



Full wwPDB EM Validation Report ⓘ

Aug 6, 2026 – 12:19 PM JST

PDB ID : 7VZV / pdb_00007vzv
EMDB ID : EMD-32230
Title : Active state CI from Q10 dataset, Subclass 1
Authors : Gu, J.K.; Yang, M.J.
Deposited on : 2021-11-16
Resolution : 3.20 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:

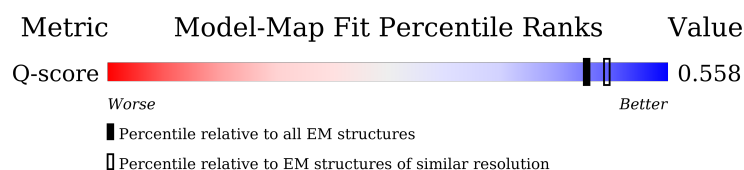
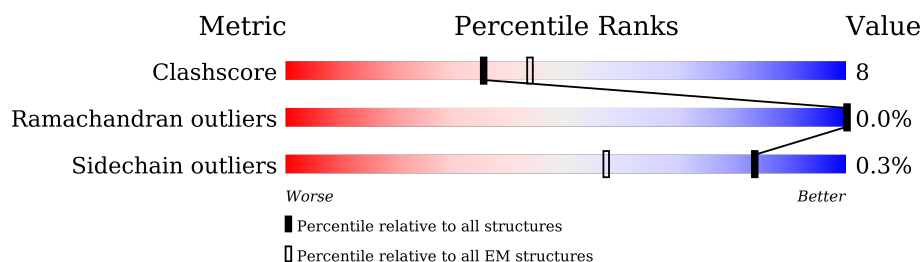
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using 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) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	A	433	
2	B	176	
3	C	156	
4	E	115	

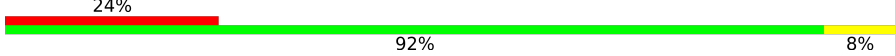
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Mol	Chain	Length	Quality of chain
5	F	86	
6	G	88	
6	X	88	
7	H	112	
8	I	112	
9	J	342	
10	K	43	
11	L	125	
12	M	690	
13	N	144	
14	O	217	
15	P	208	
16	Q	430	
17	S	70	
18	T	96	
19	U	83	
20	V	140	
21	W	142	
22	Y	67	
23	Z	80	
24	a	138	
25	b	126	
26	c	156	
27	d	175	
28	e	104	

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Mol	Chain	Length	Quality of chain
29	f	49	
30	g	121	
31	h	105	
32	i	347	
33	j	115	
34	k	98	
35	l	606	
36	m	175	
37	n	56	
38	o	128	
39	p	178	
40	r	459	
41	s	318	
42	u	171	
43	v	124	
44	w	320	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
45	SF4	A	501	-	-	X	-

2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 68183 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] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	433	Total	C	N	O	S	0	0
			3330	2103	593	614	20		

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	176	Total	C	N	O	S	0	0
			1412	887	243	269	13		

- Molecule 3 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	156	Total	C	N	O	S	0	0
			1248	794	227	213	14		

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	115	Total	C	N	O	S	0	0
			971	619	179	168	5		

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	86	Total	C	N	O	S	0	0
			687	432	129	124	2		

- Molecule 6 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	88	Total	C	N	O	S	0	0
			690	446	102	137	5		
6	X	88	Total	C	N	O	S	0	0
			694	447	103	139	5		

- Molecule 7 is a protein called Complex I subunit B13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	112	Total	C	N	O	S	0	0
			910	588	154	165	3		

- Molecule 8 is a protein called Complex I-B14.5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	97	Total	C	N	O	S	0	0
			780	491	147	139	3		

- Molecule 9 is a protein called NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	342	Total	C	N	O	S	0	0
			2751	1783	481	478	9		

- Molecule 10 is a protein called Complex I-9kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	43	Total	C	N	O	S	0	0
			366	228	68	69	1		

- Molecule 11 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	125	Total	C	N	O	S	0	0
			1016	642	181	190	3		

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	690	Total	C	N	O	S	0	0
			5296	3320	923	1014	39		

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	144	Total	C	N	O	S	0	0
			1204	770	218	212	4		

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	217	Total	C	N	O	S	0	0
			1671	1065	281	315	10		

- Molecule 15 is a protein called Complex I-30kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	208	Total	C	N	O	S	0	0
			1738	1124	298	314	2		

- Molecule 16 is a protein called Complex I-49kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	430	Total	C	N	O	S	0	0
			3459	2212	594	629	24		

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	70	Total	C	N	O	S	0	0
			566	364	103	94	5		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	96	Total	C	N	O	S	0	0
			741	452	140	146	3		

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

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

- Molecule 20 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

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

- Molecule 21 is a protein called Complex I-B16.6.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	142	Total	C	N	O	S	0	0
			1161	749	197	206	9		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Y	67	Total	C	N	O	S	0	0
			584	385	95	103	1		

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

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

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

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

- Molecule 25 is a protein called Complex I-B17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	98	Total	C	N	O	S	0	0
			819	537	144	137	1		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	156	Total	C	N	O	S	0	0
			1315	853	213	241	8		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

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

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

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

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	49	Total	C	N	O	0	0
			378	246	65	67		

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

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

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	h	105	Total	C	N	O	S	0	0
			863	548	161	148	6		

- Molecule 32 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	i	347	Total	C	N	O	S	0	0
			2706	1779	419	462	46		

- Molecule 33 is a protein called NADH-ubiquinone oxidoreductase chain 3.

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

- Molecule 34 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

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

- Molecule 35 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	606	Total	C	N	O	S	0	0
			4812	3190	745	826	51		

- Molecule 36 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	175	Total	C	N	O	S	0	0
			1291	861	188	229	13		

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	56	Total	C	N	O	S	0	0
			479	311	88	79	1		

- Molecule 38 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

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

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	178	Total	C	N	O	S	0	0
			1534	982	279	265	8		

- Molecule 40 is a protein called NADH-ubiquinone oxidoreductase chain 4.

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

- Molecule 41 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	s	318	Total	C	N	O	S	0	0
			2508	1678	385	424	21		

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

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

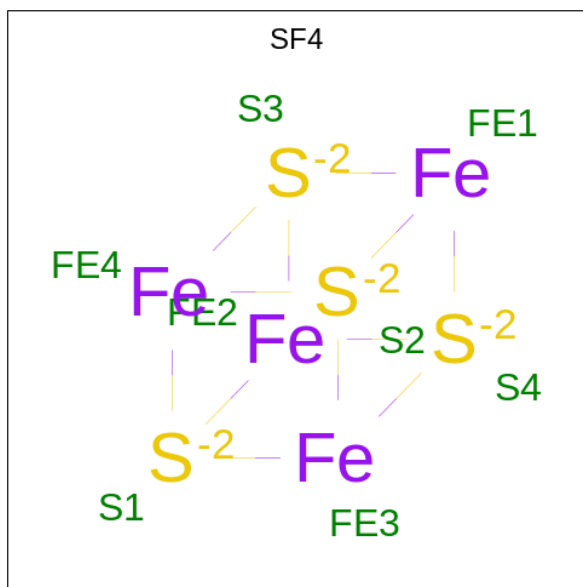
- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

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

- Molecule 44 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

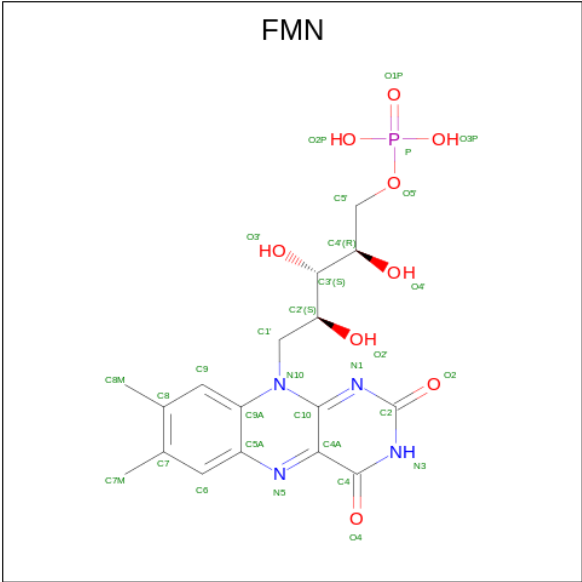
Mol	Chain	Residues	Atoms					AltConf	Trace
44	w	320	Total	C	N	O	S	0	0
			2590	1649	440	491	10		

- Molecule 45 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



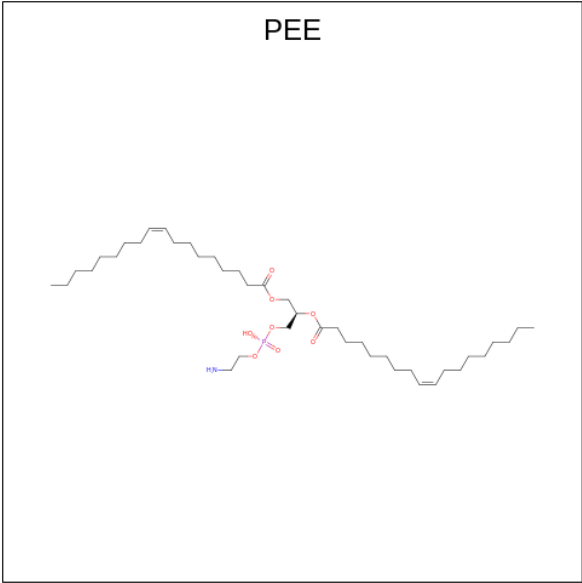
Mol	Chain	Residues	Atoms			AltConf
45	A	1	Total	Fe	S	0
			8	4	4	
45	B	1	Total	Fe	S	0
			8	4	4	
45	B	1	Total	Fe	S	0
			8	4	4	
45	C	1	Total	Fe	S	0
			8	4	4	
45	M	1	Total	Fe	S	0
			8	4	4	
45	M	1	Total	Fe	S	0
			8	4	4	

- Molecule 46 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
46	A	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 47 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).



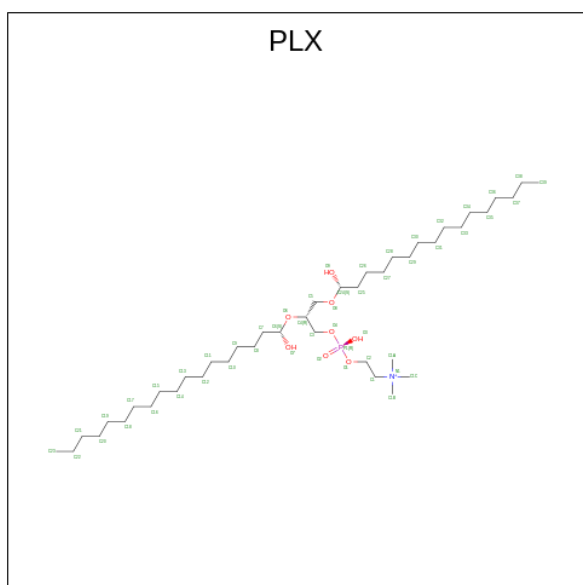
Mol	Chain	Residues	Atoms					AltConf
47	C	1	Total	C	N	O	P	0
			47	37	1	8	1	
47	Q	1	Total	C	N	O	P	0
			47	37	1	8	1	

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

- Molecule 48 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: C₄₂H₈₉NO₈P) (labeled as "Ligand of Interest" by depositor).



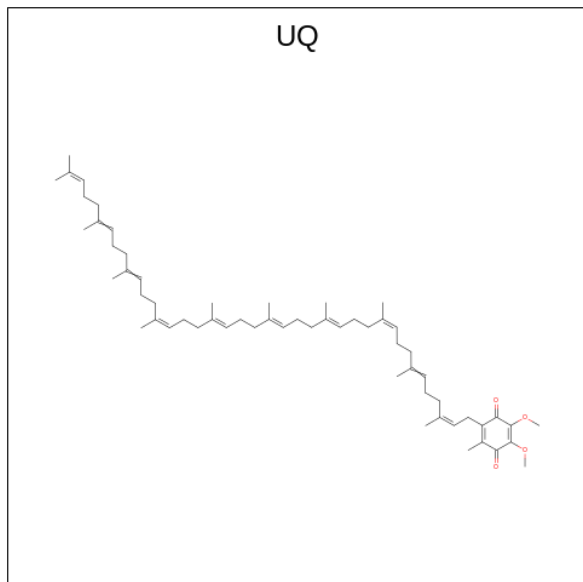
Mol	Chain	Residues	Atoms					AltConf
48	C	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	J	1	Total	C	N	O	P	0
			52	42	1	8	1	

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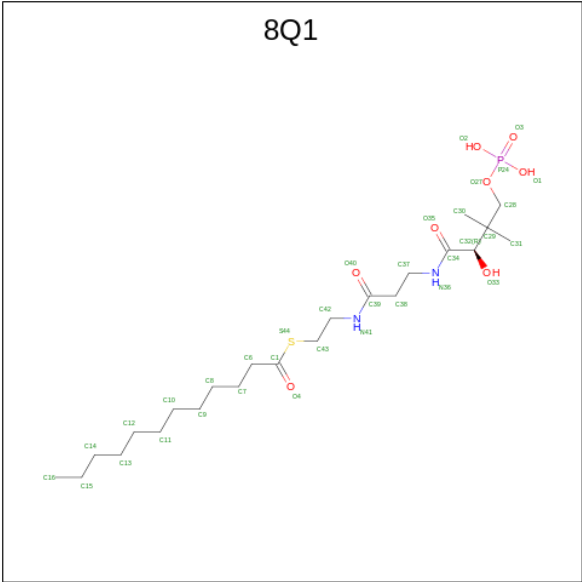
Mol	Chain	Residues	Atoms					AltConf
48	N	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	a	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	g	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	j	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	r	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 49 is Coenzyme Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-isomer (CCD ID: UQ) (formula: C₅₉H₉₀O₄) (labeled as "Ligand of Interest" by depositor).



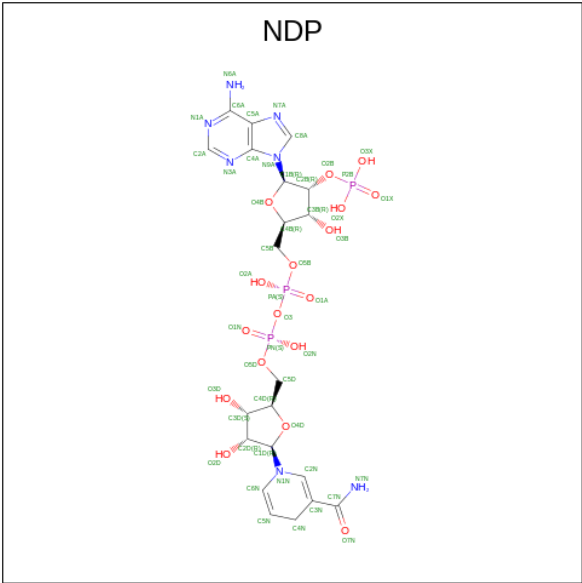
Mol	Chain	Residues	Atoms			AltConf
49	C	1	Total	C	O	0
			63	59	4	
49	J	1	Total	C	O	0
			33	29	4	

- Molecule 50 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (CCD ID: 8Q1) (formula: C₂₃H₄₅N₂O₈PS) (labeled as "Ligand of Interest" by depositor).



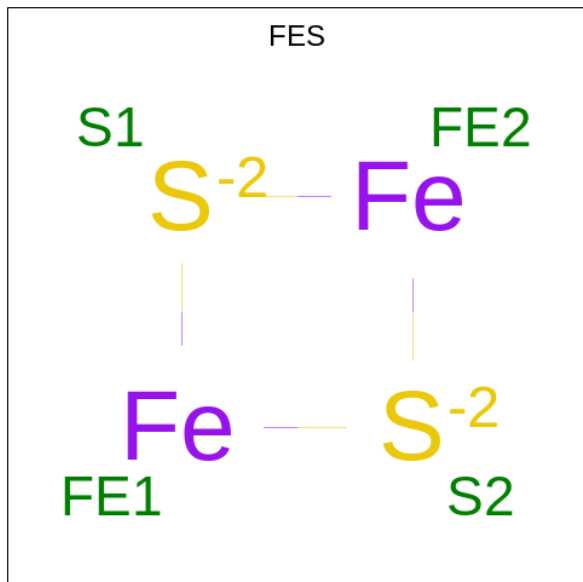
Mol	Chain	Residues	Atoms						AltConf
50	G	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	
50	X	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

- Molecule 51 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
51	J	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 52 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).

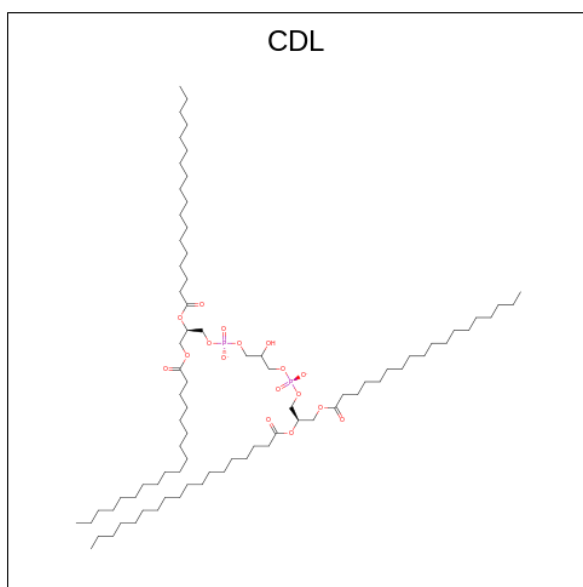


Mol	Chain	Residues	Atoms			AltConf
52	M	1	Total	Fe	S	0
			4	2	2	
52	O	1	Total	Fe	S	0
			4	2	2	

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
53	M	1	Total	Mg	0
			1	1	

- Molecule 54 is CARDIOLIPIN (CCD ID: CDL) (formula: $\text{C}_{81}\text{H}_{156}\text{O}_{17}\text{P}_2$) (labeled as "Ligand of Interest" by depositor).

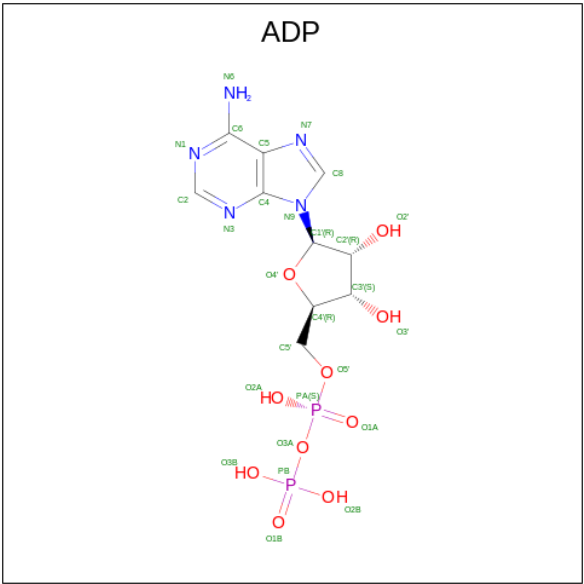


Mol	Chain	Residues	Atoms				AltConf
54	N	1	Total	C	O	P	0
			51	32	17	2	
54	V	1	Total	C	O	P	0
			94	75	17	2	
54	V	1	Total	C	O	P	0
			100	81	17	2	
54	a	1	Total	C	O	P	0
			100	81	17	2	
54	l	1	Total	C	O	P	0
			99	80	17	2	
54	l	1	Total	C	O	P	0
			100	81	17	2	
54	m	1	Total	C	O	P	0
			100	81	17	2	
54	n	1	Total	C	O	P	0
			55	36	17	2	
54	r	1	Total	C	O	P	0
			100	81	17	2	
54	s	1	Total	C	O	P	0
			89	70	17	2	

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
55	T	1	Total	Zn	0
			1	1	

- Molecule 56 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



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

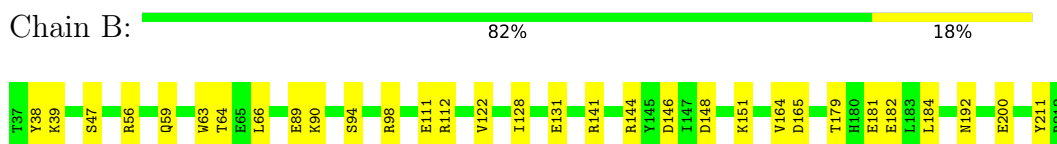
3 Residue-property plots

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.

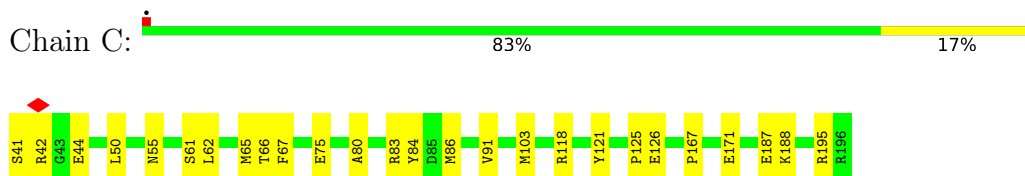
- Molecule 1: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



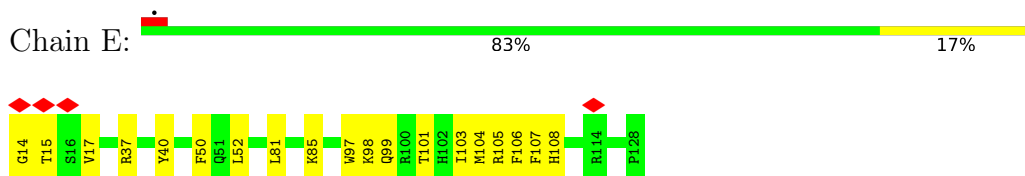
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial



- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial



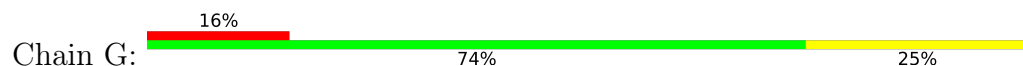
- Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



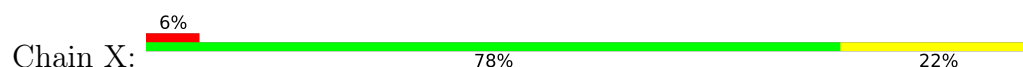
- Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2



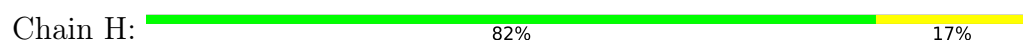
- Molecule 6: Acyl carrier protein



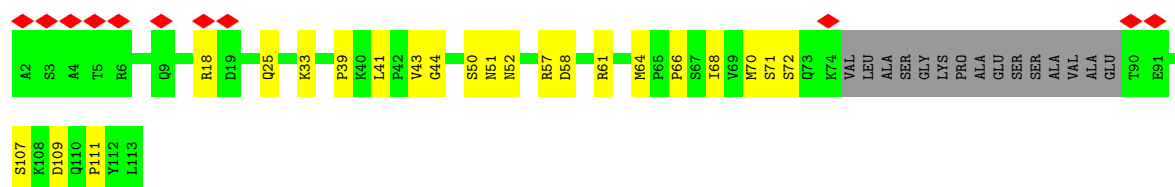
- Molecule 6: Acyl carrier protein



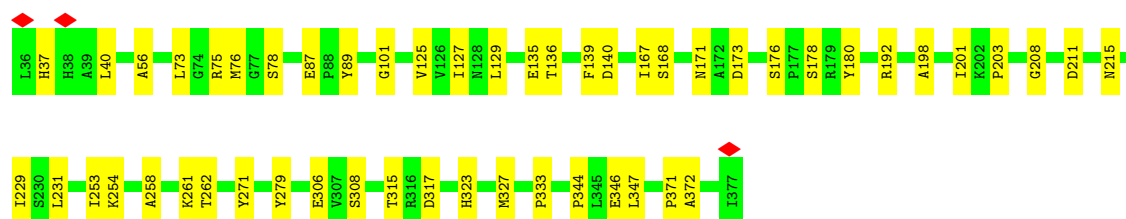
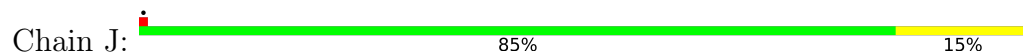
- Molecule 7: Complex I subunit B13



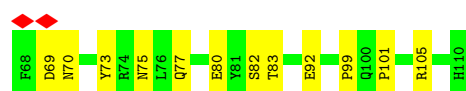
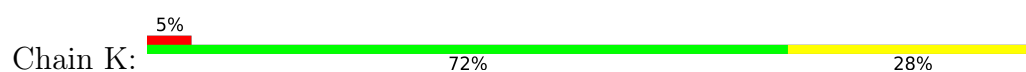
- Molecule 8: Complex I-B14.5a



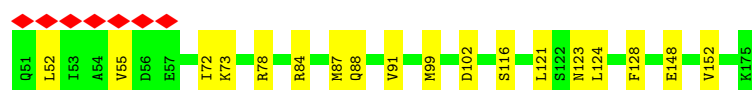
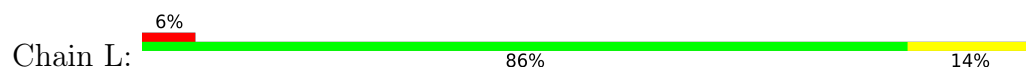
- Molecule 9: NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 9, mitochondrial



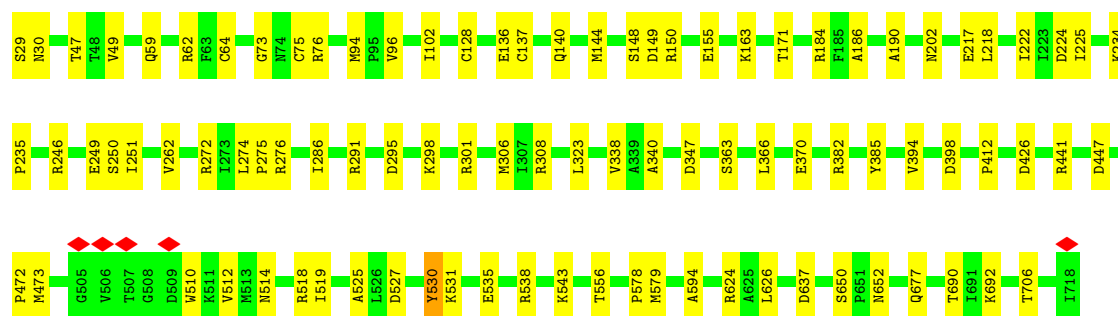
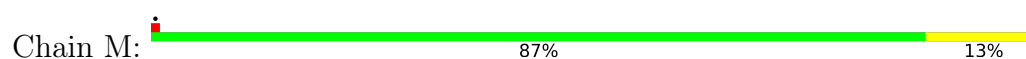
- Molecule 10: Complex I-9kD



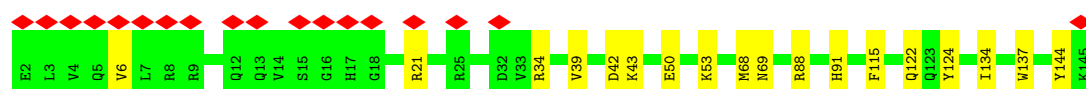
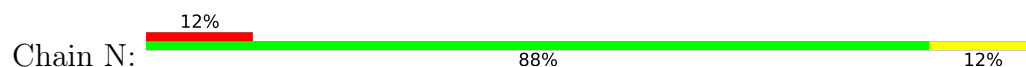
- Molecule 11: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial



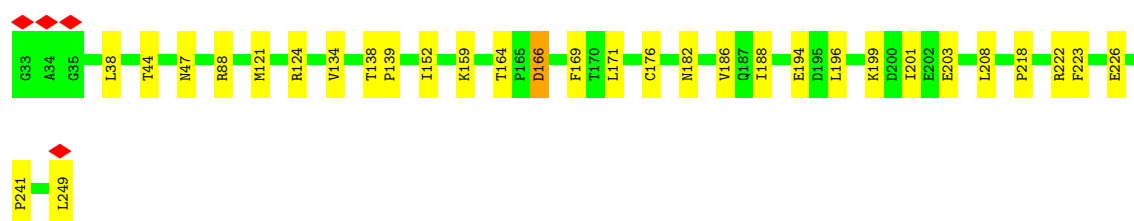
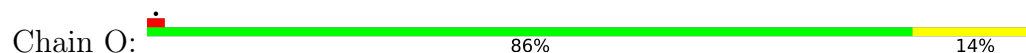
- Molecule 12: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial



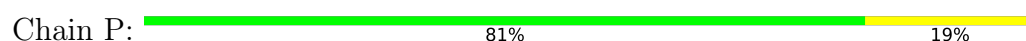
- Molecule 13: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

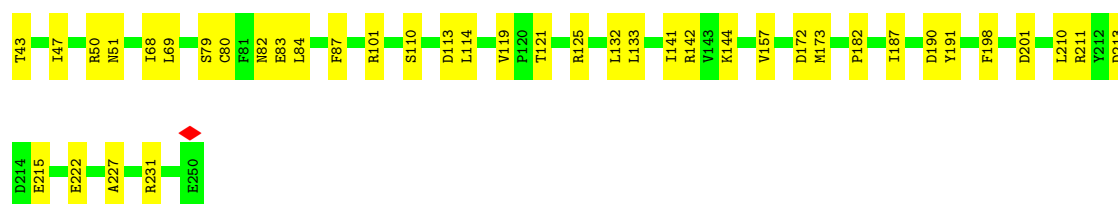


- Molecule 14: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial

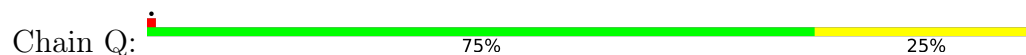


- Molecule 15: Complex I-30kD

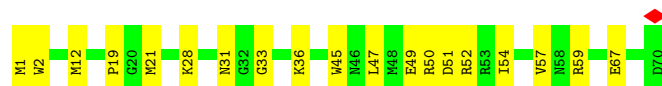




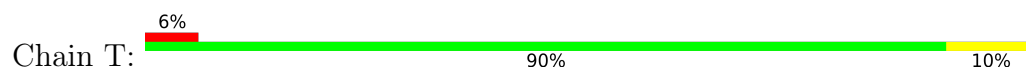
• Molecule 16: Complex I-49kD



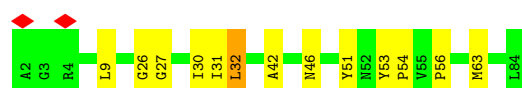
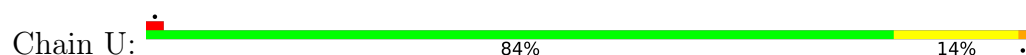
• Molecule 17: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



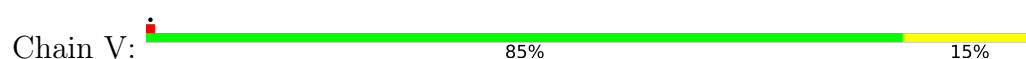
• Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial

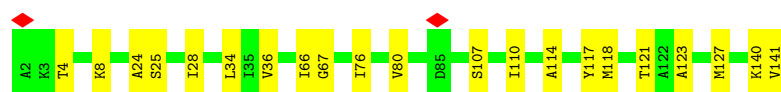


• Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

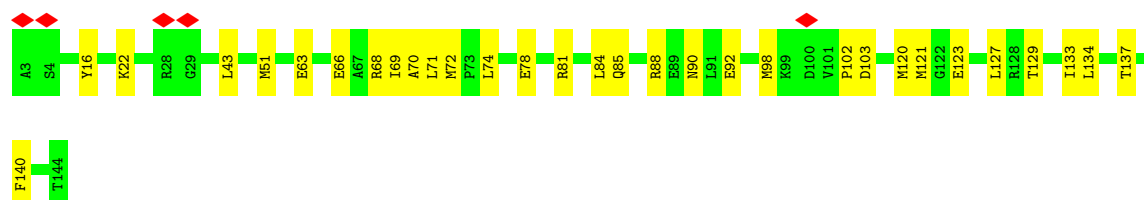
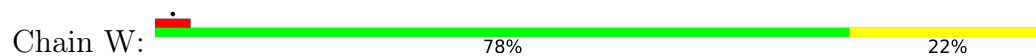


• Molecule 20: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

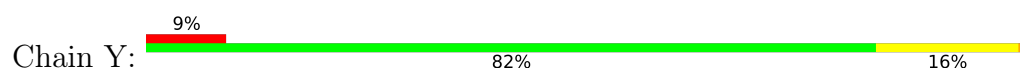




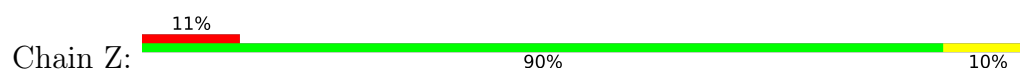
• Molecule 21: Complex I-B16.6



• Molecule 22: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



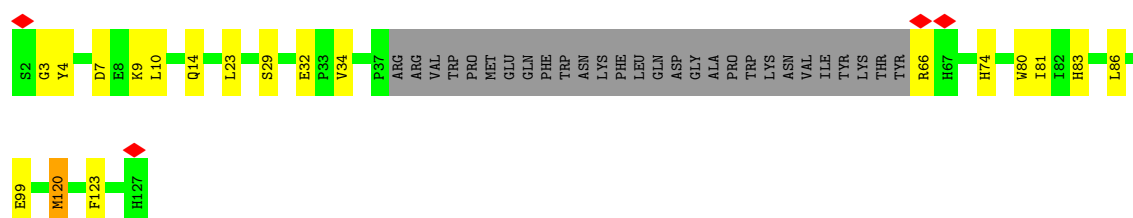
• Molecule 23: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3



• Molecule 24: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



• Molecule 25: Complex I-B17



- Molecule 26: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

Chain c:  83% 17%



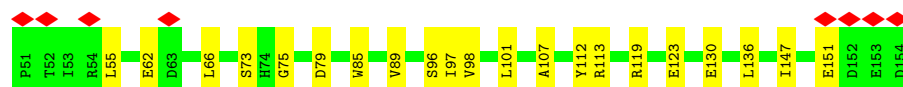
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10

Chain d:  84% 16%

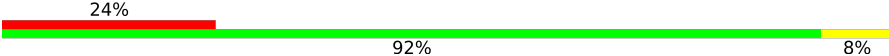


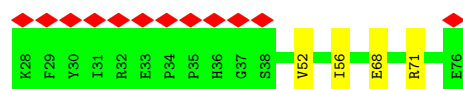
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial

Chain e:  8% 80% 20%



- Molecule 29: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

Chain f:  24% 92% 8%



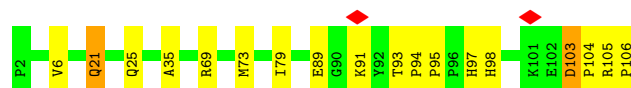
- Molecule 30: NADH dehydrogenase [ubiquinone] 1 subunit C2

Chain g:  89% 11%



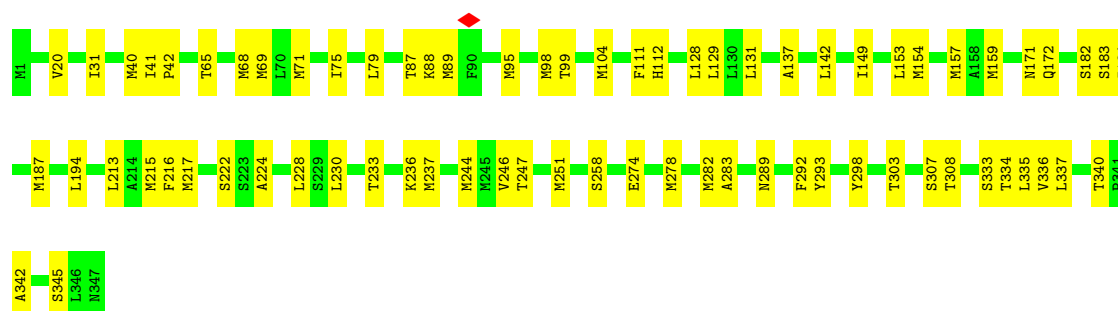
- Molecule 31: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

Chain h:  83% 15% 2%

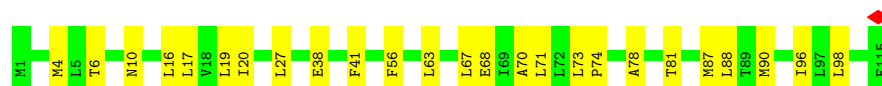
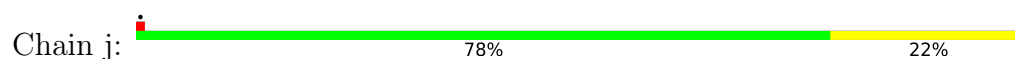


- Molecule 32: NADH-ubiquinone oxidoreductase chain 2

Chain i:  79% 21%



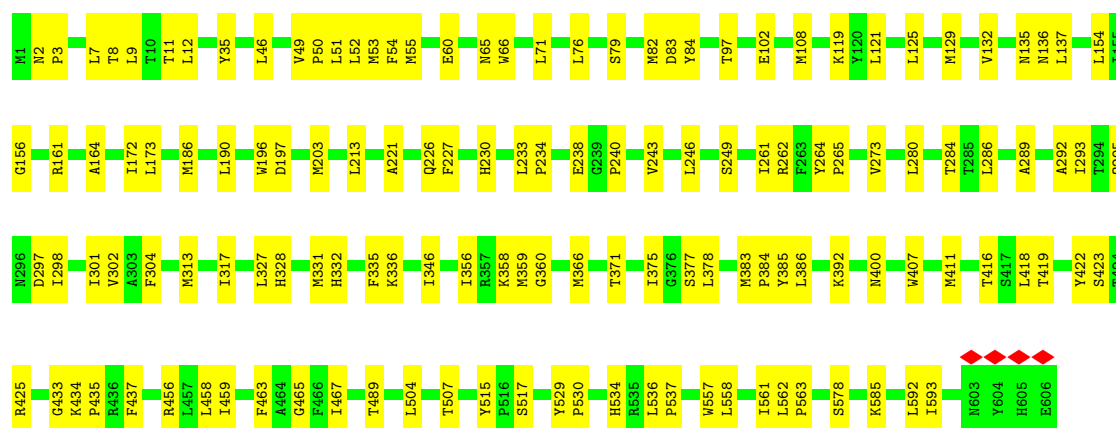
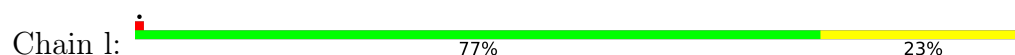
- Molecule 33: NADH-ubiquinone oxidoreductase chain 3



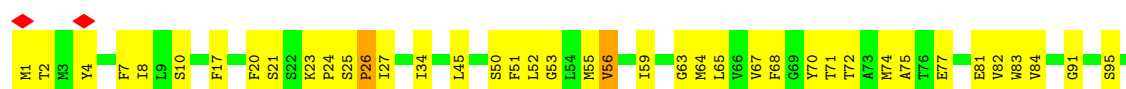
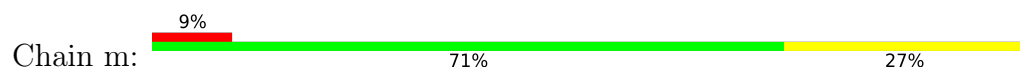
- Molecule 34: NADH-ubiquinone oxidoreductase chain 4L

