	r	504	CDL	C35-C36-C37-C38
32	r	505	CDL	C14-C15-C16-C17
32	l	701	CDL	CB7-C71-C72-C73
32	a	201	CDL	C73-C74-C75-C76
32	i	401	CDL	C52-C53-C54-C55
33	a	202	PLX	C14-C15-C16-C17
33	g	201	PLX	C25-C26-C27-C28
30	b	201	PEE	C33-C34-C35-C36
32	l	701	CDL	C37-C38-C39-C40
32	r	505	CDL	C43-C44-C45-C46
33	a	202	PLX	C11-C12-C13-C14
33	a	202	PLX	C28-C29-C30-C31
33	j	201	PLX	C10-C11-C12-C13
33	j	201	PLX	C7-C8-C9-C10
33	r	502	PLX	C14-C15-C16-C17
33	r	502	PLX	C10-C11-C12-C13
33	r	503	PLX	C33-C34-C35-C36
32	a	201	CDL	C52-C53-C54-C55
32	g	202	CDL	C55-C56-C57-C58
32	g	202	CDL	C59-C60-C61-C62
33	j	201	PLX	C25-C26-C27-C28
33	r	503	PLX	C14-C15-C16-C17
33	r	503	PLX	C27-C28-C29-C30
32	a	201	CDL	OB9-CB7-OB8-CB6
32	l	701	CDL	C39-C40-C41-C42
32	r	505	CDL	C73-C74-C75-C76
32	l	701	CDL	C40-C41-C42-C43
32	r	504	CDL	C20-C21-C22-C23
32	r	504	CDL	C74-C75-C76-C77
32	r	505	CDL	C35-C36-C37-C38
32	r	505	CDL	C52-C53-C54-C55
33	r	503	PLX	C25-C26-C27-C28
32	a	201	CDL	CB5-C51-C52-C53

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Mol	Chain	Res	Type	Atoms
30	r	501	PEE	C13-C14-C15-C16
32	a	201	CDL	C35-C36-C37-C38
32	a	201	CDL	C71-C72-C73-C74
32	l	701	CDL	C55-C56-C57-C58
32	l	701	CDL	C60-C61-C62-C63
32	l	701	CDL	C73-C74-C75-C76
32	r	504	CDL	C73-C74-C75-C76
32	r	504	CDL	C75-C76-C77-C78
32	r	505	CDL	C37-C38-C39-C40
32	r	505	CDL	C59-C60-C61-C62
32	r	505	CDL	C75-C76-C77-C78
32	l	701	CDL	C72-C73-C74-C75
32	r	505	CDL	C74-C75-C76-C77
33	a	202	PLX	C25-C26-C27-C28
33	a	202	PLX	C31-C32-C33-C34
33	a	202	PLX	C33-C34-C35-C36
32	g	202	CDL	C73-C74-C75-C76
32	l	701	CDL	C33-C34-C35-C36
32	r	505	CDL	C79-C80-C81-C82
32	a	201	CDL	C55-C56-C57-C58
30	b	201	PEE	C32-C33-C34-C35
32	r	504	CDL	C71-C72-C73-C74
30	m	201	PEE	C11-C12-C13-C14
32	g	202	CDL	C12-C13-C14-C15
32	i	401	CDL	C11-C12-C13-C14
32	r	504	CDL	C59-C60-C61-C62
32	l	701	CDL	C62-C63-C64-C65
32	r	504	CDL	C56-C57-C58-C59
33	a	202	PLX	C13-C14-C15-C16
33	a	202	PLX	O7-C6-C7-C8
33	a	202	PLX	O9-C24-C25-C26
32	r	504	CDL	C32-C33-C34-C35
32	r	505	CDL	C62-C63-C64-C65
33	r	503	PLX	C29-C30-C31-C32
30	r	501	PEE	C39-C40-C41-C42
32	r	504	CDL	C11-C12-C13-C14
32	r	505	CDL	CB5-C51-C52-C53
30	b	201	PEE	C22-C23-C24-C25
30	r	501	PEE	C31-C32-C33-C34
32	l	701	CDL	C74-C75-C76-C77
33	a	202	PLX	C10-C11-C12-C13
33	r	503	PLX	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
32	i	401	CDL	C32-C33-C34-C35
33	r	503	PLX	C2-C1-N1-C1B
30	U	101	PEE	C31-C32-C33-C34
32	i	401	CDL	C33-C34-C35-C36
32	r	505	CDL	C33-C34-C35-C36
32	r	504	CDL	C71-CB7-OB8-CB6
32	l	701	CDL	C56-C57-C58-C59
32	r	504	CDL	C14-C15-C16-C17
33	j	201	PLX	C12-C13-C14-C15
33	r	502	PLX	C7-C8-C9-C10
33	r	503	PLX	C10-C11-C12-C13
30	b	201	PEE	C37-C38-C39-C40
32	r	504	CDL	OB9-CB7-OB8-CB6
33	r	502	PLX	C33-C34-C35-C36
30	l	702	PEE	C19-C20-C21-C22
30	r	501	PEE	C30-C31-C32-C33
32	r	504	CDL	C40-C41-C42-C43
33	g	201	PLX	C31-C32-C33-C34
30	U	101	PEE	C21-C22-C23-C24
33	j	201	PLX	C13-C14-C15-C16
32	l	701	CDL	C52-C53-C54-C55
30	U	101	PEE	C22-C23-C24-C25
32	r	505	CDL	C61-C62-C63-C64
33	r	502	PLX	C28-C29-C30-C31
30	U	101	PEE	C36-C37-C38-C39
32	a	201	CDL	C22-C23-C24-C25
30	U	102	PEE	C13-C14-C15-C16
32	l	701	CDL	C71-C72-C73-C74
32	r	505	CDL	C32-C33-C34-C35
33	j	201	PLX	C2-C1-N1-C1C
33	j	201	PLX	C2-C1-N1-C1B
32	a	201	CDL	C74-C75-C76-C77
32	r	505	CDL	C42-C43-C44-C45
30	i	402	PEE	C19-C20-C21-C22
30	m	201	PEE	C19-C20-C21-C22
32	i	401	CDL	C35-C36-C37-C38
33	j	201	PLX	C26-C27-C28-C29
33	r	503	PLX	C28-C29-C30-C31
30	U	102	PEE	C33-C34-C35-C36
32	a	201	CDL	C59-C60-C61-C62
33	g	201	PLX	C13-C14-C15-C16
30	U	102	PEE	C23-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
30	i	402	PEE	C18-C19-C20-C21
30	r	501	PEE	C36-C37-C38-C39
30	b	201	PEE	C4-O4P-P-O3P
32	i	401	CDL	CB2-OB2-PB2-OB5
32	r	504	CDL	CB3-OB5-PB2-OB2
30	b	201	PEE	C12-C13-C14-C15
30	i	402	PEE	C30-C31-C32-C33
33	a	202	PLX	O4-C3-C4-C5
32	l	701	CDL	CA7-C31-C32-C33
32	g	202	CDL	C60-C61-C62-C63
32	l	701	CDL	C31-C32-C33-C34
32	r	505	CDL	C82-C83-C84-C85
32	i	401	CDL	C14-C15-C16-C17
30	r	501	PEE	C40-C41-C42-C43
33	j	201	PLX	C9-C10-C11-C12
30	b	201	PEE	C1-C2-C3-O3
30	r	501	PEE	C1-C2-C3-O3
32	g	202	CDL	CA3-CA4-CA6-OA8
32	r	505	CDL	CB3-CB4-CB6-OB8
33	r	502	PLX	C3-C4-C5-O8
32	i	401	CDL	C75-C76-C77-C78
32	r	504	CDL	C60-C61-C62-C63
30	U	102	PEE	C12-C13-C14-C15
32	r	505	CDL	C55-C56-C57-C58
30	m	201	PEE	O3-C30-C31-C32
32	i	401	CDL	C73-C74-C75-C76
33	r	503	PLX	C9-C10-C11-C12
32	r	505	CDL	C17-C18-C19-C20
30	l	702	PEE	C30-C31-C32-C33
30	U	102	PEE	C34-C35-C36-C37
30	i	402	PEE	C24-C25-C26-C27
33	g	201	PLX	C27-C28-C29-C30
33	g	201	PLX	C29-C30-C31-C32
32	g	202	CDL	C54-C55-C56-C57
32	r	505	CDL	OB6-CB4-CB6-OB8
33	j	201	PLX	C14-C15-C16-C17
31	X	201	8Q1	C31-C29-C32-O33
32	i	401	CDL	CA7-C31-C32-C33
32	l	701	CDL	C82-C83-C84-C85
32	l	701	CDL	C64-C65-C66-C67
32	a	201	CDL	C32-C33-C34-C35
30	r	501	PEE	C41-C42-C43-C44

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Mol	Chain	Res	Type	Atoms
30	l	702	PEE	O3P-C1-C2-C3
32	a	201	CDL	OA5-CA3-CA4-CA6
30	U	102	PEE	C14-C15-C16-C17
33	r	503	PLX	C26-C27-C28-C29
31	X	201	8Q1	C29-C32-C34-O35
32	r	505	CDL	CA5-C11-C12-C13
30	m	201	PEE	C23-C24-C25-C26
32	r	505	CDL	C76-C77-C78-C79
33	j	201	PLX	C33-C34-C35-C36
30	i	402	PEE	C31-C32-C33-C34
32	a	201	CDL	C60-C61-C62-C63
32	r	505	CDL	C41-C42-C43-C44
30	i	402	PEE	C1-C2-C3-O3
30	l	702	PEE	C1-C2-C3-O3
32	l	701	CDL	CA3-CA4-CA6-OA8
32	l	701	CDL	CB3-CB4-CB6-OB8
32	r	505	CDL	CA3-CA4-CA6-OA8
33	r	503	PLX	C3-C4-C5-O8
33	g	201	PLX	C14-C15-C16-C17
32	r	505	CDL	C20-C21-C22-C23
32	r	504	CDL	C36-C37-C38-C39
32	g	202	CDL	C13-C14-C15-C16
33	r	503	PLX	C16-C17-C18-C19
33	j	201	PLX	O9-C24-C25-C26
32	r	504	CDL	C37-C38-C39-C40
33	g	201	PLX	C11-C12-C13-C14
30	b	201	PEE	O3P-C1-C2-O2
32	l	701	CDL	O1-C1-CB2-OB2
30	U	102	PEE	C20-C21-C22-C23
32	l	701	CDL	C17-C18-C19-C20
33	j	201	PLX	C34-C35-C36-C37
30	b	201	PEE	C23-C24-C25-C26
30	l	702	PEE	O2-C2-C3-O3
32	i	401	CDL	OB6-CB4-CB6-OB8
32	r	505	CDL	OA6-CA4-CA6-OA8
33	r	502	PLX	O6-C4-C5-O8
33	r	503	PLX	O6-C4-C5-O8
32	a	201	CDL	C14-C15-C16-C17
32	r	505	CDL	C54-C55-C56-C57
33	a	202	PLX	C27-C28-C29-C30
30	l	702	PEE	C21-C22-C23-C24
32	r	505	CDL	C63-C64-C65-C66

