



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 12:25 AM UTC

PDB ID : 7VYS / pdb_00007vys
EMDB ID : EMD-32214
Title : Membrane arm of active state CI from Q1-NADH dataset
Authors : Gu, J.K.; Yang, M.J.
Deposited on : 2021-11-15
Resolution : 2.50 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:

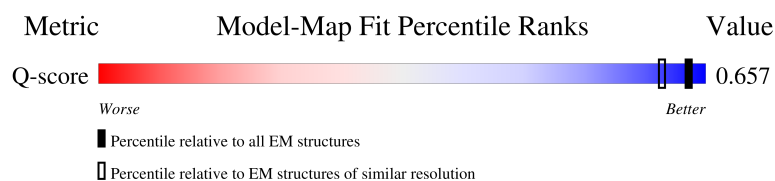
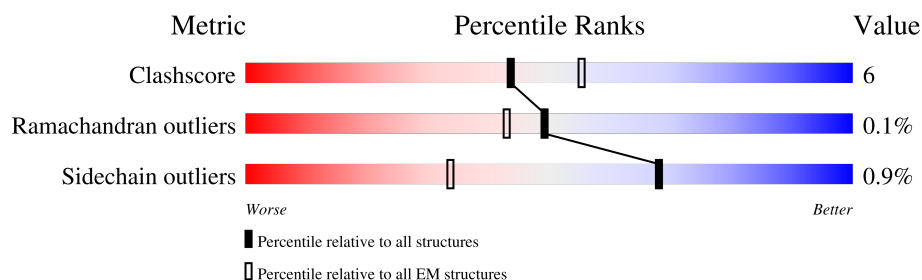
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	11% 77% 20% .
2	S	70	89% 11%
3	U	83	10% 87% 13%
4	V	140	5% 84% 15% .

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Mol	Chain	Length	Quality of chain
5	W	113	
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	122	
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	458	
26	s	318	
27	u	171	
28	v	124	
29	w	320	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 40113 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
			703	453	104	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
			1312	852	213	239	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
			378	246	65	67		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	122	Total	C	N	O	S	0	0
			1005	653	174	172	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
			1534	982	279	265	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	458	Total	C	N	O	S	0	0
			3619	2403	571	607	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
			2508	1678	385	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		

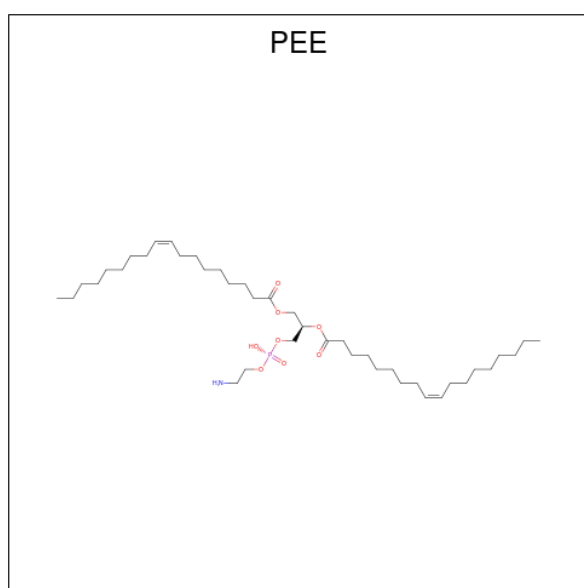
- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	v	124	Total	C	N	O	S	0	0
			1022	639	192	182	9		

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

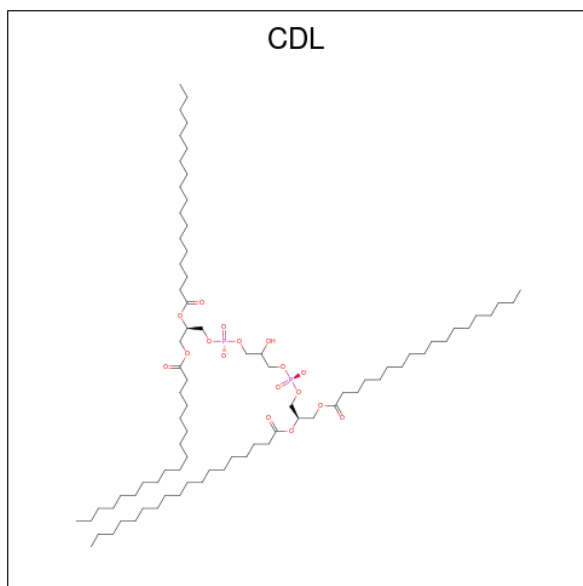
Mol	Chain	Residues	Atoms					AltConf	Trace
29	w	320	Total	C	N	O	S	0	0
			2582	1643	438	491	10		

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



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

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



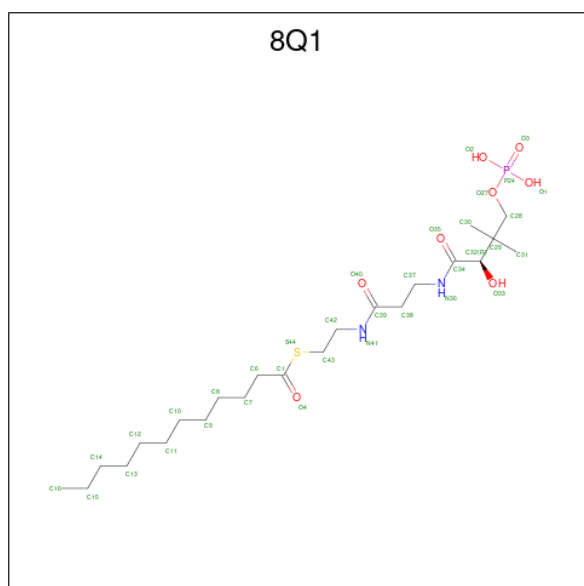
Mol	Chain	Residues	Atoms				AltConf
31	V	1	Total	C	O	P	0
			94	75	17	2	
31	V	1	Total	C	O	P	0
			100	81	17	2	

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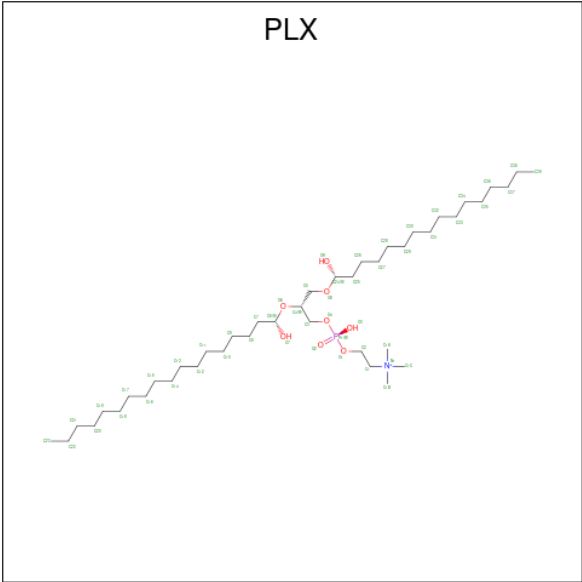
Mol	Chain	Residues	Atoms				AltConf
31	a	1	Total	C	O	P	0
			100	81	17	2	
31	i	1	Total	C	O	P	0
			100	81	17	2	
31	k	1	Total	C	O	P	0
			94	75	17	2	
31	l	1	Total	C	O	P	0
			99	80	17	2	
31	l	1	Total	C	O	P	0
			100	81	17	2	
31	s	1	Total	C	O	P	0
			89	70	17	2	
31	u	1	Total	C	O	P	0
			55	36	17	2	

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



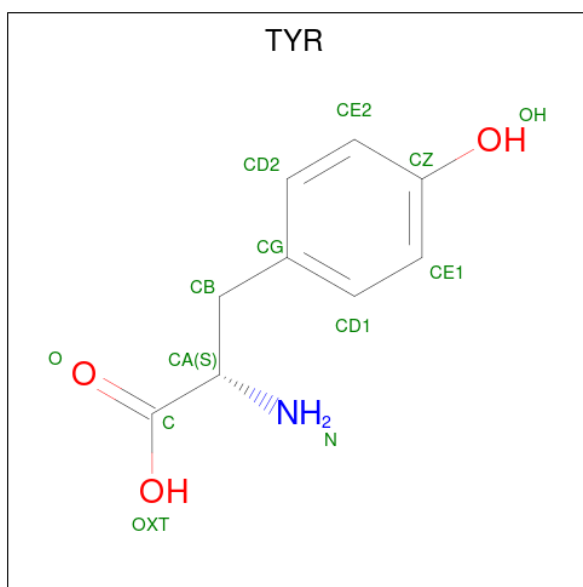
Mol	Chain	Residues	Atoms						AltConf
32	X	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

- Molecule 33 is (9R,11S)-9-({[(1S)-1-HYDROXYHEXADECYL]OXY}METHYL)-2,2-DIMETHYL-5,7,10-TRIOXA-2LAMBDA 5 -AZA-6LAMBDA 5 -PHOSPHAOCTACOSANE-6,6,11-TRIOL (CCD ID: PLX) (formula: $C_{42}H_{89}NO_8P$) (labeled as "Ligand of Interest" by depositor).



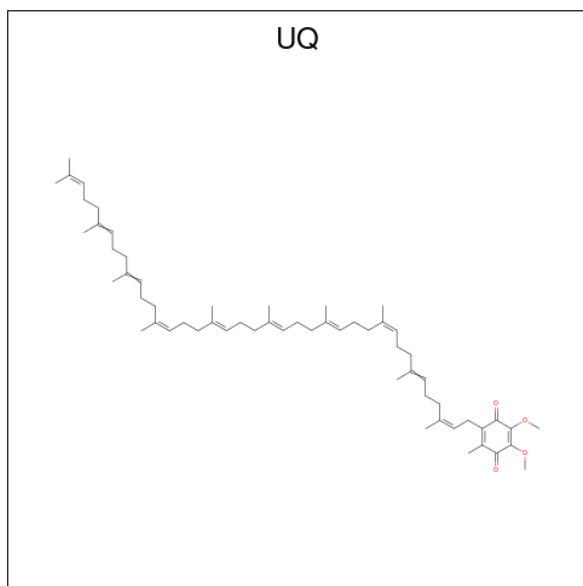
Mol	Chain	Residues	Atoms					AltConf
33	a	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	e	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	g	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	j	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	j	1	Total	C	N	O	P	0
			52	42	1	8	1	
33	r	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 34 is TYROSINE (CCD ID: TYR) (formula: C₉H₁₁NO₃).



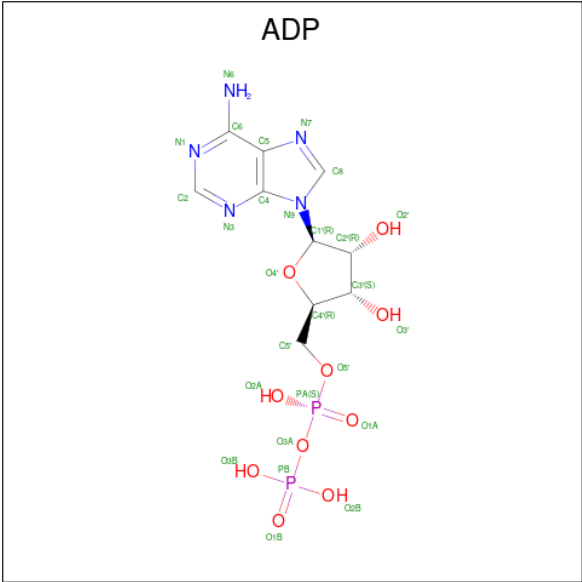
Mol	Chain	Residues	Atoms				AltConf
34	r	1	Total	C	N	O	0
			12	9	1	2	

- Molecule 35 is Coenzyme Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-isomer (CCD ID: UQ) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 36 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 37 is water.

Mol	Chain	Residues	Atoms		AltConf
37	Q	7	Total	O	0
			7	7	
37	S	5	Total	O	0
			5	5	
37	U	2	Total	O	0
			2	2	
37	V	2	Total	O	0
			2	2	
37	W	3	Total	O	0
			3	3	
37	Y	1	Total	O	0
			1	1	
37	c	4	Total	O	0
			4	4	
37	e	1	Total	O	0
			1	1	
37	h	4	Total	O	0
			4	4	
37	i	76	Total	O	0
			76	76	
37	j	31	Total	O	0
			31	31	

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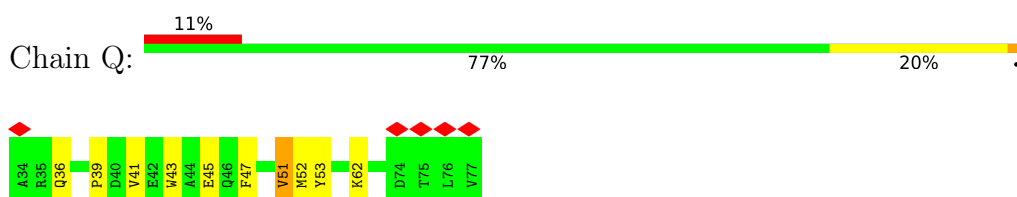
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Mol	Chain	Residues	Atoms		AltConf
37	k	29	Total 29	O 29	0
37	l	62	Total 62	O 62	0
37	m	17	Total 17	O 17	0
37	n	1	Total 1	O 1	0
37	p	2	Total 2	O 2	0
37	r	85	Total 85	O 85	0
37	s	90	Total 90	O 90	0
37	u	2	Total 2	O 2	0
37	w	1	Total 1	O 1	0

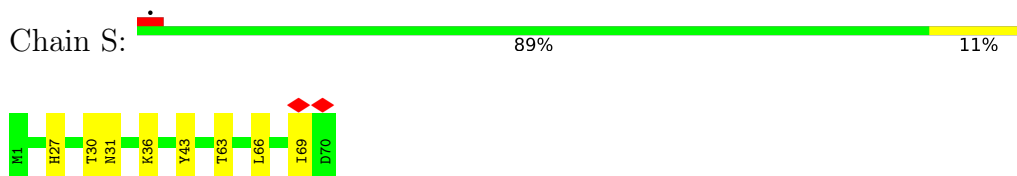
3 Residue-property plots [i](#)

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.

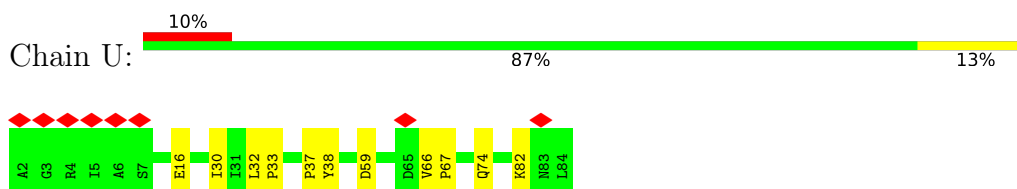
- Molecule 1: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial



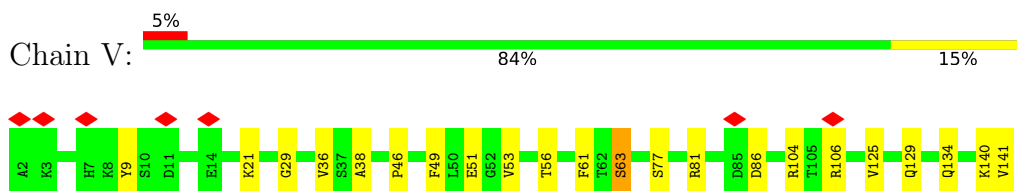
- Molecule 2: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



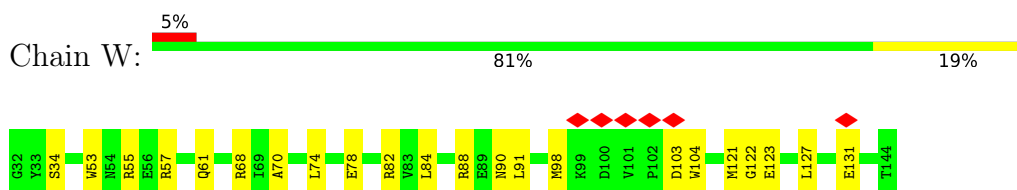
- Molecule 3: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3



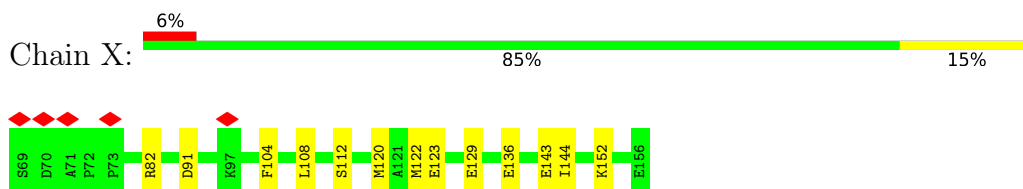
- Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11



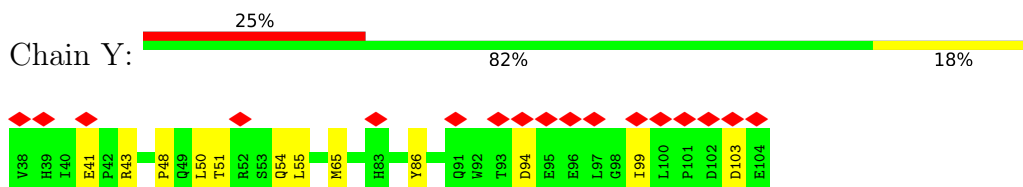
- Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13



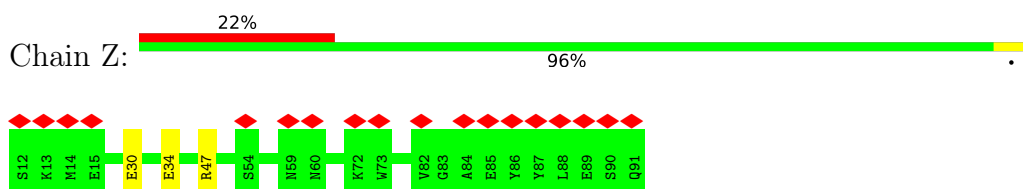
- Molecule 6: Acyl carrier protein, mitochondrial



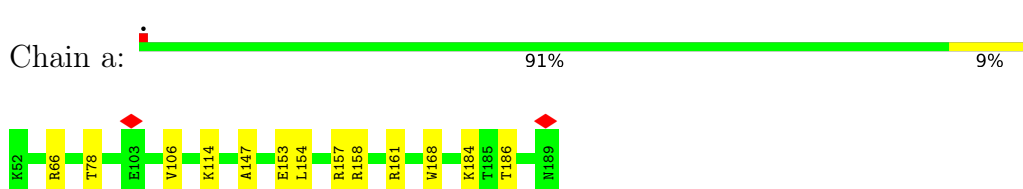
- Molecule 7: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



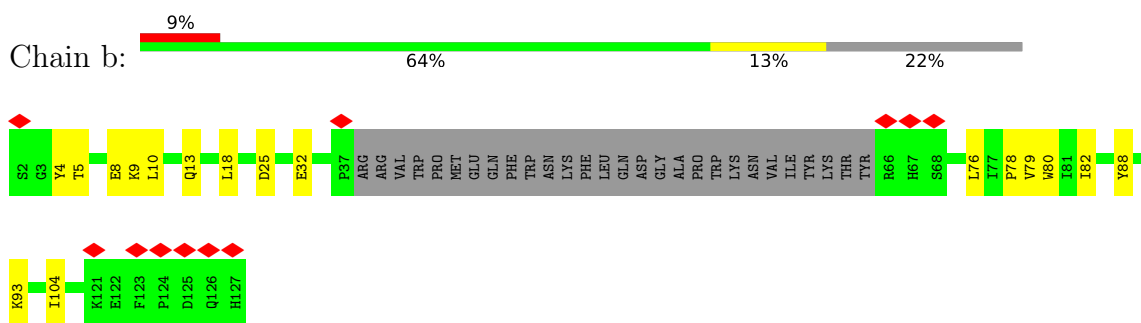
- Molecule 8: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3



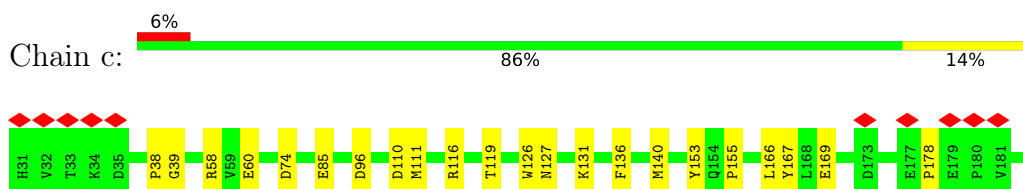
- Molecule 9: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



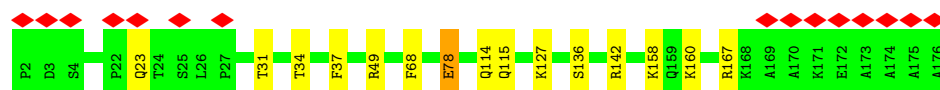
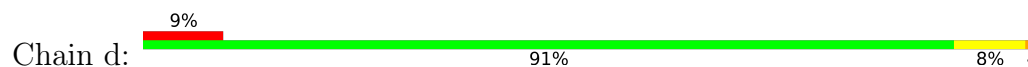
- Molecule 10: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6



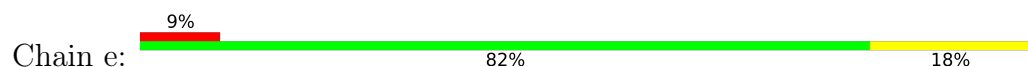
- Molecule 11: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial



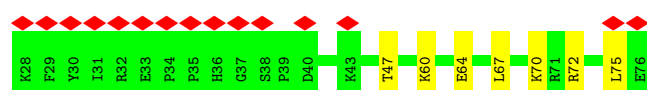
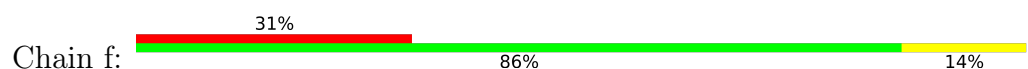
- Molecule 12: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10



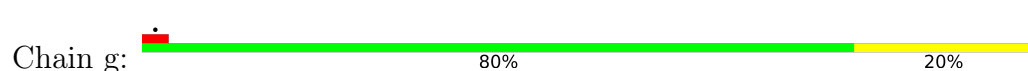
- Molecule 13: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



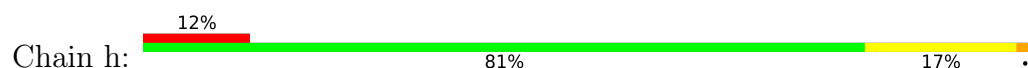
- Molecule 14: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial



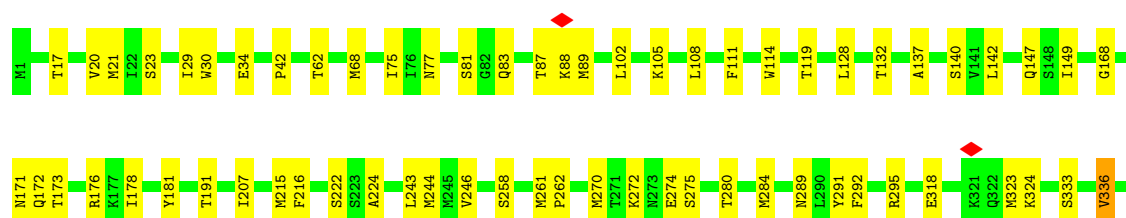
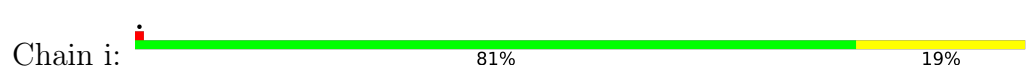
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 subunit C2



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

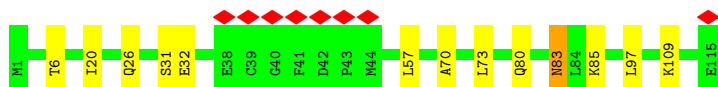
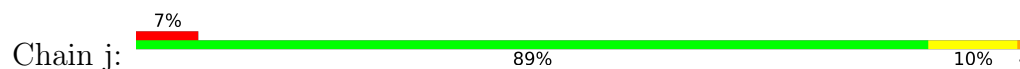


- Molecule 17: NADH-ubiquinone oxidoreductase chain 2





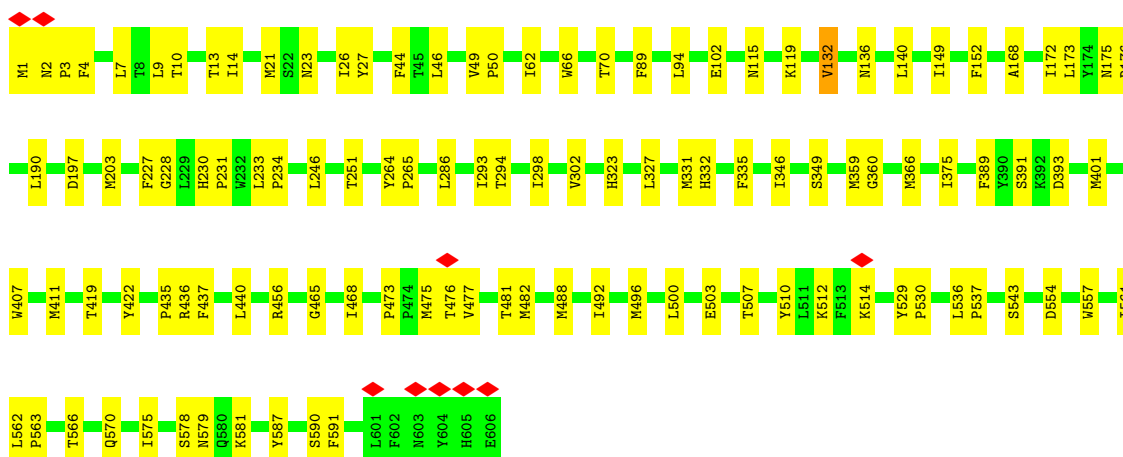
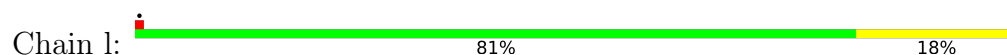
- Molecule 18: NADH-ubiquinone oxidoreductase chain 3



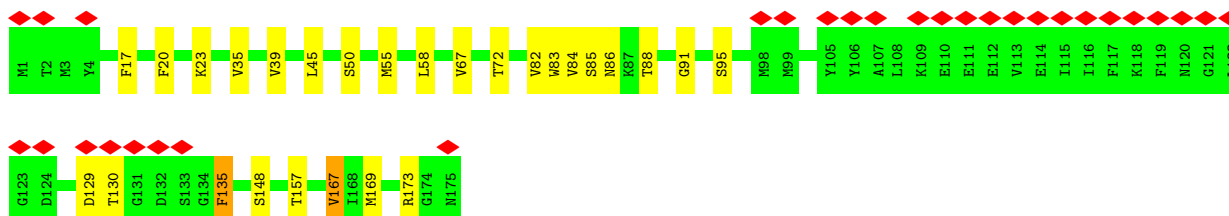
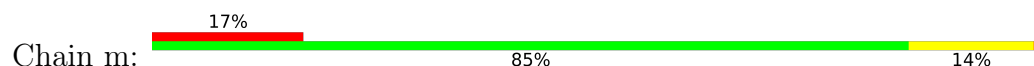
- Molecule 19: NADH-ubiquinone oxidoreductase chain 4L



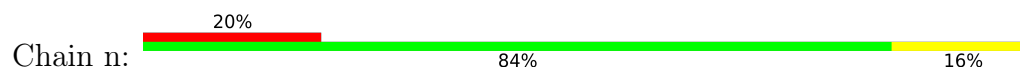
- Molecule 20: NADH-ubiquinone oxidoreductase chain 5



- Molecule 21: NADH-ubiquinone oxidoreductase chain 6

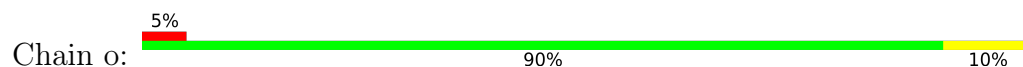


- Molecule 22: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1

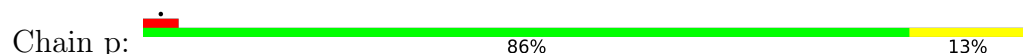




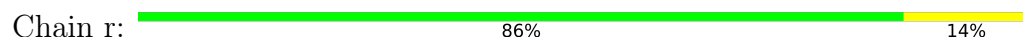
- Molecule 23: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4



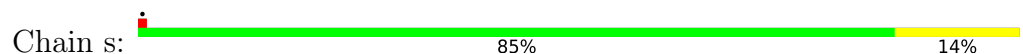
- Molecule 24: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9



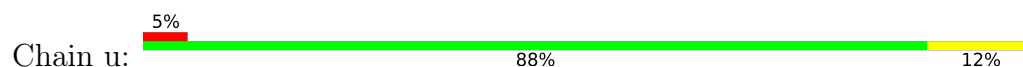
- Molecule 25: NADH-ubiquinone oxidoreductase chain 4



