



Full wwPDB EM Validation Report ⓘ

Mar 13, 2026 – 09:33 AM UTC

PDB ID : 7VYG / pdb_00007vyg
EMDB ID : EMD-32204
Title : Membrane arm of active state CI from rotenone dataset
Authors : Gu, J.K.; Yang, M.J.
Deposited on : 2021-11-14
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

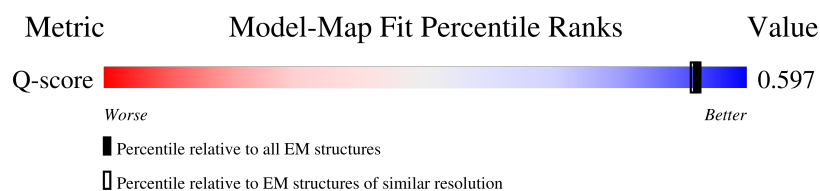
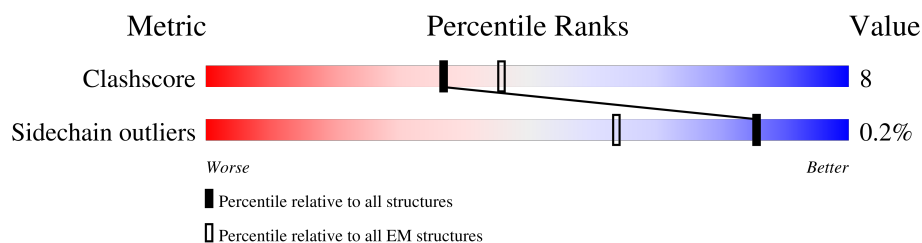
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Q	44	23% 82% 18%
2	S	70	81% 19%
3	U	83	8% 92% 8%
4	V	140	87% 13%
5	W	113	80% 20%

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Mol	Chain	Length	Quality of chain
6	X	88	
7	Y	67	
8	Z	80	
9	a	138	
10	b	126	
11	c	156	
12	d	175	
13	e	104	
14	f	49	
15	g	121	
16	h	105	
17	i	347	
18	j	115	
19	k	98	
20	l	606	
21	m	175	
22	n	56	
23	o	128	
24	p	178	
25	r	459	
26	s	318	
27	u	171	
28	v	125	
29	w	320	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
31	CDL	m	201	-	-	X	-

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 39639 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	44	Total	C	N	O	S	0	0
			363	236	60	66	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
			566	364	103	94	5		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	88	Total	C	N	O	S	0	0
			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	67	Total	C	N	O	S	0	0
			584	385	95	103	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Z	80	Total	C	N	O	S	0	0
			641	418	108	114	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	138	Total	C	N	O	S	0	0
			1151	754	195	199	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	98	Total	C	N	O	S	0	0
			819	537	144	137	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
			1315	853	213	241	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 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	e	104	Total	C	N	O	S	0	0
			867	553	142	168	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	f	49	Total	C	N	O	0	0
			377	246	65	66		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	j	115	Total	C	N	O	S	0	0
			914	615	134	158	7		

- 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	606	Total	C	N	O	S	0	0
			4816	3193	746	826	51		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	m	175	Total	C	N	O	S	0	0
			1292	863	188	228	13		

- 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 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	178	Total	C	N	O	S	0	0
			1530	980	278	264	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	318	Total	C	N	O	S	0	0
			2502	1675	382	424	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		

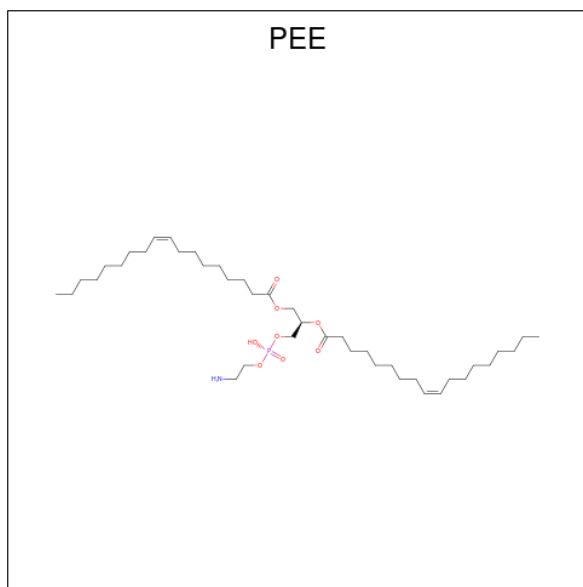
There is a discrepancy between the modelled and reference sequences:

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

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

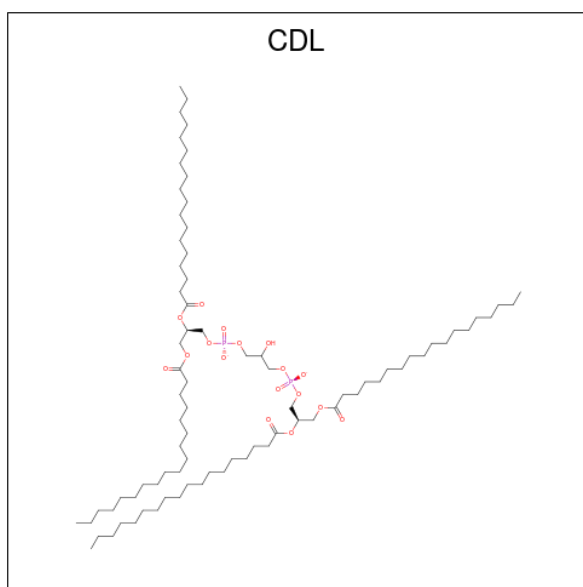
Mol	Chain	Residues	Atoms					AltConf	Trace
29	w	320	Total	C	N	O	S	0	0
			2583	1645	439	489	10		

- Molecule 30 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: C₄₁H₇₈NO₈P) (labeled as "Ligand of Interest" by depositor).



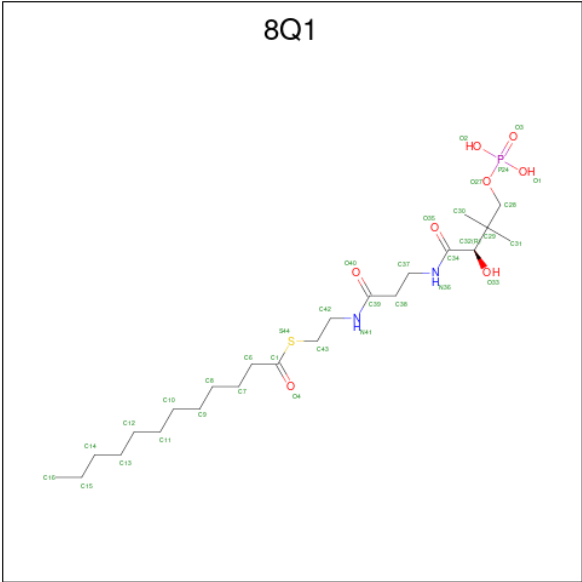
Mol	Chain	Residues	Atoms					AltConf
30	Q	1	Total	C	N	O	P	0
			47	37	1	8	1	
30	U	1	Total	C	N	O	P	0
			51	41	1	8	1	
30	W	1	Total	C	N	O	P	0
			41	31	1	8	1	
30	f	1	Total	N				0
			1	1				
30	j	1	Total	C	N	O	P	0
			51	41	1	8	1	
30	j	1	Total	N				0
			1	1				
30	l	1	Total	C	N	O	P	0
			40	30	1	8	1	
30	l	1	Total	C	N	O	P	0
			50	40	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	
30	v	1	Total	N				0
			1	1				

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



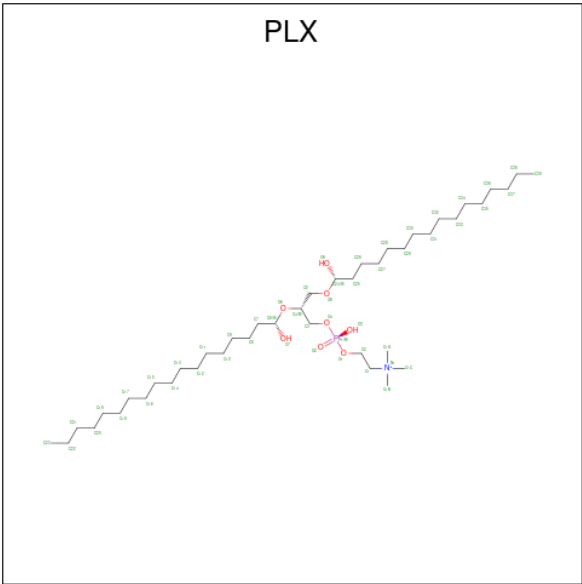
Mol	Chain	Residues	Atoms				AltConf
31	V	1	Total	C	O	P	0
			94	75	17	2	
31	V	1	Total	C	O	P	0
			100	81	17	2	
31	a	1	Total	C	O	P	0
			100	81	17	2	
31	l	1	Total	C	O	P	0
			99	80	17	2	
31	l	1	Total	C	O	P	0
			100	81	17	2	
31	m	1	Total	C	O	P	0
			95	76	17	2	
31	n	1	Total	C	O	P	0
			55	36	17	2	
31	r	1	Total	C	O	P	0
			99	80	17	2	
31	s	1	Total	C	O	P	0
			89	70	17	2	

- Molecule 32 is S-[2-(N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl)amino)ethyl] dodecanethioate (CCD ID: 8Q1) (formula: C₂₃H₄₅N₂O₈PS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
32	X	1	Total	C	N	O	P	S
			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-TRIOX (CCD ID: PLX) (formula: C₄₂H₈₉NO₈P) (labeled as "Ligand of Interest" by depositor).



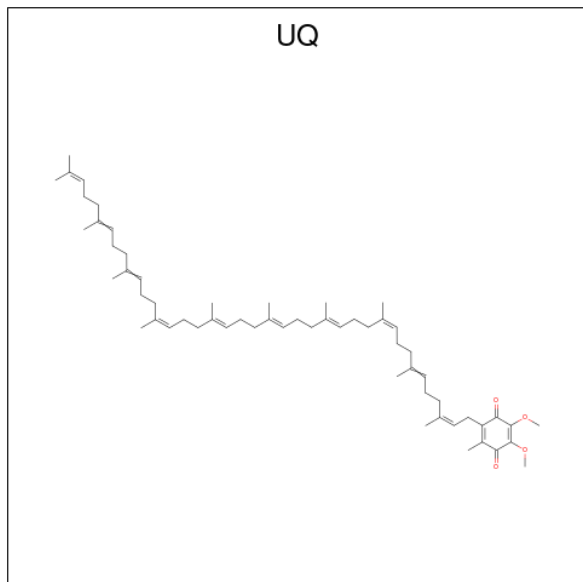
Mol	Chain	Residues	Atoms					AltConf
33	a	1	Total	C	N	O	P	
			52	42	1	8	1	0

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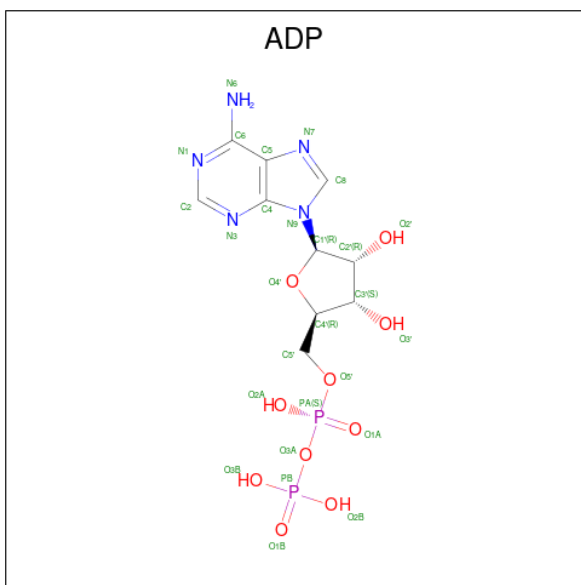
Mol	Chain	Residues	Atoms					AltConf
33	e	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	g	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	j	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	j	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	r	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 34 is Coenzyme Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-isomer (CCD ID: UQ) (formula: C₅₉H₉₀O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
34	s	1	Total	C	O	0
			38	34	4	

- Molecule 35 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).

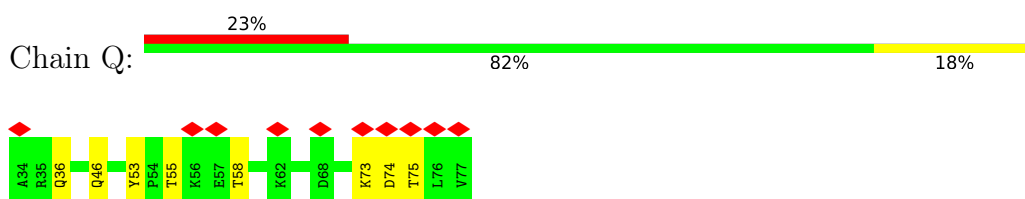


Mol	Chain	Residues	Atoms					AltConf
35	w	1	Total	C	N	O	P	0
			27	10	5	10	2	

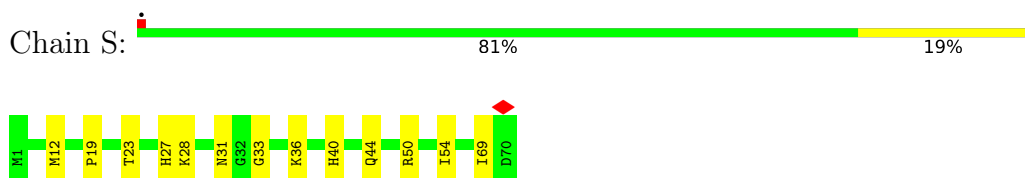
3 Residue-property plots [i](#)

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

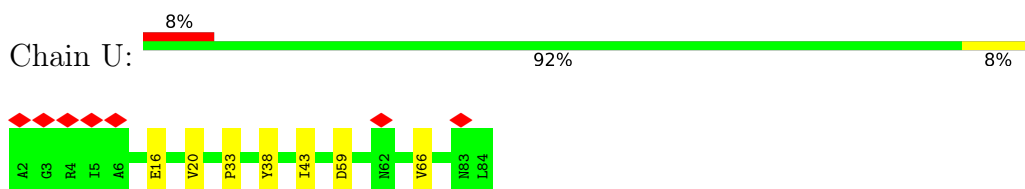
- Molecule 1: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial



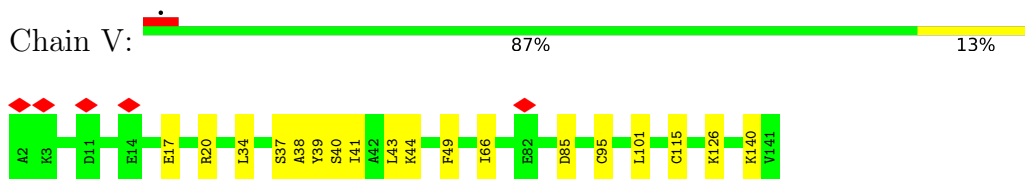
- Molecule 2: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



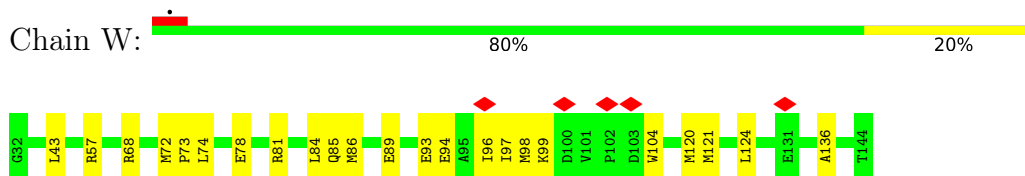
- Molecule 3: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3



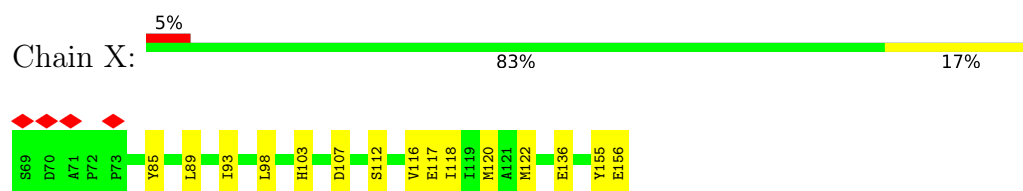
- Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11



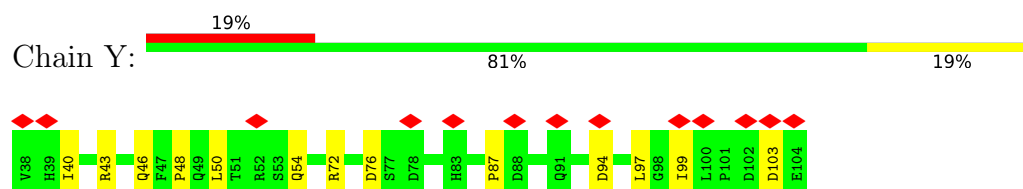
- Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13



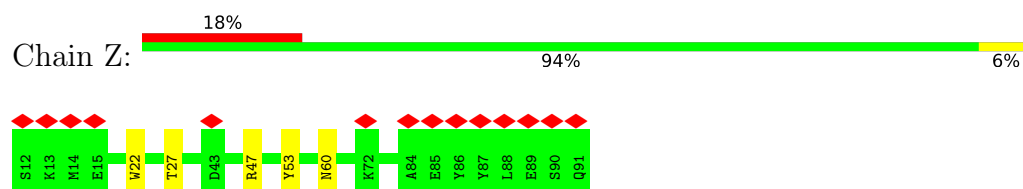
- Molecule 6: Acyl carrier protein, mitochondrial



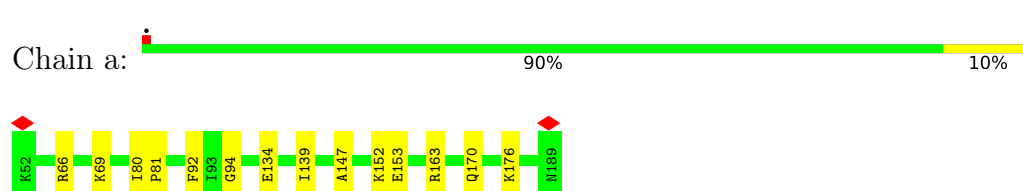
- Molecule 7: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



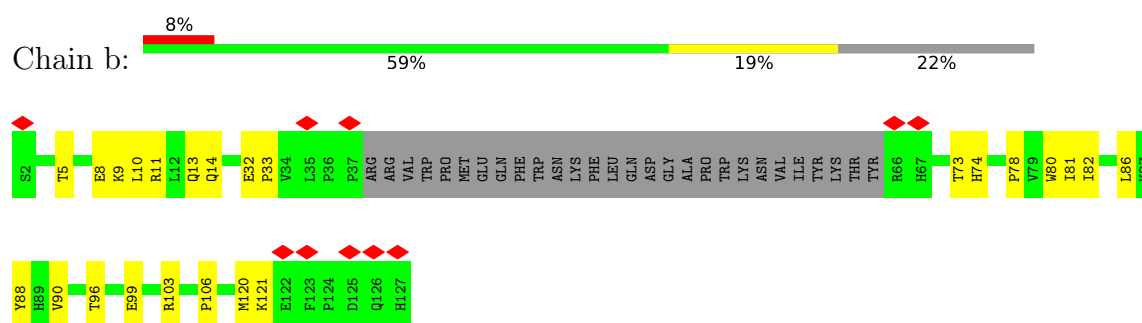
- Molecule 8: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3



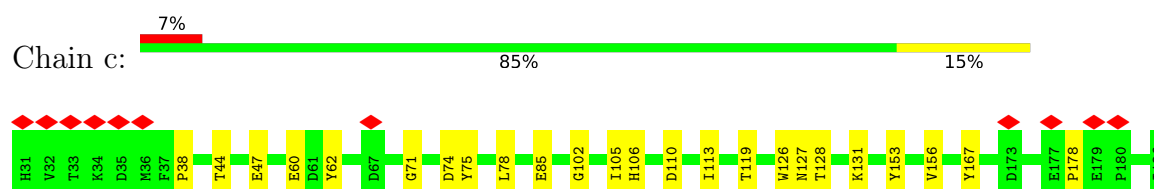
- Molecule 9: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



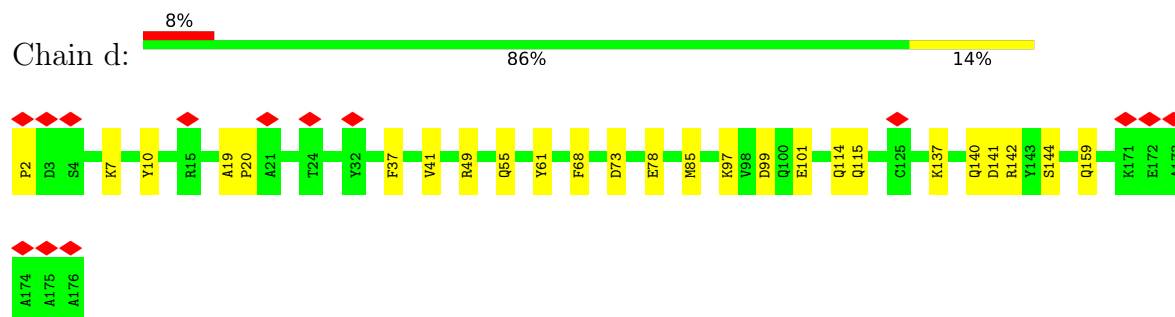
- Molecule 10: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6



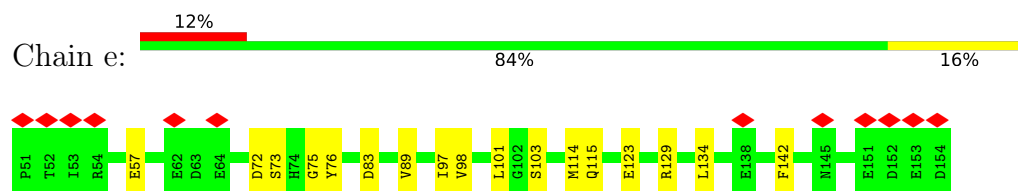
- Molecule 11: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial



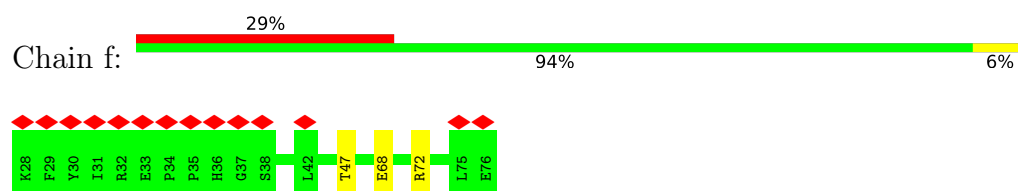
- Molecule 12: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10



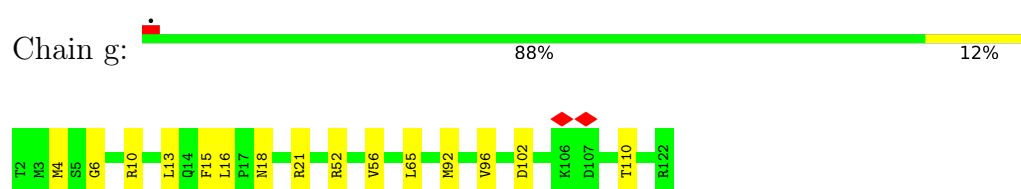
- Molecule 13: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



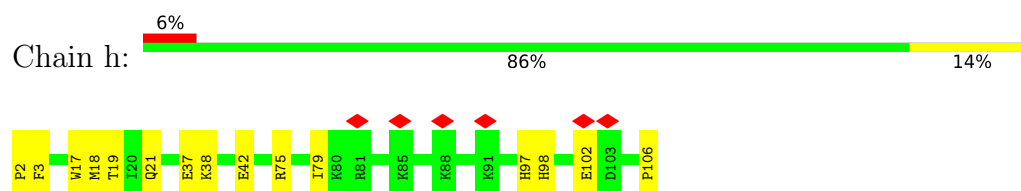
- Molecule 14: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial



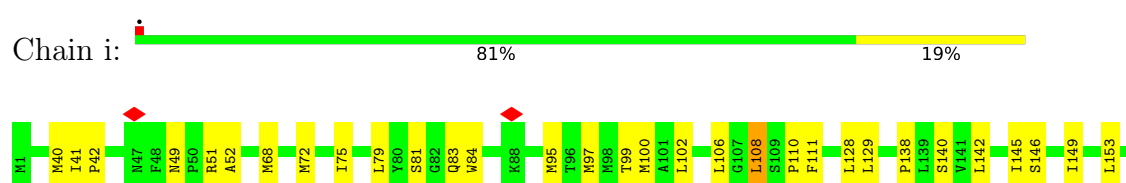
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 subunit C2

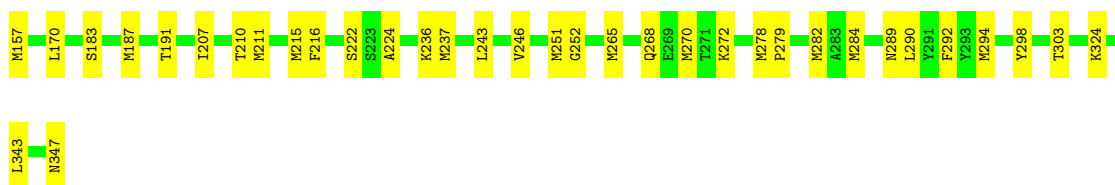


- Molecule 16: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

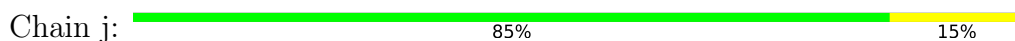


- Molecule 17: NADH-ubiquinone oxidoreductase chain 2

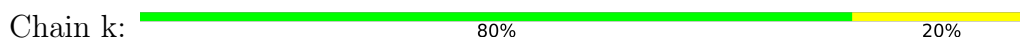




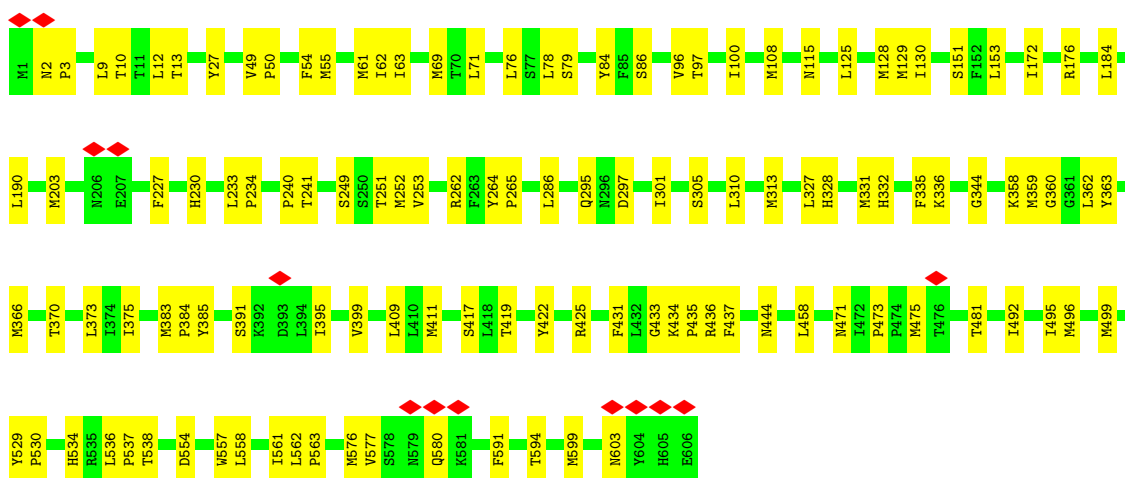
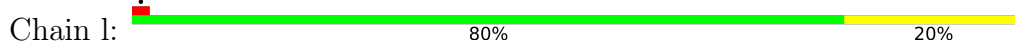
- Molecule 18: NADH-ubiquinone oxidoreductase chain 3



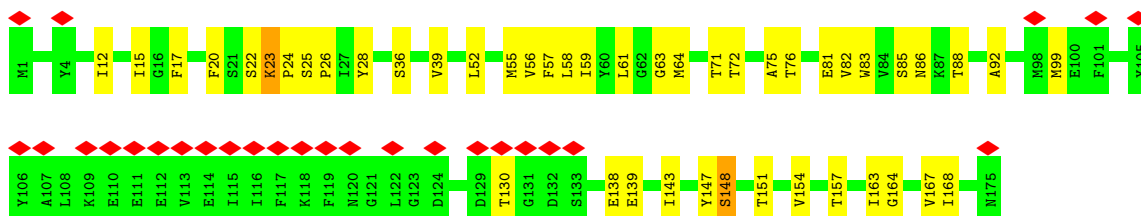
- Molecule 19: NADH-ubiquinone oxidoreductase chain 4L



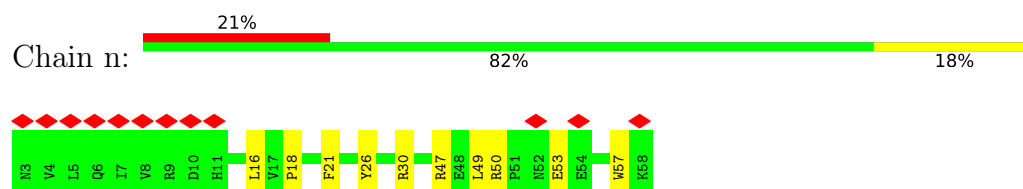
- Molecule 20: NADH-ubiquinone oxidoreductase chain 5



