Full wwPDB EM Validation Report ⓘ

May 31, 2023 – 10:19 PM JST

PDB ID	:	7VY1
EMDB ID	:	EMD-32191
Title	:	Membrane arm of deactive state CI from Q10 dataset
Authors	:	Gu, J.K.; Yang, M.J.
Deposited on	:	2021-11-13
Resolution	:	3.30 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

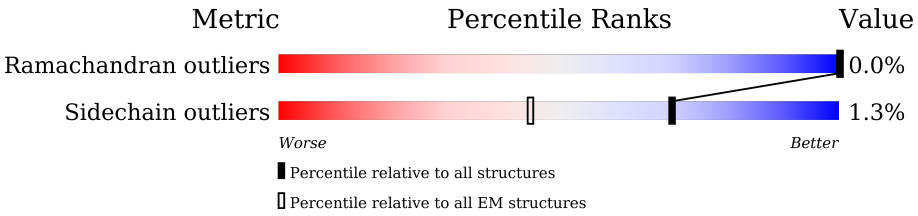
EMDB validation analysis	:	0.0.1.dev50
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.30 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)
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 >=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 <=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	473	8% 92%
2	S	70	100%
3	U	84	5% 99%
4	V	141	16% 97%
5	W	144	78% 22%
6	X	156	56% 44%
7	Y	105	10% 64% 33%
8	Z	98	18% 85% 14%
9	a	189	74% 26%

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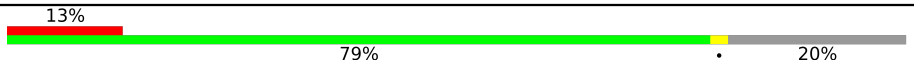
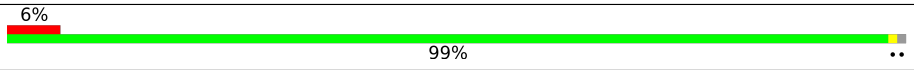
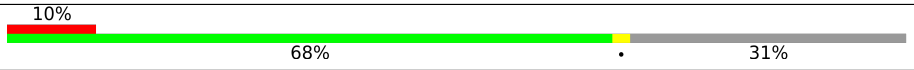
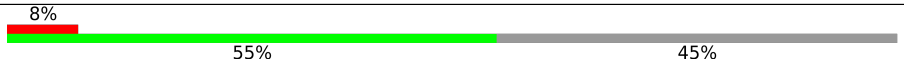
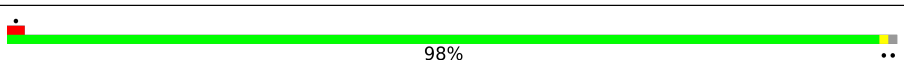
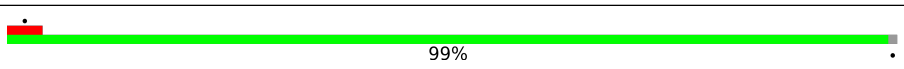
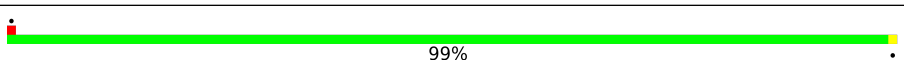
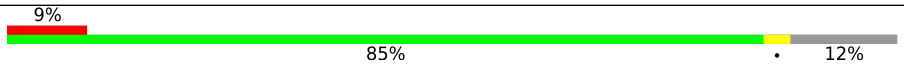
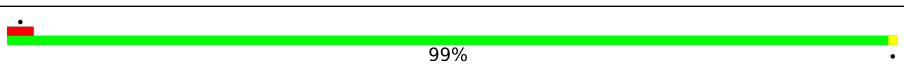
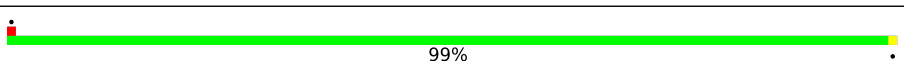
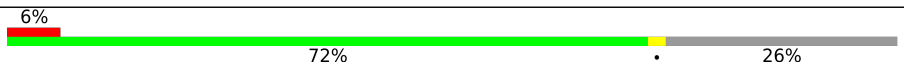
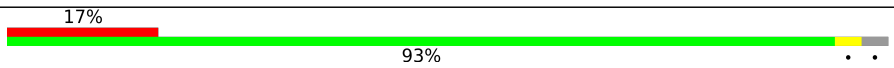
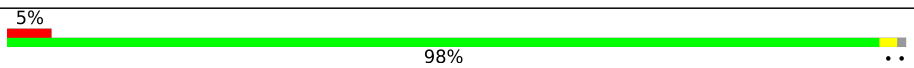
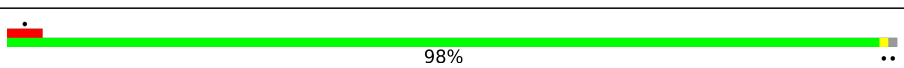
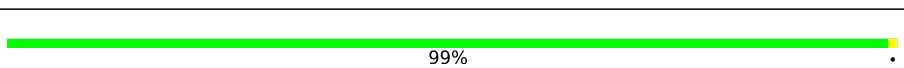
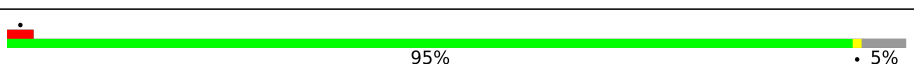
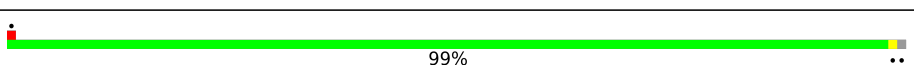
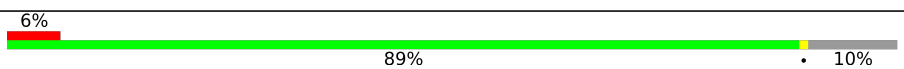
Mol	Chain	Length	Quality of chain
10	b	128	
11	c	186	
12	d	176	
13	e	154	
14	f	76	
15	g	122	
16	h	106	
17	i	347	
18	j	113	
19	k	98	
20	l	603	
21	m	175	
22	n	58	
23	o	129	
24	p	179	
25	r	459	
26	s	318	
27	u	172	
28	v	136	
29	w	357	

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 38899 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	88	Total	C	N	O	S	0	0
			699	450	103	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
			597	392	98	106	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
			1165	762	199	201	3		

- Molecule 10 is a protein called NADH dehydrogenase 1 beta subcomplex 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	103	Total	C	N	O	S	0	0
			875	571	158	145	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
			1299	843	211	237	8		

- 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 Complex I-ESSS.

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

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	?	-	CYS	deletion	UNP A0A287BMW6
e	?	-	MET	deletion	UNP A0A287BMW6
e	?	-	GLY	deletion	UNP A0A287BMW6
e	?	-	CYS	deletion	UNP A0A287BMW6
e	?	-	PRO	deletion	UNP A0A287BMW6
e	?	-	ARG	deletion	UNP A0A287BMW6
e	?	-	GLU	deletion	UNP A0A287BMW6
e	?	-	TRP	deletion	UNP A0A287BMW6
e	?	-	GLY	deletion	UNP A0A287BMW6
e	?	-	GLY	deletion	UNP A0A287BMW6

- Molecule 14 is a protein called Complex I-KFYI.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	f	42	Total	C	N	O	0	0
			344	227	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 ND3.

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
			479	311	88	79	1		

- Molecule 23 is a protein called Complex I-B15.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	o	128	Total	C	N	O	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
			1534	982	279	265	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		

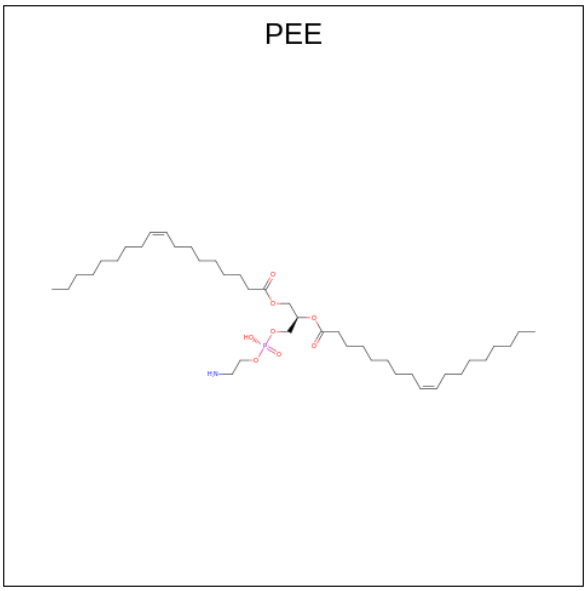
- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	v	124	Total	C	N	O	S	0	0
			1028	642	195	182	9		

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

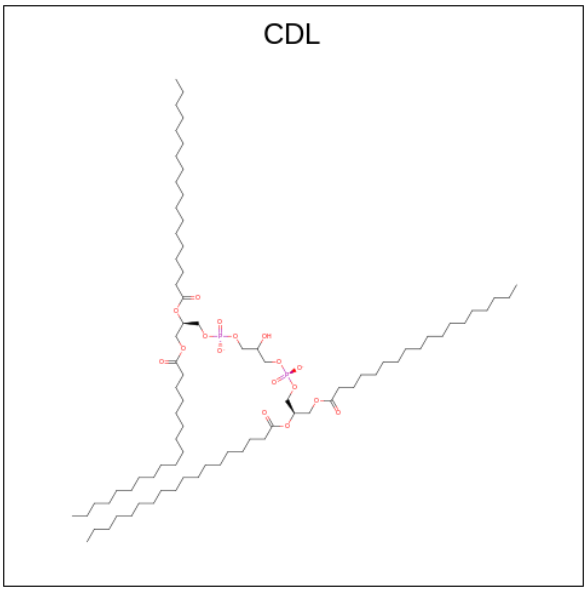
Mol	Chain	Residues	Atoms					AltConf	Trace
29	w	320	Total	C	N	O	S	0	0
			2581	1645	437	489	10		

- 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).



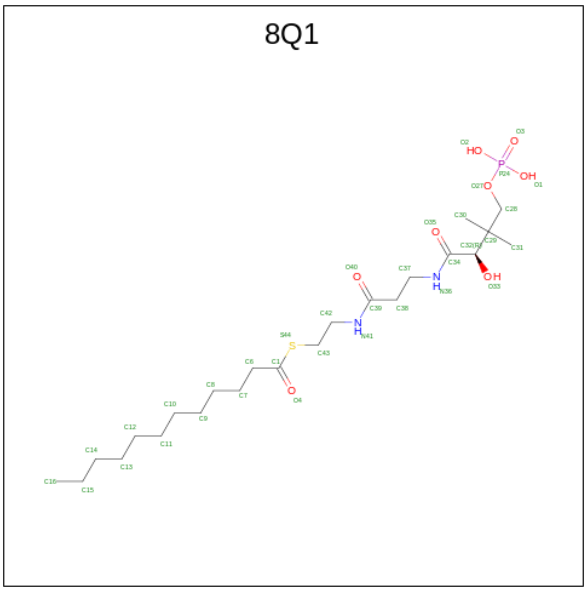
Mol	Chain	Residues	Atoms					AltConf
30	U	1	Total	C	N	O	P	0
			51	41	1	8	1	
30	W	1	Total	C	N	O	P	0
			41	31	1	8	1	
30	b	1	Total	C	N	O	P	0
			46	36	1	8	1	
30	i	1	Total	C	N	O	P	0
			47	37	1	8	1	
30	j	1	Total	C	N	O	P	0
			51	41	1	8	1	
30	l	1	Total	C	N	O	P	0
			40	30	1	8	1	
30	l	1	Total	C	N	O	P	0
			46	36	1	8	1	
30	r	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 31 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled as "Ligand of Interest" by depositor).



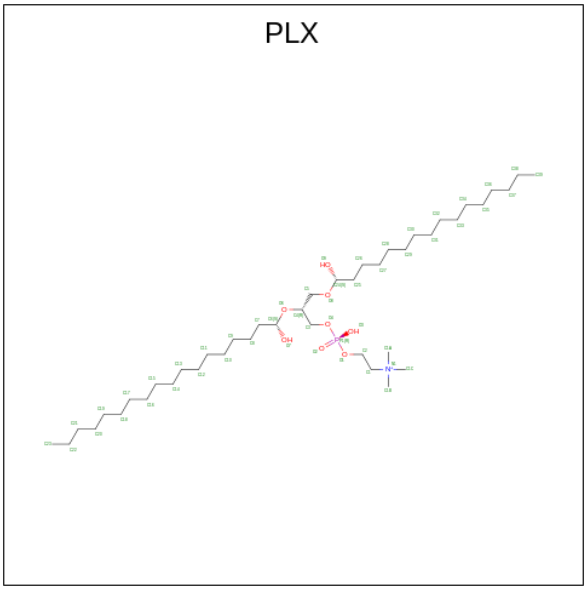
Mol	Chain	Residues	Atoms				AltConf
31	V	1	Total	C	O	P	0
			94	75	17	2	
31	a	1	Total	C	O	P	0
			91	72	17	2	
31	g	1	Total	C	O	P	0
			95	76	17	2	
31	i	1	Total	C	O	P	0
			66	47	17	2	
31	l	1	Total	C	O	P	0
			100	81	17	2	
31	o	1	Total	C	O	P	0
			68	49	17	2	
31	r	1	Total	C	O	P	0
			99	80	17	2	
31	u	1	Total	C	O	P	0
			78	59	17	2	

- Molecule 32 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta -alanyl}amino)ethyl] dodecanethioate (three-letter code: 8Q1) (formula: $C_{23}H_{45}N_2O_8PS$) (labeled as "Ligand of Interest" by depositor).



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

- 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: $C_{42}H_{89}NO_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
33	a	1	Total	C	N	O	P	0
			52	42	1	8	1	

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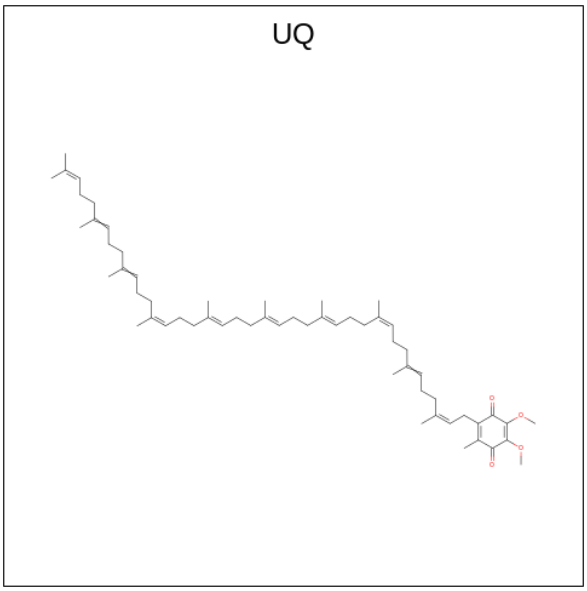
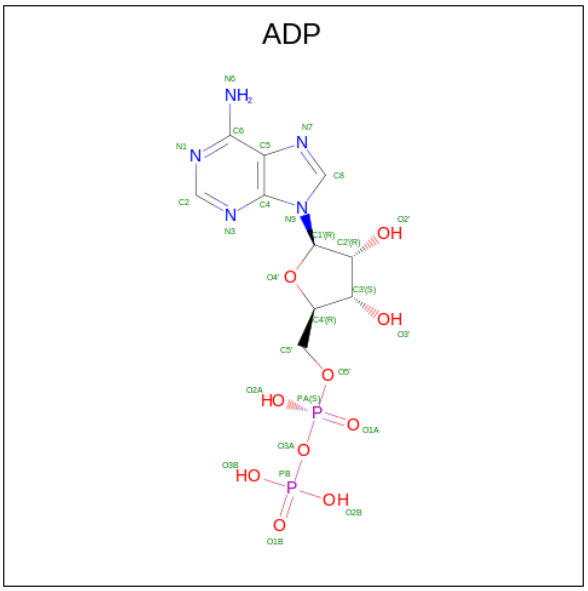
Mol	Chain	Residues	Atoms					AltConf
33	g	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	j	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	r	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	r	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 34 is Coenzyme Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-isomer (three-letter code: UQ) (formula: $C_{59}H_{90}O_4$) (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: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



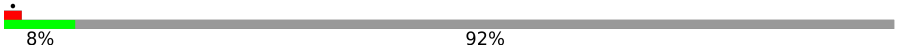
Mol	Chain	Residues	Atoms					AltConf
35	w	1	Total	C	N	O	P	0
			27	10	5	10	2	

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.

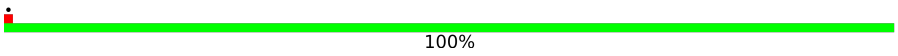
• Molecule 1: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial

Chain Q:



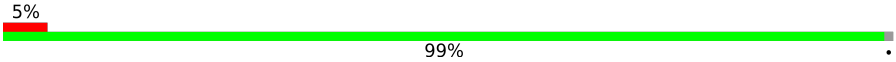
• Molecule 2: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1

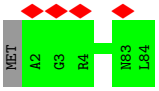
Chain S:



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

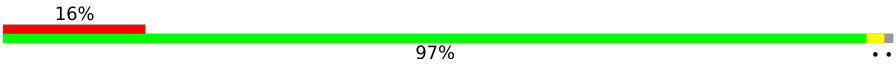
Chain U:

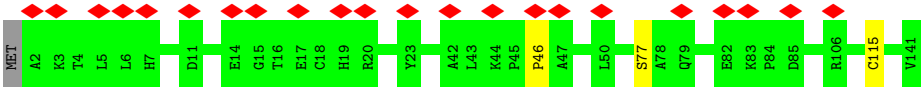




• Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

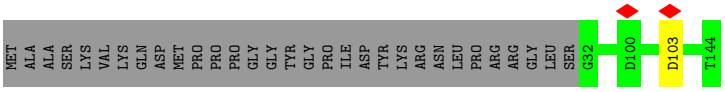
Chain V:





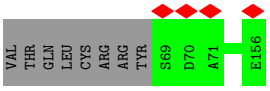
• Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13

Chain W:



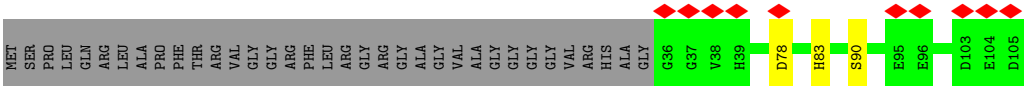
• Molecule 6: Acyl carrier protein

Chain X:



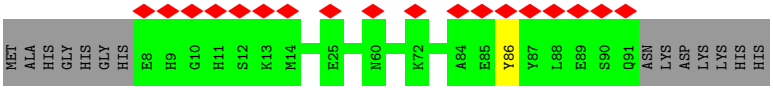
• Molecule 7: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial

Chain Y:



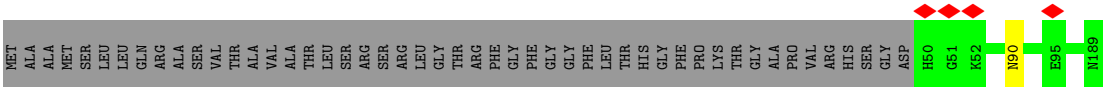
• Molecule 8: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3

Chain Z:

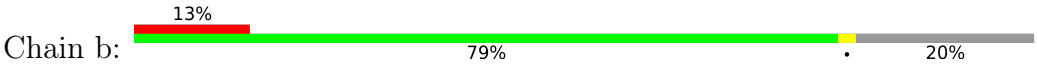


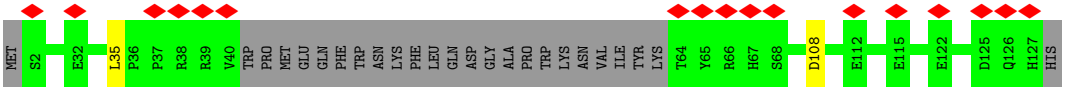
• Molecule 9: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial

Chain a:

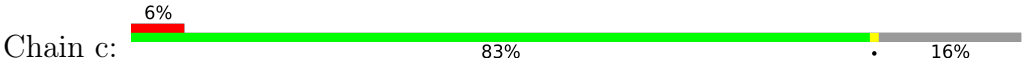


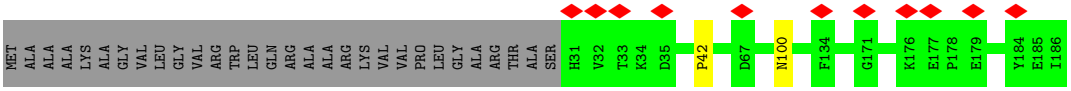
• Molecule 10: NADH dehydrogenase 1 beta subcomplex 6



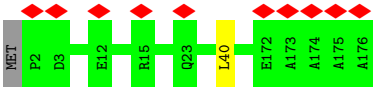


• Molecule 11: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

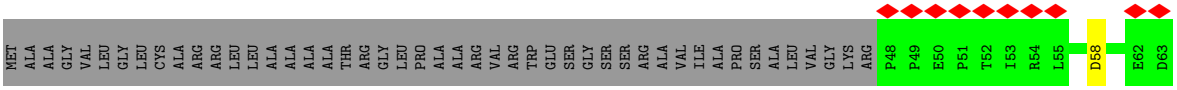


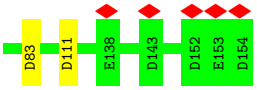


• Molecule 12: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10

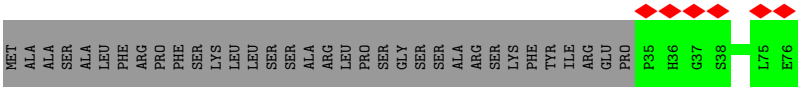


• Molecule 13: Complex I-ESSS

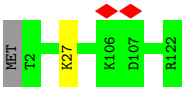




• Molecule 14: Complex I-KFYI

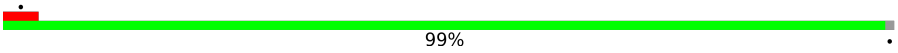


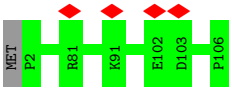
• Molecule 15: NADH dehydrogenase [ubiquinone] 1 subunit C2