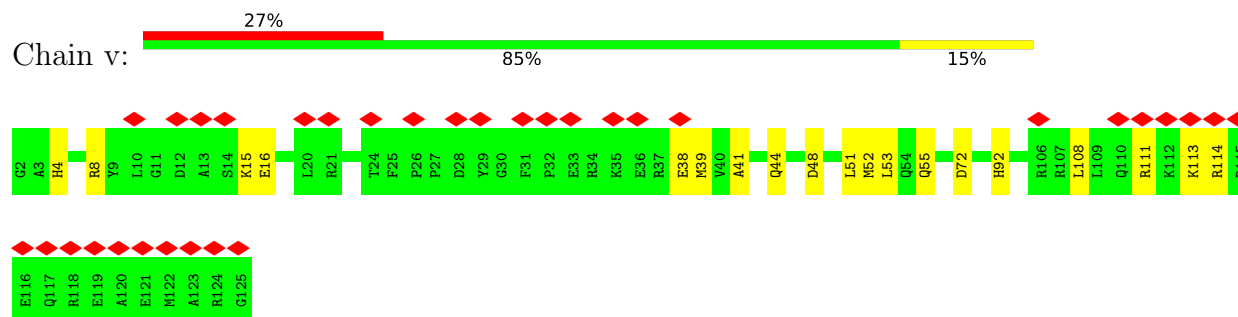
- Molecule 26: NADH-ubiquinone oxidoreductase chain 1



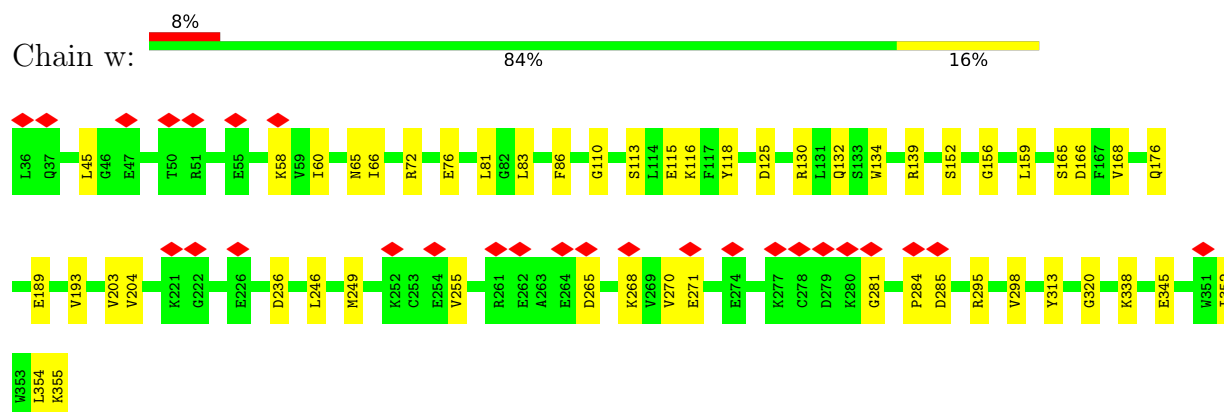
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



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



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	302353	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	0.094	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0155	Depositor
Map size (Å)	263.496, 263.496, 263.496	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.54895, 0.54895, 0.54895	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.31	0/525
2	S	0.14	0/581	0.35	0/781
3	U	0.12	0/664	0.28	0/912
4	V	0.13	0/1042	0.27	0/1411
5	W	0.15	0/973	0.33	1/1312 (0.1%)
6	X	0.12	0/715	0.29	0/967
7	Y	0.14	0/610	0.33	0/836
8	Z	0.10	0/660	0.27	0/892
9	a	0.15	0/1184	0.30	0/1603
10	b	0.15	0/844	0.35	0/1149
11	c	0.15	0/1368	0.39	0/1871
12	d	0.14	0/1494	0.30	0/2015
13	e	0.12	0/891	0.30	0/1210
14	f	0.12	0/386	0.25	0/523
15	g	0.14	0/1036	0.29	0/1401
16	h	0.24	0/889	0.85	5/1190 (0.4%)
17	i	0.17	0/2773	0.37	0/3768
18	j	0.14	0/938	0.29	0/1281
19	k	0.17	0/759	0.35	0/1029
20	l	0.16	0/4947	0.40	2/6728 (0.0%)
21	m	0.16	0/1325	0.36	0/1800
22	n	0.11	0/491	0.25	0/663
23	o	0.13	0/1092	0.29	0/1481
24	p	0.13	0/1590	0.30	0/2155
25	r	0.17	0/3710	0.35	0/5060
26	s	0.16	0/2581	0.36	0/3529
27	u	0.14	0/1436	0.33	0/1938
28	v	0.13	0/1046	0.35	0/1404
29	w	0.15	0/2642	0.34	0/3580
All	All	0.15	0/39047	0.36	8/53014 (0.0%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	h	94	PRO	CA-C-N	14.44	130.06	119.66
16	h	94	PRO	C-N-CA	14.44	130.06	119.66
16	h	92	TYR	N-CA-C	7.42	119.37	111.28
16	h	95	PRO	CA-C-N	6.82	126.62	119.05
16	h	95	PRO	C-N-CA	6.82	126.62	119.05
20	l	477	VAL	CA-C-N	5.33	125.23	119.85
20	l	477	VAL	C-N-CA	5.33	125.23	119.85
5	W	122	GLY	N-CA-C	-5.16	107.61	115.66

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	7	0
3	U	643	0	642	9	0
4	V	1021	0	1025	16	0
5	W	949	0	935	21	0
6	X	703	0	693	9	0
7	Y	584	0	529	10	0
8	Z	641	0	620	2	0
9	a	1151	0	1164	13	0
10	b	819	0	835	14	0
11	c	1312	0	1206	19	0
12	d	1461	0	1429	13	0
13	e	867	0	817	15	0
14	f	378	0	356	5	0
15	g	1005	0	999	22	0
16	h	867	0	871	29	0
17	i	2710	0	2874	47	0
18	j	914	0	951	12	0
19	k	748	0	799	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	l	4816	0	4955	89	0
21	m	1292	0	1261	25	0
22	n	479	0	486	7	0
23	o	1062	0	1072	12	0
24	p	1534	0	1470	18	0
25	r	3619	0	3830	49	0
26	s	2508	0	2607	39	0
27	u	1398	0	1374	20	0
28	v	1022	0	971	17	0
29	w	2582	0	2531	32	0
30	U	51	0	82	4	0
30	W	41	0	59	2	0
30	i	47	0	71	2	0
30	j	92	0	141	6	0
30	l	137	0	205	4	0
30	r	51	0	82	4	0
31	V	194	0	294	7	0
31	a	100	0	156	4	0
31	i	100	0	156	5	0
31	k	94	0	141	6	0
31	l	199	0	307	21	0
31	s	89	0	125	4	0
31	u	55	0	54	0	0
32	X	35	0	0	1	0
33	a	52	0	88	2	0
33	e	52	0	88	3	0
33	g	52	0	88	5	0
33	j	104	0	176	5	0
33	r	52	0	88	4	0
34	r	12	0	8	0	0
35	s	38	0	47	4	0
36	w	27	0	11	2	0
37	Q	7	0	0	0	0
37	S	5	0	0	0	0
37	U	2	0	0	0	0
37	V	2	0	0	0	0
37	W	3	0	0	0	0
37	Y	1	0	0	0	0
37	c	4	0	0	0	0
37	e	1	0	0	0	0
37	h	4	0	0	0	0
37	i	76	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	j	31	0	0	0	0
37	k	29	0	0	1	0
37	l	62	0	0	4	0
37	m	17	0	0	0	0
37	n	1	0	0	0	0
37	p	2	0	0	0	0
37	r	85	0	0	2	0
37	s	90	0	0	5	0
37	u	2	0	0	0	0
37	w	1	0	0	0	0
All	All	40113	0	40662	522	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (522) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:X:112:SER:CB	32:X:201:8Q1:O1	1.70	1.36
20:l:119:LYS:NZ	31:l:702:CDL:H511	1.55	1.21
20:l:119:LYS:HZ1	31:l:702:CDL:H511	0.97	1.10
20:l:119:LYS:NZ	31:l:702:CDL:C51	2.23	1.01
16:h:87:ILE:HG22	16:h:92:TYR:HB3	1.41	1.00
20:l:119:LYS:HZ1	31:l:702:CDL:C51	1.78	0.96
20:l:401:MET:SD	20:l:482:MET:HG2	2.11	0.89
20:l:481:THR:HG1	28:v:92:HIS:HD1	1.20	0.86
16:h:87:ILE:HG22	16:h:92:TYR:CB	2.06	0.85
16:h:87:ILE:CG2	16:h:92:TYR:HD2	1.92	0.83
26:s:287:HIS:HD2	37:s:2044:HOH:O	1.61	0.82
11:c:39:GLY:O	11:c:74:ASP:HB2	1.81	0.80
16:h:86:LEU:HA	16:h:89:GLU:OE2	1.82	0.80
5:W:88:ARG:HH11	5:W:91:LEU:HD23	1.46	0.79
16:h:87:ILE:CG2	16:h:92:TYR:CD2	2.65	0.79
25:r:400:MET:SD	37:r:638:HOH:O	2.42	0.76
20:l:119:LYS:HZ2	31:l:702:CDL:C51	1.96	0.76
11:c:127:ASN:O	11:c:131:LYS:HE3	1.86	0.75
20:l:360:GLY:HA3	20:l:435:PRO:HA	1.68	0.75
1:Q:41:VAL:O	1:Q:45:GLU:HG2	1.86	0.74
22:n:50:ARG:HB2	22:n:53:GLU:HG2	1.68	0.74
26:s:307:LEU:HA	26:s:310:MET:HE2	1.68	0.74
21:m:72:THR:HG21	26:s:133:LEU:HD21	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:167:ARG:HH21	13:e:153:GLU:HG3	1.53	0.74
20:l:492:ILE:HG23	20:l:496:MET:HE3	1.70	0.74
11:c:116:ARG:HG2	30:l:704:PEE:H49	1.69	0.73
7:Y:86:TYR:HD1	20:l:481:THR:HG22	1.52	0.73
17:i:88:LYS:HB3	37:i:576:HOH:O	1.87	0.73
22:n:47:ARG:NH2	22:n:53:GLU:OE2	2.20	0.73
24:p:35:ASP:OD1	24:p:36:LYS:N	2.23	0.72
27:u:77:HIS:HD2	27:u:114:LYS:HB3	1.54	0.72
28:v:51:LEU:O	28:v:52:MET:HG2	1.90	0.71
29:w:113:SER:HB3	29:w:116:LYS:HG2	1.72	0.71
4:V:141:VAL:O	9:a:161:ARG:NH1	2.24	0.70
20:l:227:PHE:O	20:l:230:HIS:ND1	2.25	0.69
16:h:18:MET:HE3	19:k:56:ALA:HA	1.74	0.69
20:l:228:GLY:HA3	30:l:704:PEE:H38	1.74	0.69
27:u:88:CYS:SG	27:u:103:GLN:NE2	2.66	0.69
3:U:16:GLU:HG3	30:j:201:PEE:H49	1.74	0.68
1:Q:36:GLN:NE2	25:r:137:GLY:O	2.25	0.68
9:a:154:LEU:HD21	17:i:272:LYS:HG2	1.75	0.68
20:l:492:ILE:O	20:l:496:MET:HG2	1.94	0.68
19:k:65:VAL:HG11	21:m:157:THR:HG23	1.76	0.68
31:i:402:CDL:H241	25:r:97:THR:HG21	1.77	0.67
26:s:205:SER:OG	26:s:279:ARG:NH2	2.26	0.67
25:r:198:ALA:HB2	30:r:501:PEE:H22	1.77	0.67
29:w:268:LYS:HA	29:w:271:GLU:OE2	1.95	0.67
31:V:201:CDL:H731	31:V:201:CDL:H601	1.76	0.66
15:g:52:ARG:NH1	17:i:318:GLU:OE2	2.28	0.66
5:W:61:GLN:HE22	26:s:317:GLN:H	1.41	0.66
21:m:82:VAL:HG22	21:m:85:SER:HB3	1.78	0.66
25:r:31:SER:HB3	25:r:74:PRO:HG3	1.77	0.66
5:W:98:MET:HE2	5:W:104:TRP:CD2	2.30	0.66
33:g:201:PLX:H342	17:i:261:MET:HE1	1.77	0.66
17:i:246:VAL:HG11	31:i:402:CDL:H392	1.78	0.66
11:c:58:ARG:NH2	11:c:60:GLU:OE1	2.29	0.65
26:s:287:HIS:CD2	37:s:2044:HOH:O	2.44	0.65
16:h:97:HIS:HA	16:h:102:GLU:HB3	1.79	0.65
31:l:702:CDL:H371	25:r:369:LEU:HD23	1.78	0.65
21:m:173:ARG:HG3	21:m:173:ARG:HH11	1.60	0.65
29:w:132:GLN:NE2	29:w:166:ASP:OD1	2.30	0.65
17:i:42:PRO:HG2	21:m:167:VAL:HG22	1.77	0.65
16:h:87:ILE:HG22	16:h:92:TYR:CD2	2.31	0.65
20:l:119:LYS:NZ	31:l:702:CDL:H512	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:r:312:ALA:O	25:r:316:MET:HG3	1.97	0.64
7:Y:86:TYR:CD1	20:l:481:THR:HG22	2.32	0.64
29:w:125:ASP:O	29:w:130:ARG:NH2	2.30	0.64
33:e:201:PLX:H21	30:l:705:PEE:H2	1.79	0.64
20:l:331:MET:HE2	20:l:331:MET:HA	1.79	0.64
5:W:121:MET:HG3	21:m:130:THR:HB	1.80	0.63
29:w:285:ASP:OD1	29:w:285:ASP:O	2.16	0.63
20:l:323:HIS:ND1	20:l:475:MET:SD	2.72	0.63
15:g:15:PHE:HB2	33:g:201:PLX:H6	1.81	0.63
30:i:401:PEE:H37	30:i:401:PEE:H60	1.79	0.62
17:i:108:LEU:HD11	17:i:191:THR:HG21	1.80	0.62
29:w:72:ARG:O	29:w:76:GLU:HG2	1.99	0.62
4:V:125:VAL:O	4:V:129:GLN:HG3	1.99	0.62
2:S:27:HIS:HE1	37:s:2012:HOH:O	1.82	0.62
28:v:111:ARG:HA	28:v:114:ARG:HE	1.64	0.62
28:v:52:MET:HB2	28:v:55:GLN:HG3	1.81	0.62
26:s:209:SER:HB3	26:s:213:VAL:HA	1.82	0.61
5:W:61:GLN:NE2	26:s:317:GLN:OE1	2.33	0.61
17:i:68:MET:HE2	17:i:68:MET:HA	1.82	0.61
25:r:201:MET:HE2	30:r:501:PEE:H78	1.81	0.61
22:n:47:ARG:HH21	22:n:56:THR:HG22	1.65	0.60
23:o:56:ARG:NH2	25:r:422:HIS:O	2.34	0.60
28:v:8:ARG:HB2	28:v:16:GLU:HG2	1.82	0.60
29:w:118:TYR:OH	36:w:401:ADP:O2'	2.20	0.60
5:W:127:LEU:HB3	16:h:98:HIS:CD2	2.37	0.60
16:h:93:THR:HG22	16:h:93:THR:O	2.01	0.60
17:i:207:ILE:HD13	17:i:262:PRO:HD3	1.84	0.60
20:l:562:LEU:HB3	20:l:563:PRO:HD3	1.84	0.60
25:r:237:LYS:HD2	25:r:316:MET:HB3	1.84	0.60
29:w:204:VAL:HG21	29:w:249:MET:HG2	1.84	0.60
7:Y:94:ASP:HB3	7:Y:99:ILE:HG12	1.83	0.59
12:d:160:LYS:NZ	15:g:114:ILE:O	2.36	0.59
24:p:105:ASP:OD1	24:p:122:ARG:NH1	2.26	0.59
28:v:38:GLU:OE1	28:v:38:GLU:N	2.19	0.59
25:r:403:THR:HA	25:r:406:TYR:CE2	2.38	0.59
13:e:54:ARG:NH2	29:w:313:TYR:O	2.36	0.59
1:Q:47:PHE:HD1	1:Q:52:MET:HE1	1.68	0.58
24:p:57:MET:O	24:p:61:THR:HG23	2.02	0.58
4:V:140:LYS:HE3	9:a:158:ARG:CD	2.34	0.58
11:c:38:PRO:HG2	23:o:70:TYR:HD2	1.68	0.58
17:i:215:MET:HE1	17:i:244:MET:HG3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:l:175:ASN:ND2	37:l:805:HOH:O	2.37	0.58
19:k:17:ALA:HB2	31:k:101:CDL:H811	1.86	0.58
19:k:87:THR:HG23	19:k:89:TYR:H	1.67	0.58
4:V:36:VAL:HG22	31:V:201:CDL:H741	1.86	0.58
26:s:62:ARG:NH2	31:s:401:CDL:OA3	2.36	0.58
5:W:88:ARG:NH1	5:W:91:LEU:HD23	2.17	0.57
18:j:6:THR:HG21	26:s:87:VAL:HG11	1.86	0.57
14:f:72:ARG:NH2	15:g:18:ASN:OD1	2.33	0.57
26:s:62:ARG:HG3	26:s:68:ILE:HD13	1.87	0.57
31:s:401:CDL:H322	31:s:401:CDL:HB61	1.87	0.57
13:e:129:ARG:NH1	13:e:136:LEU:O	2.33	0.57
26:s:18:ALA:O	26:s:21:THR:OG1	2.20	0.57
25:r:306:PRO:HB3	25:r:458:LEU:HD12	1.87	0.57
20:l:7:LEU:HD22	20:l:46:LEU:HD11	1.85	0.56
15:g:56:VAL:HG21	25:r:17:MET:HE1	1.86	0.56
20:l:190:LEU:HD22	25:r:383:THR:HG21	1.87	0.56
26:s:221:ALA:O	26:s:225:MET:HG3	2.05	0.56
31:l:702:CDL:H352	25:r:361:VAL:HG13	1.88	0.56
16:h:87:ILE:CG2	16:h:92:TYR:CB	2.80	0.56
6:X:120:MET:HE1	24:p:24:LEU:HD13	1.87	0.56
26:s:63:PRO:HB2	26:s:66:SER:HB3	1.88	0.56
17:i:258:SER:HB2	17:i:336:VAL:HG12	1.88	0.56
20:l:119:LYS:NZ	31:l:702:CDL:OA3	2.37	0.55
16:h:87:ILE:HG21	16:h:92:TYR:HD2	1.70	0.55
17:i:258:SER:OG	17:i:333:SER:O	2.23	0.55
30:r:501:PEE:H79	30:r:501:PEE:H40	1.88	0.55
15:g:62:ARG:NH2	29:w:355:LYS:O	2.39	0.55
25:r:83:HIS:HE1	37:r:610:HOH:O	1.89	0.55
7:Y:86:TYR:HD1	20:l:481:THR:CG2	2.20	0.55
11:c:153:TYR:OH	28:v:8:ARG:NH1	2.38	0.55
5:W:90:ASN:ND2	5:W:123:GLU:O	2.39	0.55
20:l:419:THR:HA	20:l:422:TYR:CE2	2.41	0.55
28:v:44:GLN:OE1	28:v:44:GLN:HA	2.07	0.55
5:W:103:ASP:OD1	5:W:103:ASP:N	2.38	0.55
19:k:31:LEU:HD21	21:m:67:VAL:HG11	1.87	0.55
2:S:69:ILE:HD13	27:u:71:PHE:HB3	1.89	0.55
27:u:77:HIS:CD2	27:u:114:LYS:HB3	2.40	0.55
29:w:139:ARG:NH1	29:w:166:ASP:OD2	2.40	0.55
20:l:119:LYS:HZ2	31:l:702:CDL:H512	1.68	0.54
23:o:20:PRO:HB3	24:p:65:ARG:NH2	2.22	0.54
16:h:69:ARG:O	16:h:73:MET:HG3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:k:37:MET:HG2	37:k:207:HOH:O	2.06	0.54
20:l:476:THR:HG21	37:l:832:HOH:O	2.06	0.54
12:d:114:GLN:HG3	20:l:203:MET:HG2	1.89	0.54
16:h:86:LEU:HD12	16:h:89:GLU:OE2	2.08	0.54
17:i:30:TRP:O	17:i:34:GLU:HG2	2.07	0.54
15:g:36:MET:HE1	33:g:201:PLX:H393	1.90	0.54
17:i:289:ASN:HA	17:i:292:PHE:CE2	2.43	0.54
20:l:286:LEU:HD13	20:l:411:MET:SD	2.47	0.54
20:l:481:THR:OG1	28:v:92:HIS:ND1	2.22	0.54
27:u:83:THR:HA	27:u:86:TRP:CD1	2.43	0.54
29:w:352:ILE:HA	29:w:355:LYS:HD2	1.90	0.54
26:s:170:GLU:OE2	27:u:98:ARG:NH2	2.30	0.54
5:W:70:ALA:HB2	27:u:125:LEU:HD13	1.90	0.53
29:w:45:LEU:O	29:w:45:LEU:HD12	2.09	0.53
16:h:86:LEU:O	16:h:89:GLU:HG2	2.09	0.53
20:l:23:ASN:ND2	20:l:23:ASN:O	2.41	0.53
20:l:536:LEU:HB3	20:l:537:PRO:HD3	1.91	0.53
10:b:18:LEU:HD11	24:p:163:LEU:HD22	1.90	0.53
17:i:246:VAL:HG21	31:i:402:CDL:H362	1.90	0.53
28:v:39:MET:HE3	28:v:41:ALA:HB3	1.91	0.53
5:W:131:GLU:OE1	5:W:131:GLU:N	2.39	0.53
25:r:119:TYR:O	25:r:123:GLU:HG2	2.09	0.53
33:e:201:PLX:H102	31:l:702:CDL:H641	1.91	0.53
20:l:246:LEU:O	20:l:251:THR:OG1	2.26	0.53
20:l:66:TRP:CD1	30:l:705:PEE:H16	2.43	0.52
18:j:70:ALA:HB2	21:m:55:MET:HE2	1.90	0.52
31:a:201:CDL:H652	20:l:13:THR:HG23	1.91	0.52
13:e:97:ILE:O	13:e:101:LEU:HB2	2.10	0.52
13:e:72:ASP:OD1	13:e:72:ASP:N	2.42	0.52
20:l:359:MET:O	20:l:436:ARG:NH2	2.43	0.52
3:U:32:LEU:HB3	26:s:310:MET:SD	2.49	0.52
21:m:173:ARG:HG3	21:m:173:ARG:NH1	2.25	0.52
23:o:113:GLU:O	23:o:117:GLN:HG2	2.10	0.52
4:V:29:GLY:O	4:V:63:SER:HB3	2.10	0.51
20:l:346:ILE:HA	20:l:366:MET:HE1	1.92	0.51
4:V:46:PRO:HB2	4:V:51:GLU:HG2	1.92	0.51
11:c:38:PRO:HD3	23:o:67:ARG:HG2	1.91	0.51
17:i:243:LEU:HD23	31:i:402:CDL:H361	1.91	0.51
9:a:106:VAL:HB	22:m:50:ARG:HH21	1.76	0.51
10:b:4:TYR:HB2	10:b:9:LYS:HG3	1.93	0.51
21:m:55:MET:HE1	21:m:58:LEU:HD23	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:104:ILE:HB	28:v:48:ASP:HB3	1.93	0.51
1:Q:39:PRO:HB3	1:Q:43:TRP:CD1	2.46	0.51
7:Y:103:ASP:OD1	7:Y:103:ASP:N	2.43	0.51
20:l:173:LEU:HD12	25:r:405:LEU:HD21	1.92	0.51
24:p:47:ARG:NH2	24:p:70:GLU:OE1	2.44	0.51
27:u:76:ARG:HD2	27:u:77:HIS:CE1	2.46	0.51
1:Q:53:TYR:OH	17:i:295:ARG:NH2	2.44	0.50
21:m:17:PHE:HA	21:m:20:PHE:CE2	2.46	0.50
24:p:160:GLU:HG2	24:p:161:GLY:H	1.76	0.50
25:r:266:MET:HA	25:r:269:MET:HE3	1.93	0.50
2:S:43:TYR:CZ	5:W:68:ARG:HG3	2.46	0.50
17:i:222:SER:O	17:i:224:ALA:N	2.45	0.50
21:m:45:LEU:HD12	21:m:50:SER:HA	1.93	0.50
23:o:75:ASN:O	23:o:79:ASN:ND2	2.44	0.50
17:i:171:ASN:ND2	20:l:578:SER:OG	2.42	0.50
20:l:21:MET:HE3	20:l:26:ILE:HG21	1.92	0.50
20:l:331:MET:SD	20:l:465:GLY:HA2	2.51	0.50
29:w:81:LEU:HD21	29:w:270:VAL:HG13	1.94	0.50
11:c:96:ASP:N	11:c:96:ASP:OD1	2.44	0.50
16:h:20:ILE:HA	37:i:501:HOH:O	2.11	0.50
17:i:128:LEU:O	17:i:132:THR:OG1	2.23	0.50
31:l:702:CDL:H391	25:r:371:PRO:HD2	1.92	0.50
25:r:266:MET:O	25:r:269:MET:HG2	2.12	0.50
15:g:19:GLU:O	15:g:22:SER:OG	2.30	0.50
17:i:172:GLN:HB2	17:i:178:ILE:HG13	1.92	0.50
26:s:52:ALA:HB2	35:s:402:UQ:H23	1.93	0.50
31:V:202:CDL:H782	20:l:557:TRP:CD2	2.47	0.49
27:u:76:ARG:HD2	27:u:77:HIS:HE1	1.77	0.49
20:l:500:LEU:HD12	31:l:703:CDL:H562	1.93	0.49
24:p:108:HIS:ND1	24:p:110:SER:OG	2.31	0.49
12:d:115:GLN:HG2	20:l:62:ILE:HG12	1.93	0.49
26:s:209:SER:OG	26:s:212:ASN:OD1	2.29	0.49
5:W:74:LEU:O	5:W:78:GLU:HG3	2.12	0.49
18:j:83:ASN:OD1	18:j:83:ASN:N	2.43	0.49
17:i:81:SER:O	17:i:83:GLN:N	2.44	0.49
19:k:23:ARG:HG2	31:k:101:CDL:HB62	1.95	0.49
10:b:5:THR:OG1	10:b:8:GLU:HG3	2.13	0.49
17:i:20:VAL:HG11	17:i:137:ALA:HB1	1.94	0.49
4:V:140:LYS:HE3	9:a:158:ARG:HD2	1.93	0.49
31:V:202:CDL:HB4	23:o:82:PRO:HB2	1.94	0.49
26:s:62:ARG:HD3	37:s:2006:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:i:270:MET:O	17:i:275:SER:HB3	2.13	0.49
20:l:286:LEU:HD21	31:l:703:CDL:H812	1.95	0.49
9:a:168:TRP:HB3	15:g:3:MET:HG2	1.95	0.49
16:h:86:LEU:O	16:h:89:GLU:CG	2.61	0.48
17:i:105:LYS:NZ	37:i:510:HOH:O	2.44	0.48
20:l:510:TYR:HB3	20:l:512:LYS:HE3	1.95	0.48
24:p:55:LYS:HA	24:p:55:LYS:HD3	1.61	0.48
29:w:58:LYS:O	29:w:60:ILE:HG13	2.14	0.48
4:V:49:PHE:O	4:V:53:VAL:HG23	2.13	0.48
17:i:215:MET:HE1	17:i:244:MET:CG	2.43	0.48
20:l:503:GLU:O	20:l:507:THR:HG23	2.13	0.48
13:e:55:LEU:CD2	13:e:57:GLU:HB2	2.43	0.48
20:l:323:HIS:CE1	20:l:475:MET:SD	3.06	0.48
33:a:202:PLX:H282	25:r:37:ILE:HD11	1.96	0.48
1:Q:62:LYS:NZ	1:Q:62:LYS:HB3	2.29	0.48
11:c:110:ASP:OD1	11:c:110:ASP:N	2.46	0.48
19:k:4:VAL:O	19:k:8:ILE:HG12	2.14	0.48
20:l:176:ARG:NH2	37:l:809:HOH:O	2.45	0.48
4:V:81:ARG:NH2	4:V:86:ASP:OD2	2.47	0.48
17:i:77:ASN:HB2	17:i:89:MET:HE3	1.96	0.48
25:r:203:PHE:O	25:r:207:MET:HG2	2.14	0.48
29:w:265:ASP:N	29:w:265:ASP:OD1	2.45	0.48
5:W:61:GLN:NE2	26:s:317:GLN:H	2.09	0.47
25:r:340:ARG:HG3	25:r:340:ARG:HH11	1.78	0.47
29:w:115:GLU:OE2	29:w:115:GLU:N	2.47	0.47
17:i:147:GLN:CD	17:i:147:GLN:H	2.22	0.47
29:w:86:PHE:HB2	29:w:159:LEU:HD23	1.95	0.47
15:g:3:MET:HB3	15:g:4:MET:HG2	1.97	0.47
15:g:85:TYR:CZ	17:i:344:SER:HB2	2.50	0.47
20:l:575:ILE:HG23	20:l:579:ASN:ND2	2.30	0.47
21:m:35:VAL:O	21:m:39:VAL:HG22	2.15	0.47
2:S:31:ASN:ND2	2:S:36:LYS:HB2	2.29	0.47
17:i:128:LEU:HD12	17:i:216:PHE:HB3	1.97	0.47
33:r:502:PLX:H121	33:r:502:PLX:H92	1.65	0.47
29:w:165:SER:O	29:w:168:VAL:HG22	2.13	0.47
31:a:201:CDL:H191	31:a:201:CDL:H752	1.96	0.47
14:f:47:THR:HG23	15:g:65:LEU:HD22	1.96	0.47
15:g:101:GLU:CD	15:g:101:GLU:H	2.22	0.47
9:a:153:GLU:HG3	15:g:92:MET:HE2	1.97	0.47
25:r:168:GLN:HG3	25:r:174:LEU:HG	1.95	0.47
26:s:204:GLU:HA	26:s:208:VAL:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:u:4:ILE:HD12	27:u:4:ILE:O	2.15	0.47
4:V:134:GLN:NE2	17:i:274:GLU:HG3	2.28	0.47
15:g:52:ARG:NH2	29:w:338:LYS:O	2.48	0.47
31:s:401:CDL:H141	31:s:401:CDL:H171	1.72	0.47
17:i:62:THR:HG21	17:i:114:TRP:CD1	2.50	0.47
31:l:702:CDL:H401	25:r:445:LEU:HD22	1.96	0.47
22:n:39:ARG:HG3	22:n:57:TRP:CE2	2.50	0.47
5:W:127:LEU:CB	16:h:98:HIS:CD2	2.98	0.47
33:e:201:PLX:H382	25:r:67:VAL:HG12	1.96	0.47
14:f:70:LYS:HG2	14:f:75:LEU:HB2	1.96	0.47
18:j:32:GLU:CD	18:j:32:GLU:H	2.23	0.47
29:w:176:GLN:NE2	29:w:236:ASP:OD2	2.45	0.47
31:V:201:CDL:H742	31:V:201:CDL:H361	1.97	0.46
16:h:92:TYR:CE2	16:h:94:PRO:HB3	2.50	0.46
26:s:24:GLU:HA	26:s:271:LEU:HD13	1.95	0.46
6:X:91:ASP:OD1	8:Z:47:ARG:NH2	2.34	0.46
33:j:204:PLX:H132	33:j:204:PLX:H161	1.48	0.46
24:p:132:SER:O	24:p:136:GLU:HG3	2.16	0.46
6:X:136:GLU:OE1	24:p:18:ARG:NH2	2.49	0.46
17:i:75:ILE:HD12	19:k:40:LEU:HD22	1.97	0.46
26:s:233:MET:HE3	26:s:233:MET:HB3	1.80	0.46
17:i:119:THR:HG22	17:i:176:ARG:HB3	1.97	0.46
31:l:702:CDL:H452	25:r:445:LEU:HB3	1.97	0.46
29:w:83:LEU:HD22	29:w:156:GLY:HA3	1.98	0.46
2:S:66:LEU:HD11	27:u:74:ILE:HG22	1.97	0.46
4:V:61:PHE:HD2	4:V:104:ARG:HH21	1.64	0.46
25:r:104:LEU:HG	25:r:108:MET:HE2	1.98	0.46
26:s:214:GLU:OE2	37:s:2001:HOH:O	2.20	0.46
18:j:20:ILE:HD11	33:j:203:PLX:H201	1.97	0.46
26:s:225:MET:HG2	35:s:402:UQ:H212	1.97	0.46
16:h:87:ILE:HG22	16:h:92:TYR:CG	2.50	0.46
20:l:2:ASN:O	20:l:4:PHE:N	2.48	0.46
12:d:142:ARG:NE	13:e:138:GLU:O	2.43	0.46
23:o:53:ASP:HB3	23:o:56:ARG:HB2	1.98	0.46
17:i:291:TYR:CZ	30:i:401:PEE:H48	2.50	0.46
20:l:1:MET:O	20:l:1:MET:HG2	2.16	0.46
23:o:23:TYR:OH	24:p:68:GLU:HG3	2.15	0.46
29:w:65:ASN:OD1	29:w:66:ILE:N	2.41	0.46
31:l:702:CDL:O1	25:r:357:THR:OG1	2.31	0.45
26:s:101:GLY:O	26:s:105:MET:HG2	2.15	0.45
2:S:66:LEU:HD13	27:u:75:LYS:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:a:147:ALA:HB2	25:r:173:SER:HB2	1.98	0.45
20:l:332:HIS:HA	20:l:335:PHE:CZ	2.51	0.45
30:U:401:PEE:H77	30:U:401:PEE:H70	1.80	0.45
5:W:84:LEU:HD13	27:u:8:PRO:HG2	1.97	0.45
30:W:201:PEE:H14	30:W:201:PEE:H20	1.69	0.45
11:c:85:GLU:OE1	11:c:119:THR:OG1	2.30	0.45
21:m:83:TRP:HB2	31:s:401:CDL:H712	1.99	0.45
26:s:81:LEU:HD11	26:s:111:LEU:HG	1.98	0.45
18:j:97:LEU:HD21	33:j:204:PLX:H391	1.99	0.45
20:l:89:PHE:CD2	20:l:132:VAL:HG21	2.52	0.45
21:m:86:ASN:OD1	21:m:88:THR:N	2.50	0.45
26:s:85:MET:SD	26:s:108:MET:HB2	2.57	0.45
10:b:88:TYR:CE1	12:d:49:ARG:HG2	2.51	0.45
20:l:23:ASN:C	20:l:23:ASN:HD22	2.23	0.45
11:c:167:TYR:CD2	11:c:178:PRO:HG3	2.51	0.45
20:l:233:LEU:HB3	20:l:234:PRO:HD3	1.99	0.45
25:r:243:MET:HA	25:r:246:ILE:HG22	1.99	0.45
26:s:55:LEU:HD13	26:s:221:ALA:HB2	1.97	0.45
20:l:389:PHE:O	20:l:393:ASP:HB3	2.17	0.44
35:s:402:UQ:H221	35:s:402:UQ:H262	1.58	0.44
17:i:280:THR:O	17:i:284:MET:HG2	2.16	0.44
18:j:109:LYS:HA	18:j:109:LYS:HD3	1.89	0.44
19:k:23:ARG:HG3	21:m:23:LYS:HE2	1.99	0.44
20:l:10:THR:O	20:l:14:ILE:HG23	2.16	0.44
20:l:298:ILE:O	20:l:302:VAL:HG23	2.17	0.44
27:u:83:THR:HA	27:u:86:TRP:NE1	2.31	0.44
16:h:92:TYR:O	16:h:92:TYR:CD1	2.70	0.44
20:l:264:TYR:CD2	20:l:265:PRO:HD3	2.52	0.44
4:V:56:THR:HG21	31:k:101:CDL:H361	1.98	0.44
4:V:106:ARG:HA	4:V:106:ARG:NE	2.33	0.44
16:h:86:LEU:HA	16:h:89:GLU:HG2	1.98	0.44
17:i:23:SER:HB2	17:i:29:ILE:HG13	1.99	0.44
30:j:201:PEE:H48	30:j:201:PEE:H55	1.76	0.44
24:p:160:GLU:CD	24:p:160:GLU:H	2.26	0.44
25:r:3:LYS:HB3	25:r:3:LYS:HE2	1.82	0.44
25:r:346:ARG:O	25:r:419:TYR:HA	2.18	0.44
26:s:199:ASP:OD1	26:s:199:ASP:N	2.50	0.44
4:V:9:TYR:O	4:V:21:LYS:NZ	2.49	0.44
17:i:68:MET:HE1	19:k:37:MET:HE2	2.00	0.44
30:j:201:PEE:H59	30:j:201:PEE:H64	1.85	0.44
4:V:38:ALA:HA	31:k:101:CDL:H212	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:X:123:GLU:HG2	6:X:129:GLU:HA	1.98	0.44
11:c:167:TYR:CG	11:c:178:PRO:HG3	2.53	0.44
33:r:502:PLX:H101	33:r:502:PLX:H72	1.69	0.44
11:c:166:LEU:HB3	11:c:169:GLU:HB2	1.99	0.44
20:l:435:PRO:HB3	20:l:437:PHE:CZ	2.52	0.44
31:V:202:CDL:H792	31:V:202:CDL:H761	1.74	0.44
7:Y:43:ARG:HG3	7:Y:48:PRO:HA	2.00	0.44
11:c:111:MET:HE1	20:l:543:SER:HB2	1.99	0.44
21:m:45:LEU:CD1	21:m:50:SER:HA	2.47	0.44
25:r:307:TRP:HA	25:r:310:MET:HE2	2.00	0.44
22:n:17:VAL:HG13	25:r:7:PRO:HB3	2.00	0.44
20:l:136:ASN:HA	20:l:197:ASP:HA	1.99	0.43
5:W:55:ARG:NH2	26:s:311:THR:O	2.49	0.43
15:g:48:ASN:HB3	15:g:55:VAL:HA	2.00	0.43
20:l:44:PHE:HB2	20:l:94:LEU:HB3	1.99	0.43
20:l:293:ILE:HG13	20:l:294:THR:HG23	2.00	0.43
25:r:19:LYS:HG3	25:r:20:HIS:N	2.33	0.43
30:U:401:PEE:H14	30:U:401:PEE:H20	1.80	0.43
5:W:127:LEU:HB3	16:h:98:HIS:HD2	1.82	0.43
11:c:136:PHE:O	11:c:140:MET:HG2	2.19	0.43
13:e:92:PHE:O	13:e:96:SER:HB2	2.18	0.43
16:h:2:PRO:HA	17:i:140:SER:HB2	1.99	0.43
20:l:529:TYR:HB3	20:l:530:PRO:HD3	2.00	0.43
9:a:157:ARG:HG2	15:g:3:MET:HE2	2.01	0.43
23:o:31:LYS:HB3	23:o:31:LYS:HE3	1.57	0.43
25:r:210:TYR:CG	25:r:268:GLY:HA3	2.54	0.43
3:U:66:VAL:O	27:u:130:LYS:HE3	2.18	0.43
20:l:27:TYR:O	20:l:115:ASN:ND2	2.43	0.43
30:r:501:PEE:H68	30:r:501:PEE:H62	1.84	0.43
28:v:15:LYS:HG2	28:v:113:LYS:HE2	2.01	0.43
5:W:82:ARG:NH1	16:h:106:PRO:O	2.51	0.43
6:X:143:GLU:HG2	10:b:4:TYR:HE2	1.83	0.43
11:c:38:PRO:HG2	23:o:70:TYR:CD2	2.52	0.43
12:d:37:PHE:CE1	20:l:3:PRO:HB3	2.54	0.43
12:d:68:PHE:HD1	22:n:44:LEU:HD11	1.84	0.43
18:j:83:ASN:HD21	21:m:148:SER:HB2	1.84	0.43
23:o:50:GLN:O	23:o:56:ARG:HD3	2.18	0.43
26:s:313:SER:O	26:s:313:SER:OG	2.28	0.43
33:r:502:PLX:H1C3	33:r:502:PLX:H22	1.75	0.43
2:S:63:THR:HG23	27:u:21:SER:HB2	1.99	0.43
31:a:201:CDL:H441	31:a:201:CDL:H411	1.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:r:133:ILE:HD11	25:r:231:LEU:HD11	2.01	0.43
6:X:104:PHE:HD1	6:X:108:LEU:HD12	1.84	0.43
12:d:37:PHE:CD1	20:l:3:PRO:HB3	2.54	0.43
14:f:70:LYS:HA	14:f:75:LEU:HD23	2.01	0.43
20:l:293:ILE:HD12	31:l:703:CDL:H521	2.00	0.43
26:s:152:SER:HA	26:s:155:LEU:HD12	1.99	0.43
29:w:139:ARG:HH12	36:w:401:ADP:HN61	1.67	0.43
3:U:59:ASP:HB3	27:u:132:LYS:HG3	2.01	0.42
31:a:201:CDL:H362	10:b:80:TRP:HB3	2.01	0.42
20:l:327:LEU:HD23	20:l:391:SER:HB3	2.00	0.42
21:m:129:ASP:OD1	21:m:129:ASP:N	2.50	0.42
29:w:189:GLU:O	29:w:193:VAL:HG22	2.19	0.42
11:c:39:GLY:C	11:c:74:ASP:HB2	2.41	0.42
14:f:60:LYS:O	14:f:64:GLU:HG3	2.19	0.42
16:h:24:GLU:OE2	16:h:24:GLU:HA	2.19	0.42
16:h:89:GLU:CD	16:h:91:LYS:HE2	2.44	0.42
25:r:373:ILE:HA	25:r:376:ILE:HD12	2.00	0.42
26:s:2:PHE:O	26:s:6:ILE:HG13	2.20	0.42
31:i:402:CDL:H352	31:i:402:CDL:H381	1.79	0.42
30:j:201:PEE:H26	26:s:295:PRO:HB3	2.01	0.42
31:l:702:CDL:H342	31:l:702:CDL:H372	1.79	0.42
25:r:8:THR:O	25:r:11:LEU:HB2	2.19	0.42
1:Q:52:MET:HE2	17:i:173:THR:HG22	2.02	0.42
3:U:82:LYS:NZ	3:U:82:LYS:HB3	2.34	0.42
30:W:201:PEE:H41	21:m:35:VAL:HG13	2.00	0.42
12:d:78:GLU:HG2	15:g:108:LYS:HB3	2.00	0.42
13:e:79:ASP:HB3	13:e:82:VAL:HB	2.01	0.42
20:l:473:PRO:HG2	20:l:475:MET:HE3	2.01	0.42
4:V:140:LYS:HE3	9:a:158:ARG:HD3	2.01	0.42
27:u:74:ILE:HD13	27:u:74:ILE:HA	1.89	0.42
29:w:295:ARG:HA	29:w:298:VAL:HG22	2.01	0.42
6:X:122:MET:HG3	6:X:144:ILE:HG21	2.01	0.42
15:g:5:SER:OG	33:g:201:PLX:H1A1	2.19	0.42
17:i:324:LYS:HA	17:i:324:LYS:HD3	1.90	0.42
20:l:49:VAL:HB	20:l:50:PRO:HD3	2.01	0.42
3:U:67:PRO:HG3	3:U:74:GLN:C	2.45	0.42
31:V:202:CDL:OB7	31:V:202:CDL:O1	2.31	0.42
16:h:86:LEU:C	16:h:89:GLU:HG2	2.44	0.42
27:u:47:ARG:HA	27:u:47:ARG:HD2	1.87	0.42
3:U:33:PRO:HA	26:s:310:MET:HG2	2.01	0.42
11:c:126:TRP:O	11:c:127:ASN:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:i:168:GLY:HA3	17:i:181:TYR:CE1	2.55	0.42
20:l:230:HIS:N	20:l:231:PRO:HD3	2.35	0.42
20:l:331:MET:HE1	20:l:468:ILE:HD12	2.01	0.42
20:l:514:LYS:HB3	20:l:514:LYS:HE3	1.69	0.42
7:Y:51:THR:O	7:Y:54:GLN:HG2	2.19	0.42
10:b:32:GLU:OE1	24:p:115:TYR:HA	2.20	0.42
15:g:33:LEU:HD22	15:g:71:VAL:HG13	2.02	0.42
19:k:5:TYR:CG	19:k:43:MET:HE1	2.55	0.42
20:l:475:MET:HB3	28:v:52:MET:HE2	2.02	0.42
20:l:587:TYR:HA	20:l:590:SER:HB3	2.01	0.42
31:l:703:CDL:H201	31:l:703:CDL:H172	1.69	0.42
21:m:82:VAL:HG23	21:m:84:VAL:H	1.85	0.42
10:b:78:PRO:O	10:b:82:ILE:HG12	2.19	0.41
33:g:201:PLX:H332	17:i:342:ALA:HB3	2.01	0.41
16:h:83:ARG:CG	16:h:92:TYR:CE2	3.03	0.41
18:j:73:LEU:HD12	21:m:55:MET:SD	2.60	0.41
20:l:152:PHE:CD1	20:l:168:ALA:HB1	2.55	0.41
9:a:78:THR:HG21	13:e:96:SER:HA	2.02	0.41
20:l:149:ILE:HD13	20:l:149:ILE:HA	1.85	0.41
10:b:76:LEU:O	10:b:79:VAL:HG12	2.21	0.41
20:l:172:ILE:HD13	37:l:844:HOH:O	2.19	0.41
25:r:71:TRP:O	25:r:74:PRO:HD2	2.20	0.41
35:s:402:UQ:H202	35:s:402:UQ:H172	1.76	0.41
1:Q:47:PHE:CD1	1:Q:52:MET:HE1	2.53	0.41
30:U:401:PEE:H55	30:U:401:PEE:H61	1.60	0.41
7:Y:51:THR:O	7:Y:55:LEU:HD12	2.21	0.41
7:Y:65:MET:SD	20:l:375:ILE:HG12	2.61	0.41
9:a:184:LYS:C	9:a:186:THR:H	2.29	0.41
20:l:566:THR:O	20:l:570:GLN:HG2	2.21	0.41
12:d:23:GLN:HB2	28:v:72:ASP:HB3	2.01	0.41
13:e:73:SER:C	13:e:75:GLY:H	2.28	0.41
20:l:557:TRP:O	20:l:561:ILE:HG12	2.20	0.41
29:w:110:GLY:HA2	29:w:134:TRP:CE2	2.55	0.41
9:a:66:ARG:HH12	13:e:72:ASP:HB2	1.86	0.41
33:j:204:PLX:H342	33:j:204:PLX:H372	1.79	0.41
31:k:101:CDL:H161	31:k:101:CDL:H191	1.82	0.41
29:w:281:GLY:O	29:w:284:PRO:HD2	2.21	0.41
1:Q:51:VAL:HG13	1:Q:52:MET:O	2.21	0.41
3:U:30:ILE:HD12	30:j:201:PEE:H43	2.03	0.41
11:c:155:PRO:HD3	28:v:4:HIS:CE1	2.56	0.41
18:j:80:GLN:HG3	26:s:318:SER:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:l:102:GLU:OE1	20:l:456:ARG:NH2	2.40	0.41
21:m:91:GLY:O	21:m:95:SER:OG	2.28	0.41
29:w:72:ARG:HG3	29:w:72:ARG:HH11	1.86	0.41
29:w:246:LEU:HD22	29:w:255:VAL:HG11	2.03	0.41
15:g:107:ASP:OD1	15:g:107:ASP:N	2.54	0.41
5:W:68:ARG:HD2	21:m:135:PHE:CD2	2.55	0.41
10:b:25:ASP:OD2	24:p:125:TRP:NE1	2.34	0.41
13:e:55:LEU:HD11	29:w:320:GLY:HA2	2.03	0.41
13:e:76:TYR:HB2	13:e:83:ASP:OD1	2.21	0.41
17:i:111:PHE:HA	20:l:591:PHE:CE1	2.56	0.41
20:l:488:MET:HE2	20:l:488:MET:HA	2.02	0.41
24:p:174:PRO:O	24:p:175:ARG:HB2	2.21	0.41
25:r:186:LEU:HD23	25:r:186:LEU:HA	1.93	0.41
25:r:206:LYS:HA	25:r:206:LYS:HD2	1.87	0.41
25:r:449:LEU:HD23	25:r:449:LEU:HA	1.89	0.41
28:v:113:LYS:HB3	28:v:113:LYS:HE3	1.80	0.41
8:Z:30:GLU:O	8:Z:34:GLU:HG3	2.21	0.41
13:e:89:VAL:HG21	25:r:25:ILE:HG23	2.02	0.41
30:j:201:PEE:H35	30:j:201:PEE:H30	1.90	0.41
3:U:37:PRO:HG2	3:U:38:TYR:CD1	2.56	0.40
33:a:202:PLX:H91	25:r:40:SER:HB3	2.02	0.40
12:d:158:LYS:HG3	15:g:118:PHE:CE2	2.56	0.40
17:i:102:LEU:HD13	17:i:142:LEU:HG	2.03	0.40
17:i:17:THR:O	17:i:21:MET:HG3	2.20	0.40
33:r:502:PLX:H6	33:r:502:PLX:H51	1.36	0.40
29:w:345:GLU:HB3	29:w:352:ILE:HD12	2.03	0.40
18:j:85:LYS:HZ3	18:j:85:LYS:HG3	1.83	0.40
20:l:401:MET:HE3	20:l:401:MET:HB3	1.94	0.40
20:l:407:TRP:CZ2	20:l:411:MET:HE3	2.56	0.40
28:v:108:LEU:HD23	28:v:108:LEU:HA	1.93	0.40
30:U:401:PEE:H17	26:s:296:LEU:HD23	2.04	0.40
6:X:82:ARG:HH12	20:l:440:LEU:HD22	1.86	0.40
10:b:10:LEU:HA	10:b:13:GLN:HG3	2.04	0.40
10:b:32:GLU:HB3	24:p:115:TYR:HD1	1.86	0.40
10:b:93:LYS:HB3	10:b:93:LYS:HE3	1.68	0.40
12:d:31:THR:O	12:d:34:THR:HG22	2.21	0.40
17:i:87:THR:HB	17:i:88:LYS:H	1.78	0.40
18:j:57:LEU:HD21	21:m:169:MET:HE3	2.03	0.40
19:k:75:LEU:HD23	19:k:75:LEU:HA	1.91	0.40
31:l:703:CDL:H641	31:l:703:CDL:H612	1.69	0.40
25:r:76:MET:HE2	25:r:99:LEU:HD22	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:s:172:ILE:HG12	26:s:176:PHE:HD2	1.85	0.40
27:u:152:PRO:O	27:u:153:GLU:HB2	2.22	0.40
5:W:53:TRP:NE1	5:W:57:ARG:HD2	2.37	0.40
7:Y:41:GLU:H	7:Y:41:GLU:HG2	1.73	0.40
33:j:204:PLX:H1C3	33:j:204:PLX:H22	1.83	0.40
31:k:101:CDL:H392	31:k:101:CDL:H362	1.67	0.40
25:r:243:MET:HB3	25:r:301:ILE:HG21	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
2	S	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
3	U	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
4	V	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
5	W	111/113 (98%)	108 (97%)	3 (3%)	0	100	100
6	X	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
7	Y	65/67 (97%)	62 (95%)	3 (5%)	0	100	100
8	Z	78/80 (98%)	76 (97%)	2 (3%)	0	100	100
9	a	136/138 (99%)	132 (97%)	4 (3%)	0	100	100
10	b	94/126 (75%)	85 (90%)	9 (10%)	0	100	100
11	c	154/156 (99%)	144 (94%)	10 (6%)	0	100	100
12	d	173/175 (99%)	171 (99%)	2 (1%)	0	100	100
13	e	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
14	f	47/49 (96%)	43 (92%)	4 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	g	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
16	h	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
17	i	345/347 (99%)	330 (96%)	15 (4%)	0	100	100
18	j	113/115 (98%)	110 (97%)	3 (3%)	0	100	100
19	k	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
20	l	604/606 (100%)	584 (97%)	20 (3%)	0	100	100
21	m	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
22	n	54/56 (96%)	54 (100%)	0	0	100	100
23	o	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
24	p	176/178 (99%)	168 (96%)	7 (4%)	1 (1%)	21	38
25	r	456/458 (100%)	449 (98%)	7 (2%)	0	100	100
26	s	316/318 (99%)	306 (97%)	9 (3%)	1 (0%)	36	55
27	u	169/171 (99%)	163 (96%)	5 (3%)	1 (1%)	21	38
28	v	122/124 (98%)	115 (94%)	7 (6%)	0	100	100
29	w	318/320 (99%)	306 (96%)	12 (4%)	0	100	100
All	All	4666/4754 (98%)	4499 (96%)	164 (4%)	3 (0%)	49	68