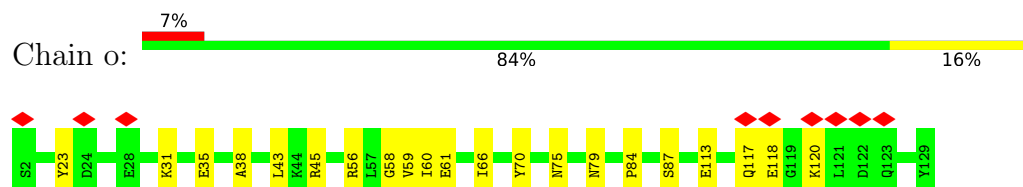
- Molecule 21: NADH-ubiquinone oxidoreductase chain 6



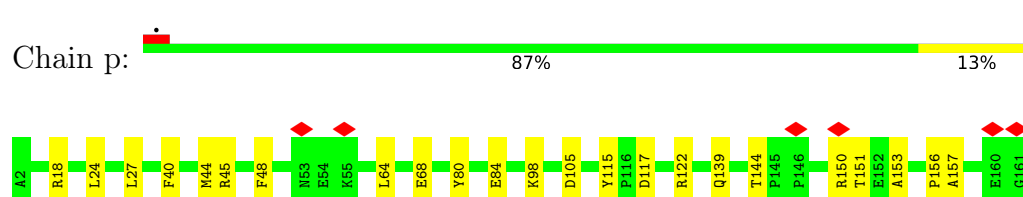
- Molecule 22: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1



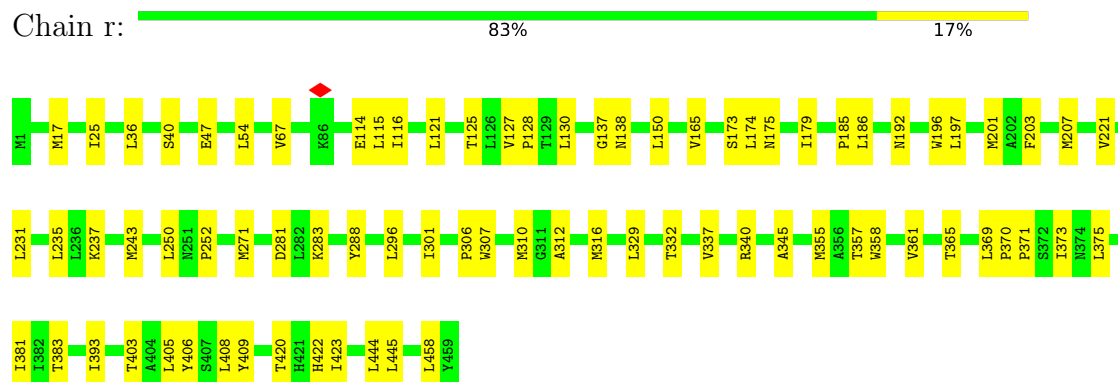
- Molecule 23: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4



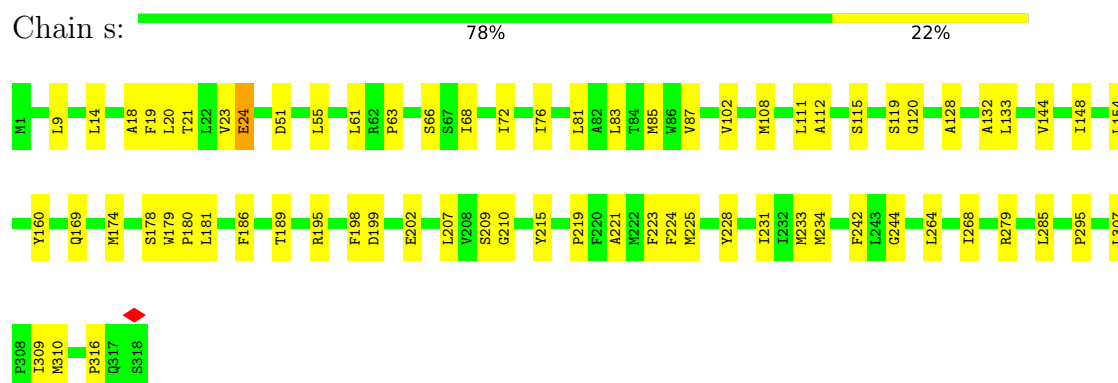
- Molecule 24: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9



- Molecule 25: NADH-ubiquinone oxidoreductase chain 4

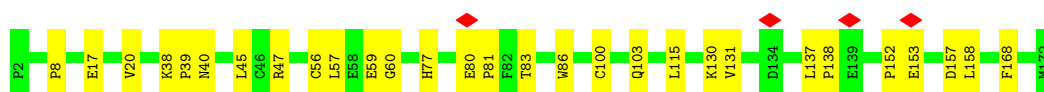


- Molecule 26: NADH-ubiquinone oxidoreductase chain 1



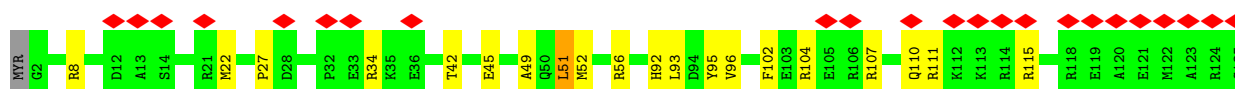
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

Chain u:  83% 17%



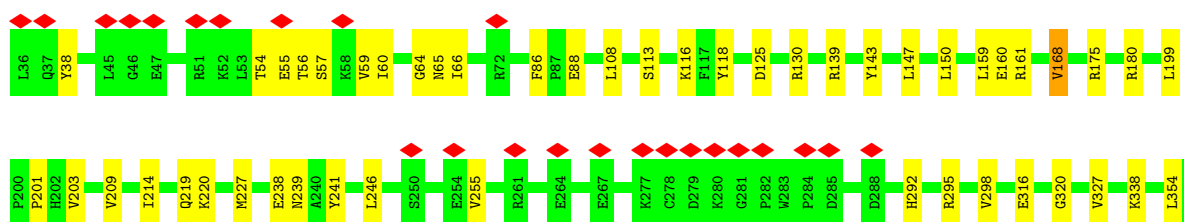
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Chain v:  18% 83% 15% ..