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

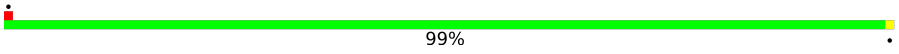
Chain h:





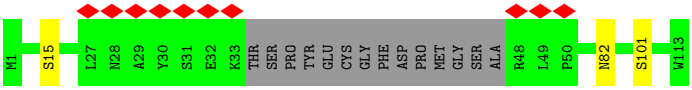
• Molecule 17: NADH-ubiquinone oxidoreductase chain 2

Chain i:



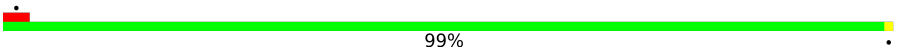
• Molecule 18: ND3

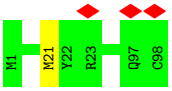
Chain j:



• Molecule 19: NADH-ubiquinone oxidoreductase chain 4L

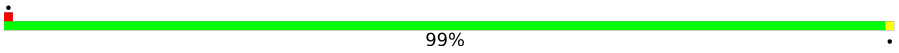
Chain k:

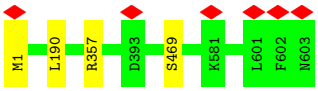




• Molecule 20: NADH-ubiquinone oxidoreductase chain 5

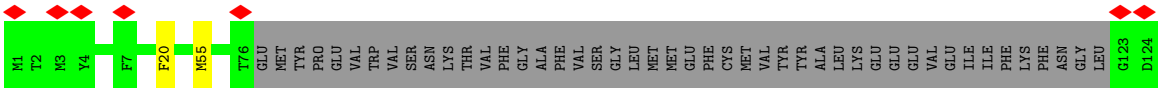
Chain l:

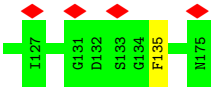




• Molecule 21: NADH-ubiquinone oxidoreductase chain 6

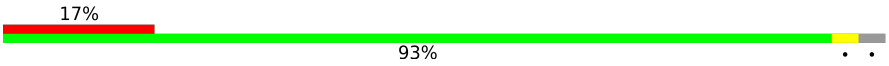
Chain m:

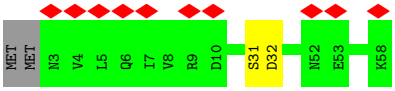




• Molecule 22: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1

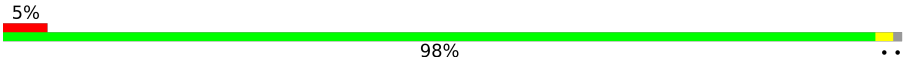
Chain n:

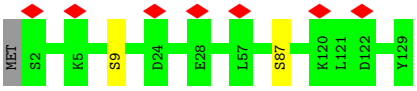




• Molecule 23: Complex I-B15

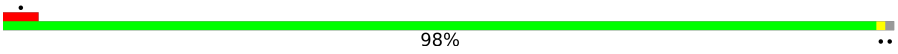
Chain o:

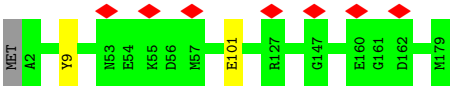




• Molecule 24: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

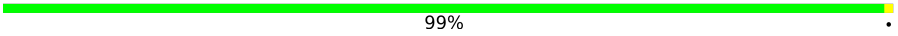
Chain p:





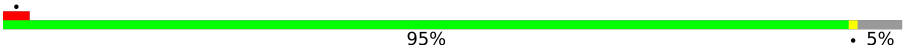
• Molecule 25: NADH-ubiquinone oxidoreductase chain 4

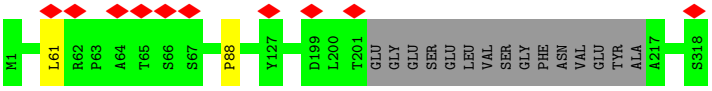
Chain r:



• Molecule 26: NADH-ubiquinone oxidoreductase chain 1

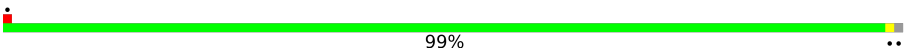
Chain s:

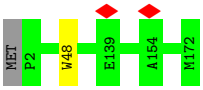




• Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

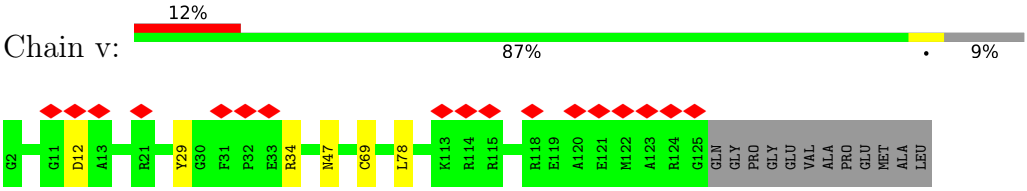
Chain u:





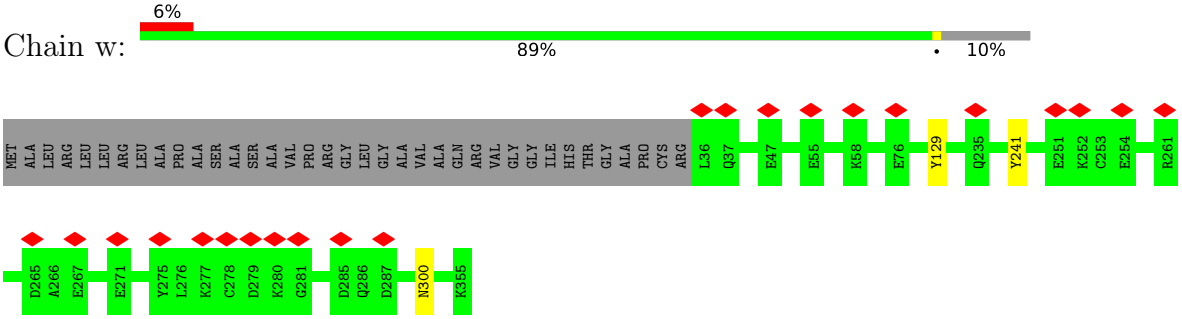
• Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Chain v:



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

Chain w:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	193234	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 ($e^-/Å^2$)	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	0.108	Depositor
Minimum map value	-0.057	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0238	Depositor
Map size (Å)	354.48602, 354.48602, 354.48602	wwPDB
Map dimensions	330, 330, 330	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0742, 1.0742, 1.0742	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: PEE, PLX, ADP, CDL, UQ, 8Q1

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	0.28	0/350	0.45	0/483
2	S	0.27	0/582	0.48	0/783
3	U	0.26	0/664	0.44	0/912
4	V	0.27	0/1042	0.48	0/1411
5	W	0.29	0/973	0.50	0/1312
6	X	0.27	0/711	0.44	0/963
7	Y	0.26	0/623	0.45	0/853
8	Z	0.25	0/695	0.47	0/939
9	a	0.29	0/1199	0.48	0/1623
10	b	0.27	0/902	0.51	0/1227
11	c	0.29	0/1355	0.48	0/1857
12	d	0.28	0/1494	0.51	0/2015
13	e	0.26	0/916	0.53	2/1246 (0.2%)
14	f	0.25	0/353	0.43	0/477
15	g	0.29	0/1031	0.47	0/1394
16	h	0.26	0/889	0.47	0/1190
17	i	0.27	0/2773	0.45	0/3768
18	j	0.27	0/819	0.46	0/1117
19	k	0.27	0/759	0.44	0/1029
20	l	0.28	0/4914	0.45	0/6683
21	m	0.30	0/973	0.50	0/1320
22	n	0.25	0/491	0.50	0/663
23	o	0.28	0/1092	0.51	0/1481
24	p	0.28	0/1590	0.51	0/2155
25	r	0.28	0/3723	0.46	0/5078
26	s	0.28	0/2464	0.47	0/3369
27	u	0.27	0/1436	0.48	0/1938
28	v	0.28	0/1052	0.55	0/1411
29	w	0.28	0/2641	0.47	0/3577
All	All	0.28	0/38506	0.48	2/52274 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	e	83	ASP	CB-CG-OD1	5.88	123.59	118.30
13	e	83	ASP	CB-CG-OD2	-5.08	113.72	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	38/473 (8%)	37 (97%)	1 (3%)	0	100	100
2	S	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
3	U	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
4	V	138/141 (98%)	129 (94%)	8 (6%)	1 (1%)	22	54
5	W	111/144 (77%)	109 (98%)	2 (2%)	0	100	100
6	X	86/156 (55%)	83 (96%)	3 (4%)	0	100	100
7	Y	68/105 (65%)	64 (94%)	4 (6%)	0	100	100
8	Z	82/98 (84%)	79 (96%)	3 (4%)	0	100	100
9	a	138/189 (73%)	134 (97%)	4 (3%)	0	100	100
10	b	99/128 (77%)	97 (98%)	2 (2%)	0	100	100
11	c	154/186 (83%)	142 (92%)	11 (7%)	1 (1%)	25	57
12	d	173/176 (98%)	169 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	e	105/154 (68%)	102 (97%)	3 (3%)	0	100	100
14	f	40/76 (53%)	39 (98%)	1 (2%)	0	100	100
15	g	119/122 (98%)	114 (96%)	5 (4%)	0	100	100
16	h	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
17	i	345/347 (99%)	334 (97%)	11 (3%)	0	100	100
18	j	95/113 (84%)	88 (93%)	7 (7%)	0	100	100
19	k	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
20	l	601/603 (100%)	568 (94%)	33 (6%)	0	100	100
21	m	125/175 (71%)	112 (90%)	13 (10%)	0	100	100
22	n	54/58 (93%)	54 (100%)	0	0	100	100
23	o	126/129 (98%)	122 (97%)	4 (3%)	0	100	100
24	p	176/179 (98%)	167 (95%)	9 (5%)	0	100	100
25	r	457/459 (100%)	443 (97%)	14 (3%)	0	100	100
26	s	299/318 (94%)	288 (96%)	11 (4%)	0	100	100
27	u	169/172 (98%)	160 (95%)	9 (5%)	0	100	100
28	v	122/136 (90%)	118 (97%)	4 (3%)	0	100	100
29	w	318/357 (89%)	302 (95%)	16 (5%)	0	100	100
All	All	4586/5552 (83%)	4384 (96%)	200 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	c	42	PRO
4	V	46	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Q	34/401 (8%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	S	58/58 (100%)	58 (100%)	0	100	100
3	U	69/70 (99%)	69 (100%)	0	100	100
4	V	101/102 (99%)	99 (98%)	2 (2%)	55	76
5	W	99/124 (80%)	98 (99%)	1 (1%)	76	86
6	X	78/132 (59%)	78 (100%)	0	100	100
7	Y	62/84 (74%)	59 (95%)	3 (5%)	25	56
8	Z	65/76 (86%)	64 (98%)	1 (2%)	65	81
9	a	122/158 (77%)	121 (99%)	1 (1%)	81	89
10	b	97/121 (80%)	95 (98%)	2 (2%)	53	75
11	c	137/160 (86%)	136 (99%)	1 (1%)	84	90
12	d	155/156 (99%)	154 (99%)	1 (1%)	86	91
13	e	99/129 (77%)	97 (98%)	2 (2%)	55	76
14	f	36/66 (54%)	36 (100%)	0	100	100
15	g	108/109 (99%)	107 (99%)	1 (1%)	78	87
16	h	93/94 (99%)	93 (100%)	0	100	100
17	i	311/311 (100%)	306 (98%)	5 (2%)	62	79
18	j	88/99 (89%)	85 (97%)	3 (3%)	37	65
19	k	85/85 (100%)	84 (99%)	1 (1%)	71	83
20	l	537/537 (100%)	533 (99%)	4 (1%)	84	90
21	m	99/141 (70%)	96 (97%)	3 (3%)	41	68
22	n	53/55 (96%)	51 (96%)	2 (4%)	33	62
23	o	113/114 (99%)	111 (98%)	2 (2%)	59	78
24	p	159/160 (99%)	157 (99%)	2 (1%)	69	82
25	r	410/410 (100%)	407 (99%)	3 (1%)	84	90
26	s	263/275 (96%)	261 (99%)	2 (1%)	81	89
27	u	153/154 (99%)	152 (99%)	1 (1%)	84	90
28	v	104/119 (87%)	98 (94%)	6 (6%)	20	50
29	w	281/307 (92%)	278 (99%)	3 (1%)	73	85
All	All	4069/4807 (85%)	4017 (99%)	52 (1%)	70	82

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

Mol	Chain	Res	Type
4	V	77	SER
4	V	115	CYS
5	W	103	ASP
7	Y	78	ASP
7	Y	83	HIS
7	Y	90	SER
8	Z	86	TYR
9	a	90	ASN
10	b	35	LEU
10	b	108	ASP
11	c	100	ASN
12	d	40	LEU
13	e	58	ASP
13	e	111	ASP
15	g	27	LYS
17	i	89	MET
17	i	190	MET
17	i	261	MET
17	i	269	GLU
17	i	300	SER
18	j	15	SER
18	j	82	ASN
18	j	101	SER
19	k	21	MET
20	l	1	MET
20	l	190	LEU
20	l	357	ARG
20	l	469	SER
21	m	20	PHE
21	m	55	MET
21	m	135	PHE
22	n	31	SER
22	n	32	ASP
23	o	9	SER
23	o	87	SER
24	p	9	TYR
24	p	101	GLU
25	r	57	PHE
25	r	229	MET
25	r	339	SER
26	s	61	LEU
26	s	88	PRO
27	u	48	TRP

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Mol	Chain	Res	Type
28	v	12	ASP
28	v	29	TYR
28	v	34	ARG
28	v	47	ASN
28	v	69	CYS
28	v	78	LEU
29	w	129	TYR
29	w	241	TYR
29	w	300	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
12	d	124	ASN
20	l	59	GLN
26	s	287	HIS
28	v	47	ASN
28	v	110	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

24 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	$\#\|Z\| > 2$
35	ADP	w	401	-	24,29,29	3.12	6 (25%)	29,45,45	1.43	4 (13%)
31	CDL	V	201	-	93,93,99	1.11	8 (8%)	99,105,111	0.85	4 (4%)
34	UQ	s	401	-	28,28,63	0.52	0	34,37,79	0.97	2 (5%)
30	PEE	j	201	-	50,50,50	1.15	6 (12%)	53,55,55	0.96	2 (3%)
30	PEE	i	402	-	46,46,50	1.19	6 (13%)	49,51,55	1.00	2 (4%)
30	PEE	W	201	-	40,40,50	1.13	5 (12%)	43,45,55	1.02	2 (4%)
30	PEE	U	401	-	50,50,50	1.15	6 (12%)	53,55,55	0.97	2 (3%)
32	8Q1	X	201	-	31,34,34	1.68	6 (19%)	40,43,43	1.60	6 (15%)
31	CDL	o	201	-	67,67,99	1.24	8 (11%)	73,79,111	1.01	4 (5%)
31	CDL	g	202	-	94,94,99	1.10	8 (8%)	100,106,111	0.88	4 (4%)
30	PEE	l	701	-	39,39,50	1.31	6 (15%)	41,44,55	1.05	2 (4%)
33	PLX	g	201	-	51,51,51	1.13	3 (5%)	55,59,59	0.62	1 (1%)
31	CDL	r	504	-	98,98,99	1.08	8 (8%)	104,110,111	0.91	4 (3%)
31	CDL	u	201	-	77,77,99	1.20	8 (10%)	83,89,111	0.96	4 (4%)
33	PLX	r	503	-	51,51,51	1.13	3 (5%)	55,59,59	0.59	1 (1%)
31	CDL	l	702	-	99,99,99	1.08	9 (9%)	105,111,111	0.85	4 (3%)
31	CDL	a	201	-	90,90,99	1.12	8 (8%)	96,102,111	0.94	4 (4%)
30	PEE	l	703	-	45,45,50	1.22	6 (13%)	48,50,55	0.97	2 (4%)
33	PLX	r	502	-	51,51,51	1.12	4 (7%)	55,59,59	0.64	1 (1%)
33	PLX	a	202	-	51,51,51	0.63	0	55,59,59	0.66	0
33	PLX	j	202	-	51,51,51	1.14	3 (5%)	55,59,59	0.60	1 (1%)
30	PEE	r	501	-	50,50,50	1.16	6 (12%)	53,55,55	0.98	2 (3%)
30	PEE	b	201	-	45,45,50	1.22	5 (11%)	48,50,55	0.98	2 (4%)
31	CDL	i	401	-	65,65,99	1.26	8 (12%)	71,77,111	1.03	4 (5%)

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
35	ADP	w	401	-	-	4/12/32/32	0/3/3/3
31	CDL	V	201	-	-	50/104/104/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	UQ	s	401	-	-	8/21/45/87	0/1/1/1
30	PEE	j	201	-	-	26/54/54/54	-
30	PEE	i	402	-	-	19/50/50/54	-
30	PEE	W	201	-	-	20/44/44/54	-
30	PEE	U	401	-	-	24/54/54/54	-
32	8Q1	X	201	-	-	17/41/41/41	-
31	CDL	o	201	-	-	42/78/78/110	-
31	CDL	g	202	-	-	60/105/105/110	-
30	PEE	l	701	-	-	30/43/43/54	-
33	PLX	g	201	-	-	23/55/55/55	-
31	CDL	r	504	-	-	53/109/109/110	-
31	CDL	u	201	-	-	38/88/88/110	-
33	PLX	r	503	-	-	34/55/55/55	-
31	CDL	l	702	-	-	55/110/110/110	-
31	CDL	a	201	-	-	47/101/101/110	-
30	PEE	l	703	-	-	23/49/49/54	-
33	PLX	r	502	-	-	23/55/55/55	-
33	PLX	a	202	-	-	12/55/55/55	-
33	PLX	j	202	-	-	28/55/55/55	-
30	PEE	r	501	-	-	29/54/54/54	-
30	PEE	b	201	-	-	28/49/49/54	-
31	CDL	i	401	-	-	41/76/76/110	-