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	s	208	VAL
27	u	152	PRO
24	p	174	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Q	38/38 (100%)	37 (97%)	1 (3%)	40	68
2	S	57/58 (98%)	56 (98%)	1 (2%)	51	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	U	69/69 (100%)	69 (100%)	0	100	100
4	V	101/101 (100%)	99 (98%)	2 (2%)	48	75
5	W	99/99 (100%)	98 (99%)	1 (1%)	68	86
6	X	79/81 (98%)	78 (99%)	1 (1%)	61	82
7	Y	62/62 (100%)	61 (98%)	1 (2%)	55	79
8	Z	62/62 (100%)	62 (100%)	0	100	100
9	a	121/121 (100%)	120 (99%)	1 (1%)	73	88
10	b	90/119 (76%)	90 (100%)	0	100	100
11	c	140/141 (99%)	140 (100%)	0	100	100
12	d	155/155 (100%)	152 (98%)	3 (2%)	50	76
13	e	96/96 (100%)	96 (100%)	0	100	100
14	f	36/45 (80%)	35 (97%)	1 (3%)	38	66
15	g	108/109 (99%)	106 (98%)	2 (2%)	50	76
16	h	93/93 (100%)	92 (99%)	1 (1%)	65	84
17	i	311/311 (100%)	308 (99%)	3 (1%)	68	86
18	j	100/100 (100%)	97 (97%)	3 (3%)	36	64
19	k	85/85 (100%)	85 (100%)	0	100	100
20	l	540/540 (100%)	533 (99%)	7 (1%)	61	82
21	m	129/141 (92%)	127 (98%)	2 (2%)	55	79
22	n	53/53 (100%)	52 (98%)	1 (2%)	50	76
23	o	113/113 (100%)	113 (100%)	0	100	100
24	p	159/159 (100%)	158 (99%)	1 (1%)	78	91
25	r	409/409 (100%)	408 (100%)	1 (0%)	87	95
26	s	275/275 (100%)	274 (100%)	1 (0%)	84	93
27	u	153/153 (100%)	152 (99%)	1 (1%)	76	89
28	v	103/111 (93%)	102 (99%)	1 (1%)	68	86
29	w	281/283 (99%)	278 (99%)	3 (1%)	65	84
All	All	4117/4182 (98%)	4078 (99%)	39 (1%)	68	87

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Q	51	VAL

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Mol	Chain	Res	Type
2	S	30	THR
4	V	63	SER
4	V	77	SER
5	W	34	SER
6	X	152	LYS
7	Y	50	LEU
9	a	114	LYS
12	d	78	GLU
12	d	127	LYS
12	d	136	SER
14	f	67	LEU
15	g	69	SER
15	g	97	LYS
16	h	21	GLN
17	i	149	ILE
17	i	323	MET
17	i	336	VAL
18	j	26	GLN
18	j	31	SER
18	j	83	ASN
20	l	9	LEU
20	l	70	THR
20	l	132	VAL
20	l	140	LEU
20	l	349	SER
20	l	554	ASP
20	l	581	LYS
21	m	135	PHE
21	m	167	VAL
22	n	4	VAL
24	p	69	GLU
25	r	179	ILE
26	s	40	VAL
27	u	106	LYS
28	v	53	LEU
29	w	152	SER
29	w	203	VAL
29	w	354	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
2	S	27	HIS
2	S	68	ASN
3	U	11	ASN
3	U	52	ASN
3	U	71	GLN
4	V	129	GLN
5	W	61	GLN
5	W	76	GLN
6	X	142	GLN
12	d	134	GLN
13	e	140	ASN
15	g	63	GLN
15	g	90	HIS
17	i	36	ASN
17	i	77	ASN
17	i	134	GLN
17	i	150	ASN
19	k	57	ASN
19	k	92	ASN
20	l	226	GLN
20	l	296	ASN
23	o	50	GLN
23	o	79	ASN
24	p	62	GLN
25	r	43	ASN
25	r	44	GLN
25	r	51	ASN
25	r	83	HIS
25	r	192	ASN
25	r	366	ASN
25	r	399	ASN
26	s	194	ASN
26	s	287	HIS
27	u	30	HIS
27	u	65	GLN
27	u	77	HIS
27	u	163	HIS
28	v	55	GLN
29	w	132	GLN
29	w	300	ASN