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

Chain w:  8% 85% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	111024	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.197	Depositor
Minimum map value	-0.106	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.031	Depositor
Map size ($\text{\AA}$)	333.002, 333.002, 333.002	wwPDB
Map dimensions	310, 310, 310	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0742, 1.0742, 1.0742	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEE, PLX, UQ, CDL, ADP, 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	0.14	0/380	0.34	0/525
2	S	0.14	0/581	0.39	0/781
3	U	0.12	0/664	0.28	0/912
4	V	0.13	0/1042	0.26	0/1411
5	W	0.16	0/973	0.34	0/1312
6	X	0.12	0/711	0.28	0/963
7	Y	0.13	0/610	0.31	0/836
8	Z	0.11	0/660	0.28	0/892
9	a	0.13	0/1184	0.30	0/1603
10	b	0.15	0/844	0.39	0/1149
11	c	0.12	0/1371	0.32	0/1875
12	d	0.13	0/1494	0.29	0/2015
13	e	0.13	0/891	0.29	0/1210
14	f	0.10	0/385	0.25	0/522
15	g	0.13	0/1031	0.30	0/1394
16	h	0.13	0/889	0.31	0/1190
17	i	0.18	0/2773	0.36	0/3768
18	j	0.18	0/938	0.36	0/1281
19	k	0.18	0/759	0.40	0/1029
20	l	0.15	0/4947	0.34	0/6728
21	m	0.25	0/1325	0.54	1/1800 (0.1%)
22	n	0.13	0/491	0.29	0/663
23	o	0.14	0/1092	0.31	0/1481
24	p	0.13	0/1586	0.29	0/2150
25	r	0.17	0/3723	0.34	0/5078
26	s	0.20	0/2575	0.42	0/3522
27	u	0.14	0/1436	0.34	0/1938
28	v	0.12	0/1052	0.35	2/1411 (0.1%)
29	w	0.13	0/2643	0.29	0/3580
All	All	0.15	0/39050	0.34	3/53019 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
28	v	51	LEU	CA-C-N	5.26	133.41	122.41
28	v	51	LEU	C-N-CA	5.26	133.41	122.41
21	m	148	SER	N-CA-C	5.03	116.84	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	363	0	332	9	0
2	S	566	0	561	8	0
3	U	643	0	642	6	0
4	V	1021	0	1025	13	0
5	W	949	0	935	21	0
6	X	699	0	682	10	0
7	Y	584	0	529	11	0
8	Z	641	0	620	6	0
9	a	1151	0	1164	12	0
10	b	819	0	835	21	0
11	c	1315	0	1208	15	0
12	d	1461	0	1429	21	0
13	e	867	0	817	13	0
14	f	377	0	353	4	0
15	g	1000	0	994	15	0
16	h	867	0	871	15	0
17	i	2710	0	2874	51	0
18	j	914	0	951	18	0
19	k	748	0	799	23	0
20	l	4816	0	4955	93	0
21	m	1292	0	1261	52	0
22	n	479	0	486	8	0
23	o	1062	0	1072	16	0
24	p	1530	0	1464	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	r	3631	0	3839	61	0
26	s	2502	0	2596	52	0
27	u	1398	0	1374	22	0
28	v	1028	0	982	15	0
29	w	2583	0	2540	33	0
30	Q	47	0	71	7	0
30	U	51	0	82	2	0
30	W	41	0	59	1	0
30	f	1	0	0	0	0
30	j	52	0	82	3	0
30	l	136	0	200	11	0
30	r	51	0	82	5	0
30	v	1	0	0	0	0
31	V	194	0	294	15	0
31	a	100	0	156	3	0
31	l	199	0	307	16	0
31	m	95	0	143	34	0
31	n	55	0	54	1	0
31	r	99	0	151	7	0
31	s	89	0	125	7	0
32	X	35	0	0	0	0
33	a	52	0	88	2	0
33	e	52	0	88	5	0
33	g	52	0	88	7	0
33	j	104	0	176	5	0
33	r	52	0	88	4	0
34	s	38	0	47	3	0
35	w	27	0	11	1	0
All	All	39639	0	40582	612	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (612) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:m:201:CDL:C39	31:m:201:CDL:H272	1.90	1.00
21:m:55:MET:HE3	21:m:55:MET:HA	1.43	0.98
21:m:64:MET:HE2	21:m:64:MET:HA	1.52	0.91
21:m:23:LYS:HZ3	31:m:201:CDL:H711	1.34	0.91
18:j:63:LEU:HD21	21:m:63:GLY:HA2	1.51	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:l:383:MET:HE3	20:l:384:PRO:HD2	1.59	0.84
21:m:23:LYS:NZ	31:m:201:CDL:C71	2.40	0.84
21:m:23:LYS:NZ	31:m:201:CDL:H711	1.91	0.84
19:k:28:SER:HB3	21:m:23:LYS:HG2	1.64	0.80
20:l:190:LEU:HD23	25:r:383:THR:HG21	1.67	0.77
31:m:201:CDL:H272	31:m:201:CDL:C40	2.14	0.77
29:w:168:VAL:HG21	29:w:241:TYR:CE1	2.20	0.76
31:m:201:CDL:H272	31:m:201:CDL:H392	1.67	0.76
25:r:237:LYS:HD2	25:r:316:MET:HB3	1.67	0.76
20:l:360:GLY:HA3	20:l:435:PRO:HA	1.67	0.75
21:m:23:LYS:HZ1	31:m:201:CDL:C71	1.99	0.75
20:l:363:TYR:HA	20:l:370:THR:HG21	1.67	0.75
17:i:236:LYS:HG3	17:i:237:MET:HG3	1.69	0.74
18:j:69:ILE:O	18:j:73:LEU:HG	1.89	0.73
31:m:201:CDL:HA22	31:m:201:CDL:OA6	1.88	0.73
22:n:26:TYR:HH	22:n:30:ARG:HH21	1.37	0.72
17:i:42:PRO:HG3	21:m:167:VAL:HG13	1.70	0.72
17:i:207:ILE:HG22	17:i:211:MET:HE2	1.71	0.72
20:l:295:GLN:O	20:l:425:ARG:NH1	2.22	0.72
31:m:201:CDL:OA8	31:m:201:CDL:H142	1.90	0.71
26:s:21:THR:HG21	26:s:224:PHE:HE2	1.54	0.71
29:w:57:SER:HB3	29:w:150:LEU:HD11	1.72	0.70
20:l:473:PRO:HG2	20:l:475:MET:HE2	1.73	0.70
26:s:85:MET:HB3	26:s:233:MET:HG3	1.74	0.70
18:j:73:LEU:HD12	21:m:55:MET:SD	2.32	0.69
29:w:125:ASP:O	29:w:130:ARG:NH2	2.26	0.68
1:Q:53:TYR:CE1	30:Q:101:PEE:H3	2.29	0.68
19:k:21:MET:SD	31:m:201:CDL:H721	2.34	0.68
17:i:49:ASN:O	17:i:52:ALA:N	2.26	0.66
18:j:18:VAL:HG11	26:s:76:ILE:HD11	1.77	0.66
5:W:121:MET:HE2	5:W:136:ALA:HB1	1.78	0.66
15:g:56:VAL:HG21	25:r:17:MET:HE1	1.78	0.66
26:s:195:ARG:HD3	26:s:231:ILE:HD11	1.78	0.65
30:l:704:PEE:H28	30:l:704:PEE:H73	1.79	0.65
29:w:54:THR:HG23	29:w:56:THR:HG22	1.79	0.65
21:m:139:GLU:O	21:m:143:ILE:HG13	1.96	0.65
9:a:152:LYS:HD3	15:g:96:VAL:HG21	1.79	0.65
21:m:72:THR:HG21	26:s:133:LEU:HD21	1.79	0.65
21:m:88:THR:HG21	31:m:201:CDL:OB4	1.97	0.64
30:l:704:PEE:H68	30:l:704:PEE:H22	1.79	0.64
23:o:75:ASN:O	23:o:79:ASN:ND2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:l:703:CDL:H431	31:l:703:CDL:H642	1.80	0.63
20:l:10:THR:HA	20:l:13:THR:HG22	1.79	0.63
10:b:14:GLN:HE22	24:p:157:ALA:HB3	1.62	0.63
18:j:6:THR:HG21	26:s:87:VAL:HG11	1.80	0.63
21:m:55:MET:HE1	21:m:58:LEU:HD23	1.81	0.63
23:o:118:GLU:O	23:o:120:LYS:NZ	2.29	0.62
21:m:26:PRO:HB2	21:m:71:THR:CG2	2.28	0.62
21:m:55:MET:HA	21:m:55:MET:CE	2.22	0.62
20:l:495:ILE:HG22	20:l:499:MET:HE2	1.81	0.62
21:m:26:PRO:HB2	21:m:71:THR:HG21	1.81	0.62
20:l:577:VAL:O	20:l:580:GLN:NE2	2.29	0.62
17:i:270:MET:HE3	17:i:279:PRO:HG3	1.81	0.61
25:r:337:VAL:HG11	25:r:345:ALA:HB2	1.81	0.61
27:u:137:LEU:HD12	27:u:138:PRO:HD2	1.82	0.61
6:X:117:GLU:OE2	24:p:45:ARG:NH1	2.33	0.61
24:p:105:ASP:OD1	24:p:122:ARG:NH1	2.32	0.61
15:g:4:MET:O	15:g:10:ARG:NH1	2.33	0.61
26:s:63:PRO:HB2	26:s:66:SER:HB3	1.80	0.61
20:l:419:THR:HA	20:l:422:TYR:CE2	2.36	0.61
23:o:59:VAL:HG22	25:r:423:ILE:HG12	1.83	0.60
4:V:17:GLU:OE1	4:V:20:ARG:NH1	2.31	0.60
31:m:201:CDL:H222	31:m:201:CDL:H342	1.83	0.60
25:r:231:LEU:HD23	25:r:235:LEU:HD12	1.81	0.60
27:u:152:PRO:O	27:u:153:GLU:HG2	2.01	0.60
31:m:201:CDL:H811	31:m:201:CDL:C62	2.31	0.60
12:d:101:GLU:OE2	13:e:115:GLN:NE2	2.34	0.60
7:Y:97:LEU:HB3	28:v:104:ARG:HB2	1.82	0.60
16:h:18:MET:HE3	19:k:56:ALA:HA	1.82	0.59
26:s:85:MET:HE1	26:s:108:MET:HB3	1.84	0.59
19:k:18:GLY:O	21:m:23:LYS:HE2	2.02	0.59
28:v:51:LEU:O	28:v:52:MET:HG3	2.01	0.59
10:b:80:TRP:CD1	12:d:41:VAL:HG23	2.37	0.59
21:m:57:PHE:CZ	21:m:61:LEU:HD11	2.37	0.59
25:r:370:PRO:HG3	25:r:375:LEU:HD22	1.84	0.59
2:S:12:MET:HE3	26:s:20:LEU:HB2	1.84	0.59
18:j:63:LEU:CD2	21:m:63:GLY:HA2	2.30	0.59
22:n:47:ARG:NH2	22:n:53:GLU:OE2	2.36	0.59
26:s:81:LEU:HD11	26:s:111:LEU:HG	1.85	0.59
18:j:50:PRO:HA	21:m:76:THR:HG21	1.85	0.59
26:s:221:ALA:O	26:s:225:MET:HG3	2.03	0.59
4:V:44:LYS:NZ	31:V:201:CDL:OB4	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:202:PLX:H92	25:r:40:SER:HB3	1.85	0.58
12:d:114:GLN:HG3	20:l:203:MET:HG2	1.84	0.58
5:W:85:GLN:O	5:W:89:GLU:HG3	2.03	0.58
10:b:80:TRP:HD1	12:d:41:VAL:HG23	1.68	0.58
10:b:9:LYS:HG2	10:b:13:GLN:HE22	1.69	0.58
24:p:139:GLN:NE2	24:p:156:PRO:O	2.36	0.58
29:w:118:TYR:OH	35:w:401:ADP:O2'	2.22	0.58
31:m:201:CDL:H142	31:m:201:CDL:CA5	2.34	0.58
24:p:151:THR:HG22	24:p:153:ALA:H	1.69	0.58
25:r:312:ALA:O	25:r:316:MET:HG3	2.04	0.57
5:W:98:MET:HE3	16:h:79:ILE:HD13	1.84	0.57
7:Y:97:LEU:HD12	28:v:107:ARG:HH21	1.68	0.57
20:l:286:LEU:HD22	20:l:411:MET:SD	2.44	0.57
15:g:13:LEU:HA	33:g:201:PLX:H32	1.87	0.57
28:v:27:PRO:O	28:v:34:ARG:NH1	2.37	0.57
5:W:84:LEU:HD12	27:u:57:LEU:HD21	1.87	0.57
20:l:128:MET:HE1	20:l:252:MET:HA	1.87	0.57
31:m:201:CDL:OA3	31:m:201:CDL:H1	2.05	0.57
19:k:23:ARG:NH1	21:m:81:GLU:OE1	2.36	0.57
6:X:136:GLU:OE2	24:p:18:ARG:NH1	2.38	0.56
25:r:307:TRP:HA	25:r:310:MET:HE2	1.86	0.56
15:g:52:ARG:NH2	29:w:338:LYS:O	2.38	0.56
17:i:268:GLN:HA	25:r:165:VAL:HG11	1.87	0.56
20:l:71:LEU:HD12	25:r:310:MET:HE1	1.86	0.56
20:l:359:MET:O	20:l:436:ARG:NH2	2.38	0.56
31:a:201:CDL:H751	13:e:103:SER:HB2	1.87	0.56
21:m:99:MET:SD	31:m:201:CDL:H781	2.45	0.56
1:Q:53:TYR:CZ	30:Q:101:PEE:H3	2.41	0.55
21:m:64:MET:HA	21:m:64:MET:CE	2.25	0.55
20:l:375:ILE:HD12	20:l:458:LEU:HD11	1.89	0.55
9:a:134:GLU:OE1	22:n:57:TRP:NE1	2.23	0.55
16:h:18:MET:HE1	19:k:59:MET:HB3	1.87	0.55
25:r:403:THR:HA	25:r:406:TYR:CE2	2.41	0.55
5:W:89:GLU:O	5:W:93:GLU:HG2	2.07	0.55
25:r:127:VAL:HG23	25:r:128:PRO:HD3	1.89	0.55
25:r:201:MET:HE2	30:r:501:PEE:H77	1.88	0.55
10:b:103:ARG:NH1	28:v:49:ALA:O	2.41	0.54
17:i:252:GLY:HA3	17:i:290:LEU:HD13	1.89	0.54
21:m:64:MET:HE2	21:m:64:MET:CA	2.32	0.54
20:l:327:LEU:O	20:l:331:MET:HG2	2.07	0.54
23:o:45:ARG:HH12	24:p:144:THR:HG21	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:r:243:MET:HB3	25:r:301:ILE:HG21	1.88	0.54
25:r:185:PRO:HB3	25:r:252:PRO:HD3	1.87	0.54
20:l:481:THR:HG1	28:v:92:HIS:HD1	1.52	0.54
20:l:55:MET:HE2	20:l:471:ASN:HB3	1.89	0.54
15:g:15:PHE:O	15:g:16:LEU:HD22	2.07	0.54
25:r:420:THR:HB	25:r:423:ILE:HD12	1.90	0.54
30:r:501:PEE:H71	30:r:501:PEE:H34	1.90	0.54
9:a:66:ARG:HA	9:a:69:LYS:HE3	1.90	0.54
31:m:201:CDL:CA5	31:m:201:CDL:C14	2.86	0.54
5:W:74:LEU:O	5:W:78:GLU:HG3	2.08	0.54
31:l:702:CDL:H822	31:l:702:CDL:H631	1.90	0.54
29:w:116:LYS:NZ	29:w:125:ASP:OD2	2.34	0.54
31:l:703:CDL:H561	31:l:703:CDL:H342	1.89	0.53
31:m:201:CDL:C40	31:m:201:CDL:C27	2.86	0.53
26:s:178:SER:HB2	26:s:181:LEU:HD12	1.89	0.53
26:s:207:LEU:O	26:s:209:SER:N	2.41	0.53
1:Q:53:TYR:OH	30:Q:101:PEE:H3	2.08	0.53
17:i:84:TRP:HH2	19:k:59:MET:HE3	1.73	0.53
17:i:128:LEU:HD12	17:i:216:PHE:HB3	1.91	0.53
19:k:21:MET:HE1	31:m:201:CDL:H601	1.89	0.53
21:m:17:PHE:HA	21:m:20:PHE:CE2	2.43	0.53
12:d:10:TYR:OH	13:e:123:GLU:OE2	2.26	0.52
16:h:106:PRO:HG2	27:u:17:GLU:HB3	1.91	0.52
19:k:65:VAL:HG11	21:m:157:THR:HG23	1.90	0.52
17:i:84:TRP:CH2	19:k:59:MET:HE3	2.44	0.52
27:u:83:THR:HA	27:u:86:TRP:CD1	2.43	0.52
18:j:33:LYS:HD3	26:s:61:LEU:HD21	1.91	0.52
29:w:168:VAL:HG21	29:w:241:TYR:HE1	1.71	0.52
12:d:137:LYS:NZ	12:d:141:ASP:OD2	2.42	0.52
29:w:246:LEU:HD22	29:w:255:VAL:HG11	1.90	0.52
12:d:140:GLN:O	12:d:144:SER:HB2	2.08	0.52
17:i:102:LEU:HD13	17:i:142:LEU:HG	1.92	0.52
21:m:23:LYS:NZ	31:m:201:CDL:CB7	2.72	0.52
9:a:139:ILE:HG23	25:r:54:LEU:HD23	1.92	0.52
20:l:227:PHE:O	20:l:230:HIS:ND1	2.42	0.52
33:g:201:PLX:H12	16:h:2:PRO:HD2	1.92	0.52
25:r:196:TRP:CD1	25:r:250:LEU:HB3	2.45	0.52
27:u:157:ASP:OD1	27:u:158:LEU:N	2.43	0.52
27:u:77:HIS:CE1	27:u:115:LEU:HD21	2.45	0.52
17:i:268:GLN:NE2	17:i:272:LYS:HE3	2.25	0.52
33:j:204:PLX:H341	33:j:204:PLX:H152	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:28:LYS:O	2:S:33:GLY:N	2.42	0.52
3:U:33:PRO:HA	26:s:310:MET:HG2	1.92	0.52
7:Y:103:ASP:OD1	7:Y:103:ASP:N	2.42	0.52
12:d:115:GLN:HG2	20:l:62:ILE:HG12	1.91	0.52
20:l:538:THR:HA	30:l:704:PEE:H59	1.91	0.52
20:l:233:LEU:HB3	20:l:234:PRO:HD3	1.92	0.51
25:r:306:PRO:HB3	25:r:458:LEU:HD12	1.92	0.51
28:v:22:MET:HE1	28:v:102:PHE:HA	1.92	0.51
33:g:201:PLX:H233	17:i:207:ILE:HD13	1.92	0.51
17:i:79:LEU:HB2	19:k:47:ILE:HD13	1.92	0.51
20:l:370:THR:HG22	20:l:431:PHE:CD1	2.45	0.51
2:S:69:ILE:HD11	27:u:20:VAL:HG13	1.92	0.51
31:V:201:CDL:H661	20:l:594:THR:HG23	1.92	0.51
17:i:100:MET:HE3	17:i:153:LEU:HD21	1.92	0.51
6:X:155:TYR:CD2	6:X:156:GLU:HG3	2.46	0.51
22:n:26:TYR:OH	22:n:30:ARG:NH2	2.20	0.51
30:r:501:PEE:H81	33:r:502:PLX:H393	1.93	0.51
31:V:202:CDL:H712	31:V:202:CDL:H521	1.93	0.51
5:W:68:ARG:CZ	5:W:72:MET:HE2	2.41	0.51
17:i:222:SER:O	17:i:224:ALA:N	2.44	0.51
20:l:358:LYS:HG3	24:p:80:TYR:CE1	2.46	0.51
11:c:153:TYR:OH	28:v:8:ARG:NH1	2.44	0.50
12:d:2:PRO:O	12:d:7:LYS:NZ	2.39	0.50
25:r:130:LEU:HD22	25:r:150:LEU:HD13	1.92	0.50
29:w:180:ARG:NH1	29:w:316:GLU:OE2	2.44	0.50
17:i:110:PRO:HG2	20:l:594:THR:HG21	1.93	0.50
19:k:76:SER:O	19:k:79:VAL:HG12	2.11	0.50
17:i:298:TYR:O	17:i:303:THR:OG1	2.29	0.50
25:r:373:ILE:HD11	25:r:444:LEU:HD23	1.93	0.50
20:l:264:TYR:CD2	20:l:265:PRO:HD3	2.47	0.50
29:w:219:GLN:NE2	29:w:227:MET:SD	2.85	0.50
31:l:702:CDL:H621	31:l:702:CDL:H432	1.93	0.50
18:j:71:LEU:O	21:m:147:TYR:OH	2.26	0.50
20:l:362:LEU:HD22	20:l:366:MET:HE2	1.93	0.50
31:l:702:CDL:H371	25:r:369:LEU:HD23	1.94	0.50
31:m:201:CDL:C62	31:m:201:CDL:C81	2.89	0.50
21:m:55:MET:O	21:m:59:ILE:HG12	2.12	0.50
17:i:289:ASN:HA	17:i:292:PHE:CE2	2.47	0.50
8:Z:60:ASN:HD22	20:l:433:GLY:H	1.58	0.49
20:l:562:LEU:HB3	20:l:563:PRO:HD3	1.92	0.49
24:p:64:LEU:O	24:p:68:GLU:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:r:329:LEU:O	25:r:332:THR:OG1	2.28	0.49
31:r:503:CDL:H332	31:r:503:CDL:H231	1.93	0.49
30:j:201:PEE:H26	26:s:295:PRO:HB3	1.93	0.49
17:i:294:MET:HE2	25:r:130:LEU:HD21	1.94	0.49
20:l:108:MET:CE	20:l:240:PRO:HB3	2.43	0.49
17:i:170:LEU:HD23	17:i:292:PHE:HB3	1.93	0.49
17:i:215:MET:HB2	17:i:251:MET:HE1	1.94	0.49
20:l:253:VAL:HB	20:l:310:LEU:HD11	1.94	0.49
31:a:201:CDL:H852	33:e:201:PLX:H232	1.94	0.49
21:m:164:GLY:O	21:m:168:ILE:HG12	2.13	0.49
4:V:38:ALA:HA	31:m:201:CDL:H232	1.94	0.49
6:X:85:TYR:OH	8:Z:22:TRP:NE1	2.32	0.49
18:j:73:LEU:O	26:s:160:TYR:OH	2.27	0.49
17:i:75:ILE:HD12	19:k:40:LEU:HD22	1.95	0.49
26:s:85:MET:HE1	26:s:108:MET:CB	2.43	0.49
27:u:59:GLU:N	27:u:59:GLU:OE1	2.46	0.49
17:i:99:THR:HG22	17:i:157:MET:HE1	1.95	0.49
4:V:40:SER:HA	31:V:201:CDL:HB61	1.95	0.49
17:i:153:LEU:HG	17:i:157:MET:HE2	1.94	0.49
26:s:14:LEU:HD21	26:s:83:LEU:HD21	1.94	0.49
26:s:174:MET:HB3	26:s:242:PHE:HA	1.94	0.49
29:w:168:VAL:HG11	29:w:241:TYR:CE1	2.47	0.49
31:V:201:CDL:H512	20:l:576:MET:HG2	1.95	0.49
20:l:599:MET:O	20:l:603:ASN:HB3	2.13	0.49
31:l:703:CDL:H612	31:l:703:CDL:H641	1.62	0.49
9:a:153:GLU:HG3	15:g:92:MET:HE2	1.95	0.48
25:r:221:VAL:HA	25:r:283:LYS:HD3	1.95	0.48
17:i:246:VAL:HG21	31:r:503:CDL:H362	1.95	0.48
26:s:186:PHE:O	26:s:189:THR:OG1	2.31	0.48
9:a:94:GLY:O	12:d:61:TYR:OH	2.30	0.48
31:V:202:CDL:H732	23:o:87:SER:HB3	1.94	0.48
5:W:121:MET:HE3	21:m:130:THR:HB	1.96	0.48
10:b:10:LEU:O	10:b:14:GLN:HG3	2.14	0.48
17:i:68:MET:HE1	19:k:37:MET:SD	2.53	0.48
20:l:373:LEU:HD22	20:l:431:PHE:HE2	1.78	0.48
20:l:536:LEU:HB3	20:l:537:PRO:HD3	1.96	0.48
31:n:101:CDL:H741	31:n:101:CDL:H711	1.70	0.48
5:W:93:GLU:O	5:W:97:ILE:HD12	2.13	0.48
6:X:120:MET:HE1	24:p:24:LEU:HB3	1.95	0.48
18:j:53:MET:HE3	18:j:56:PHE:HA	1.94	0.48
21:m:26:PRO:HG2	21:m:75:ALA:HB1	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:w:54:THR:O	29:w:55:GLU:HG3	2.14	0.48
33:j:203:PLX:H32	33:j:203:PLX:H6	1.56	0.48
20:l:69:MET:HE2	20:l:76:LEU:HD12	1.95	0.48
21:m:23:LYS:HZ1	31:m:201:CDL:CB7	2.25	0.48
26:s:19:PHE:O	26:s:23:VAL:HG23	2.13	0.48
26:s:21:THR:CG2	26:s:224:PHE:CE2	2.97	0.48
5:W:94:GLU:HG2	16:h:79:ILE:HD12	1.96	0.48
11:c:71:GLY:HA2	23:o:79:ASN:HB2	1.95	0.48
20:l:108:MET:HE3	20:l:240:PRO:HB3	1.94	0.48
17:i:72:MET:HE2	19:k:12:PHE:CG	2.49	0.48
20:l:313:MET:HG3	20:l:328:HIS:HD2	1.79	0.48
31:m:201:CDL:C27	31:m:201:CDL:H401	2.44	0.48
4:V:34:LEU:HD22	31:m:201:CDL:H261	1.95	0.48
17:i:265:MET:HE2	17:i:343:LEU:HD21	1.96	0.48
20:l:190:LEU:HD21	25:r:307:TRP:CH2	2.49	0.48
5:W:68:ARG:O	5:W:72:MET:HG3	2.14	0.47
33:g:201:PLX:H232	17:i:210:THR:HG21	1.95	0.47
17:i:108:LEU:HD11	17:i:191:THR:HG21	1.96	0.47
20:l:27:TYR:O	20:l:115:ASN:ND2	2.44	0.47
27:u:80:GLU:HB2	27:u:81:PRO:HD3	1.95	0.47
14:f:47:THR:HG23	15:g:65:LEU:HD22	1.96	0.47
18:j:93:PHE:CZ	18:j:97:LEU:HD11	2.48	0.47
20:l:529:TYR:HB3	20:l:530:PRO:HD3	1.96	0.47
22:n:50:ARG:HB2	22:n:53:GLU:HG2	1.96	0.47
26:s:144:VAL:O	26:s:148:ILE:HD12	2.13	0.47
33:e:201:PLX:H202	31:l:702:CDL:H812	1.95	0.47
29:w:86:PHE:HB2	29:w:159:LEU:HD23	1.96	0.47
26:s:264:LEU:O	26:s:268:ILE:HG12	2.14	0.47
26:s:24:GLU:OE1	26:s:228:TYR:OH	2.26	0.47
26:s:189:THR:HG22	26:s:234:MET:HE3	1.97	0.47
7:Y:50:LEU:HB3	7:Y:54:GLN:HE21	1.79	0.47
13:e:72:ASP:OD1	13:e:72:ASP:N	2.47	0.47
20:l:366:MET:O	20:l:370:THR:HG23	2.15	0.47
31:l:702:CDL:H312	31:l:702:CDL:HA61	1.69	0.47
23:o:56:ARG:NH1	23:o:58:GLY:O	2.47	0.47
29:w:88:GLU:HG3	29:w:139:ARG:HH12	1.79	0.47
7:Y:43:ARG:HB3	7:Y:46:GLN:HB2	1.97	0.47
23:o:23:TYR:OH	24:p:68:GLU:HG3	2.15	0.47
31:r:503:CDL:H342	31:r:503:CDL:H181	1.97	0.47
25:r:365:THR:HG21	25:r:444:LEU:HD13	1.97	0.47
1:Q:74:ASP:OD1	1:Q:74:ASP:N	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:c:102:GLY:HA3	23:o:43:LEU:HD22	1.96	0.47
20:l:69:MET:HE3	20:l:71:LEU:HD21	1.95	0.47
26:s:55:LEU:HD13	26:s:221:ALA:HB2	1.97	0.47
29:w:60:ILE:HG12	29:w:203:VAL:HB	1.96	0.47
5:W:120:MET:O	5:W:121:MET:HB3	2.15	0.47
13:e:97:ILE:O	13:e:101:LEU:HB2	2.14	0.47
20:l:78:LEU:HD11	31:l:702:CDL:H261	1.96	0.47
31:a:201:CDL:H541	30:l:705:PEE:H16	1.97	0.46
19:k:4:VAL:O	19:k:8:ILE:HG12	2.14	0.46
33:g:201:PLX:H112	33:g:201:PLX:H81	1.46	0.46
31:s:401:CDL:H322	31:s:401:CDL:HB61	1.97	0.46
9:a:163:ARG:NH1	15:g:102:ASP:OD2	2.44	0.46
20:l:86:SER:OG	20:l:262:ARG:NH2	2.47	0.46
31:m:201:CDL:H272	31:m:201:CDL:H391	1.86	0.46
7:Y:76:ASP:O	20:l:385:TYR:OH	2.21	0.46
13:e:89:VAL:HG21	25:r:25:ILE:HG23	1.96	0.46
20:l:561:ILE:HG13	20:l:562:LEU:H	1.80	0.46
31:V:201:CDL:H762	31:V:201:CDL:H401	1.97	0.46
31:s:401:CDL:H332	31:s:401:CDL:H182	1.98	0.46
7:Y:43:ARG:HD3	7:Y:48:PRO:HA	1.98	0.46
17:i:95:MET:HE1	17:i:145:ILE:HD12	1.97	0.46
17:i:278:MET:O	17:i:282:MET:HG3	2.16	0.46
11:c:78:LEU:HD12	11:c:106:HIS:HA	1.98	0.46
12:d:85:MET:HE2	12:d:85:MET:HB3	1.79	0.46
33:e:201:PLX:H21	30:l:705:PEE:H3	1.96	0.46
33:j:203:PLX:H252	33:j:203:PLX:H281	1.54	0.46
26:s:21:THR:CG2	26:s:224:PHE:HE2	2.23	0.46
17:i:41:ILE:HG13	19:k:73:LEU:HD21	1.96	0.46
21:m:92:ALA:HB1	31:m:201:CDL:H731	1.98	0.46
26:s:202:GLU:HA	26:s:210:GLY:HA3	1.98	0.46
31:s:401:CDL:H371	31:s:401:CDL:H341	1.59	0.46
28:v:111:ARG:O	28:v:115:ARG:HG2	2.16	0.46
4:V:49:PHE:CD1	31:m:201:CDL:H312	2.51	0.46
30:U:401:PEE:H55	30:U:401:PEE:H61	1.66	0.45
5:W:81:ARG:HH21	27:u:60:GLY:C	2.24	0.45
11:c:156:VAL:HG11	28:v:95:TYR:CZ	2.51	0.45
21:m:82:VAL:HG22	21:m:85:SER:HB3	1.98	0.45
26:s:21:THR:HG21	26:s:224:PHE:CE2	2.42	0.45
23:o:38:ALA:HB2	24:p:150:ARG:HD3	1.99	0.45
25:r:281:ASP:OD1	25:r:340:ARG:HB3	2.15	0.45
33:r:502:PLX:H122	33:r:502:PLX:H92	1.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:503:CDL:H791	31:r:503:CDL:H761	1.79	0.45
1:Q:73:LYS:HE2	1:Q:75:THR:HG22	1.97	0.45
5:W:96:ILE:O	5:W:99:LYS:HE3	2.16	0.45
10:b:90:VAL:O	10:b:96:THR:OG1	2.31	0.45
5:W:73:PRO:HG2	27:u:40:ASN:HB3	1.96	0.45
33:j:204:PLX:H311	33:j:204:PLX:H281	1.72	0.45
11:c:167:TYR:CD2	11:c:178:PRO:HG3	2.52	0.45
16:h:19:THR:HA	17:i:84:TRP:HB2	1.97	0.45
25:r:138:ASN:C	25:r:138:ASN:HD22	2.23	0.45
26:s:198:PHE:CD1	26:s:285:LEU:HD13	2.51	0.45
29:w:175:ARG:HH22	29:w:239:ASN:HD22	1.64	0.45
12:d:73:ASP:OD1	12:d:73:ASP:N	2.48	0.45
13:e:98:VAL:HG22	25:r:36:LEU:HB2	1.98	0.45
17:i:146:SER:HA	17:i:149:ILE:HD12	1.98	0.45
20:l:97:THR:HG21	20:l:125:LEU:HD22	1.99	0.45
26:s:102:VAL:HG11	26:s:154:LEU:HD11	1.99	0.45
29:w:38:TYR:HH	29:w:292:HIS:HD1	1.64	0.45
24:p:98:LYS:HG2	24:p:178:PRO:HG3	1.98	0.45
25:r:203:PHE:O	25:r:207:MET:HG2	2.16	0.45
31:s:401:CDL:H171	31:s:401:CDL:H141	1.66	0.45
20:l:305:SER:HB2	20:l:422:TYR:CE1	2.52	0.45
25:r:114:GLU:HG2	25:r:175:ASN:HA	1.99	0.45
25:r:115:LEU:HD12	25:r:174:LEU:HD22	1.99	0.45
14:f:72:ARG:NH2	15:g:18:ASN:OD1	2.50	0.45
33:g:201:PLX:H361	33:g:201:PLX:H311	1.98	0.45
30:j:201:PEE:H59	30:j:201:PEE:H64	1.75	0.45
19:k:25:HIS:ND1	19:k:88:ASP:OD1	2.39	0.45
20:l:530:PRO:O	20:l:534:HIS:HB2	2.16	0.45
10:b:5:THR:OG1	10:b:8:GLU:HG3	2.18	0.44
11:c:38:PRO:HG2	23:o:70:TYR:HD2	1.81	0.44
20:l:435:PRO:HB3	20:l:437:PHE:CZ	2.51	0.44
30:l:701:PEE:H14	30:l:701:PEE:H20	1.69	0.44
31:l:702:CDL:H452	25:r:445:LEU:HB3	2.00	0.44
3:U:43:ILE:HG12	18:j:84:LEU:HB2	1.99	0.44
5:W:94:GLU:OE2	5:W:104:TRP:NE1	2.42	0.44
7:Y:72:ARG:HB3	20:l:385:TYR:CD1	2.52	0.44
13:e:76:TYR:HB2	13:e:83:ASP:OD1	2.17	0.44
31:V:202:CDL:H742	31:V:202:CDL:H601	1.99	0.44
21:m:23:LYS:HZ3	31:m:201:CDL:C71	2.07	0.44
21:m:138:GLU:N	21:m:138:GLU:OE1	2.51	0.44
30:U:401:PEE:H21	30:U:401:PEE:H15	1.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:53:TYR:CE1	20:l:434:LYS:HG3	2.53	0.44
9:a:92:PHE:HD1	12:d:55:GLN:HE21	1.66	0.44
13:e:57:GLU:OE1	29:w:320:GLY:HA3	2.16	0.44
16:h:75:ARG:O	16:h:79:ILE:HG12	2.18	0.44
21:m:23:LYS:HZ1	31:m:201:CDL:H712	1.76	0.44
2:S:40:HIS:N	2:S:44:GLN:OE1	2.50	0.44
6:X:118:ILE:O	6:X:122:MET:HG2	2.17	0.44
16:h:2:PRO:HA	17:i:140:SER:HB2	2.00	0.44
25:r:271:MET:HE2	25:r:271:MET:HA	2.00	0.44
34:s:402:UQ:H221	34:s:402:UQ:H262	1.66	0.44
29:w:65:ASN:OD1	29:w:66:ILE:N	2.44	0.44
1:Q:36:GLN:NE2	25:r:137:GLY:O	2.47	0.44
30:Q:101:PEE:H46	17:i:284:MET:HE2	1.99	0.44
3:U:66:VAL:O	27:u:130:LYS:HE3	2.18	0.44
5:W:86:MET:SD	5:W:124:LEU:HB3	2.58	0.44
20:l:69:MET:HG3	20:l:71:LEU:CD2	2.47	0.44
20:l:295:GLN:HB2	20:l:301:ILE:HG12	1.99	0.44
21:m:52:LEU:O	21:m:56:VAL:HG12	2.16	0.44
33:r:502:PLX:H22	33:r:502:PLX:H1C3	1.70	0.44
28:v:93:LEU:HA	28:v:96:VAL:HG12	1.99	0.44
3:U:16:GLU:O	3:U:20:VAL:HG23	2.18	0.44
10:b:99:GLU:HG2	20:l:61:MET:HG2	1.99	0.44
20:l:331:MET:HG3	20:l:391:SER:HB3	1.99	0.44
31:V:202:CDL:H142	31:V:202:CDL:H111	1.70	0.44
31:V:202:CDL:H312	23:o:84:PRO:HB3	1.99	0.44
21:m:163:ILE:O	21:m:167:VAL:HG23	2.17	0.44
28:v:42:THR:OG1	28:v:45:GLU:HG3	2.17	0.44
29:w:64:GLY:O	29:w:161:ARG:NH2	2.42	0.44
4:V:37:SER:O	4:V:41:ILE:HG12	2.18	0.44
6:X:93:ILE:HG21	6:X:98:LEU:HD13	1.99	0.44
11:c:60:GLU:OE1	11:c:60:GLU:N	2.47	0.44
33:g:201:PLX:H101	33:g:201:PLX:H132	1.57	0.44
20:l:128:MET:HE3	20:l:251:THR:HG22	2.00	0.44
23:o:60:ILE:HD12	25:r:422:HIS:HB2	1.99	0.44
12:d:99:ASP:OD2	12:d:142:ARG:NH1	2.51	0.43
33:j:203:PLX:H272	33:j:203:PLX:H301	1.51	0.43
17:i:111:PHE:HA	20:l:591:PHE:CE1	2.53	0.43
17:i:324:LYS:HA	17:i:324:LYS:HD3	1.89	0.43
20:l:492:ILE:O	20:l:496:MET:HG2	2.18	0.43
25:r:186:LEU:HD23	25:r:192:ASN:HB3	2.00	0.43
25:r:357:THR:O	25:r:361:VAL:HG23	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:31:ASN:CG	2:S:36:LYS:HB2	2.44	0.43
9:a:147:ALA:HB2	25:r:173:SER:HB3	1.99	0.43
17:i:40:MET:HE1	17:i:129:LEU:HD22	1.99	0.43
19:k:21:MET:SD	31:m:201:CDL:C72	3.05	0.43
19:k:76:SER:OG	21:m:168:ILE:HD12	2.18	0.43
25:r:306:PRO:O	25:r:310:MET:HG3	2.18	0.43
29:w:295:ARG:HA	29:w:298:VAL:HG22	2.00	0.43
27:u:45:LEU:HD22	27:u:131:VAL:HB	2.01	0.43
27:u:100:CYS:HB2	27:u:103:GLN:OE1	2.19	0.43
30:Q:101:PEE:H1	30:Q:101:PEE:H14	1.65	0.43
20:l:332:HIS:HA	20:l:335:PHE:CZ	2.53	0.43
26:s:179:TRP:CG	26:s:180:PRO:HD3	2.53	0.43
26:s:215:TYR:HD1	26:s:219:PRO:HB2	1.83	0.43
11:c:85:GLU:OE1	11:c:119:THR:OG1	2.33	0.43
17:i:49:ASN:O	17:i:51:ARG:N	2.51	0.43
19:k:45:THR:HG23	21:m:52:LEU:HD13	2.01	0.43
20:l:54:PHE:CZ	20:l:84:TYR:HB2	2.53	0.43
21:m:15:ILE:HG21	31:s:401:CDL:H841	2.01	0.43
25:r:296:LEU:HG	25:r:381:ILE:HG21	2.01	0.43
29:w:143:TYR:OH	29:w:199:LEU:O	2.27	0.43
29:w:354:LEU:HD23	29:w:354:LEU:HA	1.90	0.43
3:U:59:ASP:OD2	27:u:130:LYS:HD3	2.18	0.43
10:b:11:ARG:HB2	24:p:156:PRO:HB3	1.99	0.43
16:h:38:LYS:HE2	16:h:42:GLU:OE2	2.18	0.43
31:l:703:CDL:H351	31:l:703:CDL:H382	1.50	0.43
31:m:201:CDL:H222	31:m:201:CDL:H331	1.99	0.43
1:Q:55:THR:HB	1:Q:58:THR:HB	2.00	0.43
6:X:89:LEU:HD22	8:Z:47:ARG:HB3	2.01	0.43
9:a:80:ILE:HB	9:a:81:PRO:HD3	2.01	0.43
20:l:249:SER:OG	20:l:336:LYS:HG3	2.18	0.43
23:o:113:GLU:O	23:o:117:GLN:HG2	2.18	0.43
26:s:112:ALA:O	26:s:115:SER:OG	2.33	0.43
2:S:19:PRO:HB3	26:s:9:LEU:HD12	2.01	0.43
4:V:39:TYR:HB3	31:V:201:CDL:H712	2.01	0.43
10:b:88:TYR:CE1	12:d:49:ARG:HG2	2.54	0.43
11:c:44:THR:OG1	11:c:47:GLU:HG3	2.18	0.43
20:l:399:VAL:HG12	20:l:409:LEU:HD13	2.01	0.43
25:r:406:TYR:O	25:r:409:TYR:HB3	2.19	0.43
29:w:108:LEU:HD23	29:w:327:VAL:HG13	2.01	0.43
10:b:106:PRO:HG2	10:b:120:MET:HE2	2.01	0.43
10:b:121:LYS:HD3	10:b:121:LYS:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:l:395:ILE:O	20:l:399:VAL:HG23	2.18	0.43
21:m:12:ILE:HG23	31:s:401:CDL:H842	2.01	0.43
21:m:28:TYR:HB3	21:m:83:TRP:CH2	2.54	0.43
31:r:503:CDL:H541	31:r:503:CDL:H511	1.68	0.43
4:V:43:LEU:HD13	31:V:201:CDL:H522	2.01	0.42
16:h:17:TRP:CD1	16:h:17:TRP:H	2.36	0.42
20:l:332:HIS:HA	20:l:335:PHE:CE2	2.54	0.42
25:r:116:ILE:HG13	27:u:168:PHE:CD1	2.54	0.42
26:s:68:ILE:O	26:s:72:ILE:HG12	2.18	0.42
34:s:402:UQ:H152	34:s:402:UQ:H121	1.81	0.42
31:V:202:CDL:H781	31:V:202:CDL:H812	1.78	0.42
8:Z:27:THR:HB	8:Z:53:TYR:CD2	2.55	0.42
8:Z:27:THR:HB	8:Z:53:TYR:HD2	1.83	0.42
18:j:50:PRO:CA	21:m:76:THR:HG21	2.47	0.42
20:l:12:LEU:HD22	20:l:129:MET:HB3	2.01	0.42
20:l:554:ASP:OD2	25:r:288:TYR:OH	2.29	0.42
24:p:27:LEU:HD11	24:p:40:PHE:HB3	2.01	0.42
10:b:32:GLU:HB2	10:b:33:PRO:HD3	2.01	0.42
33:e:201:PLX:H362	25:r:67:VAL:HG12	2.01	0.42
30:l:705:PEE:H33	30:l:705:PEE:H40	1.87	0.42
27:u:38:LYS:HB3	27:u:39:PRO:HD3	2.01	0.42
31:V:202:CDL:H872	20:l:558:LEU:HD21	2.01	0.42
10:b:99:GLU:HG2	20:l:61:MET:HE2	2.01	0.42
17:i:243:LEU:HD23	31:r:503:CDL:H361	2.00	0.42
20:l:176:ARG:HA	20:l:176:ARG:HD3	1.76	0.42
26:s:120:GLY:HA2	26:s:128:ALA:HB1	2.01	0.42
29:w:59:VAL:HG12	29:w:201:PRO:HB3	2.02	0.42
10:b:86:LEU:HD11	20:l:9:LEU:HD12	2.01	0.42
20:l:151:SER:HB2	20:l:252:MET:SD	2.60	0.42
31:l:702:CDL:H611	31:l:702:CDL:H581	1.67	0.42
21:m:86:ASN:OD1	21:m:88:THR:HG22	2.20	0.42
25:r:174:LEU:HA	25:r:179:ILE:HD11	2.01	0.42
11:c:110:ASP:HA	11:c:113:ILE:HG23	2.00	0.42
12:d:37:PHE:CD2	20:l:3:PRO:HB3	2.55	0.42
33:e:201:PLX:H111	31:l:702:CDL:H641	2.01	0.42
17:i:81:SER:O	17:i:83:GLN:N	2.50	0.42
30:r:501:PEE:H62	30:r:501:PEE:H68	1.91	0.42
27:u:47:ARG:HD2	27:u:47:ARG:HA	1.82	0.42
9:a:170:GLN:HB2	15:g:6:GLY:O	2.19	0.42
12:d:159:GLN:NE2	13:e:142:PHE:O	2.37	0.42
19:k:37:MET:HE2	19:k:67:ALA:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:l:702:CDL:H841	31:l:702:CDL:H811	1.63	0.42
28:v:107:ARG:HA	28:v:110:GLN:HG3	2.01	0.42
29:w:168:VAL:HG11	29:w:241:TYR:CD1	2.55	0.42
30:j:201:PEE:H22	30:j:201:PEE:H27	1.89	0.42
20:l:417:SER:OG	31:l:703:CDL:H581	2.20	0.42
25:r:355:MET:HE2	25:r:358:TRP:HD1	1.85	0.42
5:W:57:ARG:HB3	26:s:316:PRO:HG3	2.00	0.42
12:d:68:PHE:CE1	13:e:114:MET:HE1	2.55	0.42
13:e:129:ARG:HG2	13:e:134:LEU:HD12	2.01	0.42
25:r:197:LEU:HD13	30:r:501:PEE:H70	2.01	0.42
33:r:502:PLX:H72	33:r:502:PLX:H101	1.51	0.42
28:v:52:MET:O	28:v:56:ARG:HG3	2.19	0.42
29:w:113:SER:HB3	29:w:116:LYS:HB3	2.02	0.42
4:V:66:ILE:HD11	4:V:101:LEU:HD13	2.02	0.42
9:a:176:LYS:HE2	9:a:176:LYS:HB3	1.70	0.42
10:b:81:ILE:HG23	30:l:705:PEE:H58	2.01	0.42
16:h:97:HIS:HB2	16:h:102:GLU:HB2	2.02	0.42
17:i:97:MET:HE3	20:l:599:MET:HE3	2.02	0.42
20:l:241:THR:HG21	20:l:344:GLY:HA3	2.00	0.42
26:s:18:ALA:O	26:s:21:THR:OG1	2.34	0.42
4:V:85:ASP:HA	4:V:126:LYS:NZ	2.35	0.41
30:W:201:PEE:H47	30:W:201:PEE:H39	1.75	0.41
7:Y:94:ASP:HA	7:Y:99:ILE:HD13	2.02	0.41
11:c:126:TRP:C	11:c:128:THR:H	2.27	0.41
11:c:127:ASN:O	11:c:131:LYS:HE2	2.20	0.41
25:r:174:LEU:HD23	25:r:179:ILE:HD11	2.01	0.41
26:s:199:ASP:OD1	26:s:279:ARG:NE	2.47	0.41
29:w:88:GLU:N	29:w:160:GLU:HG3	2.34	0.41
14:f:68:GLU:HG2	15:g:21:ARG:HE	1.85	0.41
20:l:297:ASP:O	20:l:301:ILE:HG13	2.20	0.41
26:s:81:LEU:O	26:s:85:MET:HG2	2.20	0.41
26:s:120:GLY:HA3	26:s:132:ALA:HB2	2.02	0.41
29:w:209:VAL:HB	29:w:214:ILE:HD11	2.02	0.41
6:X:103:HIS:O	6:X:107:ASP:HB2	2.20	0.41
20:l:557:TRP:O	20:l:561:ILE:HG12	2.20	0.41
29:w:220:LYS:HB2	29:w:220:LYS:HE3	1.67	0.41
2:S:23:THR:HG22	2:S:27:HIS:CD2	2.56	0.41
4:V:95:CYS:HA	4:V:115:CYS:HA	2.02	0.41
5:W:84:LEU:HD13	27:u:8:PRO:HG2	2.01	0.41
12:d:97:LYS:NZ	25:r:47:GLU:OE2	2.37	0.41
17:i:268:GLN:HG3	27:u:168:PHE:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:k:56:ALA:O	19:k:59:MET:HG3	2.20	0.41
20:l:130:ILE:HD13	31:l:702:CDL:H252	2.02	0.41
20:l:153:LEU:HD23	20:l:153:LEU:HA	1.91	0.41
21:m:24:PRO:O	21:m:25:SER:C	2.62	0.41
24:p:84:GLU:OE1	24:p:84:GLU:N	2.53	0.41
5:W:43:LEU:HG	26:s:179:TRP:HE1	1.85	0.41
20:l:2:ASN:OD1	20:l:2:ASN:N	2.53	0.41
22:n:49:LEU:HD22	22:n:53:GLU:HG3	2.03	0.41
26:s:307:LEU:HA	26:s:310:MET:HE3	2.02	0.41
2:S:50:ARG:O	2:S:54:ILE:HG12	2.19	0.41
6:X:112:SER:O	6:X:116:VAL:HG23	2.21	0.41
10:b:73:THR:HG23	10:b:74:HIS:ND1	2.36	0.41
16:h:21:GLN:HG2	16:h:37:GLU:OE1	2.21	0.41
31:m:201:CDL:H131	31:m:201:CDL:H161	1.37	0.41
31:r:503:CDL:H641	31:r:503:CDL:H612	1.82	0.41
29:w:65:ASN:HD22	29:w:238:GLU:HG3	1.86	0.41
1:Q:46:GLN:HB3	30:Q:101:PEE:N	2.36	0.41
11:c:75:TYR:OH	11:c:105:ILE:O	2.24	0.41
13:e:73:SER:C	13:e:75:GLY:H	2.28	0.41
30:l:705:PEE:H60	30:l:705:PEE:H55	1.86	0.41
31:m:201:CDL:H531	31:m:201:CDL:H561	1.68	0.41
12:d:78:GLU:HA	15:g:110:THR:HA	2.03	0.41
20:l:96:VAL:O	20:l:100:ILE:HG12	2.21	0.41
23:o:61:GLU:OE2	23:o:66:ILE:HD11	2.21	0.41
31:s:401:CDL:H771	31:s:401:CDL:H801	1.80	0.41
31:V:201:CDL:H372	31:V:201:CDL:H341	1.52	0.41
7:Y:40:ILE:HD11	20:l:444:ASN:HB2	2.03	0.41
10:b:32:GLU:OE2	24:p:117:ASP:HB2	2.21	0.41
16:h:2:PRO:HB2	16:h:3:PHE:H	1.66	0.41
17:i:183:SER:O	17:i:187:MET:HG2	2.20	0.41
20:l:63:ILE:O	20:l:79:SER:HA	2.21	0.41
20:l:128:MET:CE	20:l:252:MET:HA	2.51	0.41
20:l:561:ILE:HG13	20:l:562:LEU:N	2.36	0.41
22:n:18:PRO:O	22:n:21:PHE:HB3	2.21	0.41
25:r:121:LEU:O	25:r:125:THR:HG23	2.21	0.41
25:r:201:MET:HE3	25:r:201:MET:HB3	1.96	0.41
26:s:85:MET:CB	26:s:233:MET:HG3	2.48	0.41
14:f:68:GLU:OE2	14:f:72:ARG:HG3	2.21	0.41
20:l:184:LEU:HD13	25:r:393:ILE:HG21	2.03	0.41
30:l:704:PEE:H58	30:l:704:PEE:H53	1.76	0.41
21:m:36:SER:HA	21:m:39:VAL:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:p:44:MET:HE3	24:p:48:PHE:CE1	2.56	0.41
29:w:147:LEU:HD23	29:w:147:LEU:HA	1.90	0.41
1:Q:53:TYR:OH	30:Q:101:PEE:C1	2.69	0.40
7:Y:87:PRO:HG3	28:v:96:VAL:HG23	2.03	0.40
33:a:202:PLX:H22	33:a:202:PLX:H1C3	1.73	0.40
11:c:62:TYR:OH	11:c:74:ASP:OD1	2.36	0.40
18:j:66:ASP:O	18:j:69:ILE:HG12	2.21	0.40
18:j:90:MET:SD	21:m:151:THR:HG23	2.61	0.40
20:l:49:VAL:HB	20:l:50:PRO:HD3	2.03	0.40
23:o:31:LYS:O	23:o:35:GLU:HG2	2.20	0.40
5:W:93:GLU:HG3	16:h:98:HIS:CD2	2.56	0.40
10:b:32:GLU:HB3	24:p:115:TYR:HD1	1.86	0.40
17:i:207:ILE:O	17:i:211:MET:HG3	2.21	0.40
20:l:172:ILE:HG21	25:r:408:LEU:HD12	2.02	0.40
25:r:221:VAL:HG22	25:r:283:LYS:HB3	2.03	0.40
26:s:51:ASP:HB3	34:s:402:UQ:H161	2.03	0.40
3:U:38:TYR:HB2	26:s:310:MET:O	2.21	0.40
10:b:78:PRO:O	10:b:82:ILE:HG12	2.22	0.40
15:g:10:ARG:NH2	17:i:347:ASN:O	2.47	0.40
18:j:87:MET:HE1	26:s:309:ILE:HD11	2.02	0.40
22:n:16:LEU:HD23	22:n:16:LEU:HA	1.91	0.40
26:s:119:SER:HG	26:s:223:PHE:HZ	1.64	0.40
4:V:140:LYS:HB3	4:V:140:LYS:HE2	1.79	0.40
12:d:19:ALA:HA	12:d:20:PRO:HD3	1.96	0.40
17:i:41:ILE:HD13	17:i:41:ILE:HA	1.93	0.40
17:i:106:LEU:HG	17:i:138:PRO:HB2	2.03	0.40
18:j:94:LEU:HD13	21:m:154:VAL:HG13	2.02	0.40
27:u:56:CYS:HB2	27:u:59:GLU:OE1	2.22	0.40
15:g:92:MET:O	15:g:96:VAL:HG23	2.21	0.40
20:l:249:SER:HG	20:l:336:LYS:HG3	1.85	0.40
30:l:704:PEE:H55	25:r:405:LEU:HD13	2.03	0.40
25:r:370:PRO:HA	25:r:371:PRO:HA	1.85	0.40
26:s:169:GLN:HB2	26:s:244:GLY:HA3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	a	63/121 (52%)	63 (100%)	0	100	100
10	b	90/119 (76%)	90 (100%)	0	100	100
11	c	141/141 (100%)	141 (100%)	0	100	100
12	d	75/155 (48%)	75 (100%)	0	100	100
13	e	72/96 (75%)	72 (100%)	0	100	100
14	f	35/45 (78%)	35 (100%)	0	100	100
15	g	108/108 (100%)	108 (100%)	0	100	100
16	h	87/93 (94%)	87 (100%)	0	100	100
17	i	268/311 (86%)	267 (100%)	1 (0%)	84	94
18	j	100/100 (100%)	100 (100%)	0	100	100
19	k	85/85 (100%)	85 (100%)	0	100	100
20	l	540/540 (100%)	540 (100%)	0	100	100
21	m	129/141 (92%)	126 (98%)	3 (2%)	44	76
22	n	53/53 (100%)	53 (100%)	0	100	100
23	o	113/113 (100%)	113 (100%)	0	100	100
24	p	158/159 (99%)	158 (100%)	0	100	100
25	r	410/410 (100%)	410 (100%)	0	100	100
26	s	274/275 (100%)	273 (100%)	1 (0%)	84	94
27	u	153/153 (100%)	153 (100%)	0	100	100
28	v	104/111 (94%)	104 (100%)	0	100	100
29	w	281/283 (99%)	280 (100%)	1 (0%)	84	94
All	All	3339/3612 (92%)	3333 (100%)	6 (0%)	85	96