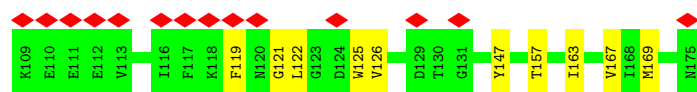


- Molecule 35: NADH-ubiquinone oxidoreductase chain 5

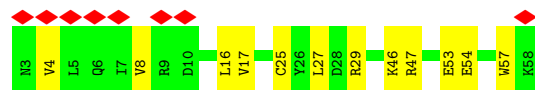
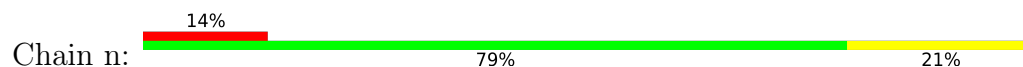


- Molecule 36: NADH-ubiquinone oxidoreductase chain 6

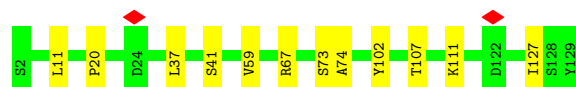
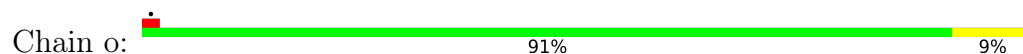




- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1



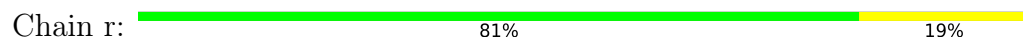
- Molecule 38: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4



- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

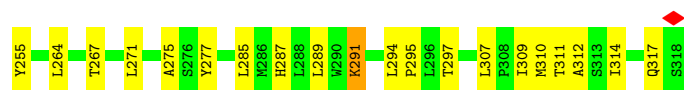


- Molecule 40: NADH-ubiquinone oxidoreductase chain 4

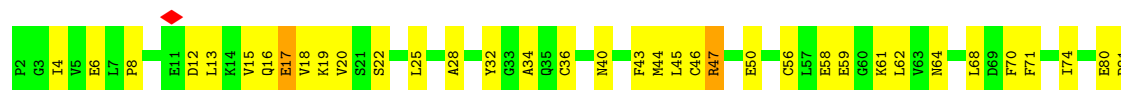


- Molecule 41: NADH-ubiquinone oxidoreductase chain 1

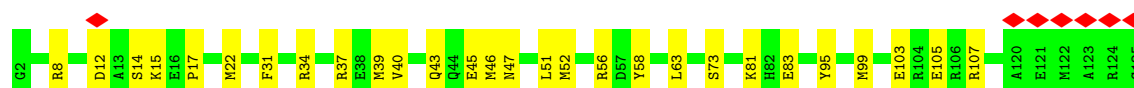
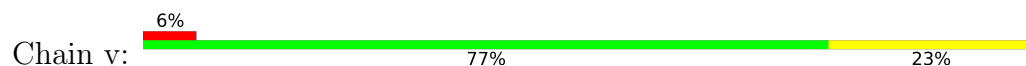




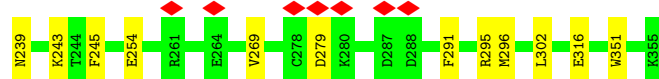
- Molecule 42: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



- Molecule 43: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



- Molecule 44: 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	122532	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	0.213	Depositor
Minimum map value	-0.072	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0205	Depositor
Map size (Å)	354.48602, 354.48602, 354.48602	wwPDB
Map dimensions	330, 330, 330	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0742, 1.0742, 1.0742	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 8Q1, SF4, FES, ADP, ZN, MG, UQ, PLX, 2MR, NDP, CDL, PEE, FMN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.13	0/3406	0.28	0/4603
2	B	0.15	0/1443	0.28	0/1952
3	C	0.14	0/1279	0.27	0/1730
4	E	0.17	0/995	0.41	2/1340 (0.1%)
5	F	0.12	0/698	0.32	0/940
6	G	0.18	0/702	0.52	0/952
6	X	0.14	0/705	0.34	0/954
7	H	0.15	0/929	0.35	0/1258
8	I	0.15	0/798	0.37	0/1079
9	J	0.14	0/2828	0.31	0/3834
10	K	0.10	0/377	0.25	0/509
11	L	0.14	0/1039	0.27	0/1403
12	M	0.14	0/5384	0.29	0/7295
13	N	0.14	0/1245	0.31	0/1694
14	O	0.13	0/1711	0.30	0/2328
15	P	0.15	0/1789	0.29	0/2436
16	Q	0.18	0/3538	0.37	0/4796
17	S	0.16	0/581	0.35	0/781
18	T	0.11	0/755	0.24	0/1018
19	U	0.12	0/664	0.25	0/912
20	V	0.12	0/1042	0.29	0/1411
21	W	0.18	0/1192	0.35	0/1610
22	Y	0.16	0/610	0.46	0/836
23	Z	0.14	0/660	0.29	0/892
24	a	0.15	0/1184	0.35	0/1603
25	b	0.15	0/844	0.36	0/1149
26	c	0.13	0/1371	0.30	0/1875
27	d	0.13	0/1494	0.27	0/2015
28	e	0.14	0/891	0.33	0/1210
29	f	0.13	0/386	0.31	0/523
30	g	0.13	0/1031	0.29	0/1394
31	h	0.19	0/885	0.65	6/1185 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	i	0.17	0/2769	0.35	0/3764
33	j	0.15	0/938	0.30	0/1281
34	k	0.17	0/759	0.34	0/1029
35	l	0.15	0/4943	0.33	0/6724
36	m	0.19	0/1323	0.40	0/1797
37	n	0.14	0/491	0.31	0/663
38	o	0.12	0/1092	0.24	0/1481
39	p	0.14	0/1590	0.29	0/2155
40	r	0.16	0/3723	0.32	0/5078
41	s	0.22	0/2581	0.46	1/3529 (0.0%)
42	u	0.22	0/1436	0.54	2/1938 (0.1%)
43	v	0.13	0/1052	0.34	0/1411
44	w	0.12	0/2650	0.28	0/3588
All	All	0.15	0/67803	0.34	11/91955 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	h	103	ASP	CA-C-N	7.67	127.82	120.31
31	h	103	ASP	C-N-CA	7.67	127.82	120.31
31	h	94	PRO	CA-C-N	6.83	127.42	120.38
31	h	94	PRO	C-N-CA	6.83	127.42	120.38
41	s	291	LYS	N-CA-C	6.07	117.98	111.36
42	u	135	ARG	CA-C-N	5.95	125.71	119.76
42	u	135	ARG	C-N-CA	5.95	125.71	119.76
4	E	107	PHE	N-CA-C	5.68	117.48	111.28
31	h	95	PRO	CA-C-N	5.60	125.27	119.05
31	h	95	PRO	C-N-CA	5.60	125.27	119.05
4	E	97	TRP	N-CA-C	-5.51	105.35	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3330	0	3292	59	0
2	B	1412	0	1363	23	0
3	C	1248	0	1254	20	0
4	E	971	0	975	14	0
5	F	687	0	700	15	0
6	G	690	0	669	14	0
6	X	694	0	674	14	0
7	H	910	0	950	12	0
8	I	780	0	808	18	0
9	J	2751	0	2773	37	0
10	K	366	0	338	11	0
11	L	1016	0	1016	13	0
12	M	5296	0	5326	59	0
13	N	1204	0	1162	16	0
14	O	1671	0	1673	23	0
15	P	1738	0	1693	26	0
16	Q	3459	0	3396	80	0
17	S	566	0	561	19	0
18	T	741	0	702	9	0
19	U	643	0	642	12	0
20	V	1021	0	1025	14	0
21	W	1161	0	1144	31	0
22	Y	584	0	529	12	0
23	Z	641	0	620	7	0
24	a	1151	0	1164	16	0
25	b	819	0	835	19	0
26	c	1315	0	1208	21	0
27	d	1461	0	1429	24	0
28	e	867	0	817	19	0
29	f	378	0	356	2	0
30	g	1000	0	994	10	0
31	h	863	0	867	18	0
32	i	2706	0	2863	49	0
33	j	914	0	951	25	0
34	k	748	0	799	30	0
35	l	4812	0	4944	96	0
36	m	1291	0	1265	59	0
37	n	479	0	486	9	0
38	o	1062	0	1072	9	0
39	p	1534	0	1470	15	0
40	r	3631	0	3839	63	0
41	s	2508	0	2607	80	0
42	u	1398	0	1374	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	v	1028	0	982	25	0
44	w	2590	0	2553	30	0
45	A	8	0	0	2	0
45	B	16	0	0	0	0
45	C	8	0	0	0	0
45	M	16	0	0	0	0
46	A	31	0	19	3	0
47	C	47	0	71	1	0
47	Q	98	0	153	5	0
47	W	41	0	59	2	0
47	b	46	0	69	2	0
47	j	92	0	141	3	0
47	l	91	0	136	4	0
47	r	51	0	82	2	0
48	C	52	0	88	2	0
48	J	52	0	88	3	0
48	N	52	0	88	2	0
48	a	52	0	88	1	0
48	g	52	0	88	5	0
48	j	52	0	88	3	0
48	r	52	0	88	5	0
49	C	63	0	90	6	0
49	J	33	0	39	2	0
50	G	35	0	0	0	0
50	X	35	0	0	1	0
51	J	48	0	25	3	0
52	M	4	0	0	0	0
52	O	4	0	0	0	0
53	M	1	0	0	0	0
54	N	51	0	46	3	0
54	V	194	0	294	10	0
54	a	100	0	156	3	0
54	l	199	0	307	18	0
54	m	100	0	156	9	0
54	n	55	0	54	3	0
54	r	100	0	156	8	0
54	s	89	0	125	4	0
55	T	1	0	0	0	0
56	w	27	0	11	1	0
All	All	68183	0	68965	1081	0