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 ⓘ

28 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
30	PEE	W	201	-	40,40,50	1.16	5 (12%)	43,45,55	1.01	2 (4%)
30	PEE	l	704	-	50,50,50	1.18	6 (12%)	53,55,55	0.95	2 (3%)
35	UQ	s	402	-	38,38,63	3.62	9 (23%)	48,49,79	2.81	17 (35%)
33	PLX	j	204	-	51,51,51	1.20	4 (7%)	53,59,59	0.65	1 (1%)
33	PLX	r	502	-	51,51,51	1.21	5 (9%)	53,59,59	0.62	1 (1%)
34	TYR	r	503	-	11,12,13	0.45	0	10,15,17	0.20	0
31	CDL	V	202	-	99,99,99	1.11	8 (8%)	105,111,111	0.89	4 (3%)
30	PEE	l	701	-	39,39,50	1.33	6 (15%)	42,44,55	1.13	3 (7%)
31	CDL	u	201	-	54,54,99	1.39	9 (16%)	60,66,111	1.08	4 (6%)
33	PLX	j	203	-	51,51,51	1.20	4 (7%)	53,59,59	0.63	1 (1%)
31	CDL	l	703	-	99,99,99	1.11	8 (8%)	105,111,111	0.92	5 (4%)
30	PEE	U	401	-	50,50,50	1.18	6 (12%)	53,55,55	1.01	2 (3%)
31	CDL	s	401	-	88,88,99	1.16	8 (9%)	94,100,111	0.94	5 (5%)
31	CDL	l	702	-	98,98,99	1.12	9 (9%)	104,110,111	0.90	4 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	PEE	j	201	-	50,50,50	1.18	6 (12%)	53,55,55	0.97	2 (3%)
33	PLX	g	201	-	51,51,51	1.19	4 (7%)	53,59,59	0.65	1 (1%)
36	ADP	w	401	-	28,29,29	3.18	9 (32%)	43,45,45	1.90	8 (18%)
30	PEE	i	401	-	46,46,50	1.22	6 (13%)	49,51,55	1.02	2 (4%)
31	CDL	a	201	-	99,99,99	1.11	8 (8%)	105,111,111	0.88	4 (3%)
33	PLX	a	202	-	51,51,51	1.21	4 (7%)	53,59,59	0.62	1 (1%)
30	PEE	r	501	-	50,50,50	1.18	6 (12%)	53,55,55	0.98	2 (3%)
32	8Q1	X	201	-	32,34,34	1.63	6 (18%)	39,43,43	1.65	5 (12%)
31	CDL	k	101	-	93,93,99	1.14	8 (8%)	99,105,111	0.87	4 (4%)
30	PEE	j	202	-	40,40,50	1.17	5 (12%)	43,45,55	1.06	2 (4%)
33	PLX	e	201	-	51,51,51	1.21	5 (9%)	53,59,59	0.54	1 (1%)
31	CDL	V	201	-	93,93,99	1.14	8 (8%)	99,105,111	0.84	4 (4%)
31	CDL	i	402	-	99,99,99	1.11	8 (8%)	105,111,111	0.86	4 (3%)
30	PEE	l	705	-	45,45,50	1.25	6 (13%)	48,50,55	1.00	2 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	PEE	W	201	-	-	21/44/44/54	-
30	PEE	l	704	-	-	26/54/54/54	-
35	UQ	s	402	-	-	13/33/57/87	0/1/1/1
33	PLX	j	204	-	-	24/55/55/55	-
33	PLX	r	502	-	-	31/55/55/55	-
34	TYR	r	503	-	-	0/5/6/8	0/1/1/1
31	CDL	V	202	-	-	60/110/110/110	-
30	PEE	l	701	-	-	17/43/43/54	-
31	CDL	u	201	-	-	26/65/65/110	-
33	PLX	j	203	-	-	37/55/55/55	-
31	CDL	l	703	-	-	54/110/110/110	-
30	PEE	U	401	-	-	22/54/54/54	-
31	CDL	s	401	-	-	46/99/99/110	-
31	CDL	l	702	-	-	57/109/109/110	-
30	PEE	j	201	-	-	20/54/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	PLX	g	201	-	-	32/55/55/55	-
36	ADP	w	401	-	-	6/16/32/32	0/3/3/3
30	PEE	i	401	-	-	22/50/50/54	-
31	CDL	a	201	-	-	54/110/110/110	-
33	PLX	a	202	-	-	31/55/55/55	-
30	PEE	r	501	-	-	25/54/54/54	-
32	8Q1	X	201	-	-	12/41/41/41	-
31	CDL	k	101	-	-	49/104/104/110	-
30	PEE	j	202	-	-	24/44/44/54	-
33	PLX	e	201	-	-	29/55/55/55	-
31	CDL	V	201	-	-	54/104/104/110	-
31	CDL	i	402	-	-	58/110/110/110	-
30	PEE	l	705	-	-	17/49/49/54	-

All (176) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	s	402	UQ	C18-C19	9.97	1.56	1.33
35	s	402	UQ	C13-C14	9.58	1.55	1.33
35	s	402	UQ	C23-C24	9.44	1.54	1.33
35	s	402	UQ	C8-C9	9.36	1.54	1.33
36	w	401	ADP	C3'-C4'	-8.96	1.30	1.53
36	w	401	ADP	O4'-C4'	7.79	1.62	1.45
35	s	402	UQ	C28-C29	7.30	1.54	1.32
36	w	401	ADP	PA-O3A	6.53	1.66	1.59
36	w	401	ADP	C6-N6	5.42	1.48	1.34
32	X	201	8Q1	C39-N41	5.13	1.45	1.33
32	X	201	8Q1	C34-N36	5.07	1.45	1.33
36	w	401	ADP	O4'-C1'	-4.57	1.31	1.42
30	l	701	PEE	C18-C19	3.84	1.53	1.31
30	l	705	PEE	C18-C19	3.83	1.53	1.31
30	l	704	PEE	C18-C19	3.82	1.53	1.31
30	U	401	PEE	C18-C19	3.81	1.53	1.31
30	j	202	PEE	C18-C19	3.81	1.53	1.31
30	j	201	PEE	C18-C19	3.80	1.53	1.31
30	r	501	PEE	C18-C19	3.80	1.53	1.31
30	W	201	PEE	C18-C19	3.78	1.53	1.31
30	i	401	PEE	C18-C19	3.77	1.53	1.31
30	r	501	PEE	C39-C38	3.74	1.53	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	j	201	PEE	C39-C38	3.74	1.52	1.31
30	l	701	PEE	C39-C38	3.73	1.52	1.31
30	i	401	PEE	C39-C38	3.73	1.52	1.31
30	U	401	PEE	C39-C38	3.73	1.52	1.31
30	l	705	PEE	C39-C38	3.71	1.52	1.31
30	l	704	PEE	C39-C38	3.71	1.52	1.31
31	u	201	CDL	OA8-CA7	3.48	1.43	1.33
31	V	201	CDL	OA8-CA7	3.47	1.43	1.33
31	i	402	CDL	OA8-CA7	3.46	1.43	1.33
31	a	201	CDL	OA8-CA7	3.46	1.43	1.33
31	l	703	CDL	OA8-CA7	3.45	1.43	1.33
31	s	401	CDL	OA8-CA7	3.43	1.43	1.33
31	V	202	CDL	OA8-CA7	3.43	1.43	1.33
31	l	702	CDL	OA8-CA7	3.43	1.43	1.33
31	k	101	CDL	OA8-CA7	3.40	1.43	1.33
36	w	401	ADP	C8-N9	-3.35	1.31	1.37
31	k	101	CDL	OA6-CA5	3.29	1.43	1.34
36	w	401	ADP	O2'-C2'	-3.21	1.35	1.43
31	a	201	CDL	OB6-CB5	3.08	1.43	1.34
31	V	201	CDL	OA6-CA5	3.07	1.43	1.34
31	s	401	CDL	OB6-CB5	3.05	1.42	1.34
31	i	402	CDL	OB6-CB5	3.03	1.42	1.34
31	l	702	CDL	OB6-CB5	3.03	1.42	1.34
31	l	702	CDL	OB8-CB7	3.02	1.42	1.33
31	k	101	CDL	OB6-CB5	3.02	1.42	1.34
31	u	201	CDL	OB6-CB5	3.02	1.42	1.34
31	i	402	CDL	OB8-CB7	3.01	1.42	1.33
31	s	401	CDL	OA6-CA5	3.01	1.42	1.34
31	a	201	CDL	OB8-CB7	3.00	1.42	1.33
31	l	703	CDL	OB8-CB7	3.00	1.42	1.33
31	u	201	CDL	OA6-CA5	2.99	1.42	1.34
31	V	202	CDL	OB6-CB5	2.98	1.42	1.34
31	u	201	CDL	OB8-CB7	2.97	1.42	1.33
31	l	702	CDL	OA6-CA5	2.97	1.42	1.34
31	l	703	CDL	OB6-CB5	2.97	1.42	1.34
36	w	401	ADP	O3'-C3'	2.96	1.50	1.43
31	V	201	CDL	OB8-CB7	2.96	1.42	1.33
31	V	201	CDL	OB6-CB5	2.96	1.42	1.34
31	i	402	CDL	OA6-CA5	2.94	1.42	1.34
31	V	202	CDL	OA6-CA5	2.93	1.42	1.34
31	k	101	CDL	OB8-CB7	2.93	1.41	1.33
31	a	201	CDL	OA6-CA5	2.93	1.42	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	s	401	CDL	OB8-CB7	2.91	1.41	1.33
31	l	703	CDL	OA6-CA5	2.90	1.42	1.34
33	g	201	PLX	O6-C4	-2.89	1.40	1.44
31	V	202	CDL	OB8-CB7	2.88	1.41	1.33
33	a	202	PLX	O6-C4	-2.81	1.41	1.44
33	e	201	PLX	O6-C4	-2.76	1.41	1.44
33	j	203	PLX	O6-C4	-2.74	1.41	1.44
30	U	401	PEE	O2-C2	-2.69	1.40	1.46
35	s	402	UQ	C6-C1	2.67	1.54	1.46
33	j	204	PLX	O6-C4	-2.63	1.41	1.44
30	W	201	PEE	O2-C2	-2.62	1.40	1.46
31	V	202	CDL	OA6-CA4	-2.59	1.40	1.46
30	l	704	PEE	O2-C2	-2.58	1.40	1.46
31	a	201	CDL	OA6-CA4	-2.57	1.40	1.46
30	i	401	PEE	O2-C2	-2.56	1.40	1.46
31	u	201	CDL	OA6-CA4	-2.56	1.40	1.46
30	l	705	PEE	O2-C2	-2.55	1.40	1.46
31	i	402	CDL	OA6-CA4	-2.54	1.40	1.46
30	j	201	PEE	O2-C2	-2.51	1.40	1.46
30	j	202	PEE	O3-C30	2.51	1.40	1.33
30	l	705	PEE	O3-C30	2.50	1.40	1.33
31	l	703	CDL	OA6-CA4	-2.50	1.40	1.46
30	l	701	PEE	O3-C30	2.49	1.40	1.33
31	l	702	CDL	OA6-CA4	-2.49	1.40	1.46
30	j	202	PEE	O2-C2	-2.49	1.40	1.46
30	r	501	PEE	O2-C2	-2.49	1.40	1.46
33	j	204	PLX	C7-C6	2.49	1.55	1.50
31	s	401	CDL	OA6-CA4	-2.48	1.40	1.46
30	l	701	PEE	O2-C2	-2.47	1.40	1.46
32	X	201	8Q1	C1-S44	2.46	1.82	1.76
33	r	502	PLX	C7-C6	2.46	1.55	1.50
30	j	201	PEE	O3-C30	2.46	1.40	1.33
33	r	502	PLX	O6-C4	-2.45	1.41	1.44
32	X	201	8Q1	C6-C1	2.43	1.53	1.50
30	U	401	PEE	O3-C30	2.41	1.40	1.33
30	W	201	PEE	O3-C30	2.40	1.40	1.33
36	w	401	ADP	C5-N7	-2.39	1.34	1.39
31	k	101	CDL	OB6-CB4	-2.38	1.41	1.46
31	u	201	CDL	OB6-CB4	-2.38	1.41	1.46
30	i	401	PEE	O3-C30	2.38	1.40	1.33
31	l	702	CDL	OB6-CB4	-2.37	1.41	1.46
33	j	203	PLX	C7-C6	2.36	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	a	202	PLX	C7-C6	2.36	1.55	1.50
31	V	202	CDL	OB6-CB4	-2.34	1.41	1.46
33	e	201	PLX	C7-C6	2.34	1.55	1.50
30	l	704	PEE	O3-C30	2.34	1.40	1.33
30	l	705	PEE	O2-C10	2.33	1.40	1.34
31	V	201	CDL	OB6-CB4	-2.33	1.41	1.46
31	s	401	CDL	OB6-CB4	-2.33	1.41	1.46
31	V	201	CDL	OA6-CA4	-2.33	1.41	1.46
31	V	202	CDL	PB2-OB2	2.33	1.68	1.59
30	i	401	PEE	O2-C10	2.33	1.40	1.34
31	i	402	CDL	OB6-CB4	-2.33	1.41	1.46
33	g	201	PLX	C7-C6	2.32	1.55	1.50
32	X	201	8Q1	O35-C34	-2.32	1.18	1.23
30	r	501	PEE	O3-C30	2.31	1.40	1.33
31	l	703	CDL	OB6-CB4	-2.31	1.41	1.46
30	l	701	PEE	O2-C10	2.31	1.40	1.34
30	l	704	PEE	O3-C3	-2.30	1.40	1.45
30	r	501	PEE	O2-C10	2.28	1.40	1.34
31	u	201	CDL	PB2-OB2	2.28	1.68	1.59
32	X	201	8Q1	O40-C39	-2.27	1.18	1.23
30	W	201	PEE	O2-C10	2.27	1.40	1.34
30	j	201	PEE	O2-C10	2.27	1.40	1.34
31	a	201	CDL	PB2-OB5	2.26	1.68	1.59
30	j	202	PEE	O2-C10	2.26	1.40	1.34
30	r	501	PEE	O3-C3	-2.26	1.40	1.45
31	s	401	CDL	PB2-OB2	2.26	1.68	1.59
31	a	201	CDL	OB6-CB4	-2.26	1.41	1.46
31	i	402	CDL	PB2-OB2	2.26	1.68	1.59
31	V	201	CDL	PB2-OB2	2.26	1.68	1.59
31	l	702	CDL	PB2-OB5	2.25	1.68	1.59
30	l	704	PEE	O2-C10	2.23	1.40	1.34
33	a	202	PLX	P1-O4	2.22	1.68	1.59
31	V	201	CDL	PB2-OB5	2.22	1.68	1.59
31	l	702	CDL	PB2-OB2	2.22	1.68	1.59
31	l	703	CDL	PB2-OB5	2.22	1.68	1.59
31	u	201	CDL	PB2-OB5	2.21	1.68	1.59
30	U	401	PEE	O2-C10	2.21	1.40	1.34
33	j	204	PLX	P1-O4	2.20	1.68	1.59
35	s	402	UQ	C7-C8	2.20	1.54	1.50
33	r	502	PLX	P1-O4	2.20	1.68	1.59
31	i	402	CDL	PB2-OB5	2.20	1.68	1.59
30	W	201	PEE	O3-C3	-2.20	1.40	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	i	401	PEE	O3-C3	-2.19	1.40	1.45
31	V	202	CDL	PB2-OB5	2.18	1.67	1.59
31	l	703	CDL	PB2-OB2	2.17	1.67	1.59
30	U	401	PEE	O3-C3	-2.16	1.40	1.45
33	e	201	PLX	P1-O4	2.16	1.67	1.59
33	g	201	PLX	P1-O4	2.15	1.67	1.59
31	a	201	CDL	PB2-OB2	2.15	1.67	1.59
31	s	401	CDL	PB2-OB5	2.14	1.67	1.59
31	k	101	CDL	PB2-OB5	2.14	1.67	1.59
31	k	101	CDL	PB2-OB2	2.14	1.67	1.59
33	r	502	PLX	P1-O1	2.13	1.67	1.59
30	j	201	PEE	O3-C3	-2.12	1.40	1.45
31	k	101	CDL	OA6-CA4	-2.12	1.41	1.46
30	l	701	PEE	O3-C3	-2.10	1.40	1.45
33	j	203	PLX	P1-O1	2.10	1.67	1.59
35	s	402	UQ	O3-CM3	-2.09	1.40	1.45
33	a	202	PLX	P1-O1	2.09	1.67	1.59
35	s	402	UQ	O4-C4	-2.09	1.18	1.23
33	j	204	PLX	P1-O1	2.09	1.67	1.59
33	r	502	PLX	C25-C24	2.08	1.55	1.50
33	j	203	PLX	P1-O4	2.07	1.67	1.59
31	l	702	CDL	C11-CA5	2.04	1.56	1.50
30	j	202	PEE	O3-C3	-2.04	1.40	1.45
30	l	705	PEE	O3-C3	-2.03	1.40	1.45
33	e	201	PLX	P1-O1	2.03	1.67	1.59
33	g	201	PLX	P1-O1	2.02	1.67	1.59
33	e	201	PLX	C1-C2	2.02	1.57	1.51
31	u	201	CDL	C11-CA5	2.01	1.56	1.50

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	s	402	UQ	C7-C8-C9	-8.13	112.83	126.83
35	s	402	UQ	C17-C18-C19	-6.39	113.00	127.62
35	s	402	UQ	C12-C13-C14	-6.22	113.38	127.62
32	X	201	8Q1	C6-C1-S44	6.16	120.75	113.40
35	s	402	UQ	C22-C23-C24	-5.78	114.38	127.62
36	w	401	ADP	C5-C4-N3	-5.40	119.28	126.72
36	w	401	ADP	N3-C2-N1	-4.59	121.63	128.58
35	s	402	UQ	C10-C9-C8	-4.32	112.54	123.63
35	s	402	UQ	C27-C28-C29	-4.29	113.32	127.64
30	j	202	PEE	O2-C10-C11	4.25	120.68	111.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	s	402	UQ	C25-C24-C23	-4.23	112.75	123.63
31	l	702	CDL	OA6-CA5-C11	4.22	120.62	111.48
36	w	401	ADP	N3-C4-N9	4.22	134.35	127.17
31	a	201	CDL	OB6-CB5-C51	4.19	120.55	111.48
31	l	703	CDL	OA6-CA5-C11	4.13	120.42	111.48
31	s	401	CDL	OA6-CA5-C11	4.13	120.41	111.48
30	l	701	PEE	O2-C10-C11	4.12	120.39	111.48
35	s	402	UQ	C20-C19-C18	-4.10	113.11	123.63
31	l	703	CDL	OB6-CB5-C51	4.08	120.32	111.48
30	l	705	PEE	O2-C10-C11	4.08	120.30	111.48
30	j	201	PEE	O2-C10-C11	4.07	120.29	111.48
30	r	501	PEE	O2-C10-C11	4.05	120.24	111.48
31	i	402	CDL	OA6-CA5-C11	3.99	120.11	111.48
31	V	202	CDL	OB6-CB5-C51	3.96	120.04	111.48
31	s	401	CDL	OB6-CB5-C51	3.95	120.03	111.48
30	i	401	PEE	O2-C10-C11	3.94	120.00	111.48
31	V	202	CDL	OA6-CA5-C11	3.94	120.00	111.48
30	U	401	PEE	O2-C10-C11	3.91	119.95	111.48
35	s	402	UQ	C15-C14-C13	-3.89	113.64	123.63
31	i	402	CDL	OB6-CB5-C51	3.88	119.87	111.48
31	u	201	CDL	OB6-CB5-C51	3.85	119.81	111.48
31	V	201	CDL	OB6-CB5-C51	3.82	119.75	111.48
31	u	201	CDL	OA6-CA5-C11	3.82	119.74	111.48
31	a	201	CDL	OA6-CA5-C11	3.81	119.71	111.48
31	k	101	CDL	OB6-CB5-C51	3.79	119.69	111.48
35	s	402	UQ	C16-C14-C13	-3.79	112.67	121.17
30	W	201	PEE	O2-C10-C11	3.77	119.64	111.48
31	l	702	CDL	OB6-CB5-C51	3.76	119.61	111.48
32	X	201	8Q1	O4-C1-C6	-3.72	119.69	123.98
35	s	402	UQ	C21-C19-C18	-3.70	112.87	121.17
35	s	402	UQ	C11-C9-C8	-3.66	112.95	121.17
31	V	201	CDL	OA6-CA5-C11	3.65	119.38	111.48
30	l	704	PEE	O2-C10-C11	3.64	119.36	111.48
32	X	201	8Q1	C37-C38-C39	3.58	118.36	112.39
36	w	401	ADP	C2-N3-C4	3.58	120.56	111.83
36	w	401	ADP	N9-C8-N7	-3.53	108.93	113.94
35	s	402	UQ	C30-C29-C28	-3.34	112.64	122.66
31	k	101	CDL	OA6-CA5-C11	3.33	118.69	111.48
35	s	402	UQ	C26-C24-C23	-3.26	113.85	121.17
35	s	402	UQ	C31-C29-C28	-3.25	112.91	122.66
36	w	401	ADP	C4-N9-C8	3.19	109.08	105.74
36	w	401	ADP	C5-N7-C8	3.18	108.44	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	U	401	PEE	O3-C30-C31	3.03	121.06	111.83
36	w	401	ADP	C4-C5-N7	-2.99	107.17	110.58
31	k	101	CDL	OA8-CA7-C31	2.98	120.92	111.83
30	l	704	PEE	O3-C30-C31	2.87	120.59	111.83
31	u	201	CDL	OA8-CA7-C31	2.84	119.76	111.15
31	V	202	CDL	OB8-CB7-C71	2.83	120.47	111.83
31	a	201	CDL	OB8-CB7-C71	2.83	120.46	111.83
31	l	702	CDL	OA8-CA7-C31	2.80	120.38	111.83
31	l	703	CDL	OB8-CB7-C71	2.80	120.37	111.83
30	j	202	PEE	O3-C30-C31	2.77	120.27	111.83
30	i	401	PEE	O3-C30-C31	2.77	120.27	111.83
31	l	703	CDL	OA8-CA7-C31	2.75	120.22	111.83
30	l	701	PEE	O3-C30-C31	2.73	120.17	111.83
31	k	101	CDL	OB8-CB7-C71	2.71	120.11	111.83
31	l	702	CDL	OB8-CB7-C71	2.71	120.09	111.83
30	W	201	PEE	O3-C30-C31	2.71	120.09	111.83
31	i	402	CDL	OA8-CA7-C31	2.70	120.07	111.83
31	s	401	CDL	OA8-CA7-C31	2.68	120.01	111.83
31	V	201	CDL	OB8-CB7-C71	2.68	120.00	111.83
31	u	201	CDL	OB8-CB7-C71	2.68	120.00	111.83
31	V	202	CDL	OA8-CA7-C31	2.67	119.98	111.83
30	r	501	PEE	O3-C30-C31	2.65	119.91	111.83
31	V	201	CDL	OA8-CA7-C31	2.64	119.89	111.83
30	l	705	PEE	O3-C30-C31	2.64	119.87	111.83
31	i	402	CDL	OB8-CB7-C71	2.62	119.83	111.83
31	a	201	CDL	OA8-CA7-C31	2.62	119.83	111.83
30	j	201	PEE	O3-C30-C31	2.58	119.70	111.83
33	r	502	PLX	C1A-N1-C1	2.56	120.07	109.91
35	s	402	UQ	C7-C6-C5	-2.54	120.54	124.89
31	s	401	CDL	OB8-CB7-C71	2.49	119.44	111.83
32	X	201	8Q1	O4-C1-S44	-2.45	119.56	122.68
33	j	204	PLX	C1A-N1-C1	2.43	119.58	109.91
35	s	402	UQ	CM5-C5-C6	-2.43	120.46	124.45
33	a	202	PLX	C1A-N1-C1	2.43	119.55	109.91
33	g	201	PLX	C1A-N1-C1	2.42	119.52	109.91
33	j	203	PLX	C1A-N1-C1	2.38	119.36	109.91
30	l	701	PEE	C20-C19-C18	-2.32	112.47	126.42
32	X	201	8Q1	C43-S44-C1	2.24	108.47	101.84
33	e	201	PLX	C1A-N1-C1	2.22	118.73	109.91
31	l	703	CDL	CB4-OB6-CB5	-2.10	112.78	117.80
31	s	401	CDL	CA4-OA6-CA5	-2.06	112.86	117.80

There are no chirality outliers.

All (867) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	i	401	PEE	C11-C10-O2-C2
30	i	401	PEE	O4-C10-O2-C2
30	i	401	PEE	C4-O4P-P-O3P
30	i	401	PEE	C4-O4P-P-O1P
30	j	202	PEE	C11-C10-O2-C2
30	j	202	PEE	C1-O3P-P-O2P
30	j	202	PEE	C1-O3P-P-O1P
30	j	202	PEE	C4-O4P-P-O3P
30	j	202	PEE	C4-O4P-P-O2P
30	j	202	PEE	C4-O4P-P-O1P
30	j	202	PEE	O4P-C4-C5-N
30	l	704	PEE	O3P-C1-C2-O2
30	l	705	PEE	O4P-C4-C5-N
30	r	501	PEE	C1-O3P-P-O4P
30	r	501	PEE	C4-O4P-P-O3P
30	r	501	PEE	C4-O4P-P-O2P
30	r	501	PEE	C5-C4-O4P-P
31	V	201	CDL	CB2-OB2-PB2-OB3
31	V	201	CDL	CB2-OB2-PB2-OB5
31	V	201	CDL	OB5-CB3-CB4-OB6
31	V	202	CDL	CA3-OA5-PA1-OA2
31	V	202	CDL	CA3-OA5-PA1-OA3
31	V	202	CDL	CA3-OA5-PA1-OA4
31	V	202	CDL	CB2-OB2-PB2-OB3
31	V	202	CDL	OB5-CB3-CB4-OB6
31	a	201	CDL	CB2-C1-CA2-OA2
31	a	201	CDL	CA2-C1-CB2-OB2
31	a	201	CDL	CA2-OA2-PA1-OA3
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	OB7-CB5-OB6-CB4
31	i	402	CDL	CA3-OA5-PA1-OA2
31	i	402	CDL	CB2-OB2-PB2-OB3
31	i	402	CDL	CB2-OB2-PB2-OB4
31	i	402	CDL	CB2-OB2-PB2-OB5
31	i	402	CDL	CB3-OB5-PB2-OB3
31	i	402	CDL	C51-CB5-OB6-CB4
31	k	101	CDL	CA2-OA2-PA1-OA3
31	k	101	CDL	CA3-OA5-PA1-OA2
31	k	101	CDL	CA3-OA5-PA1-OA3
31	k	101	CDL	CA3-OA5-PA1-OA4

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Mol	Chain	Res	Type	Atoms
31	l	702	CDL	CA2-OA2-PA1-OA3
31	l	702	CDL	CA2-OA2-PA1-OA4
31	l	702	CDL	CA2-OA2-PA1-OA5
31	l	702	CDL	CB3-OB5-PB2-OB2
31	l	702	CDL	CB3-OB5-PB2-OB3
31	l	702	CDL	CB3-OB5-PB2-OB4
31	l	702	CDL	OB5-CB3-CB4-OB6
31	l	703	CDL	CB2-C1-CA2-OA2
31	l	703	CDL	CA2-C1-CB2-OB2
31	l	703	CDL	CA3-OA5-PA1-OA2
31	l	703	CDL	CA3-OA5-PA1-OA3
31	l	703	CDL	CA3-OA5-PA1-OA4
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	s	401	CDL	CA2-C1-CB2-OB2
31	s	401	CDL	CA2-OA2-PA1-OA3
31	s	401	CDL	OA5-CA3-CA4-OA6
31	s	401	CDL	OA9-CA7-OA8-CA6
31	s	401	CDL	C31-CA7-OA8-CA6
31	u	201	CDL	CA3-OA5-PA1-OA2
31	u	201	CDL	CA3-OA5-PA1-OA3
31	u	201	CDL	CA3-OA5-PA1-OA4
32	X	201	8Q1	C1-C6-C7-C8
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-O2
33	a	202	PLX	N1-C1-C2-O1
33	a	202	PLX	O9-C24-O8-C5
33	a	202	PLX	O9-C24-C25-C26
33	e	201	PLX	O7-C6-O6-C4
33	e	201	PLX	O9-C24-O8-C5
33	g	201	PLX	C3-O4-P1-O1
33	g	201	PLX	C3-O4-P1-O2
33	g	201	PLX	C3-O4-P1-O3
33	g	201	PLX	C2-O1-P1-O4
33	g	201	PLX	C2-O1-P1-O3
33	j	203	PLX	O7-C6-O6-C4

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Mol	Chain	Res	Type	Atoms
33	j	203	PLX	C2-O1-P1-O4
33	j	203	PLX	C2-O1-P1-O2
33	j	203	PLX	N1-C1-C2-O1
33	j	203	PLX	O8-C24-C25-C26
33	j	204	PLX	O7-C6-C7-C8
33	j	204	PLX	O9-C24-O8-C5
33	r	502	PLX	O7-C6-C7-C8
33	r	502	PLX	C5-C4-O6-C6
33	r	502	PLX	C2-O1-P1-O4
33	r	502	PLX	C2-O1-P1-O2
33	r	502	PLX	O9-C24-C25-C26
35	s	402	UQ	C7-C8-C9-C10
35	s	402	UQ	C7-C8-C9-C11
35	s	402	UQ	C12-C13-C14-C16
35	s	402	UQ	C17-C18-C19-C21
36	w	401	ADP	C5'-O5'-PA-O2A
36	w	401	ADP	O4'-C4'-C5'-O5'
30	j	201	PEE	O5-C30-O3-C3
31	l	702	CDL	OA9-CA7-OA8-CA6
30	j	201	PEE	C31-C30-O3-C3
31	l	702	CDL	C31-CA7-OA8-CA6
30	j	202	PEE	O4-C10-O2-C2
30	l	704	PEE	O4-C10-O2-C2
30	l	705	PEE	O4-C10-O2-C2
31	i	402	CDL	OB7-CB5-OB6-CB4
31	l	702	CDL	C71-CB7-OB8-CB6
31	l	703	CDL	C71-CB7-OB8-CB6
30	l	704	PEE	C11-C10-O2-C2
30	l	705	PEE	C11-C10-O2-C2
31	a	201	CDL	C51-CB5-OB6-CB4
35	s	402	UQ	C18-C19-C21-C22
35	s	402	UQ	C23-C24-C26-C27
30	W	201	PEE	C31-C30-O3-C3
35	s	402	UQ	C22-C23-C24-C25
30	l	701	PEE	C17-C18-C19-C20
30	l	705	PEE	C37-C38-C39-C40
30	i	401	PEE	O5-C30-O3-C3
31	V	201	CDL	O1-C1-CB2-OB2
31	a	201	CDL	O1-C1-CA2-OA2
31	i	402	CDL	O1-C1-CA2-OA2
31	l	702	CDL	O1-C1-CA2-OA2
31	l	703	CDL	O1-C1-CA2-OA2