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	i	108	LEU

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Mol	Chain	Res	Type
21	m	22	SER
21	m	23	LYS
21	m	148	SER
26	s	24	GLU
29	w	168	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
9	a	170	GLN
10	b	67	HIS
12	d	55	GLN
13	e	86	ASN
13	e	145	ASN
14	f	61	GLN
16	h	70	GLN
16	h	97	HIS
17	i	134	GLN
17	i	172	GLN
17	i	174	GLN
18	j	83	ASN
19	k	91	GLN
20	l	59	GLN
20	l	135	ASN
20	l	192	HIS
20	l	199	GLN
20	l	470	ASN
20	l	479	ASN
21	m	175	ASN
25	r	175	ASN
25	r	338	HIS
26	s	250	HIS
27	u	30	HIS
28	v	44	GLN
28	v	82	HIS
28	v	84	GLN
29	w	188	ASN
29	w	323	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 29 ligands modelled in this entry, 3 are modelled with single atom - leaving 26 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
33	PLX	r	502	-	51,51,51	1.21	5 (9%)	53,59,59	0.61	1 (1%)
31	CDL	l	702	-	98,98,99	1.11	8 (8%)	104,110,111	0.91	4 (3%)
31	CDL	r	503	-	98,98,99	1.11	8 (8%)	104,110,111	0.87	4 (3%)
30	PEE	l	704	-	49,49,50	1.19	6 (12%)	52,54,55	0.95	2 (3%)
30	PEE	U	401	-	50,50,50	1.18	6 (12%)	53,55,55	1.01	2 (3%)
33	PLX	e	201	-	51,51,51	1.21	5 (9%)	53,59,59	0.55	1 (1%)
33	PLX	j	204	-	51,51,51	1.20	4 (7%)	53,59,59	0.62	1 (1%)
30	PEE	l	705	-	45,45,50	1.24	6 (13%)	48,50,55	0.97	2 (4%)
31	CDL	n	101	-	54,54,99	1.38	9 (16%)	60,66,111	1.11	4 (6%)
34	UQ	s	402	-	38,38,63	3.63	11 (28%)	48,49,79	2.75	17 (35%)
31	CDL	m	201	-	94,94,99	0.94	4 (4%)	100,106,111	1.04	7 (7%)
31	CDL	V	202	-	99,99,99	1.11	8 (8%)	105,111,111	0.89	4 (3%)
33	PLX	j	203	-	51,51,51	1.20	4 (7%)	53,59,59	0.61	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	CDL	V	201	-	93,93,99	1.14	9 (9%)	99,105,111	0.89	4 (4%)
30	PEE	Q	101	-	46,46,50	1.23	6 (13%)	49,51,55	1.04	2 (4%)
30	PEE	r	501	-	50,50,50	1.18	6 (12%)	53,55,55	0.99	2 (3%)
33	PLX	a	202	-	51,51,51	1.21	4 (7%)	53,59,59	0.60	1 (1%)
30	PEE	l	701	-	39,39,50	1.33	6 (15%)	42,44,55	1.11	3 (7%)
33	PLX	g	201	-	51,51,51	1.20	4 (7%)	53,59,59	0.65	1 (1%)
30	PEE	j	201	-	50,50,50	1.18	6 (12%)	53,55,55	0.96	2 (3%)
32	8Q1	X	201	-	32,34,34	1.62	6 (18%)	39,43,43	1.59	6 (15%)
35	ADP	w	401	-	28,29,29	3.18	9 (32%)	43,45,45	1.91	9 (20%)
31	CDL	s	401	-	88,88,99	1.16	9 (10%)	94,100,111	0.94	4 (4%)
30	PEE	W	201	-	40,40,50	1.16	5 (12%)	43,45,55	1.04	2 (4%)
31	CDL	a	201	-	99,99,99	1.11	8 (8%)	105,111,111	0.86	4 (3%)
31	CDL	l	703	-	99,99,99	1.11	8 (8%)	105,111,111	0.88	4 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	PLX	r	502	-	-	22/55/55/55	-
31	CDL	l	702	-	-	54/109/109/110	-
31	CDL	r	503	-	-	55/109/109/110	-
30	PEE	l	704	-	-	28/53/53/54	-
30	PEE	U	401	-	-	22/54/54/54	-
33	PLX	e	201	-	-	30/55/55/55	-
33	PLX	j	204	-	-	31/55/55/55	-
30	PEE	l	705	-	-	26/49/49/54	-
31	CDL	n	101	-	-	29/65/65/110	-
34	UQ	s	402	-	-	12/33/57/87	0/1/1/1
31	CDL	m	201	-	-	59/105/105/110	-
31	CDL	V	202	-	-	59/110/110/110	-
33	PLX	j	203	-	-	27/55/55/55	-
31	CDL	V	201	-	-	61/104/104/110	-
30	PEE	Q	101	-	-	23/50/50/54	-
30	PEE	r	501	-	-	25/54/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	PLX	a	202	-	-	30/55/55/55	-
30	PEE	l	701	-	-	24/43/43/54	-
33	PLX	g	201	-	-	36/55/55/55	-
30	PEE	j	201	-	-	24/54/54/54	-
32	8Q1	X	201	-	-	21/41/41/41	-
35	ADP	w	401	-	-	6/16/32/32	0/3/3/3
31	CDL	s	401	-	-	49/99/99/110	-
30	PEE	W	201	-	-	25/44/44/54	-
31	CDL	a	201	-	-	58/110/110/110	-
31	CDL	l	703	-	-	47/110/110/110	-

All (170) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	s	402	UQ	C18-C19	10.03	1.56	1.33
34	s	402	UQ	C13-C14	9.61	1.55	1.33
34	s	402	UQ	C23-C24	9.38	1.54	1.33
34	s	402	UQ	C8-C9	9.29	1.54	1.33
35	w	401	ADP	C3'-C4'	-8.98	1.30	1.53
35	w	401	ADP	O4'-C4'	7.70	1.62	1.45
34	s	402	UQ	C28-C29	7.35	1.54	1.32
35	w	401	ADP	PA-O3A	6.63	1.66	1.59
35	w	401	ADP	C6-N6	5.39	1.48	1.34
32	X	201	8Q1	C34-N36	5.05	1.45	1.33
32	X	201	8Q1	C39-N41	5.04	1.45	1.33
35	w	401	ADP	O4'-C1'	-4.54	1.31	1.42
31	m	201	CDL	OA8-CA7	4.27	1.45	1.33
31	m	201	CDL	OA6-CA5	4.20	1.46	1.34
31	m	201	CDL	OB8-CB7	4.18	1.45	1.33
31	m	201	CDL	OB6-CB5	3.93	1.45	1.34
30	l	701	PEE	C18-C19	3.83	1.53	1.31
30	U	401	PEE	C18-C19	3.81	1.53	1.31
30	l	704	PEE	C18-C19	3.81	1.53	1.31
30	l	705	PEE	C18-C19	3.81	1.53	1.31
30	j	201	PEE	C18-C19	3.80	1.53	1.31
30	W	201	PEE	C18-C19	3.79	1.53	1.31
30	r	501	PEE	C18-C19	3.79	1.53	1.31
30	Q	101	PEE	C18-C19	3.79	1.53	1.31
30	U	401	PEE	C39-C38	3.74	1.52	1.31
30	r	501	PEE	C39-C38	3.74	1.52	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	l	701	PEE	C39-C38	3.73	1.52	1.31
30	l	705	PEE	C39-C38	3.73	1.52	1.31
30	Q	101	PEE	C39-C38	3.72	1.52	1.31
30	j	201	PEE	C39-C38	3.70	1.52	1.31
30	l	704	PEE	C39-C38	3.69	1.52	1.31
31	n	101	CDL	OA8-CA7	3.48	1.43	1.33
31	l	703	CDL	OA8-CA7	3.47	1.43	1.33
31	V	201	CDL	OA8-CA7	3.45	1.43	1.33
31	l	702	CDL	OA8-CA7	3.44	1.43	1.33
31	V	202	CDL	OA8-CA7	3.41	1.43	1.33
31	s	401	CDL	OA8-CA7	3.41	1.43	1.33
31	a	201	CDL	OA8-CA7	3.40	1.43	1.33
35	w	401	ADP	C8-N9	-3.37	1.31	1.37
31	r	503	CDL	OA8-CA7	3.35	1.43	1.33
35	w	401	ADP	O2'-C2'	-3.20	1.35	1.43
31	a	201	CDL	OB6-CB5	3.09	1.43	1.34
31	s	401	CDL	OB6-CB5	3.09	1.43	1.34
31	V	201	CDL	OA6-CA5	3.07	1.43	1.34
31	r	503	CDL	OB6-CB5	3.05	1.42	1.34
31	a	201	CDL	OB8-CB7	3.02	1.42	1.33
31	l	702	CDL	OB8-CB7	3.02	1.42	1.33
31	r	503	CDL	OB8-CB7	3.01	1.42	1.33
31	V	201	CDL	OB6-CB5	3.00	1.42	1.34
31	l	703	CDL	OB8-CB7	2.99	1.42	1.33
31	l	703	CDL	OB6-CB5	2.98	1.42	1.34
31	a	201	CDL	OA6-CA5	2.97	1.42	1.34
31	s	401	CDL	OA6-CA5	2.97	1.42	1.34
33	g	201	PLX	O6-C4	-2.97	1.40	1.44
35	w	401	ADP	O3'-C3'	2.97	1.50	1.43
31	V	201	CDL	OB8-CB7	2.97	1.42	1.33
31	n	101	CDL	OB6-CB5	2.96	1.42	1.34
31	l	703	CDL	OA6-CA5	2.96	1.42	1.34
31	V	202	CDL	OB6-CB5	2.94	1.42	1.34
31	l	702	CDL	OB6-CB5	2.94	1.42	1.34
31	V	202	CDL	OB8-CB7	2.94	1.41	1.33
31	n	101	CDL	OB8-CB7	2.93	1.41	1.33
31	n	101	CDL	OA6-CA5	2.93	1.42	1.34
31	V	202	CDL	OA6-CA5	2.92	1.42	1.34
31	s	401	CDL	OB8-CB7	2.88	1.41	1.33
31	r	503	CDL	OA6-CA5	2.87	1.42	1.34
31	l	702	CDL	OA6-CA5	2.87	1.42	1.34
33	r	502	PLX	O6-C4	-2.81	1.41	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	a	202	PLX	O6-C4	-2.79	1.41	1.44
33	e	201	PLX	O6-C4	-2.72	1.41	1.44
34	s	402	UQ	C6-C1	2.72	1.54	1.46
31	r	503	CDL	OA6-CA4	-2.67	1.40	1.46
30	l	705	PEE	O2-C2	-2.66	1.40	1.46
30	U	401	PEE	O2-C2	-2.65	1.40	1.46
31	l	702	CDL	OA6-CA4	-2.63	1.40	1.46
30	r	501	PEE	O2-C2	-2.62	1.40	1.46
30	j	201	PEE	O2-C2	-2.61	1.40	1.46
30	W	201	PEE	O2-C2	-2.59	1.40	1.46
31	n	101	CDL	OA6-CA4	-2.58	1.40	1.46
31	s	401	CDL	OA6-CA4	-2.58	1.40	1.46
30	Q	101	PEE	O2-C2	-2.57	1.40	1.46
31	a	201	CDL	OA6-CA4	-2.57	1.40	1.46
33	j	204	PLX	O6-C4	-2.56	1.41	1.44
31	V	202	CDL	OA6-CA4	-2.56	1.40	1.46
30	l	705	PEE	O3-C30	2.54	1.40	1.33
30	l	704	PEE	O2-C2	-2.53	1.40	1.46
31	l	703	CDL	OA6-CA4	-2.53	1.40	1.46
30	j	201	PEE	O3-C30	2.47	1.40	1.33
30	l	701	PEE	O3-C30	2.46	1.40	1.33
33	j	203	PLX	C7-C6	2.45	1.55	1.50
33	e	201	PLX	C7-C6	2.45	1.55	1.50
30	l	701	PEE	O2-C2	-2.43	1.40	1.46
32	X	201	8Q1	C1-S44	2.43	1.82	1.76
31	l	703	CDL	OB6-CB4	-2.43	1.40	1.46
30	l	704	PEE	O3-C30	2.42	1.40	1.33
33	j	204	PLX	C7-C6	2.42	1.55	1.50
30	U	401	PEE	O3-C30	2.41	1.40	1.33
35	w	401	ADP	C5-N7	-2.41	1.34	1.39
31	l	702	CDL	OB6-CB4	-2.41	1.40	1.46
31	V	202	CDL	OB6-CB4	-2.40	1.41	1.46
33	r	502	PLX	C7-C6	2.38	1.55	1.50
30	r	501	PEE	O3-C30	2.38	1.40	1.33
33	j	203	PLX	O6-C4	-2.38	1.41	1.44
33	a	202	PLX	C7-C6	2.38	1.55	1.50
30	Q	101	PEE	O3-C30	2.38	1.40	1.33
30	W	201	PEE	O3-C30	2.38	1.40	1.33
33	g	201	PLX	C7-C6	2.36	1.55	1.50
30	Q	101	PEE	O2-C10	2.35	1.40	1.34
31	n	101	CDL	OB6-CB4	-2.34	1.41	1.46
31	V	201	CDL	OB6-CB4	-2.34	1.41	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	l	701	PEE	O2-C10	2.33	1.40	1.34
34	s	402	UQ	C7-C8	2.32	1.54	1.50
32	X	201	8Q1	O35-C34	-2.31	1.19	1.23
32	X	201	8Q1	O40-C39	-2.30	1.18	1.23
31	a	201	CDL	OB6-CB4	-2.30	1.41	1.46
31	V	201	CDL	PB2-OB2	2.29	1.68	1.59
31	V	201	CDL	PB2-OB5	2.28	1.68	1.59
31	V	202	CDL	PB2-OB2	2.27	1.68	1.59
30	l	704	PEE	O3-C3	-2.26	1.40	1.45
30	l	704	PEE	O2-C10	2.26	1.40	1.34
30	j	201	PEE	O2-C10	2.25	1.40	1.34
31	n	101	CDL	PB2-OB2	2.25	1.68	1.59
31	V	201	CDL	OA6-CA4	-2.25	1.41	1.46
31	r	503	CDL	PB2-OB2	2.25	1.68	1.59
31	r	503	CDL	OB6-CB4	-2.25	1.41	1.46
31	l	703	CDL	PB2-OB2	2.25	1.68	1.59
31	s	401	CDL	OB6-CB4	-2.24	1.41	1.46
30	U	401	PEE	O2-C10	2.24	1.40	1.34
30	r	501	PEE	O3-C3	-2.23	1.40	1.45
32	X	201	8Q1	C6-C1	2.23	1.53	1.50
33	j	204	PLX	P1-O4	2.23	1.68	1.59
31	r	503	CDL	PB2-OB5	2.22	1.68	1.59
30	W	201	PEE	O2-C10	2.22	1.40	1.34
30	l	705	PEE	O2-C10	2.21	1.40	1.34
31	a	201	CDL	PB2-OB2	2.21	1.68	1.59
31	l	703	CDL	PB2-OB5	2.21	1.68	1.59
31	a	201	CDL	PB2-OB5	2.20	1.68	1.59
33	a	202	PLX	P1-O4	2.20	1.68	1.59
31	V	202	CDL	PB2-OB5	2.20	1.68	1.59
31	s	401	CDL	PB2-OB2	2.20	1.68	1.59
31	n	101	CDL	PB2-OB5	2.19	1.68	1.59
30	W	201	PEE	O3-C3	-2.18	1.40	1.45
30	r	501	PEE	O2-C10	2.18	1.40	1.34
31	s	401	CDL	PB2-OB5	2.17	1.67	1.59
31	l	702	CDL	PB2-OB2	2.17	1.67	1.59
30	l	701	PEE	O3-C3	-2.17	1.40	1.45
31	l	702	CDL	PB2-OB5	2.16	1.67	1.59
33	r	502	PLX	P1-O4	2.15	1.67	1.59
30	j	201	PEE	O3-C3	-2.15	1.40	1.45
33	e	201	PLX	P1-O4	2.15	1.67	1.59
30	Q	101	PEE	O3-C3	-2.15	1.40	1.45
34	s	402	UQ	O4-C4	-2.14	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	g	201	PLX	P1-O4	2.13	1.67	1.59
33	j	203	PLX	P1-O4	2.12	1.67	1.59
30	U	401	PEE	O3-C3	-2.11	1.40	1.45
33	j	204	PLX	P1-O1	2.11	1.67	1.59
34	s	402	UQ	O3-CM3	-2.11	1.40	1.45
33	r	502	PLX	P1-O1	2.11	1.67	1.59
33	j	203	PLX	P1-O1	2.05	1.67	1.59
30	l	705	PEE	O3-C3	-2.04	1.40	1.45
31	V	201	CDL	C11-CA5	2.04	1.56	1.50
33	g	201	PLX	P1-O1	2.04	1.67	1.59
34	s	402	UQ	C21-C19	2.03	1.55	1.51
33	e	201	PLX	P1-O1	2.03	1.67	1.59
31	s	401	CDL	C11-CA5	2.02	1.56	1.50
33	a	202	PLX	P1-O1	2.02	1.67	1.59
33	r	502	PLX	C25-C24	2.02	1.55	1.50
34	s	402	UQ	O1-C1	-2.02	1.18	1.23
31	n	101	CDL	C11-CA5	2.02	1.56	1.50
33	e	201	PLX	C1-C2	2.00	1.57	1.51

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	s	402	UQ	C7-C8-C9	-8.02	113.01	126.83
34	s	402	UQ	C22-C23-C24	-6.28	113.26	127.62
34	s	402	UQ	C12-C13-C14	-6.26	113.29	127.62
34	s	402	UQ	C17-C18-C19	-5.95	114.00	127.62
32	X	201	8Q1	C6-C1-S44	5.87	120.40	113.40
35	w	401	ADP	C5-C4-N3	-5.49	119.16	126.72
35	w	401	ADP	N3-C2-N1	-4.62	121.58	128.58
34	s	402	UQ	C27-C28-C29	-4.47	112.74	127.64
35	w	401	ADP	N3-C4-N9	4.34	134.55	127.17
34	s	402	UQ	C10-C9-C8	-4.32	112.55	123.63
34	s	402	UQ	C25-C24-C23	-4.28	112.64	123.63
30	Q	101	PEE	O2-C10-C11	4.24	120.65	111.48
30	r	501	PEE	O2-C10-C11	4.09	120.32	111.48
30	l	701	PEE	O2-C10-C11	4.08	120.30	111.48
31	m	201	CDL	OB6-CB5-C51	4.06	120.27	111.48
31	a	201	CDL	OB6-CB5-C51	4.05	120.25	111.48
31	s	401	CDL	OB6-CB5-C51	4.04	120.21	111.48
31	V	202	CDL	OA6-CA5-C11	4.02	120.18	111.48
31	V	201	CDL	OA6-CA5-C11	4.01	120.17	111.48
31	s	401	CDL	OA6-CA5-C11	4.01	120.16	111.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	W	201	PEE	O2-C10-C11	4.00	120.14	111.48
31	l	702	CDL	OB6-CB5-C51	4.00	120.13	111.48
31	l	702	CDL	OA6-CA5-C11	3.99	120.12	111.48
31	l	703	CDL	OB6-CB5-C51	3.98	120.09	111.48
31	V	201	CDL	OB6-CB5-C51	3.98	120.08	111.48
34	s	402	UQ	C20-C19-C18	-3.97	113.43	123.63
31	V	202	CDL	OB6-CB5-C51	3.94	120.01	111.48
31	l	703	CDL	OA6-CA5-C11	3.94	120.00	111.48
31	n	101	CDL	OA6-CA5-C11	3.93	119.99	111.48
30	U	401	PEE	O2-C10-C11	3.93	119.97	111.48
31	r	503	CDL	OA6-CA5-C11	3.87	119.86	111.48
30	j	201	PEE	O2-C10-C11	3.85	119.82	111.48
31	r	503	CDL	OB6-CB5-C51	3.83	119.76	111.48
31	n	101	CDL	OB6-CB5-C51	3.82	119.75	111.48
30	l	704	PEE	O2-C10-C11	3.81	119.72	111.48
31	a	201	CDL	OA6-CA5-C11	3.71	119.52	111.48
32	X	201	8Q1	O4-C1-C6	-3.67	119.75	123.98
34	s	402	UQ	C15-C14-C13	-3.66	114.23	123.63
30	l	705	PEE	O2-C10-C11	3.64	119.35	111.48
34	s	402	UQ	C26-C24-C23	-3.63	113.03	121.17
31	m	201	CDL	OA6-CA5-C11	3.58	119.22	111.48
35	w	401	ADP	C2-N3-C4	3.57	120.56	111.83
35	w	401	ADP	N9-C8-N7	-3.57	108.87	113.94
34	s	402	UQ	C21-C19-C18	-3.52	113.26	121.17
34	s	402	UQ	C11-C9-C8	-3.31	113.74	121.17
34	s	402	UQ	C30-C29-C28	-3.29	112.78	122.66
35	w	401	ADP	C4-N9-C8	3.23	109.13	105.74
35	w	401	ADP	C5-N7-C8	3.22	108.51	103.45
34	s	402	UQ	C31-C29-C28	-3.16	113.16	122.66
30	U	401	PEE	O3-C30-C31	3.13	121.38	111.83
32	X	201	8Q1	C37-C38-C39	3.00	117.40	112.39
35	w	401	ADP	C4-C5-N7	-2.97	107.19	110.58
31	m	201	CDL	OB8-CB7-C71	2.95	120.83	111.83
31	n	101	CDL	OA8-CA7-C31	2.89	119.93	111.15
31	V	202	CDL	OB8-CB7-C71	2.85	120.52	111.83
31	l	702	CDL	OA8-CA7-C31	2.81	120.42	111.83
31	s	401	CDL	OA8-CA7-C31	2.80	120.38	111.83
30	Q	101	PEE	O3-C30-C31	2.80	120.37	111.83
30	l	704	PEE	O3-C30-C31	2.80	120.36	111.83
31	n	101	CDL	OB8-CB7-C71	2.79	120.35	111.83
31	l	703	CDL	OB8-CB7-C71	2.79	120.34	111.83
30	r	501	PEE	O3-C30-C31	2.79	120.33	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	s	402	UQ	C16-C14-C13	-2.78	114.92	121.17
31	m	201	CDL	OA8-CA7-C31	2.77	120.29	111.83
31	V	201	CDL	OB8-CB7-C71	2.77	120.29	111.83
31	a	201	CDL	OB8-CB7-C71	2.77	120.28	111.83
30	l	705	PEE	O3-C30-C31	2.74	120.19	111.83
30	W	201	PEE	O3-C30-C31	2.74	120.18	111.83
30	j	201	PEE	O3-C30-C31	2.73	120.16	111.83
31	l	702	CDL	OB8-CB7-C71	2.72	120.14	111.83
31	r	503	CDL	OB8-CB7-C71	2.71	120.10	111.83
31	l	703	CDL	OA8-CA7-C31	2.71	120.09	111.83
31	s	401	CDL	OB8-CB7-C71	2.70	120.08	111.83
30	l	701	PEE	O3-C30-C31	2.66	119.96	111.83
31	r	503	CDL	OA8-CA7-C31	2.66	119.95	111.83
31	V	202	CDL	OA8-CA7-C31	2.63	119.86	111.83
31	a	201	CDL	OA8-CA7-C31	2.58	119.71	111.83
33	g	201	PLX	C1A-N1-C1	2.57	120.14	109.91
31	V	201	CDL	OA8-CA7-C31	2.53	119.55	111.83
33	r	502	PLX	C1A-N1-C1	2.47	119.72	109.91
34	s	402	UQ	C7-C6-C5	-2.46	120.67	124.89
31	m	201	CDL	CB4-OB6-CB5	-2.46	111.91	117.80
33	a	202	PLX	C1A-N1-C1	2.46	119.68	109.91
34	s	402	UQ	CM5-C5-C6	-2.45	120.43	124.45
32	X	201	8Q1	C43-S44-C1	2.43	109.03	101.84
33	j	204	PLX	C1A-N1-C1	2.42	119.53	109.91
30	l	701	PEE	C20-C19-C18	-2.34	112.33	126.42
33	j	203	PLX	C1A-N1-C1	2.32	119.12	109.91
32	X	201	8Q1	O4-C1-S44	-2.23	119.85	122.68
33	e	201	PLX	C1A-N1-C1	2.18	118.58	109.91
32	X	201	8Q1	C32-C34-N36	2.09	120.44	116.48
31	m	201	CDL	OB6-CB5-OB7	-2.06	118.88	123.70
35	w	401	ADP	C2'-C3'-C4'	2.06	106.59	102.61
31	m	201	CDL	OB8-CB7-OB9	-2.04	118.52	123.63

There are no chirality outliers.