All (136) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	w	401	ADP	C3'-C4'	-8.89	1.30	1.53
35	w	401	ADP	O4'-C4'	7.66	1.62	1.45
35	w	401	ADP	O4'-C1'	-6.92	1.31	1.41
32	X	201	8Q1	C34-N36	5.37	1.45	1.33
32	X	201	8Q1	C39-N41	5.30	1.45	1.33
35	w	401	ADP	C6-N6	3.85	1.48	1.34
30	l	703	PEE	C18-C19	3.75	1.53	1.31
30	l	701	PEE	C18-C19	3.72	1.53	1.31
30	W	201	PEE	C18-C19	3.71	1.53	1.31
30	b	201	PEE	C18-C19	3.70	1.53	1.31
30	U	401	PEE	C18-C19	3.70	1.53	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	r	501	PEE	C18-C19	3.70	1.53	1.31
30	j	201	PEE	C18-C19	3.69	1.53	1.31
30	i	402	PEE	C18-C19	3.67	1.53	1.31
30	r	501	PEE	C39-C38	3.66	1.53	1.31
30	i	402	PEE	C39-C38	3.64	1.52	1.31
30	l	701	PEE	C39-C38	3.64	1.52	1.31
30	b	201	PEE	C39-C38	3.64	1.52	1.31
30	j	201	PEE	C39-C38	3.63	1.52	1.31
30	l	703	PEE	C39-C38	3.61	1.52	1.31
30	U	401	PEE	C39-C38	3.61	1.52	1.31
31	u	201	CDL	OA8-CA7	3.47	1.43	1.33
31	V	201	CDL	OA8-CA7	3.45	1.43	1.33
31	i	401	CDL	OA8-CA7	3.44	1.43	1.33
31	a	201	CDL	OA8-CA7	3.42	1.43	1.33
31	o	201	CDL	OA8-CA7	3.41	1.43	1.33
31	g	202	CDL	OA8-CA7	3.39	1.43	1.33
31	l	702	CDL	OA8-CA7	3.38	1.43	1.33
31	r	504	CDL	OA8-CA7	3.36	1.43	1.33
35	w	401	ADP	O2'-C2'	-3.24	1.35	1.43
35	w	401	ADP	O3'-C3'	3.15	1.50	1.43
31	V	201	CDL	OA6-CA5	3.11	1.43	1.34
31	i	401	CDL	OB6-CB5	3.04	1.42	1.34
31	g	202	CDL	OB6-CB5	3.02	1.42	1.34
31	l	702	CDL	OB6-CB5	3.01	1.42	1.34
31	r	504	CDL	OB6-CB5	3.01	1.42	1.34
31	g	202	CDL	OB8-CB7	2.99	1.42	1.33
31	u	201	CDL	OB8-CB7	2.99	1.42	1.33
31	l	702	CDL	OA6-CA5	2.99	1.42	1.34
31	o	201	CDL	OB6-CB5	2.96	1.42	1.34
31	r	504	CDL	OB8-CB7	2.96	1.42	1.33
31	a	201	CDL	OB6-CB5	2.95	1.42	1.34
31	i	401	CDL	OB8-CB7	2.95	1.41	1.33
31	o	201	CDL	OA6-CA5	2.95	1.42	1.34
31	l	702	CDL	OB8-CB7	2.94	1.41	1.33
31	a	201	CDL	OA6-CA5	2.94	1.42	1.34
31	a	201	CDL	OB8-CB7	2.93	1.41	1.33
31	V	201	CDL	OB8-CB7	2.93	1.41	1.33
31	V	201	CDL	OB6-CB5	2.93	1.42	1.34
31	o	201	CDL	OB8-CB7	2.93	1.41	1.33
31	g	202	CDL	OA6-CA5	2.91	1.42	1.34
31	i	401	CDL	OA6-CA5	2.90	1.42	1.34
31	u	201	CDL	OB6-CB5	2.89	1.42	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	r	504	CDL	OA6-CA5	2.89	1.42	1.34
31	u	201	CDL	OA6-CA5	2.88	1.42	1.34
33	g	201	PLX	O6-C4	-2.85	1.40	1.44
33	r	503	PLX	O6-C4	-2.81	1.40	1.44
33	j	202	PLX	O6-C4	-2.60	1.41	1.44
30	b	201	PEE	O3-C30	2.51	1.40	1.33
30	j	201	PEE	O3-C30	2.48	1.40	1.33
30	U	401	PEE	O2-C2	-2.48	1.40	1.46
31	u	201	CDL	OA6-CA4	-2.47	1.40	1.46
30	l	703	PEE	O2-C2	-2.47	1.40	1.46
30	r	501	PEE	O2-C2	-2.47	1.40	1.46
31	o	201	CDL	OA6-CA4	-2.46	1.40	1.46
31	r	504	CDL	OA6-CA4	-2.45	1.40	1.46
31	g	202	CDL	OA6-CA4	-2.45	1.40	1.46
30	i	402	PEE	O3-C30	2.45	1.40	1.33
30	j	201	PEE	O2-C2	-2.44	1.40	1.46
30	i	402	PEE	O2-C2	-2.44	1.40	1.46
30	b	201	PEE	O2-C2	-2.43	1.40	1.46
33	r	502	PLX	C7-C6	2.42	1.55	1.50
30	U	401	PEE	O3-C30	2.42	1.40	1.33
30	r	501	PEE	O3-C30	2.41	1.40	1.33
30	l	701	PEE	O3-C30	2.40	1.40	1.33
31	a	201	CDL	OA6-CA4	-2.40	1.40	1.46
31	i	401	CDL	OA6-CA4	-2.40	1.40	1.46
30	l	701	PEE	O2-C10	2.37	1.41	1.34
30	l	703	PEE	O3-C30	2.36	1.40	1.33
33	j	202	PLX	C7-C6	2.36	1.55	1.50
30	W	201	PEE	O2-C2	-2.35	1.40	1.46
31	l	702	CDL	OA6-CA4	-2.35	1.40	1.46
33	g	201	PLX	C7-C6	2.33	1.55	1.50
30	W	201	PEE	O3-C30	2.32	1.40	1.33
33	r	503	PLX	C7-C6	2.30	1.55	1.50
30	l	701	PEE	O2-C2	-2.30	1.40	1.46
32	X	201	8Q1	O35-C34	-2.30	1.18	1.23
32	X	201	8Q1	C1-S44	2.28	1.81	1.76
30	U	401	PEE	O2-C10	2.28	1.40	1.34
30	b	201	PEE	O2-C10	2.28	1.40	1.34
31	V	201	CDL	OB6-CB4	-2.25	1.41	1.46
32	X	201	8Q1	C6-C1	2.25	1.53	1.50
30	W	201	PEE	O2-C10	2.25	1.40	1.34
31	o	201	CDL	OB6-CB4	-2.25	1.41	1.46
30	l	703	PEE	O2-C10	2.24	1.40	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	l	703	PEE	O3-C3	-2.23	1.40	1.45
30	j	201	PEE	O2-C10	2.23	1.40	1.34
31	l	702	CDL	OB6-CB4	-2.23	1.41	1.46
30	r	501	PEE	O2-C10	2.23	1.40	1.34
31	o	201	CDL	PB2-OB2	2.23	1.68	1.59
30	i	402	PEE	O2-C10	2.22	1.40	1.34
31	a	201	CDL	OB6-CB4	-2.22	1.41	1.46
31	u	201	CDL	OB6-CB4	-2.22	1.41	1.46
32	X	201	8Q1	O40-C39	-2.22	1.18	1.23
31	r	504	CDL	OB6-CB4	-2.21	1.41	1.46
31	g	202	CDL	PB2-OB5	2.21	1.68	1.59
33	r	502	PLX	O6-C4	-2.20	1.41	1.44
30	W	201	PEE	O3-C3	-2.20	1.40	1.45
31	u	201	CDL	PB2-OB2	2.19	1.68	1.59
31	V	201	CDL	PB2-OB2	2.19	1.68	1.59
31	i	401	CDL	PB2-OB2	2.19	1.68	1.59
33	j	202	PLX	P1-O4	2.16	1.68	1.59
31	r	504	CDL	PB2-OB2	2.16	1.68	1.59
31	l	702	CDL	PB2-OB2	2.16	1.68	1.59
31	i	401	CDL	PB2-OB5	2.15	1.68	1.59
31	g	202	CDL	PB2-OB2	2.15	1.68	1.59
31	i	401	CDL	OB6-CB4	-2.15	1.41	1.46
31	u	201	CDL	PB2-OB5	2.15	1.68	1.59
31	a	201	CDL	PB2-OB2	2.14	1.68	1.59
30	j	201	PEE	O3-C3	-2.13	1.40	1.45
31	o	201	CDL	PB2-OB5	2.13	1.67	1.59
31	r	504	CDL	PB2-OB5	2.13	1.67	1.59
31	V	201	CDL	PB2-OB5	2.12	1.67	1.59
31	g	202	CDL	OB6-CB4	-2.12	1.41	1.46
31	V	201	CDL	OA6-CA4	-2.12	1.41	1.46
33	r	502	PLX	P1-O4	2.10	1.67	1.59
30	l	701	PEE	O3-C3	-2.09	1.40	1.45
30	r	501	PEE	O3-C3	-2.09	1.40	1.45
31	l	702	CDL	PB2-OB5	2.09	1.67	1.59
33	r	503	PLX	P1-O4	2.07	1.67	1.59
31	a	201	CDL	PB2-OB5	2.07	1.67	1.59
33	g	201	PLX	P1-O4	2.05	1.67	1.59
30	U	401	PEE	O3-C3	-2.05	1.40	1.45
30	i	402	PEE	O3-C3	-2.04	1.40	1.45
31	l	702	CDL	C11-CA5	2.03	1.56	1.50
33	r	502	PLX	P1-O1	2.00	1.67	1.59

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	X	201	8Q1	C6-C1-S44	6.25	120.74	113.46
35	w	401	ADP	N3-C2-N1	-4.40	121.80	128.68
31	a	201	CDL	OA6-CA5-C11	4.31	120.78	111.50
31	r	504	CDL	OB6-CB5-C51	4.22	120.59	111.50
31	u	201	CDL	OB6-CB5-C51	4.14	120.43	111.50
30	W	201	PEE	O2-C10-C11	4.14	120.43	111.50
31	i	401	CDL	OA6-CA5-C11	4.12	120.38	111.50
31	a	201	CDL	OB6-CB5-C51	4.10	120.34	111.50
30	l	701	PEE	O2-C10-C11	4.08	120.30	111.50
31	g	202	CDL	OB6-CB5-C51	4.07	120.27	111.50
31	r	504	CDL	OA6-CA5-C11	4.03	120.19	111.50
30	U	401	PEE	O2-C10-C11	4.02	120.16	111.50
31	l	702	CDL	OA6-CA5-C11	3.99	120.11	111.50
30	j	201	PEE	O2-C10-C11	3.96	120.03	111.50
31	i	401	CDL	OB6-CB5-C51	3.94	119.98	111.50
30	b	201	PEE	O2-C10-C11	3.93	119.97	111.50
31	u	201	CDL	OA6-CA5-C11	3.92	119.94	111.50
31	o	201	CDL	OB6-CB5-C51	3.91	119.93	111.50
30	r	501	PEE	O2-C10-C11	3.90	119.91	111.50
30	i	402	PEE	O2-C10-C11	3.87	119.84	111.50
31	o	201	CDL	OA6-CA5-C11	3.83	119.75	111.50
31	g	202	CDL	OA6-CA5-C11	3.83	119.75	111.50
31	V	201	CDL	OB6-CB5-C51	3.79	119.67	111.50
30	l	703	PEE	O2-C10-C11	3.78	119.66	111.50
31	l	702	CDL	OB6-CB5-C51	3.78	119.65	111.50
31	V	201	CDL	OA6-CA5-C11	3.76	119.61	111.50
32	X	201	8Q1	O4-C1-C6	-3.51	119.84	123.99
30	r	501	PEE	O3-C30-C31	2.86	120.90	111.91
31	V	201	CDL	OB8-CB7-C71	2.80	120.71	111.91
30	U	401	PEE	O3-C30-C31	2.76	120.56	111.91
31	a	201	CDL	OB8-CB7-C71	2.73	120.47	111.91
31	u	201	CDL	OB8-CB7-C71	2.73	120.46	111.91
30	i	402	PEE	O3-C30-C31	2.72	120.46	111.91
35	w	401	ADP	PA-O3A-PB	-2.70	123.57	132.83
31	o	201	CDL	OB8-CB7-C71	2.69	120.36	111.91
31	i	401	CDL	OB8-CB7-C71	2.68	120.32	111.91
30	b	201	PEE	O3-C30-C31	2.65	120.22	111.91
31	r	504	CDL	OB8-CB7-C71	2.64	120.20	111.91
31	r	504	CDL	OA8-CA7-C31	2.62	120.13	111.91
31	i	401	CDL	OA8-CA7-C31	2.60	120.08	111.91
30	j	201	PEE	O3-C30-C31	2.59	120.03	111.91
30	l	703	PEE	O3-C30-C31	2.58	120.00	111.91
31	l	702	CDL	OA8-CA7-C31	2.58	119.99	111.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
31	g	202	CDL	OB8-CB7-C71	2.56	119.94	111.91
30	l	701	PEE	O3-C30-C31	2.56	119.93	111.91
31	l	702	CDL	OB8-CB7-C71	2.54	119.88	111.91
31	g	202	CDL	OA8-CA7-C31	2.54	119.87	111.91
31	u	201	CDL	OA8-CA7-C31	2.54	119.87	111.91
31	o	201	CDL	OA8-CA7-C31	2.52	119.80	111.91
35	w	401	ADP	O4'-C1'-C2'	-2.49	103.28	106.93
31	V	201	CDL	OA8-CA7-C31	2.46	119.64	111.91
32	X	201	8Q1	O4-C1-S44	-2.46	119.42	122.61
33	r	502	PLX	C1A-N1-C1	2.46	119.98	109.92
33	r	503	PLX	C1A-N1-C1	2.45	119.93	109.92
30	W	201	PEE	O3-C30-C31	2.44	119.57	111.91
31	a	201	CDL	OA8-CA7-C31	2.43	119.54	111.91
32	X	201	8Q1	C38-C39-N41	2.42	120.50	116.42
33	j	202	PLX	C1A-N1-C1	2.41	119.80	109.92
33	g	201	PLX	C1A-N1-C1	2.41	119.77	109.92
32	X	201	8Q1	C37-C38-C39	2.36	116.29	112.36
34	s	401	UQ	C7-C6-C1	2.25	121.19	118.48
35	w	401	ADP	C4-C5-N7	-2.18	107.12	109.40
32	X	201	8Q1	C43-S44-C1	2.12	108.48	101.87
34	s	401	UQ	C6-C5-C4	2.08	120.83	119.18

There are no chirality outliers.

All (734) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	W	201	PEE	C4-O4P-P-O1P
30	b	201	PEE	C37-C38-C39-C40
30	i	402	PEE	C11-C10-O2-C2
30	j	201	PEE	C1-O3P-P-O2P
30	j	201	PEE	C1-O3P-P-O1P
30	j	201	PEE	C4-O4P-P-O3P
30	j	201	PEE	C4-O4P-P-O2P
30	l	701	PEE	O3P-C1-C2-O2
30	l	701	PEE	C4-O4P-P-O1P
30	r	501	PEE	C1-O3P-P-O1P
30	r	501	PEE	C4-O4P-P-O3P
30	r	501	PEE	C4-O4P-P-O2P
30	r	501	PEE	C4-O4P-P-O1P
31	V	201	CDL	CA2-C1-CB2-OB2
31	V	201	CDL	CA2-OA2-PA1-OA4
31	V	201	CDL	CB2-OB2-PB2-OB4

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Mol	Chain	Res	Type	Atoms
31	V	201	CDL	CB3-OB5-PB2-OB2
31	V	201	CDL	CB3-OB5-PB2-OB3
31	V	201	CDL	CB3-OB5-PB2-OB4
31	a	201	CDL	CA2-OA2-PA1-OA3
31	a	201	CDL	CA2-OA2-PA1-OA4
31	a	201	CDL	CA2-OA2-PA1-OA5
31	a	201	CDL	CA3-OA5-PA1-OA2
31	a	201	CDL	CB2-OB2-PB2-OB3
31	a	201	CDL	CB3-OB5-PB2-OB3
31	g	202	CDL	CA2-OA2-PA1-OA3
31	g	202	CDL	CA2-OA2-PA1-OA4
31	g	202	CDL	CA3-OA5-PA1-OA2
31	g	202	CDL	CA3-OA5-PA1-OA4
31	g	202	CDL	CB2-OB2-PB2-OB3
31	g	202	CDL	CB3-OB5-PB2-OB3
31	g	202	CDL	CB3-OB5-PB2-OB4
31	i	401	CDL	CA2-OA2-PA1-OA5
31	i	401	CDL	CA3-OA5-PA1-OA3
31	i	401	CDL	CB2-OB2-PB2-OB4
31	l	702	CDL	O1-C1-CA2-OA2
31	l	702	CDL	CA2-C1-CB2-OB2
31	l	702	CDL	OA6-CA4-CA6-OA8
31	l	702	CDL	CB2-OB2-PB2-OB3
31	l	702	CDL	CB2-OB2-PB2-OB4
31	l	702	CDL	CB2-OB2-PB2-OB5
31	l	702	CDL	OB6-CB4-CB6-OB8
31	o	201	CDL	O1-C1-CA2-OA2
31	o	201	CDL	CA2-OA2-PA1-OA5
31	o	201	CDL	CB3-OB5-PB2-OB2
31	o	201	CDL	CB3-OB5-PB2-OB3
31	o	201	CDL	CB3-OB5-PB2-OB4
31	o	201	CDL	OB6-CB4-CB6-OB8
31	r	504	CDL	O1-C1-CA2-OA2
31	r	504	CDL	CA2-C1-CB2-OB2
31	r	504	CDL	CB2-OB2-PB2-OB3
31	r	504	CDL	CB2-OB2-PB2-OB4
31	r	504	CDL	CB3-OB5-PB2-OB3
31	u	201	CDL	O1-C1-CA2-OA2
31	u	201	CDL	CA2-OA2-PA1-OA3
31	u	201	CDL	CA2-OA2-PA1-OA4
31	u	201	CDL	CB2-OB2-PB2-OB3
31	u	201	CDL	CB3-OB5-PB2-OB3

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Mol	Chain	Res	Type	Atoms
32	X	201	8Q1	C1-C6-C7-C8
32	X	201	8Q1	C28-C29-C32-C34
32	X	201	8Q1	C28-C29-C32-O33
32	X	201	8Q1	C30-C29-C32-C34
32	X	201	8Q1	C30-C29-C32-O33
32	X	201	8Q1	C31-C29-C32-C34
32	X	201	8Q1	C31-C29-C32-O33
32	X	201	8Q1	C29-C32-C34-O35
32	X	201	8Q1	N36-C37-C38-C39
32	X	201	8Q1	C42-C43-S44-C1
32	X	201	8Q1	C28-O27-P24-O3
32	X	201	8Q1	C28-O27-P24-O2
32	X	201	8Q1	C28-O27-P24-O1
33	a	202	PLX	O9-C24-O8-C5
33	g	201	PLX	C25-C24-O8-C5
33	j	202	PLX	O7-C6-C7-C8
33	j	202	PLX	O9-C24-C25-C26
33	r	502	PLX	O7-C6-O6-C4
33	r	502	PLX	C5-C4-O6-C6
33	r	502	PLX	O9-C24-O8-C5
33	r	502	PLX	O9-C24-C25-C26
33	r	503	PLX	O7-C6-O6-C4
33	r	503	PLX	C3-O4-P1-O2
33	r	503	PLX	C3-O4-P1-O3
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
34	s	401	UQ	C1-C6-C7-C8
34	s	401	UQ	C5-C6-C7-C8
34	s	401	UQ	C9-C11-C12-C13
35	w	401	ADP	C5'-O5'-PA-O1A
35	w	401	ADP	C5'-O5'-PA-O2A
35	w	401	ADP	C5'-O5'-PA-O3A
31	i	401	CDL	OA9-CA7-OA8-CA6
31	r	504	CDL	OA9-CA7-OA8-CA6
30	i	402	PEE	O4-C10-O2-C2
30	l	703	PEE	O4-C10-O2-C2
31	g	202	CDL	C71-CB7-OB8-CB6
31	i	401	CDL	C31-CA7-OA8-CA6
31	r	504	CDL	C31-CA7-OA8-CA6

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Mol	Chain	Res	Type	Atoms
30	l	703	PEE	C11-C10-O2-C2
30	U	401	PEE	C37-C38-C39-C40
30	j	201	PEE	C17-C18-C19-C20
30	l	701	PEE	C17-C18-C19-C20
30	l	703	PEE	O5-C30-O3-C3
31	V	201	CDL	O1-C1-CA2-OA2
31	a	201	CDL	O1-C1-CB2-OB2
31	l	702	CDL	O1-C1-CB2-OB2
31	r	504	CDL	O1-C1-CB2-OB2
30	b	201	PEE	C31-C30-O3-C3
31	l	702	CDL	C71-CB7-OB8-CB6
31	l	702	CDL	C75-C76-C77-C78
30	b	201	PEE	O5-C30-O3-C3
31	g	202	CDL	OB9-CB7-OB8-CB6
30	U	401	PEE	C11-C10-O2-C2
31	V	201	CDL	C11-CA5-OA6-CA4
31	u	201	CDL	C71-C72-C73-C74
33	r	502	PLX	C9-C10-C11-C12
31	V	201	CDL	C59-C60-C61-C62
31	l	702	CDL	C59-C60-C61-C62
31	o	201	CDL	C72-C73-C74-C75
31	u	201	CDL	C75-C76-C77-C78
33	g	201	PLX	C10-C11-C12-C13
33	j	202	PLX	C28-C29-C30-C31
33	r	503	PLX	C12-C13-C14-C15
30	l	703	PEE	C31-C30-O3-C3
30	U	401	PEE	O4-C10-O2-C2
31	V	201	CDL	C11-C12-C13-C14
31	u	201	CDL	C52-C53-C54-C55
31	l	702	CDL	OB9-CB7-OB8-CB6
31	l	702	CDL	C11-C12-C13-C14
31	l	702	CDL	C35-C36-C37-C38
30	l	701	PEE	C31-C30-O3-C3
33	r	502	PLX	C30-C31-C32-C33
31	V	201	CDL	C32-C33-C34-C35
31	V	201	CDL	C62-C63-C64-C65
31	a	201	CDL	CA2-C1-CB2-OB2
31	g	202	CDL	CB2-C1-CA2-OA2
31	i	401	CDL	CB2-C1-CA2-OA2
31	l	702	CDL	CB2-C1-CA2-OA2
31	o	201	CDL	CB2-C1-CA2-OA2
31	o	201	CDL	CA2-C1-CB2-OB2

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Mol	Chain	Res	Type	Atoms
31	u	201	CDL	CB2-C1-CA2-OA2
31	u	201	CDL	CA2-C1-CB2-OB2
30	W	201	PEE	C31-C30-O3-C3
30	j	201	PEE	C31-C30-O3-C3
31	r	504	CDL	C55-C56-C57-C58
30	l	703	PEE	O3P-C1-C2-O2
31	g	202	CDL	C76-C77-C78-C79
31	a	201	CDL	O1-C1-CA2-OA2
31	i	401	CDL	O1-C1-CA2-OA2
31	u	201	CDL	O1-C1-CB2-OB2
31	g	202	CDL	C74-C75-C76-C77
33	j	202	PLX	C15-C16-C17-C18
30	l	701	PEE	C11-C12-C13-C14
31	V	201	CDL	OA7-CA5-OA6-CA4
30	j	201	PEE	C11-C10-O2-C2
33	r	502	PLX	C11-C12-C13-C14
31	r	504	CDL	CB7-C71-C72-C73
33	g	201	PLX	C12-C13-C14-C15
30	j	201	PEE	C19-C20-C21-C22
30	i	402	PEE	C30-C31-C32-C33
30	l	703	PEE	C30-C31-C32-C33
31	V	201	CDL	CB7-C71-C72-C73
31	a	201	CDL	CA5-C11-C12-C13
31	i	401	CDL	CB7-C71-C72-C73
31	o	201	CDL	CB7-C71-C72-C73
31	i	401	CDL	C14-C15-C16-C17
31	r	504	CDL	C58-C59-C60-C61
31	g	202	CDL	CA7-C31-C32-C33
30	l	703	PEE	C33-C34-C35-C36
30	r	501	PEE	C11-C10-O2-C2
30	j	201	PEE	C32-C33-C34-C35
30	j	201	PEE	O5-C30-O3-C3
31	g	202	CDL	CA5-C11-C12-C13
30	j	201	PEE	C34-C35-C36-C37
31	g	202	CDL	CB5-C51-C52-C53
31	V	201	CDL	O1-C1-CB2-OB2
31	g	202	CDL	O1-C1-CA2-OA2
31	o	201	CDL	O1-C1-CB2-OB2
30	l	701	PEE	O5-C30-O3-C3
31	u	201	CDL	CB7-C71-C72-C73
31	l	702	CDL	C39-C40-C41-C42
31	u	201	CDL	C17-C18-C19-C20