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Mol	Chain	Res	Type	Atoms
31	l	703	CDL	O1-C1-CB2-OB2
31	u	201	CDL	O1-C1-CA2-OA2
31	l	702	CDL	OB9-CB7-OB8-CB6
31	l	703	CDL	OB9-CB7-OB8-CB6
31	V	201	CDL	C11-CA5-OA6-CA4
35	s	402	UQ	C27-C28-C29-C31
30	i	401	PEE	C31-C30-O3-C3
30	l	701	PEE	C31-C30-O3-C3
35	s	402	UQ	C14-C16-C17-C18
31	V	201	CDL	C11-C12-C13-C14
30	W	201	PEE	O5-C30-O3-C3
30	l	701	PEE	O5-C30-O3-C3
33	j	204	PLX	C13-C14-C15-C16
31	V	201	CDL	C62-C63-C64-C65
30	U	401	PEE	C17-C18-C19-C20
30	j	201	PEE	C17-C18-C19-C20
30	r	501	PEE	C17-C18-C19-C20
31	l	702	CDL	C18-C19-C20-C21
35	s	402	UQ	C22-C23-C24-C26
33	r	502	PLX	C9-C10-C11-C12
31	l	703	CDL	C35-C36-C37-C38
31	V	201	CDL	OA7-CA5-OA6-CA4
31	V	201	CDL	CB2-C1-CA2-OA2
31	V	201	CDL	CA2-C1-CB2-OB2
31	V	202	CDL	CA2-C1-CB2-OB2
31	l	702	CDL	CB2-C1-CA2-OA2
31	V	202	CDL	C31-CA7-OA8-CA6
33	r	502	PLX	C11-C12-C13-C14
30	U	401	PEE	C11-C12-C13-C14
31	l	702	CDL	C58-C59-C60-C61
33	g	201	PLX	C2-C1-N1-C1B
33	g	201	PLX	C2-C1-N1-C1A
33	r	502	PLX	C7-C8-C9-C10
31	a	201	CDL	O1-C1-CB2-OB2
31	a	201	CDL	C34-C35-C36-C37
31	s	401	CDL	CB7-C71-C72-C73
31	V	202	CDL	OA9-CA7-OA8-CA6
31	V	202	CDL	C82-C83-C84-C85
30	U	401	PEE	O2-C2-C3-O3
31	V	201	CDL	C31-CA7-OA8-CA6
30	W	201	PEE	C10-C11-C12-C13
31	s	401	CDL	CA7-C31-C32-C33

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Mol	Chain	Res	Type	Atoms
30	l	705	PEE	C34-C35-C36-C37
31	u	201	CDL	CB5-C51-C52-C53
31	s	401	CDL	C14-C15-C16-C17
31	V	201	CDL	CB7-C71-C72-C73
31	l	702	CDL	CB5-C51-C52-C53
31	l	703	CDL	CB7-C71-C72-C73
31	V	202	CDL	C51-CB5-OB6-CB4
31	k	101	CDL	CA7-C31-C32-C33
31	l	702	CDL	CB7-C71-C72-C73
30	U	401	PEE	C34-C35-C36-C37
31	l	703	CDL	C37-C38-C39-C40
31	V	201	CDL	O1-C1-CA2-OA2
31	V	202	CDL	O1-C1-CB2-OB2
31	s	401	CDL	O1-C1-CB2-OB2
30	r	501	PEE	C10-C11-C12-C13
33	j	203	PLX	C25-C26-C27-C28
30	l	704	PEE	C31-C30-O3-C3
31	V	201	CDL	OA9-CA7-OA8-CA6
31	V	201	CDL	CB5-C51-C52-C53
31	k	101	CDL	CA5-C11-C12-C13
31	V	202	CDL	OB7-CB5-OB6-CB4
31	i	402	CDL	CB2-C1-CA2-OA2
31	u	201	CDL	CB2-C1-CA2-OA2
31	l	703	CDL	C61-C62-C63-C64
30	j	201	PEE	C31-C32-C33-C34
36	w	401	ADP	C3'-C4'-C5'-O5'
31	k	101	CDL	C71-CB7-OB8-CB6
33	r	502	PLX	O6-C6-C7-C8
31	l	703	CDL	C51-CB5-OB6-CB4
30	i	401	PEE	C30-C31-C32-C33
31	u	201	CDL	C75-C76-C77-C78
31	u	201	CDL	CB7-C71-C72-C73
33	j	203	PLX	C34-C35-C36-C37
31	k	101	CDL	C36-C37-C38-C39
31	l	703	CDL	OB7-CB5-OB6-CB4
30	W	201	PEE	C11-C10-O2-C2
30	l	705	PEE	C21-C22-C23-C24
31	i	402	CDL	C74-C75-C76-C77
31	l	702	CDL	C81-C82-C83-C84
30	W	201	PEE	C11-C12-C13-C14
33	j	204	PLX	C34-C35-C36-C37
30	l	704	PEE	O5-C30-O3-C3

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Mol	Chain	Res	Type	Atoms
31	i	402	CDL	C62-C63-C64-C65
31	l	702	CDL	C75-C76-C77-C78
33	g	201	PLX	C9-C10-C11-C12
31	V	201	CDL	C37-C38-C39-C40
31	a	201	CDL	C62-C63-C64-C65
31	k	101	CDL	C20-C21-C22-C23
31	s	401	CDL	C52-C53-C54-C55
32	X	201	8Q1	C12-C13-C14-C15
30	j	202	PEE	C23-C24-C25-C26
30	l	705	PEE	C13-C14-C15-C16
31	V	201	CDL	C55-C56-C57-C58
31	l	702	CDL	C74-C75-C76-C77
33	j	204	PLX	C12-C13-C14-C15
30	U	401	PEE	C31-C30-O3-C3
33	e	201	PLX	O9-C24-C25-C26
33	j	203	PLX	O9-C24-C25-C26
31	k	101	CDL	C75-C76-C77-C78
31	l	702	CDL	C14-C15-C16-C17
31	l	702	CDL	C37-C38-C39-C40
31	l	702	CDL	C62-C63-C64-C65
31	l	702	CDL	C71-C72-C73-C74
31	u	201	CDL	C71-C72-C73-C74
30	j	201	PEE	C13-C14-C15-C16
31	V	202	CDL	C40-C41-C42-C43
31	V	202	CDL	C53-C54-C55-C56
33	j	204	PLX	C33-C34-C35-C36
33	r	502	PLX	C11-C10-C9-C8
33	r	502	PLX	C33-C34-C35-C36
30	j	201	PEE	C14-C15-C16-C17
31	V	202	CDL	C14-C15-C16-C17
31	l	702	CDL	C59-C60-C61-C62
31	l	703	CDL	C11-C12-C13-C14
33	e	201	PLX	C14-C15-C16-C17
33	j	203	PLX	C31-C32-C33-C34
31	V	201	CDL	C73-C74-C75-C76
31	V	201	CDL	C59-C60-C61-C62
31	s	401	CDL	C71-C72-C73-C74
31	a	201	CDL	C60-C61-C62-C63
31	k	101	CDL	C71-C72-C73-C74
33	g	201	PLX	C25-C26-C27-C28
33	r	502	PLX	C27-C28-C29-C30
31	V	202	CDL	CA5-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
31	i	402	CDL	CA7-C31-C32-C33
30	j	202	PEE	C12-C13-C14-C15
30	r	501	PEE	C14-C15-C16-C17
31	V	201	CDL	C56-C57-C58-C59
31	V	201	CDL	C75-C76-C77-C78
31	a	201	CDL	C54-C55-C56-C57
31	k	101	CDL	C15-C16-C17-C18
31	l	702	CDL	C31-C32-C33-C34
31	s	401	CDL	C73-C74-C75-C76
31	u	201	CDL	C56-C57-C58-C59
33	e	201	PLX	C13-C14-C15-C16
33	j	204	PLX	C14-C15-C16-C17
30	j	202	PEE	C11-C12-C13-C14
31	l	702	CDL	C51-C52-C53-C54
31	s	401	CDL	C32-C33-C34-C35
31	k	101	CDL	OB9-CB7-OB8-CB6
31	V	201	CDL	C19-C20-C21-C22
31	a	201	CDL	C21-C22-C23-C24
31	i	402	CDL	C34-C35-C36-C37
33	a	202	PLX	C12-C13-C14-C15
31	V	202	CDL	CB3-CB4-CB6-OB8
31	V	202	CDL	C75-C76-C77-C78
31	l	702	CDL	C16-C17-C18-C19
31	s	401	CDL	C59-C60-C61-C62
32	X	201	8Q1	C11-C10-C9-C8
33	a	202	PLX	C7-C8-C9-C10
33	j	204	PLX	C25-C26-C27-C28
31	l	703	CDL	CB5-C51-C52-C53
31	V	202	CDL	C32-C33-C34-C35
31	l	703	CDL	C51-C52-C53-C54
31	u	201	CDL	C52-C53-C54-C55
33	e	201	PLX	C25-C26-C27-C28
33	g	201	PLX	C14-C15-C16-C17
33	j	203	PLX	C11-C10-C9-C8
30	r	501	PEE	C21-C22-C23-C24
31	V	201	CDL	C31-C32-C33-C34
31	i	402	CDL	C43-C44-C45-C46
31	i	402	CDL	C57-C58-C59-C60
33	a	202	PLX	C13-C14-C15-C16
31	l	703	CDL	C75-C76-C77-C78
33	g	201	PLX	C2-C1-N1-C1C
31	V	201	CDL	C32-C33-C34-C35

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Mol	Chain	Res	Type	Atoms
31	V	202	CDL	C17-C18-C19-C20
31	l	702	CDL	C35-C36-C37-C38
31	u	201	CDL	C54-C55-C56-C57
33	r	502	PLX	C28-C29-C30-C31
30	r	501	PEE	C20-C21-C22-C23
31	a	201	CDL	C22-C23-C24-C25
31	s	401	CDL	C51-C52-C53-C54
33	a	202	PLX	C34-C35-C36-C37
33	j	204	PLX	C7-C8-C9-C10
31	a	201	CDL	C11-CA5-OA6-CA4
31	l	703	CDL	C11-CA5-OA6-CA4
30	l	704	PEE	C15-C16-C17-C18
30	j	201	PEE	C37-C38-C39-C40
31	i	402	CDL	C52-C53-C54-C55
31	k	101	CDL	C37-C38-C39-C40
31	u	201	CDL	C73-C74-C75-C76
33	g	201	PLX	C28-C29-C30-C31
33	j	203	PLX	C13-C14-C15-C16
31	i	402	CDL	C14-C15-C16-C17
33	a	202	PLX	C31-C32-C33-C34
33	j	203	PLX	C14-C15-C16-C17
30	W	201	PEE	O4-C10-O2-C2
31	i	402	CDL	C12-C13-C14-C15
33	j	203	PLX	C27-C28-C29-C30
31	V	202	CDL	C12-C13-C14-C15
31	V	202	CDL	C37-C38-C39-C40
31	V	202	CDL	C42-C43-C44-C45
30	j	202	PEE	C31-C30-O3-C3
31	V	202	CDL	C81-C82-C83-C84
31	i	402	CDL	C75-C76-C77-C78
30	i	401	PEE	C21-C22-C23-C24
33	r	502	PLX	C18-C19-C20-C21
33	e	201	PLX	C10-C11-C12-C13
33	j	204	PLX	C10-C11-C12-C13
30	U	401	PEE	O5-C30-O3-C3
31	a	201	CDL	C11-C12-C13-C14
31	l	702	CDL	C11-C12-C13-C14
33	g	201	PLX	C27-C28-C29-C30
30	l	701	PEE	C10-C11-C12-C13
31	l	702	CDL	C82-C83-C84-C85
31	k	101	CDL	C76-C77-C78-C79
31	l	702	CDL	C52-C53-C54-C55

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Mol	Chain	Res	Type	Atoms
31	s	401	CDL	C37-C38-C39-C40
30	U	401	PEE	C11-C10-O2-C2
30	l	701	PEE	C11-C10-O2-C2
31	s	401	CDL	C11-CA5-OA6-CA4
31	s	401	CDL	C51-CB5-OB6-CB4
31	i	402	CDL	CB7-C71-C72-C73
31	l	703	CDL	OA7-CA5-OA6-CA4
31	s	401	CDL	OB7-CB5-OB6-CB4
31	V	201	CDL	C53-C54-C55-C56
31	i	402	CDL	C41-C42-C43-C44
31	s	401	CDL	C75-C76-C77-C78
33	a	202	PLX	C14-C15-C16-C17
33	e	201	PLX	C29-C30-C31-C32
33	g	201	PLX	C30-C31-C32-C33
30	i	401	PEE	C19-C20-C21-C22
31	a	201	CDL	C35-C36-C37-C38
31	l	703	CDL	C17-C18-C19-C20
31	a	201	CDL	C51-C52-C53-C54
31	i	402	CDL	CB5-C51-C52-C53
31	u	201	CDL	C55-C56-C57-C58
33	j	203	PLX	C10-C11-C12-C13
31	k	101	CDL	C21-C22-C23-C24
30	W	201	PEE	C21-C22-C23-C24
31	i	402	CDL	C37-C38-C39-C40
33	a	202	PLX	C9-C10-C11-C12
33	j	204	PLX	C30-C31-C32-C33
31	V	202	CDL	C11-C12-C13-C14
33	g	201	PLX	C32-C33-C34-C35
33	j	203	PLX	C33-C34-C35-C36
33	r	502	PLX	C13-C14-C15-C16
33	e	201	PLX	C33-C34-C35-C36
31	l	702	CDL	C36-C37-C38-C39
33	g	201	PLX	C11-C10-C9-C8
33	e	201	PLX	C11-C10-C9-C8
30	l	701	PEE	O4-C10-O2-C2
31	k	101	CDL	OA5-CA3-CA4-OA6
31	s	401	CDL	C82-C83-C84-C85
31	l	702	CDL	C56-C57-C58-C59
31	s	401	CDL	C36-C37-C38-C39
31	k	101	CDL	C32-C33-C34-C35
31	a	201	CDL	CB5-C51-C52-C53
30	i	401	PEE	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
30	l	705	PEE	C15-C16-C17-C18
31	V	202	CDL	OB6-CB4-CB6-OB8
31	l	702	CDL	OA6-CA4-CA6-OA8
31	l	702	CDL	OB6-CB4-CB6-OB8
31	s	401	CDL	OB6-CB4-CB6-OB8
31	u	201	CDL	OA6-CA4-CA6-OA8
33	g	201	PLX	C10-C11-C12-C13
30	U	401	PEE	C23-C24-C25-C26
31	k	101	CDL	C52-C53-C54-C55
33	a	202	PLX	C25-C26-C27-C28
33	e	201	PLX	C27-C28-C29-C30
30	U	401	PEE	C38-C39-C40-C41
31	l	703	CDL	C40-C41-C42-C43
31	l	703	CDL	C73-C74-C75-C76
31	k	101	CDL	C42-C43-C44-C45
31	l	703	CDL	C32-C33-C34-C35
31	l	703	CDL	C55-C56-C57-C58
31	s	401	CDL	C35-C36-C37-C38
31	i	402	CDL	C32-C33-C34-C35
31	k	101	CDL	C16-C17-C18-C19
33	j	203	PLX	C18-C19-C20-C21
30	W	201	PEE	C23-C24-C25-C26
33	j	203	PLX	C26-C27-C28-C29
33	j	204	PLX	C11-C12-C13-C14
33	r	502	PLX	C30-C31-C32-C33
30	j	202	PEE	O5-C30-O3-C3
31	l	703	CDL	C14-C15-C16-C17
31	l	703	CDL	C57-C58-C59-C60
31	i	402	CDL	C17-C18-C19-C20
31	k	101	CDL	C34-C35-C36-C37
31	V	201	CDL	C14-C15-C16-C17
30	r	501	PEE	C40-C41-C42-C43
31	V	202	CDL	C76-C77-C78-C79
31	l	702	CDL	OB5-CB3-CB4-CB6
31	s	401	CDL	OA5-CA3-CA4-CA6
30	U	401	PEE	O4-C10-O2-C2
31	a	201	CDL	OA7-CA5-OA6-CA4
31	s	401	CDL	OA7-CA5-OA6-CA4
31	V	201	CDL	C71-C72-C73-C74
31	V	202	CDL	C54-C55-C56-C57
31	i	402	CDL	C71-C72-C73-C74
31	V	201	CDL	C51-CB5-OB6-CB4

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Mol	Chain	Res	Type	Atoms
30	r	501	PEE	C12-C13-C14-C15
30	l	704	PEE	C44-C45-C46-C47
30	r	501	PEE	C36-C37-C38-C39
31	k	101	CDL	C82-C83-C84-C85
31	V	202	CDL	CB7-C71-C72-C73
30	U	401	PEE	C1-C2-C3-O3
31	V	201	CDL	CA3-CA4-CA6-OA8
31	l	703	CDL	CA3-CA4-CA6-OA8
33	a	202	PLX	C3-C4-C5-O8
33	e	201	PLX	C3-C4-C5-O8
30	U	401	PEE	C13-C14-C15-C16
30	l	704	PEE	C11-C12-C13-C14
31	i	402	CDL	C59-C60-C61-C62
30	U	401	PEE	C35-C36-C37-C38
30	j	202	PEE	C15-C16-C17-C18
30	r	501	PEE	C15-C16-C17-C18
30	W	201	PEE	C13-C14-C15-C16
31	i	402	CDL	C54-C55-C56-C57
31	s	401	CDL	C31-C32-C33-C34
31	k	101	CDL	CB5-C51-C52-C53
33	j	204	PLX	C28-C29-C30-C31
31	i	402	CDL	C84-C85-C86-C87
31	a	201	CDL	C37-C38-C39-C40
33	g	201	PLX	C12-C13-C14-C15
33	j	203	PLX	C30-C31-C32-C33
31	V	202	CDL	C34-C35-C36-C37
31	a	201	CDL	C33-C34-C35-C36
31	u	201	CDL	C74-C75-C76-C77
31	i	402	CDL	C60-C61-C62-C63
33	e	201	PLX	C11-C12-C13-C14
31	u	201	CDL	C72-C73-C74-C75
33	a	202	PLX	C27-C28-C29-C30
30	W	201	PEE	C19-C20-C21-C22
30	W	201	PEE	C15-C16-C17-C18
30	l	704	PEE	C21-C22-C23-C24
31	k	101	CDL	C23-C24-C25-C26
33	e	201	PLX	C26-C27-C28-C29
31	s	401	CDL	C11-C12-C13-C14
30	j	201	PEE	C34-C35-C36-C37
30	j	201	PEE	C36-C37-C38-C39
31	V	201	CDL	OA5-CA3-CA4-OA6
31	i	402	CDL	C63-C64-C65-C66

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Mol	Chain	Res	Type	Atoms
31	l	703	CDL	C19-C20-C21-C22
31	l	703	CDL	C71-C72-C73-C74
33	j	203	PLX	C7-C8-C9-C10
31	a	201	CDL	C42-C43-C44-C45
31	a	201	CDL	C71-C72-C73-C74
33	r	502	PLX	C25-C26-C27-C28
31	a	201	CDL	C52-C53-C54-C55
31	a	201	CDL	C81-C82-C83-C84
31	s	401	CDL	C56-C57-C58-C59
33	a	202	PLX	C16-C17-C18-C19
30	l	701	PEE	O2-C2-C3-O3
31	l	703	CDL	OA6-CA4-CA6-OA8
33	r	502	PLX	O6-C4-C5-O8
31	V	201	CDL	C44-C45-C46-C47
31	k	101	CDL	C33-C34-C35-C36
31	a	201	CDL	C44-C45-C46-C47
32	X	201	8Q1	C13-C14-C15-C16
31	l	702	CDL	C40-C41-C42-C43
33	r	502	PLX	C14-C15-C16-C17
33	a	202	PLX	C11-C12-C13-C14
31	a	201	CDL	C71-CB7-OB8-CB6
30	r	501	PEE	C31-C32-C33-C34
31	l	702	CDL	C73-C74-C75-C76
31	i	402	CDL	C77-C78-C79-C80
31	k	101	CDL	C43-C44-C45-C46
33	j	204	PLX	C9-C10-C11-C12
31	a	201	CDL	C14-C15-C16-C17
31	V	201	CDL	C1-CB2-OB2-PB2
31	V	201	CDL	C51-C52-C53-C54
31	i	402	CDL	C53-C54-C55-C56
33	a	202	PLX	C15-C16-C17-C18
30	l	704	PEE	C19-C20-C21-C22
30	l	704	PEE	O3P-C1-C2-C3
31	V	202	CDL	OB5-CB3-CB4-CB6
31	k	101	CDL	OA5-CA3-CA4-CA6
33	j	203	PLX	O4-C3-C4-C5
30	j	202	PEE	C10-C11-C12-C13
31	a	201	CDL	C32-C33-C34-C35
31	k	101	CDL	C78-C79-C80-C81
30	j	201	PEE	C23-C24-C25-C26
31	l	703	CDL	C39-C40-C41-C42
31	s	401	CDL	C58-C59-C60-C61

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Mol	Chain	Res	Type	Atoms
33	g	201	PLX	C7-C8-C9-C10
33	j	203	PLX	C12-C13-C14-C15
31	V	201	CDL	C54-C55-C56-C57
31	V	202	CDL	C74-C75-C76-C77
31	a	201	CDL	C64-C65-C66-C67
31	i	402	CDL	C83-C84-C85-C86
31	V	202	CDL	C39-C40-C41-C42
31	a	201	CDL	C84-C85-C86-C87
30	W	201	PEE	C1-C2-C3-O3
30	l	704	PEE	C1-C2-C3-O3
30	l	705	PEE	C1-C2-C3-O3
31	l	702	CDL	CA3-CA4-CA6-OA8
31	l	702	CDL	CB3-CB4-CB6-OB8
31	s	401	CDL	CB3-CB4-CB6-OB8
31	u	201	CDL	CA3-CA4-CA6-OA8
33	j	203	PLX	C3-C4-C5-O8
30	U	401	PEE	C41-C42-C43-C44
30	l	701	PEE	C34-C35-C36-C37
31	s	401	CDL	C34-C35-C36-C37
30	i	401	PEE	C11-C12-C13-C14
31	i	402	CDL	C64-C65-C66-C67
31	l	703	CDL	OA5-CA3-CA4-OA6
33	j	203	PLX	O4-C3-C4-O6
30	l	704	PEE	C31-C32-C33-C34
31	V	202	CDL	C59-C60-C61-C62
30	j	201	PEE	C21-C22-C23-C24
31	V	202	CDL	C1-CB2-OB2-PB2
31	l	702	CDL	CA7-C31-C32-C33
31	l	703	CDL	C18-C19-C20-C21
31	V	202	CDL	C64-C65-C66-C67
31	V	201	CDL	C74-C75-C76-C77
30	j	202	PEE	O2-C2-C3-O3
31	V	201	CDL	OA6-CA4-CA6-OA8
31	i	402	CDL	OA6-CA4-CA6-OA8
31	k	101	CDL	OB6-CB4-CB6-OB8
33	j	203	PLX	O6-C4-C5-O8
31	l	703	CDL	C64-C65-C66-C67
32	X	201	8Q1	C6-C7-C8-C9
32	X	201	8Q1	C7-C8-C9-C10
33	r	502	PLX	C16-C17-C18-C19
33	e	201	PLX	O8-C24-C25-C26
33	r	502	PLX	O8-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
31	V	202	CDL	C31-C32-C33-C34
30	U	401	PEE	C30-C31-C32-C33
31	a	201	CDL	CA5-C11-C12-C13
31	l	703	CDL	CA5-C11-C12-C13
31	s	401	CDL	CB5-C51-C52-C53
31	V	202	CDL	C72-C73-C74-C75
31	k	101	CDL	C12-C13-C14-C15
30	i	401	PEE	C18-C19-C20-C21
30	r	501	PEE	C38-C39-C40-C41
30	l	701	PEE	C18-C19-C20-C21
33	g	201	PLX	C17-C18-C19-C20
31	V	202	CDL	C62-C63-C64-C65
31	V	202	CDL	CB2-C1-CA2-OA2
31	V	202	CDL	C71-CB7-OB8-CB6
30	i	401	PEE	O3P-C1-C2-C3
31	V	201	CDL	OB5-CB3-CB4-CB6
31	l	703	CDL	OA5-CA3-CA4-CA6
31	V	201	CDL	C64-C65-C66-C67
33	e	201	PLX	C18-C19-C20-C21
31	k	101	CDL	C11-C12-C13-C14
30	j	202	PEE	C24-C25-C26-C27
33	g	201	PLX	C20-C21-C22-C23
30	U	401	PEE	C42-C43-C44-C45
31	a	201	CDL	C23-C24-C25-C26
31	V	201	CDL	OB7-CB5-OB6-CB4
31	a	201	CDL	OB9-CB7-OB8-CB6
31	k	101	CDL	C81-C82-C83-C84
30	j	201	PEE	C44-C45-C46-C47
31	i	402	CDL	C11-C12-C13-C14
31	V	201	CDL	CA6-CA4-OA6-CA5
31	s	401	CDL	C17-C18-C19-C20
30	i	401	PEE	C24-C25-C26-C27
31	a	201	CDL	C82-C83-C84-C85
33	e	201	PLX	C7-C8-C9-C10
33	j	204	PLX	C31-C32-C33-C34
31	i	402	CDL	C72-C71-CB7-OB8
31	a	201	CDL	OA5-CA3-CA4-OA6
33	g	201	PLX	O4-C3-C4-O6
33	g	201	PLX	C33-C34-C35-C36
31	k	101	CDL	CB3-CB4-CB6-OB8
31	l	703	CDL	C38-C39-C40-C41
33	j	203	PLX	C1-C2-O1-P1

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Mol	Chain	Res	Type	Atoms
30	W	201	PEE	O2-C2-C3-O3
30	l	704	PEE	O2-C2-C3-O3
30	l	705	PEE	O2-C2-C3-O3
31	l	703	CDL	OB6-CB4-CB6-OB8
33	a	202	PLX	O6-C4-C5-O8
33	e	201	PLX	O6-C4-C5-O8
31	s	401	CDL	C55-C56-C57-C58
31	V	202	CDL	OB9-CB7-OB8-CB6
30	j	201	PEE	C22-C23-C24-C25
31	l	702	CDL	C21-C22-C23-C24
31	l	702	CDL	C54-C55-C56-C57
31	s	401	CDL	C57-C58-C59-C60
33	j	203	PLX	C2-C1-N1-C1A
31	s	401	CDL	C12-C13-C14-C15
30	U	401	PEE	C20-C21-C22-C23
31	V	201	CDL	C21-C22-C23-C24
31	a	201	CDL	C72-C73-C74-C75
33	g	201	PLX	C13-C14-C15-C16
30	W	201	PEE	C22-C23-C24-C25
31	i	402	CDL	C33-C34-C35-C36
31	u	201	CDL	CA2-C1-CB2-OB2
31	V	202	CDL	O1-C1-CA2-OA2
33	e	201	PLX	C28-C29-C30-C31
30	r	501	PEE	C41-C42-C43-C44
33	e	201	PLX	C24-C25-C26-C27
31	a	201	CDL	C61-C62-C63-C64
30	r	501	PEE	C22-C23-C24-C25
31	V	201	CDL	C52-C53-C54-C55
31	V	201	CDL	C12-C13-C14-C15
33	a	202	PLX	C25-C24-O8-C5
33	j	203	PLX	C2-C1-N1-C1B
31	i	402	CDL	C71-CB7-OB8-CB6
33	r	502	PLX	C12-C13-C14-C15
30	j	201	PEE	C38-C39-C40-C41
31	i	402	CDL	C55-C56-C57-C58
31	V	202	CDL	C52-C53-C54-C55
31	V	201	CDL	OA5-CA3-CA4-CA6
33	e	201	PLX	O4-C3-C4-C5
33	g	201	PLX	O4-C3-C4-C5
33	a	202	PLX	C19-C20-C21-C22
30	j	201	PEE	C40-C41-C42-C43
31	k	101	CDL	C14-C15-C16-C17

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Mol	Chain	Res	Type	Atoms
31	i	402	CDL	C76-C77-C78-C79
30	W	201	PEE	C17-C18-C19-C20
31	V	201	CDL	CA7-C31-C32-C33
31	a	201	CDL	C17-C18-C19-C20
31	l	703	CDL	C12-C13-C14-C15
30	j	202	PEE	C18-C19-C20-C21
32	X	201	8Q1	C42-C43-S44-C1
31	i	402	CDL	OB9-CB7-OB8-CB6
33	j	204	PLX	O6-C6-C7-C8
33	e	201	PLX	O4-C3-C4-O6
30	W	201	PEE	C12-C13-C14-C15
31	l	702	CDL	C78-C79-C80-C81
31	i	402	CDL	C15-C16-C17-C18
30	i	401	PEE	C16-C17-C18-C19
31	s	401	CDL	C39-C40-C41-C42
31	V	202	CDL	C55-C56-C57-C58
33	j	204	PLX	O6-C4-C5-O8
30	j	202	PEE	C1-C2-C3-O3
31	i	402	CDL	CA3-CA4-CA6-OA8
32	X	201	8Q1	C43-C42-N41-C39
33	g	201	PLX	C3-C4-C5-O8
33	r	502	PLX	C3-C4-C5-O8
31	k	101	CDL	C84-C85-C86-C87
30	l	701	PEE	C16-C17-C18-C19
30	l	704	PEE	C36-C37-C38-C39
31	i	402	CDL	C35-C36-C37-C38
33	e	201	PLX	C32-C33-C34-C35
30	U	401	PEE	C1-O3P-P-O1P
30	W	201	PEE	C4-O4P-P-O3P
30	W	201	PEE	C4-O4P-P-O2P
30	W	201	PEE	C4-O4P-P-O1P
30	W	201	PEE	O4P-C4-C5-N
30	i	401	PEE	C4-O4P-P-O2P
30	j	201	PEE	C1-O3P-P-O1P
30	j	202	PEE	C1-O3P-P-O4P
30	l	704	PEE	C4-O4P-P-O3P
30	l	704	PEE	C4-O4P-P-O2P
30	r	501	PEE	C1-O3P-P-O1P
31	V	201	CDL	CA2-OA2-PA1-OA3
31	V	201	CDL	CB2-OB2-PB2-OB4
31	V	202	CDL	CA2-OA2-PA1-OA3
31	V	202	CDL	CB2-OB2-PB2-OB5