All (883) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	Q	101	PEE	C11-C10-O2-C2
30	Q	101	PEE	O4-C10-O2-C2
30	Q	101	PEE	C1-O3P-P-O2P
30	Q	101	PEE	C1-O3P-P-O1P
30	Q	101	PEE	C1-O3P-P-O4P

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Mol	Chain	Res	Type	Atoms
30	Q	101	PEE	C4-O4P-P-O1P
30	Q	101	PEE	O4P-C4-C5-N
30	U	401	PEE	C11-C10-O2-C2
30	W	201	PEE	C1-O3P-P-O2P
30	W	201	PEE	C1-O3P-P-O1P
30	W	201	PEE	C1-O3P-P-O4P
30	W	201	PEE	C4-O4P-P-O2P
30	W	201	PEE	O4P-C4-C5-N
30	j	201	PEE	C1-O3P-P-O1P
30	j	201	PEE	C1-O3P-P-O4P
30	j	201	PEE	C4-O4P-P-O3P
30	l	701	PEE	C1-O3P-P-O1P
30	l	701	PEE	C1-O3P-P-O4P
30	l	701	PEE	C4-O4P-P-O3P
30	l	701	PEE	C4-O4P-P-O2P
30	l	704	PEE	C4-O4P-P-O3P
30	l	705	PEE	C1-O3P-P-O1P
30	r	501	PEE	C1-O3P-P-O2P
30	r	501	PEE	C1-O3P-P-O1P
30	r	501	PEE	C1-O3P-P-O4P
31	V	201	CDL	O1-C1-CA2-OA2
31	V	201	CDL	CA2-OA2-PA1-OA3
31	V	201	CDL	CA2-OA2-PA1-OA4
31	V	201	CDL	CA2-OA2-PA1-OA5
31	V	201	CDL	OA7-CA5-OA6-CA4
31	V	201	CDL	CB2-OB2-PB2-OB3
31	V	201	CDL	CB2-OB2-PB2-OB4
31	V	201	CDL	CB2-OB2-PB2-OB5
31	V	201	CDL	CB3-OB5-PB2-OB2
31	V	201	CDL	CB3-OB5-PB2-OB4
31	V	202	CDL	CA2-C1-CB2-OB2
31	V	202	CDL	OA6-CA4-CA6-OA8
31	V	202	CDL	CB2-OB2-PB2-OB3
31	V	202	CDL	CB2-OB2-PB2-OB5
31	V	202	CDL	CB3-OB5-PB2-OB2
31	V	202	CDL	CB3-OB5-PB2-OB3
31	V	202	CDL	CB3-OB5-PB2-OB4
31	V	202	CDL	OB6-CB4-CB6-OB8
31	a	201	CDL	CB2-OB2-PB2-OB3
31	a	201	CDL	CB2-OB2-PB2-OB4
31	a	201	CDL	CB2-OB2-PB2-OB5
31	a	201	CDL	CB3-OB5-PB2-OB2

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Mol	Chain	Res	Type	Atoms
31	a	201	CDL	CB3-OB5-PB2-OB3
31	a	201	CDL	CB3-OB5-PB2-OB4
31	a	201	CDL	C51-CB5-OB6-CB4
31	l	702	CDL	O1-C1-CA2-OA2
31	l	702	CDL	OA6-CA4-CA6-OA8
31	l	702	CDL	OA9-CA7-OA8-CA6
31	l	702	CDL	C31-CA7-OA8-CA6
31	l	702	CDL	CB2-OB2-PB2-OB4
31	l	702	CDL	CB2-OB2-PB2-OB5
31	l	702	CDL	CB3-OB5-PB2-OB2
31	l	702	CDL	CB3-OB5-PB2-OB3
31	l	703	CDL	O1-C1-CB2-OB2
31	l	703	CDL	CB2-OB2-PB2-OB3
31	l	703	CDL	CB2-OB2-PB2-OB4
31	l	703	CDL	CB2-OB2-PB2-OB5
31	l	703	CDL	CB3-OB5-PB2-OB3
31	l	703	CDL	CB3-OB5-PB2-OB4
31	m	201	CDL	C1-CA2-OA2-PA1
31	m	201	CDL	CA3-OA5-PA1-OA2
31	m	201	CDL	CA3-OA5-PA1-OA3
31	m	201	CDL	CA3-OA5-PA1-OA4
31	m	201	CDL	CB2-OB2-PB2-OB3
31	n	101	CDL	CB2-C1-CA2-OA2
31	n	101	CDL	CA2-OA2-PA1-OA4
31	n	101	CDL	CA2-OA2-PA1-OA5
31	n	101	CDL	OA5-CA3-CA4-OA6
31	n	101	CDL	CB2-OB2-PB2-OB3
31	n	101	CDL	CB2-OB2-PB2-OB4
31	n	101	CDL	CB2-OB2-PB2-OB5
31	n	101	CDL	CB3-OB5-PB2-OB2
31	n	101	CDL	CB3-OB5-PB2-OB4
31	r	503	CDL	CB2-C1-CA2-OA2
31	r	503	CDL	CA2-OA2-PA1-OA3
31	r	503	CDL	CA2-OA2-PA1-OA5
31	r	503	CDL	CA3-OA5-PA1-OA2
31	r	503	CDL	CA3-OA5-PA1-OA3
31	r	503	CDL	CB3-OB5-PB2-OB3
31	r	503	CDL	C51-CB5-OB6-CB4
31	s	401	CDL	O1-C1-CA2-OA2
31	s	401	CDL	CB2-C1-CA2-OA2
31	s	401	CDL	CA2-C1-CB2-OB2
31	s	401	CDL	CA2-OA2-PA1-OA3

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Mol	Chain	Res	Type	Atoms
31	s	401	CDL	CA2-OA2-PA1-OA4
31	s	401	CDL	CA2-OA2-PA1-OA5
31	s	401	CDL	CA3-OA5-PA1-OA3
31	s	401	CDL	OB6-CB4-CB6-OB8
32	X	201	8Q1	O4-C1-S44-C43
32	X	201	8Q1	C6-C1-S44-C43
32	X	201	8Q1	C28-C29-C32-C34
32	X	201	8Q1	C31-C29-C32-C34
32	X	201	8Q1	O33-C32-C34-N36
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	O7-C6-O6-C4
33	a	202	PLX	C3-O4-P1-O2
33	a	202	PLX	C3-O4-P1-O3
33	a	202	PLX	C2-O1-P1-O4
33	a	202	PLX	C2-O1-P1-O2
33	a	202	PLX	C2-O1-P1-O3
33	e	201	PLX	O7-C6-O6-C4
33	e	201	PLX	O9-C24-O8-C5
33	g	201	PLX	O7-C6-O6-C4
33	g	201	PLX	C3-O4-P1-O2
33	g	201	PLX	C2-O1-P1-O4
33	g	201	PLX	C2-O1-P1-O2
33	g	201	PLX	C2-O1-P1-O3
33	j	203	PLX	O7-C6-C7-C8
33	j	203	PLX	O7-C6-O6-C4
33	j	203	PLX	C3-C4-O6-C6
33	j	204	PLX	O7-C6-C7-C8
33	j	204	PLX	C3-O4-P1-O1
33	j	204	PLX	C2-O1-P1-O4
33	j	204	PLX	C2-O1-P1-O2
33	j	204	PLX	O9-C24-O8-C5
33	r	502	PLX	O6-C6-C7-C8
33	r	502	PLX	O9-C24-C25-C26
34	s	402	UQ	C7-C8-C9-C11
34	s	402	UQ	C17-C18-C19-C21
34	s	402	UQ	C18-C19-C21-C22
34	s	402	UQ	C22-C23-C24-C26
35	w	401	ADP	C5'-O5'-PA-O1A
35	w	401	ADP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
35	w	401	ADP	C5'-O5'-PA-O3A
31	m	201	CDL	OA9-CA7-OA8-CA6
31	s	401	CDL	OA9-CA7-OA8-CA6
30	U	401	PEE	O4-C10-O2-C2
30	j	201	PEE	O4-C10-O2-C2
30	l	704	PEE	O4-C10-O2-C2
31	r	503	CDL	OB7-CB5-OB6-CB4
30	j	201	PEE	C11-C10-O2-C2
31	V	201	CDL	C11-CA5-OA6-CA4
30	Q	101	PEE	O5-C30-O3-C3
30	l	704	PEE	C31-C30-O3-C3
30	l	705	PEE	C31-C30-O3-C3
31	V	201	CDL	C31-CA7-OA8-CA6
31	l	703	CDL	C71-CB7-OB8-CB6
31	m	201	CDL	C31-CA7-OA8-CA6
31	s	401	CDL	C31-CA7-OA8-CA6
34	s	402	UQ	C7-C8-C9-C10
30	j	201	PEE	C17-C18-C19-C20
30	r	501	PEE	C17-C18-C19-C20
30	l	705	PEE	O5-C30-O3-C3
31	a	201	CDL	OB7-CB5-OB6-CB4
31	l	702	CDL	O1-C1-CB2-OB2
31	n	101	CDL	O1-C1-CA2-OA2
31	n	101	CDL	O1-C1-CB2-OB2
31	r	503	CDL	O1-C1-CA2-OA2
31	s	401	CDL	O1-C1-CB2-OB2
30	Q	101	PEE	C31-C30-O3-C3
30	l	704	PEE	O5-C30-O3-C3
30	l	701	PEE	C11-C10-O2-C2
30	l	704	PEE	C11-C10-O2-C2
31	V	201	CDL	OA9-CA7-OA8-CA6
31	l	703	CDL	OB9-CB7-OB8-CB6
34	s	402	UQ	C14-C16-C17-C18
31	V	202	CDL	C37-C38-C39-C40
30	l	705	PEE	C37-C38-C39-C40
33	j	203	PLX	C27-C28-C29-C30
31	s	401	CDL	C52-C53-C54-C55
33	j	203	PLX	C25-C26-C27-C28
33	r	502	PLX	C9-C10-C11-C12
31	a	201	CDL	CA2-C1-CB2-OB2
31	l	702	CDL	CA2-C1-CB2-OB2
31	l	703	CDL	CA2-C1-CB2-OB2

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Mol	Chain	Res	Type	Atoms
31	m	201	CDL	CB2-C1-CA2-OA2
31	n	101	CDL	CA2-C1-CB2-OB2
30	j	201	PEE	C31-C30-O3-C3
30	l	701	PEE	C31-C30-O3-C3
31	r	503	CDL	C71-CB7-OB8-CB6
33	r	502	PLX	C7-C8-C9-C10
31	m	201	CDL	C13-C14-C15-C16
31	m	201	CDL	C38-C39-C40-C41
33	g	201	PLX	C11-C10-C9-C8
31	n	101	CDL	C71-C72-C73-C74
33	g	201	PLX	C10-C11-C12-C13
31	V	201	CDL	C62-C63-C64-C65
31	V	202	CDL	CB7-C71-C72-C73
31	l	703	CDL	CA7-C31-C32-C33
31	V	202	CDL	O1-C1-CB2-OB2
31	m	201	CDL	O1-C1-CA2-OA2
30	l	701	PEE	O5-C30-O3-C3
31	l	703	CDL	CB5-C51-C52-C53
31	r	503	CDL	OB9-CB7-OB8-CB6
31	s	401	CDL	C82-C83-C84-C85
30	l	701	PEE	O4-C10-O2-C2
33	g	201	PLX	O6-C4-C5-O8
31	a	201	CDL	C71-CB7-OB8-CB6
31	V	201	CDL	CA7-C31-C32-C33
31	s	401	CDL	CB7-C71-C72-C73
31	m	201	CDL	C53-C54-C55-C56
33	j	204	PLX	C28-C29-C30-C31
30	l	701	PEE	C11-C12-C13-C14
31	a	201	CDL	CA5-C11-C12-C13
31	l	703	CDL	C17-C18-C19-C20
31	V	202	CDL	C11-C12-C13-C14
31	l	702	CDL	C81-C82-C83-C84
33	j	204	PLX	C13-C14-C15-C16
34	s	402	UQ	C27-C28-C29-C31
33	j	204	PLX	C32-C33-C34-C35
31	l	703	CDL	C12-C13-C14-C15
31	l	703	CDL	C39-C40-C41-C42
31	V	201	CDL	CB7-C71-C72-C73
31	n	101	CDL	CB7-C71-C72-C73
31	r	503	CDL	CB7-C71-C72-C73
31	l	702	CDL	CA7-C31-C32-C33
31	l	702	CDL	CB7-C71-C72-C73

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Mol	Chain	Res	Type	Atoms
31	m	201	CDL	CA7-C31-C32-C33
31	s	401	CDL	C34-C35-C36-C37
30	r	501	PEE	C12-C13-C14-C15
31	l	703	CDL	C35-C36-C37-C38
31	l	703	CDL	C51-C52-C53-C54
31	V	202	CDL	O1-C1-CA2-OA2
31	a	201	CDL	O1-C1-CB2-OB2
31	l	702	CDL	C71-CB7-OB8-CB6
30	j	201	PEE	O5-C30-O3-C3
30	W	201	PEE	C10-C11-C12-C13
31	n	101	CDL	CB5-C51-C52-C53
31	s	401	CDL	CB5-C51-C52-C53
31	V	201	CDL	C34-C35-C36-C37
30	Q	101	PEE	C37-C38-C39-C40
30	l	701	PEE	C17-C18-C19-C20
30	l	701	PEE	C10-C11-C12-C13
33	r	502	PLX	C31-C32-C33-C34
31	V	201	CDL	C71-CB7-OB8-CB6
31	s	401	CDL	C71-CB7-OB8-CB6
30	U	401	PEE	C34-C35-C36-C37
31	V	201	CDL	CB2-C1-CA2-OA2
31	l	702	CDL	CB2-C1-CA2-OA2
30	W	201	PEE	C31-C30-O3-C3
31	m	201	CDL	C71-CB7-OB8-CB6
30	r	501	PEE	C41-C42-C43-C44
31	a	201	CDL	C34-C35-C36-C37
31	l	702	CDL	C34-C35-C36-C37
33	j	204	PLX	O6-C6-C7-C8
31	V	201	CDL	C51-CB5-OB6-CB4
33	g	201	PLX	C17-C18-C19-C20
31	V	201	CDL	OB7-CB5-OB6-CB4
30	U	401	PEE	C17-C18-C19-C20
31	l	703	CDL	C41-C42-C43-C44
31	a	201	CDL	OB9-CB7-OB8-CB6
31	l	703	CDL	CA5-C11-C12-C13
31	V	202	CDL	C57-C58-C59-C60
31	l	702	CDL	OB9-CB7-OB8-CB6
31	l	702	CDL	OA5-CA3-CA4-OA6
31	r	503	CDL	C51-C52-C53-C54
31	l	703	CDL	C61-C62-C63-C64
31	V	201	CDL	OB9-CB7-OB8-CB6
31	m	201	CDL	OB9-CB7-OB8-CB6

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Mol	Chain	Res	Type	Atoms
31	s	401	CDL	OB9-CB7-OB8-CB6
33	j	204	PLX	C7-C8-C9-C10
30	W	201	PEE	C11-C12-C13-C14
31	V	201	CDL	C17-C18-C19-C20
31	V	201	CDL	C56-C57-C58-C59
31	V	202	CDL	C55-C56-C57-C58
31	m	201	CDL	C21-C22-C23-C24
30	l	704	PEE	C30-C31-C32-C33
31	V	202	CDL	C14-C15-C16-C17
33	e	201	PLX	C13-C14-C15-C16
33	g	201	PLX	C25-C26-C27-C28
33	g	201	PLX	O9-C24-C25-C26
33	r	502	PLX	O7-C6-C7-C8
31	V	202	CDL	C17-C18-C19-C20
31	V	202	CDL	C52-C53-C54-C55
31	m	201	CDL	C32-C33-C34-C35
31	m	201	CDL	C34-C35-C36-C37
31	n	101	CDL	C55-C56-C57-C58
31	r	503	CDL	C31-C32-C33-C34
31	r	503	CDL	C32-C33-C34-C35
33	a	202	PLX	C9-C10-C11-C12
33	e	201	PLX	C10-C11-C12-C13
33	g	201	PLX	C14-C15-C16-C17
33	j	203	PLX	C26-C27-C28-C29
33	j	203	PLX	C31-C32-C33-C34
31	V	201	CDL	C37-C38-C39-C40
31	l	703	CDL	C74-C75-C76-C77
33	a	202	PLX	C28-C29-C30-C31
30	l	705	PEE	C22-C23-C24-C25
31	l	702	CDL	C62-C63-C64-C65
31	l	703	CDL	C32-C33-C34-C35
31	s	401	CDL	C14-C15-C16-C17
33	j	204	PLX	C11-C12-C13-C14
31	V	201	CDL	C35-C36-C37-C38
31	l	702	CDL	C52-C53-C54-C55
31	l	702	CDL	C59-C60-C61-C62
31	m	201	CDL	C76-C77-C78-C79
31	n	101	CDL	C52-C53-C54-C55
31	s	401	CDL	C59-C60-C61-C62
33	g	201	PLX	C9-C10-C11-C12
33	j	203	PLX	C9-C10-C11-C12
31	l	702	CDL	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
31	a	201	CDL	C22-C23-C24-C25
31	a	201	CDL	C35-C36-C37-C38
31	l	702	CDL	C58-C59-C60-C61
31	m	201	CDL	C33-C34-C35-C36
33	j	204	PLX	C25-C26-C27-C28
31	r	503	CDL	C80-C81-C82-C83
30	Q	101	PEE	C14-C15-C16-C17
33	j	203	PLX	C34-C35-C36-C37
31	m	201	CDL	C79-C80-C81-C82
33	j	203	PLX	C13-C14-C15-C16
33	j	204	PLX	C16-C17-C18-C19
31	V	201	CDL	CB3-CB4-CB6-OB8
30	l	704	PEE	C21-C22-C23-C24
30	l	705	PEE	C14-C15-C16-C17
31	V	202	CDL	C12-C13-C14-C15
31	a	201	CDL	C17-C18-C19-C20
31	n	101	CDL	C73-C74-C75-C76
31	r	503	CDL	C14-C15-C16-C17
31	r	503	CDL	C73-C74-C75-C76
33	g	201	PLX	C7-C8-C9-C10
31	V	202	CDL	CA7-C31-C32-C33
30	Q	101	PEE	C21-C22-C23-C24
30	j	201	PEE	C21-C22-C23-C24
31	V	201	CDL	C55-C56-C57-C58
31	a	201	CDL	C23-C24-C25-C26
31	a	201	CDL	C62-C63-C64-C65
31	l	702	CDL	C71-C72-C73-C74
31	m	201	CDL	C71-C72-C73-C74
31	s	401	CDL	C75-C76-C77-C78
33	e	201	PLX	C14-C15-C16-C17
33	j	204	PLX	C14-C15-C16-C17
30	W	201	PEE	O5-C30-O3-C3
30	l	701	PEE	C32-C33-C34-C35
31	V	202	CDL	C41-C42-C43-C44
31	V	202	CDL	C82-C83-C84-C85
31	l	702	CDL	C75-C76-C77-C78
30	l	704	PEE	C31-C32-C33-C34
31	V	202	CDL	C59-C60-C61-C62
31	m	201	CDL	C78-C79-C80-C81
31	s	401	CDL	C36-C37-C38-C39
31	s	401	CDL	C55-C56-C57-C58
33	e	201	PLX	C28-C29-C30-C31

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Mol	Chain	Res	Type	Atoms
30	U	401	PEE	C11-C12-C13-C14
31	r	503	CDL	C43-C44-C45-C46
31	s	401	CDL	C73-C74-C75-C76
33	g	201	PLX	C30-C31-C32-C33
33	r	502	PLX	C27-C28-C29-C30
30	r	501	PEE	C11-C10-O2-C2
33	a	202	PLX	C13-C14-C15-C16
31	m	201	CDL	C55-C56-C57-C58
31	r	503	CDL	C41-C42-C43-C44
31	l	703	CDL	C75-C76-C77-C78
33	j	204	PLX	C18-C19-C20-C21
33	a	202	PLX	C33-C34-C35-C36
33	r	502	PLX	C14-C15-C16-C17
33	g	201	PLX	C32-C33-C34-C35
33	r	502	PLX	C11-C10-C9-C8
34	s	402	UQ	C13-C14-C16-C17
30	l	701	PEE	C13-C14-C15-C16
31	a	201	CDL	C32-C33-C34-C35
31	m	201	CDL	C82-C83-C84-C85
31	r	503	CDL	C52-C53-C54-C55
31	V	201	CDL	C38-C39-C40-C41
31	l	702	CDL	C11-C12-C13-C14
33	j	204	PLX	C33-C34-C35-C36
30	l	705	PEE	C33-C34-C35-C36
33	j	203	PLX	C28-C29-C30-C31
31	l	702	CDL	C37-C38-C39-C40
31	m	201	CDL	C74-C75-C76-C77
33	e	201	PLX	C25-C26-C27-C28
30	W	201	PEE	C12-C13-C14-C15
31	V	202	CDL	C61-C62-C63-C64
31	l	703	CDL	C64-C65-C66-C67
31	V	202	CDL	C36-C37-C38-C39
31	l	702	CDL	C56-C57-C58-C59
31	V	202	CDL	C51-CB5-OB6-CB4
31	l	702	CDL	C11-CA5-OA6-CA4
31	s	401	CDL	C11-CA5-OA6-CA4
30	U	401	PEE	C20-C21-C22-C23
30	l	701	PEE	C35-C36-C37-C38
30	l	704	PEE	C39-C40-C41-C42
31	l	703	CDL	C11-C12-C13-C14
31	V	201	CDL	C11-C12-C13-C14
33	j	203	PLX	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
31	V	201	CDL	C44-C45-C46-C47
33	a	202	PLX	C10-C11-C12-C13
33	j	204	PLX	C10-C11-C12-C13
31	V	201	CDL	C74-C75-C76-C77
31	a	201	CDL	C82-C83-C84-C85
31	l	702	CDL	C82-C83-C84-C85
33	g	201	PLX	C11-C12-C13-C14
33	j	203	PLX	C16-C17-C18-C19
33	g	201	PLX	C2-C1-N1-C1A
31	V	201	CDL	C33-C34-C35-C36
30	r	501	PEE	C32-C33-C34-C35
31	n	101	CDL	C54-C55-C56-C57
31	V	201	CDL	C52-C53-C54-C55
31	m	201	CDL	C15-C16-C17-C18
30	l	704	PEE	C10-C11-C12-C13
30	r	501	PEE	O4-C10-O2-C2
31	V	202	CDL	OB7-CB5-OB6-CB4
30	l	704	PEE	O3P-C1-C2-O2
30	U	401	PEE	C23-C24-C25-C26
31	m	201	CDL	C52-C53-C54-C55
31	r	503	CDL	C55-C56-C57-C58
30	U	401	PEE	C14-C15-C16-C17
31	V	201	CDL	OB6-CB4-CB6-OB8
31	m	201	CDL	OA6-CA4-CA6-OA8
30	l	705	PEE	C31-C32-C33-C34
32	X	201	8Q1	C6-C7-C8-C9
31	V	201	CDL	C75-C76-C77-C78
31	V	202	CDL	C35-C36-C37-C38
31	a	201	CDL	C60-C61-C62-C63
31	m	201	CDL	C57-C58-C59-C60
33	a	202	PLX	C27-C28-C29-C30
31	V	201	CDL	C78-C79-C80-C81
31	l	703	CDL	C56-C57-C58-C59
33	a	202	PLX	C25-C26-C27-C28
33	j	203	PLX	C30-C31-C32-C33
31	n	101	CDL	C56-C57-C58-C59
33	r	502	PLX	C12-C13-C14-C15
31	a	201	CDL	C18-C19-C20-C21
31	m	201	CDL	C51-C52-C53-C54
30	l	704	PEE	C11-C12-C13-C14
31	l	702	CDL	C73-C74-C75-C76
31	V	201	CDL	C51-C52-C53-C54

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Mol	Chain	Res	Type	Atoms
31	r	503	CDL	C11-C12-C13-C14
31	l	702	CDL	C74-C75-C76-C77
31	l	702	CDL	C24-C25-C26-C27
31	a	201	CDL	C75-C76-C77-C78
33	e	201	PLX	C11-C12-C13-C14
33	e	201	PLX	C11-C10-C9-C8
30	U	401	PEE	C21-C22-C23-C24
30	Q	101	PEE	C19-C20-C21-C22
30	r	501	PEE	C15-C16-C17-C18
30	r	501	PEE	C39-C40-C41-C42
34	s	402	UQ	C27-C28-C29-C30
31	V	202	CDL	C15-C16-C17-C18
33	a	202	PLX	C11-C12-C13-C14
33	g	201	PLX	C28-C29-C30-C31
31	l	702	CDL	OA5-CA3-CA4-CA6
31	n	101	CDL	OA5-CA3-CA4-CA6
33	j	203	PLX	O4-C3-C4-C5
31	s	401	CDL	OA7-CA5-OA6-CA4
33	a	202	PLX	C34-C35-C36-C37
31	V	202	CDL	C75-C76-C77-C78
31	V	201	CDL	C59-C60-C61-C62
30	l	705	PEE	C30-C31-C32-C33
31	m	201	CDL	CB5-C51-C52-C53
31	m	201	CDL	CB7-C71-C72-C73
33	a	202	PLX	C7-C8-C9-C10
33	j	203	PLX	C7-C8-C9-C10
33	r	502	PLX	O8-C24-C25-C26
31	m	201	CDL	C58-C59-C60-C61
31	s	401	CDL	C60-C61-C62-C63
33	e	201	PLX	C27-C28-C29-C30
33	g	201	PLX	C27-C28-C29-C30
31	r	503	CDL	C62-C63-C64-C65
30	W	201	PEE	C1-C2-C3-O3
30	l	705	PEE	C1-C2-C3-O3
31	V	201	CDL	CA3-CA4-CA6-OA8
31	V	202	CDL	CB3-CB4-CB6-OB8
31	l	702	CDL	CA3-CA4-CA6-OA8
33	g	201	PLX	C3-C4-C5-O8
30	W	201	PEE	C24-C25-C26-C27
30	l	704	PEE	C42-C43-C44-C45
31	l	703	CDL	C73-C74-C75-C76
33	a	202	PLX	C30-C31-C32-C33

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Mol	Chain	Res	Type	Atoms
30	U	401	PEE	C15-C16-C17-C18
30	l	704	PEE	C15-C16-C17-C18
33	j	203	PLX	C33-C34-C35-C36
31	a	201	CDL	C71-C72-C73-C74
30	W	201	PEE	C21-C22-C23-C24
33	e	201	PLX	C30-C31-C32-C33
31	V	201	CDL	C15-C16-C17-C18
31	s	401	CDL	C12-C13-C14-C15
31	r	503	CDL	C37-C38-C39-C40
33	j	204	PLX	C27-C28-C29-C30
33	j	204	PLX	C30-C31-C32-C33
31	V	201	CDL	C53-C54-C55-C56
31	n	101	CDL	C51-C52-C53-C54
30	l	705	PEE	C13-C14-C15-C16
33	g	201	PLX	C18-C19-C20-C21
33	j	204	PLX	C31-C32-C33-C34
30	U	401	PEE	C35-C36-C37-C38
30	W	201	PEE	C15-C16-C17-C18
31	V	201	CDL	C14-C15-C16-C17
33	e	201	PLX	C9-C10-C11-C12
30	l	701	PEE	C33-C34-C35-C36
33	r	502	PLX	C16-C17-C18-C19
31	V	202	CDL	CB5-C51-C52-C53
31	V	201	CDL	C73-C74-C75-C76
33	e	201	PLX	C32-C33-C34-C35
33	r	502	PLX	C10-C11-C12-C13
31	V	202	CDL	CB2-C1-CA2-OA2
30	Q	101	PEE	O3P-C1-C2-O2
30	U	401	PEE	O3P-C1-C2-O2
31	m	201	CDL	OA5-CA3-CA4-OA6
31	V	201	CDL	C32-C33-C34-C35
33	e	201	PLX	C18-C19-C20-C21
31	V	202	CDL	C38-C39-C40-C41
33	g	201	PLX	C13-C14-C15-C16
31	l	703	CDL	C59-C60-C61-C62
31	s	401	CDL	C71-C72-C73-C74
31	m	201	CDL	C24-C25-C26-C27
31	V	202	CDL	C74-C75-C76-C77
33	j	203	PLX	O6-C4-C5-O8
33	r	502	PLX	O6-C4-C5-O8
31	m	201	CDL	C59-C60-C61-C62
33	g	201	PLX	C2-C1-N1-C1B

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Mol	Chain	Res	Type	Atoms
30	j	201	PEE	C32-C33-C34-C35
31	m	201	CDL	C81-C82-C83-C84
30	j	201	PEE	C36-C37-C38-C39
30	r	501	PEE	C36-C37-C38-C39
31	l	702	CDL	OA7-CA5-OA6-CA4
31	r	503	CDL	C17-C18-C19-C20
31	a	201	CDL	C84-C85-C86-C87
31	m	201	CDL	C44-C45-C46-C47
32	X	201	8Q1	C30-C29-C32-O33
32	X	201	8Q1	C31-C29-C32-O33
31	r	503	CDL	C15-C16-C17-C18
31	n	101	CDL	C71-CB7-OB8-CB6
31	a	201	CDL	C52-C53-C54-C55
33	g	201	PLX	C16-C17-C18-C19
31	r	503	CDL	C59-C60-C61-C62
31	m	201	CDL	CA4-CA3-OA5-PA1
31	r	503	CDL	C1-CB2-OB2-PB2
30	l	704	PEE	C32-C33-C34-C35
31	a	201	CDL	C31-C32-C33-C34
31	l	702	CDL	C55-C56-C57-C58
30	l	704	PEE	O3P-C1-C2-C3
31	a	201	CDL	OA5-CA3-CA4-CA6
31	l	703	CDL	OB5-CB3-CB4-CB6
31	r	503	CDL	OB5-CB3-CB4-CB6
33	e	201	PLX	C31-C32-C33-C34
30	r	501	PEE	C24-C25-C26-C27
31	l	703	CDL	C44-C45-C46-C47
31	n	101	CDL	C75-C76-C77-C78
31	V	202	CDL	C60-C61-C62-C63
33	r	502	PLX	C30-C31-C32-C33
30	U	401	PEE	C38-C39-C40-C41
30	j	201	PEE	C38-C39-C40-C41
31	l	702	CDL	C53-C54-C55-C56
30	r	501	PEE	C40-C41-C42-C43
31	r	503	CDL	C36-C37-C38-C39
31	V	201	CDL	C40-C41-C42-C43
31	s	401	CDL	C33-C34-C35-C36
33	e	201	PLX	C35-C36-C37-C38
30	r	501	PEE	C1-C2-C3-O3
31	m	201	CDL	CA3-CA4-CA6-OA8
31	s	401	CDL	CB3-CB4-CB6-OB8
33	e	201	PLX	C3-C4-C5-O8