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

All (1081) 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)
51:J:401:NDP:O4D	51:J:401:NDP:C4D	1.68	1.17
24:a:189:ASN:HD21	31:h:35:ALA:HB2	1.01	1.11
24:a:189:ASN:ND2	31:h:35:ALA:HB2	1.70	1.07
42:u:137:LEU:CD1	42:u:138:PRO:HD2	1.85	1.07
36:m:64:MET:HE2	36:m:64:MET:HA	1.32	1.05
42:u:137:LEU:HD12	42:u:138:PRO:CD	1.85	1.04
42:u:47:ARG:HH11	42:u:47:ARG:HB3	1.21	1.02
35:l:517:SER:HB3	54:l:703:CDL:HA32	1.42	0.98
36:m:52:LEU:O	36:m:56:VAL:HG12	1.66	0.95
41:s:28:LEU:CD2	41:s:275:ALA:HB2	2.00	0.91
42:u:137:LEU:HD12	42:u:138:PRO:HD2	0.93	0.88
42:u:47:ARG:HH11	42:u:47:ARG:CB	1.88	0.86
36:m:65:LEU:HD13	41:s:139:THR:HG21	1.60	0.84
35:l:517:SER:CB	54:l:703:CDL:HA32	2.07	0.83
9:J:173:ASP:HB3	9:J:176:SER:HB2	1.59	0.83
41:s:195:ARG:HD3	41:s:231:ILE:HD11	1.60	0.82
36:m:64:MET:HA	36:m:64:MET:CE	2.11	0.80
36:m:64:MET:HE2	36:m:64:MET:CA	2.12	0.80
24:a:189:ASN:HD21	31:h:35:ALA:CB	1.88	0.80
41:s:110:SER:O	41:s:113:VAL:HG12	1.83	0.79
31:h:103:ASP:OD1	31:h:104:PRO:HD2	1.84	0.77
6:G:134:ASP:HA	6:G:137:LYS:HE2	1.67	0.76
34:k:21:MET:HB3	54:m:201:CDL:HB61	1.68	0.75
3:C:125:PRO:HG2	41:s:58:LYS:HE3	1.69	0.75
25:b:14:GLN:HE22	39:p:157:ALA:H	1.35	0.74
36:m:64:MET:HB2	41:s:114:TYR:OH	1.87	0.74
42:u:16:GLN:HB3	42:u:68:LEU:HD11	1.69	0.74
40:r:191:SER:HB3	47:r:501:PEE:H3	1.68	0.74
20:V:140:LYS:NZ	32:i:274:GLU:OE2	2.21	0.74
21:W:85:GLN:OE1	31:h:105:ARG:NH1	2.20	0.74
1:A:398:ARG:HG2	1:A:403:ASP:HB3	1.70	0.74
41:s:20:LEU:HD12	41:s:20:LEU:O	1.88	0.73
15:P:43:THR:HA	15:P:47:ILE:HD12	1.71	0.73
2:B:165:ASP:OD1	16:Q:368:ARG:NH2	2.22	0.73
17:S:54:ILE:HD12	42:u:19:LYS:O	1.89	0.73
38:o:59:VAL:HG22	40:r:423:ILE:HG12	1.71	0.72
24:a:187:PRO:HB2	42:u:47:ARG:HH12	1.54	0.72
4:E:106:PHE:O	4:E:108:HIS:CD2	2.42	0.72
12:M:149:ASP:HB2	16:Q:361:ALA:HB3	1.69	0.72
34:k:6:MET:HE1	36:m:119:PHE:HA	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:u:47:ARG:HB3	42:u:47:ARG:NH1	2.03	0.71
42:u:59:GLU:N	42:u:59:GLU:OE1	2.24	0.71
9:J:346:GLU:HG2	9:J:371:PRO:HB3	1.73	0.70
32:i:104:MET:HG3	32:i:111:PHE:HB3	1.72	0.70
43:v:51:LEU:O	43:v:52:MET:HG2	1.92	0.70
54:l:702:CDL:H391	40:r:371:PRO:HD2	1.74	0.70
34:k:7:ASN:ND2	36:m:10:SER:OG	2.23	0.70
1:A:138:LEU:HD13	1:A:245:VAL:HG23	1.73	0.69
7:H:44:TYR:O	7:H:48:THR:HG22	1.91	0.69
35:l:102:GLU:OE1	35:l:456:ARG:NH2	2.25	0.69
7:H:54:GLU:O	7:H:58:MET:HG3	1.93	0.69
12:M:650:SER:OG	12:M:652:ASN:ND2	2.25	0.69
16:Q:156:GLU:OE1	16:Q:171:ARG:NH2	2.22	0.69
2:B:200:GLU:HG3	13:N:88:ARG:HD3	1.75	0.69
13:N:68:MET:HG3	13:N:69:ASN:H	1.56	0.69
37:n:54:GLU:OE2	37:n:54:GLU:N	2.26	0.69
12:M:136:GLU:OE2	12:M:272:ARG:NH2	2.24	0.68
39:p:151:THR:HG23	39:p:153:ALA:H	1.58	0.68
6:X:134:ASP:OD2	39:p:2:ALA:N	2.27	0.68
40:r:210:TYR:O	40:r:213:HIS:ND1	2.24	0.68
41:s:221:ALA:O	41:s:225:MET:HG3	1.93	0.68
3:C:103:MET:HE1	3:C:121:TYR:HB2	1.74	0.68
37:n:47:ARG:NH2	37:n:53:GLU:OE2	2.25	0.68
27:d:69:ARG:NH2	37:n:46:LYS:O	2.27	0.68
15:P:68:ILE:HG22	15:P:69:LEU:HG	1.76	0.68
2:B:89:GLU:OE2	13:N:34:ARG:NH2	2.27	0.68
1:A:174:ARG:NH1	10:K:92:GLU:OE1	2.27	0.67
16:Q:52:MET:O	32:i:171:ASN:ND2	2.25	0.67
21:W:127:LEU:HB2	31:h:98:HIS:CD2	2.30	0.67
14:O:38:LEU:O	14:O:124:ARG:NH2	2.28	0.67
24:a:86:ILE:O	24:a:90:ASN:ND2	2.27	0.67
10:K:105:ARG:NH2	12:M:426:ASP:OD2	2.26	0.67
25:b:99:GLU:OE2	35:l:2:ASN:ND2	2.28	0.67
1:A:48:ARG:NH2	14:O:226:GLU:OE1	2.27	0.67
4:E:52:LEU:HD22	4:E:104:MET:HE2	1.77	0.67
1:A:285:PRO:O	14:O:222:ARG:NH2	2.28	0.66
36:m:72:THR:HG21	41:s:133:LEU:HD21	1.77	0.66
12:M:298:LYS:HA	13:N:134:ILE:HD13	1.77	0.66
15:P:83:GLU:OE1	15:P:142:ARG:NH2	2.29	0.66
36:m:1:MET:HE3	36:m:125:TRP:HE1	1.60	0.66
17:S:57:VAL:HG13	17:S:59:ARG:HG3	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:C:303:PLX:H211	49:C:304:UQ:H551	1.78	0.66
11:L:123:ASN:OD1	12:M:246:ARG:NH2	2.29	0.66
32:i:213:LEU:O	32:i:217:MET:HG3	1.96	0.66
35:l:221:ALA:HA	35:l:226:GLN:HG2	1.78	0.65
21:W:51:MET:HE2	41:s:311:THR:HB	1.77	0.65
1:A:49:HIS:O	1:A:59:ARG:NH1	2.29	0.65
9:J:180:TYR:HB2	9:J:317:ASP:OD2	1.95	0.65
6:G:144:ILE:O	6:G:148:ILE:HG13	1.96	0.65
42:u:47:ARG:HH11	42:u:47:ARG:CG	2.09	0.65
44:w:73:LEU:HD11	44:w:269:VAL:HG21	1.79	0.65
15:P:125:ARG:NH2	15:P:201:ASP:OD1	2.29	0.65
11:L:78:ARG:NH2	12:M:249:GLU:OE1	2.30	0.65
16:Q:457:VAL:HG13	16:Q:460:GLU:HG2	1.79	0.65
17:S:49:GLU:OE1	17:S:52:ARG:NH1	2.30	0.65
54:l:702:CDL:H1O1	40:r:357:THR:HG1	1.45	0.64
1:A:152:ARG:NH2	10:K:99:PRO:O	2.30	0.64
24:a:134:GLU:OE1	37:n:57:TRP:NE1	2.28	0.64
28:e:98:VAL:HG22	40:r:36:LEU:HB2	1.79	0.64
5:F:64:LYS:NZ	5:F:76:ASN:OD1	2.31	0.64
37:n:4:VAL:O	37:n:8:VAL:HG12	1.96	0.64
12:M:472:PRO:O	12:M:510:TRP:NE1	2.30	0.64
16:Q:236:LEU:HD22	16:Q:240:LEU:HD23	1.80	0.64
19:U:27:GLY:O	19:U:31:ILE:HG13	1.98	0.64
32:i:236:LYS:HG3	32:i:237:MET:HG3	1.79	0.64
1:A:296:LEU:HD21	1:A:317:VAL:HG11	1.81	0.63
42:u:12:ASP:O	42:u:61:LYS:NZ	2.27	0.63
32:i:159:MET:HG2	32:i:278:MET:HE1	1.79	0.63
11:L:78:ARG:NE	11:L:148:GLU:OE2	2.24	0.63
24:a:170:GLN:NE2	42:u:151:ASN:OD1	2.30	0.63
41:s:117:LEU:HD21	41:s:136:VAL:HG23	1.79	0.63
1:A:263:ALA:HA	1:A:271:SER:HB3	1.81	0.63
1:A:385:CYS:HB2	45:A:501:SF4:S4	2.39	0.63
18:T:47:ASP:O	18:T:52:ARG:NH1	2.31	0.63
22:Y:78:ASP:O	22:Y:82:GLY:N	2.31	0.62
25:b:29:SER:H	25:b:32:GLU:HG3	1.64	0.62
35:l:132:VAL:O	35:l:262:ARG:NH2	2.32	0.62
8:I:18:ARG:NH2	16:Q:260:GLU:OE1	2.26	0.62
24:a:187:PRO:CB	42:u:47:ARG:HH12	2.12	0.62
13:N:42:ASP:OD1	13:N:43:LYS:N	2.31	0.62
15:P:172:ASP:OD2	15:P:187:ILE:N	2.28	0.62
5:F:24:CYS:N	5:F:58:CYS:SG	2.72	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:i:42:PRO:HG2	36:m:167:VAL:HG22	1.82	0.62
20:V:123:ALA:O	20:V:127:MET:HG3	2.00	0.61
35:l:3:PRO:HG2	35:l:53:MET:HE1	1.81	0.61
16:Q:62:LYS:HE3	16:Q:63:PRO:HD2	1.81	0.61
16:Q:99:MET:HE3	16:Q:101:LEU:HD21	1.83	0.61
16:Q:282:ASP:OD2	16:Q:437:LYS:NZ	2.34	0.61
44:w:139:ARG:NH1	44:w:166:ASP:OD2	2.30	0.61
42:u:6:GLU:OE1	42:u:6:GLU:HA	1.99	0.61
16:Q:208:GLU:OE2	16:Q:221:ARG:NH2	2.34	0.61
16:Q:216:ARG:NH1	16:Q:243:ASP:OD2	2.33	0.61
3:C:44:GLU:OE2	3:C:195:ARG:NH1	2.33	0.61
17:S:21:MET:HG2	41:s:253:GLU:HG3	1.83	0.61
40:r:325:MET:HE2	40:r:362:ALA:HB2	1.83	0.61
17:S:67:GLU:OE1	17:S:67:GLU:N	2.30	0.60
40:r:329:LEU:HG	40:r:437:MET:HE2	1.84	0.60
2:B:47:SER:O	2:B:56:ARG:NH2	2.34	0.60
12:M:624:ARG:NH2	12:M:637:ASP:OD1	2.31	0.60
27:d:99:ASP:OD2	27:d:142:ARG:NH1	2.34	0.60
48:g:201:PLX:H361	48:g:201:PLX:H311	1.82	0.60
54:l:702:CDL:H452	40:r:445:LEU:HB3	1.83	0.60
36:m:67:VAL:O	36:m:71:THR:HG23	2.01	0.60
40:r:282:LEU:HD13	40:r:342:MET:HG3	1.82	0.60
32:i:215:MET:HE1	32:i:244:MET:HG3	1.83	0.60
40:r:231:LEU:HA	40:r:235:LEU:HB2	1.84	0.60
1:A:448:GLU:O	1:A:452:GLN:HG3	2.01	0.60
20:V:117:TYR:O	20:V:121:THR:HG23	2.01	0.60
7:H:58:MET:HE3	7:H:71:GLN:HG2	1.84	0.60
6:G:123:GLU:HG2	6:G:130:ILE:HD12	1.83	0.60
36:m:25:SER:O	36:m:27:ILE:N	2.35	0.60
42:u:50:GLU:HA	42:u:50:GLU:OE1	2.01	0.60
54:r:503:CDL:H401	54:r:503:CDL:H221	1.84	0.60
33:j:90:MET:HE1	48:j:203:PLX:H272	1.84	0.59
35:l:360:GLY:HA3	35:l:435:PRO:HA	1.84	0.59
24:a:189:ASN:ND2	31:h:35:ALA:CB	2.56	0.59
42:u:83:THR:HA	42:u:86:TRP:CD1	2.37	0.59
17:S:54:ILE:CG2	31:h:106:PRO:HB3	2.33	0.59
3:C:41:SER:OG	3:C:42:ARG:N	2.31	0.59
36:m:34:ILE:HD11	41:s:114:TYR:CZ	2.38	0.59
44:w:125:ASP:O	44:w:130:ARG:NH2	2.36	0.59
16:Q:191:ALA:HB1	16:Q:196:ALA:HB3	1.85	0.59
32:i:283:ALA:HB1	40:r:158:LEU:HD13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:s:102:VAL:HG21	41:s:154:LEU:HD11	1.84	0.59
42:u:18:VAL:HG12	42:u:20:VAL:HG22	1.85	0.59
12:M:149:ASP:OD2	12:M:150:ARG:NH2	2.36	0.59
32:i:247:THR:O	32:i:251:MET:HG3	2.03	0.59
32:i:258:SER:HB2	32:i:336:VAL:HG12	1.85	0.59
35:l:517:SER:HB3	54:l:703:CDL:CA3	2.26	0.59
25:b:86:LEU:HD11	35:l:9:LEU:HD12	1.85	0.59
26:c:110:ASP:OD2	40:r:278:ARG:NE	2.30	0.59
36:m:53:GLY:HA2	36:m:56:VAL:CG1	2.33	0.58
35:l:161:ARG:NH2	35:l:238:GLU:OE2	2.35	0.58
54:l:702:CDL:H312	54:l:702:CDL:H742	1.85	0.58
42:u:16:GLN:CB	42:u:68:LEU:HD11	2.32	0.58
2:B:111:GLU:O	2:B:141:ARG:NH1	2.36	0.58
41:s:28:LEU:HD22	41:s:275:ALA:HB2	1.84	0.58
16:Q:154:ALA:HA	16:Q:398:THR:HG21	1.85	0.58
1:A:159:ARG:NH2	14:O:176:CYS:O	2.35	0.58
39:p:128:LEU:HD11	39:p:163:LEU:HD11	1.86	0.58
16:Q:387:GLU:OE2	16:Q:390:GLN:NE2	2.36	0.58
6:X:107:ASP:OD1	6:X:107:ASP:N	2.35	0.58
54:V:202:CDL:H441	54:V:202:CDL:H242	1.85	0.58
36:m:34:ILE:HD11	41:s:114:TYR:CE2	2.39	0.58
43:v:83:GLU:OE2	43:v:83:GLU:N	2.33	0.58
21:W:88:ARG:HD2	21:W:92:GLU:OE2	2.04	0.57
6:G:84:LEU:O	6:G:88:LYS:HG2	2.04	0.57
54:V:202:CDL:H591	54:V:202:CDL:H192	1.86	0.57
28:e:85:TRP:O	28:e:89:VAL:HG13	2.05	0.57
41:s:287:HIS:O	41:s:291:LYS:HB2	2.04	0.57
9:J:73:LEU:O	9:J:78:SER:OG	2.22	0.57
16:Q:302:LEU:HB2	16:Q:401:GLU:HB2	1.85	0.57
16:Q:176:GLU:OE2	16:Q:311:TYR:OH	2.20	0.57
16:Q:294:ARG:NH1	16:Q:336:GLU:OE2	2.38	0.57
54:m:201:CDL:H222	54:m:201:CDL:H331	1.86	0.57
5:F:91:LEU:O	5:F:95:LEU:HD12	2.05	0.57
14:O:188:ILE:HG21	14:O:208:LEU:HD21	1.85	0.57
31:h:21:GLN:O	31:h:25:GLN:NE2	2.37	0.57
10:K:82:SER:OG	10:K:83:THR:N	2.38	0.57
26:c:160:GLN:OE1	43:v:37:ARG:NH1	2.37	0.57
40:r:403:THR:HA	40:r:406:TYR:CE2	2.40	0.57
19:U:26:GLY:HA3	47:j:201:PEE:H37	1.87	0.56
25:b:83:HIS:HD2	27:d:45:VAL:HG21	1.67	0.56
23:Z:60:ASN:ND2	35:l:433:GLY:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:v:103:GLU:O	43:v:107:ARG:HG2	2.05	0.56
9:J:37:HIS:HE2	18:T:49:ASP:HA	1.70	0.56
12:M:163:LYS:O	12:M:171:THR:OG1	2.24	0.56
16:Q:182:ASN:OD1	16:Q:404:LYS:NZ	2.31	0.56
16:Q:312:ASP:OD1	16:Q:312:ASP:N	2.37	0.56
25:b:74:HIS:NE2	35:l:35:TYR:OH	2.31	0.56
26:c:156:VAL:HG12	43:v:99:MET:HG3	1.87	0.56
42:u:70:PHE:CE2	42:u:74:ILE:HD12	2.40	0.56
44:w:227:MET:SD	44:w:227:MET:N	2.78	0.56
2:B:211:TYR:CZ	8:I:39:PRO:HG3	2.41	0.56
3:C:167:PRO:HD3	16:Q:223:HIS:CD2	2.40	0.56
8:I:107:SER:OG	16:Q:317:ASP:OD2	2.24	0.56
14:O:182:ASN:HB3	14:O:194:GLU:HB3	1.87	0.56
6:X:111:ASP:OD1	6:X:111:ASP:N	2.39	0.56
27:d:159:GLN:O	27:d:163:MET:HG3	2.05	0.56
21:W:63:GLU:OE2	42:u:119:ARG:NH2	2.37	0.56
36:m:53:GLY:O	36:m:56:VAL:HG13	2.04	0.56
36:m:65:LEU:CD1	41:s:139:THR:HG21	2.33	0.56
35:l:419:THR:HA	35:l:422:TYR:CE2	2.41	0.56
54:l:702:CDL:H621	54:l:702:CDL:H432	1.88	0.56
9:J:171:ASN:HA	9:J:327:MET:HE2	1.88	0.56
51:J:401:NDP:N7N	51:J:401:NDP:O2N	2.39	0.56
14:O:182:ASN:ND2	14:O:194:GLU:OE1	2.39	0.56
41:s:285:LEU:HD12	41:s:289:LEU:HD23	1.87	0.56
15:P:113:ASP:OD1	15:P:114:LEU:N	2.39	0.56
35:l:119:LYS:NZ	54:l:702:CDL:OA3	2.36	0.56
41:s:215:TYR:HD1	41:s:219:PRO:HB2	1.70	0.56
1:A:98:LYS:NZ	1:A:242:VAL:O	2.29	0.55
1:A:132:ARG:HB3	1:A:165:GLU:HG3	1.86	0.55
9:J:192:ARG:NH1	9:J:198:ALA:O	2.39	0.55
16:Q:41:VAL:O	16:Q:45:GLU:HG2	2.06	0.55
35:l:136:ASN:HA	35:l:197:ASP:HA	1.87	0.55
12:M:64:CYS:O	12:M:184:ARG:NH2	2.30	0.55
35:l:97:THR:HG21	35:l:125:LEU:HD22	1.89	0.55
54:l:703:CDL:H712	54:l:703:CDL:H312	1.89	0.55
40:r:114:GLU:OE1	40:r:116:ILE:HG22	2.06	0.55
2:B:128:ILE:O	15:P:231:ARG:NH2	2.39	0.55
1:A:50:ASP:HB3	1:A:55:GLY:HA3	1.88	0.55
12:M:217:GLU:HG3	12:M:412:PRO:HB3	1.88	0.55
16:Q:99:MET:HE1	16:Q:444:LEU:HD13	1.88	0.55
17:S:54:ILE:HD12	42:u:19:LYS:C	2.31	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:b:10:LEU:O	25:b:14:GLN:HG3	2.07	0.55
35:l:190:LEU:HD12	40:r:383:THR:HG21	1.88	0.55
38:o:20:PRO:HB3	39:p:65:ARG:HH22	1.72	0.55
44:w:132:GLN:NE2	44:w:166:ASP:OD1	2.40	0.55
4:E:37:ARG:HG2	6:G:120:MET:SD	2.46	0.55
4:E:50:PHE:HE2	4:E:98:LYS:O	1.89	0.55
32:i:68:MET:HA	32:i:68:MET:HE3	1.88	0.55
20:V:34:LEU:HD22	54:m:201:CDL:H261	1.89	0.55
7:H:106:GLU:OE2	8:I:72:SER:OG	2.24	0.54
9:J:306:GLU:HG3	9:J:315:THR:HG22	1.88	0.54
20:V:4:THR:O	20:V:8:LYS:HG3	2.07	0.54
32:i:298:TYR:O	32:i:303:THR:OG1	2.25	0.54
35:l:7:LEU:HD22	35:l:46:LEU:HD11	1.87	0.54
21:W:103:ASP:OD1	21:W:103:ASP:N	2.39	0.54
54:a:201:CDL:H712	54:a:201:CDL:H172	1.89	0.54
35:l:515:TYR:OH	39:p:70:GLU:OE2	2.25	0.54
35:l:585:LYS:NZ	54:m:201:CDL:OB3	2.35	0.54
54:l:702:CDL:H801	48:r:502:PLX:H202	1.88	0.54
36:m:64:MET:CB	41:s:114:TYR:OH	2.54	0.54
40:r:216:LEU:HD23	40:r:291:VAL:HG22	1.89	0.54
41:s:28:LEU:HD21	41:s:275:ALA:HB2	1.87	0.54
42:u:47:ARG:HD3	42:u:56:CYS:HB2	1.89	0.54
16:Q:294:ARG:NH2	16:Q:401:GLU:OE2	2.40	0.54
30:g:101:GLU:OE2	30:g:101:GLU:N	2.27	0.54
32:i:68:MET:HE2	34:k:36:MET:HB3	1.89	0.54
18:T:51:ARG:HG2	18:T:54:ARG:HH21	1.71	0.54
12:M:275:PRO:HG3	12:M:286:ILE:HG12	1.90	0.54
13:N:39:VAL:HG23	13:N:50:GLU:HG2	1.89	0.54
20:V:140:LYS:HG3	20:V:141:VAL:HG23	1.89	0.54
12:M:250:SER:OG	12:M:251:ILE:N	2.40	0.54
47:Q:502:PEE:H59	41:s:277:TYR:HE2	1.72	0.54
21:W:70:ALA:HB2	42:u:125:LEU:HD13	1.90	0.54
40:r:255:ASN:OD1	40:r:256:TYR:N	2.40	0.54
26:c:162:PRO:HG3	43:v:39:MET:HE2	1.90	0.54
32:i:182:SER:HB2	32:i:293:TYR:OH	2.08	0.54
5:F:42:VAL:O	5:F:46:LYS:HG3	2.08	0.53
27:d:120:SER:HB3	43:v:56:ARG:HH22	1.73	0.53
36:m:65:LEU:HD23	36:m:65:LEU:C	2.34	0.53
16:Q:232:VAL:CG2	16:Q:356:ILE:HB	2.39	0.53
30:g:15:PHE:HB2	48:g:201:PLX:H6	1.89	0.53
34:k:65:VAL:HG11	36:m:157:THR:HG23	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:U:51:TYR:O	21:W:68:ARG:NH1	2.40	0.53
34:k:55:LEU:O	34:k:58:MET:HE3	2.08	0.53
17:S:51:ASP:CG	42:u:22:SER:HG	2.15	0.53
35:l:173:LEU:HD12	40:r:405:LEU:HD21	1.90	0.53
19:U:54:PRO:HD3	21:W:69:ILE:HD13	1.90	0.53
35:l:76:LEU:HD21	35:l:196:TRP:HE3	1.74	0.53
19:U:53:TYR:HB2	21:W:72:MET:HE1	1.91	0.53
26:c:149:ILE:HG13	26:c:150:TYR:HD1	1.74	0.53
27:d:15:ARG:HG3	27:d:15:ARG:O	2.08	0.53
36:m:82:VAL:HG13	36:m:84:VAL:H	1.72	0.53
12:M:29:SER:OG	12:M:30:ASN:N	2.39	0.53
33:j:16:LEU:O	33:j:20:ILE:HG13	2.08	0.53
35:l:261:ILE:HG12	35:l:317:ILE:HD11	1.90	0.53
41:s:21:THR:HG22	41:s:228:TYR:CE2	2.44	0.53
54:N:202:CDL:H722	54:N:202:CDL:H512	1.91	0.53
32:i:87:THR:HG23	32:i:88:LYS:HD3	1.90	0.53
33:j:63:LEU:HD21	36:m:63:GLY:HA2	1.90	0.53
35:l:121:LEU:HD22	35:l:246:LEU:HD23	1.90	0.53
17:S:51:ASP:OD2	42:u:22:SER:OG	2.24	0.53
35:l:356:ILE:HA	35:l:359:MET:HE2	1.91	0.53
44:w:129:TYR:OH	44:w:186:HIS:ND1	2.35	0.53
1:A:378:SER:OG	1:A:385:CYS:SG	2.62	0.52
4:E:17:VAL:HG21	11:L:55:VAL:HG12	1.91	0.52
54:l:702:CDL:H412	54:l:702:CDL:H602	1.90	0.52
6:G:114:ASP:HA	6:G:117:GLU:HG3	1.90	0.52
16:Q:156:GLU:OE1	16:Q:229:PRO:O	2.26	0.52
32:i:20:VAL:HG11	32:i:137:ALA:HB1	1.91	0.52
41:s:96:ILE:HG22	41:s:98:MET:HG2	1.91	0.52
22:Y:65:MET:HE1	35:l:378:LEU:HD13	1.92	0.52
6:X:139:MET:HE2	6:X:139:MET:HA	1.91	0.52
32:i:69:MET:HE1	32:i:104:MET:HE1	1.92	0.52
32:i:289:ASN:HA	32:i:292:PHE:CE2	2.45	0.52
1:A:88:ARG:NH2	1:A:273:THR:O	2.41	0.52
3:C:75:GLU:OE1	16:Q:221:ARG:NH1	2.43	0.52
41:s:87:VAL:HG12	41:s:95:LEU:HD23	1.91	0.52
19:U:30:ILE:HD11	33:j:96:ILE:HD11	1.91	0.52
24:a:78:THR:HG21	28:e:96:SER:HA	1.92	0.52
5:F:31:GLN:NE2	5:F:35:ASP:OD1	2.43	0.52
8:I:25:GLN:O	16:Q:209:LYS:NZ	2.31	0.52
10:K:80:GLU:OE2	10:K:80:GLU:N	2.43	0.52
32:i:278:MET:O	32:i:282:MET:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:C:304:UQ:HM52	16:Q:93:GLY:HA2	1.92	0.52
19:U:32:LEU:HB3	41:s:310:MET:SD	2.50	0.52
21:W:81:ARG:NH1	42:u:15:VAL:HG11	2.24	0.52
35:l:227:PHE:O	35:l:230:HIS:ND1	2.40	0.52
35:l:383:MET:SD	35:l:384:PRO:HD2	2.50	0.52
40:r:336:ARG:NH1	40:r:433:GLU:OE2	2.43	0.52
32:i:71:MET:HG3	34:k:40:LEU:HD13	1.91	0.52
2:B:144:ARG:NH1	2:B:146:ASP:OD2	2.43	0.52
6:X:155:TYR:CE1	25:b:23:LEU:HB3	2.45	0.52
1:A:295:PRO:HG2	1:A:298:GLU:HB3	1.92	0.51
2:B:98:ARG:NH2	16:Q:224:ALA:O	2.40	0.51
27:d:123:GLN:OE1	43:v:47:ASN:ND2	2.43	0.51
42:u:149:GLU:OE2	42:u:149:GLU:N	2.29	0.51
4:E:40:TYR:HB3	6:G:120:MET:HE1	1.93	0.51
10:K:83:THR:HG23	14:O:88:ARG:HH11	1.76	0.51
22:Y:76:ASP:O	35:l:385:TYR:OH	2.27	0.51
35:l:534:HIS:CD2	47:l:704:PEE:H13	2.45	0.51
42:u:34:ALA:HB2	42:u:120:PRO:HG3	1.91	0.51
43:v:43:GLN:HA	43:v:46:MET:HE2	1.92	0.51
12:M:295:ASP:OD2	12:M:706:THR:OG1	2.22	0.51
25:b:34:VAL:HG22	39:p:114:MET:HA	1.92	0.51
35:l:71:LEU:HD22	40:r:310:MET:HE1	1.91	0.51
14:O:169:PHE:HE1	14:O:208:LEU:HD23	1.75	0.51
20:V:24:ALA:O	20:V:28:ILE:HG13	2.10	0.51
35:l:327:LEU:O	35:l:331:MET:HG2	2.09	0.51
1:A:116:ASN:ND2	46:A:502:FMN:O3'	2.43	0.51
7:H:94:MET:SD	7:H:99:PRO:HG3	2.51	0.51
10:K:73:TYR:CZ	10:K:75:ASN:HB3	2.46	0.51
15:P:50:ARG:HH12	15:P:80:CYS:HB3	1.75	0.51
16:Q:96:ARG:HB3	16:Q:112:HIS:HB2	1.93	0.51
6:X:90:TYR:CE1	23:Z:44:PRO:HB2	2.46	0.51
27:d:136:SER:HB2	38:o:127:ILE:HD11	1.93	0.51
32:i:42:PRO:HG3	36:m:167:VAL:HG13	1.92	0.51
44:w:76:GLU:OE1	44:w:80:LYS:NZ	2.44	0.51
1:A:134:ASP:N	1:A:134:ASP:OD1	2.41	0.51
12:M:340:ALA:HB3	12:M:366:LEU:HD23	1.93	0.51
15:P:157:VAL:HG21	15:P:182:PRO:HD3	1.93	0.51
34:k:64:LEU:O	34:k:67:ALA:HB3	2.10	0.51
35:l:137:LEU:HD13	35:l:186:MET:HG3	1.92	0.51
41:s:24:GLU:HA	41:s:271:LEU:HD13	1.93	0.51
13:N:144:TYR:HD1	13:N:144:TYR:H	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:u:32:TYR:O	42:u:36:CYS:HB2	2.11	0.51
44:w:47:GLU:OE2	44:w:295:ARG:NH1	2.40	0.51
6:G:102:SER:O	6:G:140:CYS:HB2	2.11	0.51
7:H:19:THR:O	7:H:19:THR:OG1	2.23	0.51
12:M:308:ARG:NH2	12:M:578:PRO:O	2.44	0.51
32:i:75:ILE:HD12	34:k:40:LEU:HD22	1.93	0.51
40:r:373:ILE:HD11	40:r:444:LEU:HD23	1.93	0.51
41:s:46:LEU:HD23	41:s:49:ILE:HD12	1.93	0.51
1:A:208:GLU:OE1	1:A:210:THR:OG1	2.28	0.50
3:C:83:ARG:NH1	16:Q:212:GLU:OE2	2.32	0.50
16:Q:156:GLU:HG2	16:Q:229:PRO:O	2.12	0.50
16:Q:412:VAL:HB	16:Q:421:ARG:HB3	1.92	0.50
22:Y:43:ARG:NH1	22:Y:47:PHE:O	2.45	0.50
31:h:69:ARG:O	31:h:73:MET:HG3	2.11	0.50
3:C:84:TYR:CE1	3:C:171:GLU:HG3	2.46	0.50
3:C:126:GLU:OE1	9:J:89:TYR:OH	2.20	0.50
26:c:119:THR:HG22	38:o:11:LEU:HA	1.93	0.50
35:l:313:MET:HG3	35:l:328:HIS:HD2	1.75	0.50
39:p:105:ASP:OD1	39:p:126:LYS:NZ	2.44	0.50
40:r:72:LEU:HD21	40:r:233:ALA:HB3	1.93	0.50
16:Q:237:PRO:HD2	16:Q:240:LEU:HD22	1.93	0.50
41:s:117:LEU:CD2	41:s:136:VAL:HG23	2.42	0.50
2:B:131:GLU:HB2	2:B:144:ARG:HB3	1.94	0.50
54:l:702:CDL:H521	48:r:502:PLX:H211	1.92	0.50
19:U:56:PRO:HG2	42:u:45:LEU:HB2	1.94	0.50
32:i:112:HIS:HB2	32:i:184:ILE:HD13	1.92	0.50
32:i:342:ALA:O	32:i:345:SER:OG	2.26	0.50
35:l:51:LEU:O	35:l:55:MET:HG3	2.12	0.50
40:r:262:LEU:O	40:r:266:MET:HG3	2.11	0.50
8:I:43:VAL:HG23	8:I:44:GLY:H	1.77	0.50
32:i:142:LEU:HB3	32:i:194:LEU:HD21	1.94	0.50
34:k:44:SER:OG	34:k:59:MET:SD	2.66	0.50
40:r:420:THR:HB	40:r:423:ILE:HD12	1.93	0.50
41:s:20:LEU:HD12	41:s:20:LEU:C	2.36	0.50
5:F:83:SER:O	5:F:87:VAL:HG23	2.12	0.50
48:J:403:PLX:H142	33:j:20:ILE:HG12	1.93	0.50
14:O:152:ILE:HG21	14:O:171:LEU:HD13	1.93	0.50
12:M:222:ILE:HA	12:M:225:ILE:HG12	1.94	0.50
16:Q:184:ILE:HD11	16:Q:251:PHE:CZ	2.46	0.50
30:g:92:MET:O	30:g:96:VAL:HG12	2.12	0.50
41:s:123:SER:HB3	41:s:214:GLU:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:75:ARG:NH2	15:P:215:GLU:OE1	2.44	0.50
32:i:172:GLN:OE1	35:l:578:SER:OG	2.23	0.50
33:j:67:LEU:HD13	36:m:59:ILE:HD12	1.93	0.50
35:l:346:ILE:HA	35:l:366:MET:HE1	1.93	0.50
35:l:286:LEU:HG	35:l:411:MET:SD	2.52	0.49
44:w:180:ARG:NH2	44:w:182:GLN:OE1	2.45	0.49
13:N:21:ARG:HH11	13:N:21:ARG:HG2	1.77	0.49
16:Q:152:SER:O	16:Q:156:GLU:HG3	2.12	0.49
35:l:504:LEU:O	35:l:507:THR:OG1	2.30	0.49
21:W:88:ARG:O	21:W:88:ARG:HD3	2.13	0.49
28:e:97:ILE:O	28:e:101:LEU:HB2	2.12	0.49
28:e:151:GLU:N	28:e:151:GLU:OE2	2.43	0.49
14:O:166:ASP:OD1	14:O:166:ASP:N	2.34	0.49
33:j:71:LEU:O	36:m:147:TYR:OH	2.26	0.49
1:A:385:CYS:HB3	45:A:501:SF4:S2	2.52	0.49
17:S:50:ARG:O	17:S:54:ILE:HG23	2.12	0.49
26:c:157:GLY:HA2	43:v:22:MET:HE1	1.94	0.49
27:d:70:ARG:NH1	27:d:91:GLN:OE1	2.45	0.49
35:l:536:LEU:HB3	35:l:537:PRO:HD3	1.93	0.49
12:M:64:CYS:HB3	12:M:75:CYS:HB3	1.94	0.49
41:s:317:GLN:OE1	41:s:317:GLN:HA	2.12	0.49
6:G:104:PHE:HA	6:G:108:LEU:HB2	1.95	0.49
47:Q:501:PEE:H61	47:Q:501:PEE:H37	1.94	0.49
1:A:124:THR:HG22	1:A:353:ALA:HB2	1.95	0.49
12:M:217:GLU:HG2	12:M:218:LEU:HG	1.95	0.49
16:Q:202:TRP:CZ3	16:Q:261:MET:HG3	2.48	0.49
34:k:60:PRO:O	34:k:63:LEU:HB3	2.12	0.49
54:l:702:CDL:H581	54:l:702:CDL:H611	1.61	0.49
2:B:179:THR:OG1	2:B:182:GLU:OE2	2.30	0.49
9:J:37:HIS:NE2	18:T:48:GLY:O	2.45	0.49
14:O:164:THR:HG22	14:O:166:ASP:OD1	2.13	0.49
16:Q:139:LEU:HD13	16:Q:424:ILE:HG21	1.93	0.49
16:Q:242:ASP:OD1	21:W:16:TYR:OH	2.25	0.49
33:j:87:MET:HE1	41:s:309:ILE:HD11	1.94	0.49
35:l:298:ILE:O	35:l:302:VAL:HG23	2.13	0.49
13:N:6:VAL:HG21	54:N:202:CDL:HA31	1.95	0.49
16:Q:229:PRO:HG2	16:Q:389:TYR:OH	2.13	0.49
16:Q:375:MET:HE3	16:Q:379:ILE:HG13	1.94	0.49
16:Q:442:HIS:HB3	16:Q:446:ASP:HB2	1.94	0.49
27:d:140:GLN:O	27:d:144:SER:HB3	2.13	0.49
15:P:211:ARG:NH2	15:P:213:ASP:OD2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:133:LEU:HD21	16:Q:227:ILE:O	2.13	0.48
20:V:107:SER:HB3	20:V:110:ILE:HB	1.94	0.48
54:V:201:CDL:H352	54:V:201:CDL:H322	1.52	0.48
28:e:89:VAL:HG21	40:r:25:ILE:HG23	1.95	0.48
35:l:65:ASN:OD1	35:l:66:TRP:N	2.46	0.48
35:l:407:TRP:CZ2	35:l:411:MET:HE3	2.48	0.48
41:s:208:VAL:HG13	41:s:208:VAL:O	2.13	0.48
42:u:135:ARG:HG3	42:u:136:PRO:HD2	1.95	0.48
20:V:114:ALA:O	20:V:118:MET:HG3	2.13	0.48
35:l:52:LEU:HD23	35:l:55:MET:HE2	1.94	0.48
35:l:295:GLN:O	35:l:425:ARG:NH1	2.46	0.48
1:A:446:LEU:O	1:A:450:MET:HG3	2.13	0.48
6:G:132:ASP:O	6:G:133:ILE:HG22	2.13	0.48
12:M:186:ALA:HA	12:M:190:ALA:HB3	1.96	0.48
54:s:401:CDL:H331	54:s:401:CDL:H362	1.65	0.48
14:O:218:PRO:HD2	14:O:223:PHE:HA	1.96	0.48
17:S:54:ILE:HG21	31:h:106:PRO:HB3	1.94	0.48
6:X:82:ARG:O	6:X:86:VAL:HG12	2.12	0.48
38:o:37:LEU:O	38:o:41:SER:OG	2.30	0.48
9:J:136:THR:HG23	9:J:139:PHE:H	1.78	0.48
9:J:201:ILE:HG22	9:J:203:PRO:HD3	1.94	0.48
26:c:38:PRO:HD3	38:o:67:ARG:HG3	1.94	0.48
29:f:68:GLU:OE2	29:f:71:ARG:NH2	2.46	0.48
10:K:69:ASP:N	10:K:69:ASP:OD1	2.46	0.48
12:M:128:CYS:SG	12:M:140:GLN:NE2	2.83	0.48
16:Q:139:LEU:HD11	16:Q:424:ILE:HD13	1.95	0.48
16:Q:316:PHE:CG	16:Q:343:ILE:HD11	2.49	0.48
29:f:52:VAL:O	29:f:56:ILE:HG23	2.14	0.48
30:g:29:THR:O	54:n:101:CDL:HA31	2.14	0.48
37:n:27:LEU:HD11	54:n:101:CDL:H111	1.95	0.48
1:A:211:ALA:HB2	1:A:223:PRO:HG3	1.96	0.48
12:M:144:MET:HG3	16:Q:383:LYS:HG3	1.94	0.48
16:Q:156:GLU:CG	16:Q:229:PRO:O	2.62	0.48
18:T:67:ALA:O	18:T:71:ILE:HG22	2.14	0.48
40:r:240:GLY:O	40:r:244:MET:HG3	2.12	0.48
15:P:173:MET:HB3	15:P:198:PHE:HB2	1.94	0.48
21:W:133:ILE:O	21:W:137:THR:HG22	2.13	0.48
44:w:100:ASP:OD1	44:w:100:ASP:N	2.39	0.48
44:w:235:GLN:NE2	44:w:239:ASN:OD1	2.47	0.48
40:r:227:GLY:O	40:r:231:LEU:HD12	2.13	0.48
5:F:35:ASP:O	5:F:39:LYS:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:512:VAL:O	12:M:514:ASN:ND2	2.47	0.48
36:m:65:LEU:N	41:s:114:TYR:OH	2.47	0.48
37:n:16:LEU:HD12	40:r:14:MET:HB2	1.95	0.48
1:A:110:PRO:O	1:A:238:CYS:HB3	2.13	0.47
4:E:81:LEU:O	4:E:85:LYS:HG3	2.14	0.47
8:I:39:PRO:HB2	8:I:41:LEU:HD23	1.95	0.47
16:Q:84:PHE:HB3	16:Q:97:LEU:HB3	1.96	0.47
20:V:25:SER:OG	20:V:67:GLY:O	2.27	0.47
23:Z:25:GLU:HA	23:Z:30:GLU:HB2	1.94	0.47
25:b:123:PHE:HB3	43:v:40:VAL:HG11	1.96	0.47
41:s:70:MET:HG2	41:s:118:TRP:HB3	1.96	0.47
42:u:12:ASP:O	42:u:61:LYS:CE	2.62	0.47
5:F:20:ARG:HB2	5:F:66:TRP:HB2	1.94	0.47
12:M:306:MET:HE1	13:N:137:TRP:HZ3	1.79	0.47
21:W:66:GLU:OE1	42:u:123:GLY:N	2.40	0.47
6:X:79:ILE:HD13	6:X:148:ILE:HG22	1.95	0.47
34:k:35:GLY:HA3	36:m:20:PHE:HZ	1.80	0.47
54:N:202:CDL:H142	54:N:202:CDL:H111	1.59	0.47
26:c:158:PRO:HD3	43:v:22:MET:HE2	1.97	0.47
40:r:237:LYS:HD2	40:r:316:MET:HB3	1.95	0.47
9:J:37:HIS:O	9:J:40:LEU:N	2.35	0.47
54:V:202:CDL:H852	35:l:558:LEU:HD21	1.97	0.47
34:k:27:MET:HG2	36:m:71:THR:HG22	1.96	0.47
35:l:233:LEU:HB3	35:l:234:PRO:HD3	1.96	0.47
35:l:562:LEU:HB3	35:l:563:PRO:HD3	1.96	0.47
36:m:91:GLY:O	36:m:95:SER:OG	2.30	0.47
40:r:312:ALA:O	40:r:316:MET:HG3	2.15	0.47
54:r:503:CDL:H781	54:r:503:CDL:H381	1.97	0.47
41:s:84:THR:O	41:s:87:VAL:HG22	2.14	0.47
41:s:128:ALA:HA	41:s:211:PHE:HA	1.95	0.47
1:A:62:TRP:CD2	1:A:181:LEU:HD13	2.50	0.47
1:A:296:LEU:HD13	1:A:337:MET:HE2	1.96	0.47
6:G:143:GLU:OE1	6:G:143:GLU:N	2.35	0.47
9:J:258:ALA:HA	9:J:261:LYS:HG3	1.97	0.47
21:W:129:THR:O	21:W:133:ILE:HG13	2.14	0.47
22:Y:65:MET:HE3	35:l:386:LEU:HD11	1.97	0.47
27:d:97:LYS:NZ	28:e:113:ARG:O	2.47	0.47
27:d:110:LEU:HD11	35:l:203:MET:HE2	1.97	0.47
31:h:105:ARG:NH2	42:u:17:GLU:OE2	2.47	0.47
41:s:18:ALA:O	41:s:21:THR:OG1	2.32	0.47
2:B:148:ASP:HB3	2:B:151:LYS:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:192:ASN:ND2	18:T:61:GLU:OE2	2.39	0.47
26:c:33:THR:HG23	26:c:35:ASP:H	1.80	0.47
33:j:38:GLU:HB2	33:j:41:PHE:O	2.15	0.47
44:w:118:TYR:OH	56:w:401:ADP:O2'	2.33	0.47
9:J:279:TYR:HB2	9:J:372:ALA:HB2	1.96	0.47
26:c:156:VAL:HG11	43:v:95:TYR:CZ	2.49	0.47
28:e:130:GLU:HG3	28:e:136:LEU:HD21	1.96	0.47
30:g:4:MET:HE1	30:g:87:LEU:HD23	1.97	0.47
44:w:180:ARG:NH1	44:w:316:GLU:OE2	2.37	0.47
1:A:51:TRP:NE1	10:K:77:GLN:OE1	2.47	0.47
8:I:58:ASP:OD2	8:I:61:ARG:HB2	2.15	0.47
17:S:54:ILE:HG22	31:h:106:PRO:HB3	1.96	0.47
25:b:29:SER:HB2	25:b:32:GLU:HG2	1.97	0.47
26:c:62:TYR:OH	26:c:74:ASP:OD1	2.20	0.47
34:k:27:MET:HE2	34:k:27:MET:HB2	1.84	0.47
44:w:143:TYR:OH	44:w:199:LEU:O	2.21	0.47
1:A:81:LYS:HG2	1:A:96:GLY:HA3	1.97	0.47
9:J:129:LEU:HD23	9:J:167:ILE:HG13	1.97	0.47
26:c:153:TYR:OH	43:v:8:ARG:NH1	2.47	0.47
35:l:392:LYS:HE2	35:l:416:THR:HG23	1.97	0.47
40:r:67:VAL:HG12	48:r:502:PLX:H362	1.95	0.47
44:w:239:ASN:O	44:w:243:LYS:HB2	2.15	0.47
21:W:120:MET:HE2	36:m:126:VAL:HB	1.97	0.47
23:Z:58:ALA:O	35:l:434:LYS:NZ	2.48	0.47
41:s:22:LEU:HD12	41:s:22:LEU:O	2.15	0.47
44:w:96:SER:HA	44:w:101:GLY:HA2	1.96	0.47
5:F:61:VAL:HG23	5:F:62:GLN:H	1.80	0.46
20:V:110:ILE:HD11	47:l:701:PEE:H1	1.96	0.46
9:J:140:ASP:N	9:J:140:ASP:OD1	2.48	0.46
16:Q:106:VAL:HG21	16:Q:447:VAL:HG21	1.96	0.46
47:Q:502:PEE:H58	47:Q:502:PEE:H64	1.75	0.46
32:i:95:MET:HE2	32:i:95:MET:HA	1.96	0.46
32:i:230:LEU:O	32:i:233:THR:HG22	2.16	0.46
33:j:10:ASN:ND2	41:s:84:THR:OG1	2.37	0.46
35:l:336:LYS:HA	35:l:336:LYS:HD3	1.74	0.46
36:m:64:MET:CE	36:m:64:MET:CA	2.86	0.46
1:A:405:ARG:H	1:A:408:GLU:HG3	1.79	0.46
12:M:394:VAL:HG13	12:M:473:MET:HE1	1.96	0.46
15:P:211:ARG:NE	15:P:222:GLU:OE1	2.46	0.46
26:c:168:LEU:HD11	26:c:174:PRO:HB3	1.96	0.46
1:A:314:LEU:HD11	1:A:317:VAL:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:SER:HB2	1:A:370:LEU:HD22	1.97	0.46
9:J:178:SER:OG	9:J:317:ASP:OD1	2.28	0.46
12:M:525:ALA:O	12:M:530:TYR:HB2	2.15	0.46
27:d:160:LYS:HE2	28:e:147:ILE:HG23	1.96	0.46
35:l:293:ILE:HD13	35:l:418:LEU:HD22	1.96	0.46
54:n:101:CDL:H742	54:n:101:CDL:H772	1.40	0.46
16:Q:41:VAL:HG23	28:e:55:LEU:HD21	1.97	0.46
54:l:702:CDL:H611	54:l:702:CDL:H811	1.97	0.46
36:m:4:TYR:O	36:m:8:ILE:HG12	2.16	0.46
44:w:58:LYS:O	44:w:60:ILE:HG13	2.14	0.46
14:O:159:LYS:HD3	14:O:159:LYS:HA	1.79	0.46
20:V:76:ILE:O	20:V:80:VAL:HG13	2.15	0.46
35:l:49:VAL:HB	35:l:50:PRO:HD3	1.98	0.46
39:p:27:LEU:HD21	39:p:40:PHE:HB3	1.98	0.46
44:w:254:GLU:OE1	44:w:254:GLU:N	2.49	0.46
1:A:265:PHE:HB3	1:A:291:GLU:HG3	1.98	0.46
1:A:362:ASP:HB3	1:A:365:LYS:HB3	1.97	0.46
22:Y:97:LEU:HD12	43:v:107:ARG:HD2	1.96	0.46
30:g:36:MET:HE1	48:g:201:PLX:H393	1.97	0.46
35:l:293:ILE:HG21	35:l:418:LEU:HD22	1.97	0.46
54:r:503:CDL:H741	54:r:503:CDL:H772	1.43	0.46
54:s:401:CDL:H141	54:s:401:CDL:H171	1.55	0.46
42:u:58:GLU:OE1	42:u:58:GLU:HA	2.16	0.46
9:J:308:SER:HB2	48:J:403:PLX:H252	1.97	0.46
17:S:12:MET:HE3	41:s:264:LEU:HD22	1.97	0.46
54:a:201:CDL:H401	27:d:44:PRO:HB3	1.97	0.46
25:b:80:TRP:HD1	27:d:41:VAL:HG13	1.80	0.46
26:c:113:ILE:HG13	26:c:115:ASN:HB2	1.96	0.46
35:l:108:MET:HE1	35:l:240:PRO:HB3	1.98	0.46
35:l:172:ILE:HG21	40:r:408:LEU:HD12	1.98	0.46
35:l:295:GLN:HB2	35:l:301:ILE:HG12	1.97	0.46
40:r:357:THR:O	40:r:361:VAL:HG23	2.15	0.46
40:r:437:MET:O	40:r:441:ILE:HG22	2.16	0.46
4:E:105:ARG:NH2	15:P:210:LEU:HD21	2.31	0.46
5:F:92:GLU:O	5:F:96:SER:OG	2.26	0.46
9:J:127:ILE:HD11	9:J:253:ILE:HD11	1.98	0.46
25:b:120:MET:HB3	43:v:45:GLU:OE2	2.16	0.46
32:i:89:MET:HE1	32:i:98:MET:HE3	1.97	0.46
32:i:222:SER:O	32:i:224:ALA:N	2.49	0.46
39:p:133:TRP:O	39:p:137:VAL:HG12	2.15	0.46
41:s:215:TYR:CD1	41:s:219:PRO:HB2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:s:307:LEU:HA	41:s:310:MET:HE3	1.97	0.46
12:M:301:ARG:HD2	12:M:301:ARG:HA	1.75	0.45
32:i:307:SER:OG	32:i:308:THR:N	2.48	0.45
54:l:703:CDL:H382	54:l:703:CDL:H351	1.67	0.45
36:m:53:GLY:HA2	36:m:56:VAL:HG12	1.97	0.45
1:A:119:GLU:O	1:A:159:ARG:NH1	2.50	0.45
14:O:138:THR:HG23	14:O:139:PRO:HD3	1.98	0.45
30:g:110:THR:O	30:g:114:ILE:HG13	2.16	0.45
35:l:593:ILE:HD11	54:m:201:CDL:H192	1.97	0.45
40:r:76:MET:HE3	40:r:99:LEU:HD22	1.97	0.45
1:A:125:CYS:SG	1:A:125:CYS:O	2.75	0.45
3:C:55:ASN:ND2	3:C:187:GLU:O	2.46	0.45
17:S:19:PRO:HB3	41:s:9:LEU:HD12	1.98	0.45
41:s:155:LEU:HD23	41:s:155:LEU:HA	1.79	0.45
1:A:322:SER:HG	1:A:374:TYR:HH	1.65	0.45
2:B:122:VAL:HG21	16:Q:385:TYR:HD1	1.82	0.45
11:L:87:MET:HE3	12:M:274:LEU:HD21	1.98	0.45
19:U:46:ASN:HD21	41:s:314:ILE:HD12	1.81	0.45
21:W:98:MET:HE2	31:h:79:ILE:HA	1.99	0.45
35:l:264:TYR:CD2	35:l:265:PRO:HD3	2.51	0.45
5:F:65:LEU:HD11	5:F:91:LEU:HD13	1.98	0.45
5:F:86:GLN:O	5:F:90:THR:HG22	2.16	0.45
9:J:271:TYR:OH	9:J:346:GLU:OE2	2.29	0.45
12:M:347:ASP:CB	12:M:594:ALA:HB1	2.47	0.45
47:Q:502:PEE:H61	47:Q:502:PEE:H55	1.64	0.45
6:X:99:SER:N	6:X:102:SER:OG	2.38	0.45
22:Y:65:MET:SD	35:l:375:ILE:HG12	2.57	0.45
28:e:107:ALA:HB2	48:r:502:PLX:H24	1.97	0.45
33:j:27:LEU:HD13	41:s:59:GLU:HG3	1.98	0.45
54:r:503:CDL:H342	54:r:503:CDL:H201	1.97	0.45
1:A:157:TYR:HB2	1:A:212:LEU:HD21	1.98	0.45
12:M:262:VAL:HG23	12:M:276:ARG:HB2	1.99	0.45
14:O:44:THR:HG23	14:O:47:ASN:H	1.81	0.45
48:g:201:PLX:H181	48:g:201:PLX:H151	1.80	0.45
32:i:41:ILE:HG13	34:k:73:LEU:HD21	1.98	0.45
41:s:92:PRO:HB3	41:s:255:TYR:CD2	2.52	0.45
42:u:40:ASN:O	42:u:44:MET:HG2	2.17	0.45
43:v:39:MET:SD	43:v:58:TYR:HA	2.57	0.45
4:E:99:GLN:CD	33:j:41:PHE:HD2	2.24	0.45
8:I:109:ASP:OD1	21:W:22:LYS:NZ	2.50	0.45
9:J:168:SER:O	9:J:203:PRO:HD2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:116:SER:OG	15:P:227:ALA:O	2.27	0.45
22:Y:72:ARG:NH1	22:Y:76:ASP:OD2	2.50	0.45
32:i:142:LEU:HD22	32:i:149:ILE:HD11	1.97	0.45
35:l:561:ILE:HG13	35:l:562:LEU:H	1.82	0.45
36:m:17:PHE:O	36:m:21:SER:HB2	2.16	0.45
41:s:75:PRO:HG3	41:s:219:PRO:HB3	1.98	0.45
18:T:49:ASP:OD2	18:T:51:ARG:NH2	2.50	0.45
35:l:226:GLN:OE1	35:l:284:THR:HG21	2.17	0.45
35:l:280:LEU:O	35:l:284:THR:HG22	2.17	0.45
35:l:292:ALA:HB2	35:l:304:PHE:HB3	1.99	0.45
41:s:184:MET:HE1	41:s:297:THR:OG1	2.17	0.45
7:H:76:GLN:O	7:H:79:GLU:N	2.40	0.45
9:J:229:ILE:HB	9:J:323:HIS:CD2	2.52	0.45
19:U:63:MET:O	42:u:130:LYS:NZ	2.41	0.45
23:Z:29:LEU:HA	23:Z:32:VAL:HG12	1.99	0.45
35:l:400:ASN:HD21	35:l:489:THR:HG21	1.81	0.45
42:u:47:ARG:HA	42:u:47:ARG:HD2	1.56	0.45
49:C:304:UQ:H451	49:C:304:UQ:H471	1.76	0.45
11:L:84:ARG:NH1	11:L:88:GLN:O	2.50	0.45
11:L:121:LEU:HD22	11:L:124:LEU:HD22	1.98	0.45
21:W:74:LEU:O	21:W:78:GLU:HG3	2.17	0.45
50:X:201:8Q1:O40	50:X:201:8Q1:N36	2.50	0.45
28:e:73:SER:C	28:e:75:GLY:H	2.24	0.45
35:l:463:PHE:O	35:l:467:ILE:HG12	2.17	0.45
35:l:529:TYR:HB3	35:l:530:PRO:HD3	1.98	0.45
36:m:45:LEU:HD23	36:m:50:SER:HA	1.99	0.45
38:o:107:THR:O	38:o:111:LYS:HG3	2.17	0.45
51:J:401:NDP:H2N	51:J:401:NDP:H2D	1.77	0.44
14:O:196:LEU:HD13	14:O:201:ILE:HD13	1.99	0.44
54:V:201:CDL:H751	54:V:201:CDL:H381	1.98	0.44
32:i:128:LEU:HD12	32:i:216:PHE:HB3	1.98	0.44
33:j:70:ALA:HB2	36:m:59:ILE:HD11	1.98	0.44
36:m:17:PHE:HA	36:m:20:PHE:CE2	2.52	0.44
37:n:25:CYS:O	37:n:29:ARG:HG3	2.17	0.44
40:r:366:ASN:ND2	40:r:407:SER:OG	2.46	0.44
41:s:86:TRP:NE1	41:s:233:MET:HB2	2.32	0.44
9:J:167:ILE:HD13	9:J:201:ILE:HB	1.99	0.44
13:N:122:GLN:HA	18:T:59:GLN:HG2	1.99	0.44
15:P:132:LEU:HB2	15:P:141:ILE:HG22	1.98	0.44
27:d:37:PHE:CD1	35:l:3:PRO:HB3	2.53	0.44
36:m:26:PRO:HB2	36:m:71:THR:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:m:201:CDL:H161	54:m:201:CDL:H191	1.67	0.44
54:s:401:CDL:H401	54:s:401:CDL:H372	1.84	0.44
7:H:114:TRP:CD2	7:H:115:PRO:HA	2.52	0.44
12:M:338:VAL:O	12:M:363:SER:OG	2.31	0.44
54:V:202:CDL:H662	54:V:202:CDL:H611	2.00	0.44
25:b:29:SER:N	25:b:32:GLU:HG3	2.32	0.44
28:e:112:TYR:HD2	40:r:43:ASN:HD21	1.66	0.44
34:k:23:ARG:HG3	36:m:23:LYS:HE2	1.98	0.44
40:r:97:THR:HG21	54:r:503:CDL:H242	1.98	0.44
44:w:296:MET:HE3	44:w:296:MET:HB3	1.89	0.44
1:A:424:ILE:HG12	12:M:76:ARG:NH2	2.32	0.44
6:G:130:ILE:HG22	6:G:135:ALA:HB2	1.98	0.44
8:I:50:SER:OG	8:I:51:ASN:N	2.50	0.44
12:M:447:ASP:OD1	12:M:447:ASP:N	2.50	0.44
16:Q:236:LEU:HD22	16:Q:240:LEU:CD2	2.46	0.44
40:r:154:LEU:HD23	40:r:154:LEU:HA	1.82	0.44
54:s:401:CDL:H552	54:s:401:CDL:H221	1.98	0.44
2:B:39:LYS:NZ	16:Q:335:GLU:OE2	2.48	0.44
12:M:73:GLY:O	12:M:76:ARG:NH2	2.48	0.44
16:Q:74:ASP:OD1	16:Q:74:ASP:N	2.48	0.44
16:Q:144:MET:O	16:Q:148:GLU:HG2	2.17	0.44
36:m:24:PRO:HG3	36:m:83:TRP:NE1	2.33	0.44
54:r:503:CDL:H232	54:r:503:CDL:H782	1.99	0.44
46:A:502:FMN:O4'	46:A:502:FMN:O2'	2.31	0.44
11:L:99:MET:HE3	11:L:128:PHE:CE1	2.53	0.44
12:M:370:GLU:HG3	12:M:519:ILE:HG13	1.99	0.44
12:M:398:ASP:OD1	12:M:398:ASP:N	2.49	0.44
15:P:110:SER:HB3	15:P:133:LEU:HB3	2.00	0.44
16:Q:217:VAL:HG23	16:Q:236:LEU:HD23	1.99	0.44
17:S:28:LYS:HB3	17:S:33:GLY:HA2	1.99	0.44
47:W:201:PEE:H22	33:j:4:MET:HG2	1.99	0.44
16:Q:88:HIS:HB3	16:Q:91:ALA:HB2	1.99	0.44
22:Y:71:TRP:CE2	22:Y:75:HIS:CE1	3.06	0.44
34:k:37:MET:HG2	34:k:67:ALA:CB	2.48	0.44
35:l:213:LEU:HB3	35:l:273:VAL:HG11	2.00	0.44
40:r:196:TRP:CD1	40:r:250:LEU:HB3	2.53	0.44
40:r:299:VAL:O	40:r:303:ILE:HG23	2.17	0.44
5:F:24:CYS:O	5:F:34:ARG:NH1	2.51	0.44
13:N:68:MET:HG2	13:N:115:PHE:CD2	2.53	0.44
21:W:43:LEU:HG	41:s:179:TRP:HE1	1.83	0.44
25:b:81:ILE:HG23	47:b:201:PEE:H58	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:440:LYS:HD3	16:Q:440:LYS:HA	1.69	0.44
26:c:89:TRP:HE3	39:p:2:ALA:HB2	1.83	0.44
42:u:107:PHE:O	42:u:111:VAL:HG22	2.18	0.44
44:w:88:GLU:OE2	44:w:161:ARG:NH1	2.51	0.44
1:A:384:PRO:HB2	1:A:423:THR:HG22	1.99	0.43
7:H:11:LEU:HD12	7:H:14:LEU:HD22	2.00	0.43
48:N:201:PLX:H312	48:N:201:PLX:H342	1.66	0.43
16:Q:424:ILE:HB	16:Q:463:ARG:HD2	2.00	0.43
21:W:121:MET:HE1	21:W:137:THR:HB	2.00	0.43
32:i:334:THR:OG1	32:i:335:LEU:HG	2.18	0.43
35:l:435:PRO:HB3	35:l:437:PHE:CZ	2.52	0.43
40:r:84:LEU:HD22	40:r:87:GLU:HG3	1.99	0.43
42:u:4:ILE:HD12	42:u:4:ILE:C	2.43	0.43
1:A:36:LYS:H	1:A:36:LYS:HD2	1.83	0.43
9:J:262:THR:O	9:J:333:PRO:HD2	2.18	0.43
19:U:42:ALA:HB2	41:s:312:ALA:HA	2.00	0.43
33:j:67:LEU:N	33:j:67:LEU:HD22	2.33	0.43
35:l:557:TRP:O	35:l:561:ILE:HG12	2.17	0.43
47:r:501:PEE:H75	47:r:501:PEE:H69	1.84	0.43
1:A:390:ASP:OD2	12:M:202:ASN:ND2	2.52	0.43
2:B:63:TRP:HB3	2:B:66:LEU:HD12	2.00	0.43
2:B:184:LEU:O	13:N:124:TYR:OH	2.35	0.43
9:J:192:ARG:HA	9:J:192:ARG:HD3	1.90	0.43
12:M:47:THR:O	12:M:96:VAL:HG22	2.17	0.43
12:M:543:LYS:HE3	12:M:543:LYS:HB3	1.86	0.43
15:P:125:ARG:HH22	15:P:201:ASP:CG	2.23	0.43
15:P:190:ASP:OD1	15:P:191:TYR:N	2.52	0.43
28:e:136:LEU:HD23	28:e:136:LEU:HA	1.82	0.43
32:i:183:SER:O	32:i:187:MET:HG2	2.18	0.43
1:A:281:HIS:ND1	1:A:358:ASP:OD1	2.51	0.43
1:A:370:LEU:HD23	1:A:370:LEU:HA	1.79	0.43
4:E:14:GLY:O	4:E:15:THR:OG1	2.28	0.43
9:J:208:GLY:H	9:J:211:ASP:HB3	1.83	0.43
49:J:402:UQ:H153	49:J:402:UQ:H171	1.81	0.43
15:P:87:PHE:CE2	15:P:144:LYS:HE3	2.53	0.43
16:Q:205:GLU:HG3	16:Q:209:LYS:HE3	2.00	0.43
28:e:62:GLU:CD	28:e:62:GLU:H	2.27	0.43
33:j:17:LEU:HD23	33:j:17:LEU:HA	1.88	0.43
34:k:4:VAL:O	34:k:8:ILE:HG12	2.18	0.43
40:r:398:MET:O	40:r:402:ILE:HG13	2.17	0.43
16:Q:172:VAL:HG21	16:Q:310:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:120:MET:HE1	31:h:73:MET:HG2	2.00	0.43
24:a:67:PHE:CE2	40:r:434:ASN:HB3	2.53	0.43
48:g:201:PLX:H102	48:g:201:PLX:H71	1.51	0.43
33:j:88:LEU:HD13	41:s:309:ILE:HD12	2.00	0.43
41:s:169:GLN:HG3	41:s:244:GLY:HA3	2.01	0.43
42:u:43:PHE:HD1	42:u:59:GLU:CB	2.31	0.43
3:C:62:LEU:O	3:C:91:VAL:HA	2.18	0.43
49:C:304:UQ:HM51	49:C:304:UQ:H72	1.83	0.43
16:Q:220:ALA:HB3	16:Q:224:ALA:HA	2.00	0.43
23:Z:25:GLU:OE1	23:Z:25:GLU:N	2.46	0.43
35:l:12:LEU:HD22	35:l:129:MET:HB3	2.01	0.43
35:l:60:GLU:HB3	35:l:83:ASP:HA	2.00	0.43
40:r:369:LEU:O	40:r:372:SER:OG	2.24	0.43
41:s:87:VAL:HG23	41:s:88:PRO:HD3	2.00	0.43
41:s:139:THR:HA	41:s:142:TYR:CE2	2.54	0.43
49:C:304:UQ:H412	41:s:51:ASP:HB3	2.00	0.43
48:N:201:PLX:H1C3	48:N:201:PLX:H22	1.74	0.43
24:a:187:PRO:CB	42:u:47:ARG:NH1	2.80	0.43
27:d:90:MET:SD	40:r:47:GLU:HB3	2.58	0.43
32:i:40:MET:HE1	32:i:129:LEU:HG	2.00	0.43
33:j:6:THR:HG21	41:s:87:VAL:HG11	2.01	0.43
33:j:63:LEU:HD23	33:j:63:LEU:HA	1.87	0.43
34:k:37:MET:HG2	34:k:67:ALA:HB2	1.99	0.43
43:v:12:ASP:HB3	43:v:15:LYS:HE2	2.01	0.43
3:C:61:SER:O	3:C:61:SER:OG	2.33	0.43
3:C:66:THR:HG22	49:C:304:UQ:H102	2.00	0.43
7:H:48:THR:HA	7:H:51:ILE:HG12	1.99	0.43
12:M:234:LYS:HB3	12:M:235:PRO:HD3	2.01	0.43
21:W:84:LEU:HD13	42:u:8:PRO:HG2	2.00	0.43
54:a:201:CDL:H772	54:a:201:CDL:H201	2.00	0.43
26:c:149:ILE:HG13	26:c:150:TYR:CD1	2.53	0.43
43:v:73:SER:O	43:v:73:SER:OG	2.37	0.43
44:w:351:TRP:HA	44:w:351:TRP:CE3	2.54	0.43
3:C:167:PRO:HD3	16:Q:223:HIS:HD2	1.81	0.43
12:M:59:GLN:HG2	12:M:62:ARG:NH2	2.34	0.43
35:l:375:ILE:HD12	35:l:458:LEU:HD11	2.00	0.43
40:r:189:SER:OG	40:r:192:ASN:OD1	2.36	0.43
40:r:354:LEU:HD12	40:r:354:LEU:HA	1.91	0.43
40:r:445:LEU:HA	40:r:448:THR:HG22	2.01	0.43
2:B:112:ARG:HD3	2:B:164:VAL:O	2.19	0.43
3:C:80:ALA:HB2	3:C:86:MET:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:c:167:TYR:CD2	26:c:178:PRO:HG3	2.54	0.43
27:d:33:LEU:HD13	35:l:49:VAL:HG13	2.01	0.43
37:n:17:VAL:HG21	40:r:30:HIS:HB3	2.00	0.43
39:p:44:MET:HE2	39:p:44:MET:HB2	1.93	0.43
43:v:31:PHE:CD2	43:v:34:ARG:HD3	2.54	0.43
44:w:230:THR:HG23	44:w:233:TYR:H	1.83	0.43
5:F:45:LYS:HD2	5:F:45:LYS:HA	1.84	0.42
16:Q:450:ILE:HA	16:Q:453:THR:HG22	2.01	0.42
48:a:202:PLX:H1C3	48:a:202:PLX:H22	1.78	0.42
27:d:36:ILE:HD13	27:d:36:ILE:HA	1.92	0.42
35:l:190:LEU:HB2	35:l:196:TRP:NE1	2.34	0.42
40:r:216:LEU:HB3	40:r:217:PRO:HD3	2.01	0.42
41:s:192:GLU:C	41:s:192:GLU:OE1	2.62	0.42
1:A:60:GLY:HA2	14:O:241:PRO:HA	2.00	0.42
8:I:52:ASN:OD1	8:I:57:ARG:NE	2.52	0.42
8:I:66:PRO:HB3	15:P:79:SER:HA	2.01	0.42
14:O:199:LYS:O	14:O:203:GLU:HG3	2.19	0.42
21:W:120:MET:O	21:W:120:MET:HG2	2.18	0.42
22:Y:61:PHE:HE1	35:l:459:ILE:HD11	1.84	0.42
32:i:258:SER:HB3	32:i:333:SER:O	2.19	0.42
34:k:23:ARG:NH2	36:m:81:GLU:OE1	2.47	0.42
36:m:23:LYS:N	36:m:24:PRO:HD3	2.33	0.42
36:m:169:MET:HE3	36:m:169:MET:HB3	1.78	0.42
54:m:201:CDL:H652	54:m:201:CDL:H622	1.76	0.42
1:A:326:LEU:HD22	1:A:363:ILE:HD11	2.02	0.42
2:B:90:LYS:HG2	13:N:91:HIS:NE2	2.34	0.42
3:C:50:LEU:HD23	3:C:50:LEU:HA	1.88	0.42
15:P:84:LEU:HD23	15:P:141:ILE:HG13	2.00	0.42
21:W:134:LEU:HD21	36:m:2:THR:HB	2.01	0.42
27:d:10:TYR:OH	28:e:123:GLU:OE2	2.30	0.42
33:j:73:LEU:N	33:j:74:PRO:HD2	2.34	0.42
35:l:358:LYS:HG3	39:p:80:TYR:CE1	2.54	0.42
54:l:702:CDL:H251	54:l:702:CDL:H222	1.96	0.42
39:p:55:LYS:HE2	39:p:55:LYS:HB2	1.70	0.42
1:A:210:THR:HB	1:A:224:ARG:H	1.84	0.42
1:A:267:ARG:HH11	1:A:336:LEU:HD12	1.83	0.42
46:A:502:FMN:H9	46:A:502:FMN:H1'1	1.78	0.42
3:C:125:PRO:HG3	41:s:216:ALA:HB1	2.01	0.42
9:J:254:LYS:HE3	9:J:254:LYS:HB2	1.78	0.42
21:W:85:GLN:HB2	42:u:13:LEU:HD13	2.01	0.42
25:b:7:ASP:OD1	25:b:7:ASP:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:m:68:PHE:CD2	36:m:68:PHE:C	2.97	0.42
40:r:207:MET:HG2	40:r:298:ILE:CG1	2.49	0.42
40:r:216:LEU:HD11	40:r:220:HIS:CE1	2.54	0.42
41:s:267:THR:O	41:s:271:LEU:HG	2.19	0.42
42:u:47:ARG:NH1	42:u:47:ARG:CG	2.73	0.42
2:B:38:TYR:O	8:I:107:SER:HB2	2.19	0.42
16:Q:121:GLU:HG2	16:Q:422:CYS:O	2.19	0.42
32:i:246:VAL:HG11	54:r:503:CDL:H392	2.01	0.42
48:j:203:PLX:H132	48:j:203:PLX:H161	1.54	0.42
9:J:211:ASP:O	9:J:215:ASN:ND2	2.52	0.42
9:J:344:PRO:HG2	9:J:347:LEU:HD13	2.01	0.42
11:L:102:ASP:OD1	11:L:102:ASP:N	2.53	0.42
25:b:66:ARG:HE	25:b:66:ARG:HB3	1.77	0.42
47:j:201:PEE:H59	47:j:201:PEE:H64	1.85	0.42
39:p:71:PHE:CD2	39:p:71:PHE:C	2.97	0.42
1:A:48:ARG:HH11	10:K:70:ASN:HB3	1.85	0.42
1:A:152:ARG:CZ	10:K:101:PRO:HD3	2.49	0.42
12:M:370:GLU:OE2	12:M:518:ARG:NE	2.53	0.42
16:Q:238:LEU:HD23	16:Q:238:LEU:HA	1.81	0.42
17:S:45:TRP:CD1	21:W:140:PHE:HB2	2.55	0.42
19:U:9:LEU:HD11	47:j:201:PEE:H68	2.00	0.42
22:Y:71:TRP:CZ2	22:Y:75:HIS:CE1	3.07	0.42
40:r:22:MET:HE3	40:r:22:MET:HB3	1.80	0.42
40:r:455:LEU:HD23	40:r:455:LEU:HA	1.88	0.42
54:r:503:CDL:H632	54:r:503:CDL:H602	1.88	0.42
41:s:98:MET:HE2	41:s:101:GLY:HA2	2.02	0.42
41:s:110:SER:O	41:s:113:VAL:CG1	2.61	0.42
1:A:398:ARG:NH1	12:M:155:GLU:OE2	2.49	0.42
3:C:65:MET:HG2	3:C:67:PHE:HB2	2.02	0.42
9:J:37:HIS:NE2	18:T:49:ASP:HA	2.34	0.42
49:J:402:UQ:H221	49:J:402:UQ:H201	1.65	0.42
16:Q:244:ILE:HG22	16:Q:348:LEU:HD11	2.00	0.42
17:S:31:ASN:ND2	17:S:36:LYS:HB2	2.34	0.42
17:S:47:LEU:HD22	42:u:22:SER:HB3	2.01	0.42
20:V:66:ILE:HG21	54:V:201:CDL:H181	2.02	0.42
24:a:141:GLN:O	24:a:145:GLU:HG3	2.19	0.42
48:j:203:PLX:H22	48:j:203:PLX:H1C3	1.80	0.42
35:l:297:ASP:O	35:l:301:ILE:HG13	2.20	0.42
35:l:332:HIS:HA	35:l:335:PHE:CZ	2.55	0.42
36:m:1:MET:HE3	36:m:125:TRP:NE1	2.31	0.42
40:r:303:ILE:HD11	40:r:384:ALA:HB1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:v:17:PRO:HB3	43:v:105:GLU:HG2	2.01	0.42
12:M:535:GLU:HA	12:M:538:ARG:HG3	2.02	0.42
20:V:36:VAL:HG22	54:V:201:CDL:H742	2.02	0.42
27:d:43:ARG:HB3	27:d:44:PRO:HD3	2.02	0.42
34:k:31:LEU:HD21	36:m:67:VAL:HG11	2.01	0.42
35:l:154:LEU:HD13	35:l:243:VAL:HG22	2.01	0.42
54:l:702:CDL:H641	48:r:502:PLX:H111	2.02	0.42
40:r:269:MET:SD	40:r:399:ASN:ND2	2.93	0.42
44:w:51:ARG:HE	44:w:51:ARG:HB3	1.60	0.42
44:w:76:GLU:O	44:w:80:LYS:HG3	2.20	0.42
1:A:53:LEU:HB2	1:A:136:HIS:CE1	2.54	0.42
1:A:67:GLU:O	1:A:71:LYS:HG2	2.19	0.42
1:A:146:GLY:HA3	1:A:193:PHE:CE1	2.55	0.42
8:I:70:MET:O	8:I:70:MET:SD	2.77	0.42
9:J:231:LEU:HD23	9:J:231:LEU:HA	1.87	0.42
12:M:49:VAL:HG23	12:M:94:MET:O	2.20	0.42
12:M:366:LEU:O	12:M:531:LYS:HB3	2.20	0.42
16:Q:39:PRO:HB3	16:Q:43:TRP:CD1	2.55	0.42
17:S:1:MET:HB3	17:S:2:TRP:H	1.71	0.42
54:V:202:CDL:H321	54:V:202:CDL:H352	1.69	0.42
35:l:54:PHE:CZ	35:l:84:TYR:HB2	2.55	0.42
36:m:53:GLY:O	36:m:56:VAL:CG1	2.68	0.42
44:w:223:ASN:OD1	44:w:226:GLU:HG3	2.20	0.42
2:B:59:GLN:HG3	2:B:64:THR:HB	2.01	0.41
2:B:181:GLU:OE2	9:J:101:GLY:N	2.51	0.41
6:G:105:MET:HE2	6:G:139:MET:SD	2.60	0.41
7:H:38:ILE:O	7:H:45:ARG:NH1	2.49	0.41
15:P:119:VAL:HG12	15:P:121:THR:HG22	2.02	0.41
47:Q:501:PEE:H28	47:Q:501:PEE:H33	1.79	0.41
26:c:55:TYR:OH	26:c:74:ASP:O	2.26	0.41
31:h:89:GLU:OE1	31:h:91:LYS:HB2	2.20	0.41
33:j:73:LEU:O	41:s:160:TYR:OH	2.23	0.41
35:l:7:LEU:O	35:l:11:THR:HG23	2.20	0.41
35:l:331:MET:SD	35:l:465:GLY:HA2	2.60	0.41
3:C:118:ARG:HA	3:C:118:ARG:HD2	1.90	0.41
8:I:33:LYS:HB3	8:I:33:LYS:HE2	1.85	0.41
16:Q:217:VAL:CG2	16:Q:236:LEU:HD23	2.50	0.41
32:i:99:THR:HG23	32:i:154:MET:HE1	2.03	0.41
32:i:153:LEU:HD11	32:i:157:MET:HE3	2.03	0.41
34:k:41:PHE:O	34:k:45:THR:HG22	2.20	0.41
35:l:289:ALA:O	35:l:293:ILE:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:m:51:PHE:O	36:m:55:MET:HB2	2.20	0.41
41:s:20:LEU:HD22	41:s:232:ILE:HD11	2.01	0.41
16:Q:383:LYS:HA	16:Q:383:LYS:HD2	1.89	0.41
21:W:102:PRO:HG2	21:W:103:ASP:OD1	2.21	0.41
6:X:100:VAL:HG12	6:X:142:GLN:HB2	2.02	0.41
25:b:4:TYR:HB3	25:b:9:LYS:HG3	2.01	0.41
27:d:80:LYS:HD2	27:d:80:LYS:HA	1.79	0.41
34:k:23:ARG:HG2	54:m:201:CDL:HB62	2.02	0.41
36:m:53:GLY:CA	36:m:56:VAL:HG12	2.49	0.41
36:m:77:GLU:N	36:m:77:GLU:OE2	2.53	0.41
5:F:59:SER:O	5:F:61:VAL:N	2.53	0.41
12:M:224:ASP:OD2	12:M:291:ARG:NH2	2.33	0.41
14:O:138:THR:CG2	14:O:139:PRO:HD3	2.50	0.41
16:Q:439:SER:O	16:Q:439:SER:OG	2.38	0.41
23:Z:13:LYS:HD2	23:Z:13:LYS:HA	1.84	0.41
32:i:228:LEU:HD23	32:i:228:LEU:HA	1.90	0.41
33:j:19:LEU:HD12	33:j:19:LEU:HA	1.85	0.41
35:l:108:MET:CE	35:l:240:PRO:HB3	2.51	0.41
43:v:51:LEU:HD13	43:v:63:LEU:HD23	2.02	0.41
48:C:303:PLX:H21	48:C:303:PLX:H1C3	1.88	0.41
8:I:64:MET:HE3	15:P:80:CYS:SG	2.60	0.41
12:M:137:CYS:HB3	12:M:140:GLN:HB2	2.02	0.41
13:N:21:ARG:HG2	13:N:21:ARG:NH1	2.35	0.41
16:Q:123:LEU:O	16:Q:127:LYS:HG2	2.21	0.41
24:a:147:ALA:HB2	40:r:173:SER:HB2	2.02	0.41
31:h:93:THR:O	31:h:93:THR:OG1	2.34	0.41
32:i:131:LEU:HD12	32:i:216:PHE:CE2	2.56	0.41
36:m:4:TYR:HB3	36:m:7:PHE:HB3	2.02	0.41
42:u:25:LEU:HD23	42:u:71:PHE:HZ	1.86	0.41
4:E:52:LEU:HD11	4:E:103:ILE:HG21	2.01	0.41
9:J:56:ALA:HA	9:J:125:VAL:O	2.21	0.41
16:Q:83:ASN:O	41:s:127:TYR:OH	2.37	0.41
21:W:90:ASN:ND2	21:W:123:GLU:O	2.54	0.41
32:i:79:LEU:HD21	34:k:1:MET:SD	2.60	0.41
36:m:121:GLY:O	36:m:122:LEU:HD23	2.21	0.41
41:s:180:PRO:O	41:s:184:MET:HG3	2.21	0.41
42:u:70:PHE:CD2	42:u:70:PHE:C	2.98	0.41
42:u:80:GLU:HB3	42:u:81:PRO:HD3	2.02	0.41
43:v:12:ASP:OD1	43:v:14:SER:OG	2.37	0.41
1:A:64:LYS:HD3	14:O:249:LEU:HD23	2.03	0.41
12:M:441:ARG:HB3	12:M:441:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:134:VAL:HG22	14:O:186:VAL:HG22	2.02	0.41
15:P:101:ARG:HE	15:P:101:ARG:HB3	1.71	0.41
22:Y:61:PHE:O	22:Y:64:THR:HG22	2.21	0.41
32:i:337:LEU:O	32:i:340:THR:OG1	2.38	0.41
33:j:56:PHE:HB2	36:m:70:TYR:OH	2.21	0.41
35:l:79:SER:HB3	35:l:135:ASN:HB3	2.02	0.41
41:s:85:MET:HG2	41:s:233:MET:HE2	2.02	0.41
41:s:189:THR:HG22	41:s:234:MET:CE	2.51	0.41
41:s:285:LEU:O	41:s:289:LEU:HD23	2.21	0.41
42:u:43:PHE:HD1	42:u:59:GLU:HB2	1.85	0.41
44:w:165:SER:HB3	44:w:245:PHE:CE1	2.56	0.41
1:A:288:VAL:HG21	1:A:303:HIS:CD2	2.55	0.41
12:M:323:LEU:HD22	12:M:626:LEU:HB2	2.03	0.41
13:N:53:LYS:HD2	13:N:53:LYS:HA	1.82	0.41
6:X:89:LEU:O	6:X:89:LEU:HD23	2.20	0.41
28:e:66:LEU:HD23	28:e:66:LEU:HA	1.89	0.41
35:l:8:THR:HB	35:l:82:MET:HE3	2.03	0.41
35:l:156:GLY:HA2	35:l:164:ALA:HB1	2.02	0.41
41:s:157:ASN:ND2	41:s:159:SER:O	2.54	0.41
12:M:49:VAL:HG13	12:M:102:ILE:HD13	2.03	0.41
12:M:556:THR:HA	12:M:579:MET:HE1	2.02	0.41
12:M:690:THR:HG22	12:M:692:LYS:H	1.86	0.41
15:P:51:ASN:HB3	15:P:82:ASN:HD21	1.84	0.41
16:Q:158:LEU:HD23	16:Q:158:LEU:HA	1.88	0.41
27:d:28:ASN:OD1	27:d:30:VAL:HG22	2.20	0.41
28:e:119:ARG:HA	28:e:119:ARG:HD3	1.77	0.41
30:g:13:LEU:HD11	31:h:6:VAL:HG12	2.03	0.41
34:k:30:LEU:O	34:k:34:GLU:HG3	2.20	0.41
35:l:371:THR:O	35:l:375:ILE:HG13	2.21	0.41
35:l:377:SER:HB2	35:l:423:SER:OG	2.21	0.41
47:l:704:PEE:H58	47:l:704:PEE:H53	1.88	0.41
38:o:102:TYR:HB2	40:r:263:MET:HG3	2.03	0.41
41:s:294:LEU:HB3	41:s:295:PRO:HD3	2.03	0.41
42:u:158:LEU:HD12	42:u:158:LEU:HA	1.97	0.41
2:B:94:SER:OG	16:Q:215:GLU:OE2	2.39	0.41
8:I:68:ILE:HD11	8:I:71:SER:HB2	2.03	0.41
8:I:107:SER:HB3	8:I:111:PRO:HA	2.02	0.41
9:J:135:GLU:HG3	9:J:140:ASP:HA	2.03	0.41
12:M:382:ARG:NH2	12:M:652:ASN:OD1	2.54	0.41
12:M:385:TYR:OH	12:M:527:ASP:OD1	2.29	0.41
54:V:202:CDL:H781	54:V:202:CDL:H812	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:l:313:MET:HG3	35:l:328:HIS:CD2	2.55	0.41
40:r:118:PHE:O	40:r:122:PHE:HB3	2.21	0.41
41:s:222:MET:HE3	41:s:222:MET:HB3	1.97	0.41
44:w:279:ASP:N	44:w:279:ASP:OD1	2.51	0.41
47:C:302:PEE:H82	47:C:302:PEE:H74	1.95	0.40
7:H:77:ILE:HA	7:H:80:VAL:HG23	2.04	0.40
12:M:148:SER:OG	12:M:149:ASP:N	2.53	0.40
47:W:201:PEE:H59	41:s:108:MET:HE1	2.02	0.40
6:X:84:LEU:HD23	6:X:84:LEU:HA	1.86	0.40
24:a:133:TYR:HE1	27:d:90:MET:HG3	1.87	0.40
34:k:20:LEU:HD13	35:l:592:LEU:HB2	2.03	0.40
34:k:79:VAL:HG22	36:m:74:MET:HE1	2.04	0.40
44:w:291:PHE:HD1	44:w:291:PHE:HA	1.78	0.40
14:O:121:MET:HE2	14:O:121:MET:HB3	1.93	0.40
24:a:170:GLN:HB2	30:g:6:GLY:O	2.21	0.40
26:c:185:GLU:O	43:v:34:ARG:NE	2.54	0.40
40:r:306:PRO:O	40:r:310:MET:HG3	2.21	0.40
41:s:14:LEU:HD22	41:s:225:MET:HE2	2.03	0.40
43:v:81:LYS:HD2	43:v:81:LYS:HA	1.83	0.40
1:A:102:MET:HE2	1:A:149:MET:HB3	2.02	0.40
3:C:188:LYS:N	9:J:87:GLU:OE2	2.45	0.40
4:E:14:GLY:O	11:L:52:LEU:HD11	2.21	0.40
6:G:94:ASP:HB3	6:G:97:LYS:HB3	2.03	0.40
48:J:403:PLX:H372	48:J:403:PLX:H321	2.03	0.40
11:L:84:ARG:HD3	11:L:91:VAL:HG12	2.03	0.40
16:Q:133:LEU:CD2	16:Q:228:ARG:HD3	2.51	0.40
6:X:128:PHE:CE2	6:X:151:LYS:HD2	2.56	0.40
26:c:96:ASP:OD1	26:c:97:LEU:N	2.55	0.40
36:m:163:ILE:HD13	36:m:163:ILE:HA	1.89	0.40
44:w:302:LEU:HD23	44:w:302:LEU:HA	1.85	0.40
44:w:351:TRP:HA	44:w:351:TRP:HE3	1.85	0.40
11:L:72:ILE:HG22	11:L:73:LYS:HG3	2.03	0.40
16:Q:95:LEU:HB2	16:Q:458:PHE:CE1	2.56	0.40
16:Q:271:ARG:HD2	16:Q:271:ARG:HA	1.90	0.40
21:W:71:LEU:HD23	21:W:71:LEU:HA	1.91	0.40
6:X:137:LYS:HA	25:b:3:GLY:HA2	2.04	0.40
47:b:201:PEE:H40	47:b:201:PEE:H33	1.85	0.40
34:k:19:LEU:HD22	34:k:36:MET:HE1	2.03	0.40
47:l:704:PEE:H55	40:r:405:LEU:HD13	2.02	0.40
36:m:71:THR:HA	36:m:75:ALA:HB3	2.03	0.40
54:m:201:CDL:H462	54:m:201:CDL:H432	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:ILE:HD12	1:A:158:ILE:HA	1.81	0.40
4:E:50:PHE:CE2	4:E:98:LYS:O	2.73	0.40
4:E:106:PHE:O	4:E:108:HIS:NE2	2.54	0.40
28:e:79:ASP:OD1	28:e:79:ASP:C	2.64	0.40
30:g:4:MET:HE2	30:g:4:MET:HB3	1.99	0.40
32:i:31:ILE:HG23	34:k:66:PHE:CZ	2.57	0.40
32:i:65:THR:HG22	32:i:69:MET:HE2	2.03	0.40
32:i:79:LEU:HB2	34:k:47:ILE:HD13	2.04	0.40
33:j:68:GLU:HG3	33:j:98:LEU:HG	2.04	0.40
33:j:78:ALA:O	33:j:81:THR:HG22	2.22	0.40
36:m:34:ILE:HG13	36:m:64:MET:HG3	2.04	0.40
38:o:73:SER:OG	38:o:74:ALA:N	2.54	0.40
41:s:55:LEU:HD13	41:s:221:ALA:HB2	2.03	0.40
41:s:149:ILE:HG21	41:s:185:TRP:HB2	2.02	0.40
42:u:28:ALA:HB2	42:u:82:PHE:CE1	2.57	0.40
42:u:62:LEU:HD23	42:u:62:LEU:HA	1.91	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	A	431/433 (100%)	417 (97%)	14 (3%)	0	100	100
2	B	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
3	C	154/156 (99%)	148 (96%)	6 (4%)	0	100	100
4	E	113/115 (98%)	108 (96%)	5 (4%)	0	100	100
5	F	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
6	G	86/88 (98%)	78 (91%)	7 (8%)	1 (1%)	10	42
6	X	86/88 (98%)	81 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	H	110/112 (98%)	103 (94%)	6 (6%)	1 (1%)	14	47
8	I	93/112 (83%)	79 (85%)	14 (15%)	0	100	100
9	J	340/342 (99%)	328 (96%)	12 (4%)	0	100	100
10	K	41/43 (95%)	39 (95%)	2 (5%)	0	100	100
11	L	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
12	M	688/690 (100%)	664 (96%)	24 (4%)	0	100	100
13	N	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
14	O	215/217 (99%)	206 (96%)	9 (4%)	0	100	100
15	P	206/208 (99%)	196 (95%)	10 (5%)	0	100	100
16	Q	427/430 (99%)	414 (97%)	13 (3%)	0	100	100
17	S	68/70 (97%)	63 (93%)	5 (7%)	0	100	100
18	T	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
19	U	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
20	V	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
21	W	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
22	Y	65/67 (97%)	61 (94%)	4 (6%)	0	100	100
23	Z	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
24	a	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
25	b	94/126 (75%)	89 (95%)	5 (5%)	0	100	100
26	c	154/156 (99%)	143 (93%)	11 (7%)	0	100	100
27	d	173/175 (99%)	168 (97%)	5 (3%)	0	100	100
28	e	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
29	f	47/49 (96%)	42 (89%)	5 (11%)	0	100	100
30	g	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
31	h	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
32	i	345/347 (99%)	327 (95%)	18 (5%)	0	100	100
33	j	113/115 (98%)	108 (96%)	5 (4%)	0	100	100
34	k	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
35	l	604/606 (100%)	575 (95%)	29 (5%)	0	100	100
36	m	173/175 (99%)	164 (95%)	8 (5%)	1 (1%)	21	56
37	n	54/56 (96%)	54 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	o	126/128 (98%)	121 (96%)	5 (4%)	0	100	100
39	p	176/178 (99%)	169 (96%)	7 (4%)	0	100	100
40	r	457/459 (100%)	448 (98%)	9 (2%)	0	100	100
41	s	316/318 (99%)	303 (96%)	13 (4%)	0	100	100
42	u	169/171 (99%)	162 (96%)	6 (4%)	1 (1%)	21	56
43	v	122/124 (98%)	114 (93%)	8 (7%)	0	100	100
44	w	318/320 (99%)	305 (96%)	13 (4%)	0	100	100
All	All	8174/8312 (98%)	7838 (96%)	332 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	G	133	ILE
42	u	17	GLU
36	m	26	PRO
7	H	77	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	346/346 (100%)	346 (100%)	0	100	100
2	B	151/151 (100%)	151 (100%)	0	100	100
3	C	132/132 (100%)	132 (100%)	0	100	100
4	E	107/107 (100%)	106 (99%)	1 (1%)	70	81
5	F	75/76 (99%)	75 (100%)	0	100	100
6	G	75/81 (93%)	75 (100%)	0	100	100
6	X	76/81 (94%)	76 (100%)	0	100	100
7	H	99/99 (100%)	99 (100%)	0	100	100
8	I	87/97 (90%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	J	296/296 (100%)	295 (100%)	1 (0%)	86	88
10	K	42/42 (100%)	42 (100%)	0	100	100
11	L	113/113 (100%)	112 (99%)	1 (1%)	70	81
12	M	580/580 (100%)	578 (100%)	2 (0%)	86	88
13	N	130/130 (100%)	130 (100%)	0	100	100
14	O	183/183 (100%)	182 (100%)	1 (0%)	81	85
15	P	190/190 (100%)	190 (100%)	0	100	100
16	Q	370/370 (100%)	370 (100%)	0	100	100
17	S	57/58 (98%)	57 (100%)	0	100	100
18	T	79/79 (100%)	79 (100%)	0	100	100
19	U	69/69 (100%)	68 (99%)	1 (1%)	59	77
20	V	101/101 (100%)	101 (100%)	0	100	100
21	W	121/123 (98%)	121 (100%)	0	100	100
22	Y	62/62 (100%)	61 (98%)	1 (2%)	55	75
23	Z	62/62 (100%)	62 (100%)	0	100	100
24	a	121/121 (100%)	120 (99%)	1 (1%)	73	82
25	b	90/119 (76%)	89 (99%)	1 (1%)	65	79
26	c	141/141 (100%)	140 (99%)	1 (1%)	76	83
27	d	155/155 (100%)	155 (100%)	0	100	100
28	e	96/96 (100%)	96 (100%)	0	100	100
29	f	36/45 (80%)	36 (100%)	0	100	100
30	g	108/108 (100%)	107 (99%)	1 (1%)	70	81
31	h	92/93 (99%)	90 (98%)	2 (2%)	45	71
32	i	310/311 (100%)	310 (100%)	0	100	100
33	j	100/100 (100%)	100 (100%)	0	100	100
34	k	85/85 (100%)	85 (100%)	0	100	100
35	l	539/540 (100%)	538 (100%)	1 (0%)	87	89
36	m	130/141 (92%)	129 (99%)	1 (1%)	73	82
37	n	53/53 (100%)	53 (100%)	0	100	100
38	o	113/113 (100%)	113 (100%)	0	100	100
39	p	159/159 (100%)	159 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	r	410/410 (100%)	410 (100%)	0	100	100
41	s	275/275 (100%)	274 (100%)	1 (0%)	84	86
42	u	153/153 (100%)	149 (97%)	4 (3%)	40	69
43	v	104/111 (94%)	104 (100%)	0	100	100
44	w	283/283 (100%)	283 (100%)	0	100	100
All	All	7156/7240 (99%)	7135 (100%)	21 (0%)	84	88