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Mol	Chain	Res	Type	Atoms
30	W	201	PEE	O5-C30-O3-C3
30	j	201	PEE	C1-O3P-P-O4P
30	l	701	PEE	C1-O3P-P-O4P
30	l	701	PEE	C4-O4P-P-O3P
31	V	201	CDL	CA2-OA2-PA1-OA5
31	V	201	CDL	CA3-OA5-PA1-OA2
31	V	201	CDL	CB2-OB2-PB2-OB5
31	a	201	CDL	CB3-OB5-PB2-OB2
31	g	202	CDL	CA2-OA2-PA1-OA5
31	g	202	CDL	CB3-OB5-PB2-OB2
31	l	702	CDL	CB3-OB5-PB2-OB2
31	r	504	CDL	CA2-OA2-PA1-OA5
31	r	504	CDL	CB2-OB2-PB2-OB5
31	r	504	CDL	CB3-OB5-PB2-OB2
31	u	201	CDL	CA2-OA2-PA1-OA5
31	u	201	CDL	CB2-OB2-PB2-OB5
33	g	201	PLX	C3-O4-P1-O1
33	r	503	PLX	C3-O4-P1-O1
31	a	201	CDL	C71-CB7-OB8-CB6
31	o	201	CDL	C31-CA7-OA8-CA6
31	r	504	CDL	C71-CB7-OB8-CB6
31	a	201	CDL	C31-C32-C33-C34
31	a	201	CDL	CA7-C31-C32-C33
31	i	401	CDL	CA7-C31-C32-C33
31	V	201	CDL	CB2-C1-CA2-OA2
31	a	201	CDL	CB2-C1-CA2-OA2
31	r	504	CDL	CB2-C1-CA2-OA2
30	j	201	PEE	O4-C10-O2-C2
30	r	501	PEE	O4-C10-O2-C2
34	s	401	UQ	C12-C11-C9-C10
33	g	201	PLX	C31-C32-C33-C34
33	g	201	PLX	O8-C24-C25-C26
31	g	202	CDL	C78-C79-C80-C81
30	b	201	PEE	C31-C32-C33-C34
33	r	503	PLX	C25-C26-C27-C28
30	b	201	PEE	C11-C10-O2-C2
31	g	202	CDL	C51-CB5-OB6-CB4
30	l	703	PEE	C34-C35-C36-C37
31	a	201	CDL	C75-C76-C77-C78
31	g	202	CDL	C12-C13-C14-C15
31	g	202	CDL	C35-C36-C37-C38
31	g	202	CDL	C59-C60-C61-C62

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Mol	Chain	Res	Type	Atoms
31	r	504	CDL	C52-C53-C54-C55
30	U	401	PEE	C33-C34-C35-C36
30	i	402	PEE	C11-C12-C13-C14
31	a	201	CDL	C73-C74-C75-C76
31	g	202	CDL	C56-C57-C58-C59
31	i	401	CDL	C52-C53-C54-C55
31	l	702	CDL	C37-C38-C39-C40
33	r	502	PLX	C7-C8-C9-C10
33	r	502	PLX	C27-C28-C29-C30
30	b	201	PEE	O4-C10-O2-C2
31	g	202	CDL	OB7-CB5-OB6-CB4
30	W	201	PEE	C13-C14-C15-C16
30	b	201	PEE	C32-C33-C34-C35
31	V	201	CDL	C52-C53-C54-C55
33	r	502	PLX	C15-C16-C17-C18
33	r	503	PLX	C13-C14-C15-C16
30	r	501	PEE	C13-C14-C15-C16
31	V	201	CDL	C40-C41-C42-C43
31	r	504	CDL	C74-C75-C76-C77
33	r	503	PLX	C10-C11-C12-C13
30	j	201	PEE	C30-C31-C32-C33
31	u	201	CDL	CB5-C51-C52-C53
31	o	201	CDL	C71-CB7-OB8-CB6
31	V	201	CDL	C74-C75-C76-C77
31	a	201	CDL	C21-C22-C23-C24
31	a	201	CDL	C37-C38-C39-C40
31	i	401	CDL	C11-C12-C13-C14
31	r	504	CDL	C59-C60-C61-C62
31	r	504	CDL	C73-C74-C75-C76
31	g	202	CDL	C32-C33-C34-C35
31	l	702	CDL	C55-C56-C57-C58
31	r	504	CDL	C35-C36-C37-C38
31	u	201	CDL	C13-C14-C15-C16
31	u	201	CDL	C53-C54-C55-C56
33	g	201	PLX	C25-C26-C27-C28
31	l	702	CDL	CB5-C51-C52-C53
31	l	702	CDL	CB7-C71-C72-C73
31	g	202	CDL	C73-C74-C75-C76
31	o	201	CDL	C83-C84-C85-C86
31	r	504	CDL	C75-C76-C77-C78
31	u	201	CDL	C11-C12-C13-C14
33	r	502	PLX	C13-C14-C15-C16

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Mol	Chain	Res	Type	Atoms
30	j	201	PEE	C41-C42-C43-C44
30	l	701	PEE	C11-C10-O2-C2
31	V	201	CDL	C51-CB5-OB6-CB4
31	g	202	CDL	C72-C73-C74-C75
31	l	702	CDL	C73-C74-C75-C76
33	j	202	PLX	C10-C11-C12-C13
33	r	502	PLX	C12-C13-C14-C15
33	r	502	PLX	C31-C32-C33-C34
30	i	402	PEE	C35-C36-C37-C38
30	W	201	PEE	C23-C24-C25-C26
30	i	402	PEE	C21-C22-C23-C24
31	g	202	CDL	C17-C18-C19-C20
31	g	202	CDL	C71-C72-C73-C74
31	o	201	CDL	C71-C72-C73-C74
31	o	201	CDL	C73-C74-C75-C76
31	o	201	CDL	C75-C76-C77-C78
31	r	504	CDL	C82-C83-C84-C85
31	u	201	CDL	C55-C56-C57-C58
31	u	201	CDL	C59-C60-C61-C62
33	g	201	PLX	C9-C10-C11-C12
33	g	201	PLX	C11-C10-C9-C8
33	g	201	PLX	C27-C28-C29-C30
33	j	202	PLX	C7-C8-C9-C10
33	j	202	PLX	C25-C26-C27-C28
33	r	503	PLX	C14-C15-C16-C17
30	W	201	PEE	C33-C34-C35-C36
30	b	201	PEE	C22-C23-C24-C25
31	r	504	CDL	C56-C57-C58-C59
33	r	502	PLX	C14-C15-C16-C17
33	r	503	PLX	C27-C28-C29-C30
30	U	401	PEE	C23-C24-C25-C26
30	U	401	PEE	C20-C21-C22-C23
31	l	702	CDL	C74-C75-C76-C77
31	r	504	CDL	C11-C12-C13-C14
33	r	503	PLX	C26-C27-C28-C29
30	r	501	PEE	C10-C11-C12-C13
31	r	504	CDL	OB9-CB7-OB8-CB6
30	b	201	PEE	C34-C35-C36-C37
30	l	703	PEE	C23-C24-C25-C26
30	l	703	PEE	C11-C12-C13-C14
31	i	401	CDL	C37-C38-C39-C40
31	l	702	CDL	C72-C73-C74-C75

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Mol	Chain	Res	Type	Atoms
31	a	201	CDL	OB9-CB7-OB8-CB6
30	b	201	PEE	C13-C14-C15-C16
31	o	201	CDL	C55-C56-C57-C58
30	l	701	PEE	O4-C10-O2-C2
31	V	201	CDL	OB7-CB5-OB6-CB4
33	a	202	PLX	C25-C26-C27-C28
30	b	201	PEE	C33-C34-C35-C36
31	r	504	CDL	C61-C62-C63-C64
31	o	201	CDL	C51-CB5-OB6-CB4
33	a	202	PLX	O9-C24-C25-C26
33	g	201	PLX	O9-C24-C25-C26
31	g	202	CDL	C43-C44-C45-C46
33	g	201	PLX	C28-C29-C30-C31
30	U	401	PEE	C35-C36-C37-C38
30	U	401	PEE	C39-C40-C41-C42
30	i	402	PEE	C19-C20-C21-C22
31	o	201	CDL	OA9-CA7-OA8-CA6
30	b	201	PEE	C23-C24-C25-C26
31	a	201	CDL	C71-C72-C73-C74
33	j	202	PLX	C12-C13-C14-C15
31	r	504	CDL	C20-C21-C22-C23
33	j	202	PLX	C27-C28-C29-C30
31	o	201	CDL	OB7-CB5-OB6-CB4
30	U	401	PEE	C22-C23-C24-C25
30	l	701	PEE	C32-C33-C34-C35
31	g	202	CDL	C75-C76-C77-C78
31	l	702	CDL	C58-C59-C60-C61
33	r	503	PLX	C2-C1-N1-C1A
30	r	501	PEE	C40-C41-C42-C43
33	r	503	PLX	C31-C32-C33-C34
31	u	201	CDL	C11-CA5-OA6-CA4
31	g	202	CDL	C57-C58-C59-C60
33	j	202	PLX	C14-C15-C16-C17
31	o	201	CDL	OB9-CB7-OB8-CB6
31	g	202	CDL	CB7-C71-C72-C73
31	o	201	CDL	CA7-C31-C32-C33
31	V	201	CDL	C33-C34-C35-C36
31	V	201	CDL	C31-CA7-OA8-CA6
31	l	702	CDL	C71-C72-C73-C74
31	g	202	CDL	C41-C42-C43-C44
31	i	401	CDL	C32-C33-C34-C35
31	l	702	CDL	C56-C57-C58-C59

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Mol	Chain	Res	Type	Atoms
31	l	702	CDL	C60-C61-C62-C63
31	r	504	CDL	C32-C33-C34-C35
31	u	201	CDL	C14-C15-C16-C17
31	o	201	CDL	C54-C55-C56-C57
31	V	201	CDL	C71-CB7-OB8-CB6
30	r	501	PEE	C21-C22-C23-C24
31	i	401	CDL	C33-C34-C35-C36
33	r	503	PLX	C28-C29-C30-C31
30	U	401	PEE	C21-C22-C23-C24
30	r	501	PEE	C36-C37-C38-C39
31	g	202	CDL	C14-C15-C16-C17
30	l	703	PEE	C31-C32-C33-C34
31	g	202	CDL	C37-C38-C39-C40
33	g	201	PLX	C13-C14-C15-C16
33	r	502	PLX	C33-C34-C35-C36
31	g	202	CDL	OB6-CB4-CB6-OB8
31	i	401	CDL	OB6-CB4-CB6-OB8
30	l	703	PEE	C32-C33-C34-C35
31	V	201	CDL	C31-C32-C33-C34
31	r	504	CDL	C42-C43-C44-C45
33	r	503	PLX	C2-C1-N1-C1C
30	W	201	PEE	C22-C23-C24-C25
30	U	401	PEE	C15-C16-C17-C18
30	l	701	PEE	C35-C36-C37-C38
30	r	501	PEE	C39-C40-C41-C42
34	s	401	UQ	C12-C11-C9-C8
30	j	201	PEE	C31-C32-C33-C34
31	r	504	CDL	C14-C15-C16-C17
30	l	703	PEE	C37-C38-C39-C40
31	o	201	CDL	C74-C75-C76-C77
31	u	201	CDL	OA7-CA5-OA6-CA4
30	j	201	PEE	C22-C23-C24-C25
31	V	201	CDL	C35-C36-C37-C38
30	j	201	PEE	C36-C37-C38-C39
31	a	201	CDL	CB2-OB2-PB2-OB5
31	i	401	CDL	CA3-OA5-PA1-OA2
31	i	401	CDL	CB2-OB2-PB2-OB5
31	u	201	CDL	CB3-OB5-PB2-OB2
33	j	202	PLX	C3-O4-P1-O1
31	o	201	CDL	C82-C83-C84-C85
31	g	202	CDL	CB4-CB3-OB5-PB2
30	W	201	PEE	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
30	r	501	PEE	C12-C13-C14-C15
33	j	202	PLX	C26-C27-C28-C29
30	l	701	PEE	O3P-C1-C2-C3
30	l	703	PEE	O3P-C1-C2-C3
31	i	401	CDL	OB5-CB3-CB4-CB6
33	j	202	PLX	O4-C3-C4-C5
31	g	202	CDL	C60-C61-C62-C63
31	r	504	CDL	C23-C24-C25-C26
33	g	201	PLX	C33-C34-C35-C36
30	b	201	PEE	C10-C11-C12-C13
30	l	701	PEE	C30-C31-C32-C33
31	a	201	CDL	C76-C77-C78-C79
33	r	503	PLX	C15-C16-C17-C18
33	r	503	PLX	C29-C30-C31-C32
31	V	201	CDL	OA9-CA7-OA8-CA6
31	a	201	CDL	C52-C53-C54-C55
30	W	201	PEE	C1-C2-C3-O3
30	l	701	PEE	C1-C2-C3-O3
31	g	202	CDL	CB3-CB4-CB6-OB8
31	l	702	CDL	CA3-CA4-CA6-OA8
31	l	702	CDL	CB3-CB4-CB6-OB8
31	o	201	CDL	CB3-CB4-CB6-OB8
31	r	504	CDL	C76-C77-C78-C79
31	u	201	CDL	CA3-CA4-CA6-OA8
31	V	201	CDL	C37-C38-C39-C40
31	l	702	CDL	C41-C42-C43-C44
31	o	201	CDL	C84-C85-C86-C87
33	r	503	PLX	C16-C17-C18-C19
31	V	201	CDL	OB9-CB7-OB8-CB6
31	a	201	CDL	C43-C44-C45-C46
33	g	201	PLX	C11-C12-C13-C14
33	r	502	PLX	C16-C17-C18-C19
31	i	401	CDL	C34-C35-C36-C37
31	l	702	CDL	C14-C15-C16-C17
33	j	202	PLX	C9-C10-C11-C12
31	V	201	CDL	C54-C55-C56-C57
31	l	702	CDL	C52-C53-C54-C55
33	a	202	PLX	C7-C8-C9-C10
30	r	501	PEE	C41-C42-C43-C44
31	V	201	CDL	C14-C15-C16-C17
33	a	202	PLX	C11-C12-C13-C14
30	U	401	PEE	C31-C30-O3-C3

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Mol	Chain	Res	Type	Atoms
31	l	702	CDL	C64-C65-C66-C67
31	r	504	CDL	C36-C37-C38-C39
31	r	504	CDL	C71-C72-C73-C74
31	V	201	CDL	C58-C59-C60-C61
30	r	501	PEE	O3P-C1-C2-O2
31	a	201	CDL	OA5-CA3-CA4-OA6
30	U	401	PEE	C17-C18-C19-C20
33	r	503	PLX	C2-C1-N1-C1B
31	i	401	CDL	C73-C74-C75-C76
31	a	201	CDL	C55-C56-C57-C58
31	l	702	CDL	C54-C55-C56-C57
31	o	201	CDL	C52-C53-C54-C55
30	l	701	PEE	O2-C2-C3-O3
31	o	201	CDL	OA6-CA4-CA6-OA8
31	a	201	CDL	C14-C15-C16-C17
31	r	504	CDL	C62-C63-C64-C65
30	W	201	PEE	C11-C10-O2-C2
30	r	501	PEE	C11-C12-C13-C14
31	i	401	CDL	C71-CB7-OB8-CB6
33	r	503	PLX	C7-C8-C9-C10
33	r	503	PLX	C30-C31-C32-C33
30	i	402	PEE	O3P-C1-C2-C3
31	V	201	CDL	OB5-CB3-CB4-CB6
31	a	201	CDL	OA5-CA3-CA4-CA6
31	a	201	CDL	OB5-CB3-CB4-CB6
31	o	201	CDL	OB5-CB3-CB4-CB6
30	W	201	PEE	O3-C30-C31-C32
33	j	202	PLX	C33-C34-C35-C36
31	a	201	CDL	CB5-C51-C52-C53
31	g	202	CDL	C20-C21-C22-C23
33	j	202	PLX	C13-C14-C15-C16
30	U	401	PEE	O5-C30-O3-C3
31	g	202	CDL	C13-C14-C15-C16
33	j	202	PLX	C34-C35-C36-C37
30	l	701	PEE	C10-C11-C12-C13
30	i	402	PEE	C18-C19-C20-C21
31	g	202	CDL	C33-C34-C35-C36
33	r	503	PLX	C33-C34-C35-C36
30	b	201	PEE	C1-C2-C3-O3
30	i	402	PEE	C1-C2-C3-O3
31	i	401	CDL	CB3-CB4-CB6-OB8
33	r	502	PLX	C3-C4-C5-O8

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Mol	Chain	Res	Type	Atoms
33	r	503	PLX	C3-C4-C5-O8
30	r	501	PEE	C17-C18-C19-C20
31	r	504	CDL	C39-C40-C41-C42
31	u	201	CDL	C54-C55-C56-C57
32	X	201	8Q1	C29-C32-C34-N36
33	r	503	PLX	C5-C4-O6-C6
31	l	702	CDL	C40-C41-C42-C43
31	V	201	CDL	OB5-CB3-CB4-OB6
31	o	201	CDL	OB5-CB3-CB4-OB6
33	g	201	PLX	O4-C3-C4-O6
33	j	202	PLX	O4-C3-C4-O6
31	g	202	CDL	OA6-CA4-CA6-OA8
33	j	202	PLX	O6-C4-C5-O8
33	r	503	PLX	O6-C4-C5-O8
31	l	702	CDL	C43-C44-C45-C46
31	a	201	CDL	C60-C61-C62-C63
33	g	201	PLX	C14-C15-C16-C17
30	W	201	PEE	O4-C10-O2-C2
30	l	701	PEE	C33-C34-C35-C36
33	r	502	PLX	C28-C29-C30-C31
31	i	401	CDL	OB9-CB7-OB8-CB6
31	o	201	CDL	C32-C31-CA7-OA8
30	r	501	PEE	C38-C39-C40-C41
31	g	202	CDL	C52-C53-C54-C55
32	X	201	8Q1	O4-C1-S44-C43
30	l	701	PEE	C18-C19-C20-C21
31	g	202	CDL	C42-C43-C44-C45
33	r	503	PLX	O8-C24-C25-C26
31	i	401	CDL	OA5-CA3-CA4-CA6
30	W	201	PEE	C32-C33-C34-C35
31	r	504	CDL	C60-C61-C62-C63
32	X	201	8Q1	O33-C32-C34-N36
31	l	702	CDL	CA7-C31-C32-C33
33	r	503	PLX	C9-C10-C11-C12
30	b	201	PEE	C11-C12-C13-C14
31	V	201	CDL	CA6-CA4-OA6-CA5
32	X	201	8Q1	C6-C1-S44-C43
30	r	501	PEE	C1-C2-C3-O3
31	g	202	CDL	CA3-CA4-CA6-OA8
31	i	401	CDL	CA3-CA4-CA6-OA8
33	j	202	PLX	C3-C4-C5-O8
30	i	402	PEE	O3P-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
31	a	201	CDL	OB5-CB3-CB4-OB6
31	i	401	CDL	OA5-CA3-CA4-OA6
30	b	201	PEE	C14-C15-C16-C17
30	r	501	PEE	O2-C2-C3-O3
31	i	401	CDL	OA6-CA4-CA6-OA8
31	u	201	CDL	OA6-CA4-CA6-OA8
33	r	502	PLX	O6-C4-C5-O8
31	g	202	CDL	C55-C56-C57-C58
31	l	702	CDL	C12-C13-C14-C15
30	l	701	PEE	C13-C14-C15-C16
31	a	201	CDL	C17-C18-C19-C20
31	i	401	CDL	C75-C76-C77-C78
31	V	201	CDL	C34-C35-C36-C37
31	a	201	CDL	C36-C37-C38-C39
31	i	401	CDL	C35-C36-C37-C38
31	a	201	CDL	C54-C55-C56-C57
33	r	503	PLX	C18-C19-C20-C21
31	g	202	CDL	C54-C55-C56-C57
33	j	202	PLX	C31-C32-C33-C34
30	r	501	PEE	C1-O3P-P-O4P
31	l	702	CDL	CA3-OA5-PA1-OA2
31	g	202	CDL	C64-C65-C66-C67
33	r	503	PLX	C11-C12-C13-C14
30	b	201	PEE	C1-O3P-P-O1P
30	j	201	PEE	C4-O4P-P-O1P
30	l	701	PEE	C1-O3P-P-O2P
30	l	701	PEE	C1-O3P-P-O1P
30	l	701	PEE	C4-O4P-P-O2P
30	r	501	PEE	C1-O3P-P-O2P
31	V	201	CDL	CA3-OA5-PA1-OA4
31	a	201	CDL	CA3-OA5-PA1-OA4
31	a	201	CDL	CB2-OB2-PB2-OB4
31	g	202	CDL	CA3-OA5-PA1-OA3
31	i	401	CDL	CA2-OA2-PA1-OA4
31	i	401	CDL	CA3-OA5-PA1-OA4
31	i	401	CDL	CB2-OB2-PB2-OB3
31	i	401	CDL	CB3-OB5-PB2-OB4
31	l	702	CDL	CB3-OB5-PB2-OB3
31	l	702	CDL	CB3-OB5-PB2-OB4
31	o	201	CDL	CA2-OA2-PA1-OA4
31	o	201	CDL	CB2-OB2-PB2-OB4
31	r	504	CDL	CA2-OA2-PA1-OA3