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Mol	Chain	Res	Type	Atoms
33	j	204	PLX	C3-C4-C5-O8
30	j	201	PEE	C23-C24-C25-C26
31	a	201	CDL	C42-C43-C44-C45
30	Q	101	PEE	C24-C25-C26-C27
31	m	201	CDL	C12-C13-C14-C15
33	g	201	PLX	C12-C13-C14-C15
31	a	201	CDL	C61-C62-C63-C64
31	a	201	CDL	C15-C16-C17-C18
31	s	401	CDL	C74-C75-C76-C77
31	a	201	CDL	OB5-CB3-CB4-OB6
31	l	703	CDL	OB5-CB3-CB4-OB6
31	s	401	CDL	C80-C81-C82-C83
30	W	201	PEE	C11-C10-O2-C2
31	r	503	CDL	C82-C83-C84-C85
31	a	201	CDL	C44-C45-C46-C47
31	V	201	CDL	C54-C55-C56-C57
30	W	201	PEE	O2-C2-C3-O3
30	l	701	PEE	O2-C2-C3-O3
33	j	204	PLX	O6-C4-C5-O8
31	r	503	CDL	C12-C13-C14-C15
30	W	201	PEE	C13-C14-C15-C16
31	s	401	CDL	C11-C12-C13-C14
31	l	702	CDL	C33-C34-C35-C36
31	a	201	CDL	C14-C15-C16-C17
31	l	702	CDL	CB5-C51-C52-C53
31	r	503	CDL	CA5-C11-C12-C13
33	g	201	PLX	C2-C1-N1-C1C
30	j	201	PEE	C11-C12-C13-C14
33	r	502	PLX	C25-C26-C27-C28
30	r	501	PEE	C38-C39-C40-C41
30	j	201	PEE	C44-C45-C46-C47
31	V	202	CDL	C78-C79-C80-C81
31	a	201	CDL	CB5-C51-C52-C53
31	V	201	CDL	C64-C65-C66-C67
31	m	201	CDL	C42-C43-C44-C45
30	Q	101	PEE	O3P-C1-C2-C3
30	U	401	PEE	O3P-C1-C2-C3
30	l	701	PEE	O3P-C1-C2-C3
30	r	501	PEE	O3P-C1-C2-C3
31	a	201	CDL	OB5-CB3-CB4-CB6
31	l	703	CDL	OA5-CA3-CA4-CA6
30	U	401	PEE	C36-C37-C38-C39

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Mol	Chain	Res	Type	Atoms
31	a	201	CDL	C54-C55-C56-C57
31	m	201	CDL	C35-C36-C37-C38
30	l	704	PEE	C13-C14-C15-C16
35	w	401	ADP	PA-O3A-PB-O1B
31	l	703	CDL	C40-C41-C42-C43
31	n	101	CDL	OB9-CB7-OB8-CB6
33	e	201	PLX	C16-C17-C18-C19
33	e	201	PLX	C33-C34-C35-C36
31	V	201	CDL	CA6-CA4-OA6-CA5
31	m	201	CDL	CA3-CA4-OA6-CA5
30	l	704	PEE	C19-C20-C21-C22
33	j	203	PLX	C11-C10-C9-C8
30	W	201	PEE	O4-C10-O2-C2
30	l	705	PEE	O3P-C1-C2-O2
30	r	501	PEE	O3P-C1-C2-O2
31	V	201	CDL	OA5-CA3-CA4-OA6
31	V	202	CDL	OA5-CA3-CA4-OA6
31	a	201	CDL	OA5-CA3-CA4-OA6
31	l	703	CDL	OA5-CA3-CA4-OA6
31	r	503	CDL	OB5-CB3-CB4-OB6
33	j	204	PLX	O4-C3-C4-O6
31	a	201	CDL	C40-C41-C42-C43
31	V	202	CDL	CA3-CA4-CA6-OA8
33	a	202	PLX	C3-C4-C5-O8
33	r	502	PLX	C3-C4-C5-O8
31	a	201	CDL	C37-C38-C39-C40
32	X	201	8Q1	C30-C29-C32-C34
33	j	203	PLX	C1-C2-O1-P1
33	a	202	PLX	C35-C36-C37-C38
30	l	705	PEE	O2-C2-C3-O3
30	r	501	PEE	O2-C2-C3-O3
31	V	201	CDL	OA6-CA4-CA6-OA8
31	l	702	CDL	C38-C39-C40-C41
31	m	201	CDL	C31-C32-C33-C34
31	l	702	CDL	C17-C18-C19-C20
33	j	204	PLX	C7-C6-O6-C4
33	a	202	PLX	C32-C33-C34-C35
30	l	705	PEE	C11-C10-O2-C2
33	r	502	PLX	C11-C12-C13-C14
31	V	202	CDL	C54-C55-C56-C57
33	j	203	PLX	N1-C1-C2-O1
31	m	201	CDL	C14-C15-C16-C17

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Mol	Chain	Res	Type	Atoms
30	j	201	PEE	C42-C43-C44-C45
31	a	201	CDL	C11-C12-C13-C14
31	V	202	CDL	C62-C63-C64-C65
31	m	201	CDL	C41-C42-C43-C44
31	V	202	CDL	C39-C40-C41-C42
31	a	201	CDL	C73-C74-C75-C76
32	X	201	8Q1	O33-C32-C34-O35
33	a	202	PLX	C25-C24-O8-C5
33	g	201	PLX	C25-C24-O8-C5
33	j	203	PLX	C25-C24-O8-C5
31	l	702	CDL	C31-C32-C33-C34
31	V	201	CDL	C32-C31-CA7-OA8
31	V	201	CDL	C71-C72-C73-C74
31	l	703	CDL	C62-C63-C64-C65
31	m	201	CDL	C22-C23-C24-C25
30	l	705	PEE	O3P-C1-C2-C3
31	V	201	CDL	OA5-CA3-CA4-CA6
31	V	202	CDL	OA5-CA3-CA4-CA6
31	V	202	CDL	OB5-CB3-CB4-CB6
33	e	201	PLX	O4-C3-C4-C5
33	j	204	PLX	O4-C3-C4-C5
30	W	201	PEE	C23-C24-C25-C26
30	l	705	PEE	O4-C10-O2-C2
32	X	201	8Q1	O27-C28-C29-C31
31	V	201	CDL	C43-C44-C45-C46
31	l	703	CDL	C36-C37-C38-C39
31	r	503	CDL	C39-C40-C41-C42
31	s	401	CDL	C17-C18-C19-C20
33	a	202	PLX	C11-C10-C9-C8
31	V	202	CDL	C64-C65-C66-C67
30	l	701	PEE	O3P-C1-C2-O2
33	e	201	PLX	O4-C3-C4-O6
33	j	203	PLX	O4-C3-C4-O6
31	l	703	CDL	C15-C16-C17-C18
33	g	201	PLX	C33-C34-C35-C36
31	l	702	CDL	C51-CB5-OB6-CB4
31	m	201	CDL	C51-CB5-OB6-CB4
30	U	401	PEE	C13-C14-C15-C16
31	l	703	CDL	C43-C44-C45-C46
31	m	201	CDL	C20-C21-C22-C23
31	a	201	CDL	C51-C52-C53-C54
33	e	201	PLX	O6-C4-C5-O8

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Mol	Chain	Res	Type	Atoms
33	j	203	PLX	C3-C4-C5-O8
31	s	401	CDL	C77-C78-C79-C80
32	X	201	8Q1	O27-C28-C29-C32
33	a	202	PLX	C14-C15-C16-C17
30	U	401	PEE	C4-O4P-P-O1P
30	W	201	PEE	C4-O4P-P-O3P
30	W	201	PEE	C4-O4P-P-O1P
30	j	201	PEE	C1-O3P-P-O2P
30	j	201	PEE	C4-O4P-P-O2P
30	l	701	PEE	C1-O3P-P-O2P
30	l	704	PEE	C4-O4P-P-O2P
30	l	705	PEE	C1-O3P-P-O4P
31	V	201	CDL	CB3-OB5-PB2-OB3
31	V	202	CDL	CB2-OB2-PB2-OB4
31	a	201	CDL	CA2-OA2-PA1-OA3
31	l	702	CDL	CA2-OA2-PA1-OA3
31	l	702	CDL	CB3-OB5-PB2-OB4
31	l	703	CDL	CA3-OA5-PA1-OA3
31	l	703	CDL	CB3-OB5-PB2-OB2
31	n	101	CDL	CB3-OB5-PB2-OB3
31	r	503	CDL	CA2-OA2-PA1-OA4
31	r	503	CDL	CB2-OB2-PB2-OB3
31	r	503	CDL	CB2-OB2-PB2-OB4
31	r	503	CDL	CB2-OB2-PB2-OB5
31	r	503	CDL	CB3-OB5-PB2-OB2
31	r	503	CDL	CB3-OB5-PB2-OB4
32	X	201	8Q1	C28-C29-C32-O33
33	a	202	PLX	C3-O4-P1-O1
33	e	201	PLX	C3-C4-O6-C6
33	e	201	PLX	C5-C4-O6-C6
33	g	201	PLX	C3-O4-P1-O1
33	g	201	PLX	C3-O4-P1-O3
33	j	204	PLX	C3-O4-P1-O2
33	j	204	PLX	C2-O1-P1-O3
33	r	502	PLX	C3-C4-O6-C6
33	r	502	PLX	C5-C4-O6-C6
31	n	101	CDL	C72-C71-CB7-OB8
30	Q	101	PEE	C16-C17-C18-C19
30	l	705	PEE	C18-C19-C20-C21
30	W	201	PEE	C22-C23-C24-C25
31	l	702	CDL	OB7-CB5-OB6-CB4
31	m	201	CDL	OB7-CB5-OB6-CB4

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Mol	Chain	Res	Type	Atoms
31	r	503	CDL	C74-C75-C76-C77
33	j	203	PLX	C10-C11-C12-C13
30	r	501	PEE	C18-C19-C20-C21
31	m	201	CDL	C75-C76-C77-C78
30	l	704	PEE	C3-C2-O2-C10
30	l	705	PEE	C32-C33-C34-C35
30	U	401	PEE	C44-C45-C46-C47
31	m	201	CDL	OA5-CA3-CA4-CA6
30	Q	101	PEE	C32-C33-C34-C35
33	a	202	PLX	C26-C27-C28-C29
32	X	201	8Q1	C12-C13-C14-C15
30	j	201	PEE	C30-C31-C32-C33
31	s	401	CDL	C72-C71-CB7-OB8
34	s	402	UQ	C23-C24-C26-C27
30	U	401	PEE	C42-C43-C44-C45
33	a	202	PLX	O6-C4-C5-O8
31	s	401	CDL	C12-C11-CA5-OA6
30	l	701	PEE	C18-C19-C20-C21
31	r	503	CDL	C76-C77-C78-C79
30	r	501	PEE	C13-C14-C15-C16
31	V	202	CDL	C22-C23-C24-C25
30	l	705	PEE	C34-C35-C36-C37
30	l	705	PEE	C15-C16-C17-C18
30	l	704	PEE	C40-C41-C42-C43
31	s	401	CDL	C37-C38-C39-C40
31	l	703	CDL	C53-C54-C55-C56
30	l	705	PEE	C38-C39-C40-C41
31	n	101	CDL	C74-C75-C76-C77
31	a	201	CDL	C33-C34-C35-C36
31	l	702	CDL	C54-C55-C56-C57
34	s	402	UQ	C12-C11-C9-C10
33	a	202	PLX	O9-C24-C25-C26
33	g	201	PLX	O7-C6-C7-C8
30	l	704	PEE	C36-C37-C38-C39
30	j	201	PEE	C34-C35-C36-C37
31	V	202	CDL	C31-C32-C33-C34
31	V	202	CDL	C32-C31-CA7-OA8
30	Q	101	PEE	C11-C12-C13-C14
30	r	501	PEE	C16-C17-C18-C19
33	j	203	PLX	C14-C15-C16-C17
30	W	201	PEE	C20-C21-C22-C23
33	g	201	PLX	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
30	l	704	PEE	C41-C42-C43-C44
31	s	401	CDL	C15-C16-C17-C18
30	l	705	PEE	C16-C17-C18-C19
30	U	401	PEE	C12-C13-C14-C15
31	r	503	CDL	C42-C43-C44-C45
31	l	703	CDL	C72-C73-C74-C75
31	a	201	CDL	C16-C17-C18-C19
31	n	101	CDL	C1-CB2-OB2-PB2
31	r	503	CDL	C21-C22-C23-C24
31	l	703	CDL	C82-C83-C84-C85
31	V	201	CDL	C31-C32-C33-C34
30	l	704	PEE	C38-C39-C40-C41
30	Q	101	PEE	C22-C23-C24-C25
30	r	501	PEE	C21-C22-C23-C24
31	s	401	CDL	C56-C57-C58-C59
33	j	204	PLX	C17-C18-C19-C20
31	l	702	CDL	C84-C85-C86-C87
31	V	201	CDL	OB5-CB3-CB4-OB6
31	l	702	CDL	OB5-CB3-CB4-OB6
31	a	201	CDL	C31-CA7-OA8-CA6
31	r	503	CDL	C13-C14-C15-C16
31	V	201	CDL	CA4-CA3-OA5-PA1
30	j	201	PEE	C37-C38-C39-C40
33	j	204	PLX	C9-C10-C11-C12
31	r	503	CDL	C61-C62-C63-C64
31	l	703	CDL	C34-C35-C36-C37
31	r	503	CDL	OA6-CA4-CA6-OA8
34	s	402	UQ	C22-C23-C24-C25
31	l	703	CDL	OB7-CB5-OB6-CB4
30	l	704	PEE	C34-C35-C36-C37
31	s	401	CDL	C32-C33-C34-C35
30	Q	101	PEE	C18-C19-C20-C21
33	a	202	PLX	O6-C6-C7-C8
33	e	201	PLX	O8-C24-C25-C26
32	X	201	8Q1	C9-C10-C11-C12
33	e	201	PLX	C24-C25-C26-C27
31	V	202	CDL	C24-C25-C26-C27
31	s	401	CDL	CA5-C11-C12-C13
31	a	201	CDL	OA9-CA7-OA8-CA6
30	l	701	PEE	C16-C17-C18-C19
31	l	702	CDL	CB4-CB3-OB5-PB2
31	V	202	CDL	C81-C82-C83-C84

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Mol	Chain	Res	Type	Atoms
30	j	201	PEE	C40-C41-C42-C43
31	l	703	CDL	C14-C15-C16-C17
30	l	701	PEE	C1-C2-C3-O3
31	V	201	CDL	C57-C58-C59-C60
31	r	503	CDL	C20-C21-C22-C23
31	V	202	CDL	OB5-CB3-CB4-OB6
30	U	401	PEE	C18-C19-C20-C21
31	m	201	CDL	C52-C51-CB5-OB6
33	a	202	PLX	C12-C13-C14-C15
31	s	401	CDL	C19-C20-C21-C22
33	g	201	PLX	C31-C32-C33-C34
31	a	201	CDL	CA7-C31-C32-C33
31	a	201	CDL	C76-C77-C78-C79
31	s	401	CDL	C18-C19-C20-C21
31	V	202	CDL	C13-C14-C15-C16
31	s	401	CDL	C40-C41-C42-C43
33	j	204	PLX	C26-C27-C28-C29
30	l	704	PEE	C33-C34-C35-C36
31	V	201	CDL	C72-C73-C74-C75
33	e	201	PLX	C12-C13-C14-C15
30	W	201	PEE	C16-C17-C18-C19
31	a	201	CDL	C64-C65-C66-C67
30	l	705	PEE	C21-C22-C23-C24
30	r	501	PEE	C14-C15-C16-C17
35	w	401	ADP	PA-O3A-PB-O2B
35	w	401	ADP	PA-O3A-PB-O3B
31	V	202	CDL	C71-C72-C73-C74
31	s	401	CDL	C84-C85-C86-C87
31	a	201	CDL	C58-C59-C60-C61
30	l	701	PEE	C38-C39-C40-C41
33	g	201	PLX	O4-C3-C4-O6
30	W	201	PEE	C34-C35-C36-C37
30	l	705	PEE	C23-C24-C25-C26
30	Q	101	PEE	C36-C37-C38-C39
30	Q	101	PEE	C38-C39-C40-C41
31	l	703	CDL	C57-C58-C59-C60
31	V	202	CDL	C58-C59-C60-C61
31	m	201	CDL	C18-C19-C20-C21
30	U	401	PEE	C16-C17-C18-C19
33	a	202	PLX	C6-C7-C8-C9
31	l	702	CDL	C72-C71-CB7-OB8
31	l	703	CDL	C51-CB5-OB6-CB4

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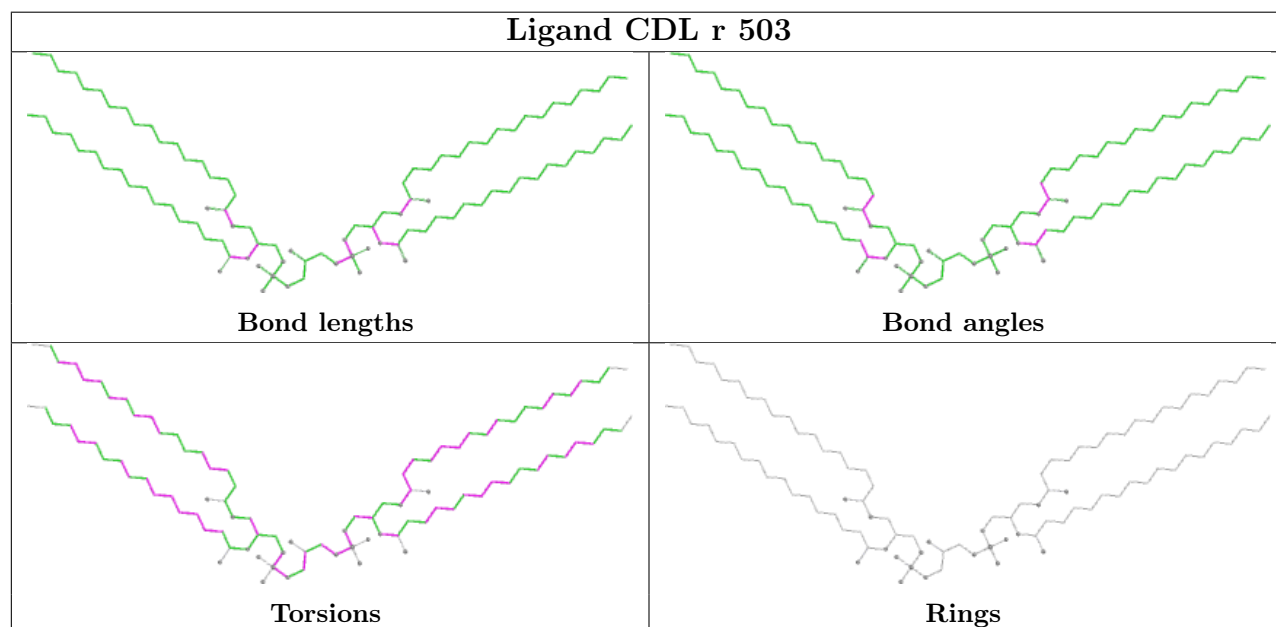
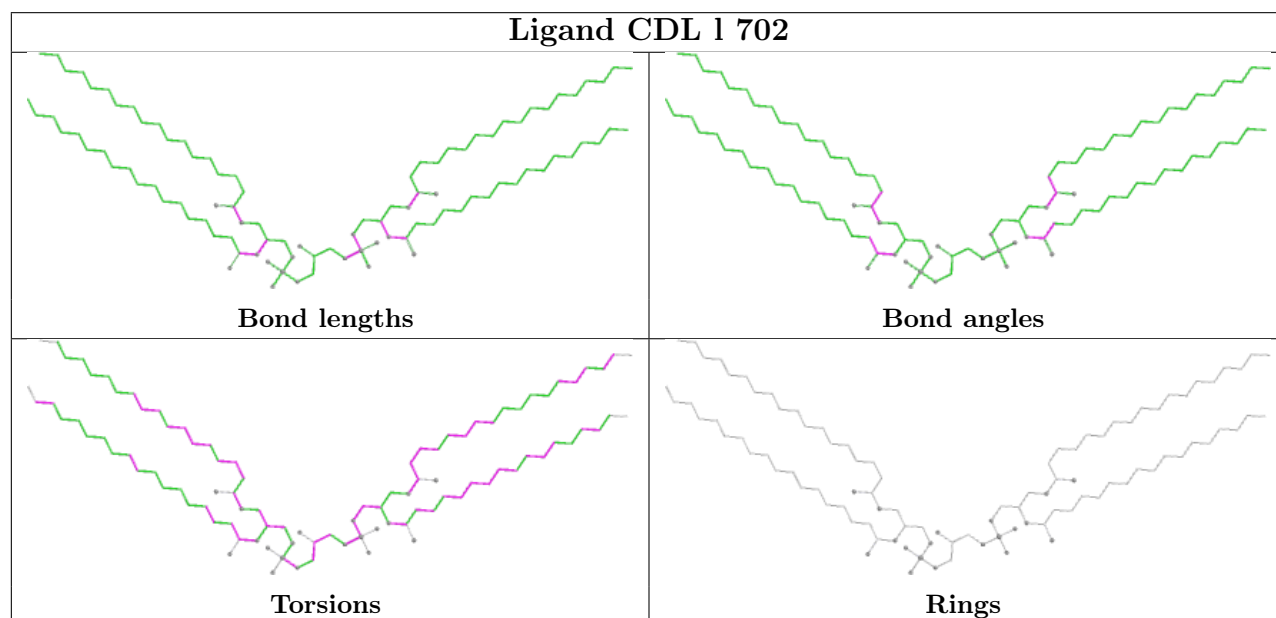
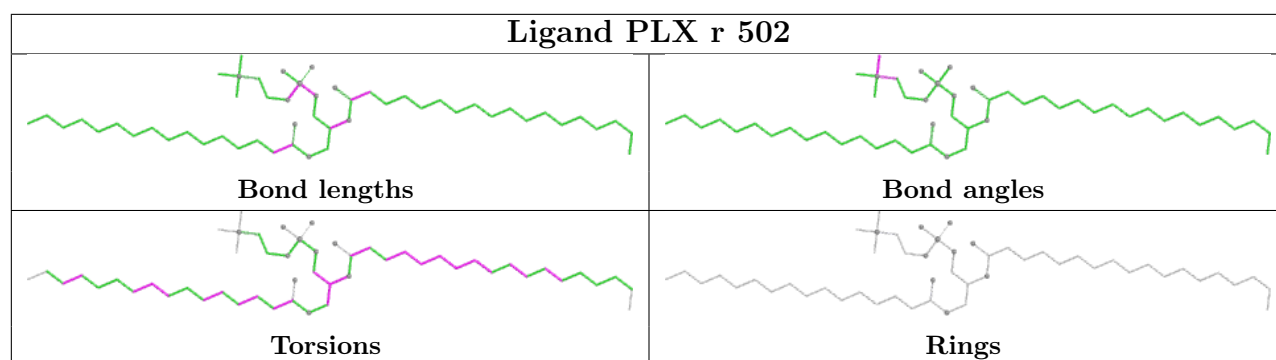
Mol	Chain	Res	Type	Atoms
30	l	704	PEE	C18-C19-C20-C21
31	r	503	CDL	C56-C57-C58-C59
31	V	202	CDL	C34-C35-C36-C37
30	l	704	PEE	C22-C23-C24-C25
31	V	202	CDL	C76-C77-C78-C79
31	a	201	CDL	C12-C11-CA5-OA6
30	j	201	PEE	O3-C30-C31-C32
31	r	503	CDL	C72-C73-C74-C75
33	j	204	PLX	C25-C24-O8-C5
30	r	501	PEE	C44-C45-C46-C47
31	m	201	CDL	C72-C71-CB7-OB8
33	r	502	PLX	C35-C36-C37-C38
31	s	401	CDL	C35-C36-C37-C38
31	r	503	CDL	C72-C71-CB7-OB8
31	r	503	CDL	C54-C55-C56-C57
31	a	201	CDL	C32-C31-CA7-OA8
32	X	201	8Q1	O27-C28-C29-C30
33	e	201	PLX	C2-C1-N1-C1B
31	V	202	CDL	C77-C78-C79-C80
31	l	702	CDL	C72-C71-CB7-OB9
33	r	502	PLX	O4-C3-C4-O6
32	X	201	8Q1	C11-C10-C9-C8
33	e	201	PLX	C2-C1-N1-C1C
31	a	201	CDL	C12-C11-CA5-OA7
33	j	203	PLX	O9-C24-O8-C5
31	m	201	CDL	C72-C71-CB7-OB9
33	g	201	PLX	C4-C5-O8-C24
31	a	201	CDL	C36-C37-C38-C39
30	l	705	PEE	C10-C11-C12-C13
31	l	702	CDL	C12-C11-CA5-OA6
33	e	201	PLX	C2-C1-N1-C1A
30	j	201	PEE	O5-C30-C31-C32
31	r	503	CDL	C72-C71-CB7-OB9
31	s	401	CDL	C31-C32-C33-C34
31	V	202	CDL	C52-C51-CB5-OB6
31	m	201	CDL	O1-C1-CB2-OB2
31	a	201	CDL	C32-C31-CA7-OA9
30	l	701	PEE	O3-C30-C31-C32

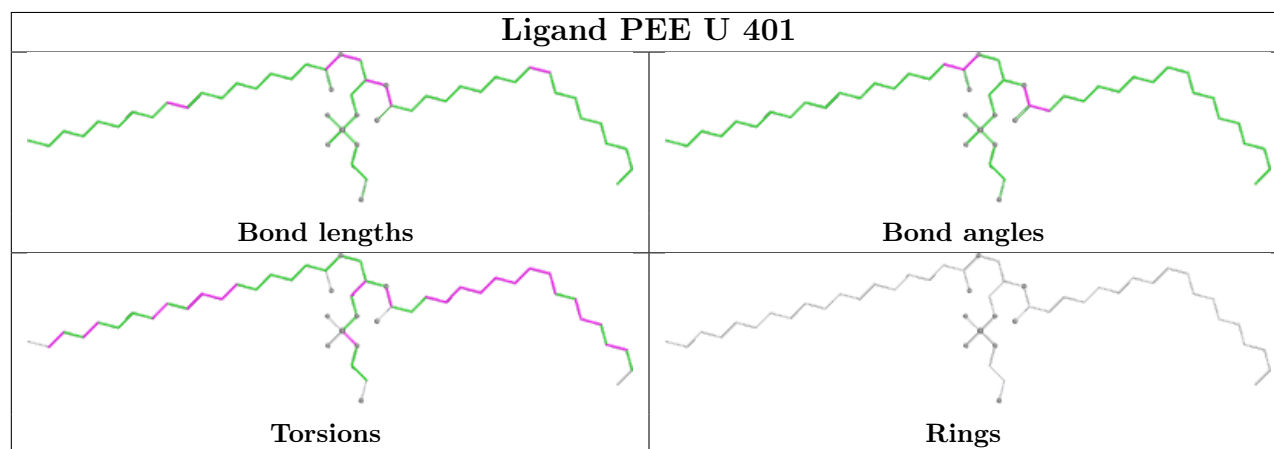
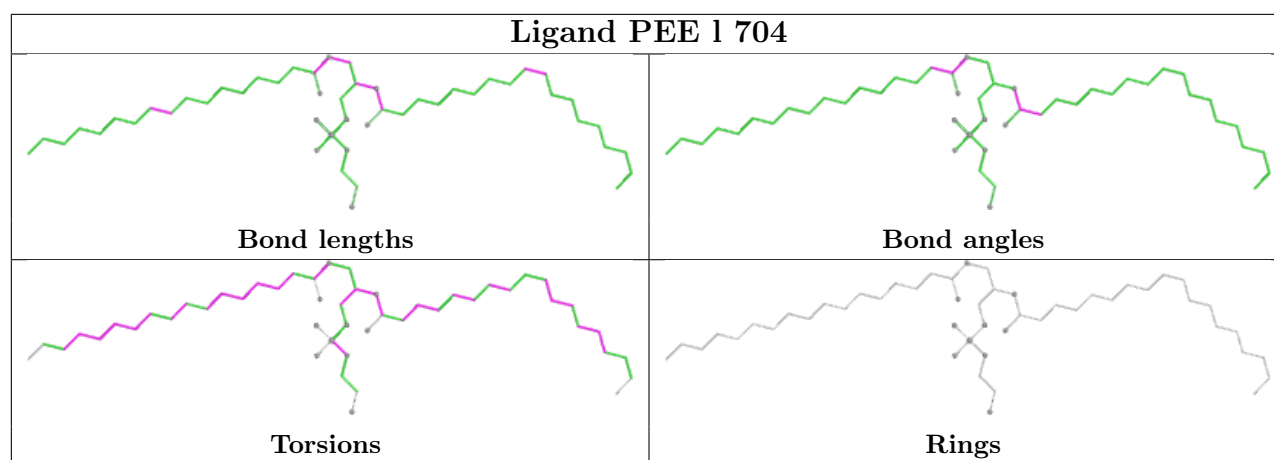
There are no ring outliers.