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	E	101	THR
9	J	76	MET
11	L	152	VAL
12	M	530	TYR
12	M	677	GLN
14	O	166	ASP
19	U	32	LEU
22	Y	78	ASP
24	a	185	THR
25	b	120	MET
26	c	122	THR
30	g	113	GLU
31	h	21	GLN
31	h	97	HIS
35	l	249	SER
36	m	56	VAL
41	s	20	LEU
42	u	46	CYS
42	u	47	ARG
42	u	64	ASN
42	u	121	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (61) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	303	HIS
4	E	108	HIS
5	F	62	GLN
5	F	73	GLN

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Mol	Chain	Res	Type
9	J	128	ASN
10	K	79	HIS
10	K	100	GLN
11	L	71	HIS
12	M	278	HIS
12	M	334	GLN
12	M	540	ASN
12	M	652	ASN
13	N	31	ASN
14	O	131	HIS
14	O	153	GLN
15	P	77	GLN
15	P	124	ASN
15	P	228	GLN
16	Q	233	HIS
16	Q	285	ASN
17	S	61	HIS
20	V	89	ASN
6	X	142	GLN
22	Y	49	GLN
22	Y	75	HIS
23	Z	21	GLN
23	Z	33	GLN
23	Z	91	GLN
24	a	90	ASN
24	a	189	ASN
25	b	26	GLN
26	c	94	HIS
26	c	127	ASN
27	d	149	HIS
32	i	83	GLN
32	i	120	GLN
32	i	144	GLN
32	i	174	GLN
32	i	316	GLN
33	j	28	ASN
34	k	7	ASN
35	l	170	GLN
35	l	309	GLN
35	l	348	HIS
35	l	447	ASN
35	l	470	ASN

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Mol	Chain	Res	Type
35	l	579	ASN
38	o	50	GLN
40	r	43	ASN
40	r	251	ASN
40	r	279	GLN
40	r	304	GLN
40	r	338	HIS
41	s	171	HIS
41	s	194	ASN
42	u	30	HIS
42	u	65	GLN
42	u	163	HIS
43	v	55	GLN
44	w	300	ASN
44	w	322	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
16	2MR	Q	118	16	10,12,13	1.96	1 (10%)	5,13,15	5.92	3 (60%)

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
16	2MR	Q	118	16	-	2/10/13/15	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	Q	118	2MR	CZ-NE	5.62	1.46	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	118	2MR	NE-CZ-NH2	12.11	130.58	119.48
16	Q	118	2MR	CD-NE-CZ	4.16	131.19	123.41
16	Q	118	2MR	CQ2-NH2-CZ	3.18	130.90	123.86

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	Q	118	2MR	NE-CD-CG-CB
16	Q	118	2MR	CA-CB-CG-CD

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 44 ligands modelled in this entry, 2 are monoatomic - leaving 42 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
46	FMN	A	502	-	33,33,33	1.10	2 (6%)	48,50,50	1.23	8 (16%)
48	PLX	N	201	-	51,51,51	1.15	4 (7%)	55,59,59	0.61	1 (1%)
45	SF4	B	301	2	0,12,12	-	-	-	-	-
50	8Q1	X	201	-	31,34,34	1.69	6 (19%)	40,43,43	1.56	8 (20%)
54	CDL	s	401	-	88,88,99	1.13	8 (9%)	94,100,111	0.91	4 (4%)
45	SF4	A	501	1	0,12,12	-	-	-	-	-
54	CDL	r	503	-	99,99,99	1.08	8 (8%)	105,111,111	0.87	4 (3%)
45	SF4	B	302	2	0,12,12	-	-	-	-	-
47	PEE	r	501	-	50,50,50	1.16	6 (12%)	53,55,55	0.96	2 (3%)
54	CDL	l	703	-	99,99,99	1.08	8 (8%)	105,111,111	0.85	4 (3%)
54	CDL	V	202	-	99,99,99	1.09	8 (8%)	105,111,111	0.87	4 (3%)
47	PEE	Q	501	-	46,46,50	1.20	6 (13%)	49,51,55	1.01	2 (4%)
48	PLX	C	303	-	51,51,51	1.14	4 (7%)	55,59,59	0.61	1 (1%)
48	PLX	J	403	-	51,51,51	1.14	4 (7%)	55,59,59	0.60	1 (1%)
54	CDL	m	201	-	99,99,99	1.09	8 (8%)	105,111,111	0.85	4 (3%)
47	PEE	l	704	-	50,50,50	1.16	6 (12%)	53,55,55	0.94	2 (3%)
47	PEE	j	202	-	40,40,50	1.15	5 (12%)	43,45,55	1.00	2 (4%)
47	PEE	b	201	-	45,45,50	1.22	6 (13%)	48,50,55	1.00	2 (4%)
45	SF4	C	301	3	0,12,12	-	-	-	-	-
45	SF4	M	802	12	0,12,12	-	-	-	-	-
56	ADP	w	401	-	27,29,29	2.97	8 (29%)	42,45,45	2.02	10 (23%)
54	CDL	l	702	-	98,98,99	1.08	8 (8%)	104,110,111	0.90	4 (3%)
51	NDP	J	401	-	49,52,52	4.39	23 (46%)	66,80,80	2.17	13 (19%)
48	PLX	j	203	-	51,51,51	1.15	4 (7%)	55,59,59	0.59	1 (1%)
47	PEE	W	201	-	40,40,50	1.14	5 (12%)	43,45,55	1.03	2 (4%)
45	SF4	M	801	12	0,12,12	-	-	-	-	-
54	CDL	n	101	-	54,54,99	1.35	8 (14%)	60,66,111	1.11	4 (6%)
48	PLX	g	201	-	51,51,51	1.13	3 (5%)	55,59,59	0.65	1 (1%)
48	PLX	a	202	-	51,51,51	1.15	4 (7%)	55,59,59	0.58	1 (1%)
48	PLX	r	502	-	51,51,51	1.14	4 (7%)	55,59,59	0.59	1 (1%)
49	UQ	J	402	-	33,33,63	3.45	9 (27%)	40,43,79	2.79	13 (32%)
49	UQ	C	304	-	63,63,63	3.66	14 (22%)	76,79,79	3.11	31 (40%)
47	PEE	C	302	-	46,46,50	1.20	6 (13%)	49,51,55	1.01	2 (4%)
50	8Q1	G	201	6	31,34,34	1.69	6 (19%)	40,43,43	1.55	7 (17%)
54	CDL	a	201	-	99,99,99	1.09	8 (8%)	105,111,111	0.85	4 (3%)
47	PEE	l	701	-	39,39,50	1.31	6 (15%)	41,44,55	1.04	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	FES	M	803	12	0,4,4	-	-	-		
52	FES	O	301	14	0,4,4	-	-	-		
54	CDL	N	202	-	50,50,99	1.41	8 (16%)	56,62,111	1.14	4 (7%)
54	CDL	V	201	-	93,93,99	1.11	9 (9%)	99,105,111	0.87	4 (4%)
47	PEE	Q	502	-	50,50,50	1.15	6 (12%)	53,55,55	0.98	2 (3%)
47	PEE	j	201	-	50,50,50	1.16	6 (12%)	53,55,55	0.96	2 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
46	FMN	A	502	-	-	5/18/18/18	0/3/3/3
48	PLX	N	201	-	-	29/55/55/55	-
50	8Q1	X	201	-	-	15/41/41/41	-
54	CDL	s	401	-	-	57/99/99/110	-
45	SF4	B	301	2	-	-	0/6/5/5
45	SF4	A	501	1	-	-	0/6/5/5
54	CDL	r	503	-	-	55/110/110/110	-
45	SF4	B	302	2	-	-	0/6/5/5
47	PEE	r	501	-	-	29/54/54/54	-
54	CDL	l	703	-	-	57/110/110/110	-
54	CDL	V	202	-	-	53/110/110/110	-
47	PEE	Q	501	-	-	21/50/50/54	-
48	PLX	C	303	-	-	29/55/55/55	-
48	PLX	J	403	-	-	34/55/55/55	-
54	CDL	m	201	-	-	66/110/110/110	-
47	PEE	l	704	-	-	25/54/54/54	-
47	PEE	j	202	-	-	20/44/44/54	-
47	PEE	b	201	-	-	28/49/49/54	-
45	SF4	C	301	3	-	-	0/6/5/5
45	SF4	M	802	12	-	-	0/6/5/5
56	ADP	w	401	-	-	3/16/32/32	0/3/3/3
54	CDL	l	702	-	-	58/109/109/110	-
51	NDP	J	401	-	-	7/34/77/77	0/4/5/5
48	PLX	j	203	-	-	28/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	PEE	W	201	-	-	23/44/44/54	-
45	SF4	M	801	12	-	-	0/6/5/5
54	CDL	n	101	-	-	29/65/65/110	-
48	PLX	g	201	-	-	29/55/55/55	-
48	PLX	r	502	-	-	28/55/55/55	-
48	PLX	a	202	-	-	30/55/55/55	-
49	UQ	J	402	-	-	15/27/51/87	0/1/1/1
49	UQ	C	304	-	-	27/63/87/87	0/1/1/1
47	PEE	C	302	-	-	33/50/50/54	-
50	8Q1	G	201	6	-	11/41/41/41	-
54	CDL	a	201	-	-	58/110/110/110	-
47	PEE	l	701	-	-	25/43/43/54	-
52	FES	M	803	12	-	-	0/1/1/1
52	FES	O	301	14	-	-	0/1/1/1
54	CDL	N	202	-	-	29/61/61/110	-
54	CDL	V	201	-	-	49/104/104/110	-
47	PEE	Q	502	-	-	21/54/54/54	-
47	PEE	j	201	-	-	25/54/54/54	-