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Mol	Chain	Res	Type	Atoms
31	r	504	CDL	CB3-OB5-PB2-OB4
31	u	201	CDL	CB2-OB2-PB2-OB4
31	u	201	CDL	CB3-OB5-PB2-OB4
33	g	201	PLX	C3-O4-P1-O3
33	j	202	PLX	C3-O4-P1-O3
30	b	201	PEE	O3P-C1-C2-C3
30	r	501	PEE	O3P-C1-C2-C3
31	l	702	CDL	OA5-CA3-CA4-CA6
33	g	201	PLX	O4-C3-C4-C5
30	r	501	PEE	C14-C15-C16-C17
31	i	401	CDL	C74-C75-C76-C77
33	g	201	PLX	C16-C17-C18-C19
33	a	202	PLX	C25-C24-O8-C5
33	j	202	PLX	C25-C24-O8-C5
31	a	201	CDL	C19-C20-C21-C22
30	b	201	PEE	O3P-C1-C2-O2
31	i	401	CDL	OB5-CB3-CB4-OB6
31	l	702	CDL	OA5-CA3-CA4-OA6
30	l	703	PEE	C14-C15-C16-C17
31	V	201	CDL	C71-C72-C73-C74
31	r	504	CDL	CA7-C31-C32-C33
31	u	201	CDL	CA5-C11-C12-C13
30	i	402	PEE	C24-C25-C26-C27
31	o	201	CDL	CA3-CA4-CA6-OA8
30	W	201	PEE	O2-C2-C3-O3
30	b	201	PEE	O2-C2-C3-O3
30	i	402	PEE	O2-C2-C3-O3
30	b	201	PEE	C16-C17-C18-C19
31	V	201	CDL	C55-C56-C57-C58
30	i	402	PEE	C2-C1-O3P-P
33	j	202	PLX	O6-C6-C7-C8
34	s	401	UQ	C14-C16-C17-C18
31	l	702	CDL	C32-C33-C34-C35
31	r	504	CDL	C34-C35-C36-C37
31	g	202	CDL	C62-C63-C64-C65
30	b	201	PEE	C38-C39-C40-C41
33	g	201	PLX	C29-C30-C31-C32
33	a	202	PLX	C13-C14-C15-C16
33	a	202	PLX	C34-C35-C36-C37
30	U	401	PEE	C11-C12-C13-C14
31	r	504	CDL	C40-C41-C42-C43
30	U	401	PEE	O3P-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
30	i	402	PEE	C31-C32-C33-C34
30	l	701	PEE	C31-C32-C33-C34
30	W	201	PEE	C18-C19-C20-C21
30	j	201	PEE	C38-C39-C40-C41
30	l	701	PEE	C38-C39-C40-C41
31	o	201	CDL	C32-C33-C34-C35
30	l	703	PEE	C4-O4P-P-O3P
31	i	401	CDL	CB3-OB5-PB2-OB2
31	l	702	CDL	CA2-OA2-PA1-OA5
33	a	202	PLX	C3-O4-P1-O1
33	a	202	PLX	C2-O1-P1-O4
31	i	401	CDL	C15-C16-C17-C18
31	i	401	CDL	C71-C72-C73-C74
31	l	702	CDL	C63-C64-C65-C66
31	g	202	CDL	C23-C24-C25-C26
31	a	201	CDL	C31-CA7-OA8-CA6
31	a	201	CDL	OA9-CA7-OA8-CA6
31	g	202	CDL	C39-C40-C41-C42
31	V	201	CDL	C53-C54-C55-C56
31	i	401	CDL	CB5-C51-C52-C53
30	b	201	PEE	C15-C16-C17-C18
30	i	402	PEE	C37-C38-C39-C40
30	b	201	PEE	C18-C19-C20-C21
30	U	401	PEE	C34-C35-C36-C37
30	U	401	PEE	C40-C41-C42-C43
31	V	201	CDL	C39-C40-C41-C42
31	V	201	CDL	C75-C76-C77-C78
30	l	701	PEE	C39-C40-C41-C42
31	u	201	CDL	C61-C62-C63-C64
31	u	201	CDL	C60-C61-C62-C63
31	g	202	CDL	C11-C12-C13-C14
33	g	201	PLX	C36-C37-C38-C39
33	j	202	PLX	C11-C12-C13-C14
31	r	504	CDL	C21-C22-C23-C24
30	l	703	PEE	C22-C23-C24-C25
31	V	201	CDL	CA3-CA4-CA6-OA8
31	r	504	CDL	C37-C38-C39-C40
31	g	202	CDL	C44-C45-C46-C47
31	g	202	CDL	C31-C32-C33-C34
31	r	504	CDL	C78-C79-C80-C81
33	a	202	PLX	C10-C11-C12-C13
33	j	202	PLX	C19-C20-C21-C22

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Mol	Chain	Res	Type	Atoms
31	u	201	CDL	C72-C73-C74-C75
30	W	201	PEE	C34-C35-C36-C37
30	U	401	PEE	O3P-C1-C2-C3
30	U	401	PEE	C32-C33-C34-C35
31	l	702	CDL	C57-C58-C59-C60
30	W	201	PEE	O5-C30-C31-C32
30	l	703	PEE	C13-C14-C15-C16
30	r	501	PEE	C31-C32-C33-C34
30	r	501	PEE	C20-C21-C22-C23
31	g	202	CDL	C51-C52-C53-C54
31	i	401	CDL	C13-C14-C15-C16
33	r	502	PLX	O8-C24-C25-C26
30	i	402	PEE	C23-C24-C25-C26
31	a	201	CDL	C15-C16-C17-C18
33	a	202	PLX	C33-C34-C35-C36
31	V	201	CDL	OB6-CB4-CB6-OB8
31	V	201	CDL	C64-C65-C66-C67
31	o	201	CDL	C80-C81-C82-C83
30	l	701	PEE	C37-C38-C39-C40
30	j	201	PEE	C39-C40-C41-C42
30	l	703	PEE	C19-C20-C21-C22
30	l	703	PEE	C15-C16-C17-C18
30	U	401	PEE	C14-C15-C16-C17
30	W	201	PEE	C16-C17-C18-C19
30	i	402	PEE	C38-C39-C40-C41
31	a	201	CDL	C35-C36-C37-C38
33	r	502	PLX	C25-C26-C27-C28
31	r	504	CDL	C54-C55-C56-C57
30	U	401	PEE	C18-C19-C20-C21
30	l	703	PEE	C36-C37-C38-C39
33	j	202	PLX	C7-C6-O6-C4
31	l	702	CDL	C31-C32-C33-C34
31	V	201	CDL	OA5-CA3-CA4-OA6
31	r	504	CDL	C17-C18-C19-C20
30	U	401	PEE	C13-C14-C15-C16
33	g	201	PLX	C6-C7-C8-C9
31	l	702	CDL	C12-C11-CA5-OA6
30	j	201	PEE	C16-C17-C18-C19
30	l	703	PEE	C16-C17-C18-C19
30	l	701	PEE	O3-C30-C31-C32
31	u	201	CDL	C72-C71-CB7-OB8
30	j	201	PEE	C15-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
30	W	201	PEE	O3P-C1-C2-C3
31	a	201	CDL	C12-C13-C14-C15
30	i	402	PEE	C36-C37-C38-C39
31	o	201	CDL	C12-C11-CA5-OA6
31	V	201	CDL	C57-C58-C59-C60
30	U	401	PEE	C44-C45-C46-C47
30	l	701	PEE	C16-C17-C18-C19
30	r	501	PEE	C30-C31-C32-C33
30	j	201	PEE	O2-C10-C11-C12
35	w	401	ADP	PB-O3A-PA-O2A
31	r	504	CDL	C72-C73-C74-C75
34	s	401	UQ	C1-C2-O2-CM2
31	g	202	CDL	C36-C37-C38-C39
33	j	202	PLX	C2-C1-N1-C1A
31	o	201	CDL	C32-C31-CA7-OA9
30	W	201	PEE	O3P-C1-C2-O2
30	l	701	PEE	O5-C30-C31-C32
31	u	201	CDL	C72-C71-CB7-OB9
31	l	702	CDL	C12-C11-CA5-OA7
30	b	201	PEE	O3-C30-C31-C32
31	o	201	CDL	C12-C11-CA5-OA7
31	r	504	CDL	CA3-OA5-PA1-OA3
31	u	201	CDL	CA3-OA5-PA1-OA3
34	s	401	UQ	C6-C7-C8-C9
31	o	201	CDL	C78-C79-C80-C81
31	l	702	CDL	OB5-CB3-CB4-CB6
30	b	201	PEE	C12-C13-C14-C15
31	a	201	CDL	C74-C75-C76-C77
30	r	501	PEE	C16-C17-C18-C19
31	l	702	CDL	C52-C51-CB5-OB6
31	a	201	CDL	C18-C19-C20-C21
30	b	201	PEE	C5-C4-O4P-P
33	r	502	PLX	C25-C24-O8-C5
31	r	504	CDL	C12-C11-CA5-OA6
30	j	201	PEE	C40-C41-C42-C43
30	l	703	PEE	C39-C40-C41-C42
33	r	502	PLX	C35-C36-C37-C38
31	r	504	CDL	C44-C45-C46-C47
31	u	201	CDL	C12-C11-CA5-OA6
31	a	201	CDL	C53-C54-C55-C56
30	j	201	PEE	O4-C10-C11-C12
31	l	702	CDL	C32-C31-CA7-OA8

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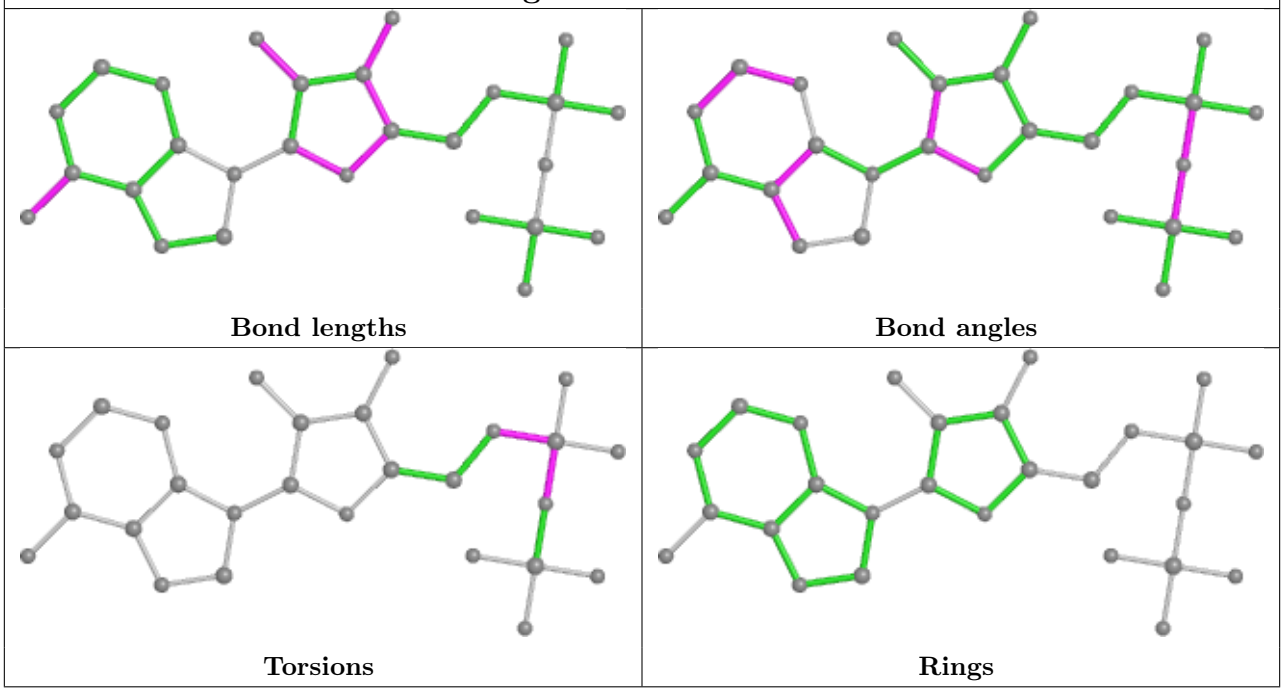
Mol	Chain	Res	Type	Atoms
31	l	702	CDL	C32-C31-CA7-OA9
30	b	201	PEE	O5-C30-C31-C32
31	r	504	CDL	C12-C11-CA5-OA7
30	r	501	PEE	C44-C45-C46-C47

There are no ring outliers.

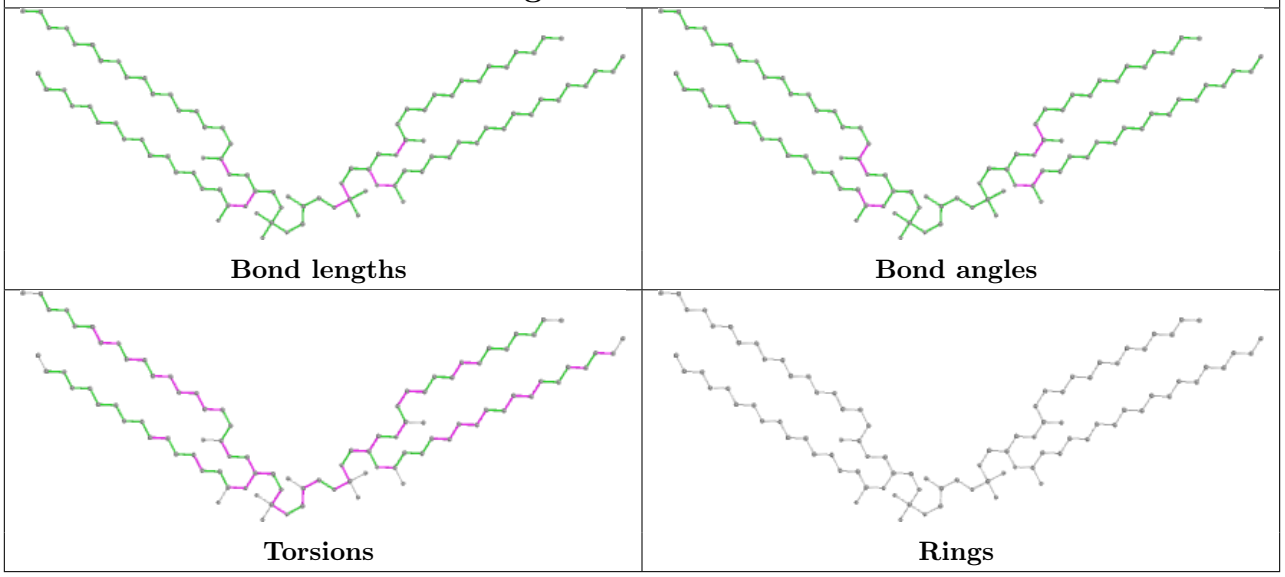
No monomer is involved in short contacts.

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 then 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.

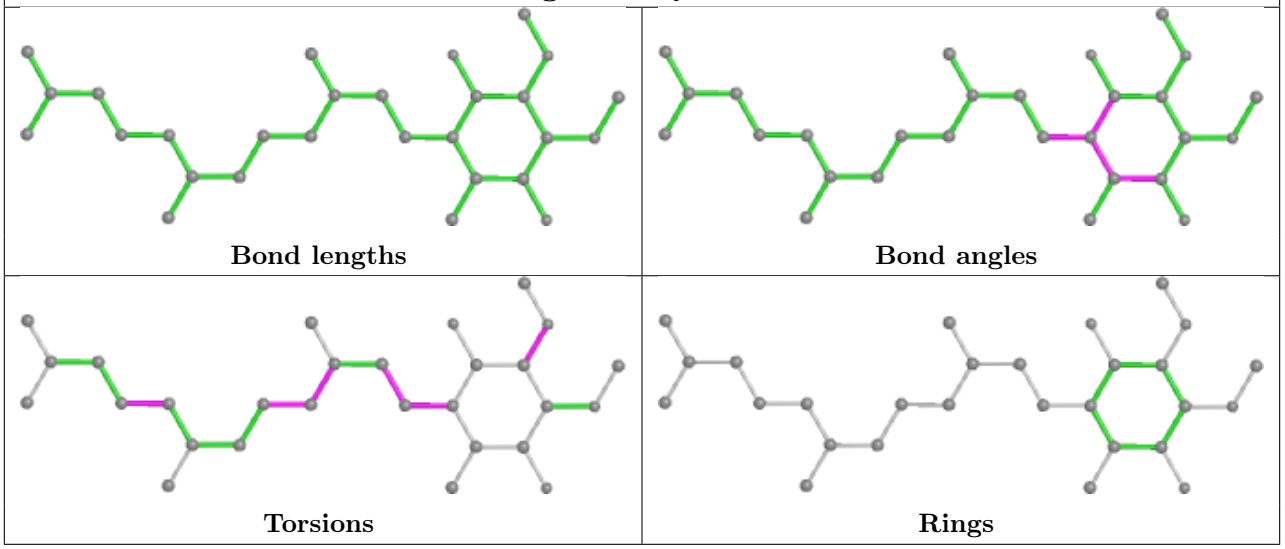
Ligand ADP w 401



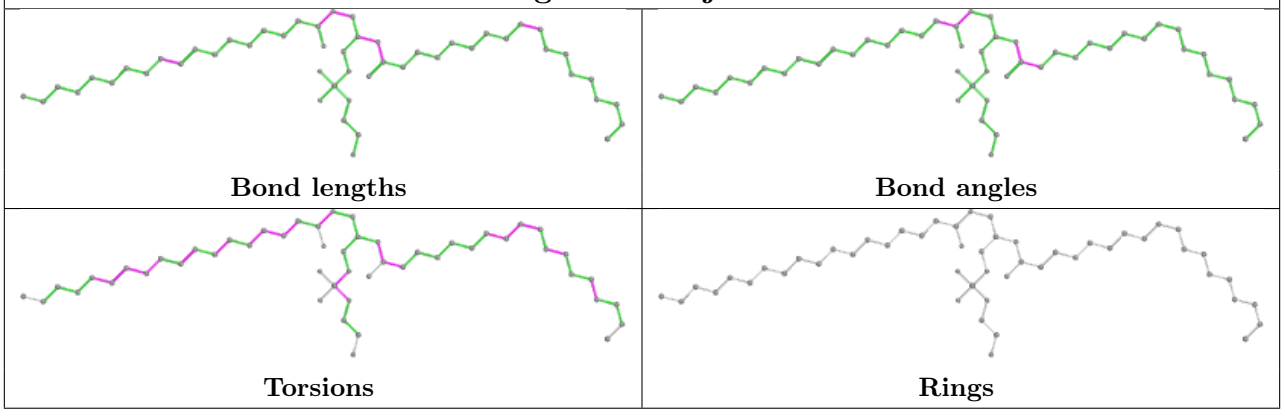
Ligand CDL V 201



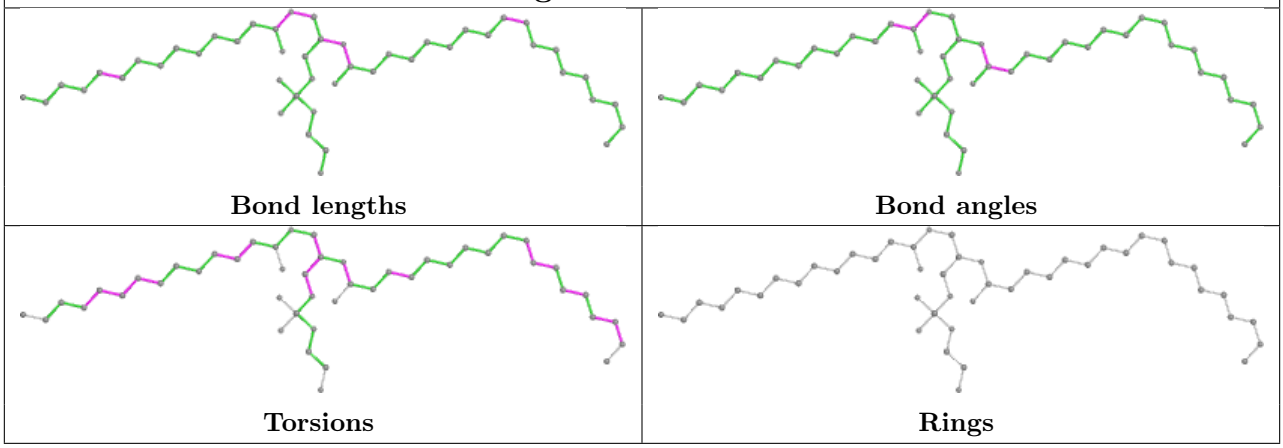
Ligand UQ s 401



Ligand PEE j 201



Ligand PEE i 402



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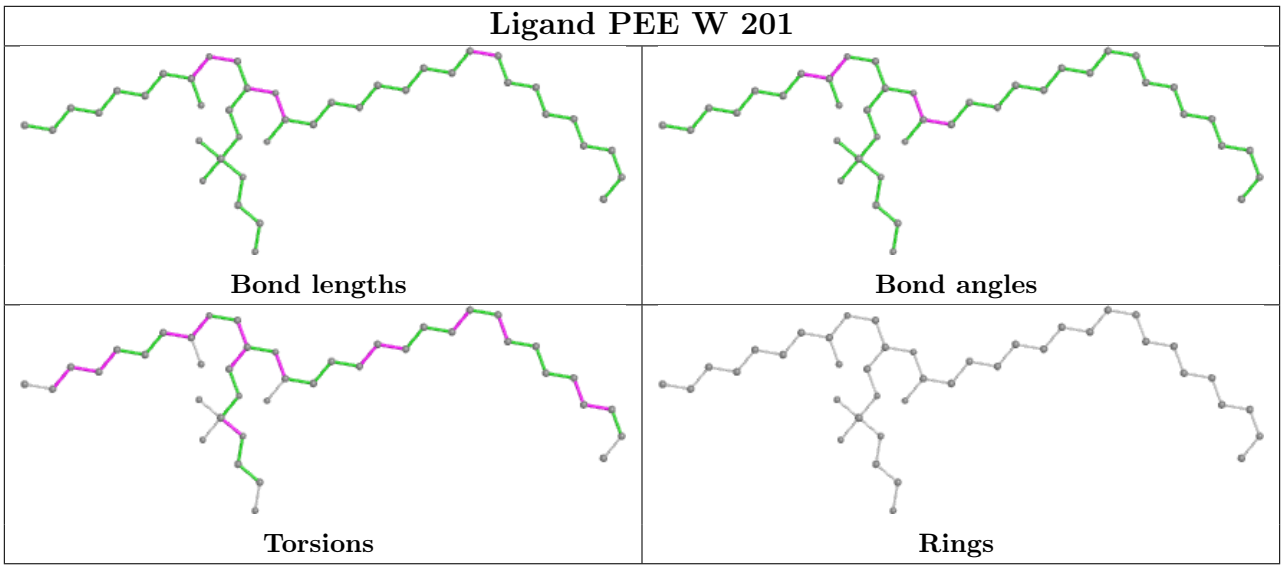