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Mol	Chain	Res	Type	Atoms
31	i	402	CDL	CA3-OA5-PA1-OA3
31	i	402	CDL	CB3-OB5-PB2-OB2
31	i	402	CDL	CB3-OB5-PB2-OB4
31	k	101	CDL	CB2-OB2-PB2-OB4
31	k	101	CDL	CB2-OB2-PB2-OB5
31	l	702	CDL	CA3-OA5-PA1-OA3
31	s	401	CDL	CB3-OB5-PB2-OB3
31	u	201	CDL	CB3-OB5-PB2-OB3
33	a	202	PLX	C3-O4-P1-O1
33	a	202	PLX	C2-O1-P1-O4
33	j	203	PLX	C3-C4-O6-C6
33	j	203	PLX	C5-C4-O6-C6
33	j	203	PLX	C3-O4-P1-O1
33	j	203	PLX	C2-O1-P1-O3
33	r	502	PLX	C3-O4-P1-O1
33	r	502	PLX	C3-O4-P1-O2
33	r	502	PLX	C3-O4-P1-O3
33	r	502	PLX	C2-O1-P1-O3
36	w	401	ADP	C5'-O5'-PA-O1A
36	w	401	ADP	C5'-O5'-PA-O3A
30	j	202	PEE	C34-C35-C36-C37
31	i	402	CDL	C21-C22-C23-C24
30	U	401	PEE	C2-C1-O3P-P
30	l	705	PEE	C2-C1-O3P-P
31	i	402	CDL	C1-CB2-OB2-PB2
31	i	402	CDL	C44-C45-C46-C47
30	l	704	PEE	C33-C34-C35-C36
31	s	401	CDL	C84-C85-C86-C87
30	l	701	PEE	C31-C32-C33-C34
31	k	101	CDL	C44-C45-C46-C47
31	k	101	CDL	CA6-CA4-OA6-CA5
30	l	705	PEE	C11-C12-C13-C14
33	e	201	PLX	C30-C31-C32-C33
30	l	704	PEE	C30-C31-C32-C33
33	g	201	PLX	C19-C20-C21-C22
33	j	203	PLX	C2-C1-N1-C1C
31	a	201	CDL	OA5-CA3-CA4-CA6
31	l	703	CDL	C44-C45-C46-C47
30	i	401	PEE	C34-C35-C36-C37
30	i	401	PEE	O3P-C1-C2-O2
33	j	204	PLX	C32-C33-C34-C35
33	r	502	PLX	C29-C30-C31-C32

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Mol	Chain	Res	Type	Atoms
33	j	203	PLX	C36-C37-C38-C39
31	k	101	CDL	C35-C36-C37-C38
31	s	401	CDL	C15-C16-C17-C18
31	i	402	CDL	C39-C40-C41-C42
30	r	501	PEE	C11-C12-C13-C14
30	l	701	PEE	O3-C30-C31-C32
30	l	701	PEE	C1-C2-C3-O3
33	j	204	PLX	C3-C4-C5-O8
33	e	201	PLX	C15-C16-C17-C18
31	l	702	CDL	C42-C43-C44-C45
31	V	202	CDL	C51-C52-C53-C54
31	V	202	CDL	CA7-C31-C32-C33
31	a	201	CDL	C40-C41-C42-C43
31	u	201	CDL	C51-C52-C53-C54
33	j	203	PLX	C35-C36-C37-C38
31	V	202	CDL	C80-C81-C82-C83
31	k	101	CDL	C56-C57-C58-C59
31	s	401	CDL	C54-C55-C56-C57
33	j	203	PLX	C29-C30-C31-C32
33	g	201	PLX	C36-C37-C38-C39
31	V	202	CDL	C13-C14-C15-C16
33	a	202	PLX	C26-C27-C28-C29
30	i	401	PEE	C12-C13-C14-C15
35	s	402	UQ	C17-C18-C19-C20
31	a	201	CDL	CA7-C31-C32-C33
31	l	702	CDL	OA5-CA3-CA4-OA6
31	V	201	CDL	C43-C44-C45-C46
31	l	702	CDL	C44-C45-C46-C47
30	r	501	PEE	C33-C34-C35-C36
30	r	501	PEE	C34-C35-C36-C37
30	l	701	PEE	C36-C37-C38-C39
30	l	704	PEE	C24-C25-C26-C27
30	U	401	PEE	C24-C25-C26-C27
31	a	201	CDL	C41-C42-C43-C44
30	l	705	PEE	C18-C19-C20-C21
31	k	101	CDL	C39-C40-C41-C42
31	V	201	CDL	CA4-CA3-OA5-PA1
33	e	201	PLX	C16-C17-C18-C19
30	j	201	PEE	C19-C20-C21-C22
31	V	202	CDL	C24-C25-C26-C27
30	j	202	PEE	C14-C15-C16-C17
30	l	704	PEE	C32-C33-C34-C35

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Mol	Chain	Res	Type	Atoms
33	j	204	PLX	C27-C28-C29-C30
31	V	201	CDL	C79-C80-C81-C82
30	j	202	PEE	C19-C20-C21-C22
31	k	101	CDL	CA4-CA3-OA5-PA1
31	u	201	CDL	OA5-CA3-CA4-CA6
33	j	203	PLX	C15-C16-C17-C18
33	e	201	PLX	C12-C13-C14-C15
33	g	201	PLX	O6-C4-C5-O8
31	l	702	CDL	C34-C35-C36-C37
31	V	202	CDL	C58-C59-C60-C61
31	V	202	CDL	C35-C36-C37-C38
33	a	202	PLX	C11-C10-C9-C8
31	l	703	CDL	C32-C31-CA7-OA8
33	a	202	PLX	O8-C24-C25-C26
33	g	201	PLX	O8-C24-C25-C26
31	u	201	CDL	O1-C1-CB2-OB2
33	j	204	PLX	C24-C25-C26-C27
31	a	201	CDL	C74-C75-C76-C77
30	l	701	PEE	C33-C34-C35-C36
35	s	402	UQ	C15-C14-C16-C17
31	l	703	CDL	CB3-CB4-CB6-OB8
33	r	502	PLX	C31-C32-C33-C34
33	j	204	PLX	C29-C30-C31-C32
31	l	703	CDL	C54-C55-C56-C57
30	W	201	PEE	C16-C17-C18-C19
30	l	705	PEE	C38-C39-C40-C41
30	j	201	PEE	O2-C10-C11-C12
31	s	401	CDL	C72-C71-CB7-OB8
30	l	705	PEE	C17-C18-C19-C20
31	V	202	CDL	C16-C17-C18-C19
31	l	702	CDL	CA5-C11-C12-C13
31	i	402	CDL	C13-C14-C15-C16
31	l	703	CDL	C33-C34-C35-C36
31	V	202	CDL	C41-C42-C43-C44
31	V	202	CDL	C84-C85-C86-C87
30	j	201	PEE	C2-C1-O3P-P
33	r	502	PLX	C4-C3-O4-P1
31	l	702	CDL	C33-C34-C35-C36
33	a	202	PLX	C29-C30-C31-C32
30	l	704	PEE	C13-C14-C15-C16
31	V	201	CDL	C72-C73-C74-C75
31	l	702	CDL	C32-C33-C34-C35

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Mol	Chain	Res	Type	Atoms
31	V	201	CDL	C60-C61-C62-C63
33	e	201	PLX	C9-C10-C11-C12
30	l	704	PEE	C16-C17-C18-C19
31	a	201	CDL	C18-C19-C20-C21
31	a	201	CDL	C56-C57-C58-C59
31	a	201	CDL	C53-C54-C55-C56
31	V	201	CDL	C17-C18-C19-C20
30	l	704	PEE	C1-C2-O2-C10
31	l	703	CDL	C59-C60-C61-C62
31	k	101	CDL	C58-C59-C60-C61
30	l	704	PEE	C38-C39-C40-C41
33	g	201	PLX	C11-C12-C13-C14
30	U	401	PEE	C18-C19-C20-C21
32	X	201	8Q1	C11-C12-C13-C14
31	l	703	CDL	C15-C16-C17-C18
30	r	501	PEE	C24-C25-C26-C27
30	l	705	PEE	O2-C10-C11-C12
31	k	101	CDL	C57-C58-C59-C60
31	s	401	CDL	O1-C1-CA2-OA2
30	l	701	PEE	C38-C39-C40-C41
31	i	402	CDL	C52-C51-CB5-OB6
31	l	703	CDL	C77-C78-C79-C80
33	j	204	PLX	C7-C6-O6-C4
31	a	201	CDL	C32-C31-CA7-OA8
31	l	702	CDL	C24-C25-C26-C27
30	j	202	PEE	O3-C30-C31-C32
30	r	501	PEE	O4-C10-O2-C2
30	i	401	PEE	C38-C39-C40-C41
31	l	703	CDL	C72-C73-C74-C75
31	u	201	CDL	C52-C51-CB5-OB6
31	k	101	CDL	C17-C18-C19-C20
33	j	204	PLX	C25-C24-O8-C5
33	j	203	PLX	C24-C25-C26-C27
31	s	401	CDL	C16-C17-C18-C19
31	V	202	CDL	C77-C78-C79-C80
31	a	201	CDL	C12-C11-CA5-OA6
31	l	702	CDL	C38-C39-C40-C41
30	i	401	PEE	C14-C15-C16-C17
30	l	704	PEE	C3-C2-O2-C10
30	i	401	PEE	C2-C1-O3P-P
33	g	201	PLX	O6-C6-C7-C8
30	l	701	PEE	O3P-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
31	k	101	CDL	C31-C32-C33-C34
31	i	402	CDL	C72-C71-CB7-OB9
33	e	201	PLX	C2-C1-N1-C1B
33	a	202	PLX	C10-C11-C12-C13
31	a	201	CDL	C32-C31-CA7-OA9
33	r	502	PLX	O9-C24-O8-C5
31	i	402	CDL	C52-C51-CB5-OB7
31	V	202	CDL	C44-C45-C46-C47
31	l	702	CDL	C52-C51-CB5-OB6
30	l	705	PEE	O4-C10-C11-C12
31	a	201	CDL	C12-C11-CA5-OA7
33	a	202	PLX	C4-C5-O8-C24
31	u	201	CDL	C52-C51-CB5-OB7
35	s	402	UQ	C24-C26-C27-C28
31	i	402	CDL	C36-C37-C38-C39
30	U	401	PEE	C21-C22-C23-C24
30	j	201	PEE	C41-C42-C43-C44
31	V	201	CDL	C32-C31-CA7-OA8
31	V	202	CDL	C63-C64-C65-C66
31	l	703	CDL	C41-C42-C43-C44
31	l	702	CDL	C52-C51-CB5-OB7
31	u	201	CDL	C12-C11-CA5-OA6
30	r	501	PEE	C11-C10-O2-C2
36	w	401	ADP	PB-O3A-PA-O2A
31	s	401	CDL	C74-C75-C76-C77
30	r	501	PEE	O2-C10-C11-C12
31	k	101	CDL	C24-C25-C26-C27

There are no ring outliers.

24 monomers are involved in 93 short contacts:

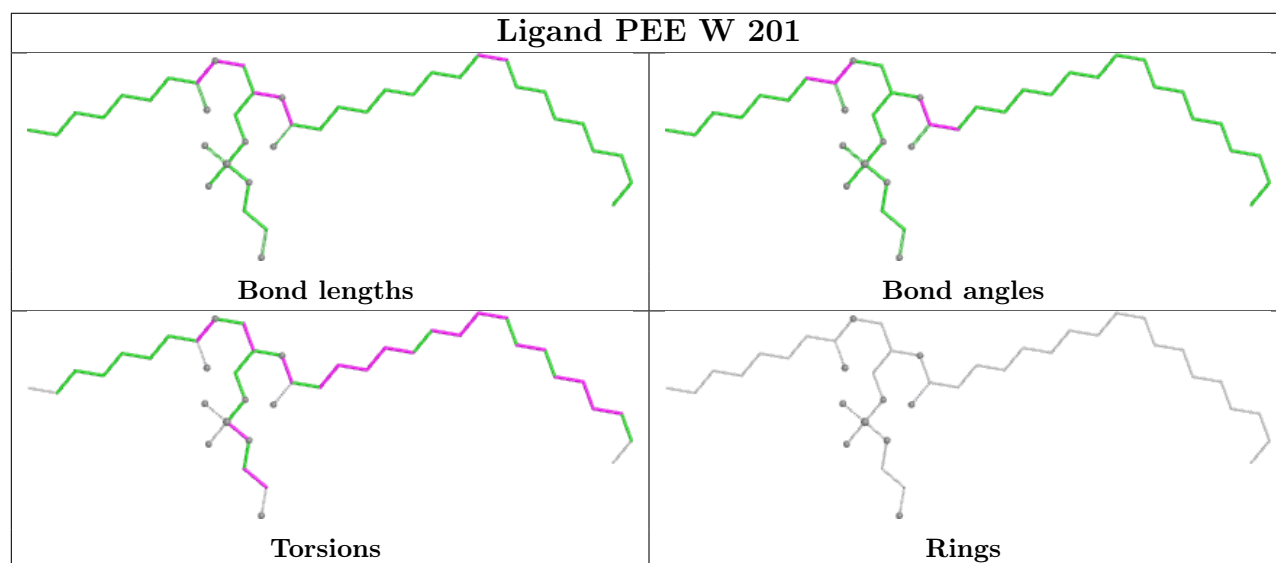
Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	W	201	PEE	2	0
30	l	704	PEE	2	0
35	s	402	UQ	4	0
33	j	204	PLX	4	0
33	r	502	PLX	4	0
31	V	202	CDL	4	0
33	j	203	PLX	1	0
31	l	703	CDL	5	0
30	U	401	PEE	4	0
31	s	401	CDL	4	0

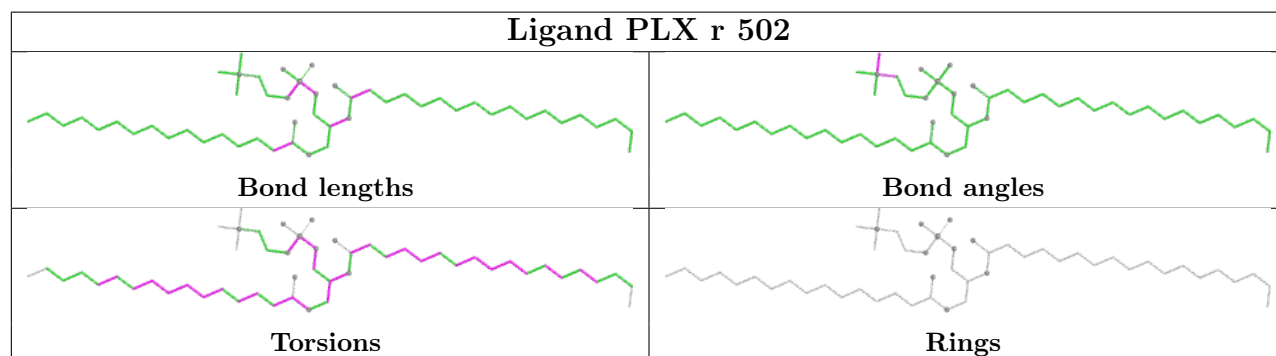
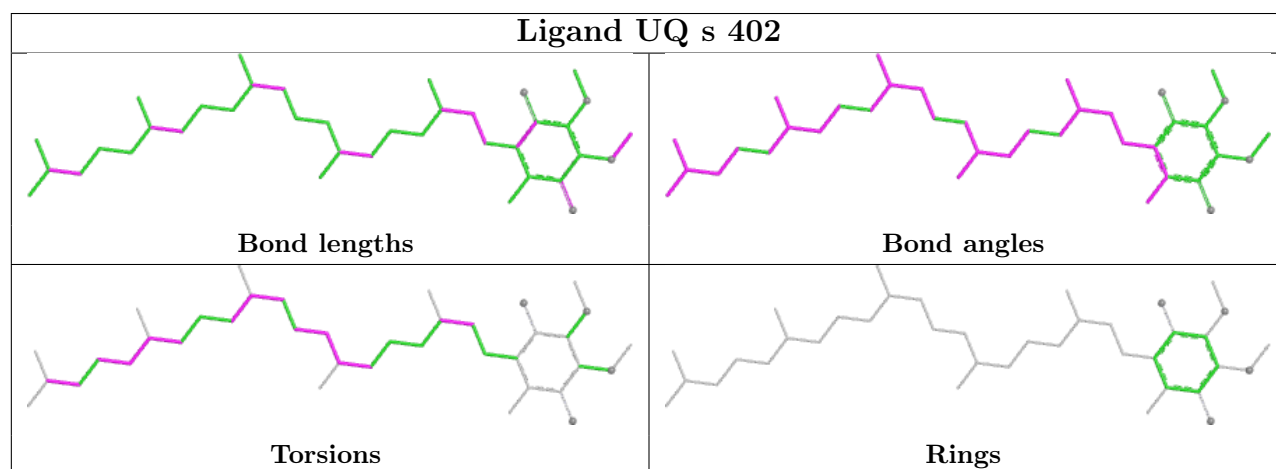
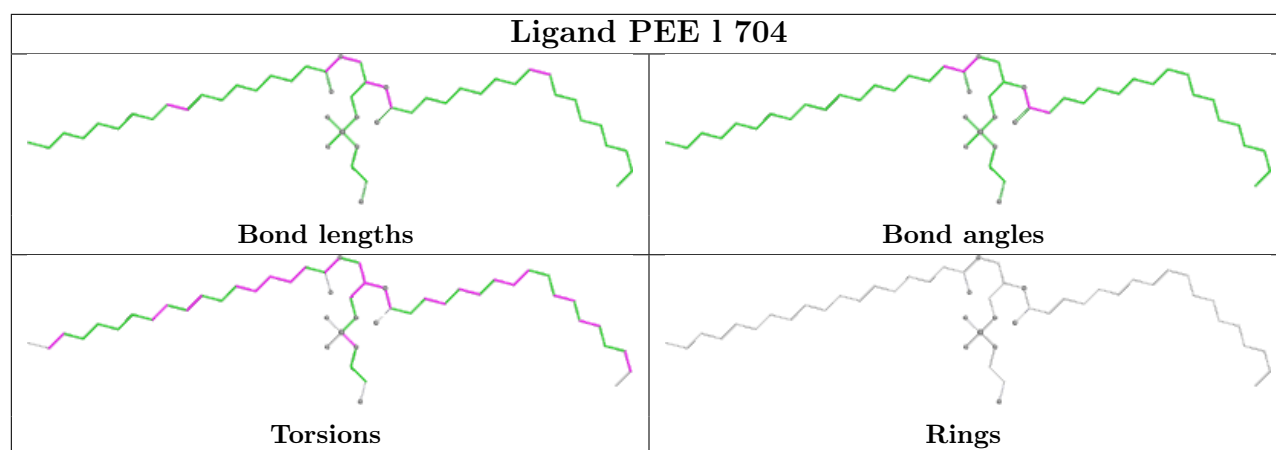
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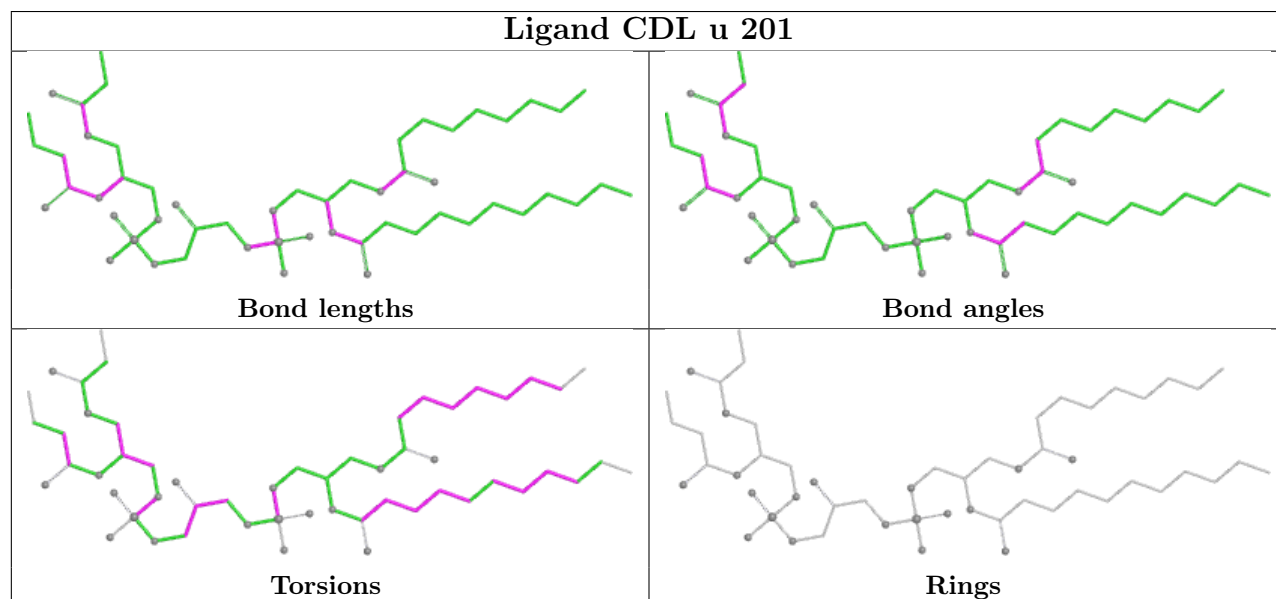
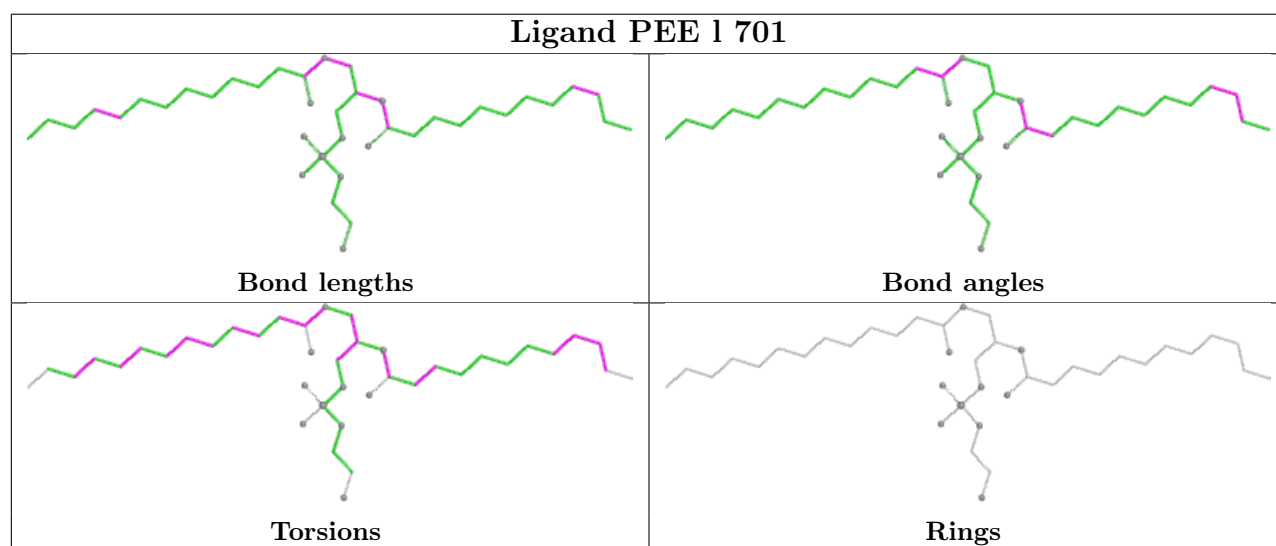
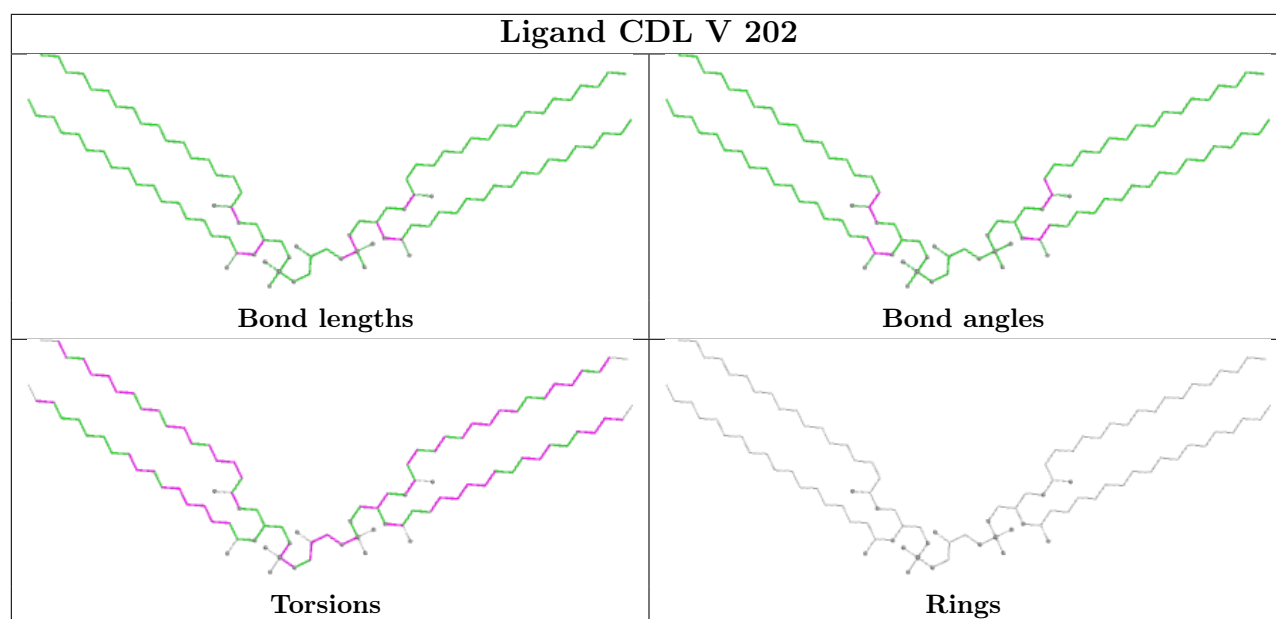
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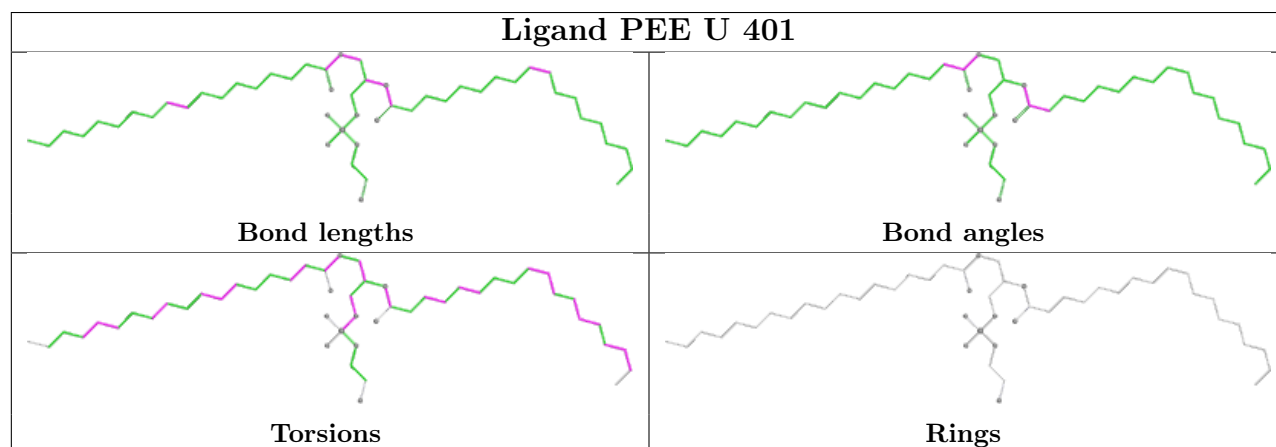
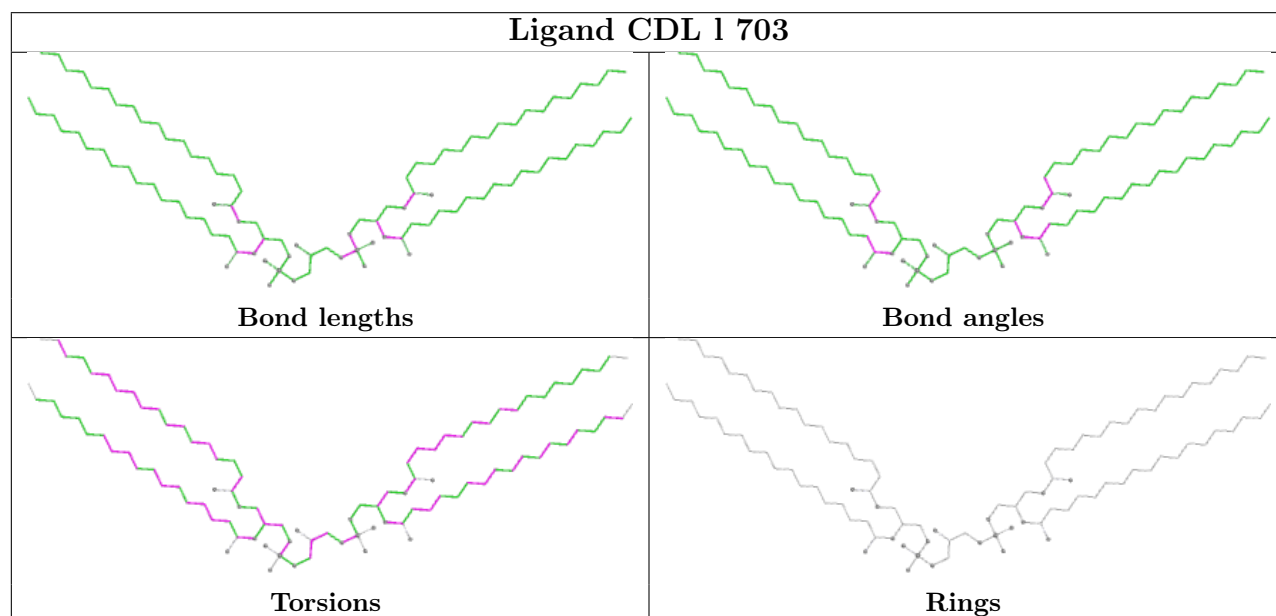
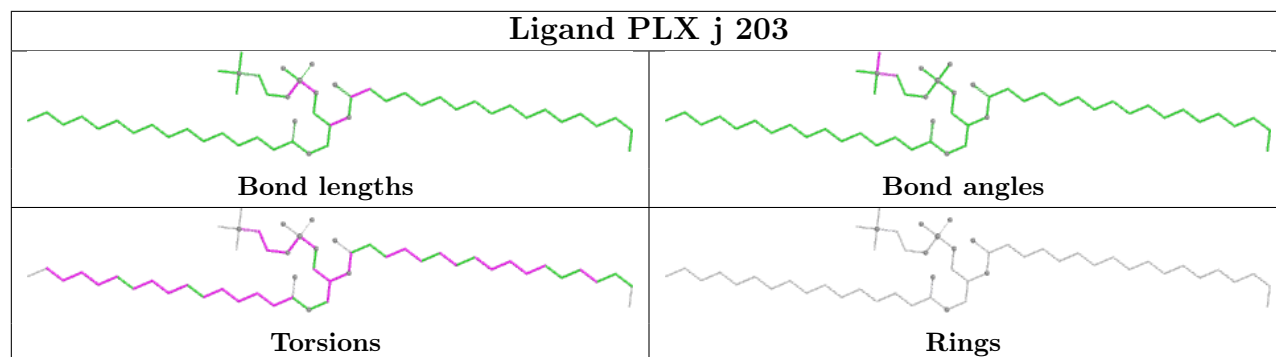
Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	l	702	CDL	16	0
30	j	201	PEE	6	0
33	g	201	PLX	5	0
36	w	401	ADP	2	0
30	i	401	PEE	2	0
31	a	201	CDL	4	0
33	a	202	PLX	2	0
30	r	501	PEE	4	0
32	X	201	8Q1	1	0
31	k	101	CDL	6	0
33	e	201	PLX	3	0
31	V	201	CDL	3	0
31	i	402	CDL	5	0
30	l	705	PEE	2	0