All (234) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	J	401	NDP	C3B-C2B	-13.02	1.23	1.52
51	J	401	NDP	C6N-C5N	12.48	1.55	1.33
51	J	401	NDP	O4D-C4D	10.61	1.68	1.45
51	J	401	NDP	C3D-C4D	-9.95	1.27	1.53
49	C	304	UQ	C18-C19	9.65	1.56	1.33
49	J	402	UQ	C18-C19	9.63	1.56	1.33
49	C	304	UQ	C13-C14	9.36	1.55	1.33
49	J	402	UQ	C13-C14	9.25	1.55	1.33
49	C	304	UQ	C23-C24	9.13	1.54	1.33
49	J	402	UQ	C8-C9	9.00	1.54	1.33
49	C	304	UQ	C8-C9	8.96	1.54	1.33
56	w	401	ADP	C3'-C4'	-8.88	1.30	1.53
49	C	304	UQ	C28-C29	8.84	1.54	1.33
49	C	304	UQ	C33-C34	8.57	1.53	1.33
49	C	304	UQ	C43-C44	8.34	1.53	1.33
49	C	304	UQ	C38-C39	8.29	1.52	1.33
51	J	401	NDP	O4B-C4B	-7.94	1.27	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	C	304	UQ	C48-C49	7.92	1.52	1.33
49	J	402	UQ	C23-C24	7.84	1.54	1.32
56	w	401	ADP	O4'-C4'	7.67	1.62	1.45
49	C	304	UQ	C53-C54	7.42	1.53	1.32
51	J	401	NDP	C2N-C3N	7.25	1.55	1.34
51	J	401	NDP	C6A-N6A	5.91	1.49	1.34
51	J	401	NDP	P2B-O2B	5.55	1.69	1.59
56	w	401	ADP	C6-N6	5.55	1.48	1.34
50	X	201	8Q1	C34-N36	5.43	1.45	1.33
50	G	201	8Q1	C34-N36	5.40	1.45	1.33
50	G	201	8Q1	C39-N41	5.30	1.45	1.33
50	X	201	8Q1	C39-N41	5.28	1.45	1.33
51	J	401	NDP	C3B-C4B	5.24	1.66	1.53
51	J	401	NDP	O4D-C1D	-4.89	1.30	1.42
51	J	401	NDP	C6N-N1N	4.80	1.49	1.37
51	J	401	NDP	O4B-C1B	4.55	1.52	1.42
51	J	401	NDP	C1B-N9A	-4.52	1.33	1.46
56	w	401	ADP	O4'-C1'	-4.49	1.31	1.42
51	J	401	NDP	O2D-C2D	-4.29	1.32	1.43
51	J	401	NDP	C7N-N7N	4.20	1.44	1.33
46	A	502	FMN	C4A-N5	3.77	1.38	1.30
47	l	704	PEE	C18-C19	3.74	1.53	1.31
47	Q	502	PEE	C18-C19	3.73	1.53	1.31
47	j	202	PEE	C18-C19	3.73	1.53	1.31
47	r	501	PEE	C18-C19	3.73	1.53	1.31
47	C	302	PEE	C18-C19	3.73	1.53	1.31
47	j	201	PEE	C18-C19	3.73	1.53	1.31
47	l	701	PEE	C18-C19	3.73	1.53	1.31
47	b	201	PEE	C18-C19	3.73	1.53	1.31
47	Q	501	PEE	C18-C19	3.71	1.53	1.31
47	W	201	PEE	C18-C19	3.71	1.53	1.31
47	C	302	PEE	C39-C38	3.65	1.52	1.31
47	l	701	PEE	C39-C38	3.65	1.52	1.31
47	b	201	PEE	C39-C38	3.63	1.52	1.31
47	r	501	PEE	C39-C38	3.63	1.52	1.31
47	l	704	PEE	C39-C38	3.63	1.52	1.31
47	Q	502	PEE	C39-C38	3.63	1.52	1.31
47	j	201	PEE	C39-C38	3.63	1.52	1.31
47	Q	501	PEE	C39-C38	3.63	1.52	1.31
54	V	201	CDL	OA8-CA7	3.46	1.43	1.33
54	V	202	CDL	OA8-CA7	3.44	1.43	1.33
54	s	401	CDL	OA8-CA7	3.43	1.43	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	N	202	CDL	OA8-CA7	3.43	1.43	1.33
54	m	201	CDL	OA8-CA7	3.42	1.43	1.33
54	l	702	CDL	OA8-CA7	3.42	1.43	1.33
54	a	201	CDL	OA8-CA7	3.40	1.43	1.33
54	n	101	CDL	OA8-CA7	3.39	1.43	1.33
54	r	503	CDL	OA8-CA7	3.38	1.43	1.33
56	w	401	ADP	O2'-C2'	-3.37	1.35	1.43
54	l	703	CDL	OA8-CA7	3.36	1.43	1.33
56	w	401	ADP	C8-N9	-3.23	1.31	1.37
56	w	401	ADP	O3'-C3'	3.12	1.50	1.43
54	m	201	CDL	OA6-CA5	3.12	1.43	1.34
51	J	401	NDP	C8A-N9A	-3.10	1.32	1.37
54	a	201	CDL	OB6-CB5	3.09	1.43	1.34
54	V	201	CDL	OA6-CA5	3.08	1.43	1.34
54	r	503	CDL	OB6-CB5	3.06	1.42	1.34
51	J	401	NDP	O3D-C3D	3.05	1.50	1.43
54	V	202	CDL	OB6-CB5	3.04	1.42	1.34
54	N	202	CDL	OB6-CB5	3.03	1.42	1.34
54	s	401	CDL	OB6-CB5	3.03	1.42	1.34
54	N	202	CDL	OB8-CB7	3.02	1.42	1.33
54	a	201	CDL	OB8-CB7	3.02	1.42	1.33
54	l	702	CDL	OB6-CB5	3.01	1.42	1.34
54	r	503	CDL	OB8-CB7	3.01	1.42	1.33
54	m	201	CDL	OB8-CB7	3.01	1.42	1.33
54	m	201	CDL	OB6-CB5	3.01	1.42	1.34
54	V	201	CDL	OB8-CB7	2.98	1.42	1.33
54	l	703	CDL	OB6-CB5	2.98	1.42	1.34
54	V	202	CDL	OA6-CA5	2.97	1.42	1.34
54	n	101	CDL	OB6-CB5	2.97	1.42	1.34
54	l	703	CDL	OA6-CA5	2.96	1.42	1.34
54	s	401	CDL	OA6-CA5	2.96	1.42	1.34
54	V	201	CDL	OB6-CB5	2.95	1.42	1.34
54	n	101	CDL	OB8-CB7	2.95	1.42	1.33
54	n	101	CDL	OA6-CA5	2.95	1.42	1.34
54	N	202	CDL	OA6-CA5	2.94	1.42	1.34
51	J	401	NDP	C7N-C3N	2.94	1.55	1.48
54	l	702	CDL	OB8-CB7	2.94	1.41	1.33
54	V	202	CDL	OB8-CB7	2.94	1.41	1.33
54	a	201	CDL	OA6-CA5	2.94	1.42	1.34
54	l	703	CDL	OB8-CB7	2.93	1.41	1.33
51	J	401	NDP	C5A-N7A	-2.93	1.33	1.39
54	s	401	CDL	OB8-CB7	2.87	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	r	503	CDL	OA6-CA5	2.84	1.42	1.34
54	l	702	CDL	OA6-CA5	2.82	1.42	1.34
48	a	202	PLX	O6-C4	-2.78	1.40	1.44
48	C	303	PLX	O6-C4	-2.74	1.40	1.44
48	r	502	PLX	O6-C4	-2.70	1.41	1.44
49	J	402	UQ	C6-C1	2.69	1.54	1.46
49	C	304	UQ	C6-C1	2.68	1.54	1.46
48	g	201	PLX	O6-C4	-2.68	1.41	1.44
48	j	203	PLX	O6-C4	-2.65	1.41	1.44
48	N	201	PLX	O6-C4	-2.63	1.41	1.44
47	l	701	PEE	O3-C30	2.48	1.40	1.33
54	r	503	CDL	OA6-CA4	-2.48	1.40	1.46
48	J	403	PLX	O6-C4	-2.47	1.41	1.44
47	r	501	PEE	O2-C2	-2.46	1.40	1.46
47	Q	502	PEE	O2-C2	-2.46	1.40	1.46
47	b	201	PEE	O3-C30	2.46	1.40	1.33
47	Q	501	PEE	O2-C2	-2.44	1.40	1.46
47	C	302	PEE	O2-C2	-2.44	1.40	1.46
47	W	201	PEE	O2-C2	-2.44	1.40	1.46
54	l	702	CDL	OA6-CA4	-2.44	1.40	1.46
47	j	201	PEE	O3-C30	2.44	1.40	1.33
47	j	202	PEE	O3-C30	2.44	1.40	1.33
48	j	203	PLX	C7-C6	2.44	1.55	1.50
47	C	302	PEE	O3-C30	2.43	1.40	1.33
54	a	201	CDL	OA6-CA4	-2.43	1.40	1.46
47	Q	502	PEE	O3-C30	2.42	1.40	1.33
47	r	501	PEE	O3-C30	2.42	1.40	1.33
47	l	704	PEE	O2-C2	-2.42	1.40	1.46
49	C	304	UQ	C7-C8	2.42	1.54	1.50
47	j	201	PEE	O2-C2	-2.41	1.40	1.46
54	n	101	CDL	OA6-CA4	-2.41	1.40	1.46
54	N	202	CDL	OA6-CA4	-2.40	1.40	1.46
47	j	202	PEE	O2-C2	-2.40	1.40	1.46
54	s	401	CDL	OA6-CA4	-2.40	1.40	1.46
54	l	703	CDL	OA6-CA4	-2.40	1.40	1.46
49	J	402	UQ	C7-C8	2.39	1.54	1.50
47	l	701	PEE	O2-C2	-2.39	1.40	1.46
54	V	202	CDL	OA6-CA4	-2.39	1.40	1.46
47	l	704	PEE	O3-C30	2.38	1.40	1.33
48	J	403	PLX	C7-C6	2.38	1.55	1.50
47	Q	501	PEE	O3-C30	2.37	1.40	1.33
47	W	201	PEE	O3-C30	2.37	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	X	201	8Q1	C1-S44	2.37	1.81	1.76
48	r	502	PLX	C7-C6	2.37	1.55	1.50
46	A	502	FMN	C10-N1	2.34	1.38	1.33
48	g	201	PLX	C7-C6	2.34	1.55	1.50
51	J	401	NDP	O2B-C2B	2.33	1.52	1.44
48	N	201	PLX	C7-C6	2.33	1.55	1.50
47	b	201	PEE	O2-C2	-2.33	1.40	1.46
50	G	201	8Q1	C1-S44	2.32	1.81	1.76
50	G	201	8Q1	O35-C34	-2.30	1.18	1.23
51	J	401	NDP	C2D-C3D	2.30	1.59	1.53
47	l	704	PEE	O2-C10	2.30	1.40	1.34
47	b	201	PEE	O2-C10	2.29	1.40	1.34
48	C	303	PLX	C7-C6	2.28	1.55	1.50
50	X	201	8Q1	O40-C39	-2.28	1.18	1.23
47	j	202	PEE	O2-C10	2.27	1.40	1.34
48	a	202	PLX	C7-C6	2.27	1.55	1.50
54	V	201	CDL	PB2-OB2	2.27	1.68	1.59
50	G	201	8Q1	O40-C39	-2.27	1.18	1.23
47	W	201	PEE	O2-C10	2.26	1.40	1.34
54	l	703	CDL	OB6-CB4	-2.26	1.41	1.46
54	V	202	CDL	PB2-OB2	2.25	1.68	1.59
56	w	401	ADP	C5-N7	-2.25	1.34	1.39
54	V	201	CDL	OB6-CB4	-2.24	1.41	1.46
50	X	201	8Q1	O35-C34	-2.24	1.18	1.23
54	n	101	CDL	OB6-CB4	-2.24	1.41	1.46
47	Q	501	PEE	O2-C10	2.24	1.40	1.34
47	j	201	PEE	O2-C10	2.24	1.40	1.34
47	l	701	PEE	O2-C10	2.23	1.40	1.34
54	N	202	CDL	PB2-OB2	2.21	1.68	1.59
49	C	304	UQ	O4-C4	-2.21	1.18	1.23
47	Q	502	PEE	O2-C10	2.21	1.40	1.34
47	r	501	PEE	O2-C10	2.21	1.40	1.34
47	C	302	PEE	O2-C10	2.20	1.40	1.34
54	n	101	CDL	PB2-OB2	2.20	1.68	1.59
47	l	704	PEE	O3-C3	-2.20	1.40	1.45
54	l	703	CDL	PB2-OB2	2.20	1.68	1.59
50	G	201	8Q1	C6-C1	2.20	1.53	1.50
54	a	201	CDL	PB2-OB2	2.20	1.68	1.59
49	J	402	UQ	O4-C4	-2.20	1.18	1.23
54	m	201	CDL	OA6-CA4	-2.19	1.41	1.46
54	l	702	CDL	PB2-OB2	2.19	1.68	1.59
54	m	201	CDL	OB6-CB4	-2.19	1.41	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	s	401	CDL	OB6-CB4	-2.19	1.41	1.46
54	s	401	CDL	PB2-OB2	2.18	1.68	1.59
54	m	201	CDL	PB2-OB2	2.18	1.68	1.59
54	a	201	CDL	PB2-OB5	2.17	1.68	1.59
48	N	201	PLX	P1-O4	2.17	1.68	1.59
54	l	702	CDL	PB2-OB5	2.16	1.68	1.59
54	r	503	CDL	PB2-OB2	2.16	1.68	1.59
54	N	202	CDL	PB2-OB5	2.16	1.68	1.59
54	l	702	CDL	OB6-CB4	-2.15	1.41	1.46
54	V	201	CDL	PB2-OB5	2.15	1.68	1.59
54	m	201	CDL	PB2-OB5	2.15	1.68	1.59
50	X	201	8Q1	C6-C1	2.14	1.53	1.50
54	V	202	CDL	PB2-OB5	2.14	1.68	1.59
54	r	503	CDL	OB6-CB4	-2.14	1.41	1.46
47	Q	501	PEE	O3-C3	-2.14	1.40	1.45
54	V	202	CDL	OB6-CB4	-2.13	1.41	1.46
54	N	202	CDL	OB6-CB4	-2.13	1.41	1.46
47	W	201	PEE	O3-C3	-2.13	1.40	1.45
48	j	203	PLX	P1-O4	2.13	1.67	1.59
54	a	201	CDL	OB6-CB4	-2.12	1.41	1.46
48	a	202	PLX	P1-O4	2.12	1.67	1.59
54	V	201	CDL	OA6-CA4	-2.12	1.41	1.46
51	J	401	NDP	O7N-C7N	-2.12	1.19	1.24
54	r	503	CDL	PB2-OB5	2.12	1.67	1.59
48	C	303	PLX	P1-O4	2.11	1.67	1.59
54	n	101	CDL	PB2-OB5	2.11	1.67	1.59
54	s	401	CDL	PB2-OB5	2.11	1.67	1.59
48	g	201	PLX	P1-O4	2.11	1.67	1.59
48	r	502	PLX	P1-O4	2.11	1.67	1.59
48	J	403	PLX	P1-O4	2.10	1.67	1.59
54	l	703	CDL	PB2-OB5	2.10	1.67	1.59
47	j	201	PEE	O3-C3	-2.10	1.40	1.45
47	r	501	PEE	O3-C3	-2.10	1.40	1.45
47	Q	502	PEE	O3-C3	-2.09	1.40	1.45
51	J	401	NDP	PA-O5B	2.08	1.67	1.59
47	b	201	PEE	O3-C3	-2.07	1.40	1.45
47	l	701	PEE	O3-C3	-2.07	1.40	1.45
47	C	302	PEE	O3-C3	-2.07	1.40	1.45
47	j	202	PEE	O3-C3	-2.07	1.40	1.45
48	N	201	PLX	P1-O1	2.06	1.67	1.59
49	J	402	UQ	O1-C1	-2.04	1.18	1.23
49	J	402	UQ	C21-C19	2.04	1.55	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	a	202	PLX	P1-O1	2.03	1.67	1.59
48	j	203	PLX	P1-O1	2.02	1.67	1.59
48	C	303	PLX	P1-O1	2.02	1.67	1.59
49	C	304	UQ	C21-C19	2.02	1.55	1.51
48	r	502	PLX	P1-O1	2.01	1.67	1.59
48	J	403	PLX	P1-O1	2.01	1.67	1.59
54	V	201	CDL	C11-CA5	2.01	1.56	1.50

All (157) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	J	401	NDP	C3N-C2N-N1N	-8.74	110.63	123.10
49	J	402	UQ	C7-C8-C9	-8.22	113.10	126.79
49	C	304	UQ	C7-C8-C9	-7.56	114.21	126.79
49	C	304	UQ	C42-C43-C44	-6.35	112.36	127.66
51	J	401	NDP	C1D-N1N-C2N	-6.33	110.56	121.11
49	J	402	UQ	C12-C13-C14	-6.21	112.71	127.66
49	C	304	UQ	C47-C48-C49	-6.15	112.84	127.66
49	C	304	UQ	C22-C23-C24	-6.08	113.01	127.66
49	J	402	UQ	C17-C18-C19	-5.96	113.32	127.66
49	C	304	UQ	C37-C38-C39	-5.96	113.32	127.66
49	C	304	UQ	C27-C28-C29	-5.91	113.44	127.66
51	J	401	NDP	C5A-C4A-N3A	-5.85	119.11	126.75
50	G	201	8Q1	C6-C1-S44	5.77	120.17	113.46
49	C	304	UQ	C12-C13-C14	-5.76	113.79	127.66
56	w	401	ADP	C5-C4-N3	-5.73	119.28	126.75
49	C	304	UQ	C32-C33-C34	-5.62	114.12	127.66
50	X	201	8Q1	C6-C1-S44	5.58	119.96	113.46
49	C	304	UQ	C17-C18-C19	-5.46	114.52	127.66
51	J	401	NDP	C1D-N1N-C6N	-4.76	110.57	120.83
49	C	304	UQ	C30-C29-C28	-4.71	111.59	123.68
56	w	401	ADP	N3-C2-N1	-4.48	121.59	128.60
49	C	304	UQ	C45-C44-C43	-4.46	112.23	123.68
49	C	304	UQ	C31-C29-C28	-4.42	112.17	121.12
56	w	401	ADP	N3-C4-N9	4.37	134.28	127.08
49	J	402	UQ	C22-C23-C24	-4.36	112.86	127.75
49	J	402	UQ	C21-C19-C18	-4.35	112.31	121.12
49	C	304	UQ	C41-C39-C38	-4.33	112.36	121.12
49	C	304	UQ	C40-C39-C38	-4.31	112.62	123.68
49	C	304	UQ	C21-C19-C18	-4.29	112.43	121.12
49	C	304	UQ	C50-C49-C48	-4.28	112.70	123.68
49	J	402	UQ	C15-C14-C13	-4.24	112.81	123.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	C	304	UQ	C20-C19-C18	-4.20	112.89	123.68
49	J	402	UQ	C20-C19-C18	-4.20	112.91	123.68
49	C	304	UQ	C10-C9-C8	-4.19	112.93	123.68
49	C	304	UQ	C51-C49-C48	-4.16	112.69	121.12
49	J	402	UQ	C11-C9-C8	-4.15	112.72	121.12
49	C	304	UQ	C52-C53-C54	-4.13	113.64	127.75
47	b	201	PEE	O2-C10-C11	4.12	120.39	111.50
49	J	402	UQ	C10-C9-C8	-4.10	113.16	123.68
54	l	702	CDL	OB6-CB5-C51	4.09	120.31	111.50
54	a	201	CDL	OB6-CB5-C51	4.08	120.29	111.50
49	C	304	UQ	C36-C34-C33	-4.07	112.88	121.12
51	J	401	NDP	N3A-C4A-N9A	4.07	133.78	127.08
47	W	201	PEE	O2-C10-C11	4.05	120.24	111.50
54	l	702	CDL	OA6-CA5-C11	4.05	120.23	111.50
54	s	401	CDL	OB6-CB5-C51	4.05	120.23	111.50
47	j	201	PEE	O2-C10-C11	4.03	120.19	111.50
47	C	302	PEE	O2-C10-C11	4.03	120.18	111.50
49	C	304	UQ	C11-C9-C8	-4.02	112.99	121.12
47	Q	502	PEE	O2-C10-C11	4.02	120.16	111.50
54	V	201	CDL	OA6-CA5-C11	4.01	120.15	111.50
54	n	101	CDL	OA6-CA5-C11	4.00	120.13	111.50
49	J	402	UQ	C16-C14-C13	-3.99	113.04	121.12
54	N	202	CDL	OB6-CB5-C51	3.99	120.11	111.50
49	C	304	UQ	C25-C24-C23	-3.99	113.44	123.68
54	s	401	CDL	OA6-CA5-C11	3.99	120.09	111.50
54	r	503	CDL	OA6-CA5-C11	3.98	120.09	111.50
49	C	304	UQ	C46-C44-C43	-3.98	113.06	121.12
47	j	202	PEE	O2-C10-C11	3.97	120.06	111.50
54	V	202	CDL	OB6-CB5-C51	3.97	120.05	111.50
51	J	401	NDP	N3A-C2A-N1A	-3.96	122.41	128.60
54	m	201	CDL	OB6-CB5-C51	3.96	120.03	111.50
54	V	202	CDL	OA6-CA5-C11	3.94	120.00	111.50
54	N	202	CDL	OA6-CA5-C11	3.94	120.00	111.50
47	r	501	PEE	O2-C10-C11	3.93	119.97	111.50
54	l	703	CDL	OA6-CA5-C11	3.91	119.92	111.50
54	V	201	CDL	OB6-CB5-C51	3.89	119.89	111.50
47	Q	501	PEE	O2-C10-C11	3.89	119.89	111.50
47	l	701	PEE	O2-C10-C11	3.89	119.87	111.50
49	C	304	UQ	C15-C14-C13	-3.86	113.77	123.68
47	l	704	PEE	O2-C10-C11	3.85	119.81	111.50
54	r	503	CDL	OB6-CB5-C51	3.83	119.75	111.50
54	n	101	CDL	OB6-CB5-C51	3.81	119.70	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	C	304	UQ	C35-C34-C33	-3.75	114.06	123.68
54	a	201	CDL	OA6-CA5-C11	3.74	119.56	111.50
56	w	401	ADP	C2-N3-C4	3.72	120.55	111.75
51	J	401	NDP	C2A-N3A-C4A	3.70	120.50	111.75
49	C	304	UQ	C26-C24-C23	-3.65	113.72	121.12
54	l	703	CDL	OB6-CB5-C51	3.64	119.35	111.50
56	w	401	ADP	N9-C8-N7	-3.63	108.95	113.91
54	m	201	CDL	OA6-CA5-C11	3.61	119.28	111.50
49	C	304	UQ	C16-C14-C13	-3.57	113.90	121.12
56	w	401	ADP	C5-N7-C8	3.47	108.44	103.51
49	C	304	UQ	C55-C54-C53	-3.39	112.84	122.65
50	G	201	8Q1	O4-C1-C6	-3.38	120.00	123.99
51	J	401	NDP	C5A-N7A-C8A	3.35	108.27	103.51
50	X	201	8Q1	O4-C1-C6	-3.35	120.03	123.99
49	J	402	UQ	C25-C24-C23	-3.31	113.07	122.65
49	J	402	UQ	C26-C24-C23	-3.31	113.07	122.65
51	J	401	NDP	N9A-C8A-N7A	-3.28	109.43	113.91
46	A	502	FMN	C4-N3-C2	-3.20	119.73	125.64
54	n	101	CDL	OA8-CA7-C31	3.18	119.71	111.38
49	C	304	UQ	C56-C54-C53	-3.12	113.63	122.65
51	J	401	NDP	C4A-C5A-N7A	-3.09	106.86	110.62
56	w	401	ADP	C4-N9-C8	3.09	109.07	105.73
51	J	401	NDP	PN-O3-PA	-2.91	122.84	132.83
56	w	401	ADP	C4-C5-N7	-2.89	107.10	110.62
50	G	201	8Q1	C37-C38-C39	2.83	117.08	112.36
47	r	501	PEE	O3-C30-C31	2.78	120.63	111.91
47	Q	502	PEE	O3-C30-C31	2.77	120.60	111.91
54	r	503	CDL	OB8-CB7-C71	2.74	120.50	111.91
49	C	304	UQ	CM5-C5-C6	-2.73	119.94	124.40
54	m	201	CDL	OB8-CB7-C71	2.72	120.45	111.91
54	m	201	CDL	OA8-CA7-C31	2.72	120.44	111.91
54	l	702	CDL	OA8-CA7-C31	2.70	120.37	111.91
46	A	502	FMN	C4A-C4-N3	2.69	120.01	113.19
54	V	202	CDL	OB8-CB7-C71	2.68	120.32	111.91
50	X	201	8Q1	C38-C39-N41	2.68	120.93	116.42
54	a	201	CDL	OB8-CB7-C71	2.66	120.26	111.91
47	W	201	PEE	O3-C30-C31	2.65	120.23	111.91
54	N	202	CDL	OA8-CA7-C31	2.65	120.23	111.91
47	Q	501	PEE	O3-C30-C31	2.64	120.20	111.91
47	C	302	PEE	O3-C30-C31	2.64	120.18	111.91
54	V	202	CDL	OA8-CA7-C31	2.63	120.15	111.91
47	j	202	PEE	O3-C30-C31	2.62	120.14	111.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	l	701	PEE	O3-C30-C31	2.62	120.12	111.91
48	g	201	PLX	C1A-N1-C1	2.62	120.62	109.92
54	l	702	CDL	OB8-CB7-C71	2.61	120.09	111.91
47	l	704	PEE	O3-C30-C31	2.60	120.08	111.91
54	n	101	CDL	OB8-CB7-C71	2.60	120.08	111.91
54	V	201	CDL	OB8-CB7-C71	2.60	120.07	111.91
54	s	401	CDL	OA8-CA7-C31	2.60	120.07	111.91
56	w	401	ADP	PA-O3A-PB	-2.59	123.94	132.83
54	N	202	CDL	OB8-CB7-C71	2.59	120.03	111.91
54	l	703	CDL	OB8-CB7-C71	2.58	120.01	111.91
47	b	201	PEE	O3-C30-C31	2.57	119.98	111.91
47	j	201	PEE	O3-C30-C31	2.57	119.97	111.91
54	a	201	CDL	OA8-CA7-C31	2.57	119.96	111.91
54	r	503	CDL	OA8-CA7-C31	2.54	119.86	111.91
46	A	502	FMN	O4-C4-C4A	-2.53	119.88	126.60
54	l	703	CDL	OA8-CA7-C31	2.51	119.79	111.91
56	w	401	ADP	C4'-O4'-C1'	-2.50	103.95	109.47
46	A	502	FMN	C4A-C10-N10	2.47	120.09	116.48
49	J	402	UQ	CM5-C5-C6	-2.46	120.38	124.40
54	s	401	CDL	OB8-CB7-C71	2.44	119.57	111.91
54	V	201	CDL	OA8-CA7-C31	2.43	119.52	111.91
50	G	201	8Q1	C38-C39-N41	2.41	120.48	116.42
51	J	401	NDP	C4A-N9A-C8A	2.41	108.34	105.73
50	X	201	8Q1	C42-N41-C39	-2.40	118.37	122.84
48	r	502	PLX	C1A-N1-C1	2.39	119.69	109.92
48	j	203	PLX	C1A-N1-C1	2.39	119.68	109.92
48	N	201	PLX	C1A-N1-C1	2.38	119.65	109.92
50	X	201	8Q1	C37-C38-C39	2.37	116.30	112.36
48	a	202	PLX	C1A-N1-C1	2.33	119.45	109.92
48	C	303	PLX	C1A-N1-C1	2.30	119.33	109.92
46	A	502	FMN	C4A-C10-N1	-2.29	119.42	124.73
48	J	403	PLX	C1A-N1-C1	2.27	119.19	109.92
51	J	401	NDP	C2B-C1B-N9A	-2.23	109.77	113.53
50	G	201	8Q1	C43-S44-C1	2.21	108.76	101.87
46	A	502	FMN	C10-C4A-N5	-2.21	120.17	124.86
50	X	201	8Q1	C43-S44-C1	2.19	108.70	101.87
50	G	201	8Q1	O4-C1-S44	-2.15	119.83	122.61
46	A	502	FMN	C9A-C5A-N5	-2.14	120.10	122.43
46	A	502	FMN	C5A-C9A-N10	2.14	120.16	117.95
50	G	201	8Q1	C42-N41-C39	-2.06	119.01	122.84
50	X	201	8Q1	C32-C34-N36	2.04	120.63	116.58
50	X	201	8Q1	O4-C1-S44	-2.00	120.01	122.61

There are no chirality outliers.

All (1051) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	A	502	FMN	N10-C1'-C2'-O2'
46	A	502	FMN	N10-C1'-C2'-C3'
46	A	502	FMN	C5'-O5'-P-O1P
46	A	502	FMN	C5'-O5'-P-O2P
47	C	302	PEE	C11-C10-O2-C2
47	C	302	PEE	C1-O3P-P-O2P
47	C	302	PEE	C1-O3P-P-O1P
47	C	302	PEE	C4-O4P-P-O1P
47	Q	501	PEE	C11-C10-O2-C2
47	Q	502	PEE	C11-C10-O2-C2
47	W	201	PEE	C5-C4-O4P-P
47	b	201	PEE	C11-C10-O2-C2
47	b	201	PEE	C37-C38-C39-C40
47	j	201	PEE	C1-O3P-P-O2P
47	j	201	PEE	C1-O3P-P-O1P
47	l	701	PEE	C11-C10-O2-C2
47	l	701	PEE	C1-O3P-P-O2P
47	l	701	PEE	C1-O3P-P-O1P
47	l	701	PEE	C1-O3P-P-O4P
47	l	704	PEE	O3P-C1-C2-O2
47	r	501	PEE	C1-O3P-P-O2P
47	r	501	PEE	C1-O3P-P-O1P
48	C	303	PLX	O6-C4-C5-O8
48	J	403	PLX	O7-C6-O6-C4
48	J	403	PLX	C2-O1-P1-O2
48	J	403	PLX	C2-O1-P1-O3
48	N	201	PLX	O7-C6-O6-C4
48	N	201	PLX	C2-O1-P1-O3
48	N	201	PLX	O9-C24-O8-C5
48	a	202	PLX	O7-C6-C7-C8
48	a	202	PLX	O7-C6-O6-C4
48	a	202	PLX	C3-O4-P1-O3
48	a	202	PLX	C2-O1-P1-O2
48	g	201	PLX	C2-O1-P1-O4
48	j	203	PLX	O7-C6-C7-C8
48	r	502	PLX	O7-C6-C7-C8
48	r	502	PLX	O7-C6-O6-C4
48	r	502	PLX	C3-O4-P1-O2
48	r	502	PLX	C3-O4-P1-O3
49	C	304	UQ	C12-C13-C14-C16

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Mol	Chain	Res	Type	Atoms
49	C	304	UQ	C16-C17-C18-C19
49	C	304	UQ	C17-C18-C19-C20
49	C	304	UQ	C17-C18-C19-C21
49	C	304	UQ	C22-C23-C24-C26
49	C	304	UQ	C27-C28-C29-C30
49	C	304	UQ	C27-C28-C29-C31
49	C	304	UQ	C32-C33-C34-C36
49	C	304	UQ	C37-C38-C39-C40
49	C	304	UQ	C42-C43-C44-C45
49	C	304	UQ	C42-C43-C44-C46
49	C	304	UQ	C47-C48-C49-C51
49	J	402	UQ	C7-C8-C9-C10
49	J	402	UQ	C7-C8-C9-C11
49	J	402	UQ	C11-C12-C13-C14
49	J	402	UQ	C12-C13-C14-C15
49	J	402	UQ	C12-C13-C14-C16
49	J	402	UQ	C14-C16-C17-C18
49	J	402	UQ	C17-C18-C19-C21
49	J	402	UQ	C19-C21-C22-C23
50	G	201	8Q1	C28-C29-C32-C34
50	G	201	8Q1	C28-C29-C32-O33
50	G	201	8Q1	C31-C29-C32-C34
50	G	201	8Q1	C31-C29-C32-O33
50	G	201	8Q1	C42-C43-S44-C1
50	G	201	8Q1	C28-O27-P24-O3
50	G	201	8Q1	C28-O27-P24-O2
50	G	201	8Q1	C28-O27-P24-O1
50	X	201	8Q1	C1-C6-C7-C8
50	X	201	8Q1	O4-C1-S44-C43
50	X	201	8Q1	C6-C1-S44-C43
50	X	201	8Q1	O33-C32-C34-N36
50	X	201	8Q1	N41-C42-C43-S44
50	X	201	8Q1	C42-C43-S44-C1
50	X	201	8Q1	C28-O27-P24-O2
50	X	201	8Q1	C28-O27-P24-O1
51	J	401	NDP	O4D-C1D-N1N-C6N
54	N	202	CDL	O1-C1-CA2-OA2
54	N	202	CDL	CB2-C1-CA2-OA2
54	N	202	CDL	O1-C1-CB2-OB2
54	N	202	CDL	CA3-OA5-PA1-OA3
54	N	202	CDL	OA5-CA3-CA4-OA6
54	N	202	CDL	CB2-OB2-PB2-OB3

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Mol	Chain	Res	Type	Atoms
54	N	202	CDL	CB2-OB2-PB2-OB4
54	N	202	CDL	CB3-OB5-PB2-OB3
54	V	201	CDL	CA2-OA2-PA1-OA5
54	V	201	CDL	C11-CA5-OA6-CA4
54	V	201	CDL	CB2-OB2-PB2-OB3
54	V	201	CDL	CB2-OB2-PB2-OB4
54	V	201	CDL	CB3-OB5-PB2-OB3
54	V	201	CDL	CB3-OB5-PB2-OB4
54	V	202	CDL	CA3-OA5-PA1-OA3
54	V	202	CDL	CB2-OB2-PB2-OB3
54	a	201	CDL	CA2-OA2-PA1-OA3
54	a	201	CDL	CB2-OB2-PB2-OB3
54	a	201	CDL	CB3-OB5-PB2-OB3
54	a	201	CDL	CB3-OB5-PB2-OB4
54	a	201	CDL	OB7-CB5-OB6-CB4
54	l	702	CDL	O1-C1-CA2-OA2
54	l	702	CDL	CA2-OA2-PA1-OA3
54	l	702	CDL	CA2-OA2-PA1-OA5
54	l	702	CDL	CB2-OB2-PB2-OB4
54	l	702	CDL	CB3-OB5-PB2-OB3
54	l	703	CDL	O1-C1-CB2-OB2
54	l	703	CDL	CA2-OA2-PA1-OA4
54	l	703	CDL	CB2-OB2-PB2-OB3
54	l	703	CDL	CB2-OB2-PB2-OB4
54	m	201	CDL	CA2-OA2-PA1-OA3
54	m	201	CDL	CA2-OA2-PA1-OA4
54	m	201	CDL	CA2-OA2-PA1-OA5
54	m	201	CDL	CA3-OA5-PA1-OA3
54	m	201	CDL	CA3-OA5-PA1-OA4
54	m	201	CDL	CB3-OB5-PB2-OB2
54	m	201	CDL	CB3-OB5-PB2-OB3
54	m	201	CDL	CB3-OB5-PB2-OB4
54	n	101	CDL	O1-C1-CB2-OB2
54	n	101	CDL	CA2-C1-CB2-OB2
54	n	101	CDL	CA2-OA2-PA1-OA3
54	n	101	CDL	OA5-CA3-CA4-OA6
54	r	503	CDL	CA2-OA2-PA1-OA3
54	r	503	CDL	CA3-OA5-PA1-OA2
54	r	503	CDL	CA3-OA5-PA1-OA3
54	r	503	CDL	CB2-OB2-PB2-OB3
54	r	503	CDL	CB2-OB2-PB2-OB4
54	r	503	CDL	CB2-OB2-PB2-OB5

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Mol	Chain	Res	Type	Atoms
54	r	503	CDL	CB3-OB5-PB2-OB3
54	r	503	CDL	CB3-OB5-PB2-OB4
54	r	503	CDL	C51-CB5-OB6-CB4
54	s	401	CDL	CB2-C1-CA2-OA2
54	s	401	CDL	CA2-OA2-PA1-OA3
54	s	401	CDL	CA2-OA2-PA1-OA4
54	s	401	CDL	CA2-OA2-PA1-OA5
54	s	401	CDL	OB6-CB4-CB6-OB8
56	w	401	ADP	C5'-O5'-PA-O2A
56	w	401	ADP	C5'-O5'-PA-O3A
54	l	702	CDL	OA9-CA7-OA8-CA6
54	s	401	CDL	OA9-CA7-OA8-CA6
47	C	302	PEE	O4-C10-O2-C2
47	Q	501	PEE	O4-C10-O2-C2
47	Q	502	PEE	O4-C10-O2-C2
47	b	201	PEE	O4-C10-O2-C2
47	l	701	PEE	O4-C10-O2-C2
54	V	201	CDL	OA7-CA5-OA6-CA4
54	V	202	CDL	OB7-CB5-OB6-CB4
54	r	503	CDL	OB7-CB5-OB6-CB4
54	s	401	CDL	C31-CA7-OA8-CA6
54	V	202	CDL	C51-CB5-OB6-CB4
54	a	201	CDL	C51-CB5-OB6-CB4
49	C	304	UQ	C25-C24-C26-C27
47	Q	501	PEE	O5-C30-O3-C3
47	l	704	PEE	C31-C30-O3-C3
54	l	702	CDL	C31-CA7-OA8-CA6
47	Q	502	PEE	C17-C18-C19-C20
47	W	201	PEE	C17-C18-C19-C20
47	j	201	PEE	C17-C18-C19-C20
47	r	501	PEE	C17-C18-C19-C20
49	J	402	UQ	C22-C23-C24-C26
49	C	304	UQ	C7-C8-C9-C10
47	l	704	PEE	O4-C10-O2-C2
48	g	201	PLX	C2-C1-N1-C1A
54	a	201	CDL	O1-C1-CA2-OA2
54	a	201	CDL	O1-C1-CB2-OB2
54	l	703	CDL	O1-C1-CA2-OA2
54	r	503	CDL	O1-C1-CA2-OA2
54	s	401	CDL	O1-C1-CA2-OA2
54	s	401	CDL	O1-C1-CB2-OB2
47	Q	501	PEE	C31-C30-O3-C3

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Mol	Chain	Res	Type	Atoms
47	l	701	PEE	C31-C30-O3-C3
54	V	201	CDL	C71-CB7-OB8-CB6
47	l	704	PEE	C11-C10-O2-C2
49	C	304	UQ	C52-C53-C54-C55
54	s	401	CDL	C37-C38-C39-C40
48	g	201	PLX	C7-C8-C9-C10
54	V	202	CDL	C11-C12-C13-C14
54	V	202	CDL	C32-C33-C34-C35
54	n	101	CDL	C74-C75-C76-C77
48	g	201	PLX	C9-C10-C11-C12
54	V	201	CDL	C59-C60-C61-C62
54	r	503	CDL	C74-C75-C76-C77
47	l	701	PEE	O5-C30-O3-C3
54	V	201	CDL	OB9-CB7-OB8-CB6
54	l	702	CDL	C16-C17-C18-C19
54	l	702	CDL	C32-C33-C34-C35
49	J	402	UQ	C12-C11-C9-C10
49	C	304	UQ	C43-C44-C46-C47
49	C	304	UQ	C48-C49-C51-C52
49	J	402	UQ	C18-C19-C21-C22
48	j	203	PLX	C13-C14-C15-C16
54	V	201	CDL	C32-C33-C34-C35
47	l	704	PEE	O5-C30-O3-C3
49	J	402	UQ	C9-C11-C12-C13
54	m	201	CDL	C73-C74-C75-C76
47	j	201	PEE	C31-C30-O3-C3
54	V	201	CDL	C62-C63-C64-C65
54	l	702	CDL	C34-C35-C36-C37
54	l	702	CDL	C55-C56-C57-C58
54	N	202	CDL	CA2-C1-CB2-OB2
54	V	202	CDL	CA2-C1-CB2-OB2
54	a	201	CDL	CA2-C1-CB2-OB2
54	l	702	CDL	CB2-C1-CA2-OA2
54	l	702	CDL	CA2-C1-CB2-OB2
54	l	703	CDL	CA2-C1-CB2-OB2
54	s	401	CDL	CA2-C1-CB2-OB2
47	j	201	PEE	O5-C30-O3-C3
48	C	303	PLX	C33-C34-C35-C36
48	N	201	PLX	C31-C32-C33-C34
54	N	202	CDL	CB7-C71-C72-C73
54	l	702	CDL	CA7-C31-C32-C33
54	l	703	CDL	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
54	V	201	CDL	OB5-CB3-CB4-OB6
54	m	201	CDL	C13-C14-C15-C16
54	V	202	CDL	O1-C1-CA2-OA2
54	l	702	CDL	O1-C1-CB2-OB2
54	V	202	CDL	OA6-CA4-CA6-OA8
48	C	303	PLX	C9-C10-C11-C12
54	s	401	CDL	C14-C15-C16-C17
54	m	201	CDL	C11-CA5-OA6-CA4
54	r	503	CDL	C60-C61-C62-C63
47	r	501	PEE	C10-C11-C12-C13
54	a	201	CDL	CA7-C31-C32-C33
54	m	201	CDL	C36-C37-C38-C39
54	l	702	CDL	CB5-C51-C52-C53
54	r	503	CDL	CA5-C11-C12-C13
54	s	401	CDL	CB5-C51-C52-C53
54	s	401	CDL	CB7-C71-C72-C73
54	s	401	CDL	C33-C34-C35-C36
49	J	402	UQ	C17-C18-C19-C20
54	a	201	CDL	CA5-C11-C12-C13
54	l	702	CDL	CB7-C71-C72-C73
54	l	703	CDL	CB5-C51-C52-C53
54	r	503	CDL	CA7-C31-C32-C33
54	s	401	CDL	CA7-C31-C32-C33
54	V	202	CDL	CB7-C71-C72-C73
54	N	202	CDL	C11-C12-C13-C14
54	l	703	CDL	C17-C18-C19-C20
49	C	304	UQ	C34-C36-C37-C38
54	m	201	CDL	OA7-CA5-OA6-CA4
47	Q	501	PEE	C37-C38-C39-C40
47	j	201	PEE	C11-C10-O2-C2
47	Q	502	PEE	C34-C35-C36-C37
54	n	101	CDL	C71-C72-C73-C74
47	C	302	PEE	C1-O3P-P-O4P
47	W	201	PEE	C4-O4P-P-O3P
47	b	201	PEE	C1-O3P-P-O4P
47	j	201	PEE	C1-O3P-P-O4P
47	l	701	PEE	C4-O4P-P-O3P
47	r	501	PEE	C1-O3P-P-O4P
48	J	403	PLX	C3-O4-P1-O1
48	J	403	PLX	C2-O1-P1-O4
48	a	202	PLX	C3-O4-P1-O1
48	r	502	PLX	C3-O4-P1-O1