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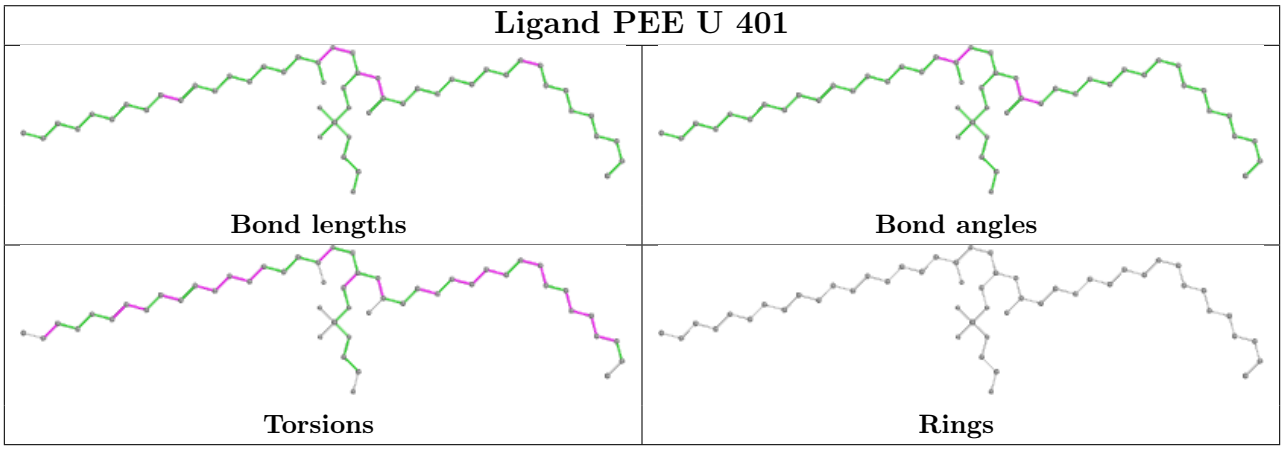
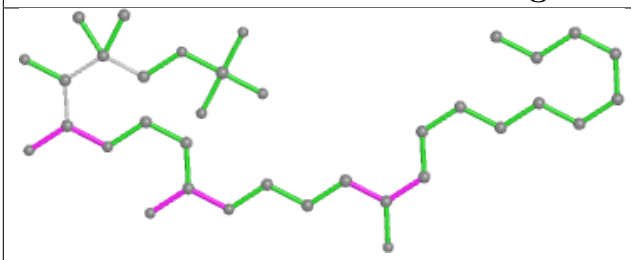
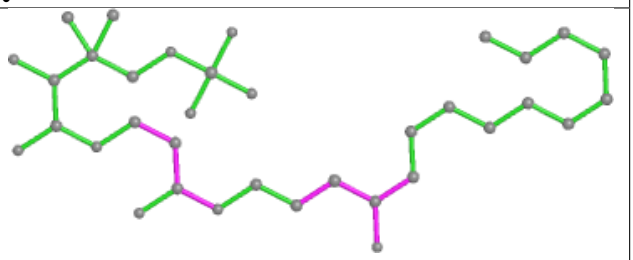