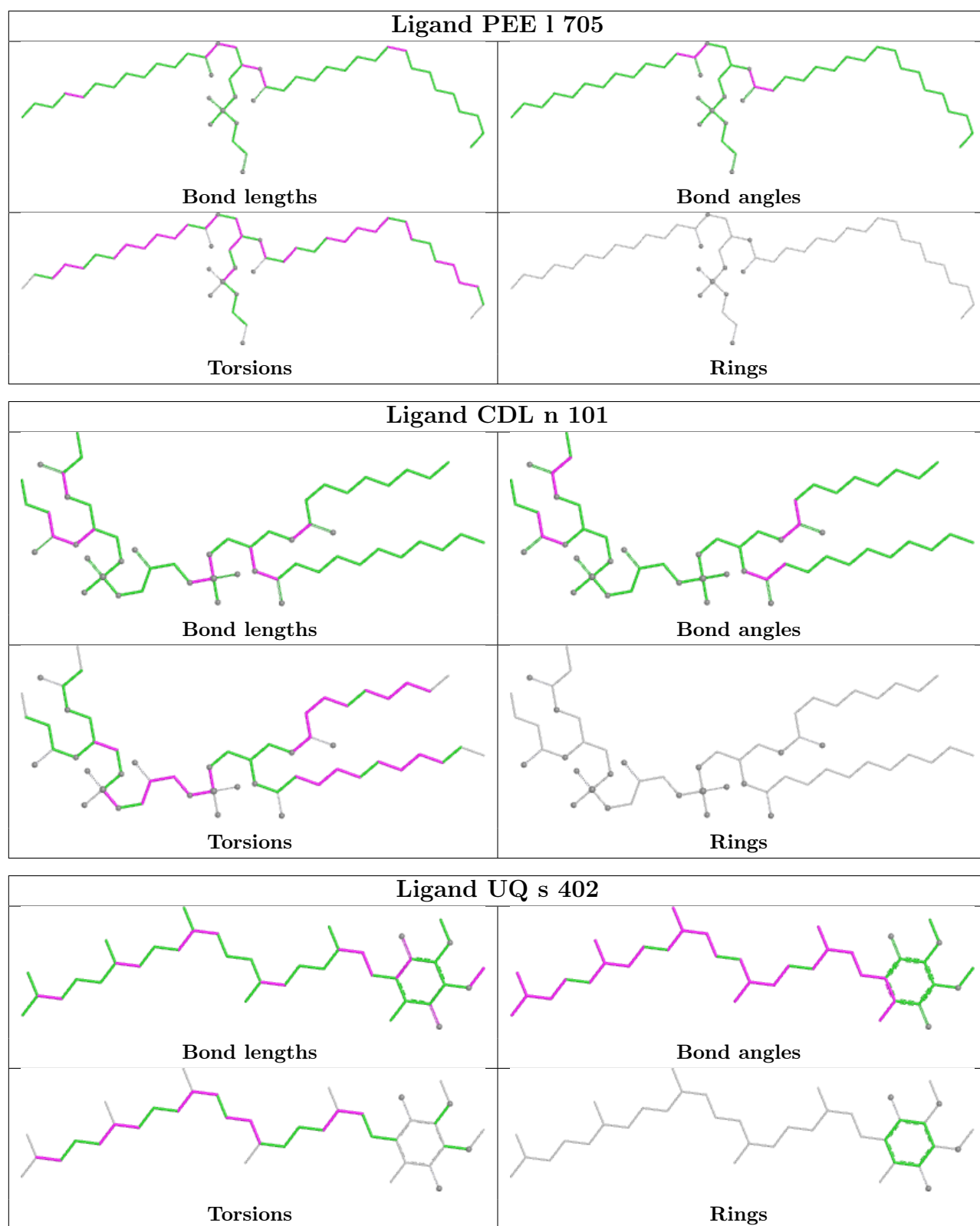
25 monomers are involved in 133 short contacts:

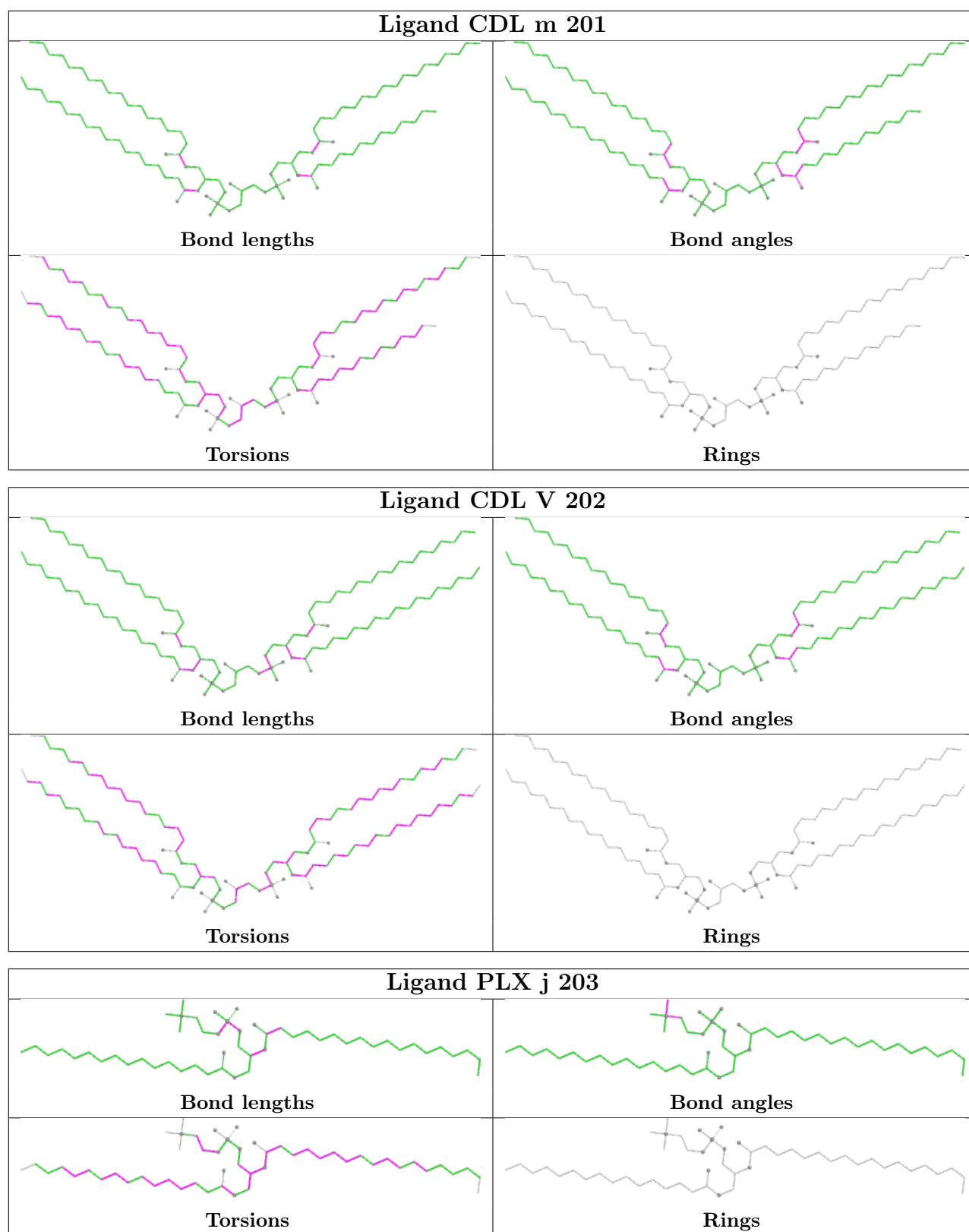
Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	r	502	PLX	4	0
31	l	702	CDL	11	0
31	r	503	CDL	7	0
30	l	704	PEE	5	0
30	U	401	PEE	2	0
33	e	201	PLX	5	0
33	j	204	PLX	2	0
30	l	705	PEE	5	0
31	n	101	CDL	1	0
34	s	402	UQ	3	0
31	m	201	CDL	34	0
31	V	202	CDL	7	0
33	j	203	PLX	3	0
31	V	201	CDL	8	0
30	Q	101	PEE	7	0
30	r	501	PEE	5	0
33	a	202	PLX	2	0
30	l	701	PEE	1	0
33	g	201	PLX	7	0
30	j	201	PEE	3	0
35	w	401	ADP	1	0
31	s	401	CDL	7	0
30	W	201	PEE	1	0
31	a	201	CDL	3	0
31	l	703	CDL	5	0

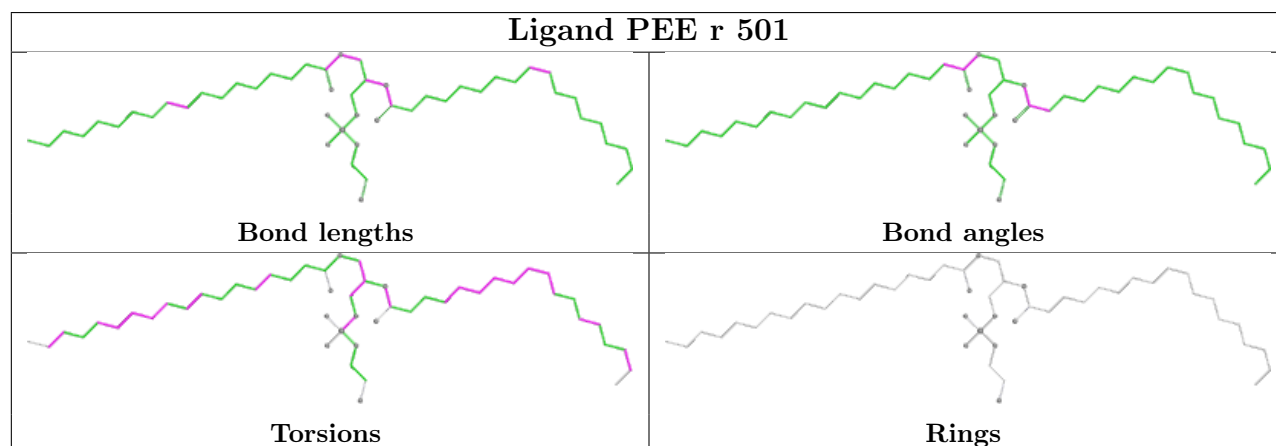
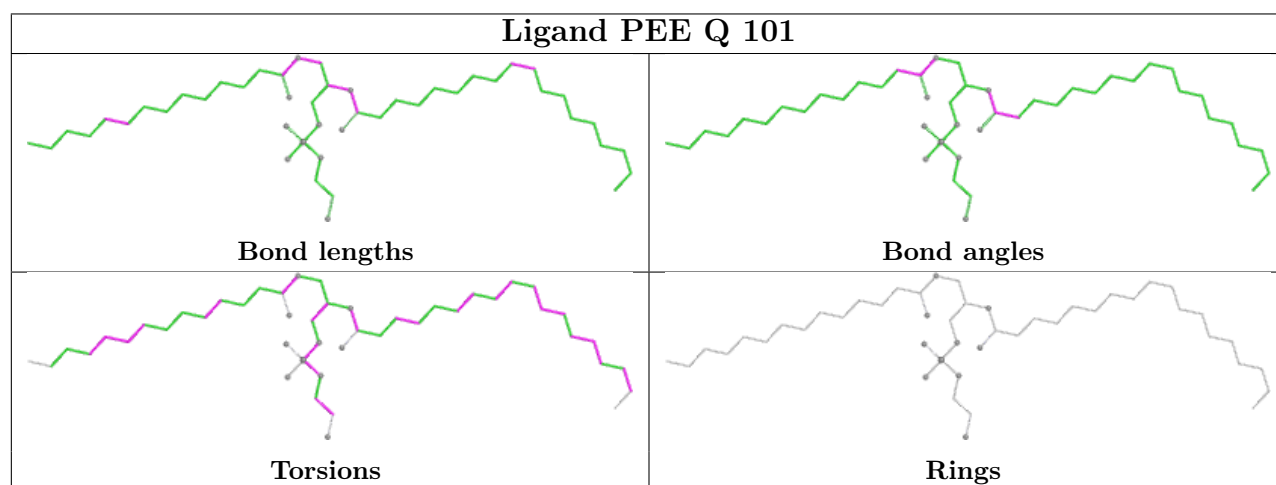
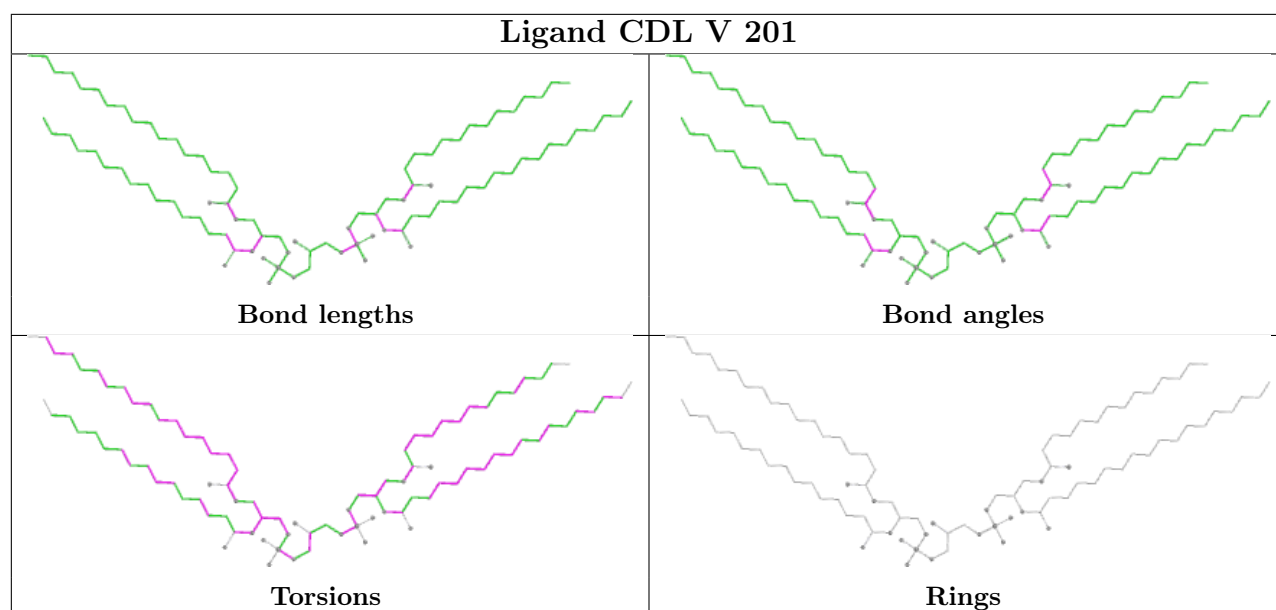
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

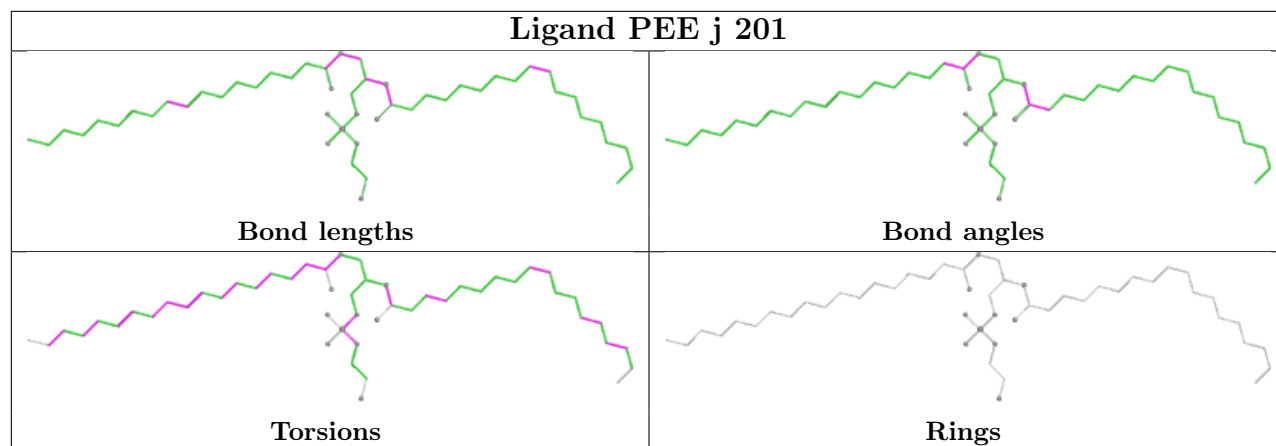
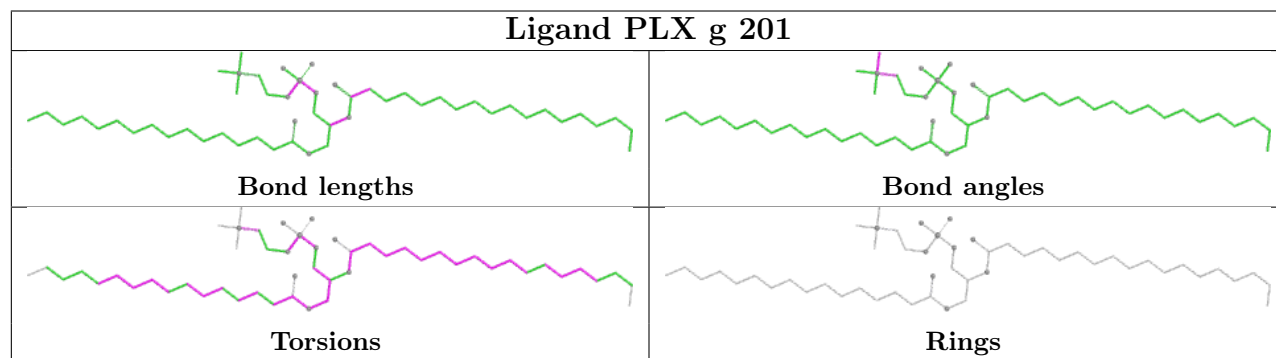
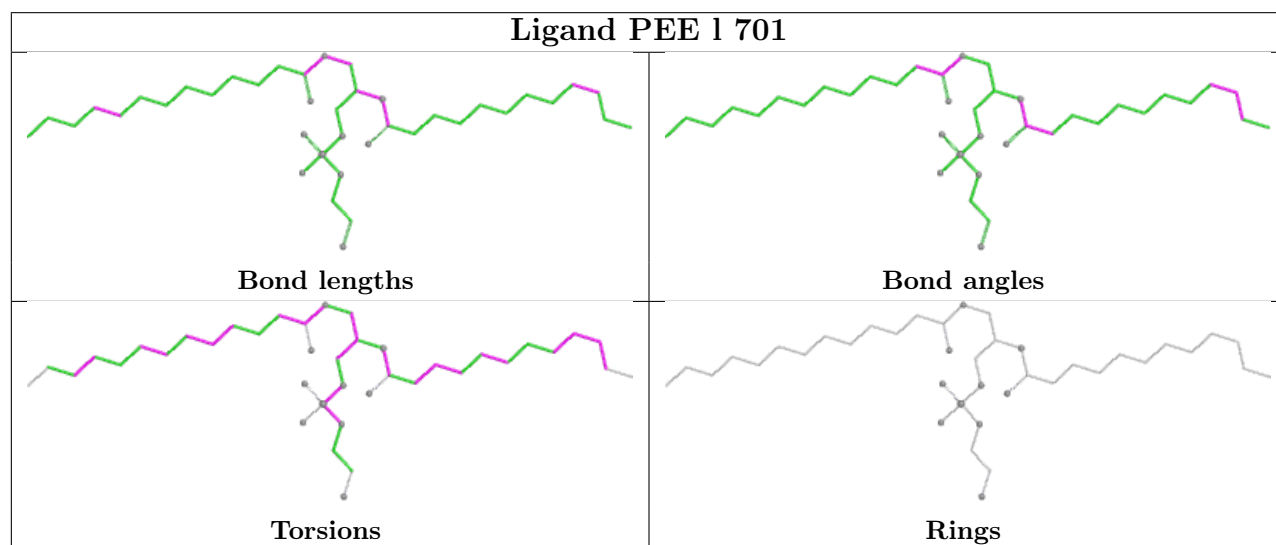
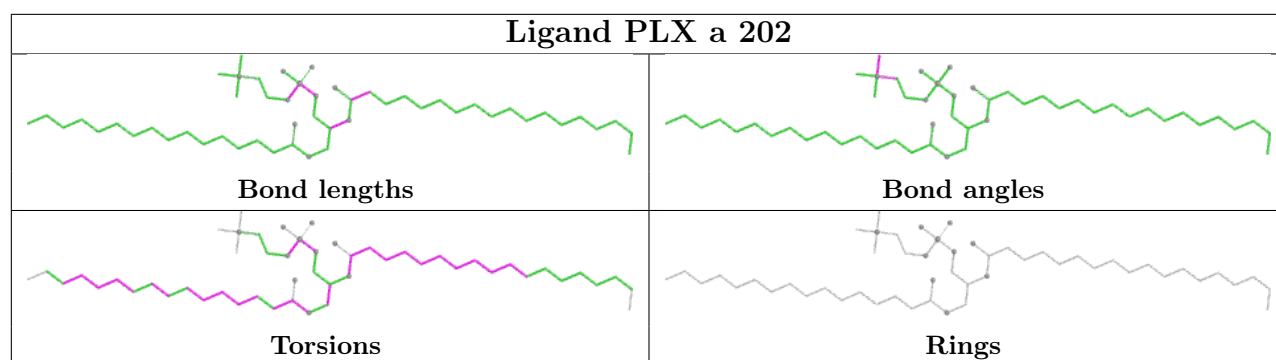


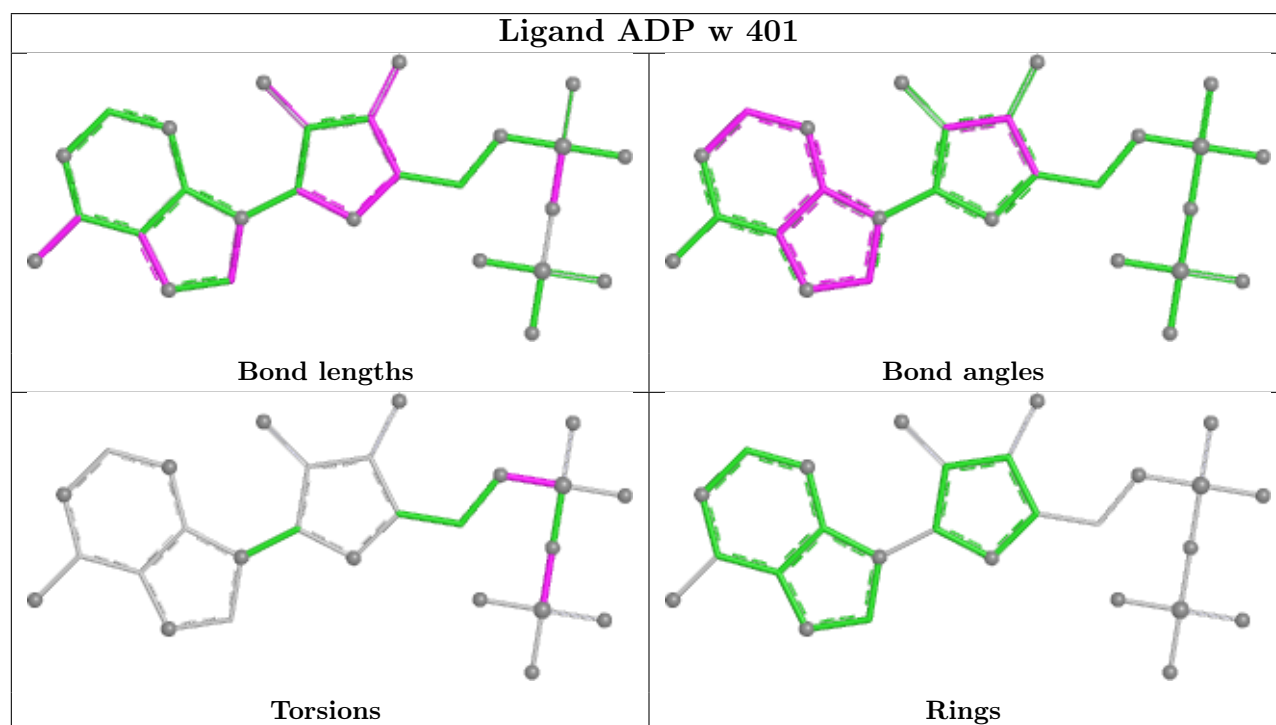
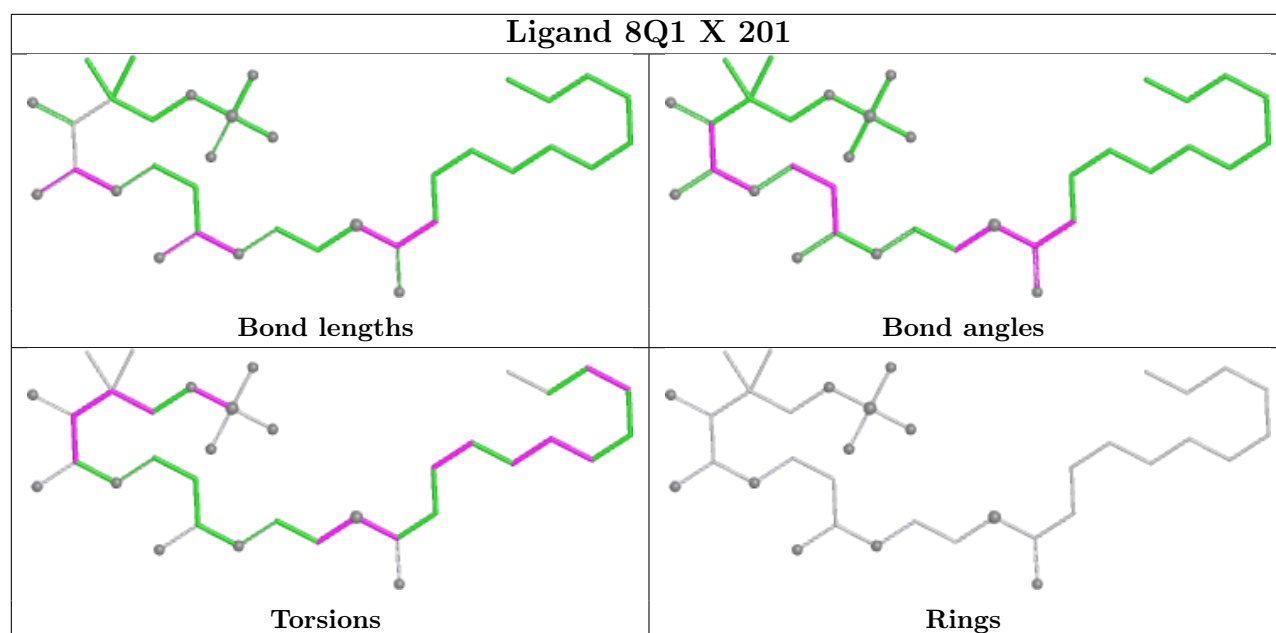


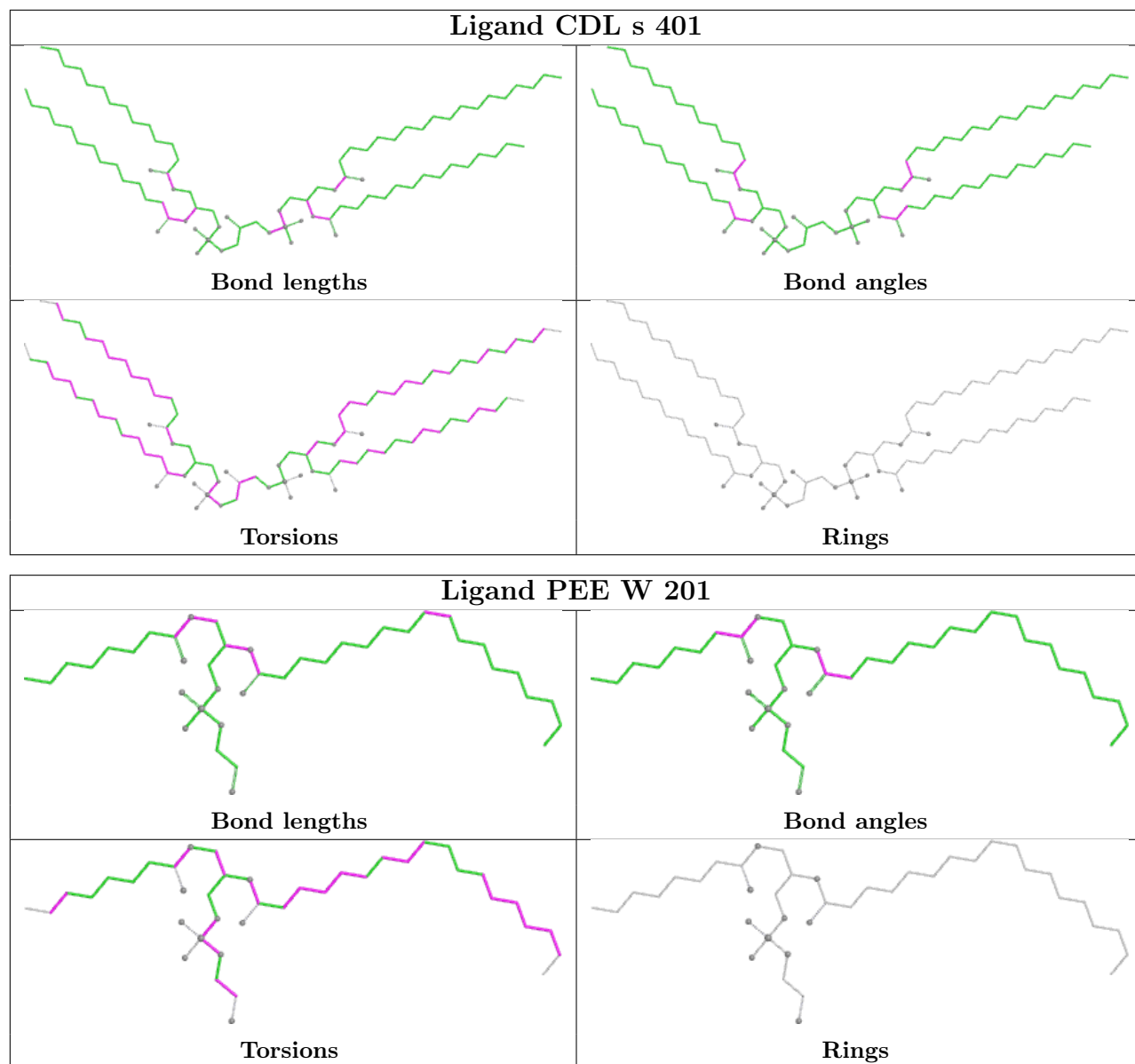


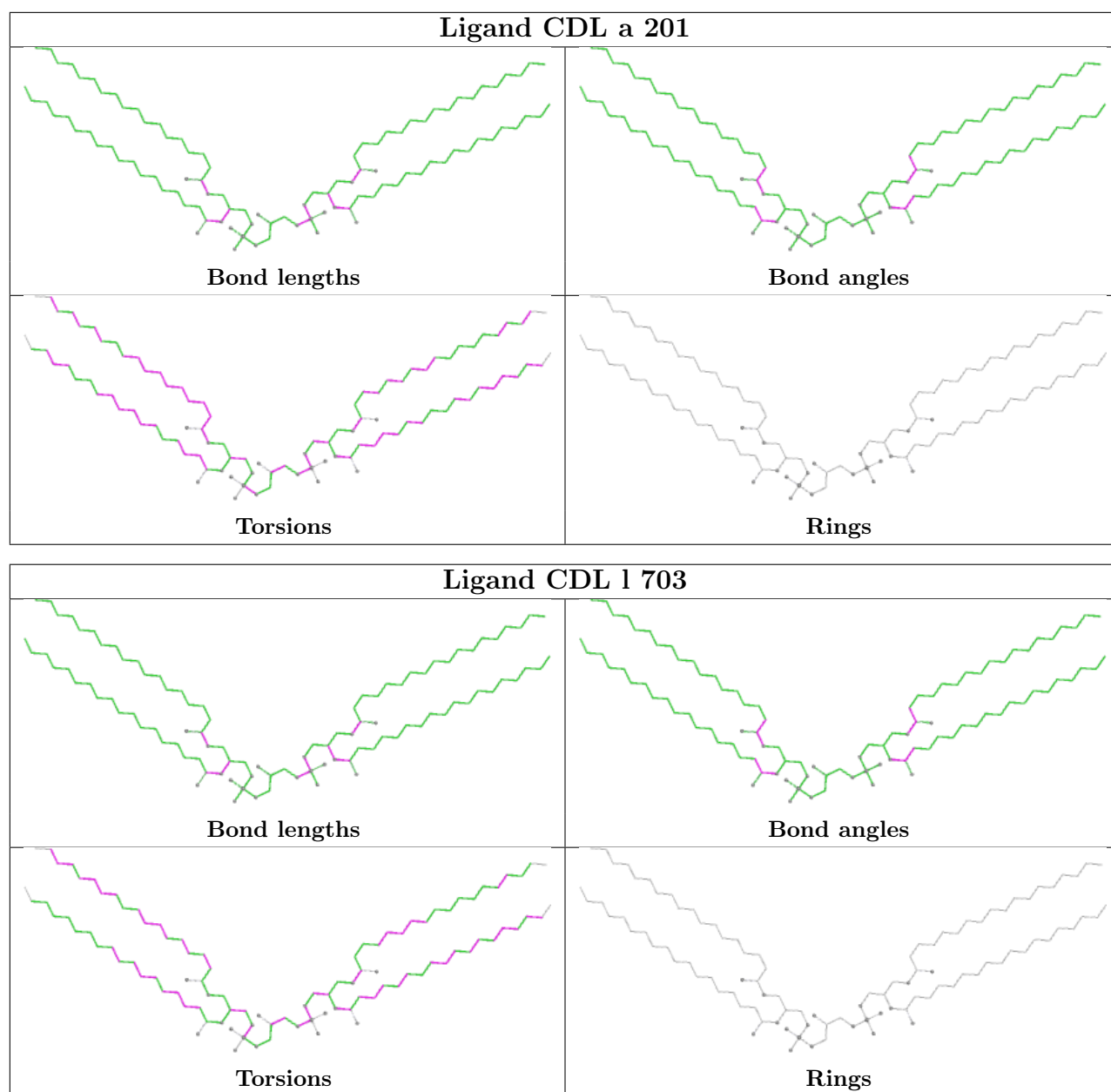












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

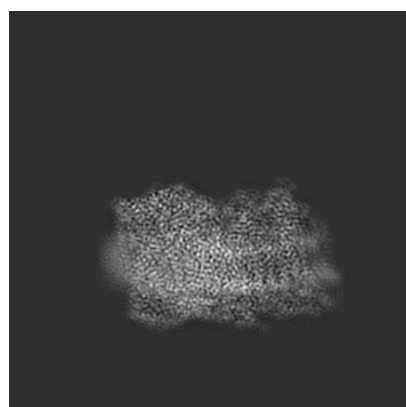
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32204. These allow visual inspection of the internal detail of the map and identification of artifacts.