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Mol	Chain	Res	Type	Atoms
54	N	202	CDL	CA2-OA2-PA1-OA5
54	N	202	CDL	CB2-OB2-PB2-OB5
54	V	201	CDL	CB2-OB2-PB2-OB5
54	V	201	CDL	CB3-OB5-PB2-OB2
54	a	201	CDL	CA2-OA2-PA1-OA5
54	a	201	CDL	CB2-OB2-PB2-OB5
54	a	201	CDL	CB3-OB5-PB2-OB2
54	l	702	CDL	CB2-OB2-PB2-OB5
54	l	702	CDL	CB3-OB5-PB2-OB2
54	l	703	CDL	CA2-OA2-PA1-OA5
54	l	703	CDL	CA3-OA5-PA1-OA2
54	l	703	CDL	CB2-OB2-PB2-OB5
54	m	201	CDL	CA3-OA5-PA1-OA2
54	n	101	CDL	CA2-OA2-PA1-OA5
54	r	503	CDL	CA2-OA2-PA1-OA5
54	r	503	CDL	CB3-OB5-PB2-OB2
54	s	401	CDL	CA3-OA5-PA1-OA2
54	s	401	CDL	CB3-OB5-PB2-OB2
47	W	201	PEE	C31-C30-O3-C3
54	V	202	CDL	C71-CB7-OB8-CB6
54	N	202	CDL	CA7-C31-C32-C33
54	l	703	CDL	CB2-C1-CA2-OA2
54	r	503	CDL	CB2-C1-CA2-OA2
47	j	201	PEE	O4-C10-O2-C2
48	g	201	PLX	C2-C1-N1-C1C
54	a	201	CDL	C71-CB7-OB8-CB6
54	l	703	CDL	C71-CB7-OB8-CB6
48	a	202	PLX	O8-C24-C25-C26
48	g	201	PLX	O6-C6-C7-C8
47	Q	502	PEE	C35-C36-C37-C38
47	b	201	PEE	C33-C34-C35-C36
54	V	201	CDL	C51-CB5-OB6-CB4
47	j	202	PEE	C23-C24-C25-C26
47	j	202	PEE	C13-C14-C15-C16
47	r	501	PEE	C31-C32-C33-C34
47	r	501	PEE	C40-C41-C42-C43
48	C	303	PLX	C17-C18-C19-C20
48	C	303	PLX	C25-C26-C27-C28
48	J	403	PLX	C7-C8-C9-C10
48	J	403	PLX	C31-C32-C33-C34
48	N	201	PLX	C29-C30-C31-C32
48	a	202	PLX	C10-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
48	a	202	PLX	C31-C32-C33-C34
48	g	201	PLX	C14-C15-C16-C17
48	j	203	PLX	C14-C15-C16-C17
48	j	203	PLX	C7-C8-C9-C10
48	j	203	PLX	C31-C32-C33-C34
48	r	502	PLX	C13-C14-C15-C16
54	V	202	CDL	C37-C38-C39-C40
54	l	703	CDL	C59-C60-C61-C62
47	Q	502	PEE	C22-C23-C24-C25
47	l	701	PEE	C11-C12-C13-C14
48	J	403	PLX	C28-C29-C30-C31
48	J	403	PLX	C34-C35-C36-C37
48	N	201	PLX	C14-C15-C16-C17
48	r	502	PLX	C25-C26-C27-C28
54	a	201	CDL	C62-C63-C64-C65
54	n	101	CDL	C52-C53-C54-C55
54	V	201	CDL	OB7-CB5-OB6-CB4
48	J	403	PLX	C30-C31-C32-C33
48	a	202	PLX	C13-C14-C15-C16
54	V	202	CDL	C33-C34-C35-C36
54	a	201	CDL	C60-C61-C62-C63
54	a	201	CDL	C75-C76-C77-C78
54	l	702	CDL	C11-C12-C13-C14
54	m	201	CDL	C61-C62-C63-C64
47	l	704	PEE	C37-C38-C39-C40
48	J	403	PLX	C14-C15-C16-C17
48	g	201	PLX	C32-C33-C34-C35
48	r	502	PLX	C27-C28-C29-C30
54	V	201	CDL	C52-C53-C54-C55
54	V	202	CDL	C82-C83-C84-C85
54	V	202	CDL	O1-C1-CB2-OB2
54	m	201	CDL	O1-C1-CA2-OA2
47	b	201	PEE	C22-C23-C24-C25
47	r	501	PEE	C21-C22-C23-C24
54	V	202	CDL	C35-C36-C37-C38
54	a	201	CDL	C17-C18-C19-C20
54	l	703	CDL	C11-C12-C13-C14
54	n	101	CDL	C71-CB7-OB8-CB6
48	C	303	PLX	C27-C28-C29-C30
48	j	203	PLX	C16-C17-C18-C19
48	j	203	PLX	C12-C13-C14-C15
48	r	502	PLX	C10-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
50	X	201	8Q1	C10-C11-C12-C13
54	V	201	CDL	C31-C32-C33-C34
54	V	201	CDL	C33-C34-C35-C36
54	V	201	CDL	C72-C73-C74-C75
54	a	201	CDL	C33-C34-C35-C36
54	n	101	CDL	C55-C56-C57-C58
54	s	401	CDL	C52-C53-C54-C55
47	W	201	PEE	C21-C22-C23-C24
48	N	201	PLX	C25-C26-C27-C28
48	N	201	PLX	C27-C28-C29-C30
48	N	201	PLX	C33-C34-C35-C36
48	a	202	PLX	C27-C28-C29-C30
48	g	201	PLX	C11-C12-C13-C14
54	l	702	CDL	C58-C59-C60-C61
54	m	201	CDL	C11-C12-C13-C14
54	r	503	CDL	C57-C58-C59-C60
47	W	201	PEE	C12-C13-C14-C15
47	r	501	PEE	C13-C14-C15-C16
47	r	501	PEE	C41-C42-C43-C44
48	g	201	PLX	C25-C26-C27-C28
54	V	201	CDL	C37-C38-C39-C40
54	a	201	CDL	C73-C74-C75-C76
54	m	201	CDL	C34-C35-C36-C37
54	m	201	CDL	C55-C56-C57-C58
54	r	503	CDL	C73-C74-C75-C76
54	V	202	CDL	OB9-CB7-OB8-CB6
47	Q	501	PEE	C21-C22-C23-C24
54	V	202	CDL	C59-C60-C61-C62
54	a	201	CDL	C37-C38-C39-C40
54	l	703	CDL	C79-C80-C81-C82
47	W	201	PEE	C11-C10-O2-C2
50	X	201	8Q1	C11-C12-C13-C14
54	V	201	CDL	C11-C12-C13-C14
54	V	202	CDL	C40-C41-C42-C43
54	V	202	CDL	C72-C73-C74-C75
54	l	702	CDL	C14-C15-C16-C17
54	l	702	CDL	C71-C72-C73-C74
54	s	401	CDL	C71-C72-C73-C74
47	W	201	PEE	C15-C16-C17-C18
48	J	403	PLX	C33-C34-C35-C36
48	j	203	PLX	C9-C10-C11-C12
50	X	201	8Q1	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
54	V	201	CDL	C40-C41-C42-C43
54	V	201	CDL	C74-C75-C76-C77
54	V	202	CDL	C42-C43-C44-C45
54	V	202	CDL	C52-C53-C54-C55
54	l	702	CDL	C74-C75-C76-C77
54	m	201	CDL	C32-C33-C34-C35
54	m	201	CDL	C71-C72-C73-C74
54	m	201	CDL	C75-C76-C77-C78
54	m	201	CDL	C79-C80-C81-C82
54	r	503	CDL	C35-C36-C37-C38
54	r	503	CDL	C71-C72-C73-C74
54	r	503	CDL	C83-C84-C85-C86
54	s	401	CDL	C55-C56-C57-C58
54	s	401	CDL	C59-C60-C61-C62
48	g	201	PLX	C2-C1-N1-C1B
47	j	202	PEE	C11-C12-C13-C14
54	N	202	CDL	C71-C72-C73-C74
54	V	201	CDL	C58-C59-C60-C61
54	l	703	CDL	C14-C15-C16-C17
54	m	201	CDL	C58-C59-C60-C61
54	r	503	CDL	C37-C38-C39-C40
48	j	203	PLX	C28-C29-C30-C31
48	j	203	PLX	C33-C34-C35-C36
54	V	202	CDL	C14-C15-C16-C17
54	l	703	CDL	CB7-C71-C72-C73
54	l	703	CDL	C73-C74-C75-C76
54	r	503	CDL	C11-C12-C13-C14
54	l	702	CDL	C71-CB7-OB8-CB6
48	J	403	PLX	C32-C33-C34-C35
48	g	201	PLX	C30-C31-C32-C33
54	V	202	CDL	C73-C74-C75-C76
47	r	501	PEE	C11-C12-C13-C14
48	C	303	PLX	C14-C15-C16-C17
50	G	201	8Q1	C12-C13-C14-C15
54	m	201	CDL	C59-C60-C61-C62
54	s	401	CDL	C75-C76-C77-C78
47	W	201	PEE	O5-C30-O3-C3
48	a	202	PLX	C14-C15-C16-C17
54	r	503	CDL	C14-C15-C16-C17
54	r	503	CDL	C32-C33-C34-C35
54	r	503	CDL	C43-C44-C45-C46
54	r	503	CDL	C62-C63-C64-C65

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Mol	Chain	Res	Type	Atoms
54	s	401	CDL	C82-C83-C84-C85
47	r	501	PEE	C1-C2-C3-O3
47	l	701	PEE	C17-C18-C19-C20
48	C	303	PLX	C7-C8-C9-C10
54	l	702	CDL	C62-C63-C64-C65
47	b	201	PEE	C10-C11-C12-C13
54	r	503	CDL	CB7-C71-C72-C73
48	j	203	PLX	C25-C26-C27-C28
48	r	502	PLX	C11-C12-C13-C14
54	V	202	CDL	C74-C75-C76-C77
54	l	702	CDL	C52-C53-C54-C55
54	a	201	CDL	OB9-CB7-OB8-CB6
49	C	304	UQ	C13-C14-C16-C17
54	s	401	CDL	C51-CB5-OB6-CB4
48	C	303	PLX	C11-C12-C13-C14
54	V	202	CDL	C17-C18-C19-C20
48	C	303	PLX	O7-C6-C7-C8
48	C	303	PLX	O9-C24-C25-C26
48	g	201	PLX	O9-C24-C25-C26
48	r	502	PLX	O9-C24-C25-C26
47	C	302	PEE	C43-C44-C45-C46
47	W	201	PEE	C13-C14-C15-C16
48	J	403	PLX	C13-C14-C15-C16
48	g	201	PLX	C27-C28-C29-C30
54	V	201	CDL	C55-C56-C57-C58
54	m	201	CDL	C41-C42-C43-C44
54	l	703	CDL	OB9-CB7-OB8-CB6
47	l	704	PEE	C31-C32-C33-C34
54	l	702	CDL	C59-C60-C61-C62
54	l	703	CDL	C74-C75-C76-C77
54	s	401	CDL	C73-C74-C75-C76
54	m	201	CDL	C14-C15-C16-C17
48	N	201	PLX	C12-C13-C14-C15
48	r	502	PLX	C30-C31-C32-C33
54	a	201	CDL	CB2-C1-CA2-OA2
54	m	201	CDL	CB2-C1-CA2-OA2
47	Q	502	PEE	C23-C24-C25-C26
48	g	201	PLX	C28-C29-C30-C31
54	r	503	CDL	C41-C42-C43-C44
47	W	201	PEE	O4-C10-O2-C2
48	N	201	PLX	C10-C11-C12-C13
54	n	101	CDL	OB9-CB7-OB8-CB6

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Mol	Chain	Res	Type	Atoms
48	J	403	PLX	C27-C28-C29-C30
48	N	201	PLX	C7-C8-C9-C10
54	l	703	CDL	C31-C32-C33-C34
54	m	201	CDL	C18-C19-C20-C21
54	l	703	CDL	C37-C38-C39-C40
54	s	401	CDL	C51-C52-C53-C54
47	j	202	PEE	C14-C15-C16-C17
48	j	203	PLX	C29-C30-C31-C32
48	r	502	PLX	C11-C10-C9-C8
54	l	703	CDL	C32-C33-C34-C35
54	s	401	CDL	C31-C32-C33-C34
54	l	702	CDL	OB9-CB7-OB8-CB6
47	l	701	PEE	C10-C11-C12-C13
54	n	101	CDL	CB5-C51-C52-C53
47	l	704	PEE	C11-C12-C13-C14
48	a	202	PLX	C25-C26-C27-C28
49	J	402	UQ	C15-C14-C16-C17
47	r	501	PEE	C14-C15-C16-C17
47	Q	501	PEE	C19-C20-C21-C22
47	l	701	PEE	C35-C36-C37-C38
47	r	501	PEE	C15-C16-C17-C18
47	r	501	PEE	C39-C40-C41-C42
54	s	401	CDL	OB7-CB5-OB6-CB4
54	m	201	CDL	C71-CB7-OB8-CB6
54	V	201	CDL	C14-C15-C16-C17
47	b	201	PEE	C31-C32-C33-C34
47	l	704	PEE	C34-C35-C36-C37
48	r	502	PLX	C14-C15-C16-C17
47	Q	502	PEE	C42-C43-C44-C45
48	g	201	PLX	C13-C14-C15-C16
54	a	201	CDL	C71-C72-C73-C74
54	r	503	CDL	C51-C52-C53-C54
48	C	303	PLX	C35-C36-C37-C38
54	V	201	CDL	C71-C72-C73-C74
50	X	201	8Q1	N36-C37-C38-C39
48	J	403	PLX	C9-C10-C11-C12
48	J	403	PLX	C35-C36-C37-C38
54	a	201	CDL	C32-C33-C34-C35
54	l	702	CDL	C75-C76-C77-C78
54	r	503	CDL	C75-C76-C77-C78
47	r	501	PEE	C11-C10-O2-C2
54	l	702	CDL	C51-CB5-OB6-CB4

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Mol	Chain	Res	Type	Atoms
47	W	201	PEE	O3P-C1-C2-O2
48	a	202	PLX	O4-C3-C4-O6
54	m	201	CDL	OA5-CA3-CA4-OA6
54	l	703	CDL	C82-C83-C84-C85
47	Q	502	PEE	C36-C37-C38-C39
54	V	202	CDL	C62-C63-C64-C65
48	a	202	PLX	O6-C4-C5-O8
48	g	201	PLX	O6-C4-C5-O8
48	a	202	PLX	C26-C27-C28-C29
54	V	202	CDL	C75-C76-C77-C78
54	s	401	CDL	C36-C37-C38-C39
48	j	203	PLX	C27-C28-C29-C30
47	l	704	PEE	C19-C20-C21-C22
54	V	202	CDL	CA7-C31-C32-C33
54	l	702	CDL	C36-C37-C38-C39
47	Q	502	PEE	C31-C32-C33-C34
54	l	702	CDL	C81-C82-C83-C84
54	m	201	CDL	C16-C17-C18-C19
54	r	503	CDL	C31-C32-C33-C34
54	s	401	CDL	C54-C55-C56-C57
47	r	501	PEE	O4-C10-O2-C2
54	l	702	CDL	OB7-CB5-OB6-CB4
54	l	703	CDL	C11-CA5-OA6-CA4
54	r	503	CDL	C77-C78-C79-C80
47	r	501	PEE	C36-C37-C38-C39
47	C	302	PEE	C4-O4P-P-O3P
47	l	704	PEE	C4-O4P-P-O3P
48	N	201	PLX	C2-O1-P1-O4
48	a	202	PLX	C2-O1-P1-O4
54	V	202	CDL	CB2-OB2-PB2-OB5
54	V	202	CDL	CB3-OB5-PB2-OB2
54	l	703	CDL	CB3-OB5-PB2-OB2
54	V	202	CDL	C34-C35-C36-C37
54	a	201	CDL	C31-C32-C33-C34
54	m	201	CDL	C60-C61-C62-C63
54	r	503	CDL	C59-C60-C61-C62
54	V	201	CDL	C1-CB2-OB2-PB2
47	W	201	PEE	C24-C25-C26-C27
48	C	303	PLX	C10-C11-C12-C13
54	V	201	CDL	OB5-CB3-CB4-CB6
54	m	201	CDL	OA5-CA3-CA4-CA6
54	n	101	CDL	OA5-CA3-CA4-CA6

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Mol	Chain	Res	Type	Atoms
54	l	702	CDL	CA5-C11-C12-C13
54	m	201	CDL	C52-C53-C54-C55
54	a	201	CDL	C15-C16-C17-C18
54	V	202	CDL	CB2-C1-CA2-OA2
47	l	704	PEE	C43-C44-C45-C46
54	m	201	CDL	C15-C16-C17-C18
54	m	201	CDL	C33-C34-C35-C36
54	r	503	CDL	C84-C85-C86-C87
48	C	303	PLX	C3-C4-C5-O8
48	J	403	PLX	C3-C4-C5-O8
48	a	202	PLX	C3-C4-C5-O8
48	j	203	PLX	C3-C4-C5-O8
54	V	202	CDL	CA3-CA4-CA6-OA8
54	V	202	CDL	C41-C42-C43-C44
54	V	202	CDL	C84-C85-C86-C87
54	m	201	CDL	CA3-CA4-CA6-OA8
54	n	101	CDL	CA3-CA4-CA6-OA8
54	V	202	CDL	C64-C65-C66-C67
54	l	702	CDL	C35-C36-C37-C38
54	l	702	CDL	C56-C57-C58-C59
54	a	201	CDL	C21-C22-C23-C24
54	l	702	CDL	C37-C38-C39-C40
54	m	201	CDL	C42-C43-C44-C45
54	l	703	CDL	C12-C11-CA5-OA6
54	m	201	CDL	OB9-CB7-OB8-CB6
50	X	201	8Q1	O33-C32-C34-O35
54	n	101	CDL	C75-C76-C77-C78
47	Q	501	PEE	C18-C19-C20-C21
47	l	704	PEE	C15-C16-C17-C18
47	j	202	PEE	C11-C10-O2-C2
47	j	201	PEE	C32-C33-C34-C35
54	a	201	CDL	C36-C37-C38-C39
47	b	201	PEE	C31-C30-O3-C3
48	r	502	PLX	C18-C19-C20-C21
48	r	502	PLX	C33-C34-C35-C36
54	m	201	CDL	CA6-CA4-OA6-CA5
54	l	702	CDL	C63-C64-C65-C66
54	s	401	CDL	C35-C36-C37-C38
50	X	201	8Q1	C28-O27-P24-O3
47	j	202	PEE	C31-C30-O3-C3
54	r	503	CDL	C71-CB7-OB8-CB6
47	j	201	PEE	C34-C35-C36-C37

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Mol	Chain	Res	Type	Atoms
54	r	503	CDL	C64-C65-C66-C67
48	g	201	PLX	C12-C13-C14-C15
47	Q	501	PEE	C10-C11-C12-C13
54	V	201	CDL	OB6-CB4-CB6-OB8
54	m	201	CDL	OB6-CB4-CB6-OB8
47	b	201	PEE	C13-C14-C15-C16
50	G	201	8Q1	C30-C29-C32-O33
48	r	502	PLX	C31-C32-C33-C34
48	r	502	PLX	C36-C37-C38-C39
54	m	201	CDL	C19-C20-C21-C22
48	r	502	PLX	C29-C30-C31-C32
54	a	201	CDL	C22-C23-C24-C25
48	N	201	PLX	C30-C31-C32-C33
54	r	503	CDL	C17-C18-C19-C20
47	Q	502	PEE	C31-C30-O3-C3
48	a	202	PLX	C9-C10-C11-C12
54	n	101	CDL	C73-C74-C75-C76
47	r	501	PEE	C20-C21-C22-C23
54	V	202	CDL	C60-C61-C62-C63
54	a	201	CDL	C52-C53-C54-C55
54	s	401	CDL	C17-C18-C19-C20
54	r	503	CDL	C15-C16-C17-C18
47	b	201	PEE	O5-C30-O3-C3
54	N	202	CDL	C71-CB7-OB8-CB6
48	a	202	PLX	C12-C13-C14-C15
54	V	201	CDL	C75-C76-C77-C78
48	g	201	PLX	C15-C16-C17-C18
48	g	201	PLX	C11-C10-C9-C8
47	Q	502	PEE	C38-C39-C40-C41
48	N	201	PLX	C13-C14-C15-C16
54	V	201	CDL	C54-C55-C56-C57
54	m	201	CDL	C62-C63-C64-C65
47	Q	501	PEE	O3P-C1-C2-C3
47	W	201	PEE	O3P-C1-C2-C3
54	a	201	CDL	OA5-CA3-CA4-CA6
54	a	201	CDL	OB5-CB3-CB4-CB6
54	l	703	CDL	OA5-CA3-CA4-CA6
49	C	304	UQ	C39-C41-C42-C43
54	s	401	CDL	C16-C17-C18-C19
47	Q	502	PEE	C44-C45-C46-C47
47	l	704	PEE	C13-C14-C15-C16
49	C	304	UQ	C52-C53-C54-C56

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Mol	Chain	Res	Type	Atoms
48	g	201	PLX	C10-C11-C12-C13
47	Q	501	PEE	C24-C25-C26-C27
47	l	704	PEE	C30-C31-C32-C33
54	m	201	CDL	CA4-CA3-OA5-PA1
54	n	101	CDL	C1-CB2-OB2-PB2
54	r	503	CDL	C1-CB2-OB2-PB2
54	s	401	CDL	C34-C35-C36-C37
47	Q	502	PEE	C12-C13-C14-C15
54	s	401	CDL	C71-CB7-OB8-CB6
47	C	302	PEE	C1-C2-C3-O3
47	Q	501	PEE	C1-C2-C3-O3
47	b	201	PEE	C1-C2-C3-O3
47	l	704	PEE	C1-C2-C3-O3
48	g	201	PLX	C3-C4-C5-O8
48	r	502	PLX	C3-C4-C5-O8
54	N	202	CDL	CA3-CA4-CA6-OA8
54	m	201	CDL	CB3-CB4-CB6-OB8
54	s	401	CDL	CB3-CB4-CB6-OB8
54	a	201	CDL	C35-C36-C37-C38
47	l	704	PEE	C23-C24-C25-C26
48	N	201	PLX	C28-C29-C30-C31
54	l	703	CDL	C33-C34-C35-C36
48	J	403	PLX	C5-C4-O6-C6
54	V	202	CDL	CA3-OA5-PA1-OA2
47	W	201	PEE	C10-C11-C12-C13
47	l	704	PEE	C32-C33-C34-C35
48	a	202	PLX	C11-C12-C13-C14
54	N	202	CDL	C52-C53-C54-C55
54	l	702	CDL	C21-C22-C23-C24
54	l	703	CDL	C44-C45-C46-C47
48	N	201	PLX	O9-C24-C25-C26
48	a	202	PLX	O9-C24-C25-C26
48	g	201	PLX	O7-C6-C7-C8
48	J	403	PLX	C10-C11-C12-C13
47	j	201	PEE	O3P-C1-C2-O2
54	a	201	CDL	OB5-CB3-CB4-OB6
54	l	703	CDL	OA5-CA3-CA4-OA6
54	m	201	CDL	OB5-CB3-CB4-OB6
48	a	202	PLX	C16-C17-C18-C19
47	j	202	PEE	C19-C20-C21-C22
54	r	503	CDL	OB9-CB7-OB8-CB6
47	j	202	PEE	O5-C30-O3-C3

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Mol	Chain	Res	Type	Atoms
47	l	701	PEE	C14-C15-C16-C17
54	l	703	CDL	C75-C76-C77-C78
48	J	403	PLX	C12-C13-C14-C15
47	b	201	PEE	O2-C2-C3-O3
48	J	403	PLX	O6-C4-C5-O8
48	r	502	PLX	O6-C4-C5-O8
54	l	703	CDL	OA6-CA4-CA6-OA8
54	m	201	CDL	C64-C65-C66-C67
49	C	304	UQ	C14-C16-C17-C18
47	j	202	PEE	O4-C10-O2-C2
54	l	703	CDL	OA7-CA5-OA6-CA4
47	j	202	PEE	C12-C13-C14-C15
54	l	703	CDL	C64-C65-C66-C67
54	N	202	CDL	OB9-CB7-OB8-CB6
54	V	202	CDL	CB5-C51-C52-C53
48	N	201	PLX	C16-C17-C18-C19
48	J	403	PLX	C25-C26-C27-C28
54	a	201	CDL	C11-C12-C13-C14
47	C	302	PEE	C15-C16-C17-C18
48	C	303	PLX	C13-C14-C15-C16
47	j	201	PEE	C23-C24-C25-C26
48	g	201	PLX	C33-C34-C35-C36
54	r	503	CDL	C54-C55-C56-C57
54	m	201	CDL	C37-C38-C39-C40
47	l	701	PEE	C18-C19-C20-C21
48	a	202	PLX	C29-C30-C31-C32
47	Q	502	PEE	O5-C30-O3-C3
48	C	303	PLX	O8-C24-C25-C26
48	j	203	PLX	O6-C6-C7-C8
54	r	503	CDL	C21-C22-C23-C24
47	C	302	PEE	O3P-C1-C2-C3
47	Q	502	PEE	O3P-C1-C2-C3
47	l	704	PEE	O3P-C1-C2-C3
54	N	202	CDL	OA5-CA3-CA4-CA6
54	V	201	CDL	OA5-CA3-CA4-CA6
54	l	703	CDL	OB5-CB3-CB4-CB6
54	s	401	CDL	OA5-CA3-CA4-CA6
48	C	303	PLX	C28-C29-C30-C31
47	j	201	PEE	C36-C37-C38-C39
47	j	201	PEE	C38-C39-C40-C41
48	a	202	PLX	C28-C29-C30-C31
48	r	502	PLX	C16-C17-C18-C19

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Mol	Chain	Res	Type	Atoms
54	l	702	CDL	C82-C83-C84-C85
47	j	201	PEE	C19-C20-C21-C22
54	s	401	CDL	C11-C12-C13-C14
48	J	403	PLX	C11-C12-C13-C14
54	m	201	CDL	C17-C18-C19-C20
51	J	401	NDP	O4B-C4B-C5B-O5B
54	r	503	CDL	C52-C53-C54-C55
54	m	201	CDL	C56-C57-C58-C59
48	C	303	PLX	C30-C31-C32-C33
48	j	203	PLX	C11-C12-C13-C14
48	r	502	PLX	C7-C8-C9-C10
50	X	201	8Q1	C6-C7-C8-C9
54	r	503	CDL	C33-C34-C35-C36
54	V	201	CDL	CA6-CA4-OA6-CA5
54	V	202	CDL	C13-C14-C15-C16
54	a	201	CDL	C84-C85-C86-C87
48	C	303	PLX	C36-C37-C38-C39
54	r	503	CDL	C42-C43-C44-C45
54	V	201	CDL	C64-C65-C66-C67
47	W	201	PEE	C1-C2-C3-O3
48	N	201	PLX	C3-C4-C5-O8
47	j	202	PEE	C31-C32-C33-C34
47	l	701	PEE	O3P-C1-C2-O2
47	r	501	PEE	O3P-C1-C2-O2
48	N	201	PLX	O4-C3-C4-O6
54	a	201	CDL	OA5-CA3-CA4-OA6
54	l	702	CDL	OB5-CB3-CB4-OB6
54	l	703	CDL	OB5-CB3-CB4-OB6
47	W	201	PEE	C34-C35-C36-C37
54	s	401	CDL	C13-C14-C15-C16
50	G	201	8Q1	C30-C29-C32-C34
48	a	202	PLX	C30-C31-C32-C33
54	s	401	CDL	OB9-CB7-OB8-CB6
54	V	201	CDL	C34-C35-C36-C37
47	Q	501	PEE	O2-C2-C3-O3
47	W	201	PEE	O2-C2-C3-O3
47	l	704	PEE	O2-C2-C3-O3
48	N	201	PLX	O6-C4-C5-O8
54	n	101	CDL	OA6-CA4-CA6-OA8
54	V	201	CDL	C31-CA7-OA8-CA6
54	l	702	CDL	C24-C25-C26-C27
54	l	703	CDL	C56-C57-C58-C59

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Mol	Chain	Res	Type	Atoms
54	s	401	CDL	C40-C41-C42-C43
54	a	201	CDL	C38-C39-C40-C41
54	l	703	CDL	C15-C16-C17-C18
54	l	703	CDL	C55-C56-C57-C58
54	V	202	CDL	C54-C55-C56-C57
47	C	302	PEE	C17-C18-C19-C20
47	C	302	PEE	C37-C38-C39-C40
47	Q	501	PEE	C32-C33-C34-C35
54	s	401	CDL	C74-C75-C76-C77
47	C	302	PEE	C32-C33-C34-C35
54	r	503	CDL	C39-C40-C41-C42
54	N	202	CDL	CB3-OB5-PB2-OB2
54	n	101	CDL	CB3-OB5-PB2-OB2
54	a	201	CDL	C54-C55-C56-C57
54	N	202	CDL	CA5-C11-C12-C13
54	l	703	CDL	C21-C22-C23-C24
47	j	202	PEE	C22-C23-C24-C25
54	a	201	CDL	C74-C75-C76-C77
47	C	302	PEE	C4-O4P-P-O2P
47	W	201	PEE	C4-O4P-P-O2P
47	W	201	PEE	C4-O4P-P-O1P
47	b	201	PEE	C1-O3P-P-O2P
47	b	201	PEE	C1-O3P-P-O1P
47	l	701	PEE	C4-O4P-P-O2P
48	J	403	PLX	C3-O4-P1-O2
48	J	403	PLX	C3-O4-P1-O3
48	N	201	PLX	C2-O1-P1-O2
48	a	202	PLX	C3-O4-P1-O2
48	a	202	PLX	C2-O1-P1-O3
48	j	203	PLX	C3-O4-P1-O3
54	N	202	CDL	CA2-OA2-PA1-OA4
54	N	202	CDL	CB3-OB5-PB2-OB4
54	V	201	CDL	CA2-OA2-PA1-OA4
54	V	201	CDL	CA3-OA5-PA1-OA3
54	V	202	CDL	CB2-OB2-PB2-OB4
54	V	202	CDL	CB3-OB5-PB2-OB3
54	V	202	CDL	CB3-OB5-PB2-OB4
54	a	201	CDL	CB2-OB2-PB2-OB4
54	l	702	CDL	CB3-OB5-PB2-OB4
54	l	703	CDL	CA3-OA5-PA1-OA4
54	l	703	CDL	CB3-OB5-PB2-OB4
54	n	101	CDL	CA2-OA2-PA1-OA4

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Mol	Chain	Res	Type	Atoms
54	n	101	CDL	CB3-OB5-PB2-OB3
54	r	503	CDL	CA2-OA2-PA1-OA4
54	s	401	CDL	CA3-OA5-PA1-OA3
54	s	401	CDL	CA3-OA5-PA1-OA4
54	s	401	CDL	CB3-OB5-PB2-OB4
56	w	401	ADP	C5'-O5'-PA-O1A
54	l	703	CDL	C12-C13-C14-C15
47	b	201	PEE	O3P-C1-C2-C3
47	l	701	PEE	O3P-C1-C2-C3
47	r	501	PEE	O3P-C1-C2-C3
48	J	403	PLX	O4-C3-C4-C5
48	N	201	PLX	O4-C3-C4-C5
54	N	202	CDL	OB5-CB3-CB4-CB6
54	s	401	CDL	C12-C13-C14-C15
54	V	202	CDL	C32-C31-CA7-OA8
54	l	703	CDL	C81-C82-C83-C84
54	m	201	CDL	C84-C85-C86-C87
47	C	302	PEE	C11-C12-C13-C14
48	C	303	PLX	C25-C24-O8-C5
48	N	201	PLX	C1-C2-O1-P1
48	g	201	PLX	C25-C24-O8-C5
48	j	203	PLX	C25-C24-O8-C5
47	Q	501	PEE	C15-C16-C17-C18
47	b	201	PEE	C15-C16-C17-C18
48	J	403	PLX	C26-C27-C28-C29
54	a	201	CDL	C16-C17-C18-C19
54	l	703	CDL	C71-C72-C73-C74
47	C	302	PEE	O3P-C1-C2-O2
47	Q	501	PEE	O3P-C1-C2-O2
47	Q	502	PEE	O3P-C1-C2-O2
47	b	201	PEE	O3P-C1-C2-O2
48	J	403	PLX	O4-C3-C4-O6
48	j	203	PLX	O4-C3-C4-O6
48	r	502	PLX	O4-C3-C4-O6
54	N	202	CDL	OB5-CB3-CB4-OB6
54	V	201	CDL	OA5-CA3-CA4-OA6
47	b	201	PEE	C16-C17-C18-C19
54	V	201	CDL	OA9-CA7-OA8-CA6
54	l	702	CDL	C72-C73-C74-C75
47	C	302	PEE	C33-C34-C35-C36
48	j	203	PLX	C18-C19-C20-C21
54	l	702	CDL	C76-C77-C78-C79

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Mol	Chain	Res	Type	Atoms
48	C	303	PLX	C18-C19-C20-C21
47	j	201	PEE	C30-C31-C32-C33
48	C	303	PLX	N1-C1-C2-O1
48	J	403	PLX	N1-C1-C2-O1
54	V	201	CDL	CB3-CB4-CB6-OB8
54	s	401	CDL	C15-C16-C17-C18
47	r	501	PEE	O2-C2-C3-O3
48	j	203	PLX	O6-C4-C5-O8
54	N	202	CDL	OA6-CA4-CA6-OA8
54	m	201	CDL	OA6-CA4-CA6-OA8
54	l	703	CDL	C62-C63-C64-C65
47	r	501	PEE	C37-C38-C39-C40
47	l	704	PEE	C14-C15-C16-C17
48	a	202	PLX	O6-C6-C7-C8
47	j	202	PEE	C24-C25-C26-C27
47	b	201	PEE	C18-C19-C20-C21
47	j	201	PEE	C16-C17-C18-C19
47	r	501	PEE	C38-C39-C40-C41
47	r	501	PEE	C23-C24-C25-C26
54	l	702	CDL	C41-C42-C43-C44
47	l	701	PEE	C32-C33-C34-C35
47	l	704	PEE	C24-C25-C26-C27
54	a	201	CDL	C64-C65-C66-C67
47	j	201	PEE	O3P-C1-C2-C3
48	a	202	PLX	O4-C3-C4-C5
48	r	502	PLX	O4-C3-C4-C5
47	Q	501	PEE	C34-C35-C36-C37
47	b	201	PEE	C23-C24-C25-C26
54	m	201	CDL	C31-C32-C33-C34
47	b	201	PEE	C14-C15-C16-C17
54	V	202	CDL	OB5-CB3-CB4-OB6
47	C	302	PEE	O2-C2-C3-O3
54	l	703	CDL	OB6-CB4-CB6-OB8
47	Q	501	PEE	C11-C12-C13-C14
48	C	303	PLX	C3-O4-P1-O1
54	N	202	CDL	CA3-OA5-PA1-OA2
54	V	202	CDL	CA2-OA2-PA1-OA5
54	n	101	CDL	CA3-OA5-PA1-OA2
54	n	101	CDL	CB2-OB2-PB2-OB5
51	J	401	NDP	C2D-C1D-N1N-C2N
47	C	302	PEE	C42-C43-C44-C45
48	J	403	PLX	C19-C20-C21-C22

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Mol	Chain	Res	Type	Atoms
54	l	702	CDL	C54-C55-C56-C57
48	C	303	PLX	C34-C35-C36-C37
54	s	401	CDL	C72-C71-CB7-OB8
48	C	303	PLX	C15-C16-C17-C18
54	V	201	CDL	CA4-CA3-OA5-PA1
54	a	201	CDL	C51-C52-C53-C54
54	s	401	CDL	C84-C85-C86-C87
47	l	701	PEE	C38-C39-C40-C41
54	l	702	CDL	C22-C23-C24-C25
54	s	401	CDL	C77-C78-C79-C80
47	Q	502	PEE	C39-C40-C41-C42
54	l	703	CDL	C12-C11-CA5-OA7
54	V	201	CDL	C21-C22-C23-C24
48	C	303	PLX	C6-C7-C8-C9
54	V	201	CDL	C53-C54-C55-C56
54	n	101	CDL	OB5-CB3-CB4-OB6
47	b	201	PEE	C20-C21-C22-C23
48	r	502	PLX	C28-C29-C30-C31
54	l	703	CDL	C43-C44-C45-C46
54	m	201	CDL	C39-C40-C41-C42
47	l	701	PEE	O2-C2-C3-O3
47	C	302	PEE	C13-C14-C15-C16
54	n	101	CDL	CB7-C71-C72-C73
48	j	203	PLX	C10-C11-C12-C13
48	r	502	PLX	C26-C27-C28-C29
47	C	302	PEE	C16-C17-C18-C19
47	W	201	PEE	C16-C17-C18-C19
54	a	201	CDL	C14-C15-C16-C17
48	C	303	PLX	C29-C30-C31-C32
49	C	304	UQ	C15-C14-C16-C17
48	a	202	PLX	C15-C16-C17-C18
48	g	201	PLX	C6-C7-C8-C9
54	l	702	CDL	C20-C21-C22-C23
47	l	704	PEE	C3-C2-O2-C10
54	V	202	CDL	C36-C37-C38-C39
48	C	303	PLX	C5-C4-O6-C6
48	N	201	PLX	C3-C4-O6-C6
48	j	203	PLX	C3-C4-O6-C6
47	j	201	PEE	C44-C45-C46-C47
47	l	701	PEE	C2-C1-O3P-P
47	l	704	PEE	C42-C43-C44-C45
54	V	202	CDL	C31-C32-C33-C34

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Mol	Chain	Res	Type	Atoms
54	l	702	CDL	C51-C52-C53-C54
54	s	401	CDL	OA5-CA3-CA4-OA6
47	C	302	PEE	C12-C13-C14-C15
54	V	202	CDL	OB5-CB3-CB4-CB6
47	C	302	PEE	C41-C42-C43-C44
54	a	201	CDL	C13-C14-C15-C16
54	a	201	CDL	C12-C13-C14-C15
47	r	501	PEE	C33-C34-C35-C36
54	a	201	CDL	C53-C54-C55-C56
54	a	201	CDL	C55-C56-C57-C58
47	Q	501	PEE	C20-C21-C22-C23
47	j	201	PEE	C41-C42-C43-C44
47	b	201	PEE	C21-C22-C23-C24
48	g	201	PLX	C18-C19-C20-C21
54	m	201	CDL	C40-C41-C42-C43
54	n	101	CDL	C72-C71-CB7-OB8
54	m	201	CDL	C20-C21-C22-C23
54	r	503	CDL	C12-C13-C14-C15
51	J	401	NDP	C3B-C4B-C5B-O5B
48	g	201	PLX	C31-C32-C33-C34
51	J	401	NDP	O4D-C1D-N1N-C2N
54	l	702	CDL	C78-C79-C80-C81
54	a	201	CDL	C43-C44-C45-C46
54	r	503	CDL	C72-C71-CB7-OB8
47	j	202	PEE	C18-C19-C20-C21
47	l	701	PEE	C16-C17-C18-C19
54	V	201	CDL	CA7-C31-C32-C33
54	a	201	CDL	C44-C45-C46-C47
48	N	201	PLX	O8-C24-C25-C26
47	C	302	PEE	C14-C15-C16-C17
54	l	702	CDL	OB5-CB3-CB4-CB6
54	m	201	CDL	OB5-CB3-CB4-CB6
54	n	101	CDL	OB5-CB3-CB4-CB6
49	C	304	UQ	C40-C39-C41-C42
49	J	402	UQ	C20-C19-C21-C22
54	a	201	CDL	C18-C19-C20-C21
49	C	304	UQ	C12-C11-C9-C8
47	W	201	PEE	O4P-C4-C5-N
47	j	202	PEE	O3-C30-C31-C32
51	J	401	NDP	O4D-C4D-C5D-O5D
46	A	502	FMN	C5'-O5'-P-O3P
54	l	702	CDL	C72-C71-CB7-OB8