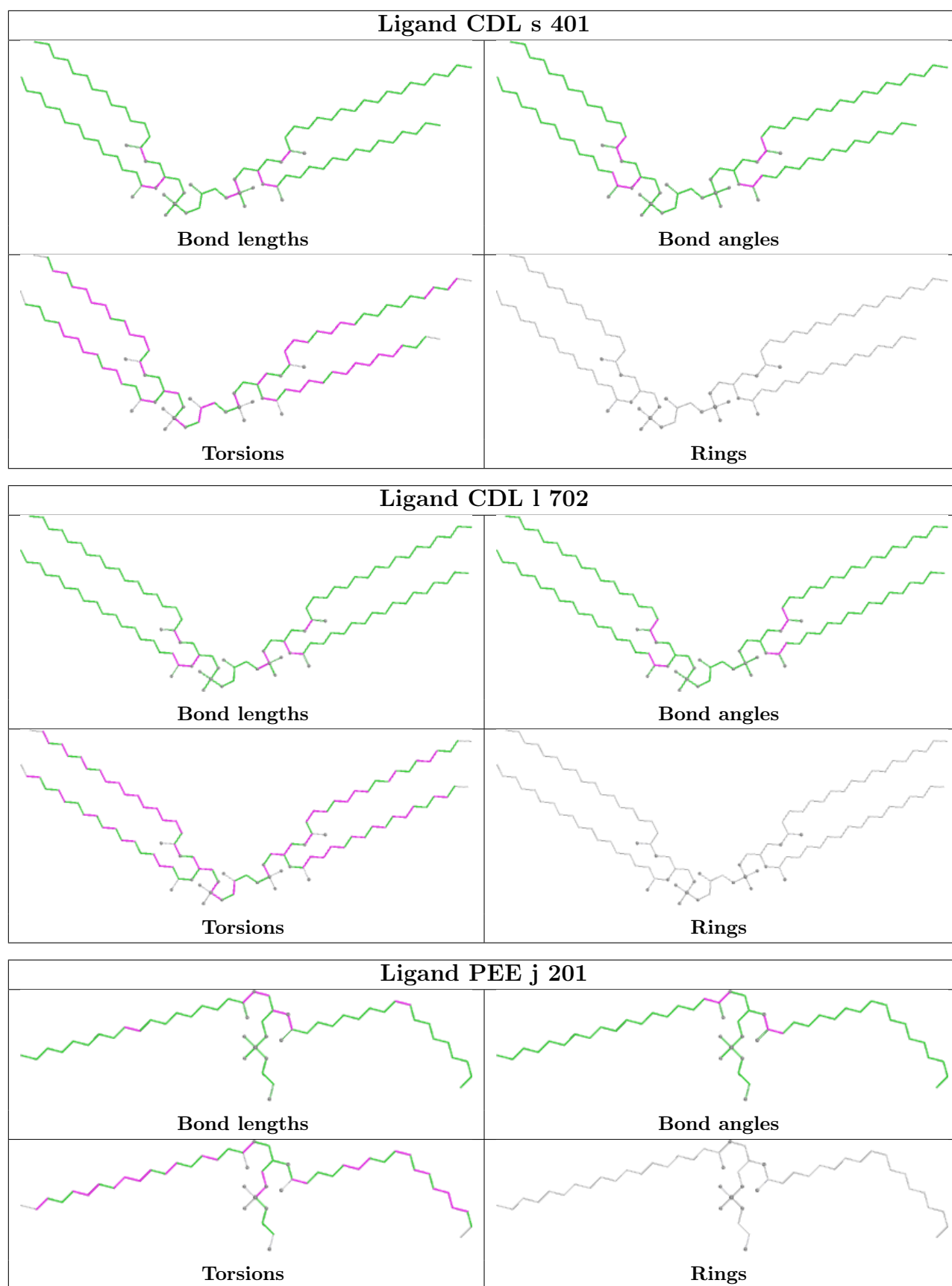
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



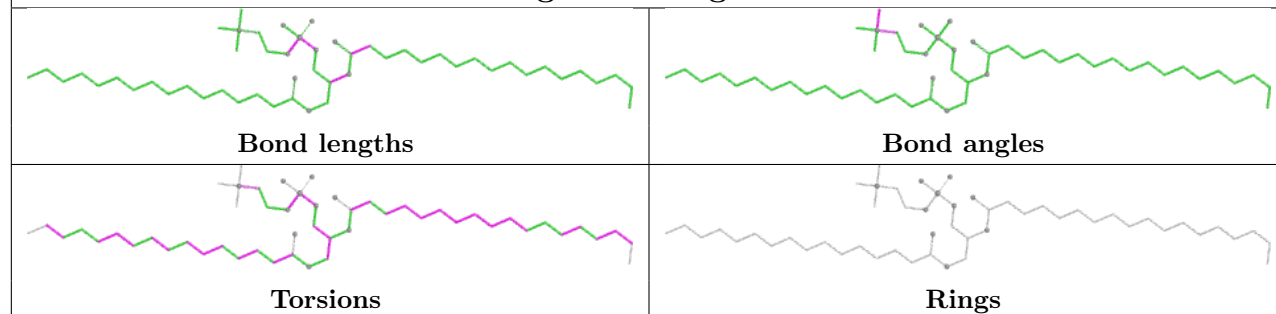




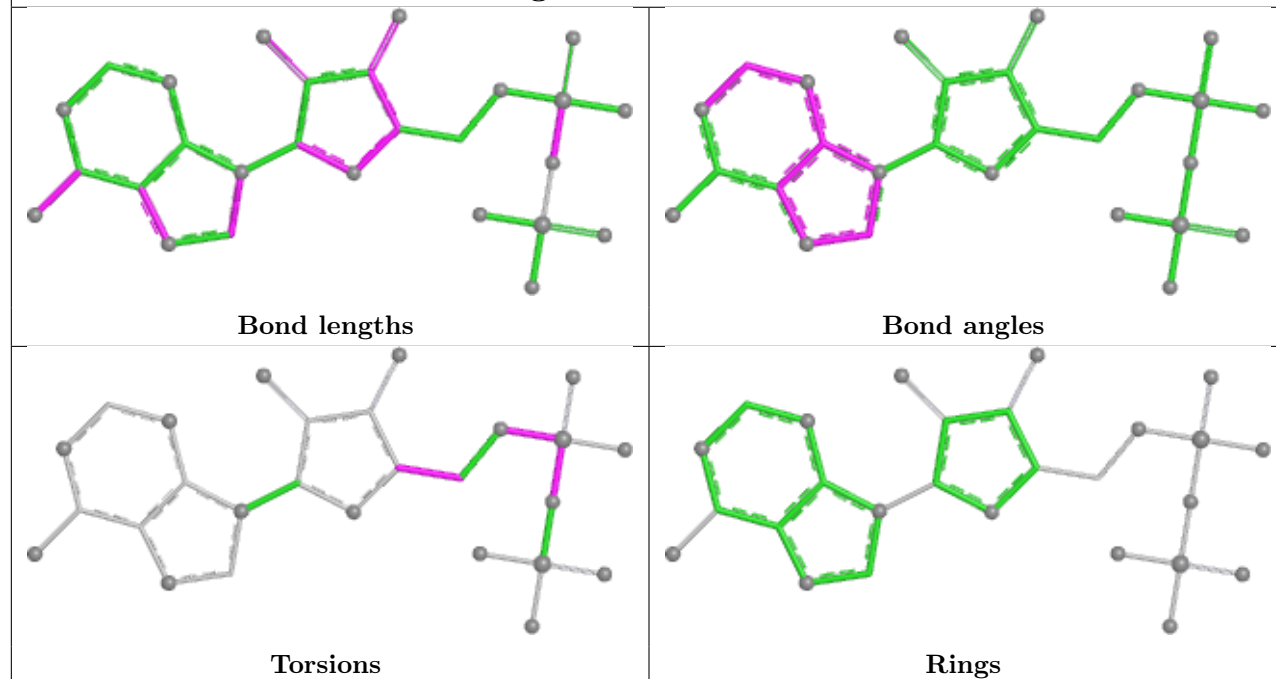




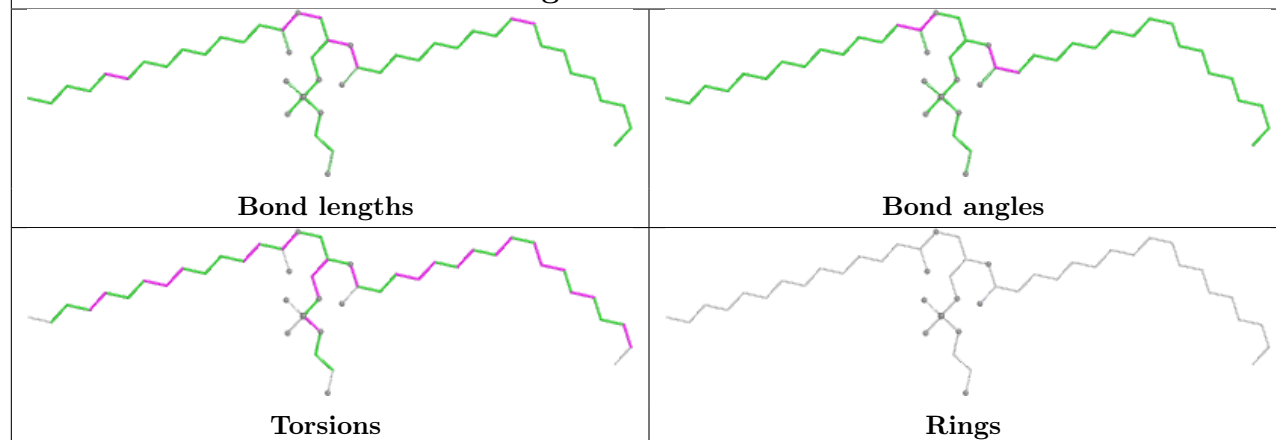
Ligand PLX g 201

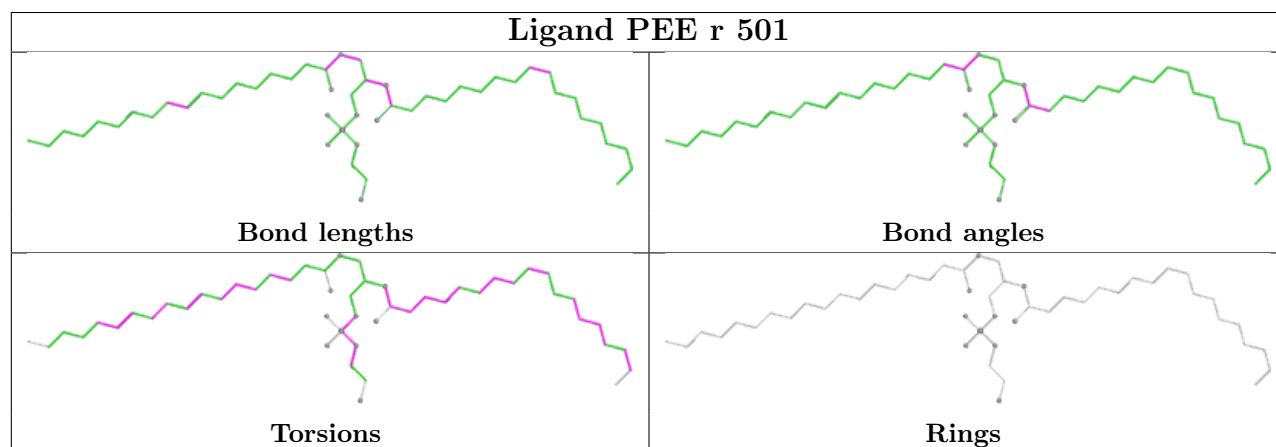
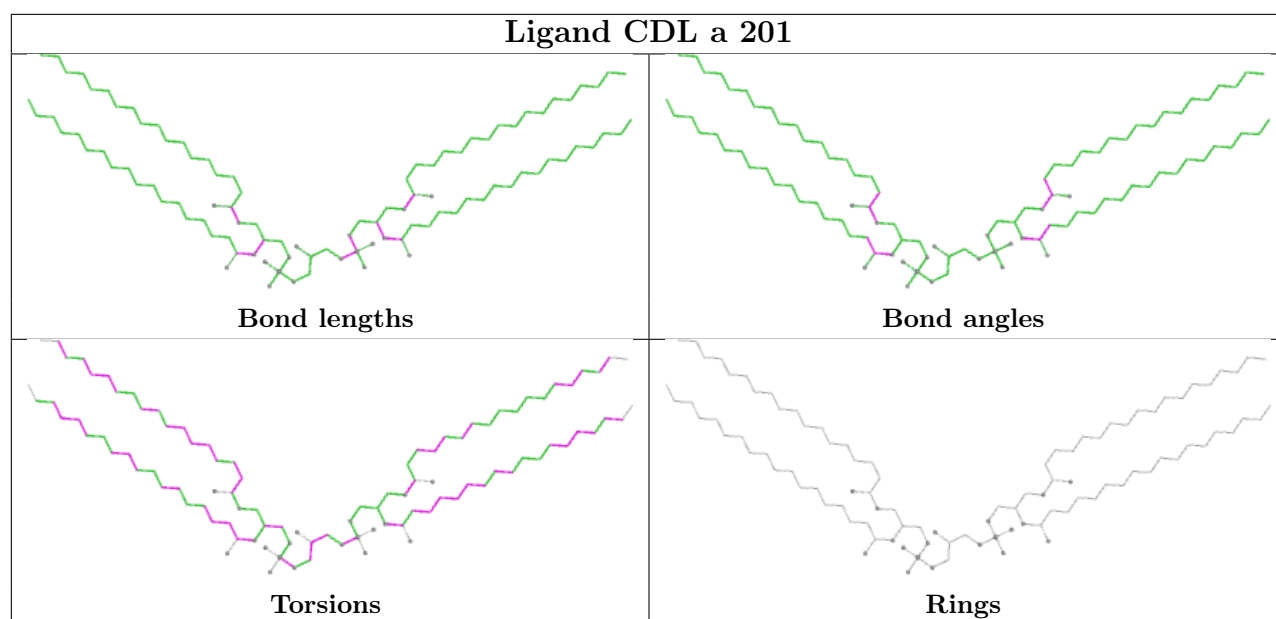


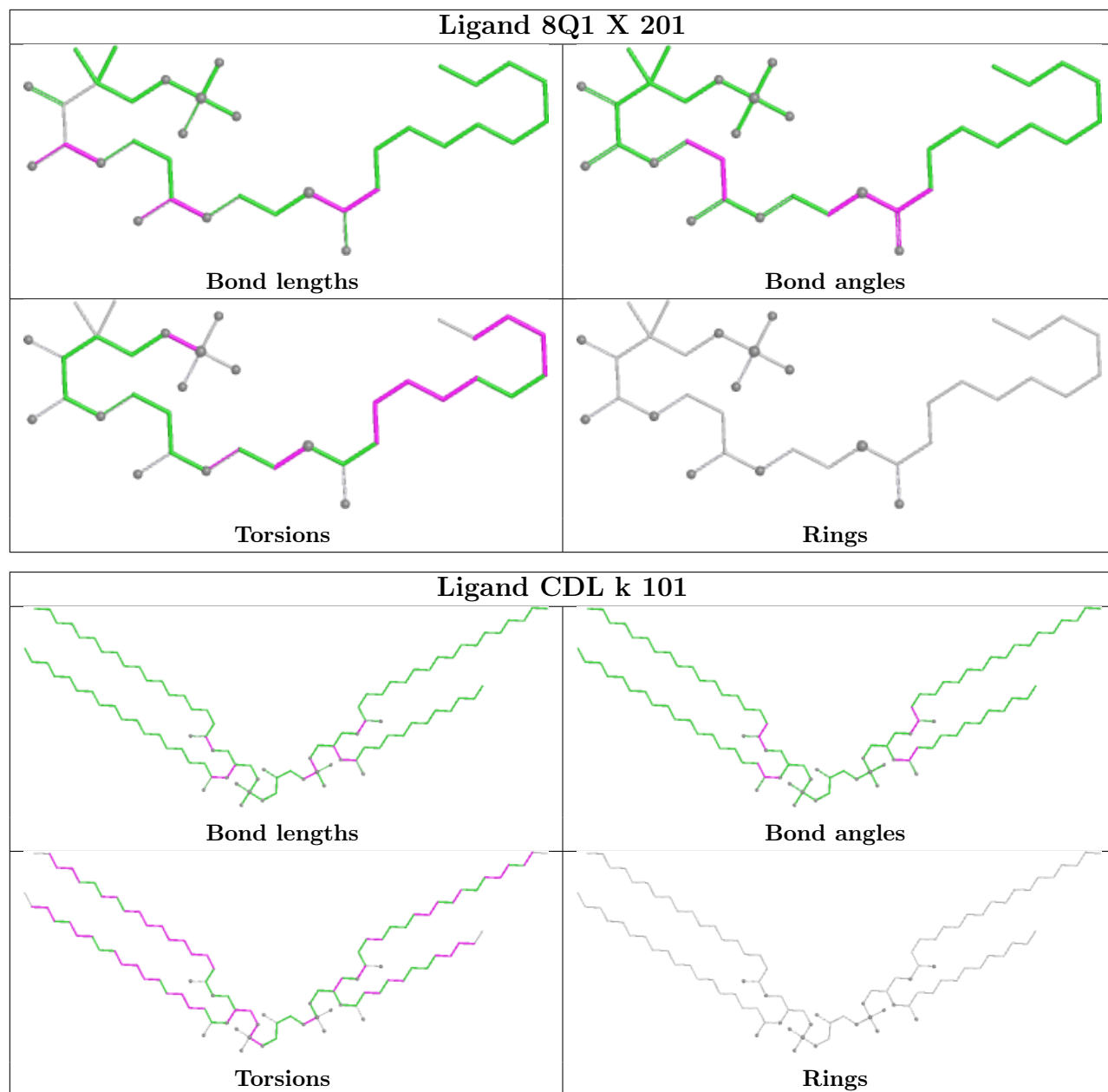
Ligand ADP w 401

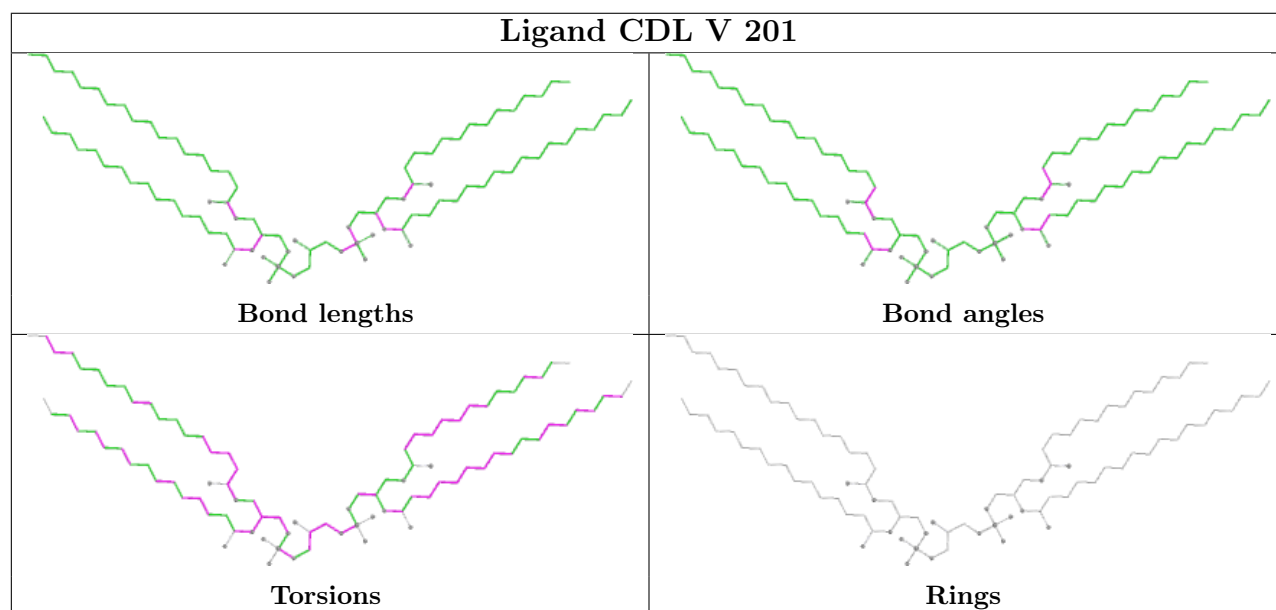
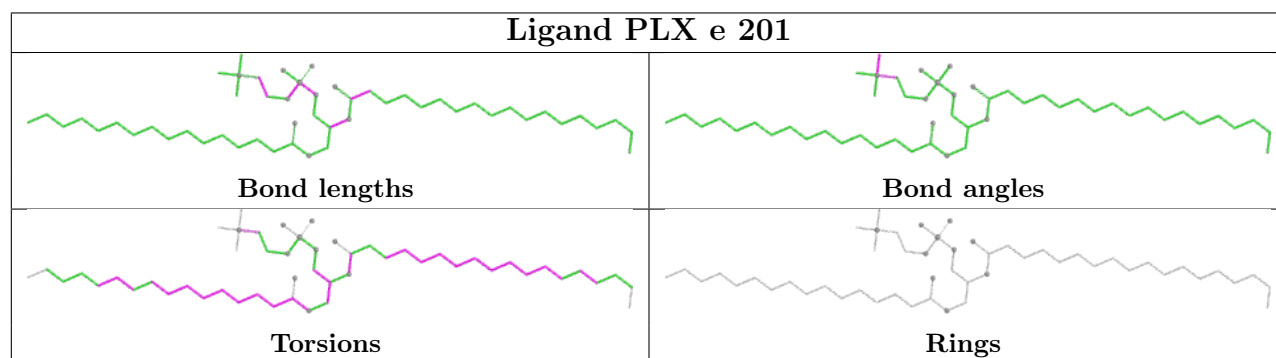
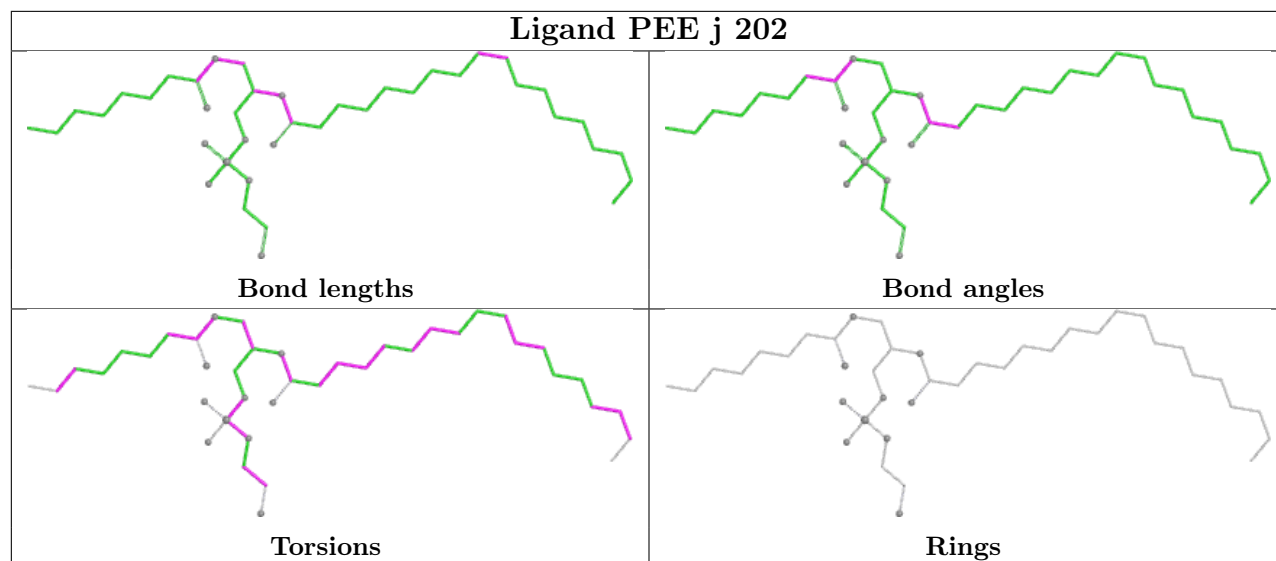


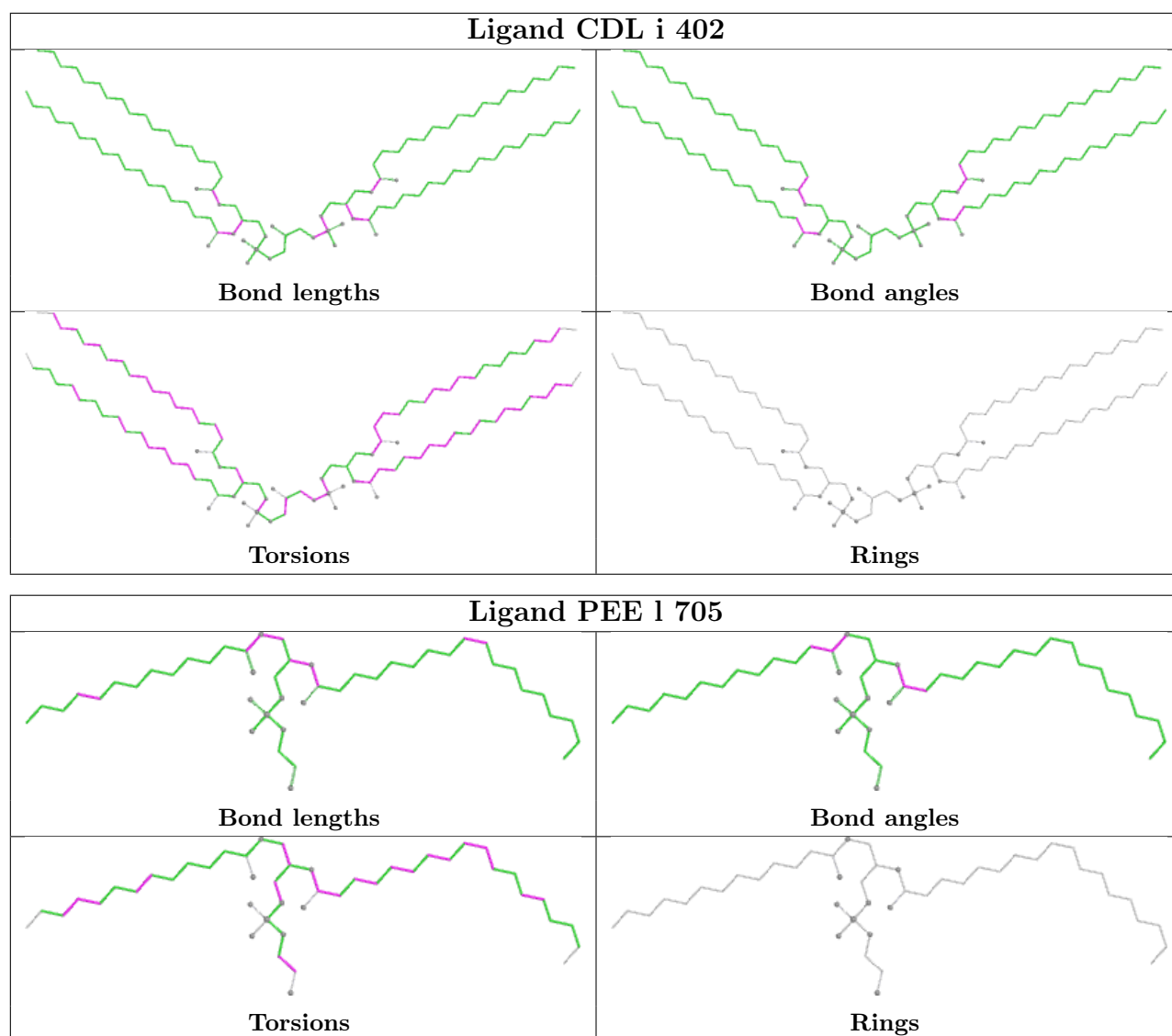
Ligand PEE i 401











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.