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Mol	Chain	Res	Type	Atoms
33	r	503	PLX	C36-C37-C38-C39
33	r	503	PLX	C31-C32-C33-C34
30	i	402	PEE	C2-C1-O3P-P
32	r	505	CDL	CB4-CB3-OB5-PB2
30	U	102	PEE	C38-C39-C40-C41
32	r	504	CDL	C42-C43-C44-C45
33	r	503	PLX	C15-C16-C17-C18
33	g	201	PLX	C36-C37-C38-C39
33	r	503	PLX	O8-C24-C25-C26
32	a	201	CDL	OB5-CB3-CB4-CB6
32	i	401	CDL	OA5-CA3-CA4-CA6
33	j	201	PLX	O4-C3-C4-C5
32	g	202	CDL	C14-C15-C16-C17
30	U	101	PEE	C15-C16-C17-C18
32	r	504	CDL	C72-C73-C74-C75
30	i	402	PEE	C32-C33-C34-C35
32	l	701	CDL	C63-C64-C65-C66
31	X	201	8Q1	O33-C32-C34-N36
30	b	201	PEE	C13-C14-C15-C16
30	m	201	PEE	C3-C2-O2-C10
30	U	101	PEE	C19-C20-C21-C22
33	g	201	PLX	C3-C4-C5-O8
30	U	102	PEE	O3P-C1-C2-O2
32	a	201	CDL	OB5-CB3-CB4-OB6
32	i	401	CDL	OA5-CA3-CA4-OA6
32	l	701	CDL	OA5-CA3-CA4-OA6
33	g	201	PLX	O4-C3-C4-O6
33	j	201	PLX	O4-C3-C4-O6
33	r	502	PLX	O4-C3-C4-O6
30	i	402	PEE	O2-C2-C3-O3
30	r	501	PEE	O2-C2-C3-O3
32	g	202	CDL	OA6-CA4-CA6-OA8
32	i	401	CDL	OA6-CA4-CA6-OA8
33	g	201	PLX	O6-C4-C5-O8
30	U	102	PEE	C15-C16-C17-C18
33	g	201	PLX	C28-C29-C30-C31
30	U	102	PEE	C31-C30-O3-C3
32	l	701	CDL	C31-CA7-OA8-CA6
30	U	101	PEE	C4-O4P-P-O3P
33	a	202	PLX	C3-O4-P1-O1
33	g	201	PLX	C3-O4-P1-O1
32	r	505	CDL	C83-C84-C85-C86

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Mol	Chain	Res	Type	Atoms
32	l	701	CDL	C58-C59-C60-C61
30	U	101	PEE	C1-O3P-P-O2P
30	U	101	PEE	C4-O4P-P-O2P
30	b	201	PEE	C4-O4P-P-O1P
30	i	402	PEE	C1-O3P-P-O1P
30	l	702	PEE	C4-O4P-P-O2P
30	r	501	PEE	C1-O3P-P-O2P
30	r	501	PEE	C1-O3P-P-O1P
30	r	501	PEE	C4-O4P-P-O1P
32	g	202	CDL	CA2-OA2-PA1-OA4
32	g	202	CDL	CB2-OB2-PB2-OB4
32	g	202	CDL	CB3-OB5-PB2-OB4
32	i	401	CDL	CA3-OA5-PA1-OA4
32	i	401	CDL	CB2-OB2-PB2-OB3
32	l	701	CDL	CB3-OB5-PB2-OB3
32	l	701	CDL	CB3-OB5-PB2-OB4
32	r	504	CDL	CA2-OA2-PA1-OA3
32	r	504	CDL	CB3-OB5-PB2-OB4
32	r	505	CDL	CB3-OB5-PB2-OB3
33	a	202	PLX	C3-O4-P1-O2
33	r	502	PLX	C3-O4-P1-O3
35	w	401	ADP	C5'-O5'-PA-O2A
30	U	102	PEE	O3P-C1-C2-C3
30	b	201	PEE	O3P-C1-C2-C3
32	l	701	CDL	OA5-CA3-CA4-CA6
33	g	201	PLX	O4-C3-C4-C5
33	r	502	PLX	O4-C3-C4-C5
32	r	505	CDL	C64-C65-C66-C67
32	g	202	CDL	C58-C59-C60-C61
32	r	505	CDL	C44-C45-C46-C47
33	r	502	PLX	C31-C32-C33-C34
30	U	101	PEE	C30-C31-C32-C33
32	r	504	CDL	CA7-C31-C32-C33
30	U	101	PEE	C38-C39-C40-C41
30	b	201	PEE	C18-C19-C20-C21
32	i	401	CDL	CA3-CA4-CA6-OA8
30	U	102	PEE	O5-C30-O3-C3
32	l	701	CDL	OA9-CA7-OA8-CA6
33	j	201	PLX	C11-C12-C13-C14
33	r	502	PLX	C15-C16-C17-C18
30	b	201	PEE	C34-C35-C36-C37
32	a	201	CDL	C21-C22-C23-C24

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Mol	Chain	Res	Type	Atoms
32	l	701	CDL	C44-C45-C46-C47
32	r	505	CDL	C13-C14-C15-C16
30	U	102	PEE	C22-C23-C24-C25
33	j	201	PLX	C31-C32-C33-C34
32	a	201	CDL	C13-C14-C15-C16
32	a	201	CDL	OA9-CA7-OA8-CA6
32	a	201	CDL	C77-C78-C79-C80
32	a	201	CDL	C31-CA7-OA8-CA6
32	g	202	CDL	C72-C73-C74-C75
33	r	503	PLX	C30-C31-C32-C33
34	s	401	UQ	C12-C11-C9-C8
32	i	401	CDL	C38-C39-C40-C41
30	U	101	PEE	O2-C2-C3-O3
30	b	201	PEE	O2-C2-C3-O3
32	g	202	CDL	CB2-OB2-PB2-OB5
32	g	202	CDL	CB3-OB5-PB2-OB2
33	j	201	PLX	C3-O4-P1-O1
33	r	503	PLX	C3-O4-P1-O1
32	r	504	CDL	C44-C45-C46-C47
33	r	502	PLX	C16-C17-C18-C19
30	r	501	PEE	C38-C39-C40-C41
30	i	402	PEE	C37-C38-C39-C40
33	a	202	PLX	C29-C30-C31-C32
30	U	101	PEE	C12-C13-C14-C15
32	r	504	CDL	C54-C55-C56-C57
30	m	201	PEE	O5-C30-C31-C32
32	g	202	CDL	C19-C20-C21-C22
30	U	102	PEE	C21-C22-C23-C24
30	l	702	PEE	C38-C39-C40-C41
33	r	502	PLX	C13-C14-C15-C16
32	r	504	CDL	C76-C77-C78-C79
33	a	202	PLX	C6-C7-C8-C9
33	j	201	PLX	O6-C6-C7-C8
33	r	503	PLX	C19-C20-C21-C22
32	r	505	CDL	C31-CA7-OA8-CA6
30	i	402	PEE	C22-C23-C24-C25
33	j	201	PLX	C18-C19-C20-C21
33	a	202	PLX	C24-C25-C26-C27
32	g	202	CDL	C11-C12-C13-C14
32	r	505	CDL	C72-C73-C74-C75
30	r	501	PEE	C24-C25-C26-C27
32	r	504	CDL	C53-C54-C55-C56

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Mol	Chain	Res	Type	Atoms
31	X	201	8Q1	C29-C32-C34-N36
30	m	201	PEE	C15-C16-C17-C18
30	m	201	PEE	C22-C23-C24-C25
32	r	504	CDL	C34-C35-C36-C37
33	r	503	PLX	C7-C8-C9-C10
30	U	101	PEE	C34-C35-C36-C37
30	r	501	PEE	C31-C30-O3-C3
33	r	502	PLX	C18-C19-C20-C21
32	r	505	CDL	OA9-CA7-OA8-CA6
30	U	102	PEE	C44-C45-C46-C47
32	g	202	CDL	C17-C18-C19-C20
32	g	202	CDL	C51-C52-C53-C54
30	r	501	PEE	O5-C30-O3-C3
33	a	202	PLX	C16-C17-C18-C19
33	j	201	PLX	C32-C33-C34-C35
32	g	202	CDL	C61-C62-C63-C64
30	r	501	PEE	C15-C16-C17-C18
32	a	201	CDL	C36-C37-C38-C39
32	i	401	CDL	C39-C40-C41-C42
33	a	202	PLX	C30-C31-C32-C33
30	U	102	PEE	C16-C17-C18-C19
30	U	101	PEE	C1-C2-C3-O3
30	b	201	PEE	C10-C11-C12-C13
30	U	101	PEE	C16-C17-C18-C19
30	m	201	PEE	C16-C17-C18-C19
30	b	201	PEE	O4P-C4-C5-N
32	r	504	CDL	C23-C24-C25-C26
30	i	402	PEE	C14-C15-C16-C17
30	U	102	PEE	C39-C40-C41-C42
32	l	701	CDL	C80-C81-C82-C83
32	l	701	CDL	C61-C62-C63-C64
30	U	102	PEE	C18-C19-C20-C21
32	r	504	CDL	C12-C11-CA5-OA6
32	r	505	CDL	C60-C61-C62-C63
30	i	402	PEE	C36-C37-C38-C39
30	l	702	PEE	C16-C17-C18-C19
30	l	702	PEE	C36-C37-C38-C39
30	l	702	PEE	O2-C10-C11-C12
33	j	201	PLX	C30-C31-C32-C33
32	a	201	CDL	C32-C31-CA7-OA8
32	a	201	CDL	C43-C44-C45-C46
32	a	201	CDL	C76-C77-C78-C79

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Mol	Chain	Res	Type	Atoms
30	m	201	PEE	C18-C19-C20-C21
30	r	501	PEE	C18-C19-C20-C21
33	j	201	PLX	C7-C6-O6-C4
32	l	701	CDL	C32-C31-CA7-OA8
32	g	202	CDL	C12-C11-CA5-OA6
30	b	201	PEE	C16-C17-C18-C19
30	b	201	PEE	C38-C39-C40-C41
30	l	702	PEE	C18-C19-C20-C21
32	l	701	CDL	C12-C11-CA5-OA6
32	r	505	CDL	C51-C52-C53-C54
30	b	201	PEE	C15-C16-C17-C18
33	g	201	PLX	C6-C7-C8-C9
30	i	402	PEE	C38-C39-C40-C41
32	l	701	CDL	C14-C15-C16-C17
32	r	505	CDL	C84-C85-C86-C87
32	g	202	CDL	C72-C71-CB7-OB8
32	a	201	CDL	C37-C38-C39-C40
32	i	401	CDL	C15-C16-C17-C18
30	b	201	PEE	C24-C25-C26-C27
35	w	401	ADP	C4'-C5'-O5'-PA
30	b	201	PEE	O3-C30-C31-C32
30	i	402	PEE	C20-C21-C22-C23
32	r	504	CDL	C17-C18-C19-C20
32	l	701	CDL	C32-C33-C34-C35
32	l	701	CDL	C57-C58-C59-C60
30	l	702	PEE	O4-C10-C11-C12
32	l	701	CDL	C12-C11-CA5-OA7
32	r	504	CDL	C12-C11-CA5-OA7
32	r	504	CDL	C12-C13-C14-C15
30	m	201	PEE	C1-C2-C3-O3
32	i	401	CDL	CB3-CB4-CB6-OB8
33	j	201	PLX	C3-C4-C5-O8
33	a	202	PLX	C19-C20-C21-C22
32	g	202	CDL	C72-C71-CB7-OB9
32	r	505	CDL	C15-C16-C17-C18
32	r	504	CDL	CA3-OA5-PA1-OA3
35	w	401	ADP	C5'-O5'-PA-O1A
32	a	201	CDL	C32-C31-CA7-OA9
32	g	202	CDL	C12-C11-CA5-OA7
32	l	701	CDL	C32-C31-CA7-OA9
32	i	401	CDL	C72-C73-C74-C75
30	U	101	PEE	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
30	b	201	PEE	O5-C30-C31-C32
32	g	202	CDL	C21-C22-C23-C24
32	a	201	CDL	C72-C71-CB7-OB8
30	l	702	PEE	C32-C33-C34-C35
32	r	505	CDL	C23-C24-C25-C26
33	g	201	PLX	C24-C25-C26-C27
32	l	701	CDL	C41-C42-C43-C44
34	s	401	UQ	C17-C18-C19-C20
32	a	201	CDL	C72-C71-CB7-OB9
30	m	201	PEE	C34-C35-C36-C37
32	l	701	CDL	C53-C54-C55-C56
33	r	503	PLX	C24-C25-C26-C27
30	U	101	PEE	O3-C30-C31-C32
32	l	701	CDL	C12-C13-C14-C15
30	U	101	PEE	C40-C41-C42-C43
32	l	701	CDL	C72-C71-CB7-OB8