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Mol	Chain	Res	Type	Atoms
54	s	401	CDL	C12-C11-CA5-OA6
49	C	304	UQ	C45-C44-C46-C47
47	l	701	PEE	O3-C30-C31-C32
47	Q	501	PEE	C17-C18-C19-C20
48	J	403	PLX	C36-C37-C38-C39
48	j	203	PLX	C30-C31-C32-C33
54	m	201	CDL	C52-C51-CB5-OB6
47	b	201	PEE	C38-C39-C40-C41
47	j	202	PEE	C16-C17-C18-C19
47	r	501	PEE	C16-C17-C18-C19
54	s	401	CDL	C60-C61-C62-C63
54	r	503	CDL	C56-C57-C58-C59
54	a	201	CDL	C32-C31-CA7-OA8
47	C	302	PEE	C18-C19-C20-C21
47	W	201	PEE	C18-C19-C20-C21
47	r	501	PEE	C18-C19-C20-C21
48	j	203	PLX	C7-C6-O6-C4
54	l	703	CDL	CA3-CA4-CA6-OA8
47	j	202	PEE	O3P-C1-C2-O2
47	C	302	PEE	O3-C30-C31-C32
54	r	503	CDL	C82-C83-C84-C85
54	s	401	CDL	C57-C58-C59-C60
48	j	203	PLX	C24-C25-C26-C27
47	C	302	PEE	C36-C37-C38-C39
47	C	302	PEE	O2-C10-C11-C12
54	a	201	CDL	C12-C11-CA5-OA6
54	r	503	CDL	OA6-CA4-CA6-OA8
54	m	201	CDL	C12-C11-CA5-OA6
48	J	403	PLX	O9-C24-C25-C26
51	J	401	NDP	C2B-O2B-P2B-O2X
47	Q	501	PEE	C22-C23-C24-C25
47	r	501	PEE	C32-C33-C34-C35
47	C	302	PEE	C38-C39-C40-C41
54	l	703	CDL	C72-C71-CB7-OB8
47	Q	502	PEE	O2-C10-C11-C12
47	j	201	PEE	O3-C30-C31-C32
54	N	202	CDL	C51-C52-C53-C54
47	Q	502	PEE	C16-C17-C18-C19
54	V	202	CDL	C44-C45-C46-C47
48	r	502	PLX	C19-C20-C21-C22
47	j	201	PEE	O2-C10-C11-C12
48	C	303	PLX	O6-C6-C7-C8

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Mol	Chain	Res	Type	Atoms
54	m	201	CDL	CA5-C11-C12-C13
54	s	401	CDL	C12-C11-CA5-OA7
54	l	702	CDL	C44-C45-C46-C47
54	V	202	CDL	C51-C52-C53-C54
47	l	704	PEE	C16-C17-C18-C19
47	C	302	PEE	O4-C10-C11-C12
54	a	201	CDL	C12-C11-CA5-OA7
54	l	702	CDL	C72-C71-CB7-OB9
48	j	203	PLX	C32-C33-C34-C35
47	j	202	PEE	O5-C30-C31-C32
48	J	403	PLX	C11-C10-C9-C8
48	N	201	PLX	C4-C3-O4-P1
54	l	702	CDL	C60-C61-C62-C63
54	m	201	CDL	C43-C44-C45-C46
47	b	201	PEE	C4-O4P-P-O1P
47	j	202	PEE	C1-O3P-P-O2P
48	g	201	PLX	C3-O4-P1-O2
54	l	702	CDL	CB2-OB2-PB2-OB3
54	m	201	CDL	CB2-OB2-PB2-OB4
54	n	101	CDL	CB2-OB2-PB2-OB3
54	n	101	CDL	CB3-OB5-PB2-OB4
47	l	701	PEE	O5-C30-C31-C32
54	m	201	CDL	C12-C11-CA5-OA7
48	j	203	PLX	O4-C3-C4-C5
54	m	201	CDL	C44-C45-C46-C47
54	m	201	CDL	C82-C83-C84-C85
48	N	201	PLX	C26-C27-C28-C29
48	N	201	PLX	C18-C19-C20-C21
54	l	703	CDL	C39-C40-C41-C42
47	C	302	PEE	O5-C30-C31-C32
54	a	201	CDL	C32-C31-CA7-OA9
54	l	703	CDL	C72-C71-CB7-OB9
54	l	703	CDL	C51-C52-C53-C54
47	Q	502	PEE	O4-C10-C11-C12
47	l	701	PEE	O2-C10-C11-C12
54	V	201	CDL	C12-C11-CA5-OA6
49	C	304	UQ	C30-C29-C31-C32
47	b	201	PEE	O3-C30-C31-C32
47	j	201	PEE	C24-C25-C26-C27
47	C	302	PEE	C44-C45-C46-C47
47	b	201	PEE	O5-C30-C31-C32
54	s	401	CDL	C56-C57-C58-C59

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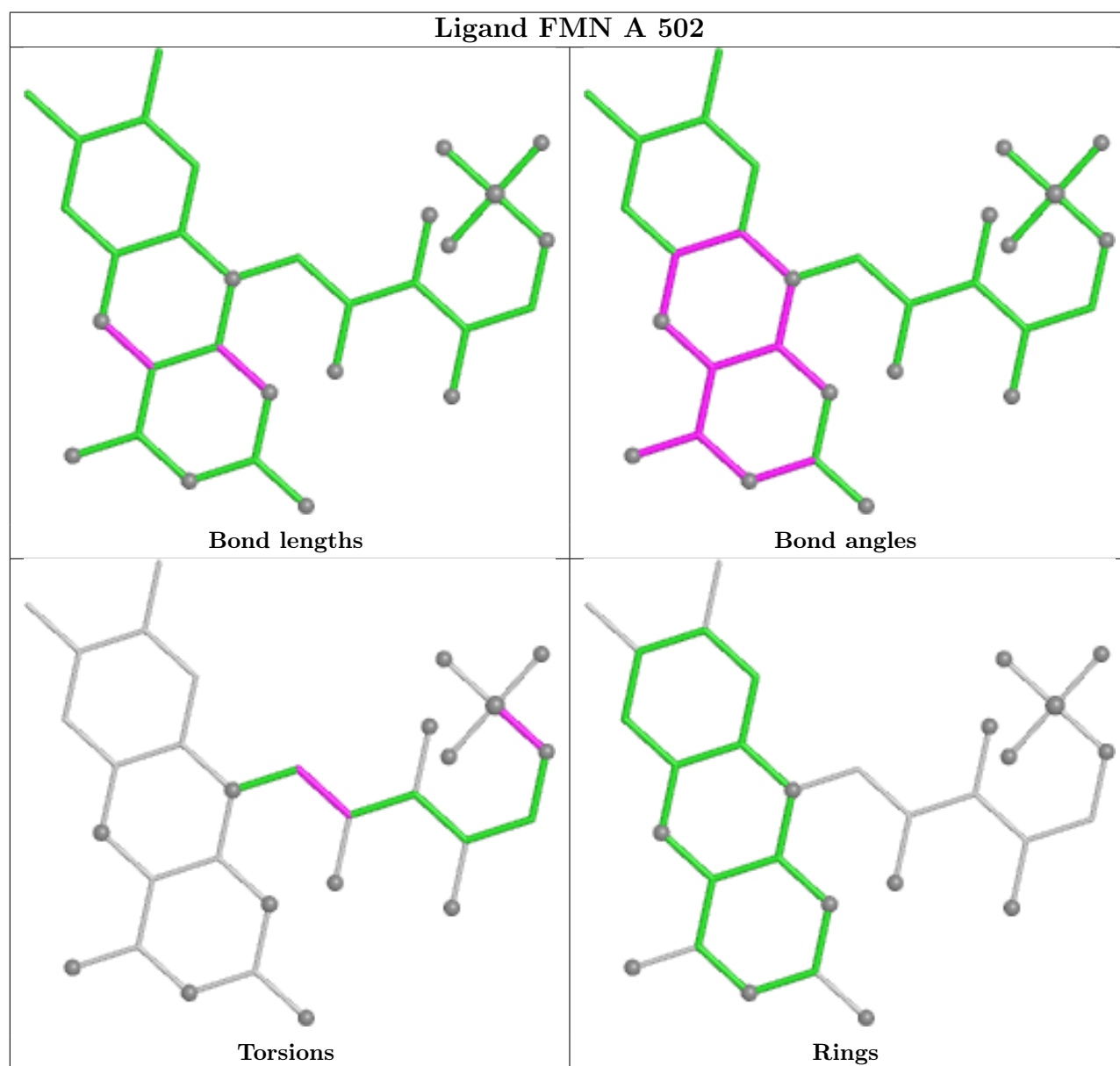
Mol	Chain	Res	Type	Atoms
47	j	202	PEE	C15-C16-C17-C18
47	j	201	PEE	O4-C10-C11-C12
47	j	201	PEE	O5-C30-C31-C32

There are no ring outliers.

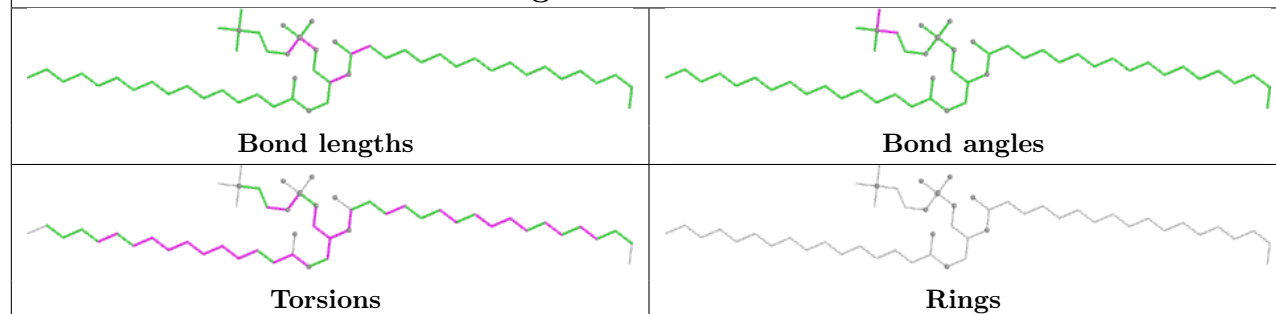
33 monomers are involved in 112 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
46	A	502	FMN	3	0
48	N	201	PLX	2	0
50	X	201	8Q1	1	0
54	s	401	CDL	4	0
45	A	501	SF4	2	0
54	r	503	CDL	8	0
47	r	501	PEE	2	0
54	l	703	CDL	5	0
54	V	202	CDL	6	0
47	Q	501	PEE	2	0
48	C	303	PLX	2	0
48	J	403	PLX	3	0
54	m	201	CDL	9	0
47	l	704	PEE	3	0
47	b	201	PEE	2	0
56	w	401	ADP	1	0
54	l	702	CDL	13	0
51	J	401	NDP	3	0
48	j	203	PLX	3	0
47	W	201	PEE	2	0
54	n	101	CDL	3	0
48	g	201	PLX	5	0
48	a	202	PLX	1	0
48	r	502	PLX	5	0
49	J	402	UQ	2	0
49	C	304	UQ	6	0
47	C	302	PEE	1	0
54	a	201	CDL	3	0
47	l	701	PEE	1	0
54	N	202	CDL	3	0
54	V	201	CDL	4	0
47	Q	502	PEE	3	0
47	j	201	PEE	3	0

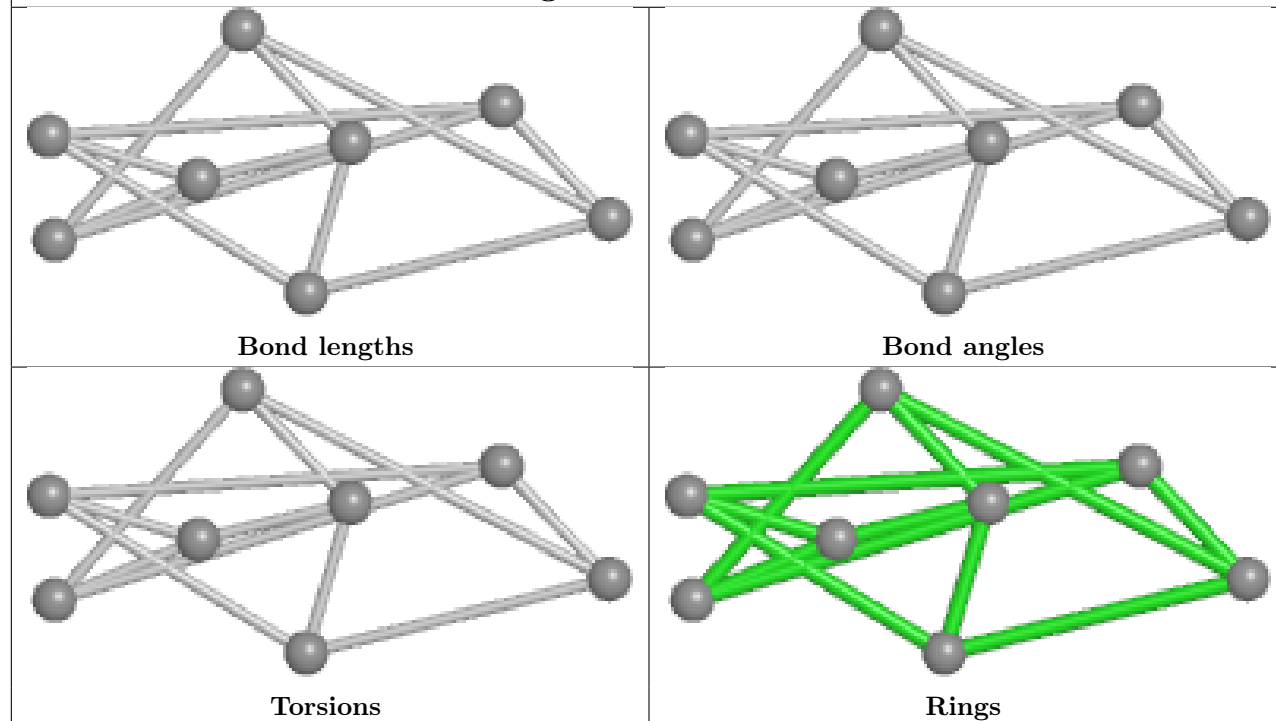
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



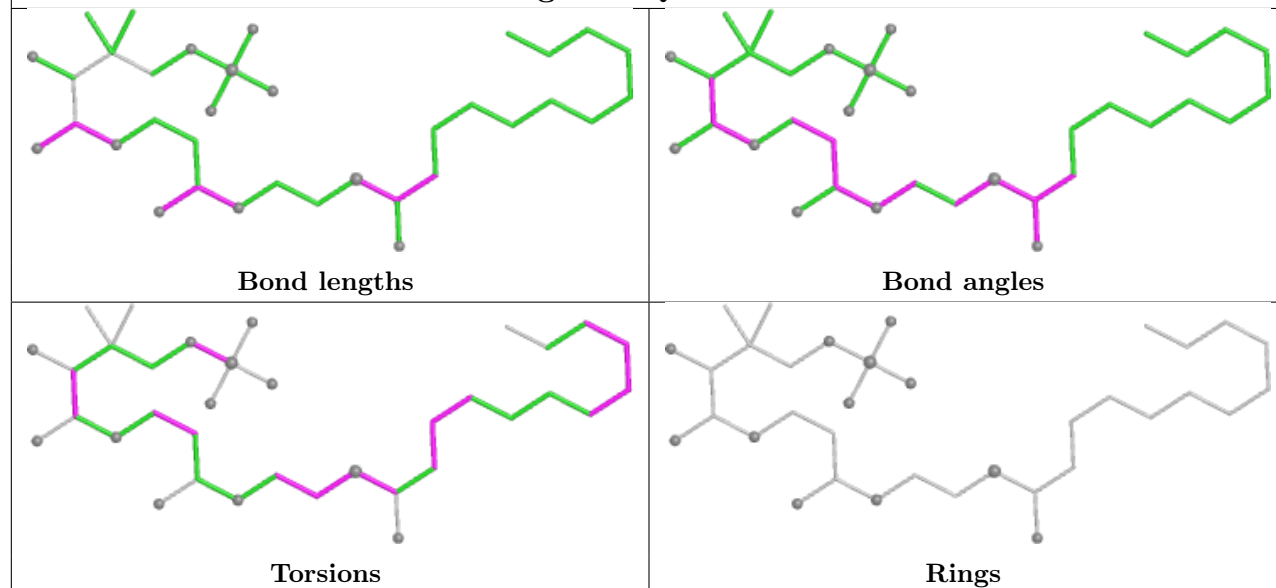
Ligand PLX N 201

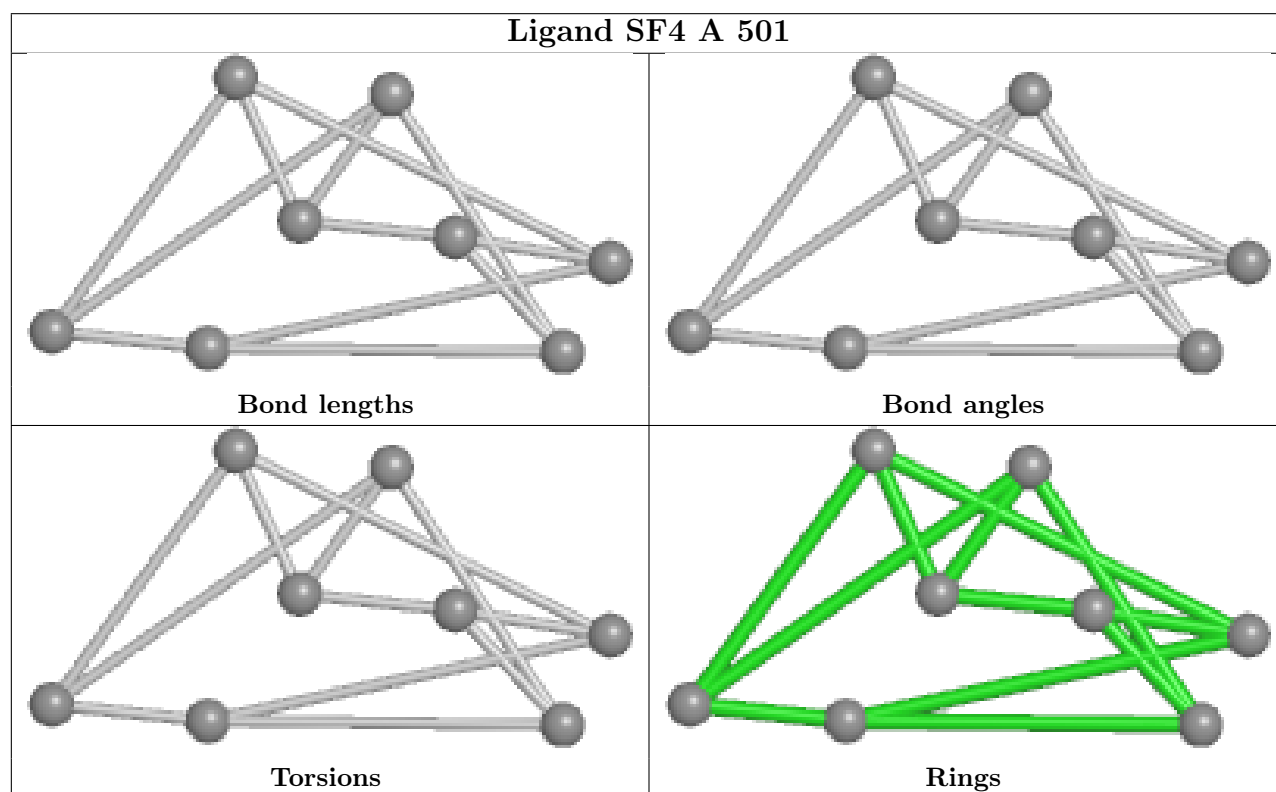
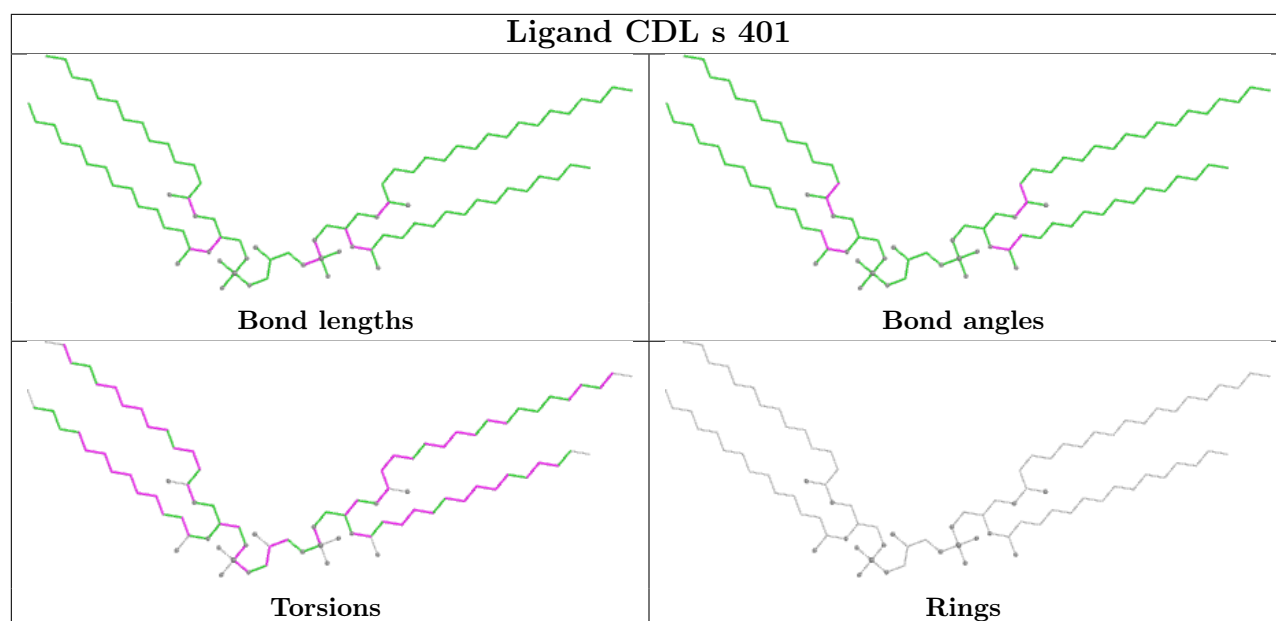


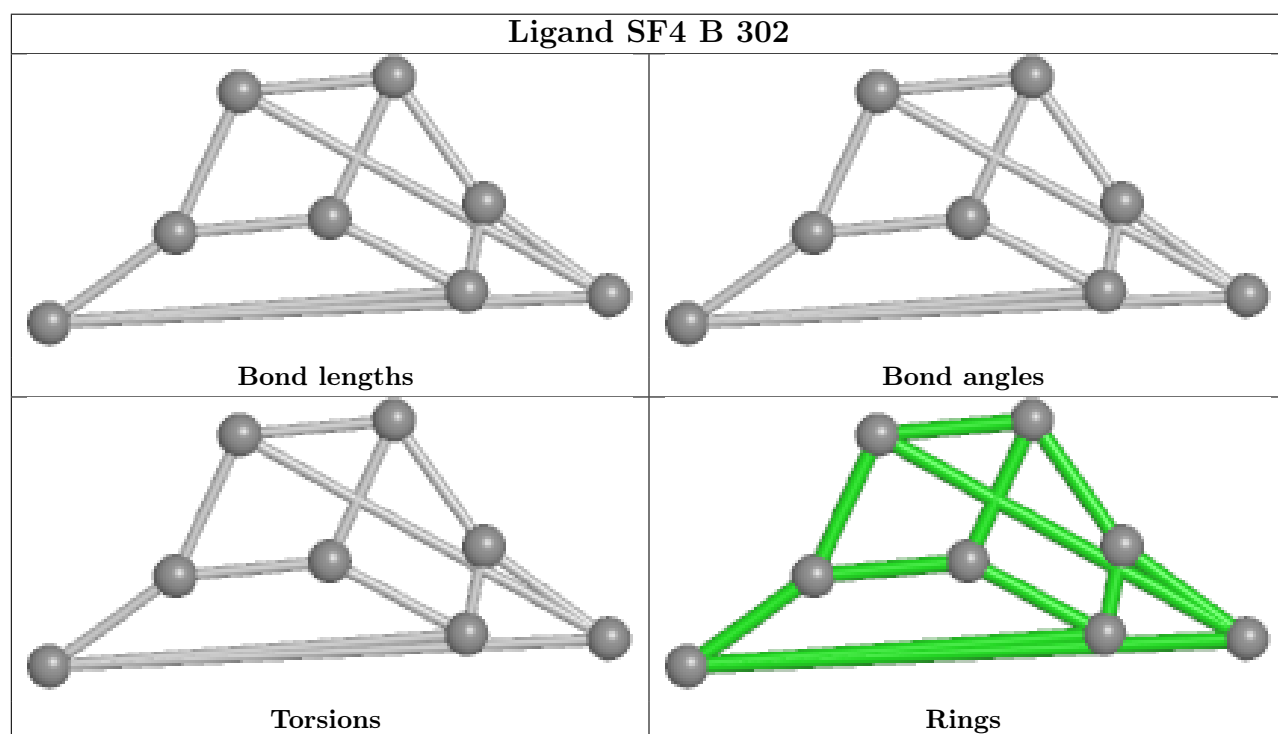
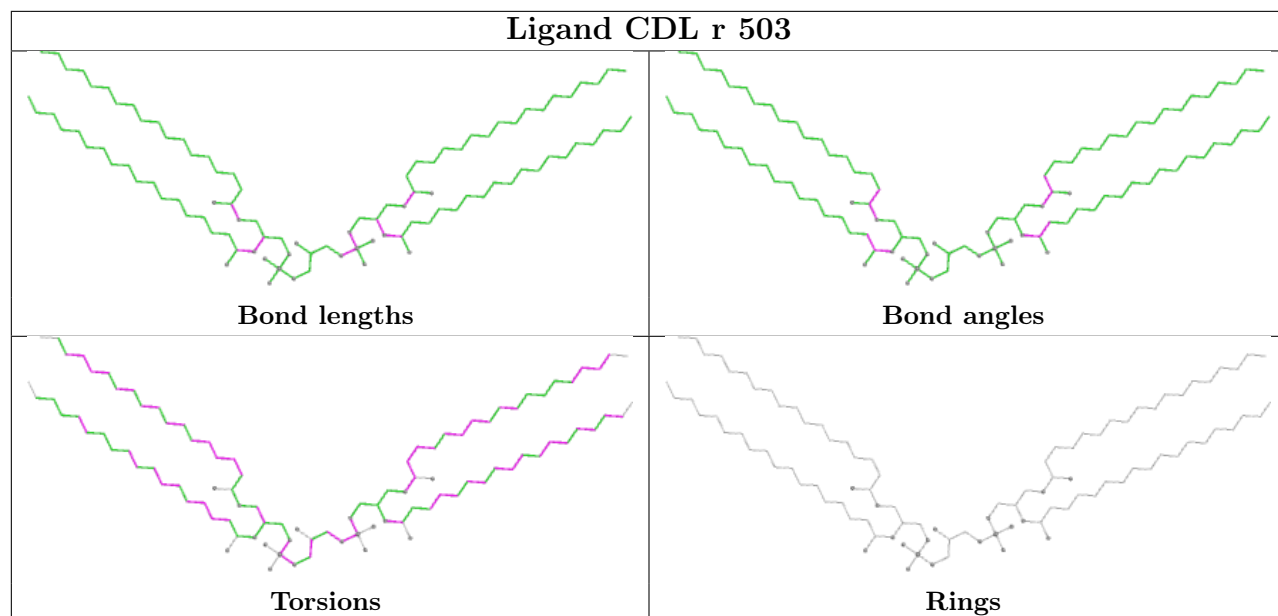
Ligand SF4 B 301

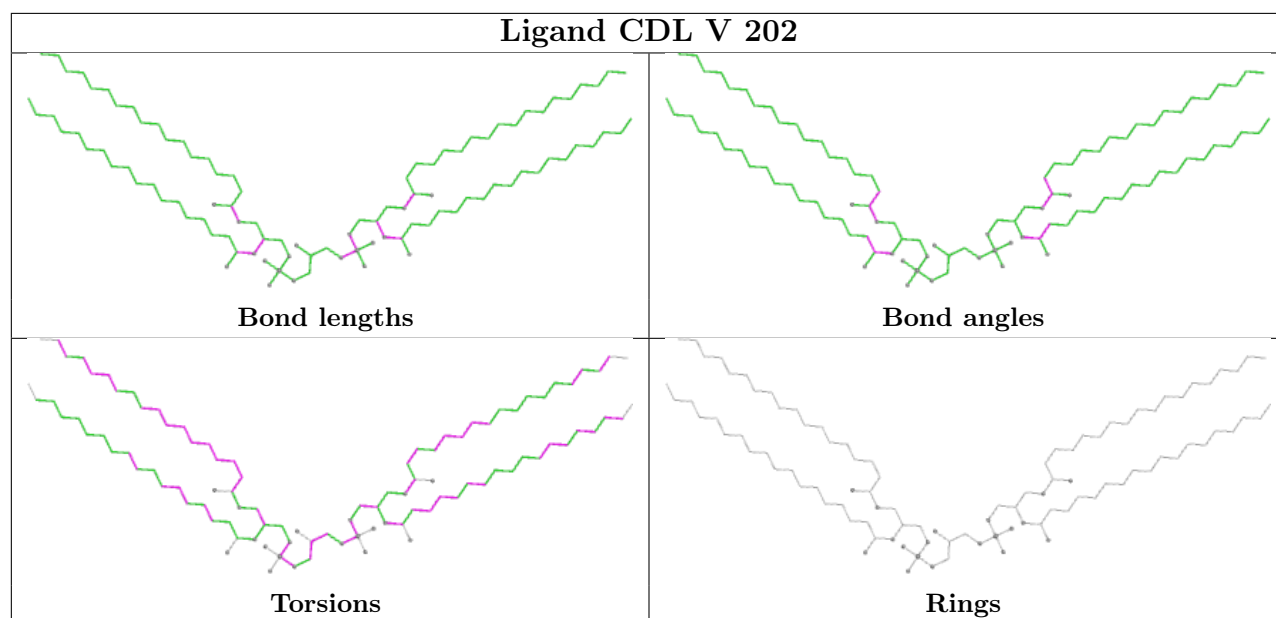
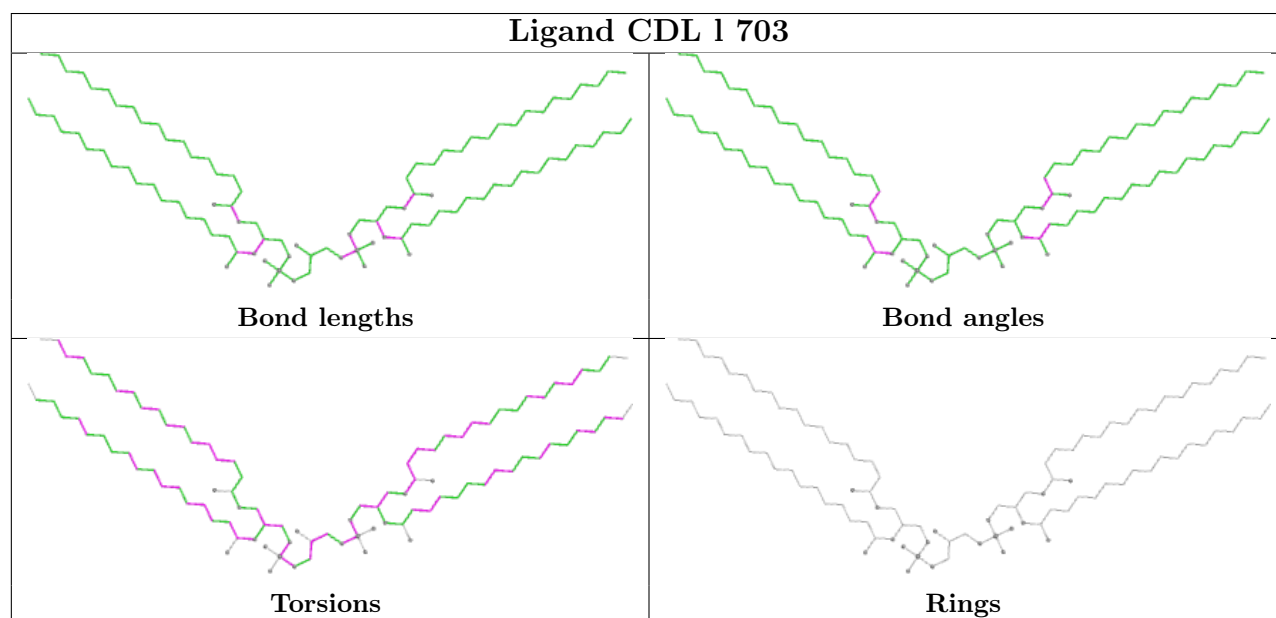
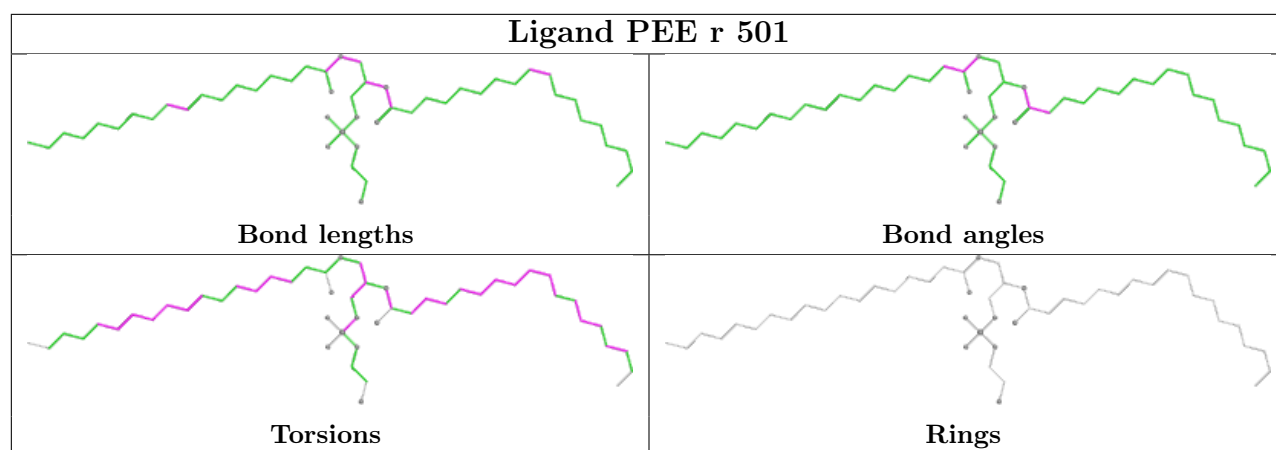