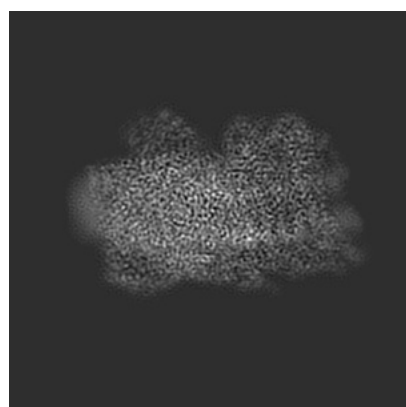
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32214. These allow visual inspection of the internal detail of the map and identification of artifacts.

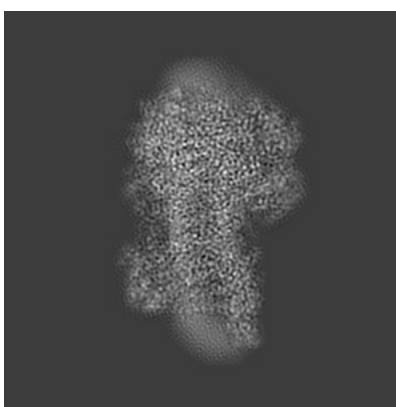
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

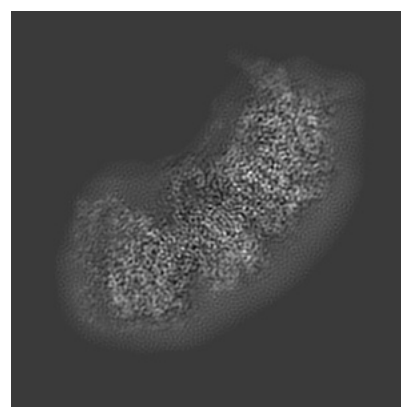
6.1.1 Primary map



X



Y

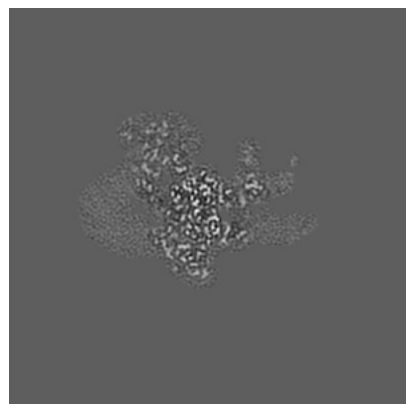


Z

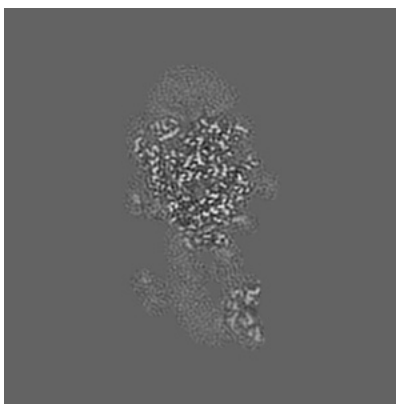
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

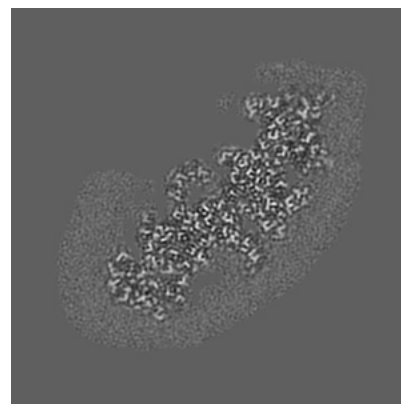
6.2.1 Primary map



X Index: 240



Y Index: 240

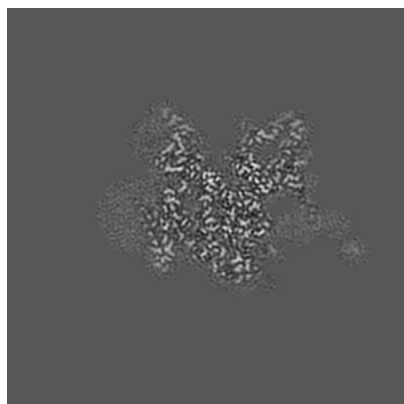


Z Index: 240

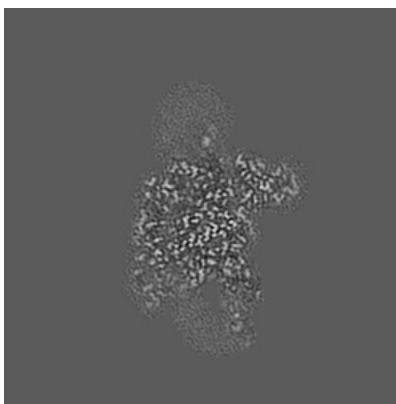
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

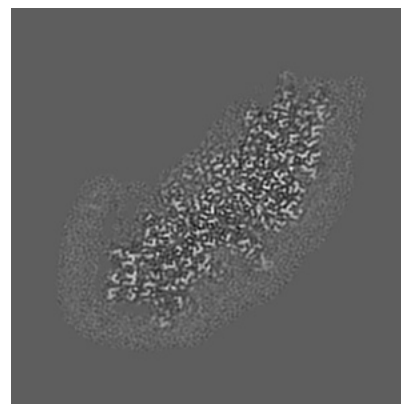
6.3.1 Primary map



X Index: 280



Y Index: 204

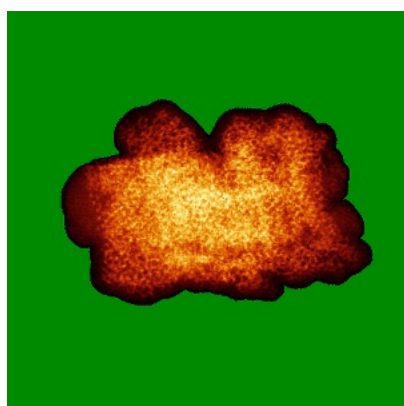


Z Index: 258

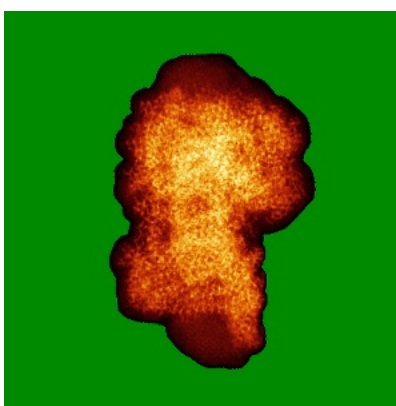
The images above show the largest variance slices of the map in three orthogonal directions.

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

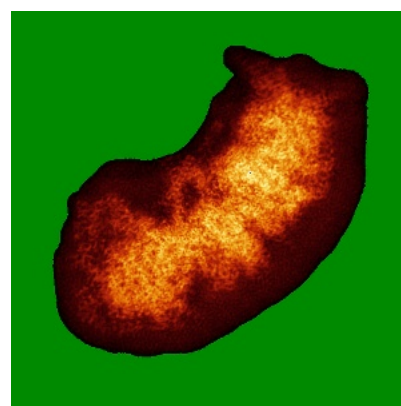
6.4.1 Primary map



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.

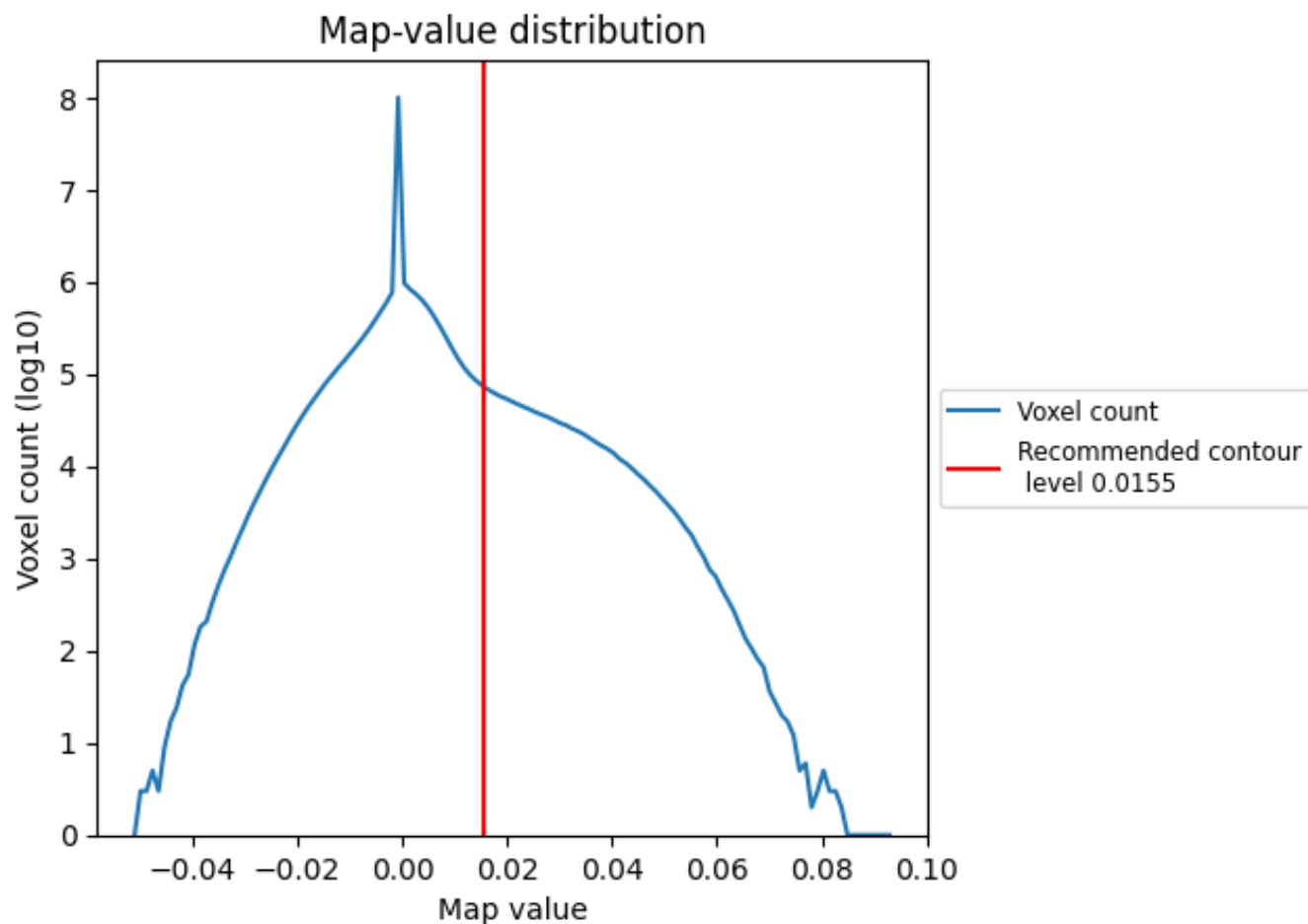
6.6 Mask visualisation

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

7 Map analysis [i](#)

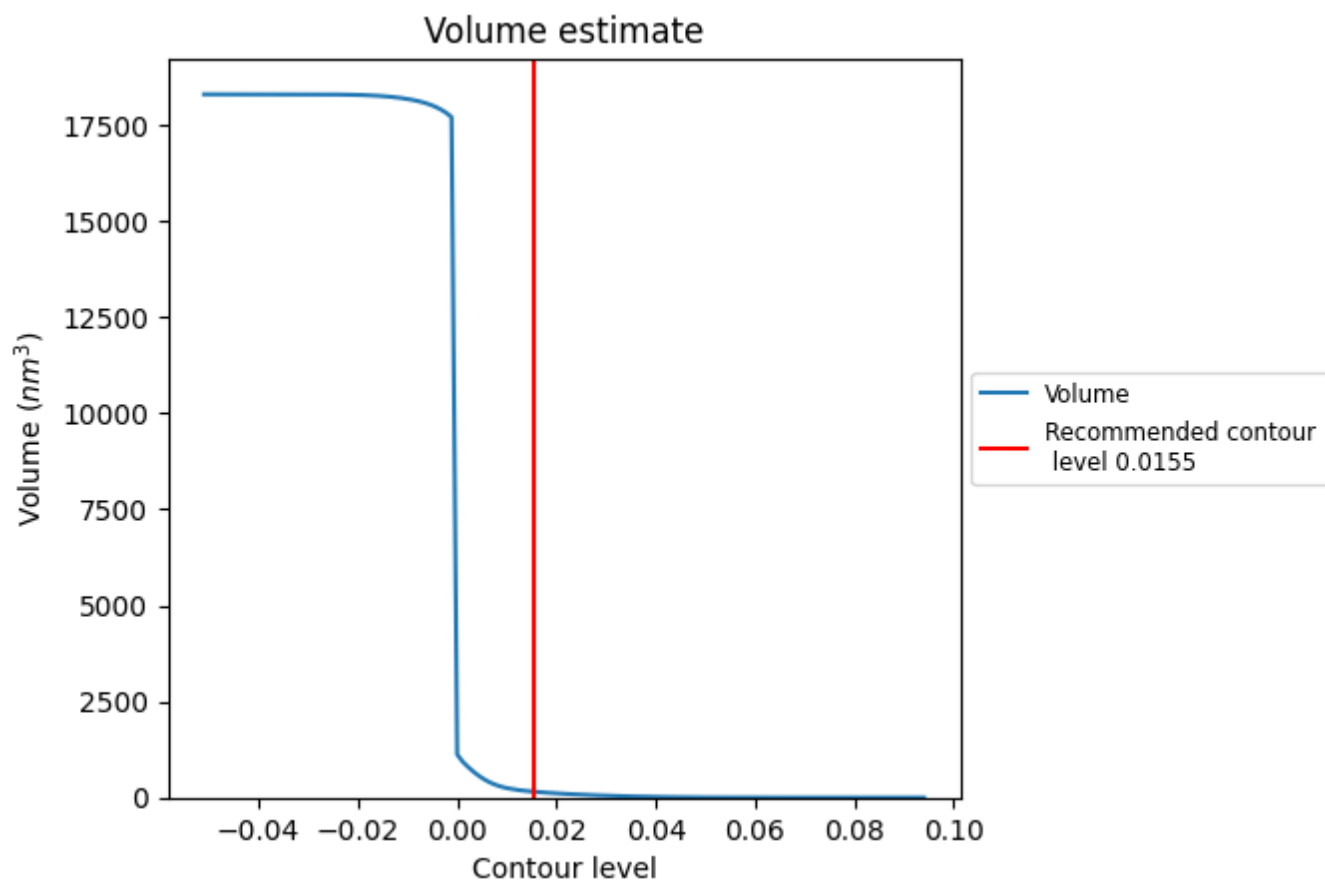
This section contains the results of statistical analysis of the map.

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.

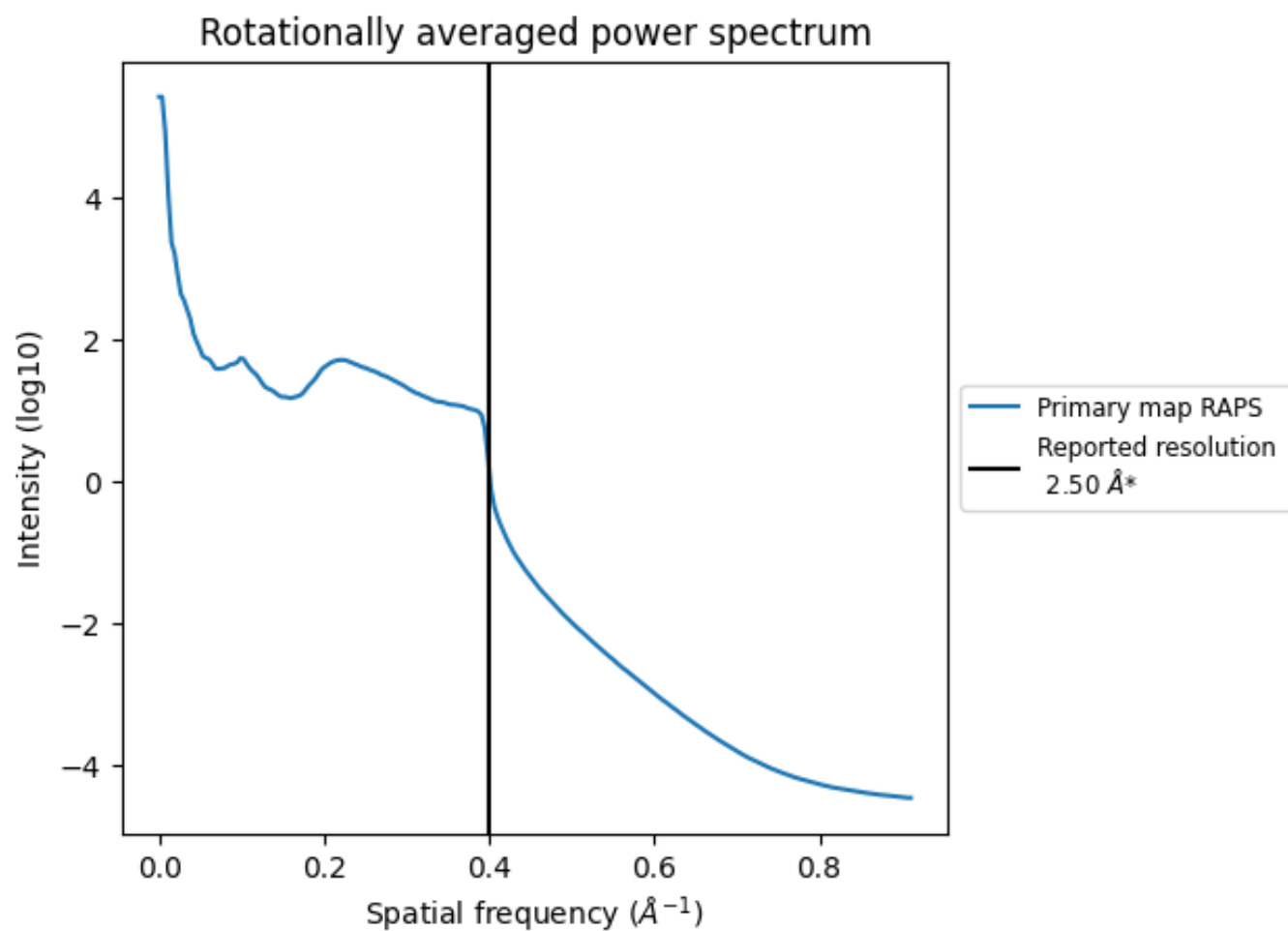
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 152 nm³; this corresponds to an approximate mass of 138 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 0.400 Å⁻¹

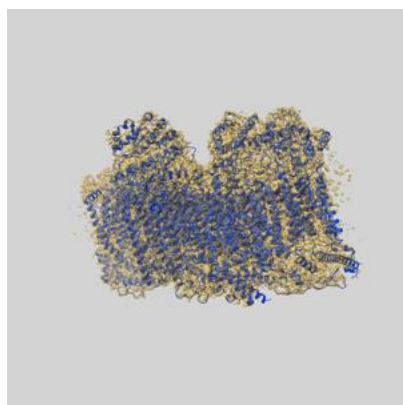
8 Fourier-Shell correlation

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

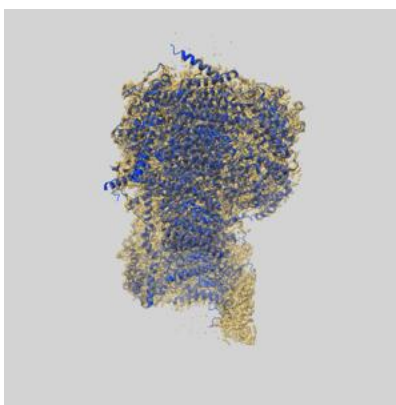
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32214 and PDB model 7VYS. Per-residue inclusion information can be found in section 3 on page 15.

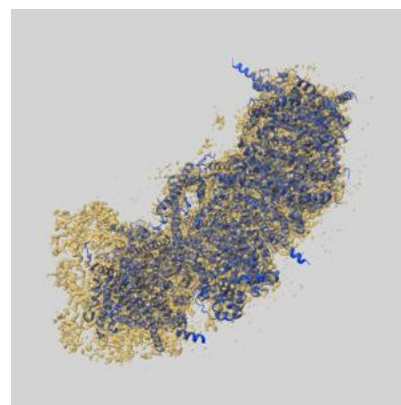
9.1 Map-model overlay [i](#)



X



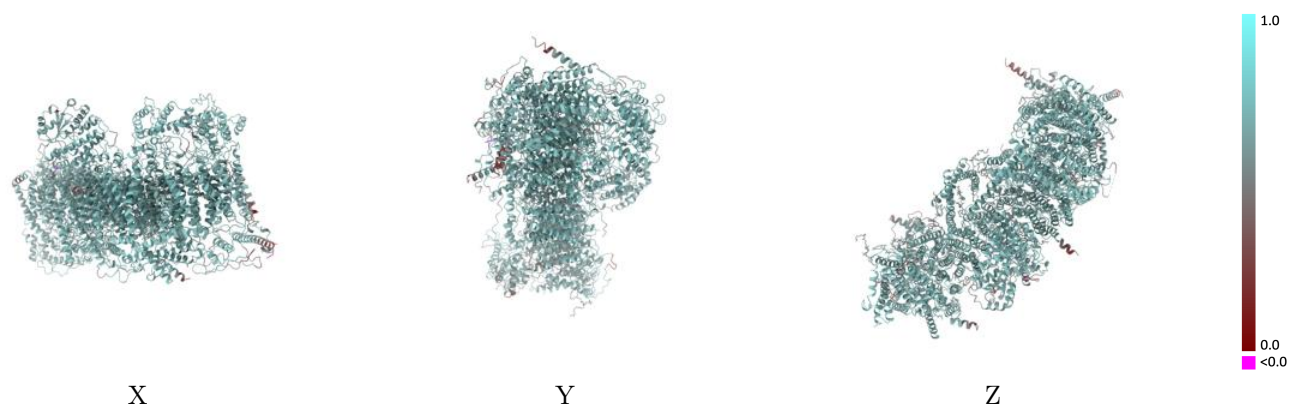
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0155 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

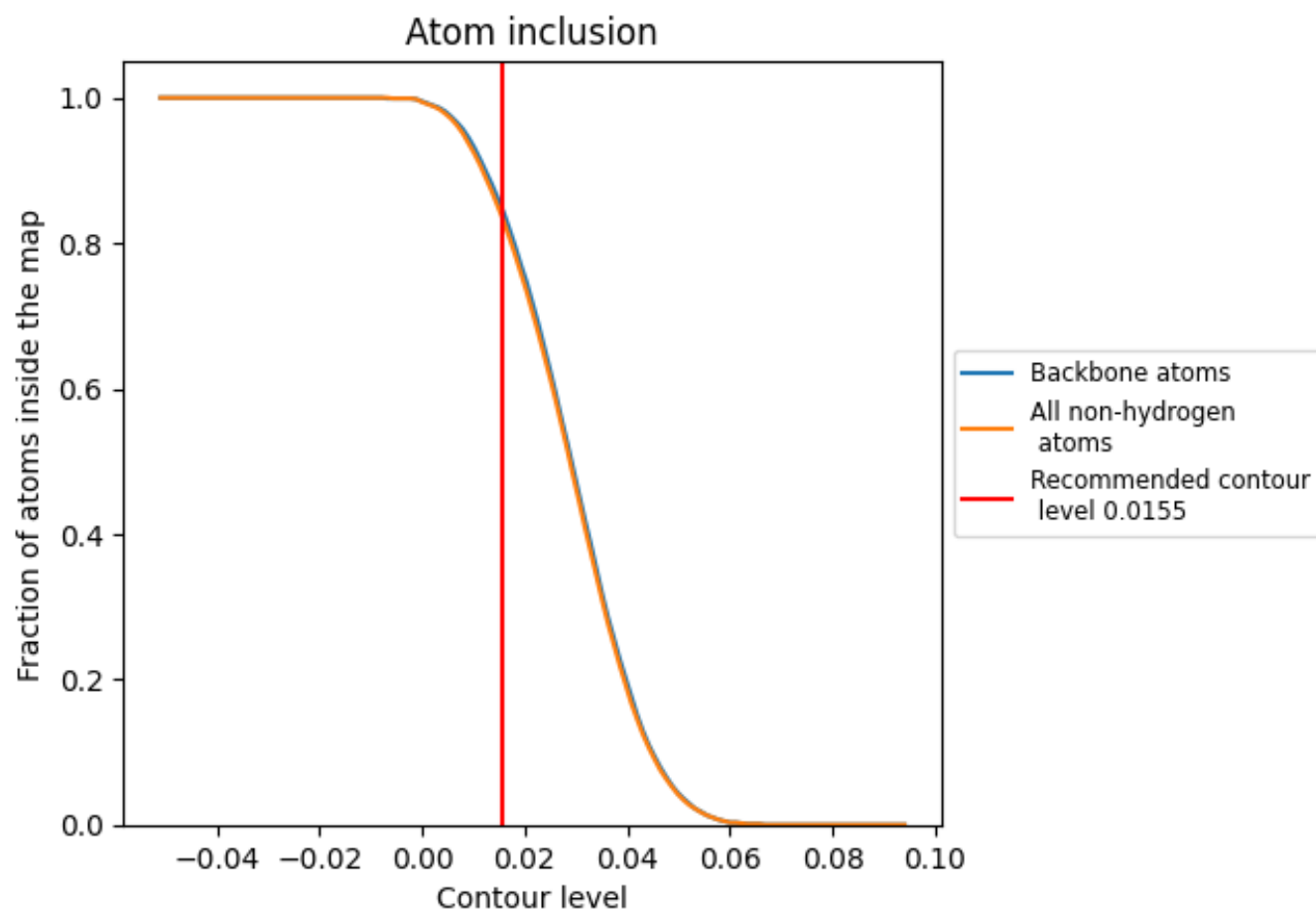


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 84% 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 (0.0155) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.6570
Q	 0.7920	 0.6450
S	 0.8910	 0.6690
U	 0.7730	 0.6340
V	 0.7440	 0.6420
W	 0.8060	 0.6410
X	 0.8100	 0.6420
Y	 0.6410	 0.5910
Z	 0.6400	 0.5810
a	 0.8610	 0.6720
b	 0.7630	 0.6220
c	 0.8470	 0.6610
d	 0.8160	 0.6550
e	 0.7940	 0.6390
f	 0.6460	 0.5870
g	 0.8920	 0.6720
h	 0.7950	 0.6430
i	 0.9390	 0.6910
j	 0.7590	 0.6310
k	 0.8970	 0.6800
l	 0.8900	 0.6700
m	 0.7970	 0.6340
n	 0.7240	 0.6140
o	 0.8520	 0.6710
p	 0.8630	 0.6660
r	 0.9610	 0.6950
s	 0.9060	 0.6770
u	 0.7750	 0.6430
v	 0.6460	 0.5850
w	 0.7730	 0.6390