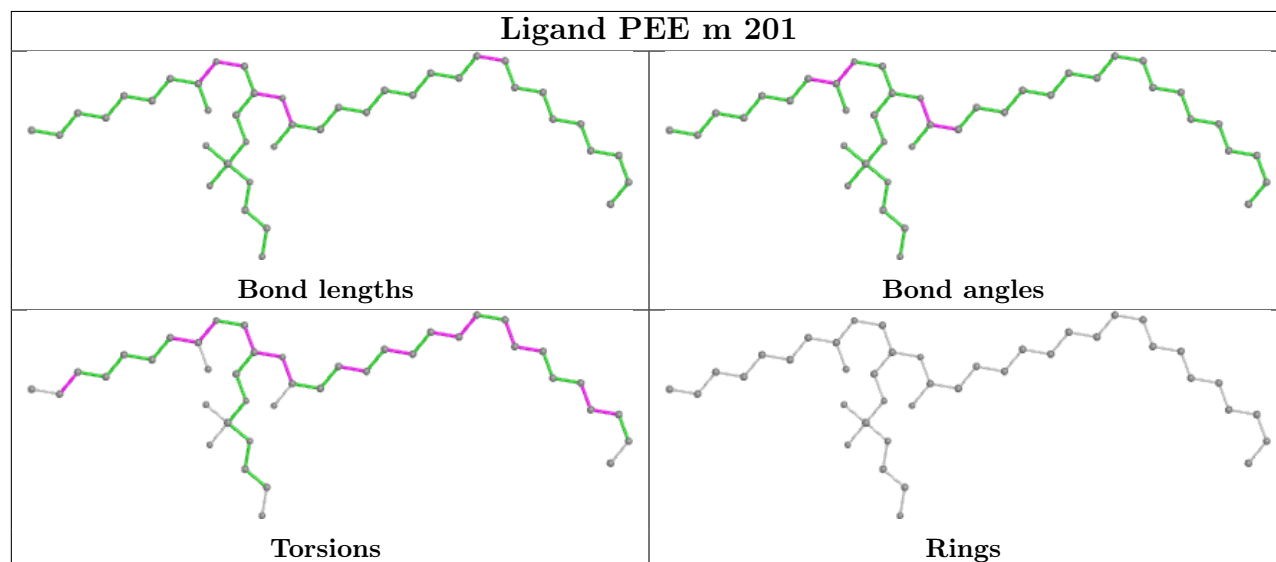
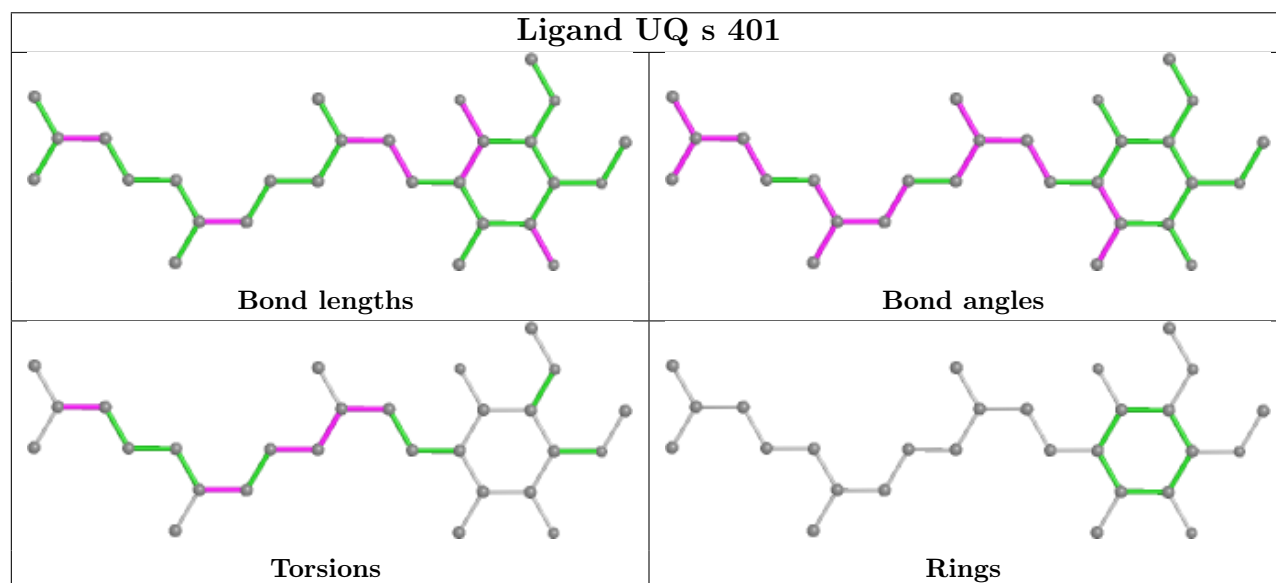
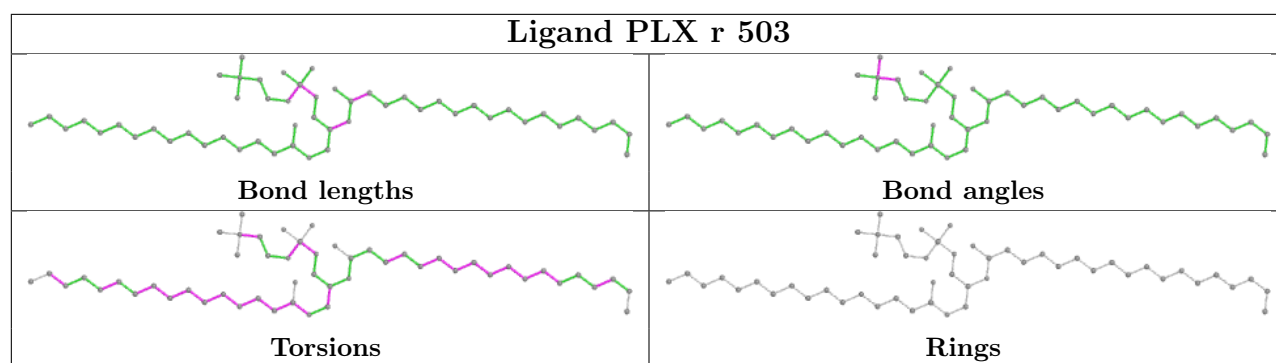
There are no ring outliers.

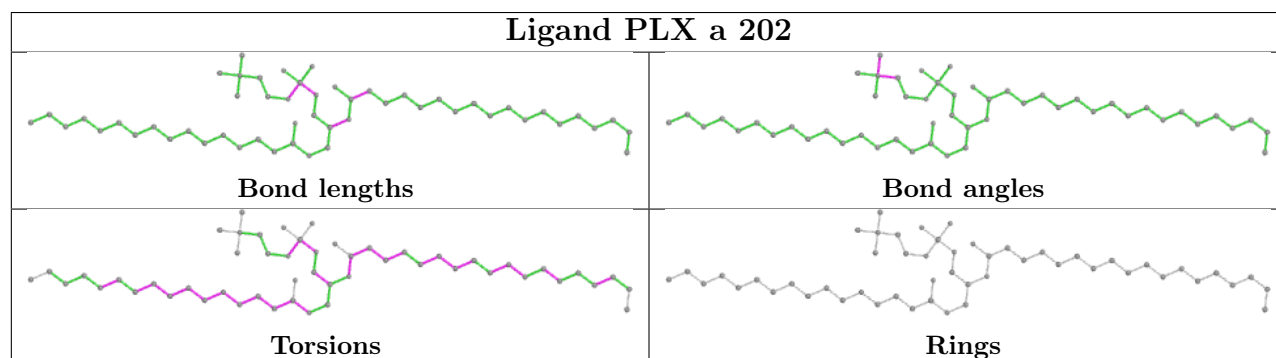
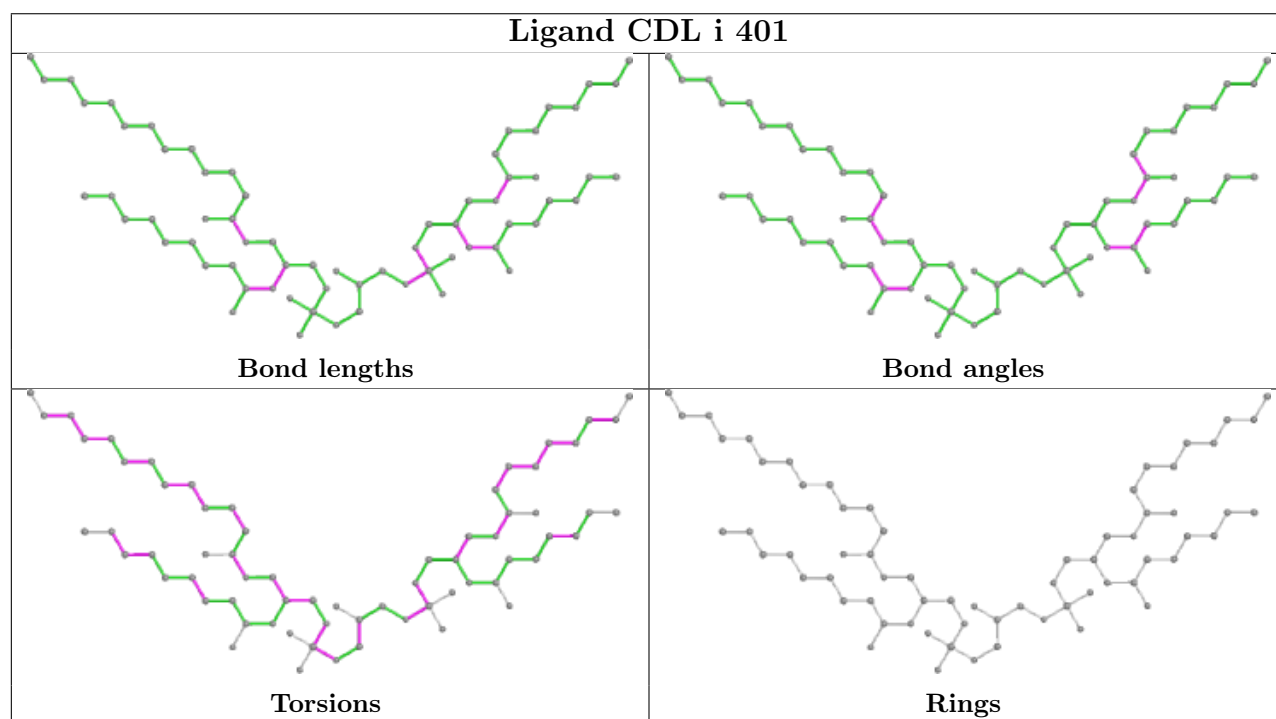
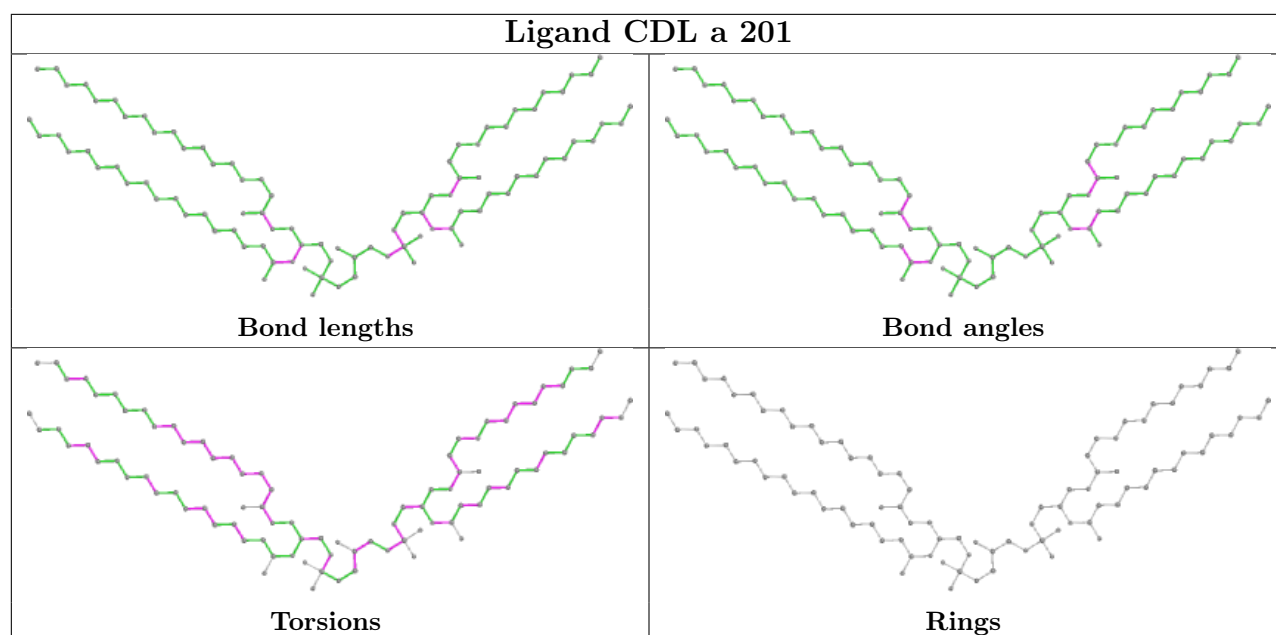
3 monomers are involved in 5 short contacts:

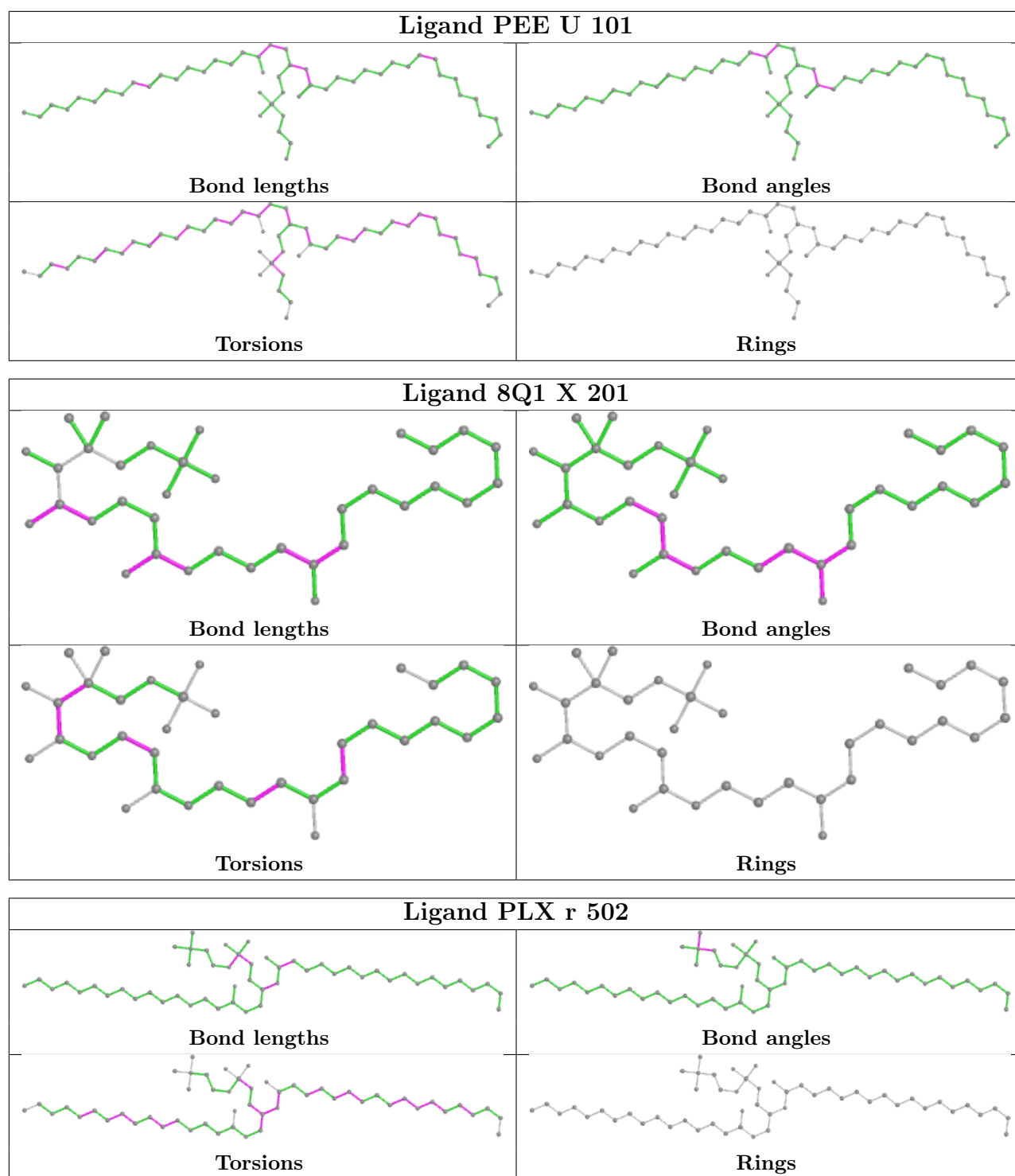
Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	U	101	PEE	1	0
31	X	201	8Q1	3	0
30	U	102	PEE	1	0

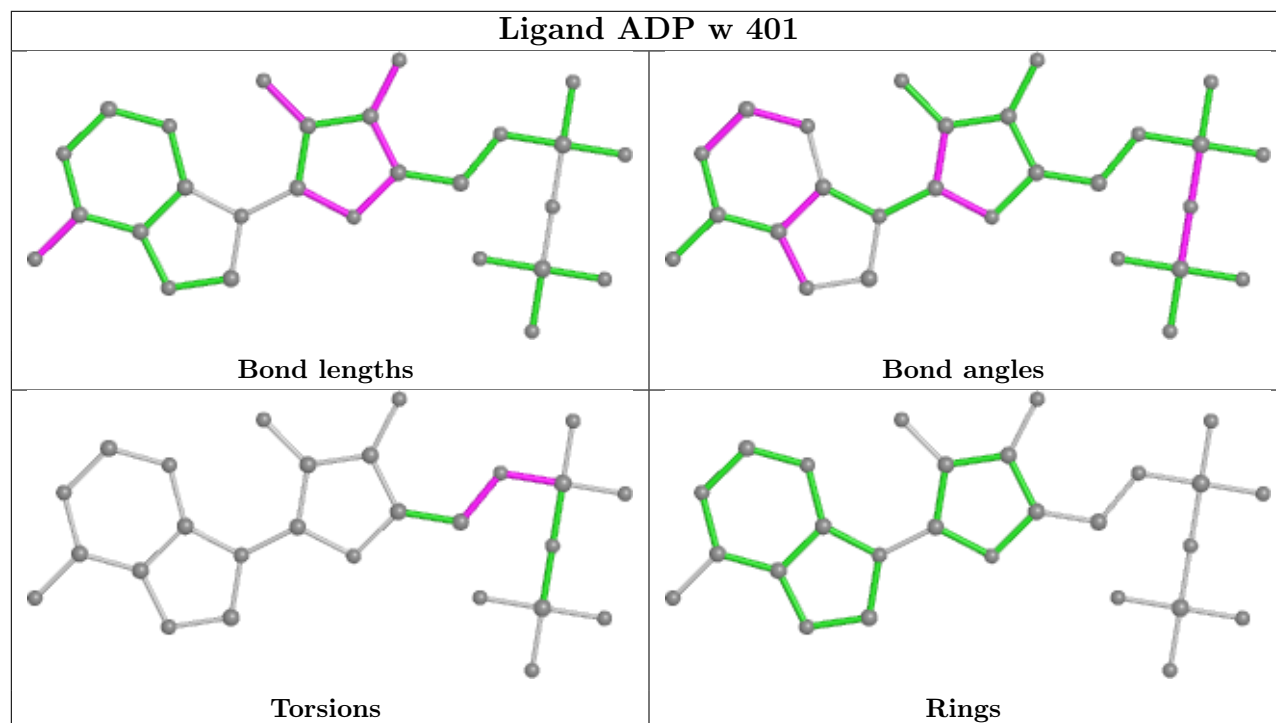
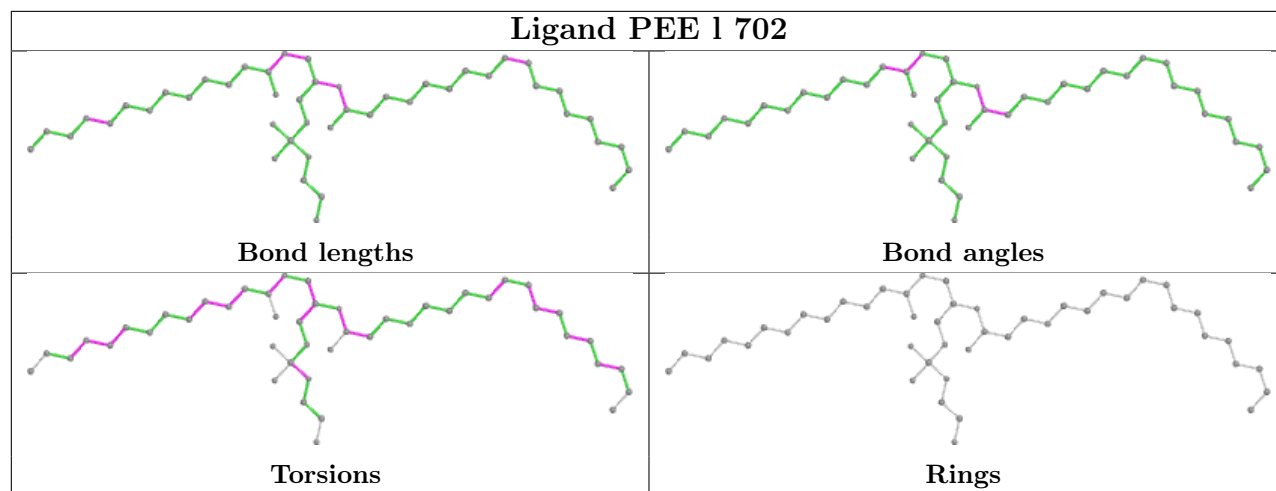
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