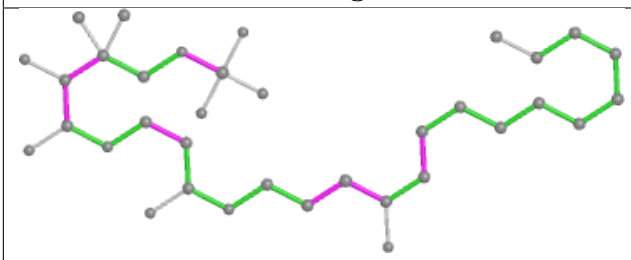
Ligand 8Q1 X 201



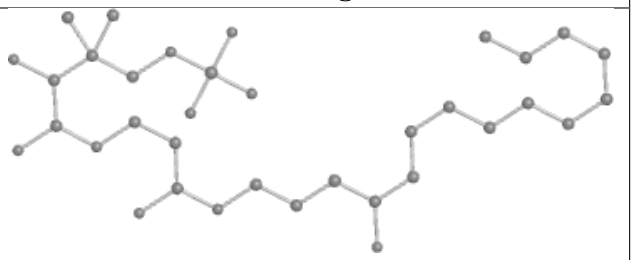
Bond lengths



Bond angles

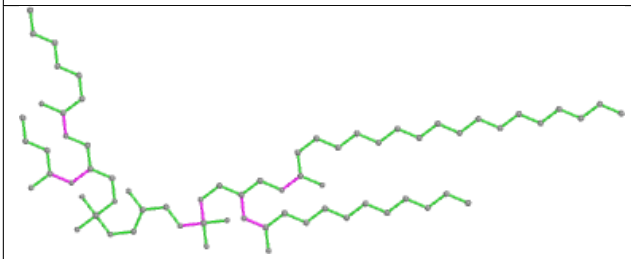


Torsions

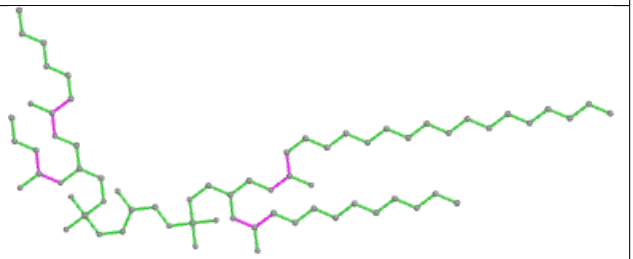


Rings

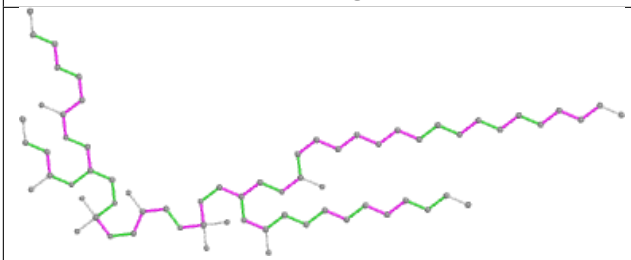
Ligand CDL o 201



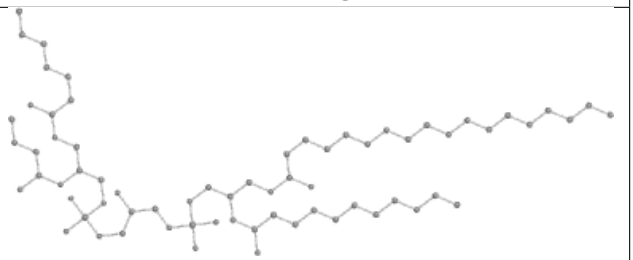
Bond lengths



Bond angles

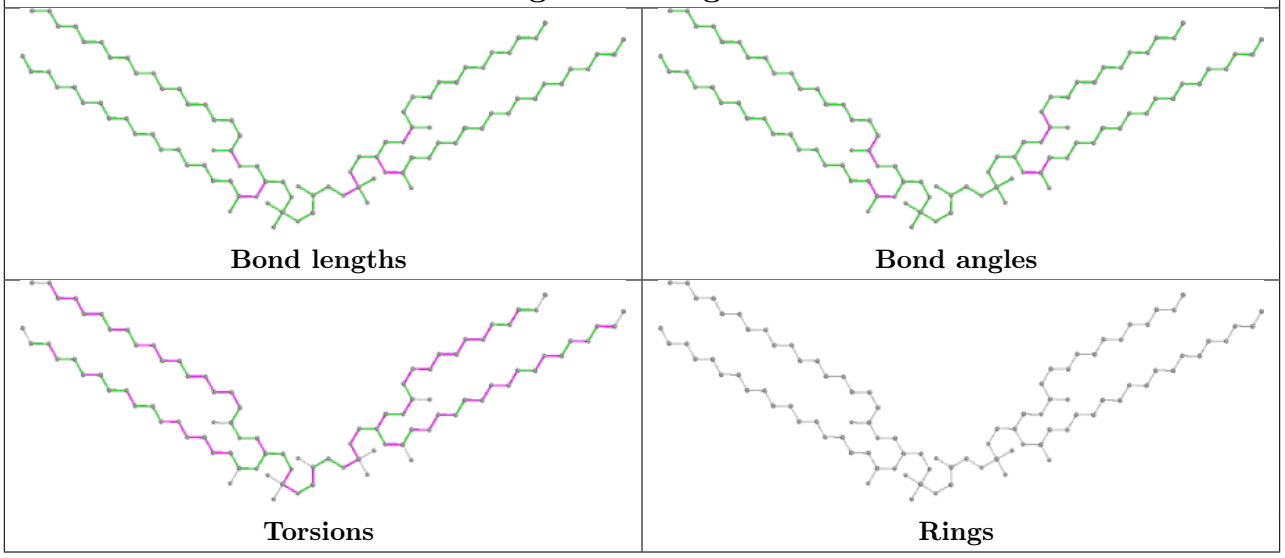


Torsions

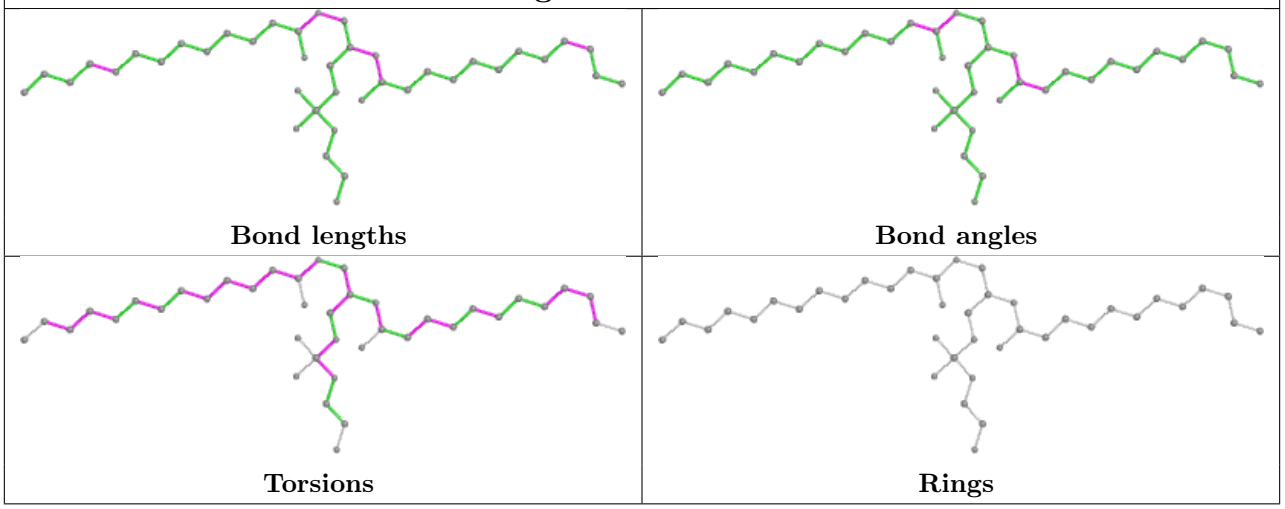


Rings

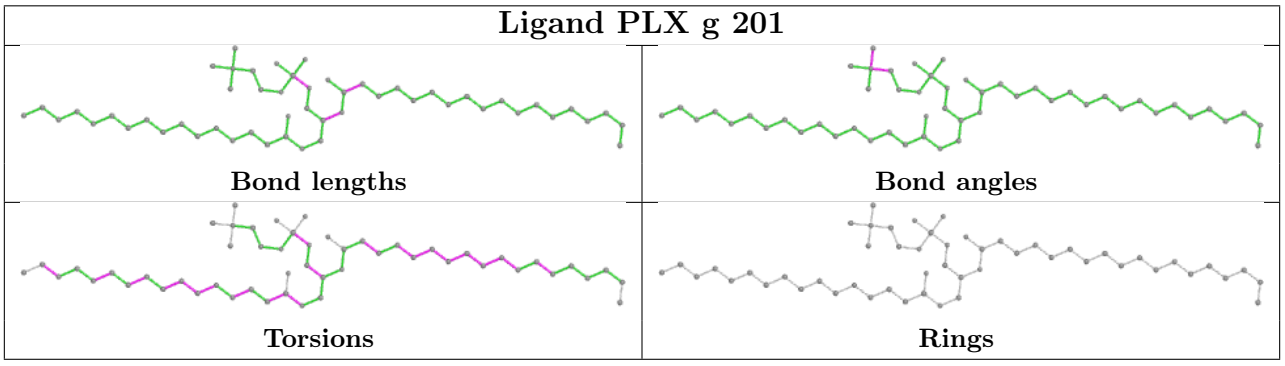
Ligand CDL g 202



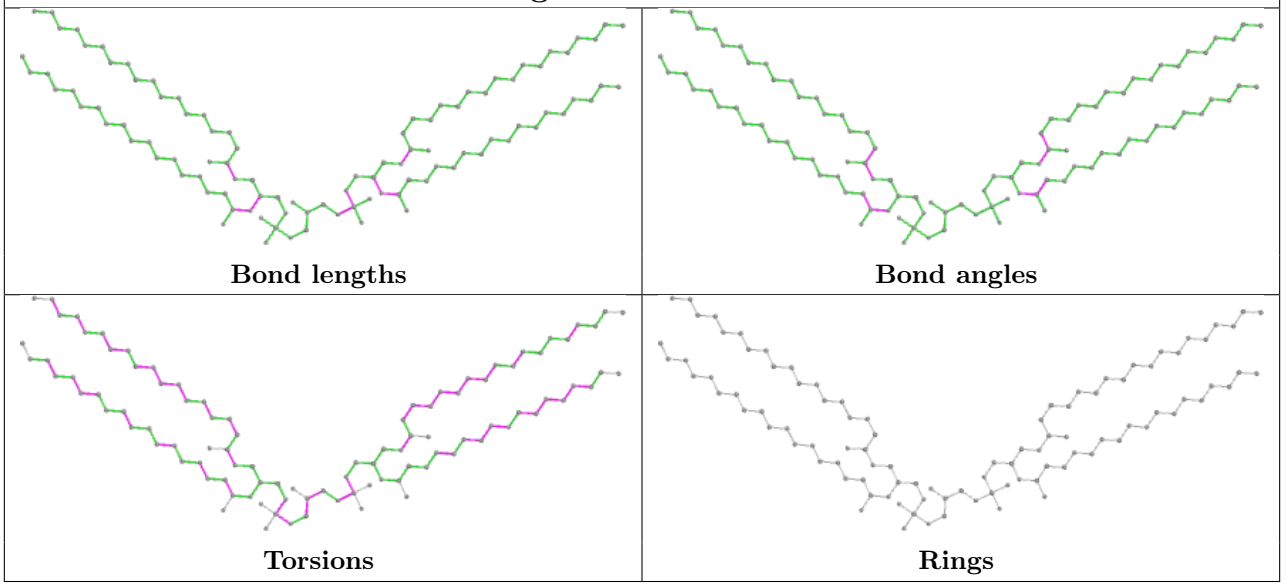
Ligand PEE l 701



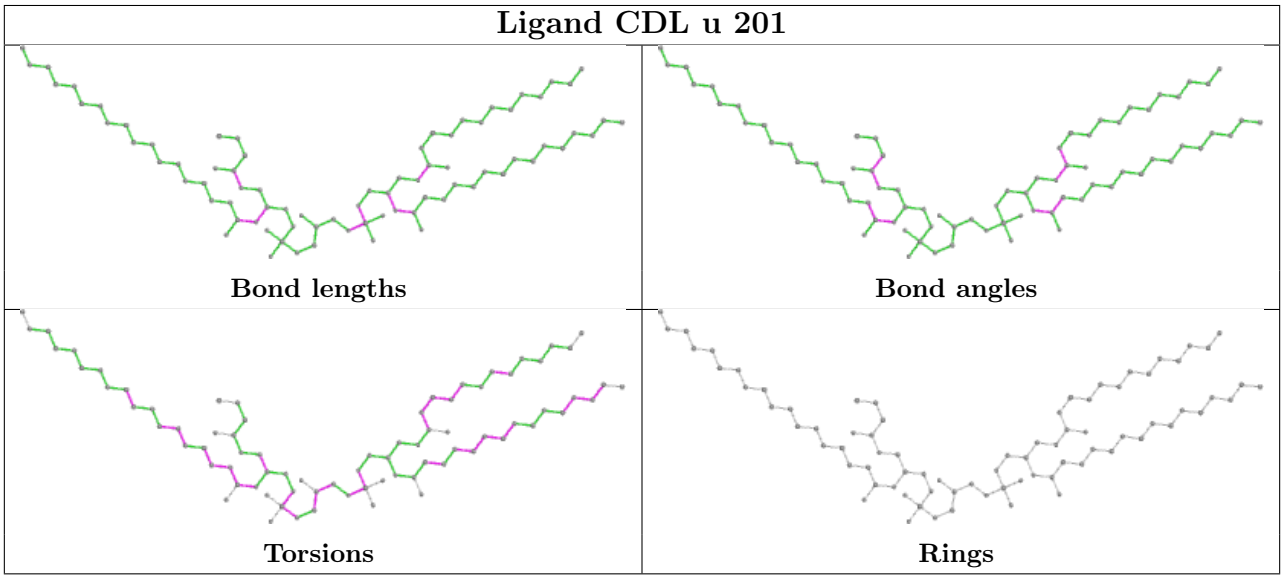
Ligand PLX g 201



Ligand CDL r 504



Ligand CDL u 201



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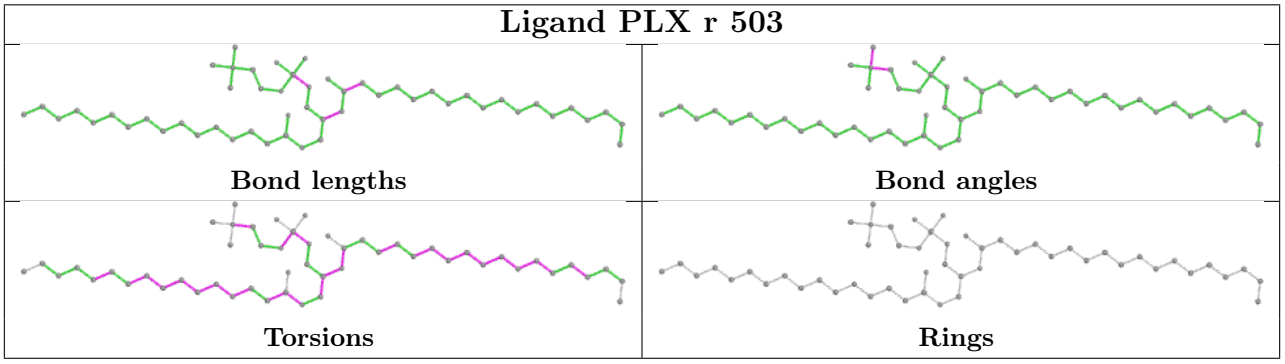
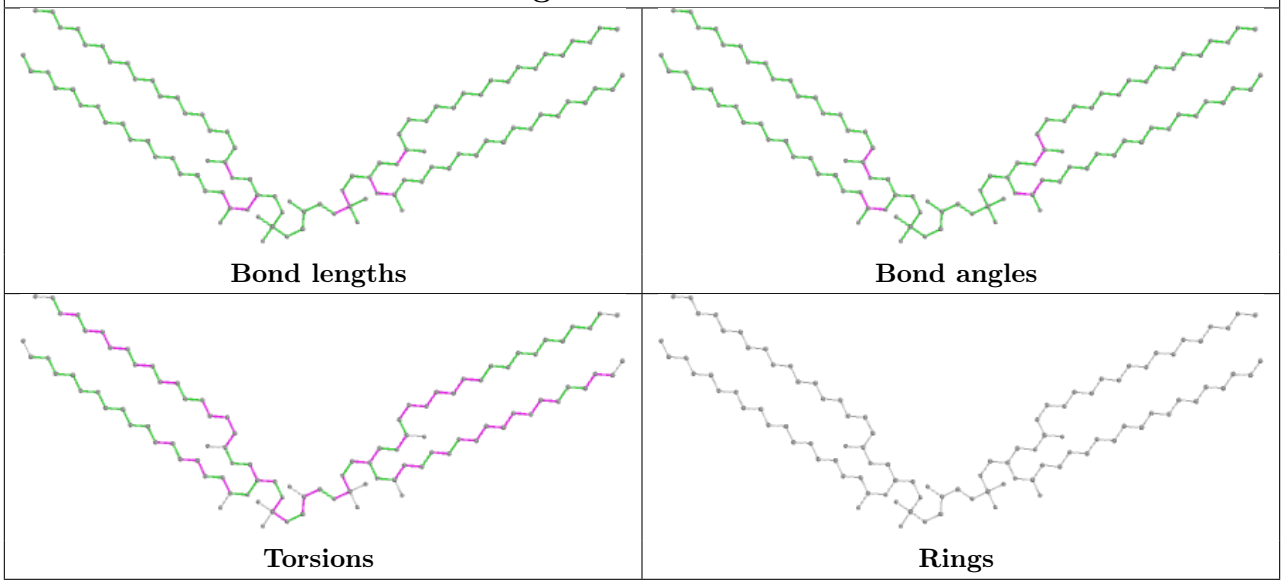
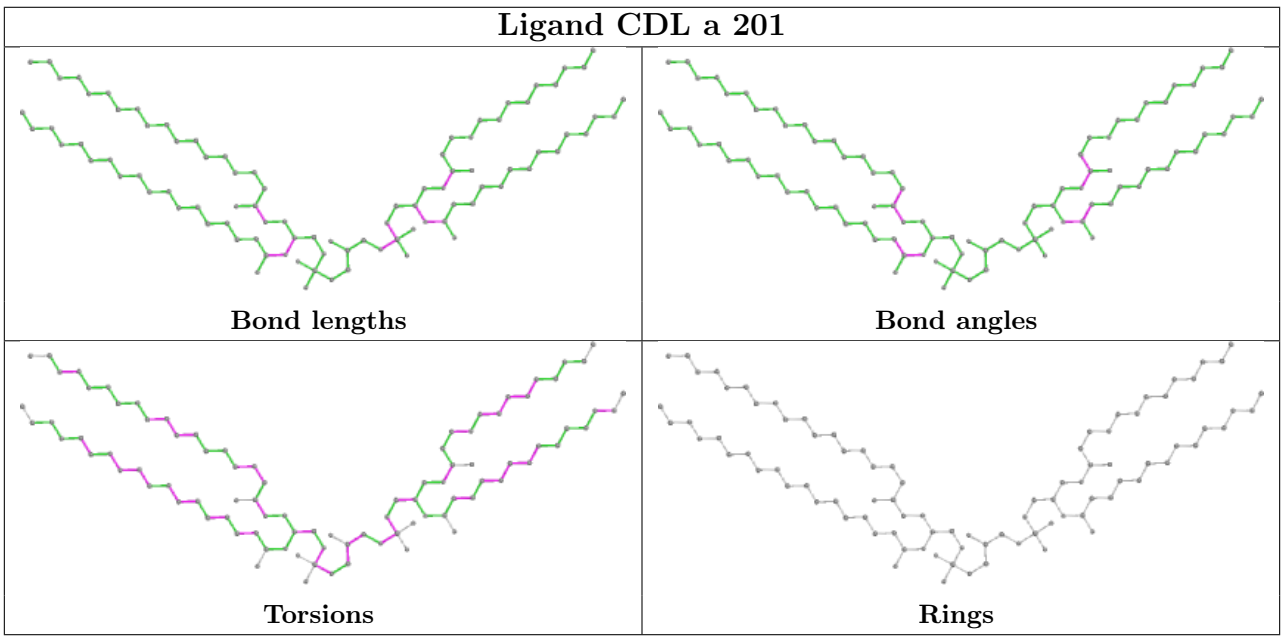


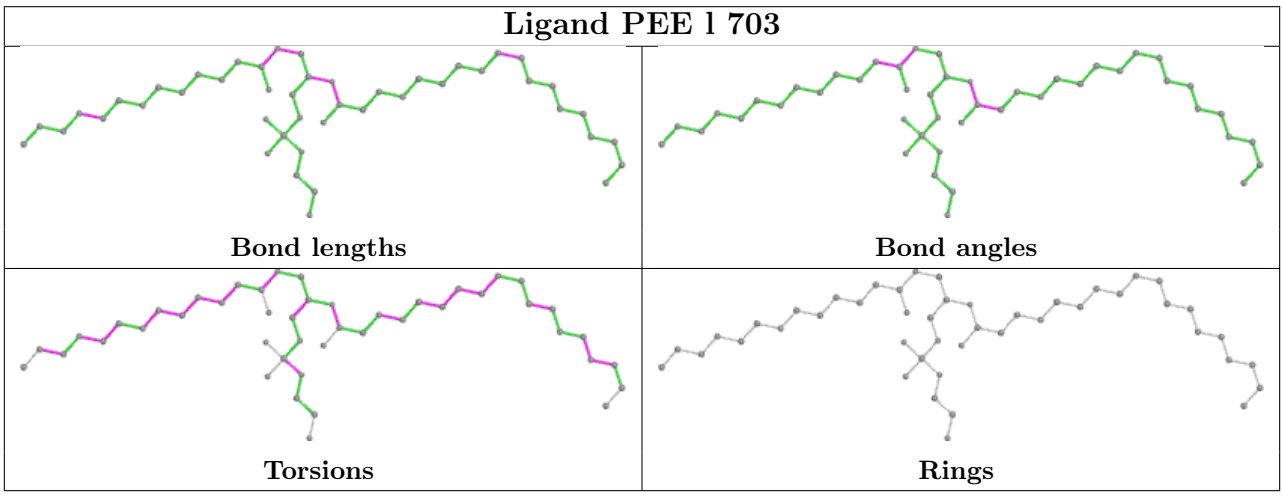
Ligand CDL l 702



Ligand CDL a 201



Ligand PEE l 703



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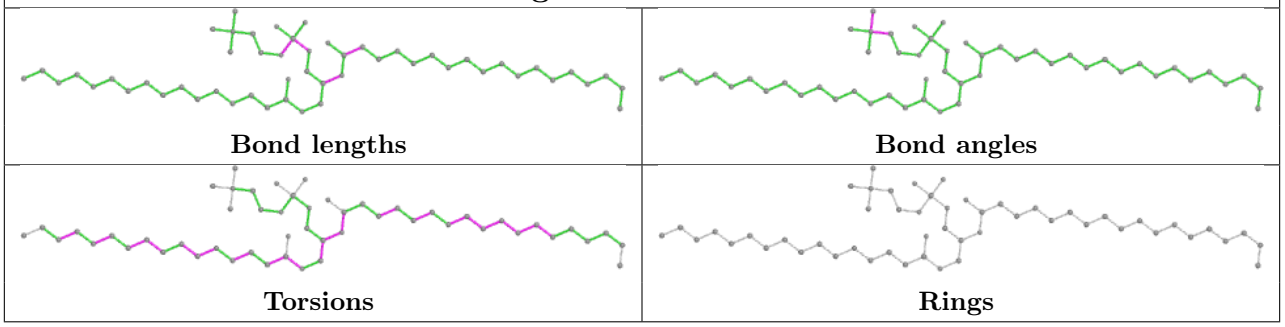

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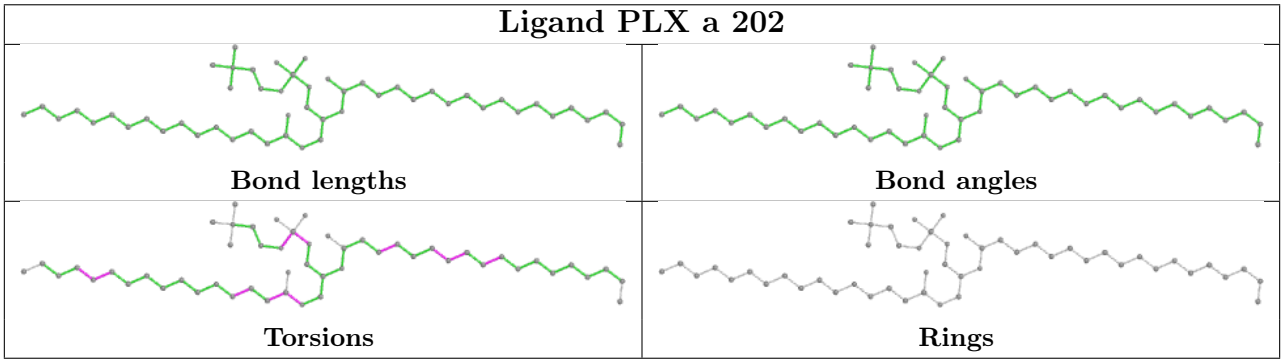

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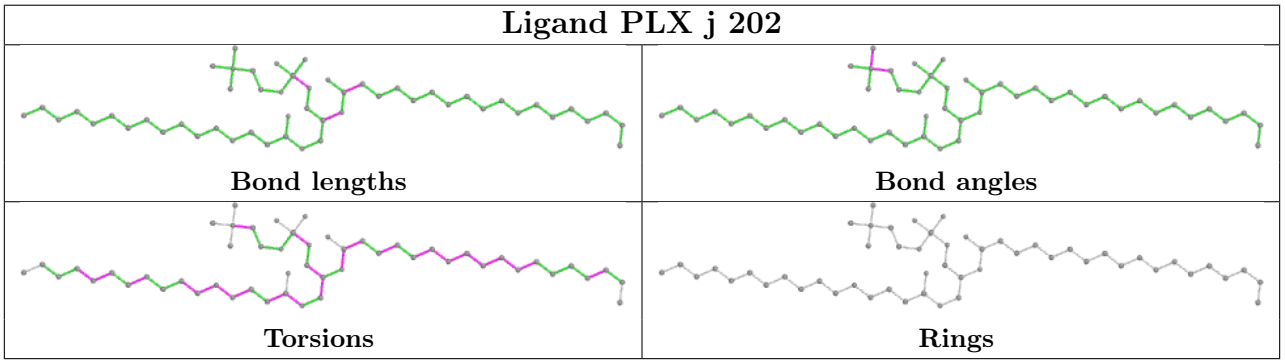

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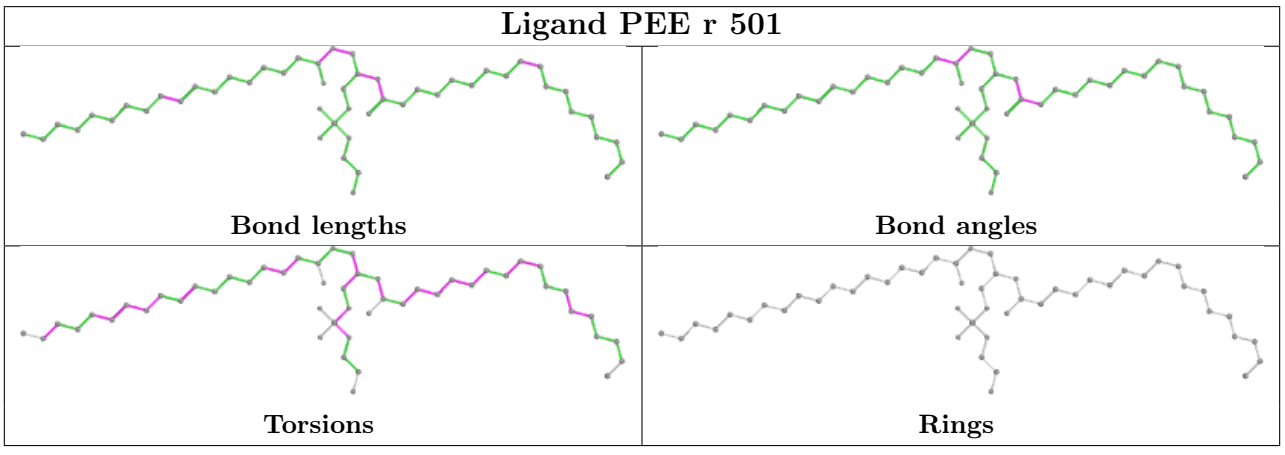
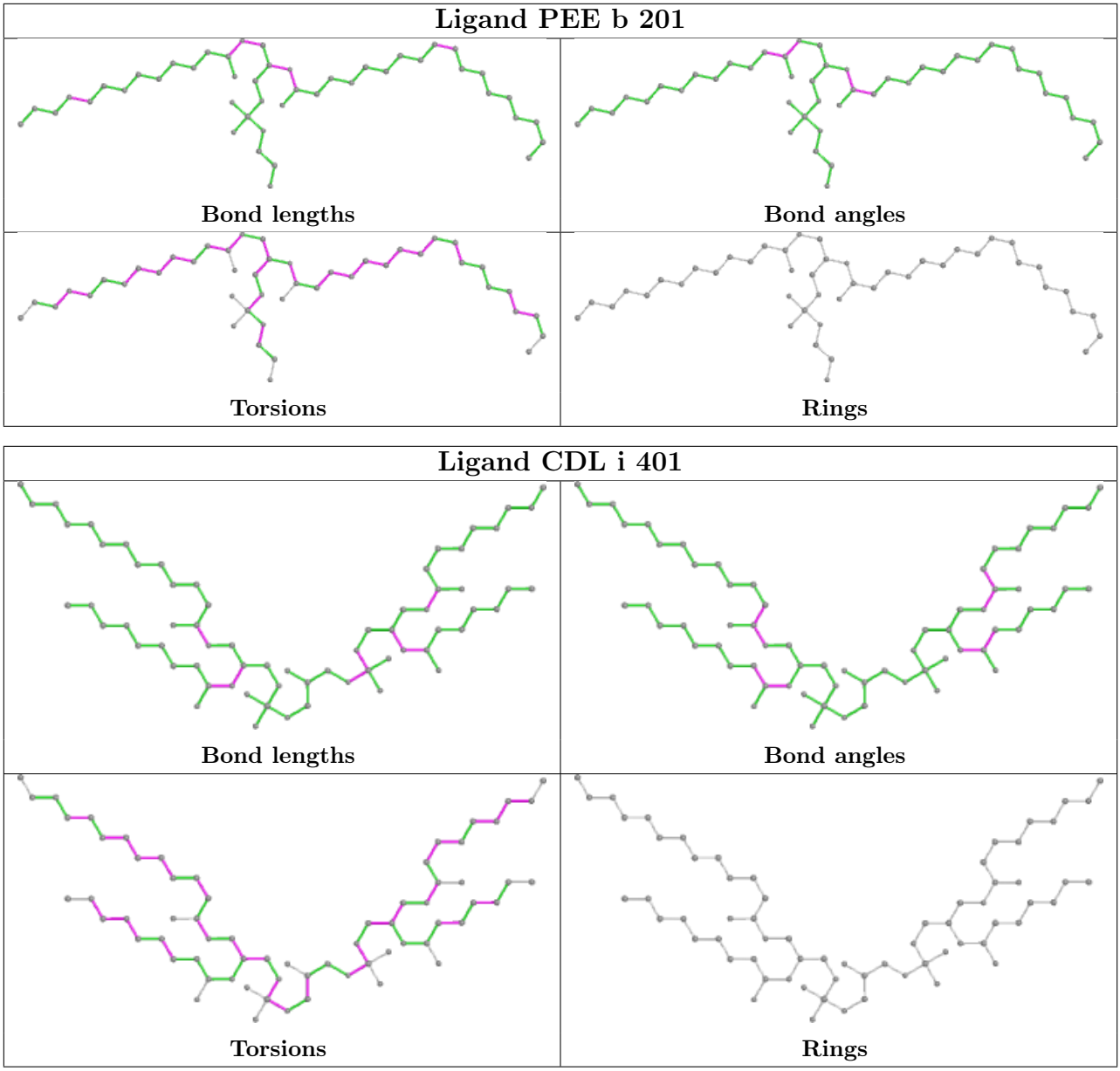




5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

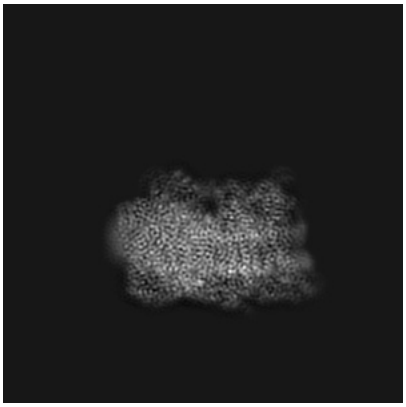
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-32191. These allow visual inspection of the internal detail of the map and identification of artifacts.

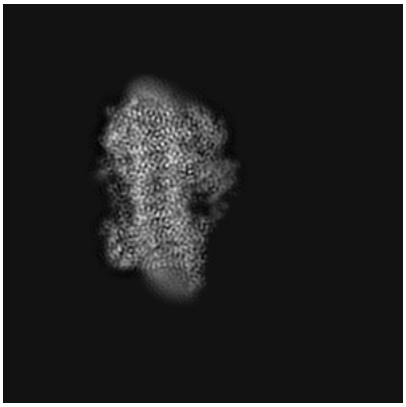
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

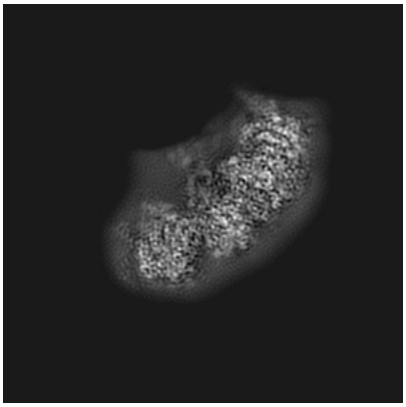
6.1.1 Primary map



X



Y

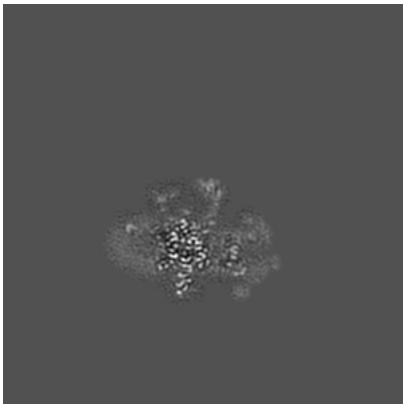


Z

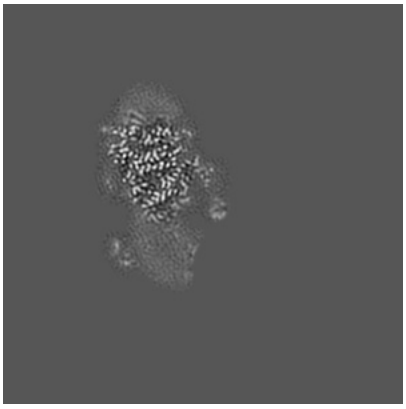
The images above show the map projected in three orthogonal directions.

6.2 Central slices

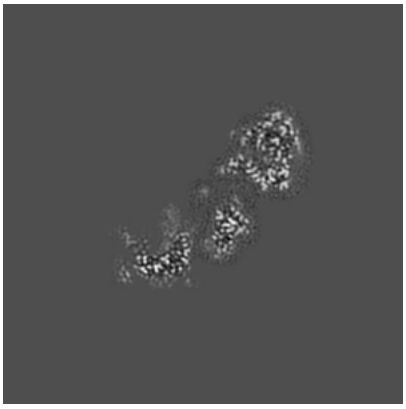
6.2.1 Primary map



X Index: 165



Y Index: 165

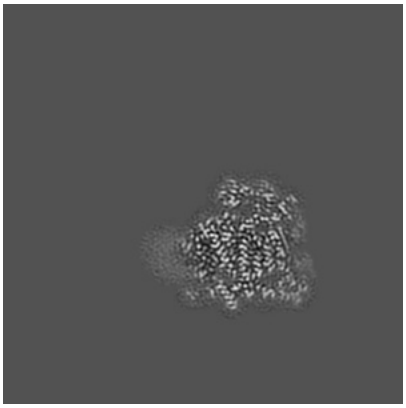


Z Index: 165

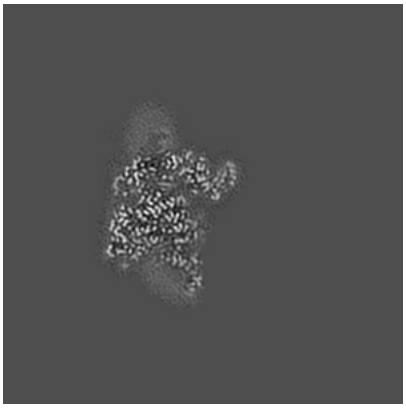
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

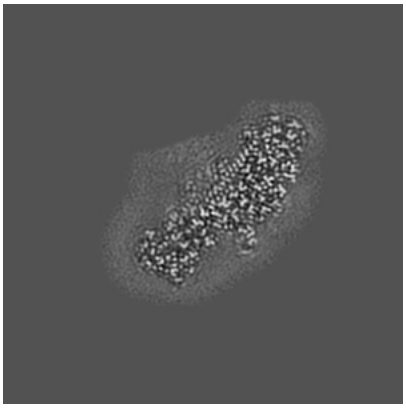
6.3.1 Primary map



X Index: 219



Y Index: 142

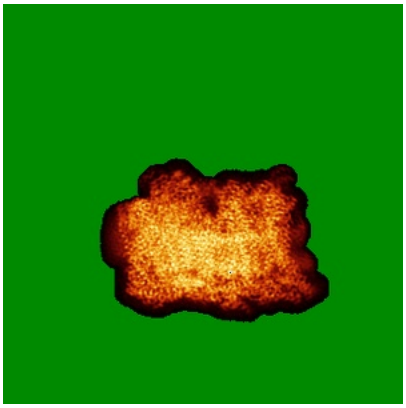


Z Index: 136

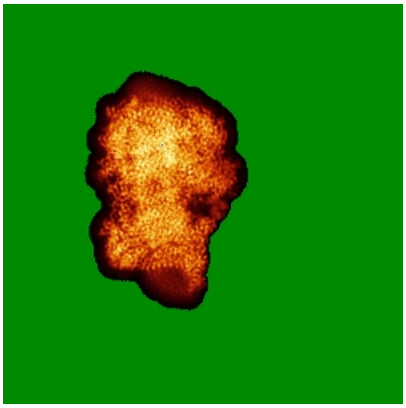
The images above show the largest variance slices of the map in three orthogonal directions.