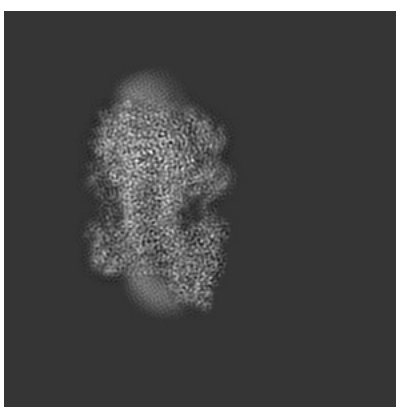
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

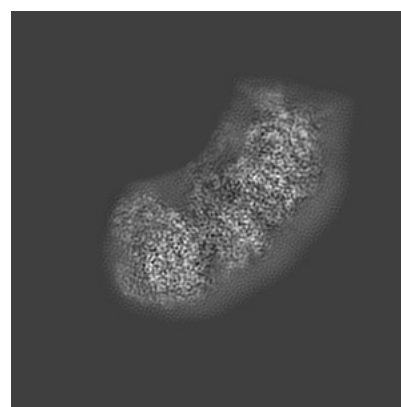
6.1.1 Primary map



X



Y

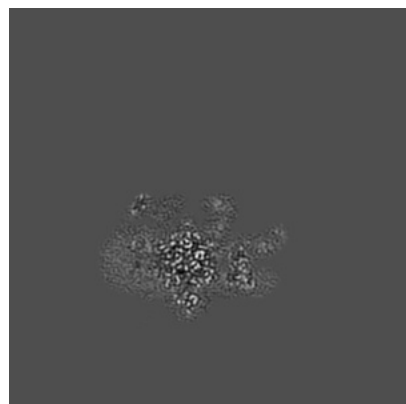


Z

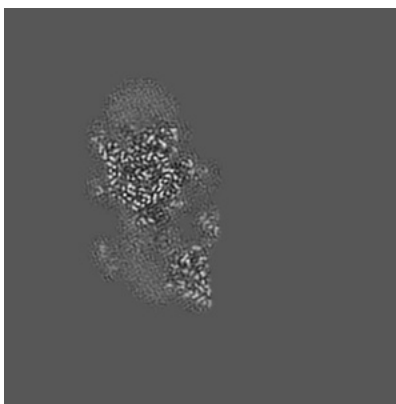
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

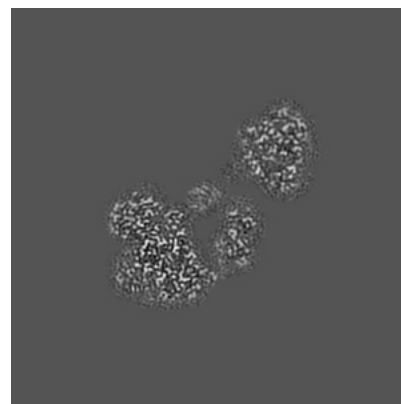
6.2.1 Primary map



X Index: 155



Y Index: 155

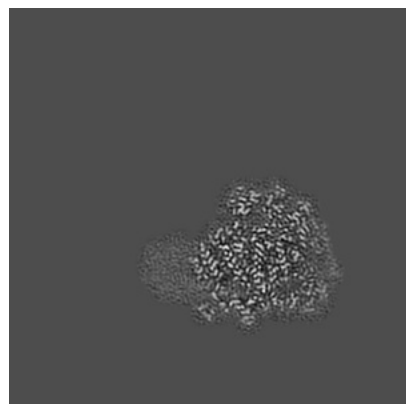


Z Index: 155

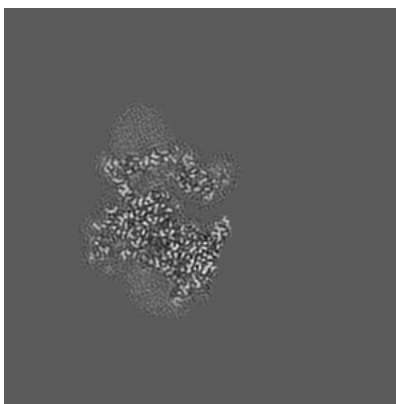
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

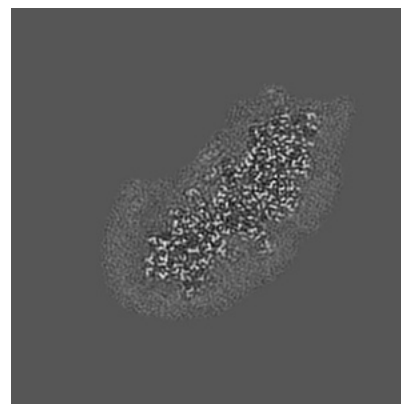
6.3.1 Primary map



X Index: 208



Y Index: 129

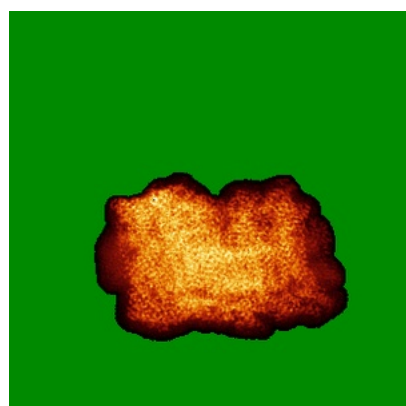


Z Index: 123

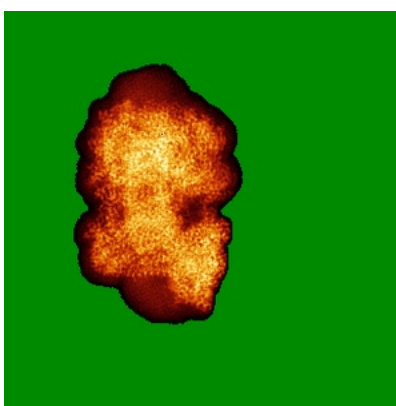
The images above show the largest variance slices of the map in three orthogonal directions.

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

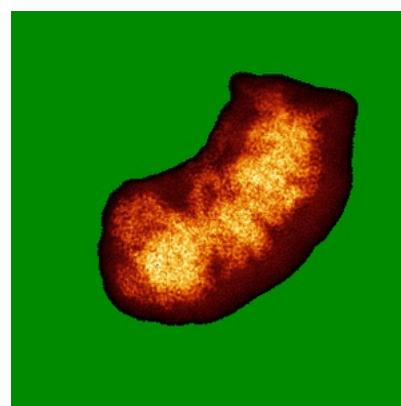
6.4.1 Primary map



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

This section was not generated.

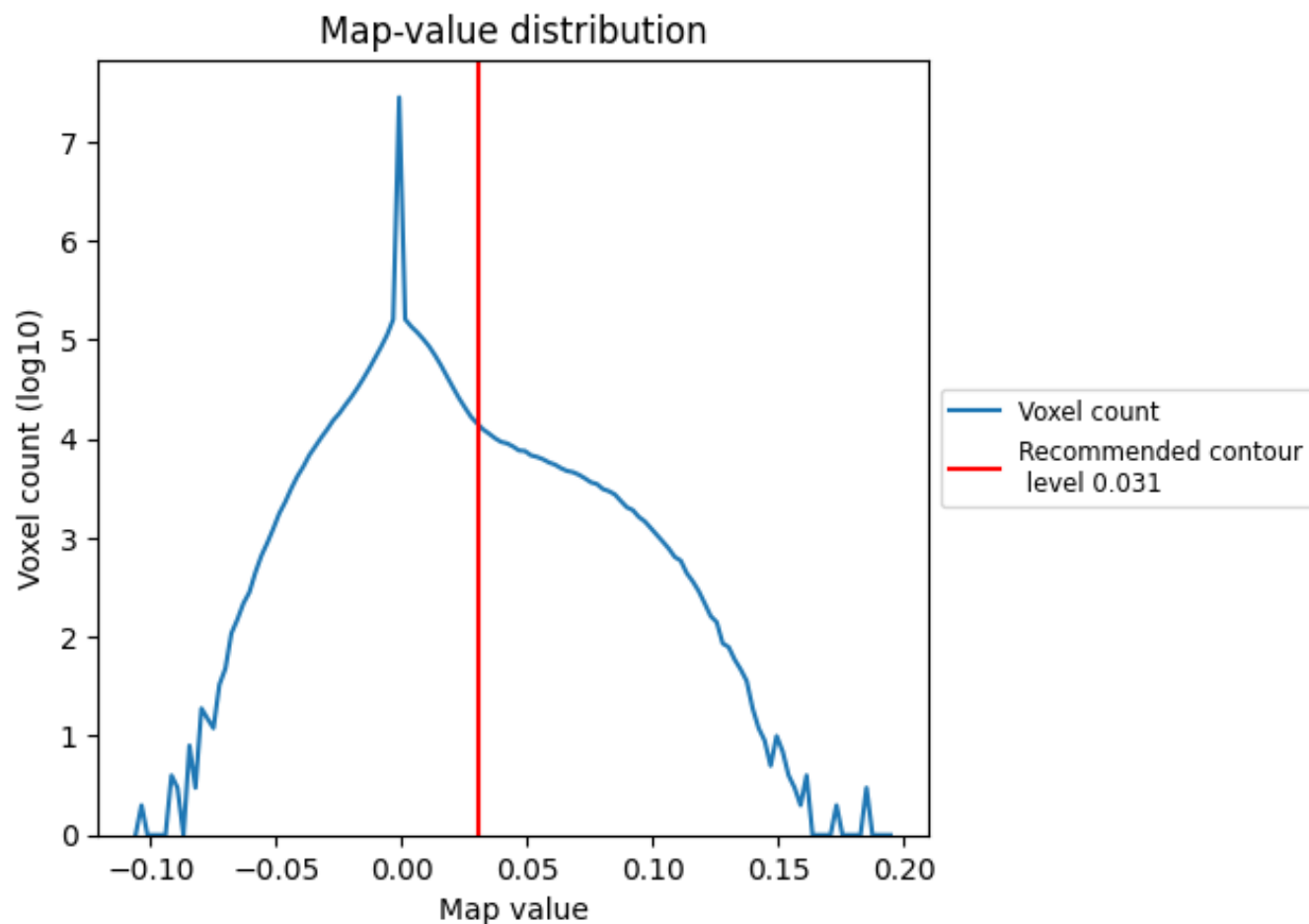
6.6 Mask visualisation

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

7 Map analysis [i](#)

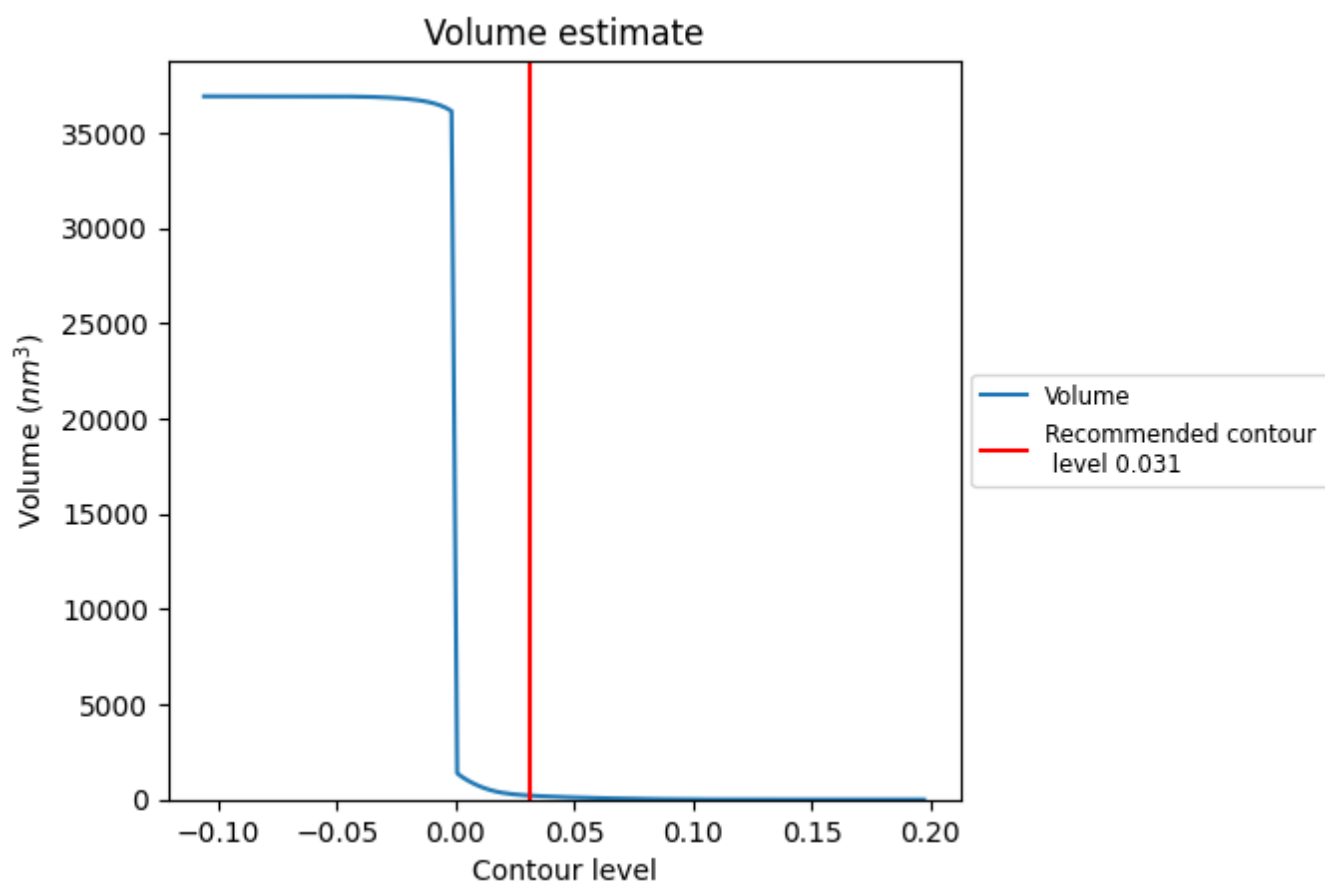
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

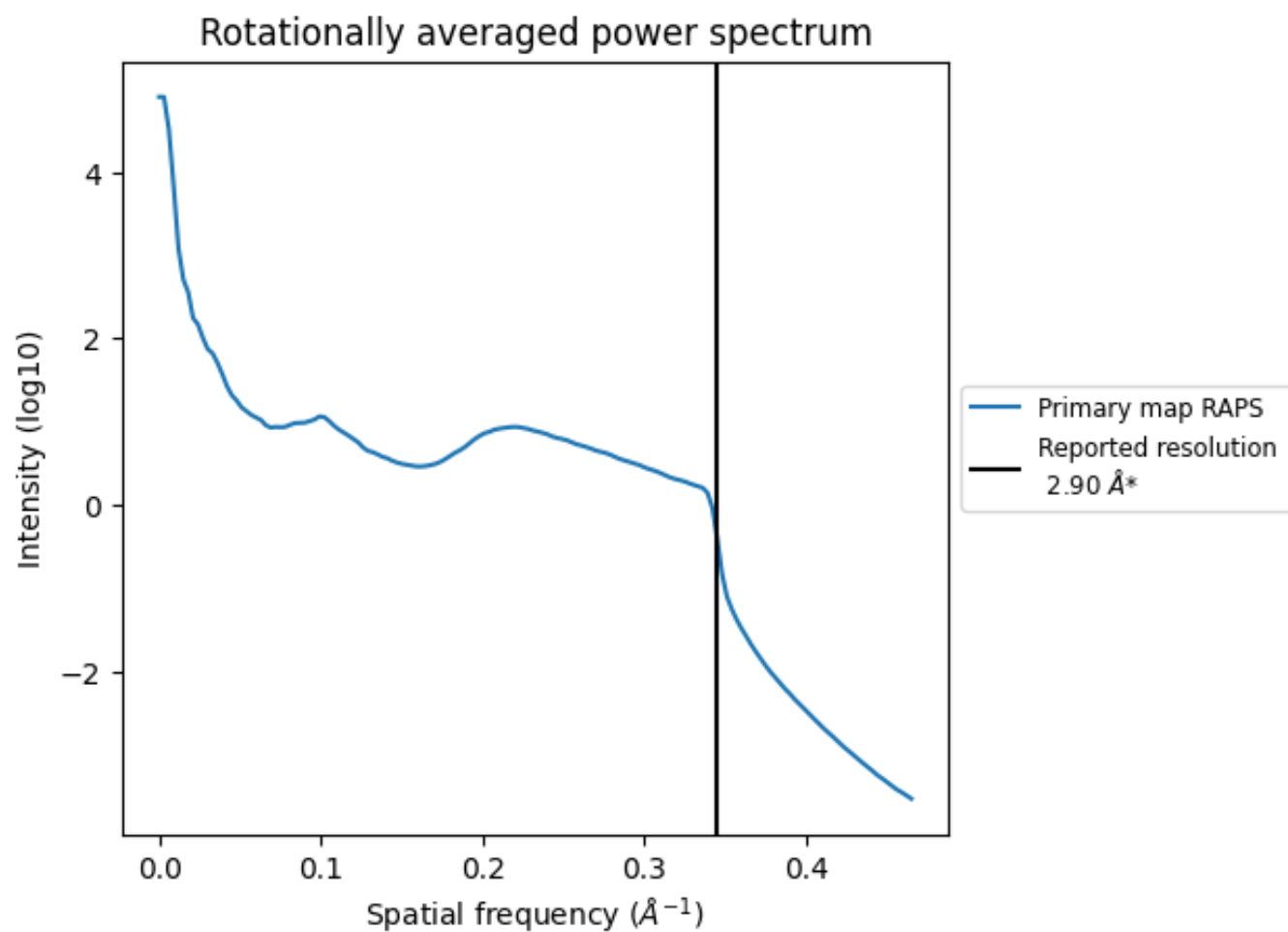
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 212 nm^3 ; this corresponds to an approximate mass of 192 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

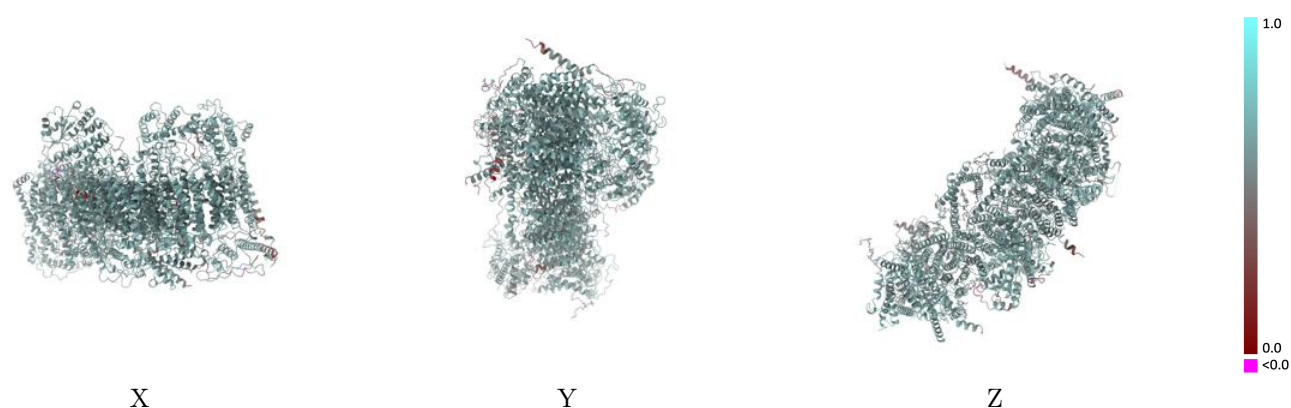
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-32204 and PDB model 7VYG. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

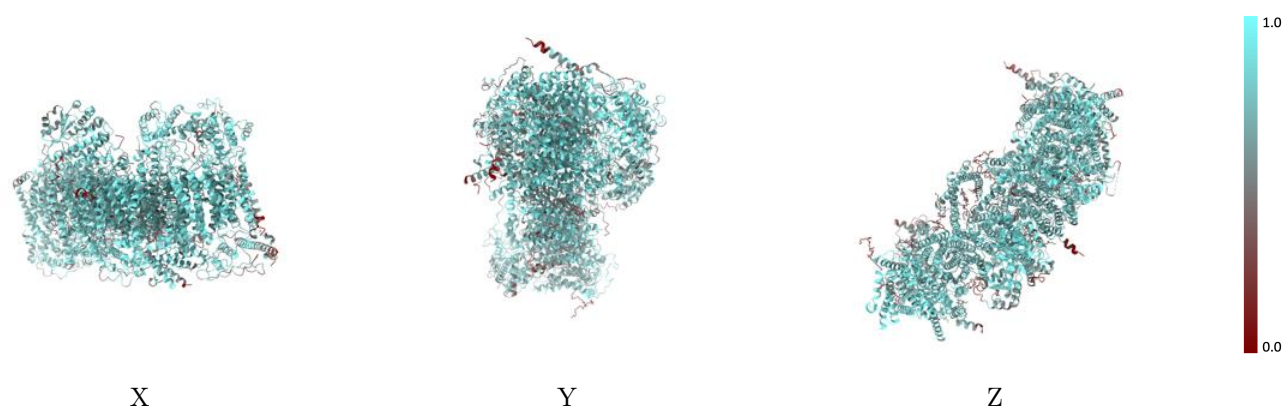
This section was not generated.

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



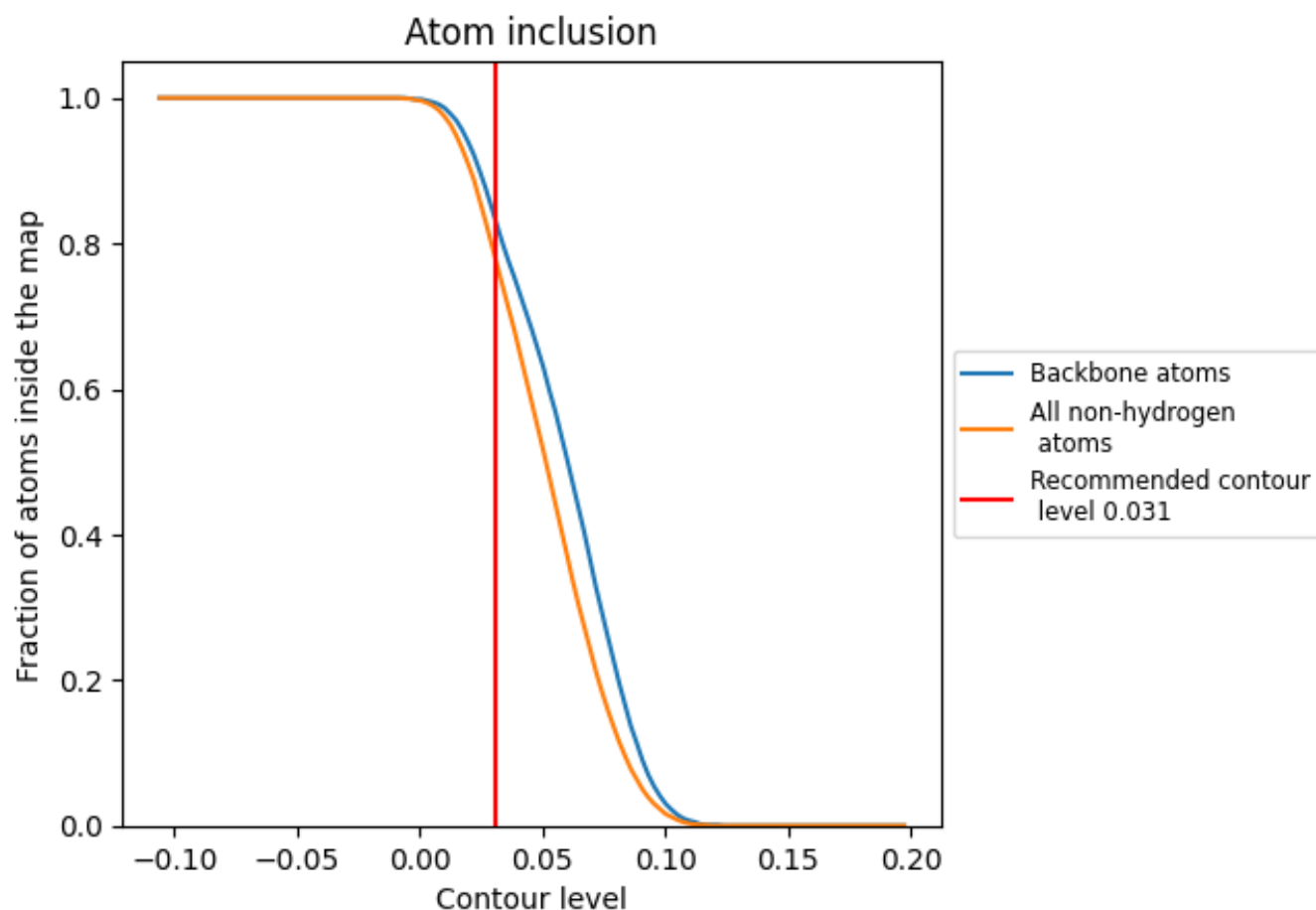
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.031).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% 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 (0.031) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7760	 0.5970
Q	 0.6450	 0.5710
S	 0.8370	 0.6080
U	 0.7370	 0.5900
V	 0.6620	 0.5830
W	 0.7810	 0.5960
X	 0.7340	 0.5850
Y	 0.6680	 0.5480
Z	 0.6210	 0.5340
a	 0.7990	 0.6160
b	 0.7230	 0.5670
c	 0.7790	 0.5980
d	 0.7390	 0.5820
e	 0.7170	 0.5880
f	 0.6000	 0.5310
g	 0.8200	 0.6070
h	 0.7620	 0.5820
i	 0.8770	 0.6260
j	 0.7430	 0.6030
k	 0.8560	 0.6180
l	 0.8060	 0.6080
m	 0.6830	 0.5680
n	 0.6320	 0.5490
o	 0.7520	 0.5930
p	 0.8040	 0.6070
r	 0.8490	 0.6210
s	 0.8340	 0.6160
u	 0.7800	 0.5890
v	 0.6780	 0.5540
w	 0.7400	 0.5850