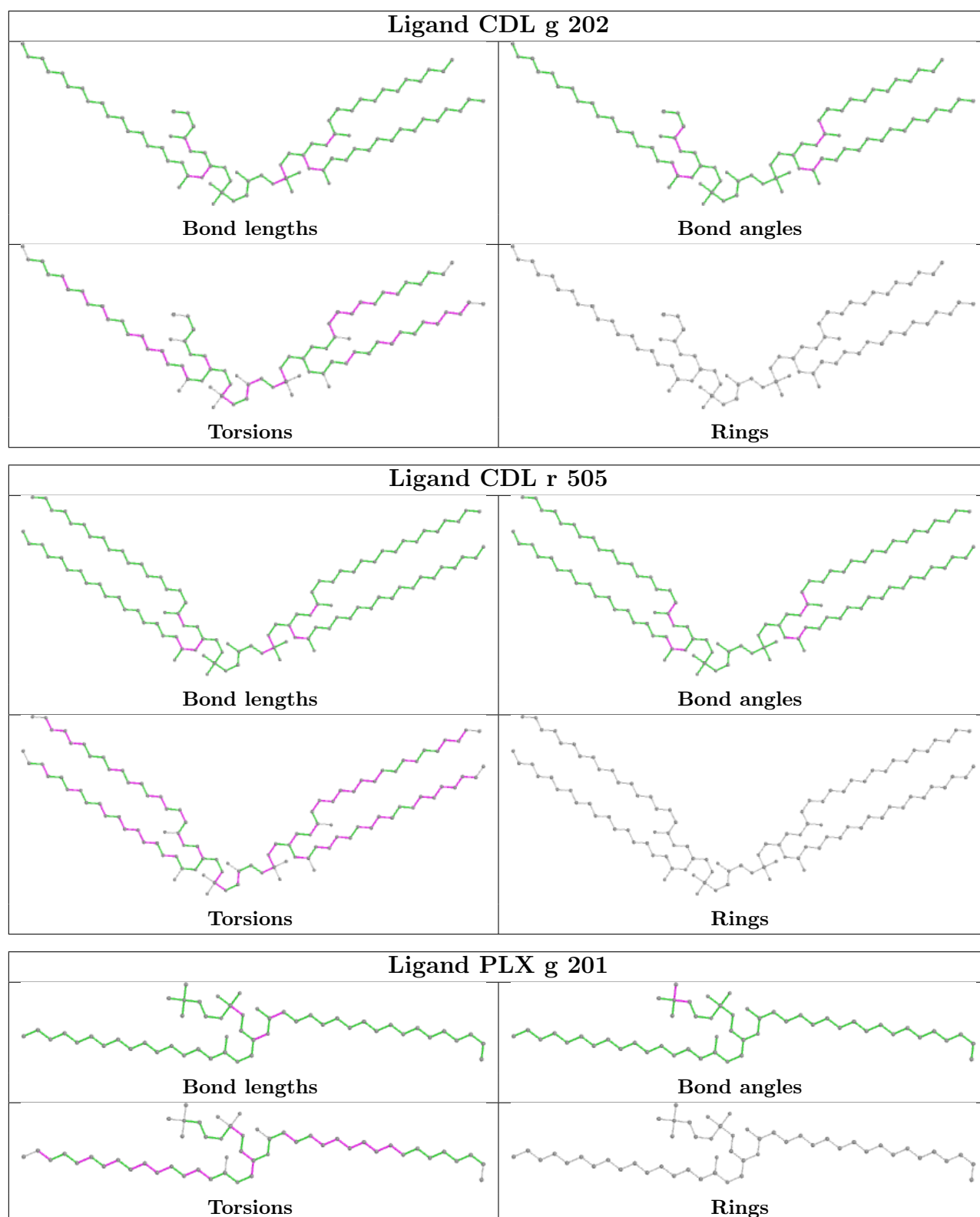


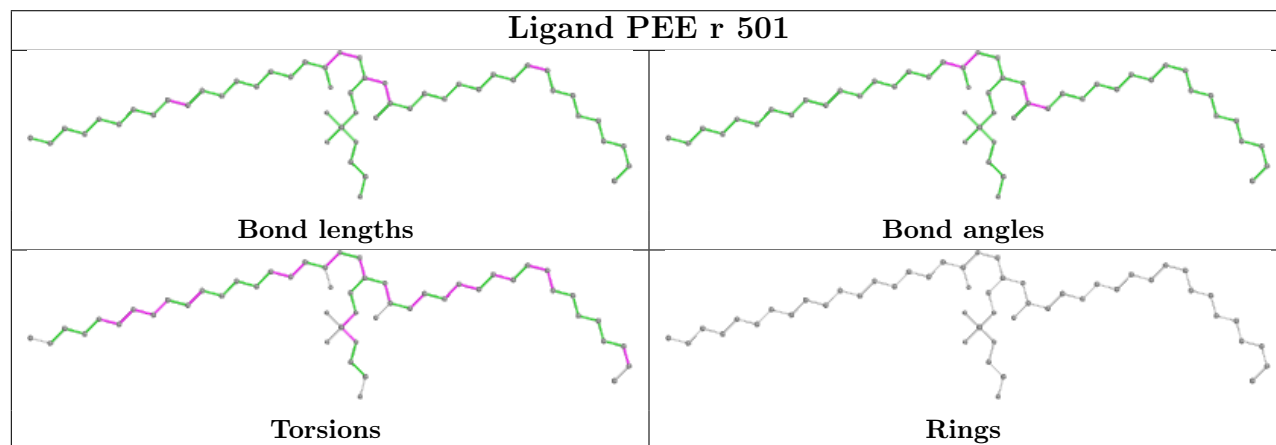
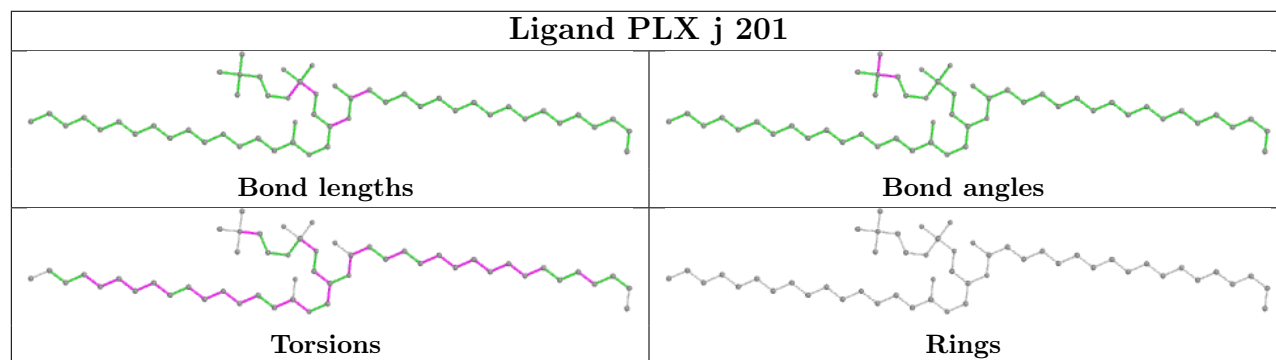
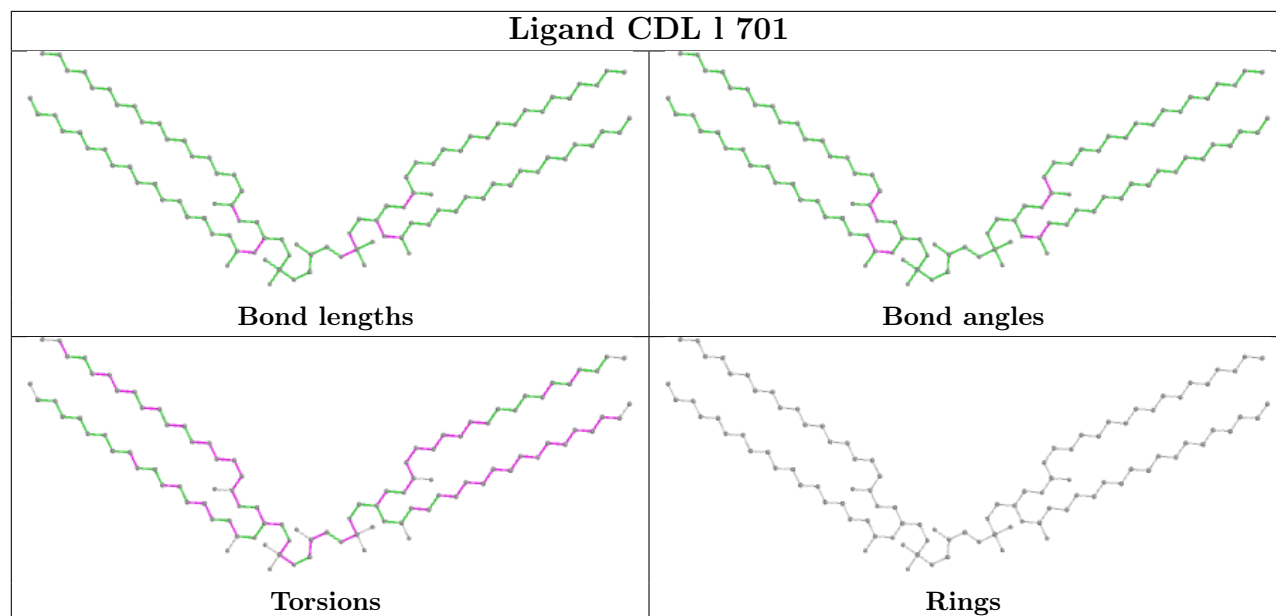