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

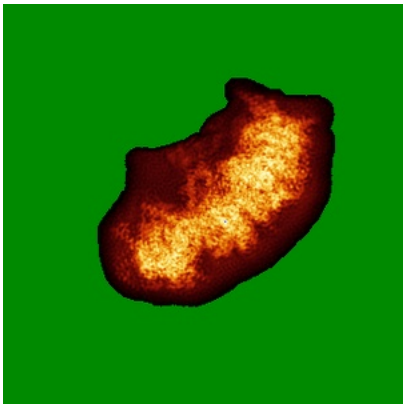
6.4.1 Primary map



X



Y

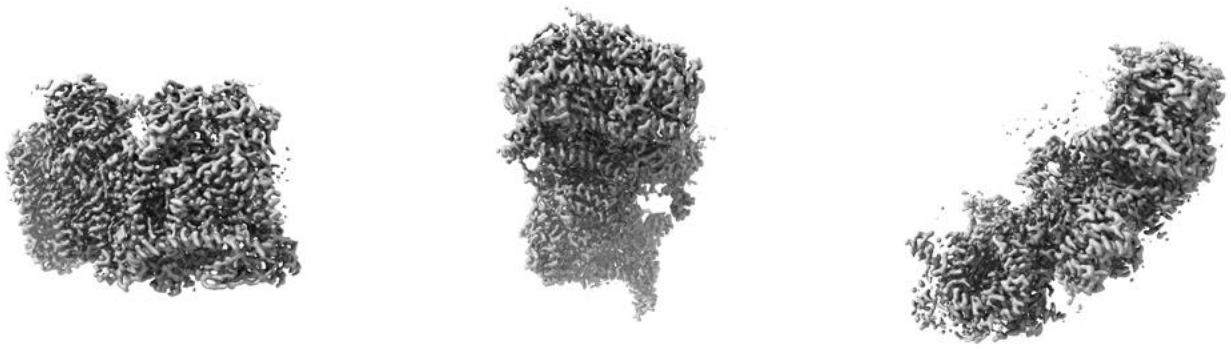


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0238. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

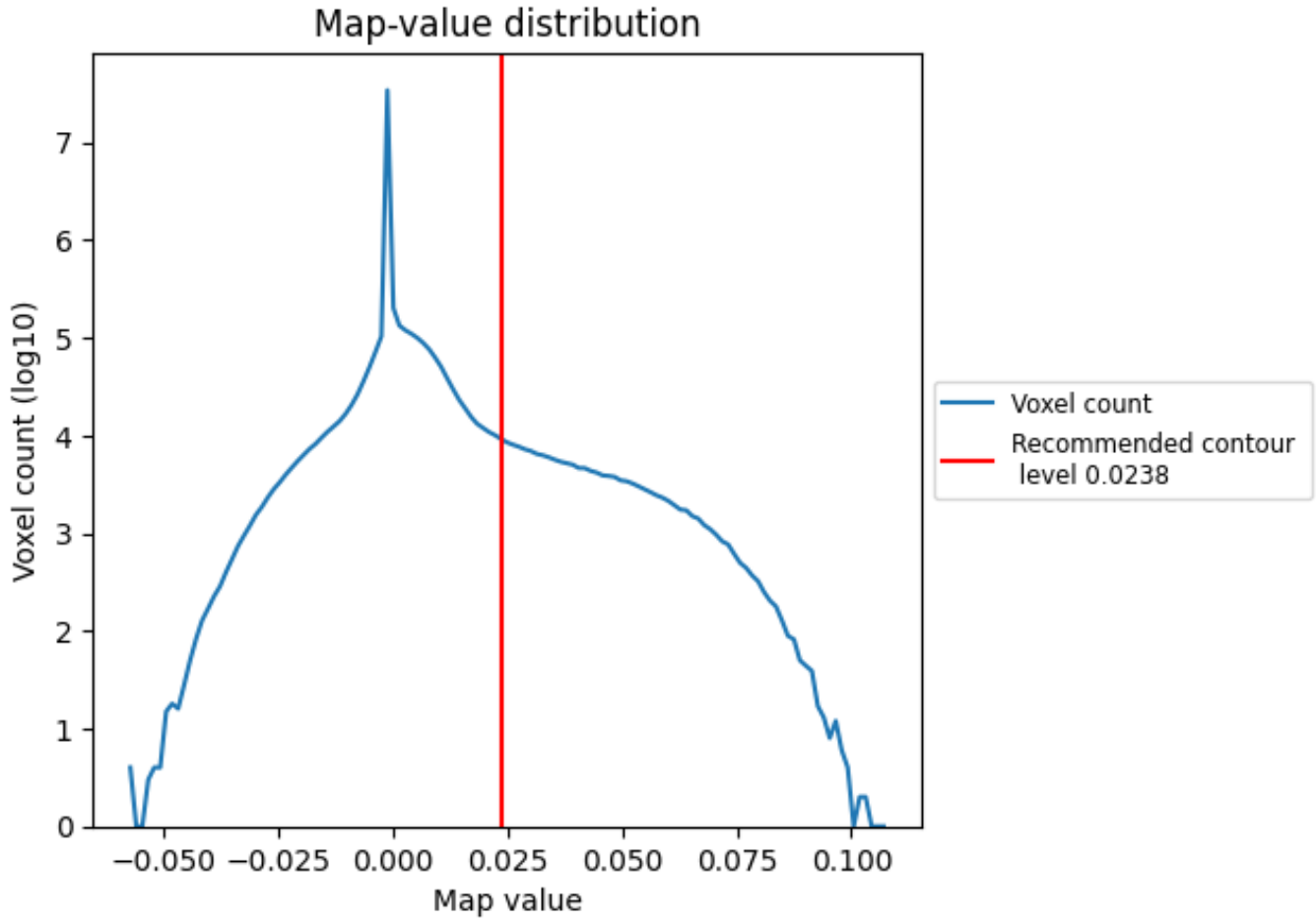
6.6 Mask visualisation (i)

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

7 Map analysis

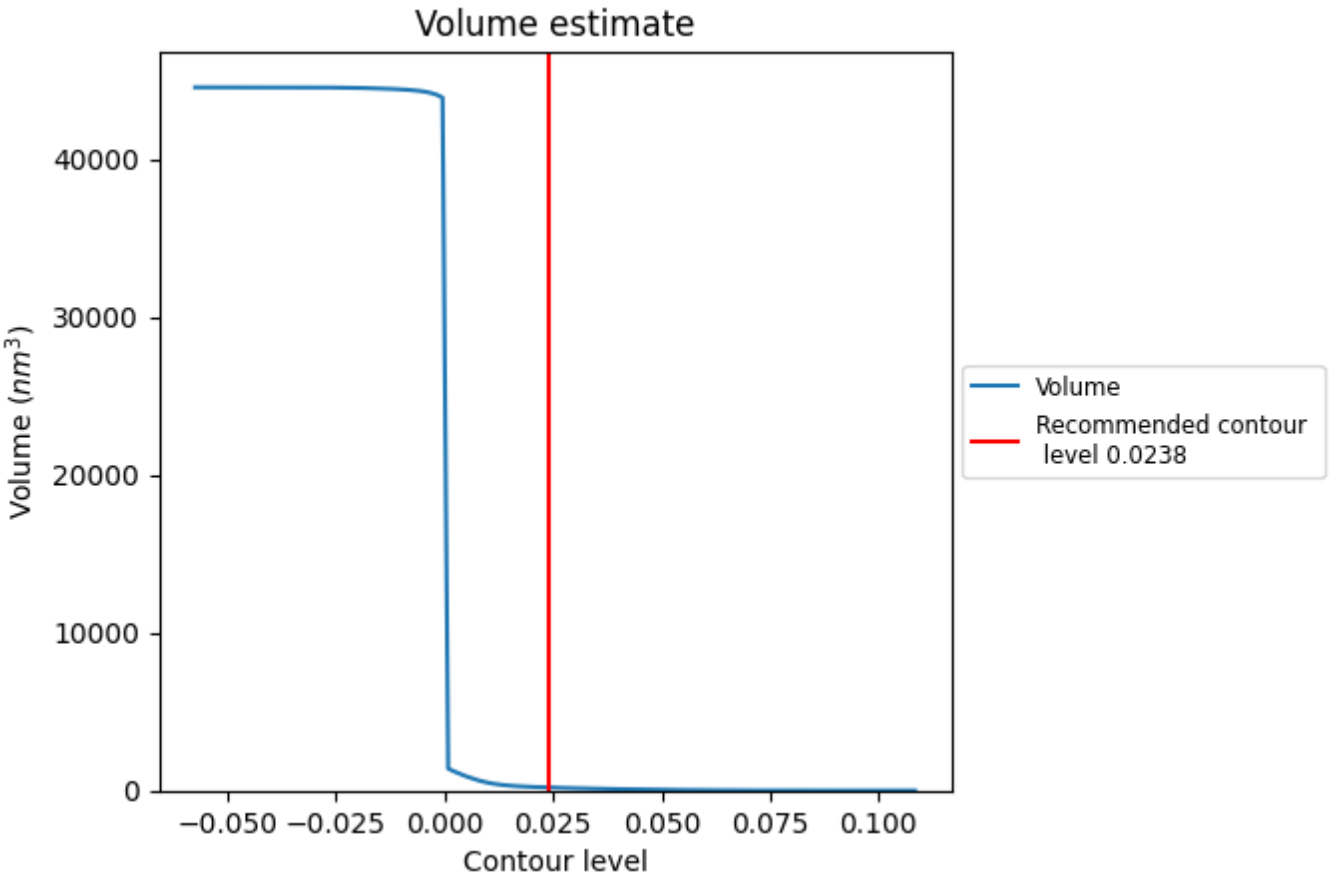
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

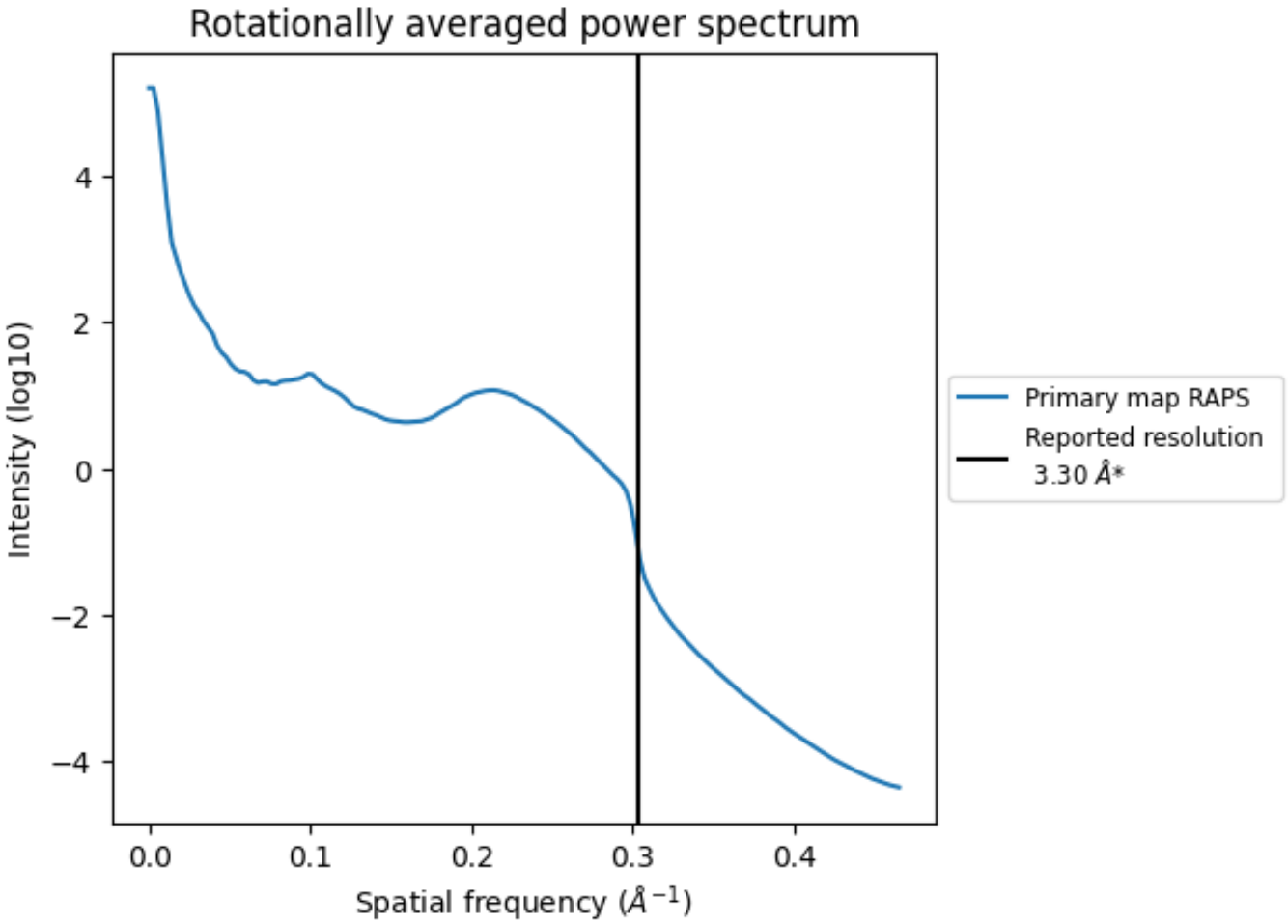
7.2 Volume estimate



The volume at the recommended contour level is 195 nm^3; this corresponds to an approximate mass of 176 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.303 $Å^{-1}$

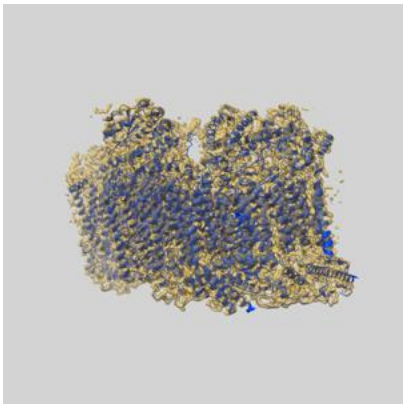
8 Fourier-Shell correlation (i)

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

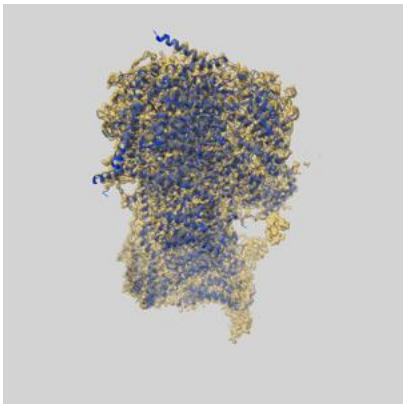
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-32191 and PDB model 7VY1. Per-residue inclusion information can be found in section 3 on page 14.

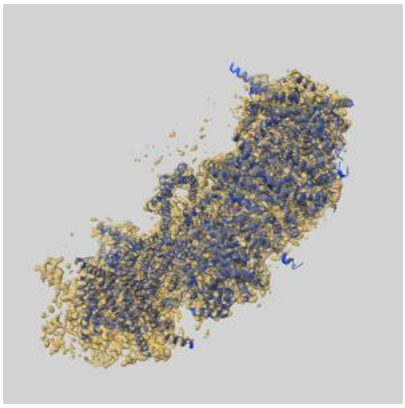
9.1 Map-model overlay



X



Y



Z

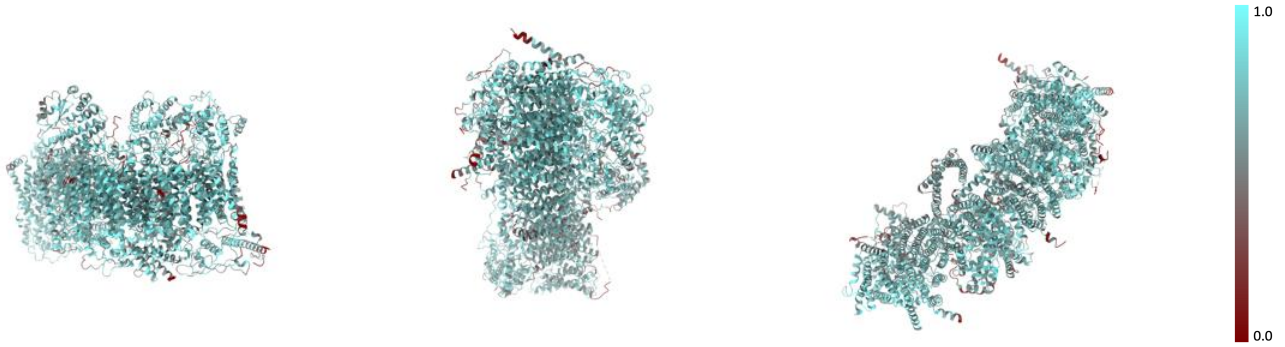
The images above show the 3D surface view of the map at the recommended contour level 0.0238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)

X Y Z

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

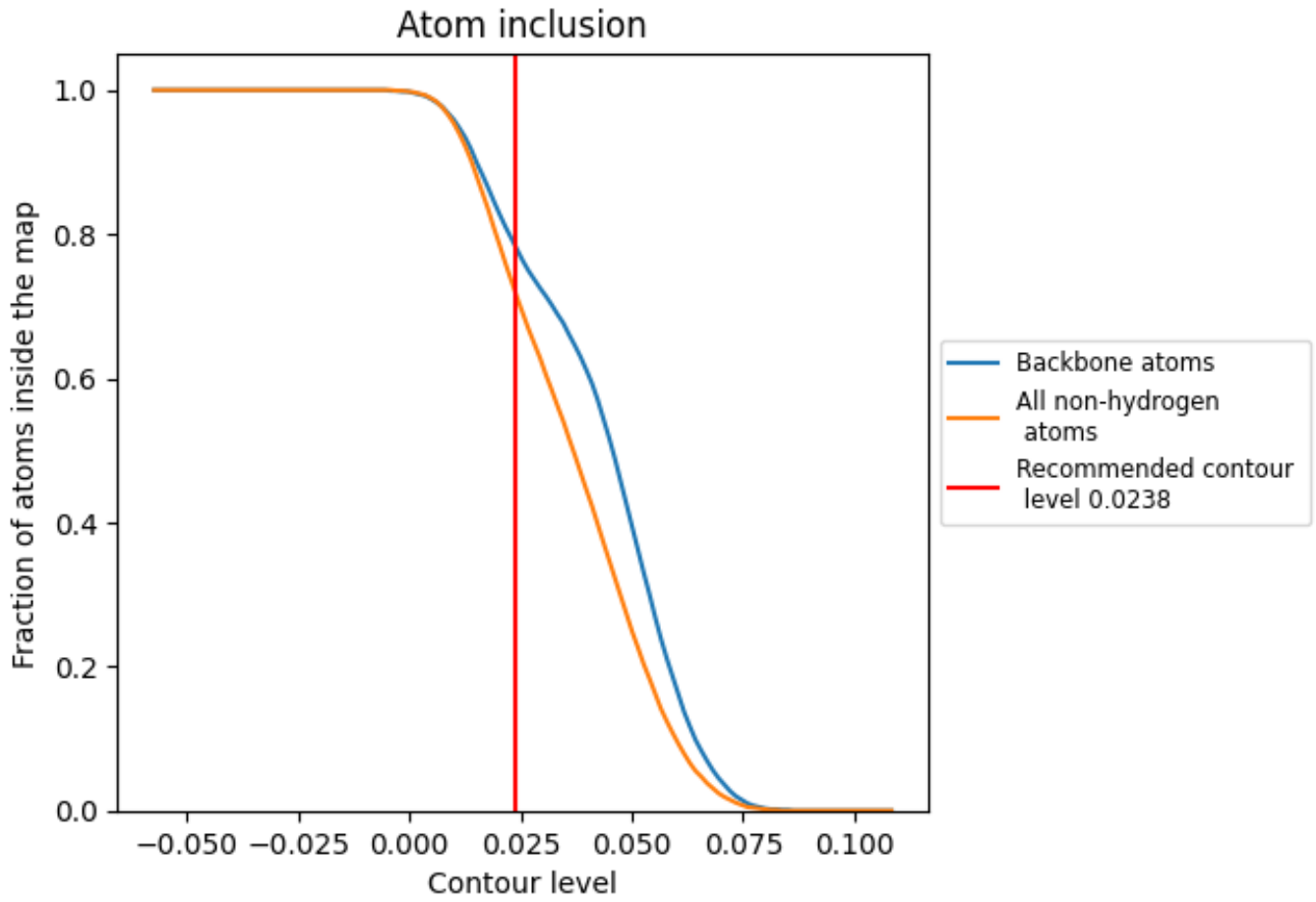
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0238).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 72% 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 (0.0238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7190	0.5380
Q	0.6230	0.5400
S	0.7880	0.5560
U	0.7530	0.5410
V	0.5390	0.5080
W	0.7690	0.5520
X	0.7090	0.5240
Y	0.6730	0.5130
Z	0.5840	0.4800
a	0.7480	0.5540
b	0.6320	0.5140
c	0.7430	0.5370
d	0.7170	0.5290
e	0.6670	0.5230
f	0.6580	0.5210
g	0.7410	0.5560
h	0.7380	0.5480
i	0.7670	0.5560
j	0.6200	0.5130
k	0.6930	0.5350
l	0.7440	0.5470
m	0.6870	0.5200
n	0.6380	0.5180
o	0.6760	0.5360
p	0.7480	0.5400
r	0.7680	0.5570
s	0.7560	0.5450
u	0.7510	0.5450
v	0.6610	0.5010
w	0.6980	0.5280