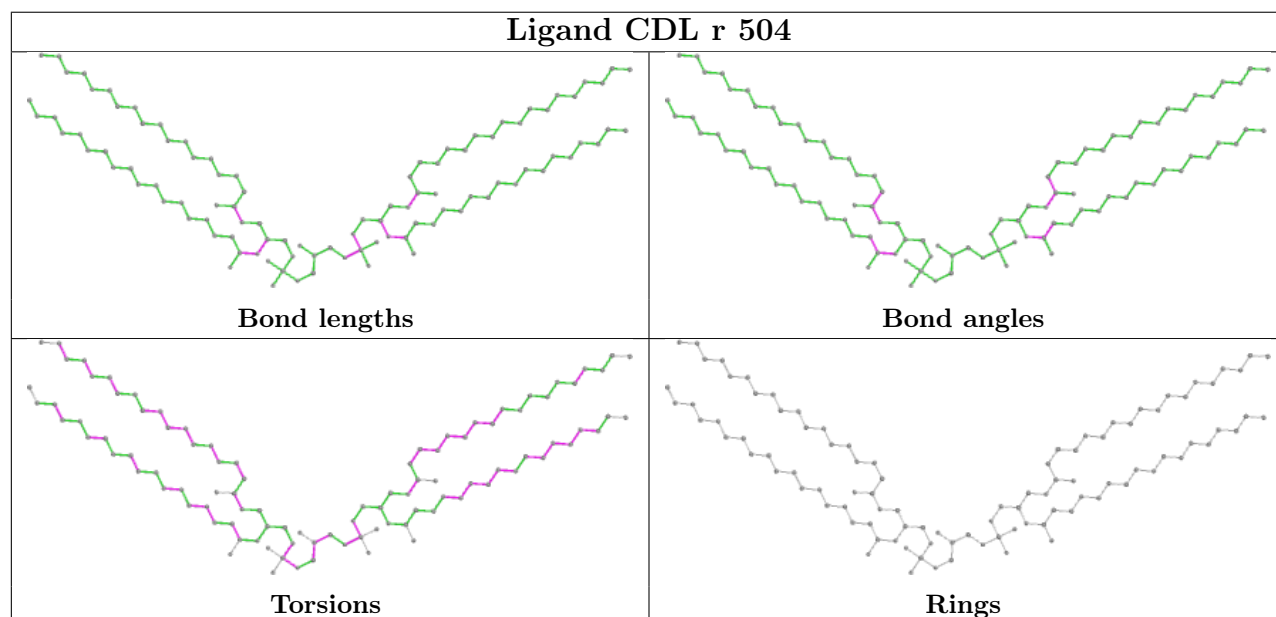
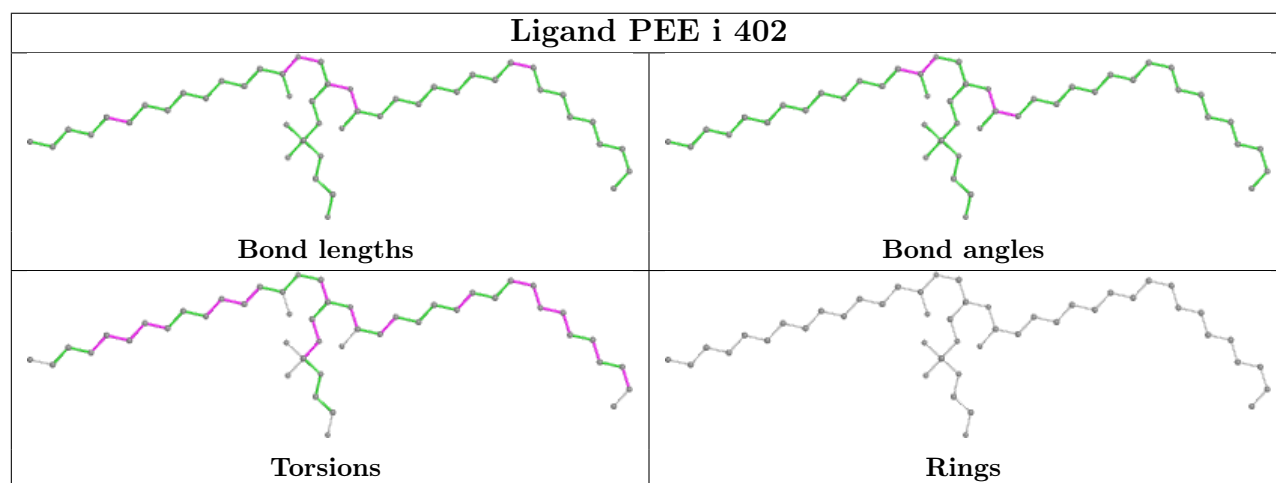
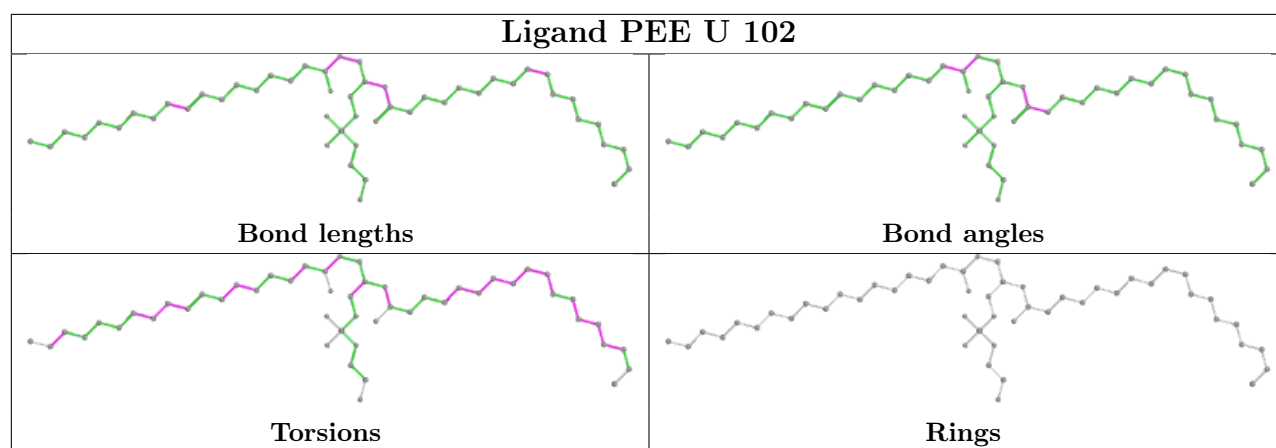


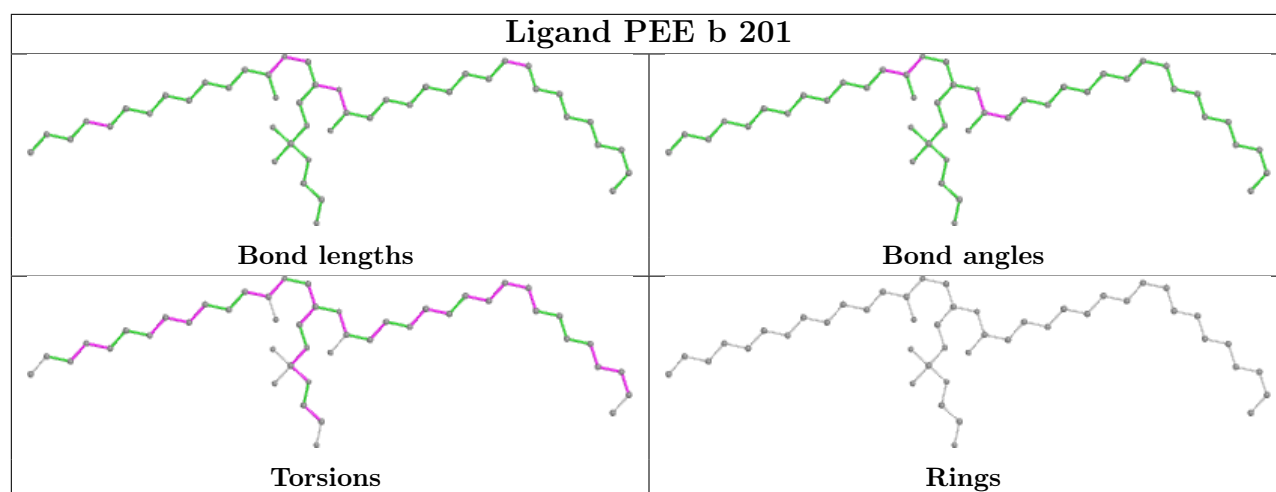












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.



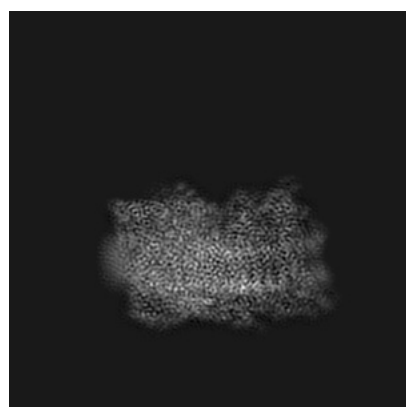
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32206. These allow visual inspection of the internal detail of the map and identification of artifacts.

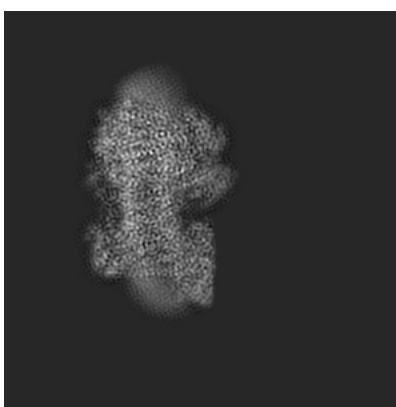
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

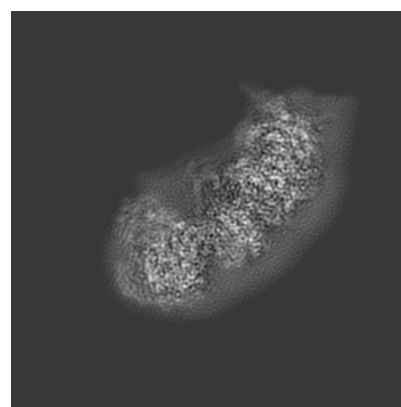
#### 6.1.1 Primary map



X



Y

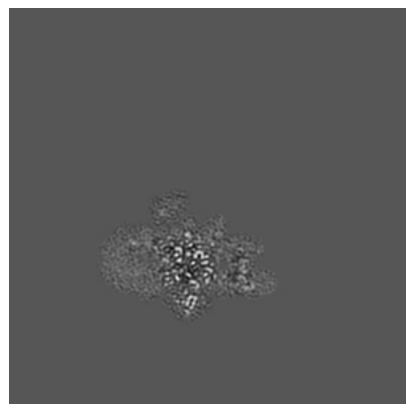


Z

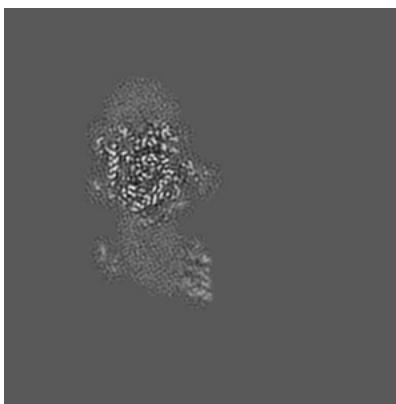
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

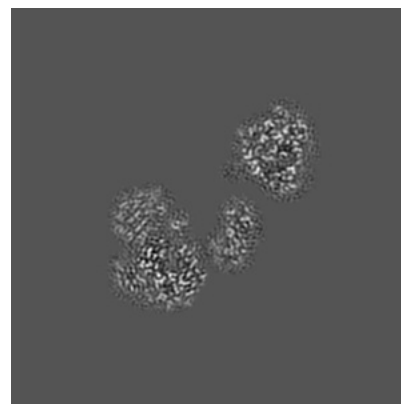
#### 6.2.1 Primary map



X Index: 155



Y Index: 155

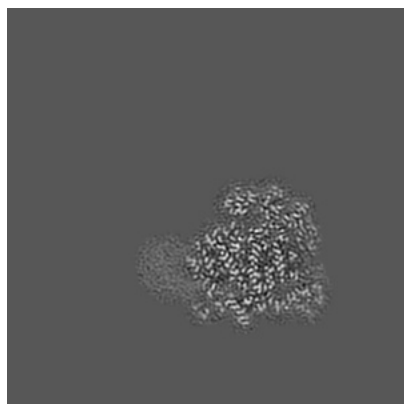


Z Index: 155

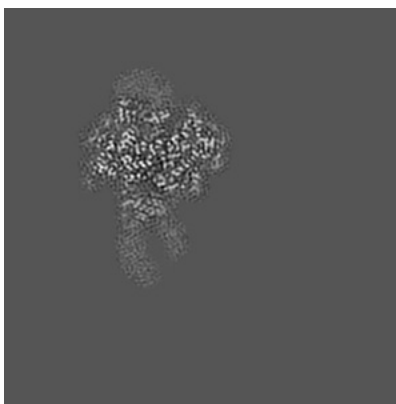
The images above show central slices of the map in three orthogonal directions.

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

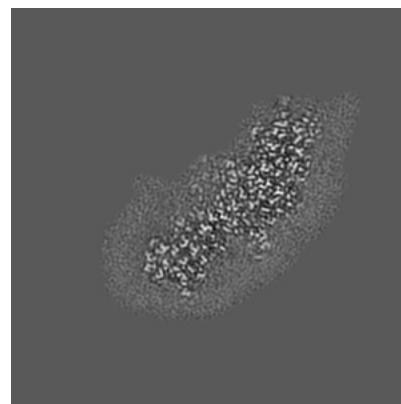
### 6.3.1 Primary map



X Index: 208



Y Index: 180

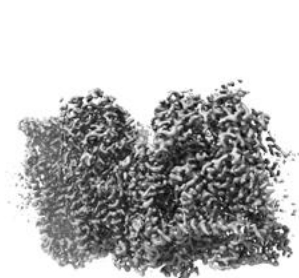


Z Index: 120

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

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

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0288. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

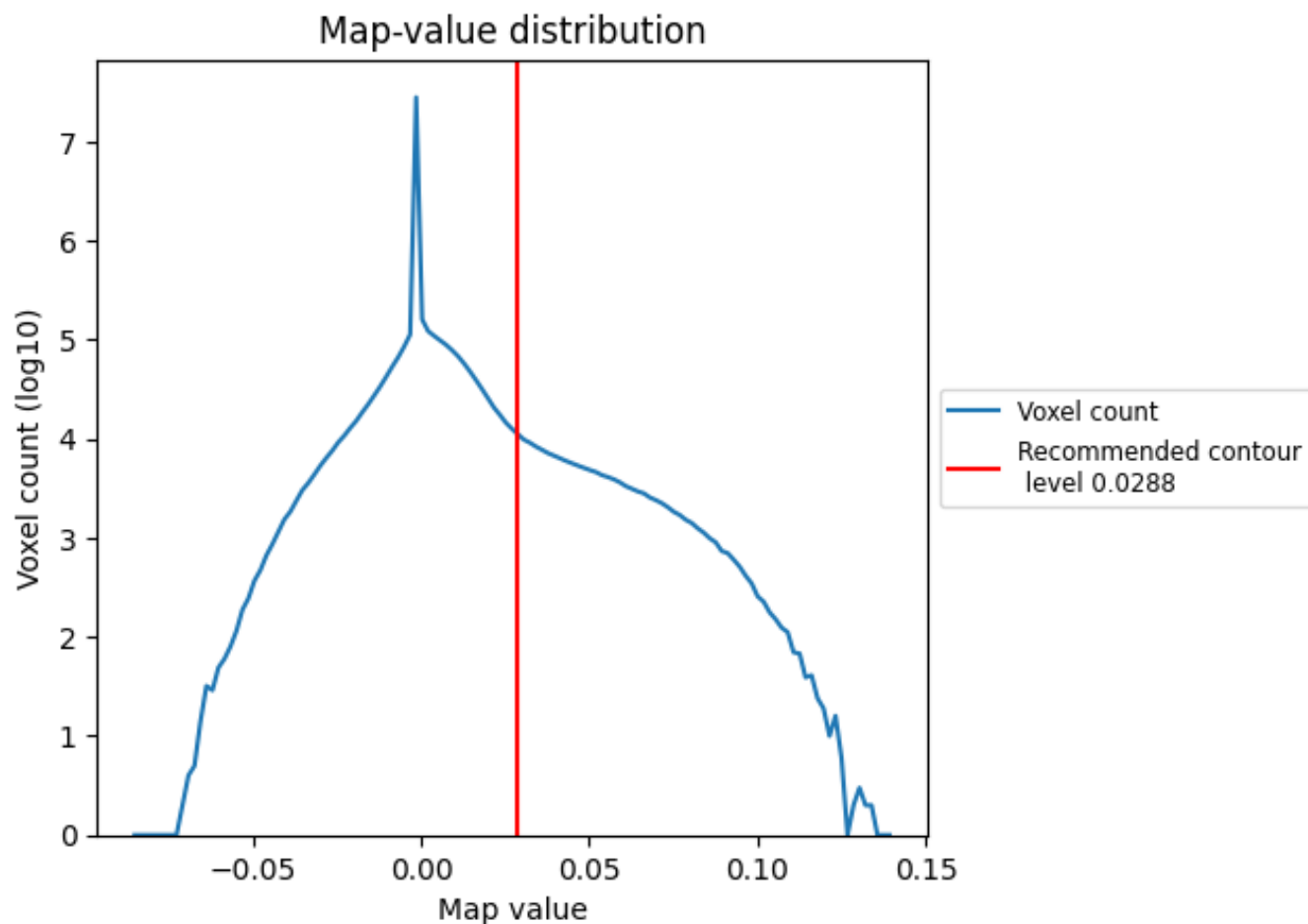
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

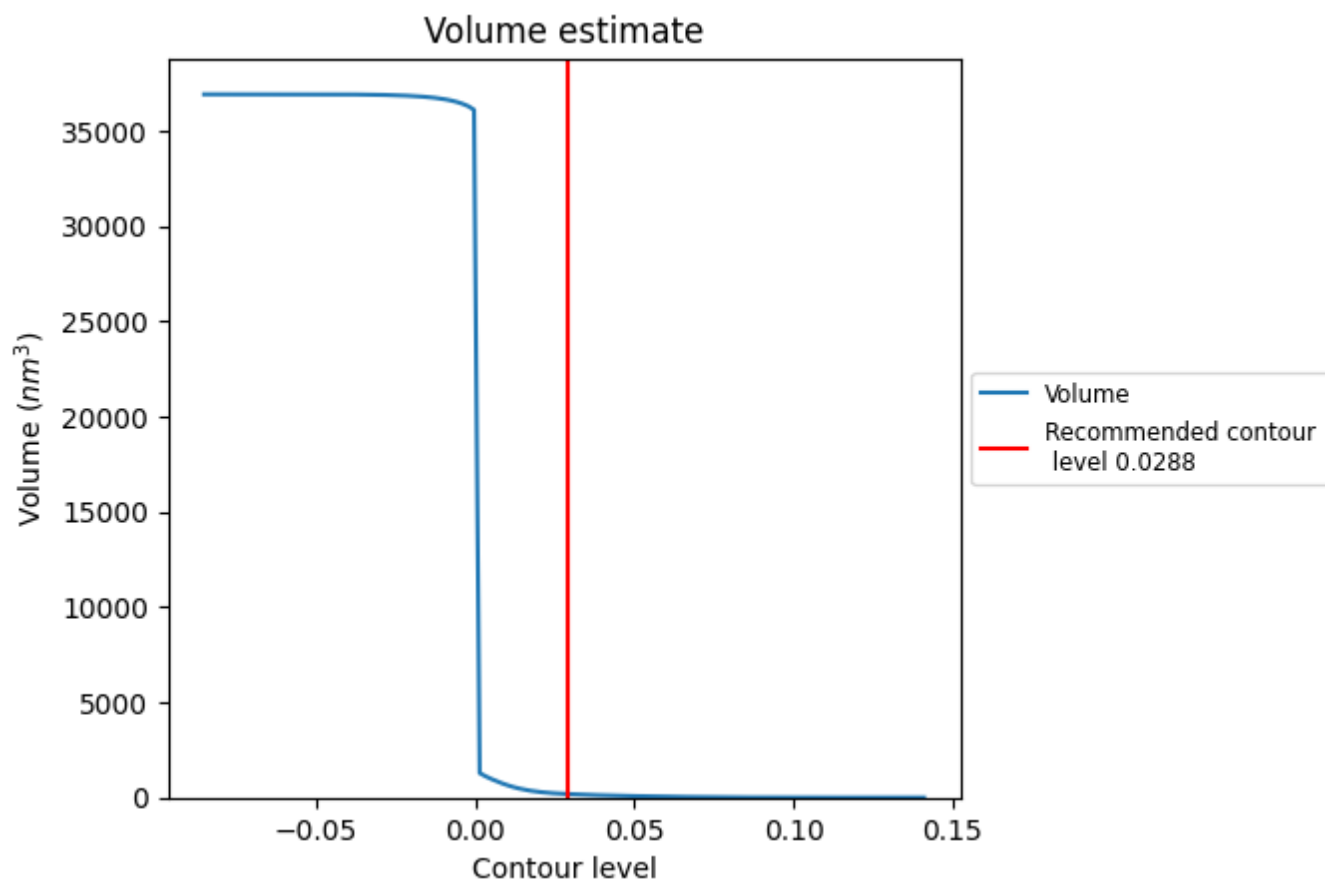
This section contains the results of statistical analysis of the map.

### 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.

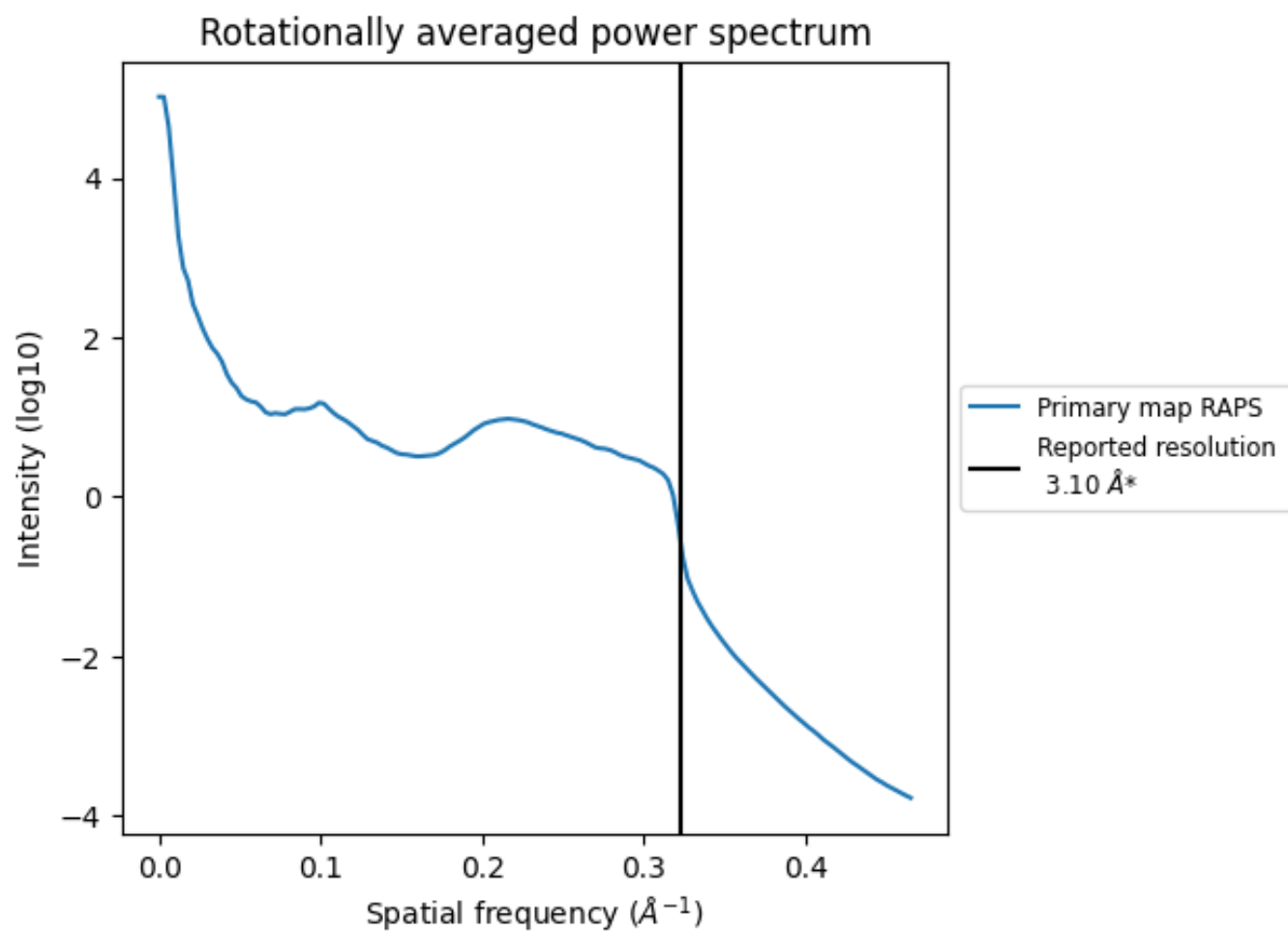
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 188  $\text{nm}^3$ ; this corresponds to an approximate mass of 169 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 0.323 Å<sup>-1</sup>

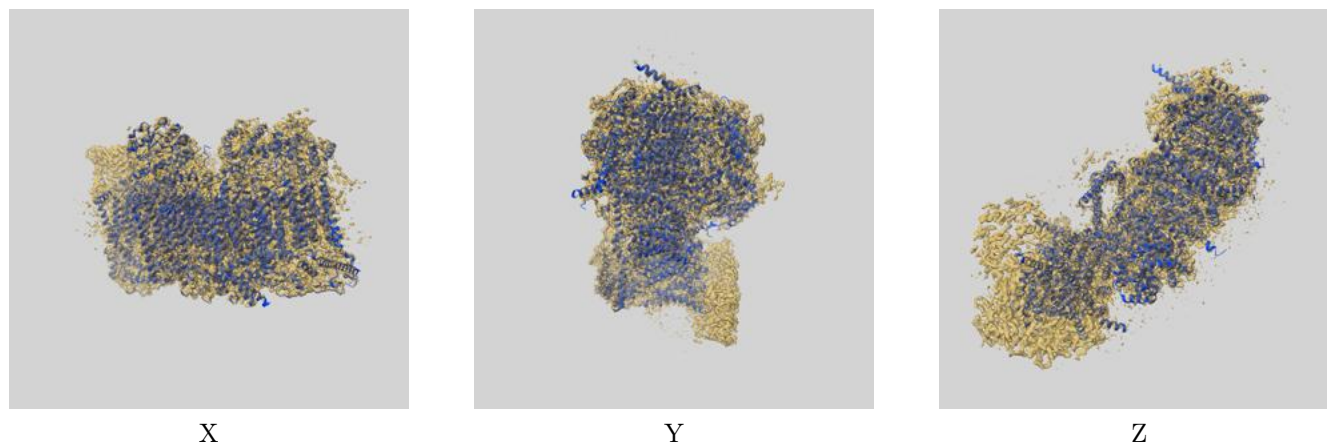
## 8 Fourier-Shell correlation ⓘ

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-32206 and PDB model 7VYI. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

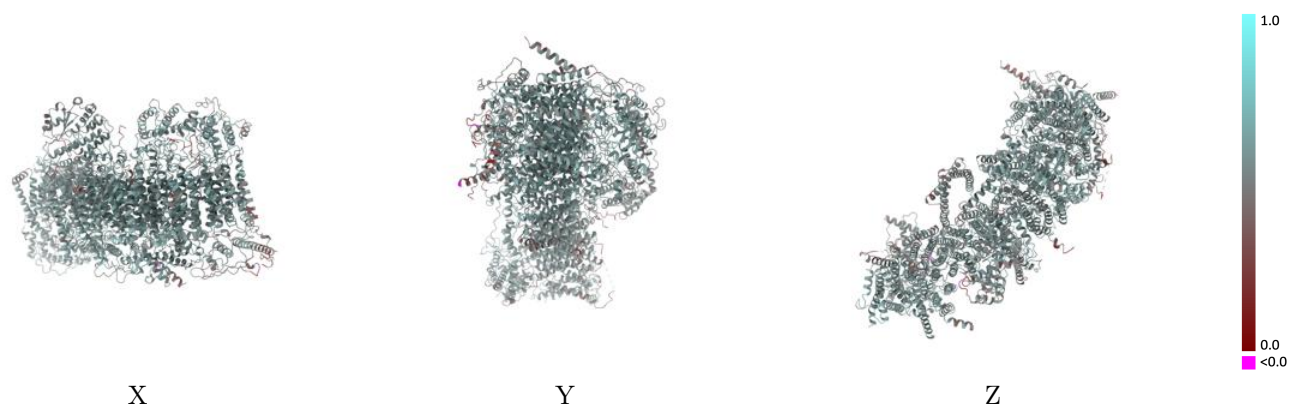
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0288 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.

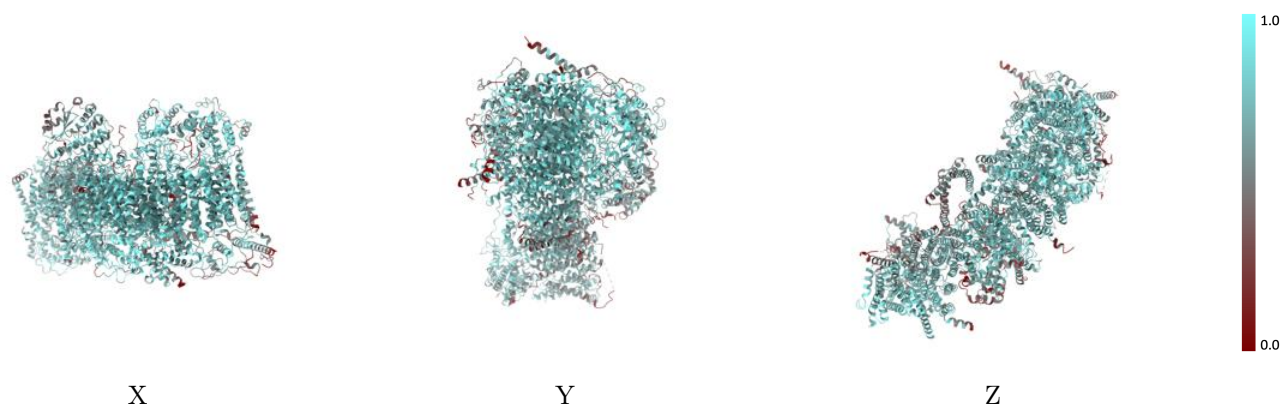


## 9.2 Q-score mapped to coordinate model [i](#)



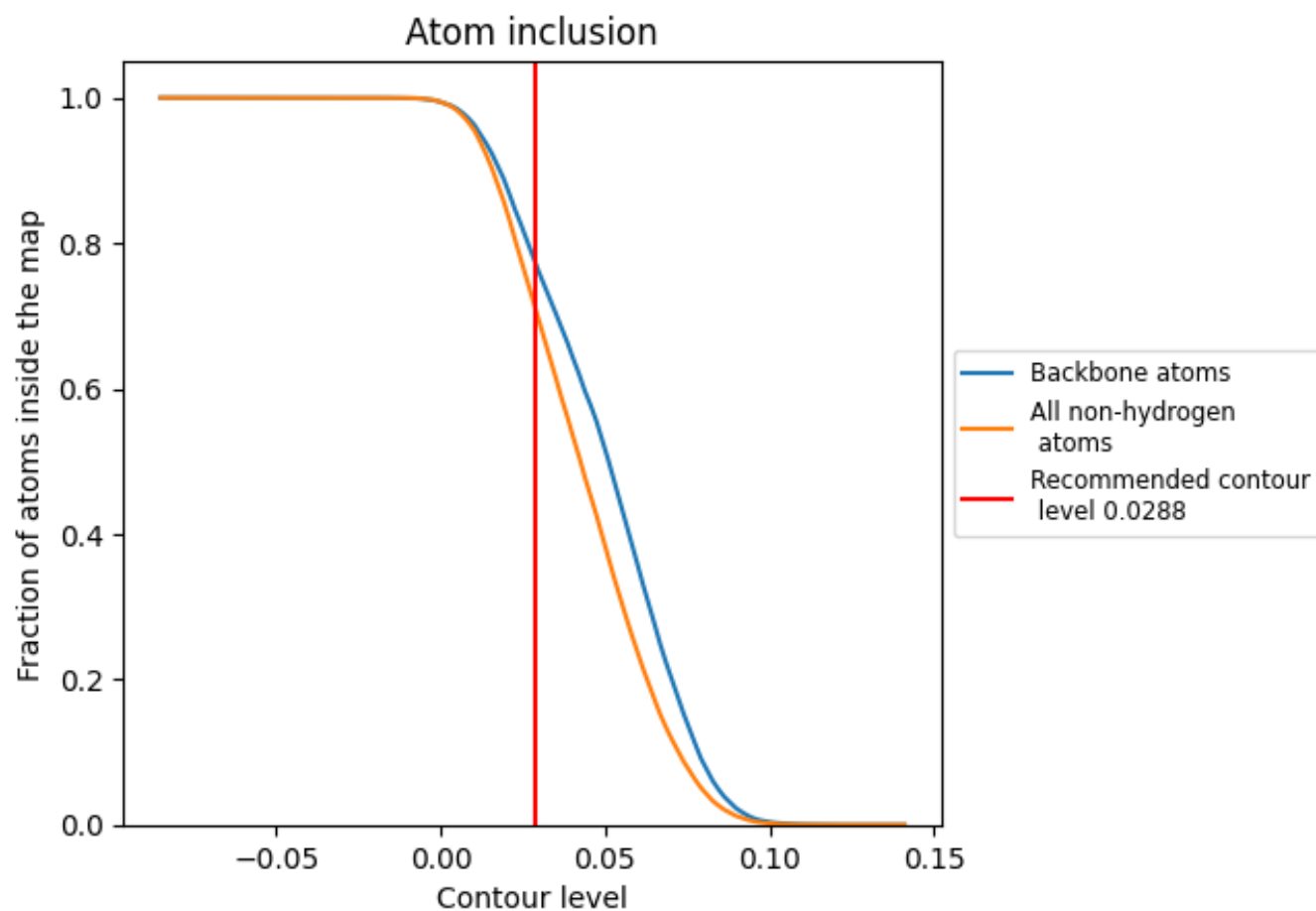
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0288).





























































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 71% 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 (0.0288) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7102	 0.5520
Q	 0.5123	 0.5020
S	 0.7740	 0.5690
U	 0.6881	 0.5550
V	 0.5135	 0.4990
W	 0.7606	 0.5670
X	 0.6842	 0.5280
Y	 0.6051	 0.4930
Z	 0.5729	 0.5080
a	 0.7522	 0.5750
b	 0.6246	 0.5250
c	 0.7316	 0.5540
d	 0.7194	 0.5460
e	 0.6697	 0.5340
f	 0.6347	 0.5250
g	 0.7498	 0.5710
h	 0.7293	 0.5600
i	 0.7827	 0.5800
j	 0.5723	 0.5130
k	 0.6792	 0.5500
l	 0.7573	 0.5680
m	 0.6279	 0.5270
n	 0.6524	 0.5250
o	 0.7182	 0.5580
p	 0.7529	 0.5650
r	 0.7848	 0.5830
s	 0.7439	 0.5640
u	 0.7387	 0.5620
v	 0.6083	 0.4870
w	 0.6224	 0.5170