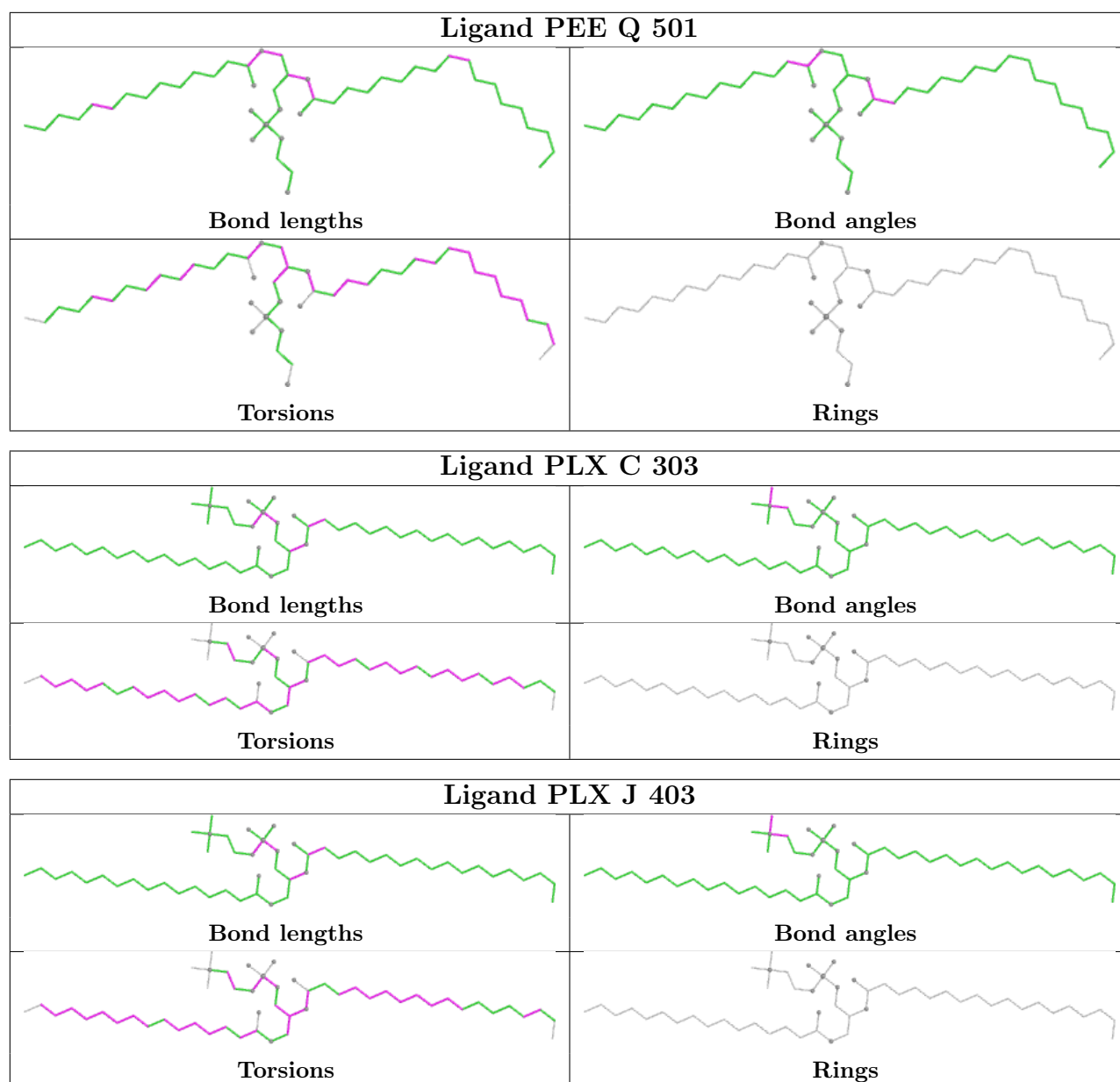
Ligand 8Q1 X 201

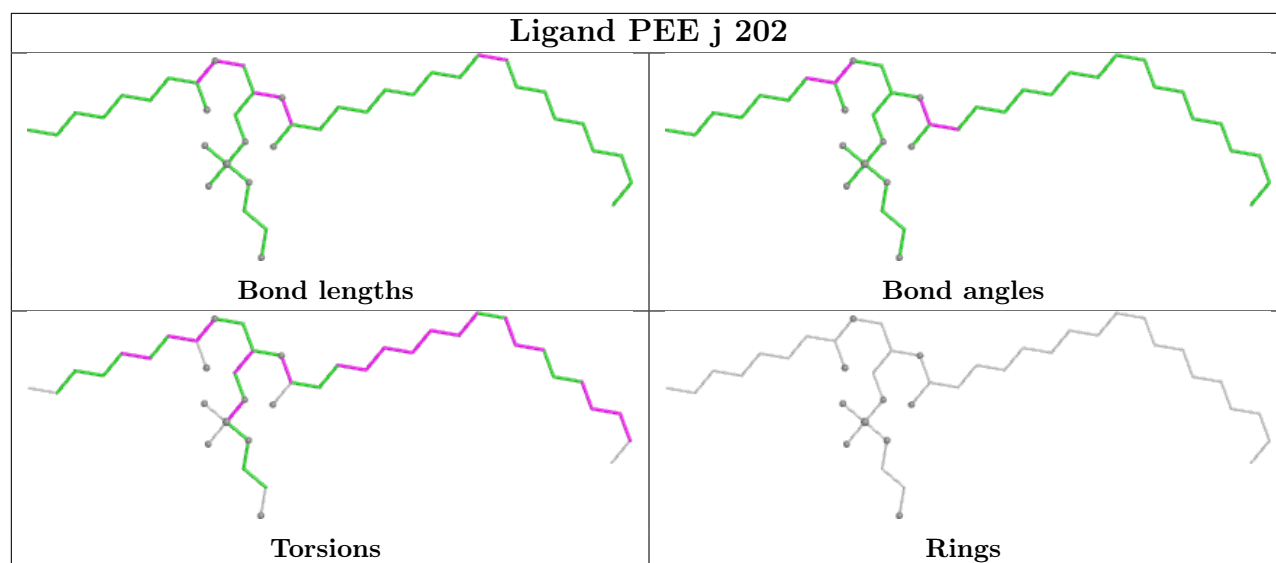
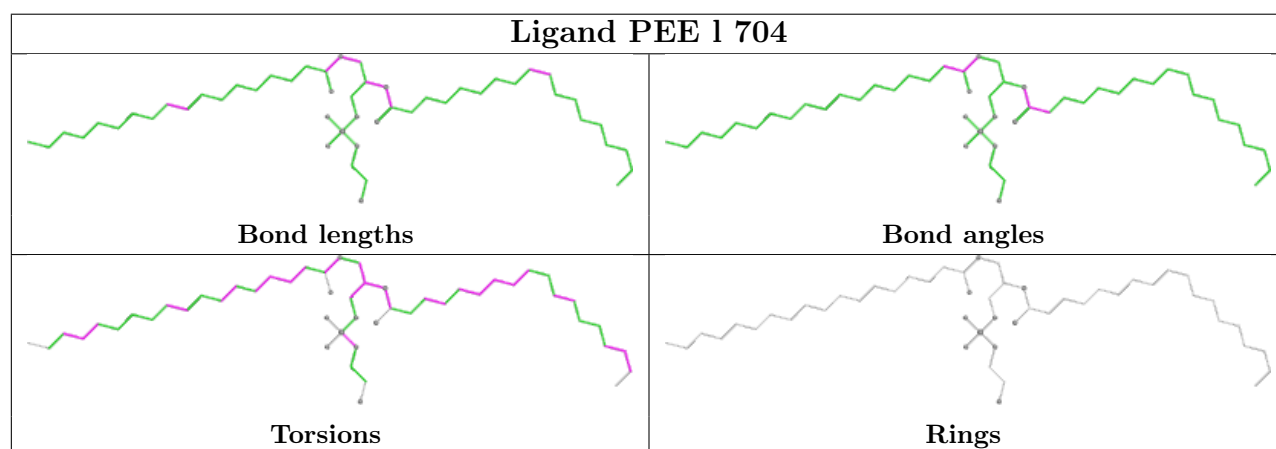
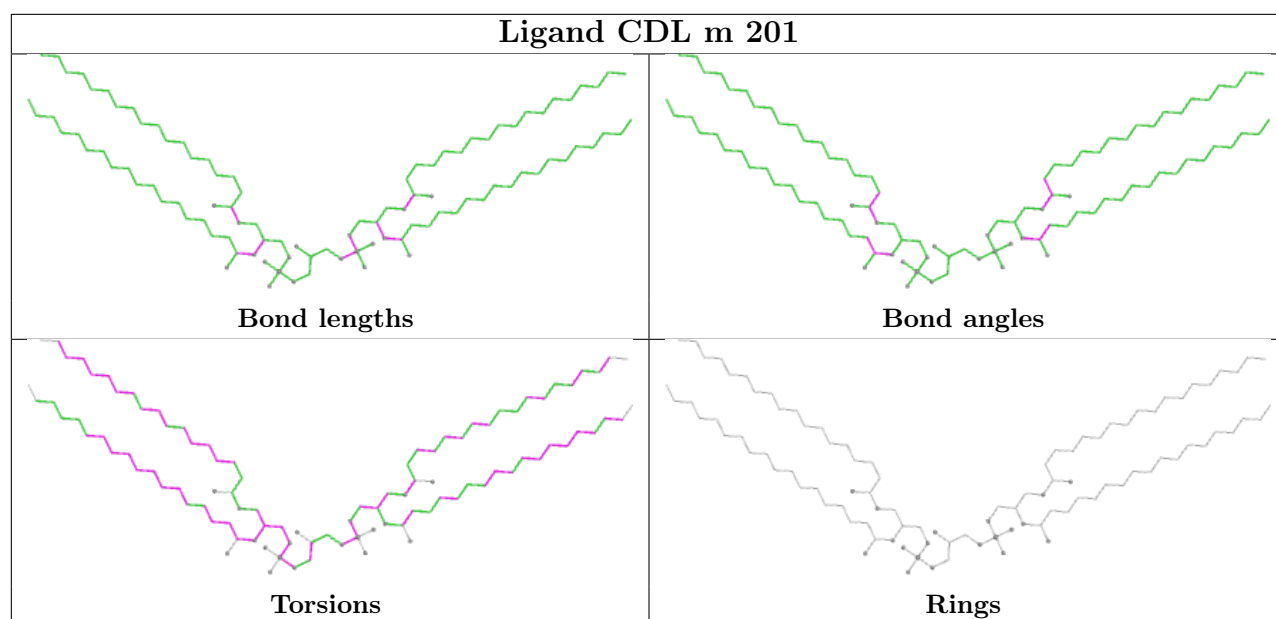


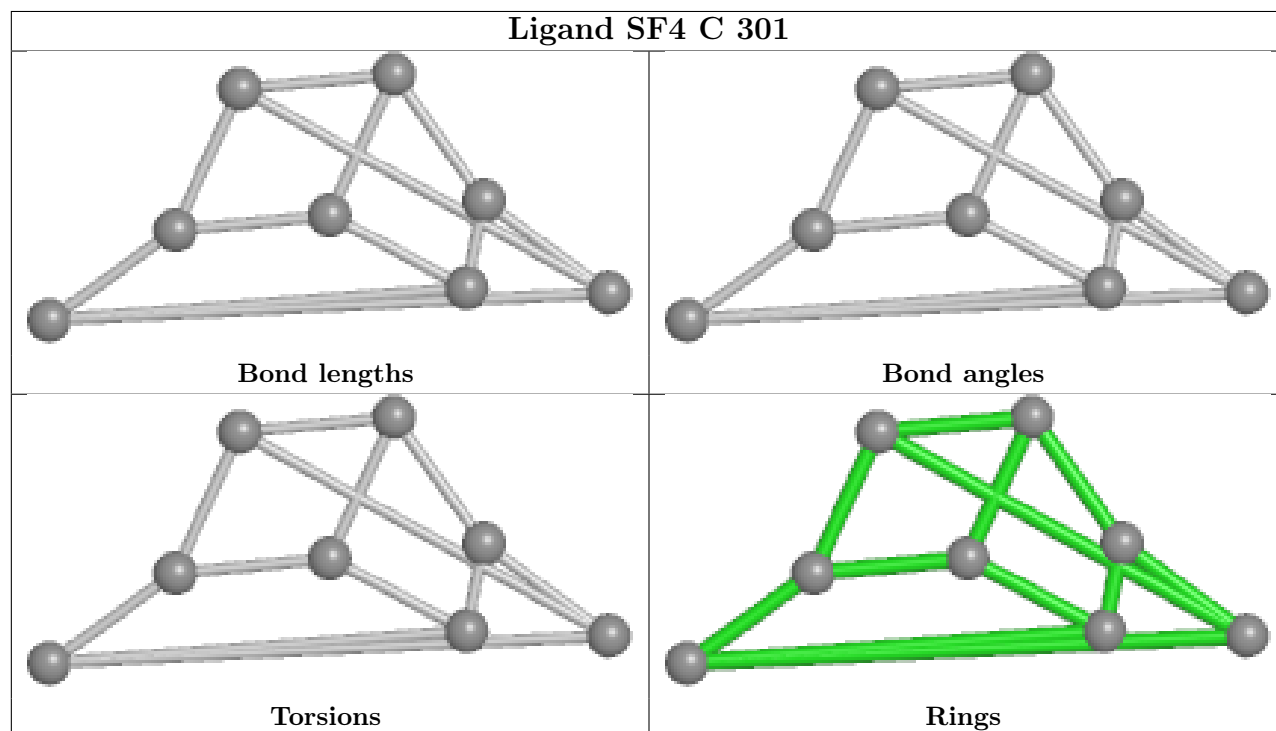
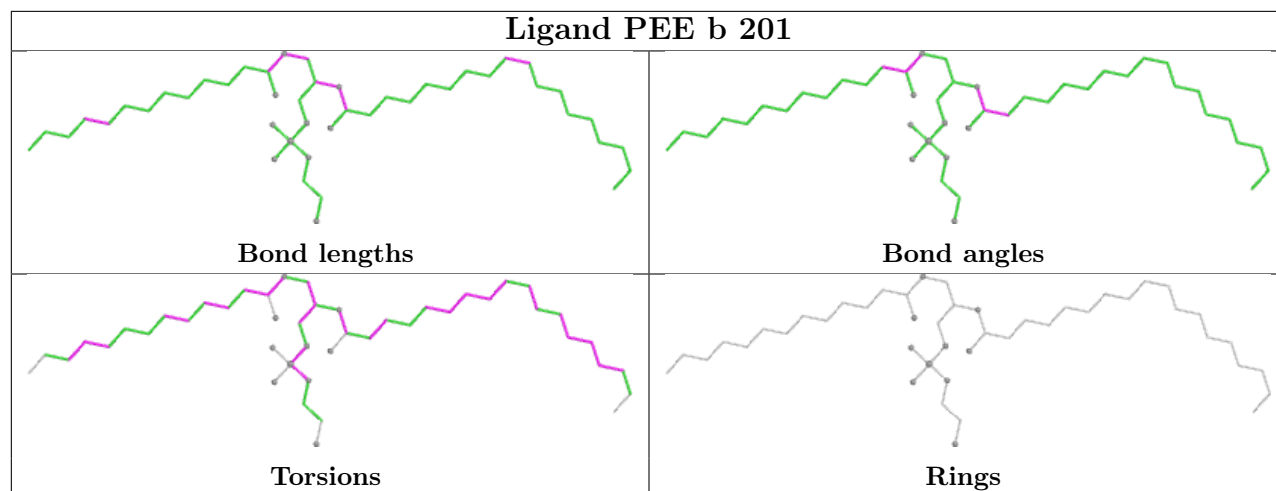




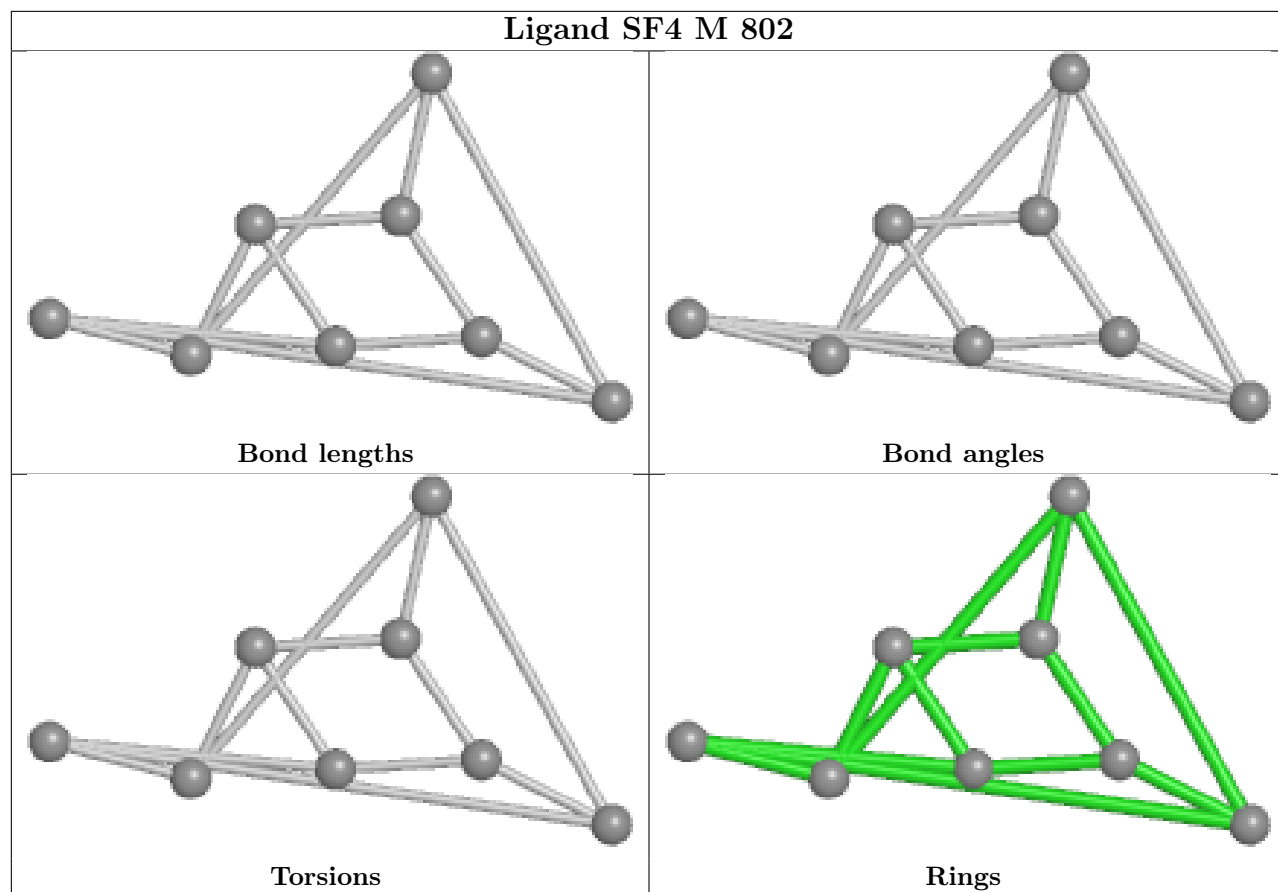




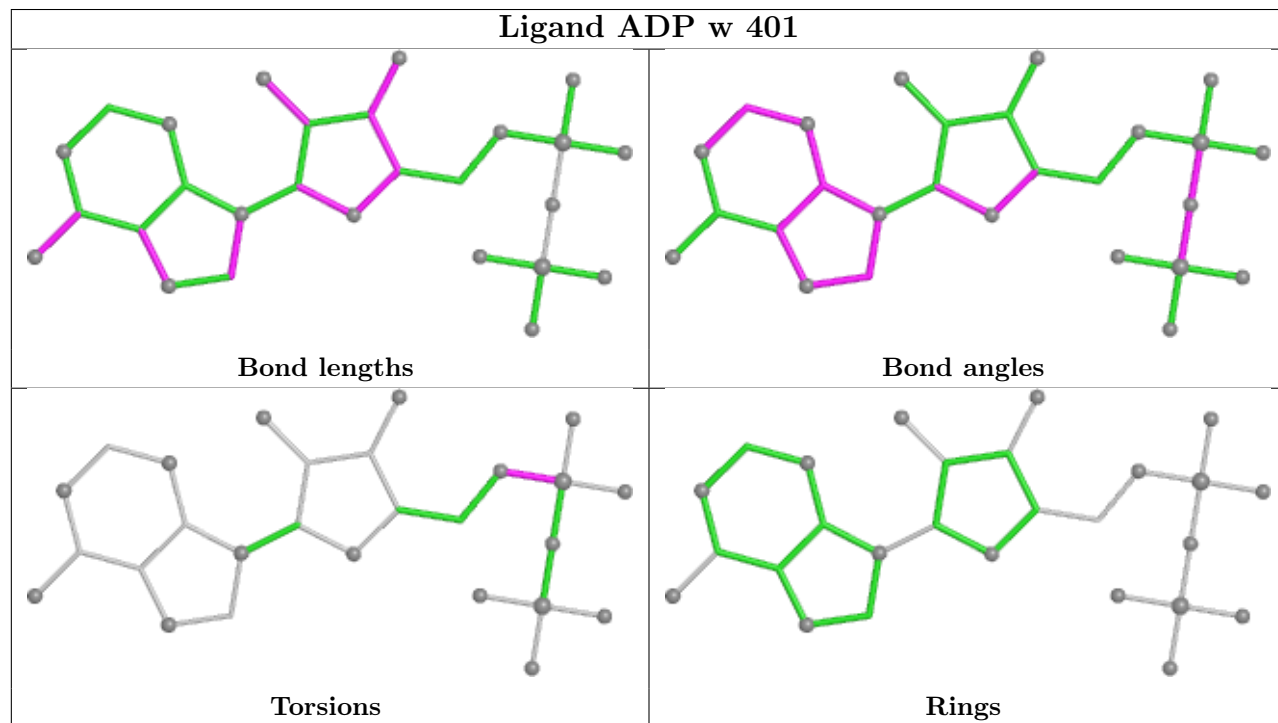


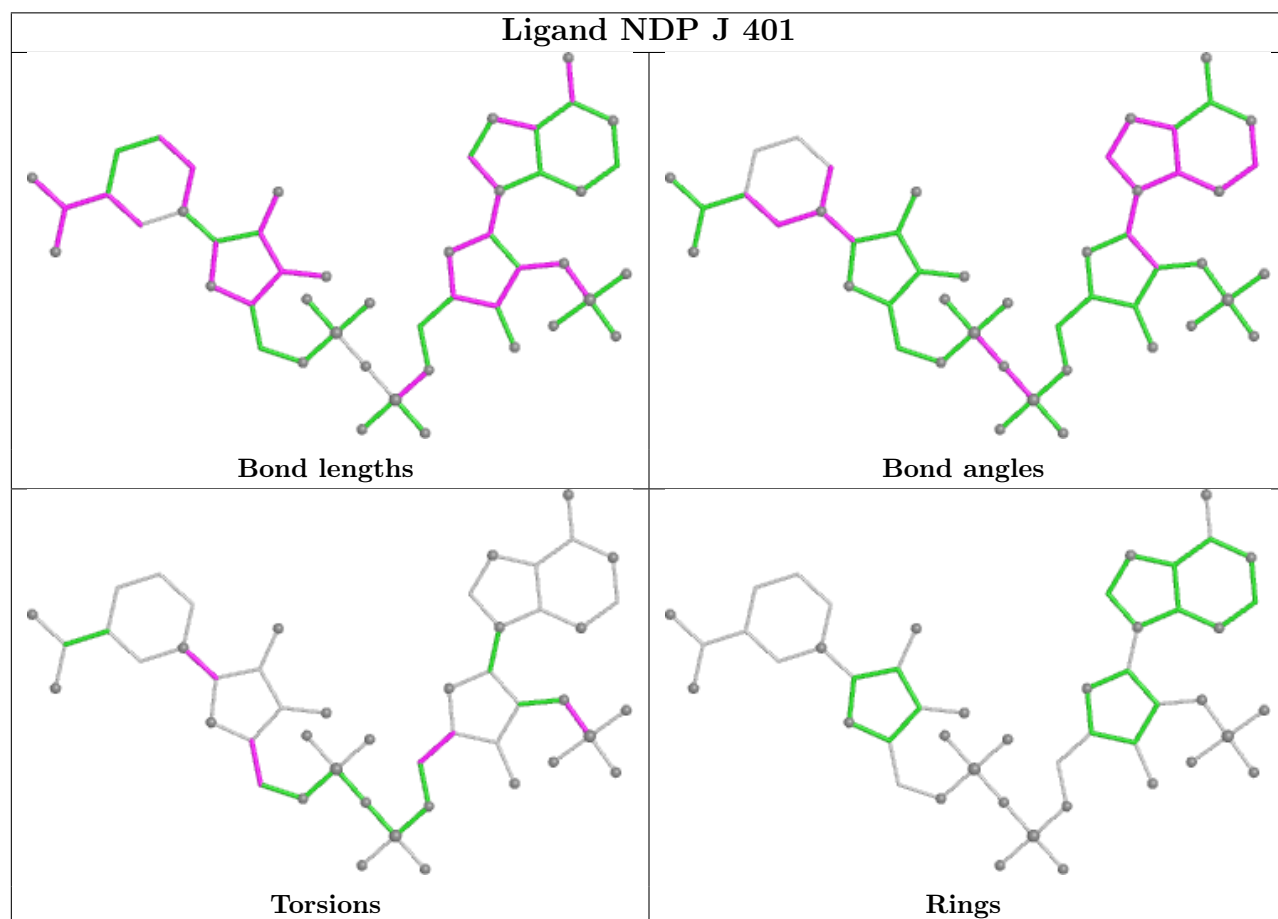
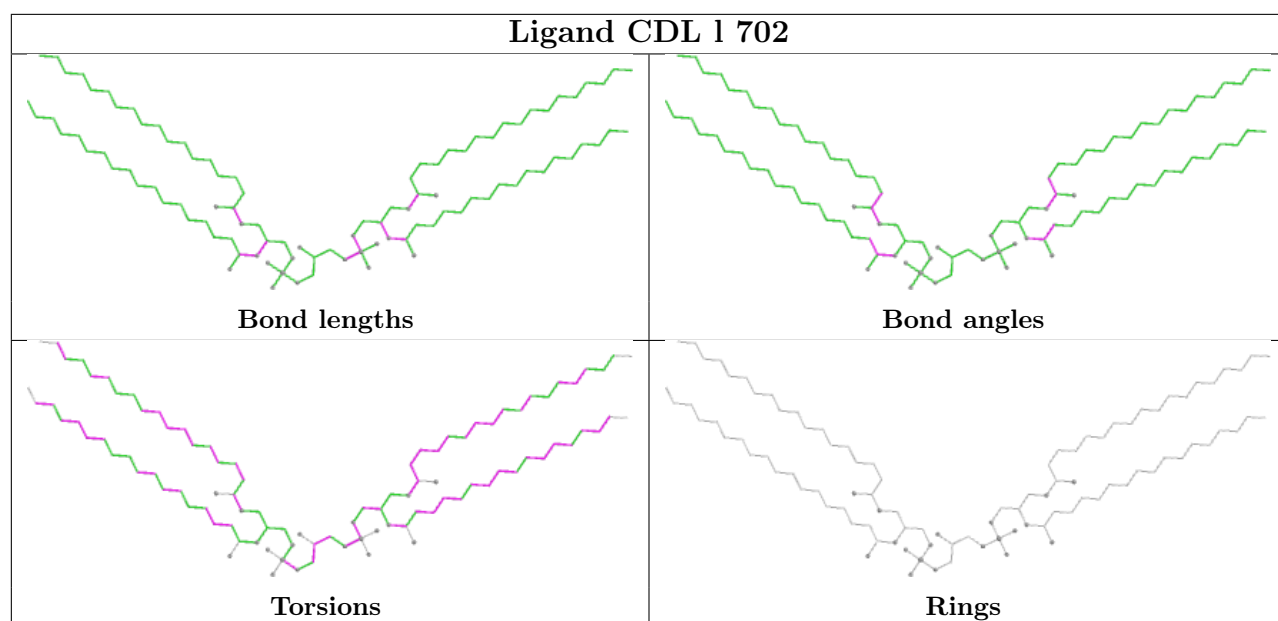


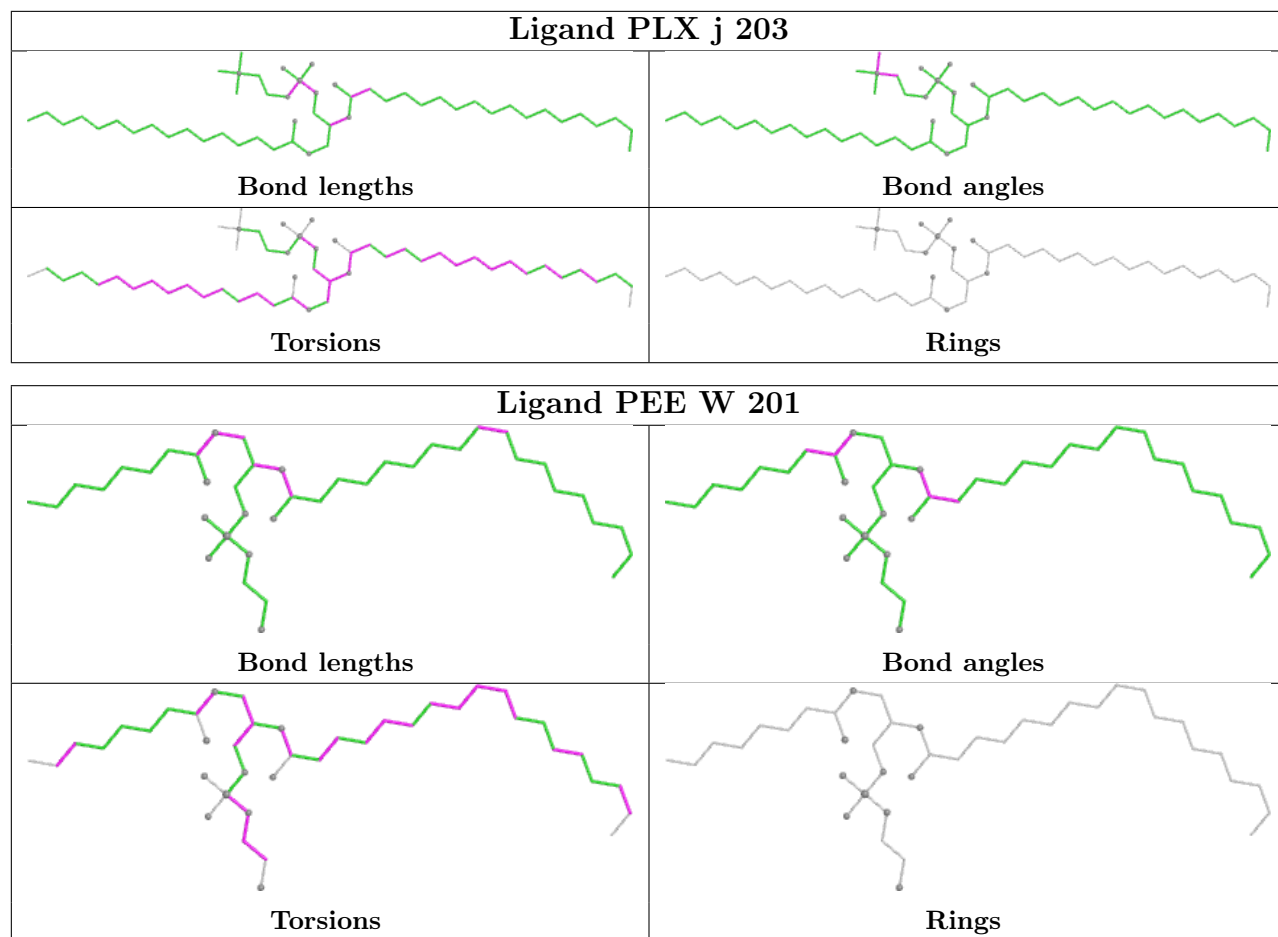
Ligand SF4 M 802



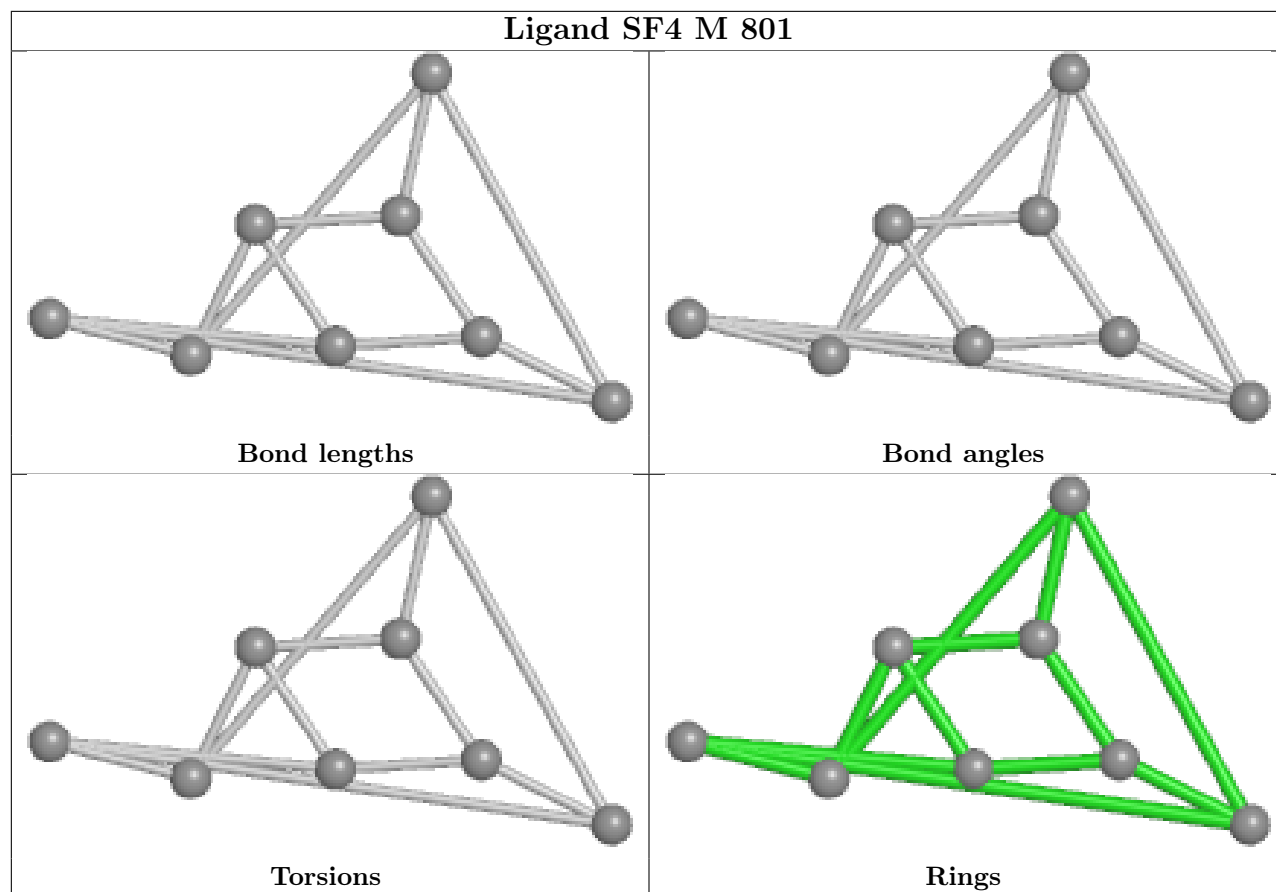
Ligand ADP w 401



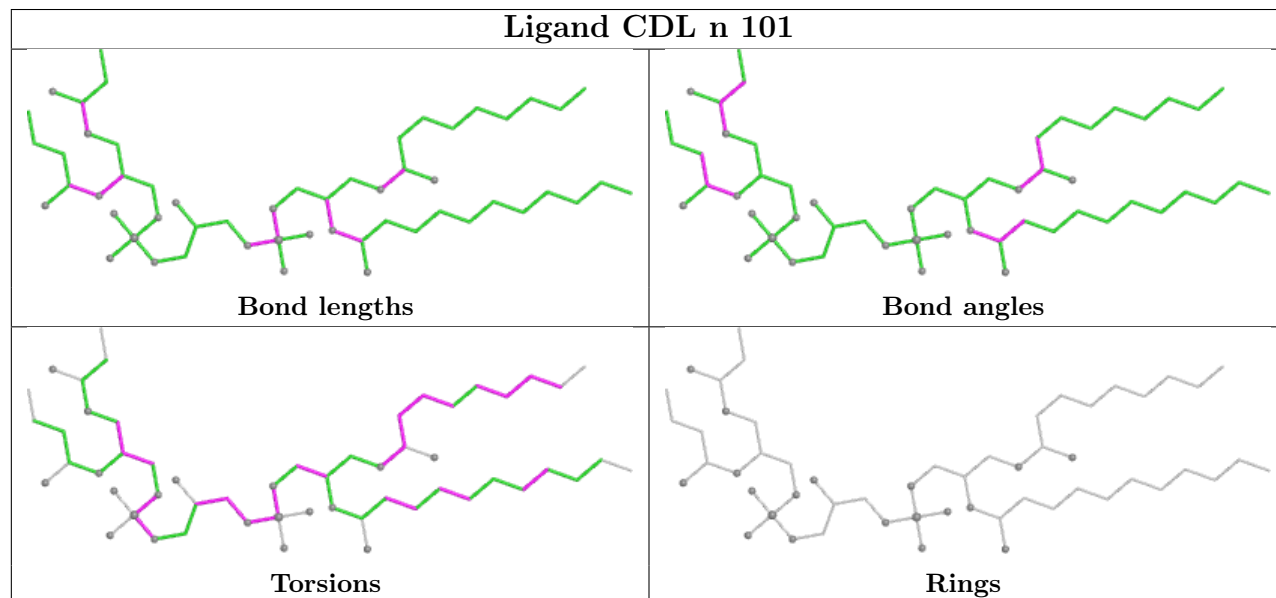


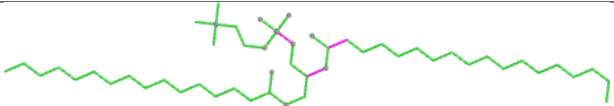
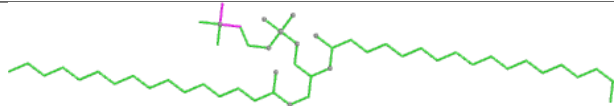
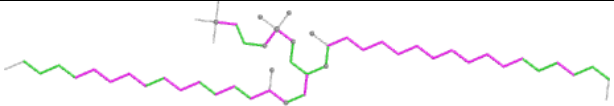
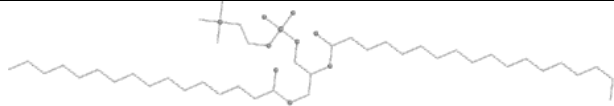
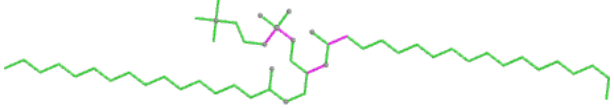
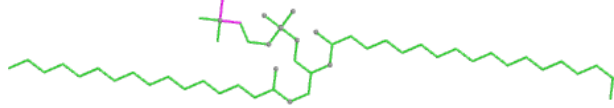
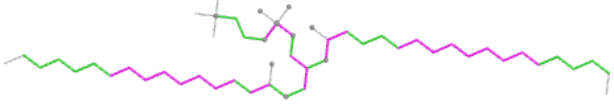
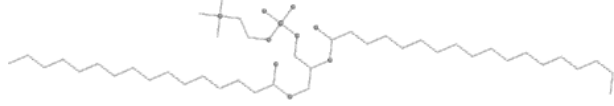
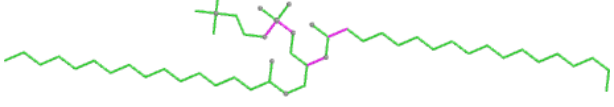
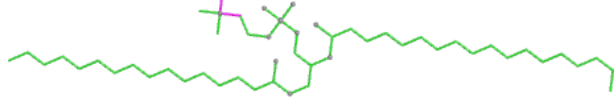
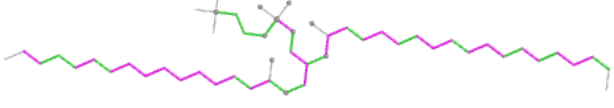
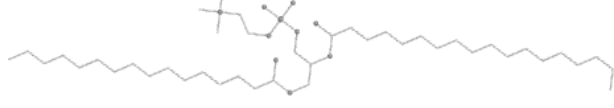
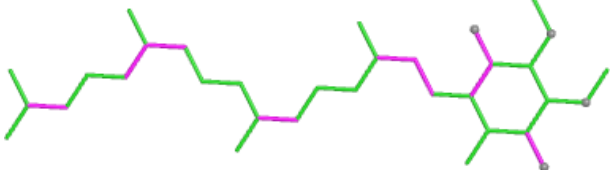
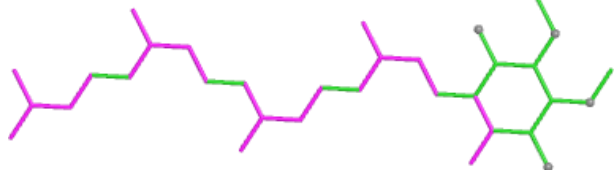
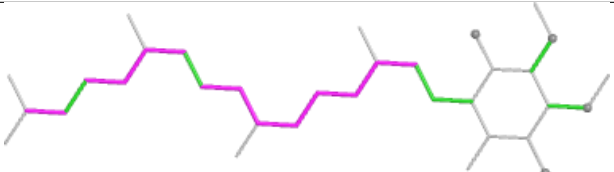
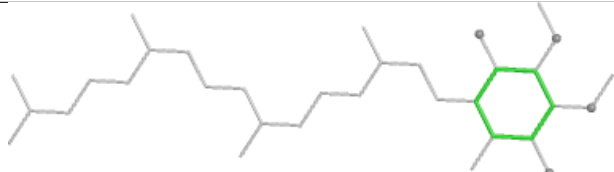


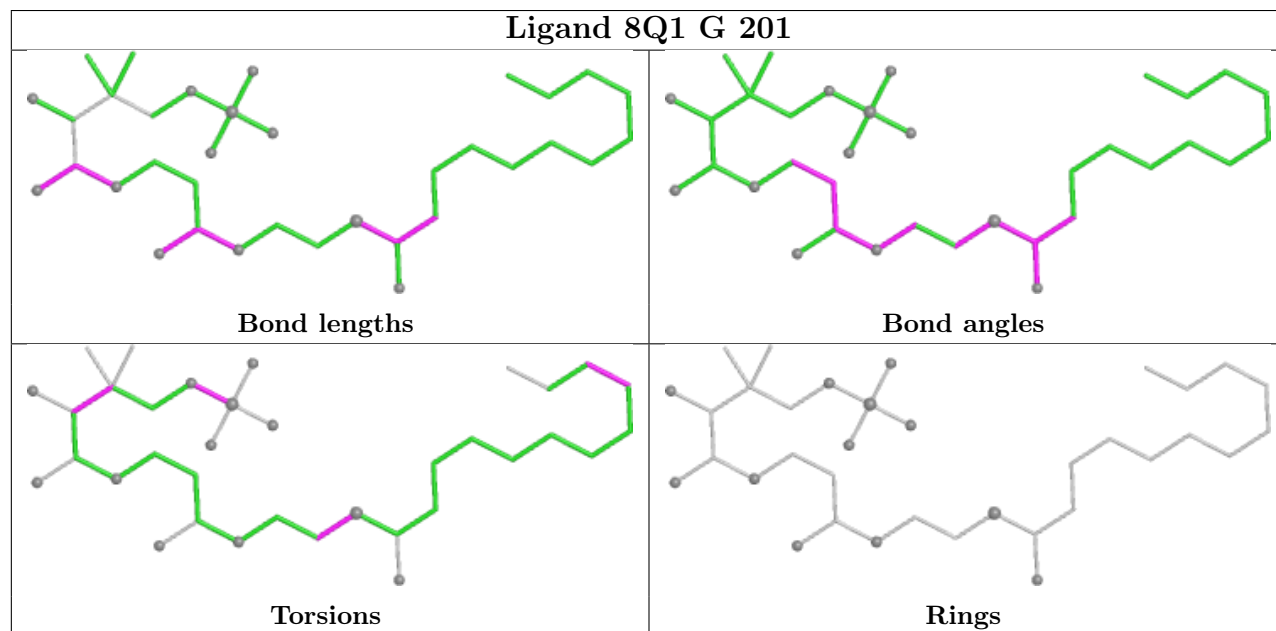
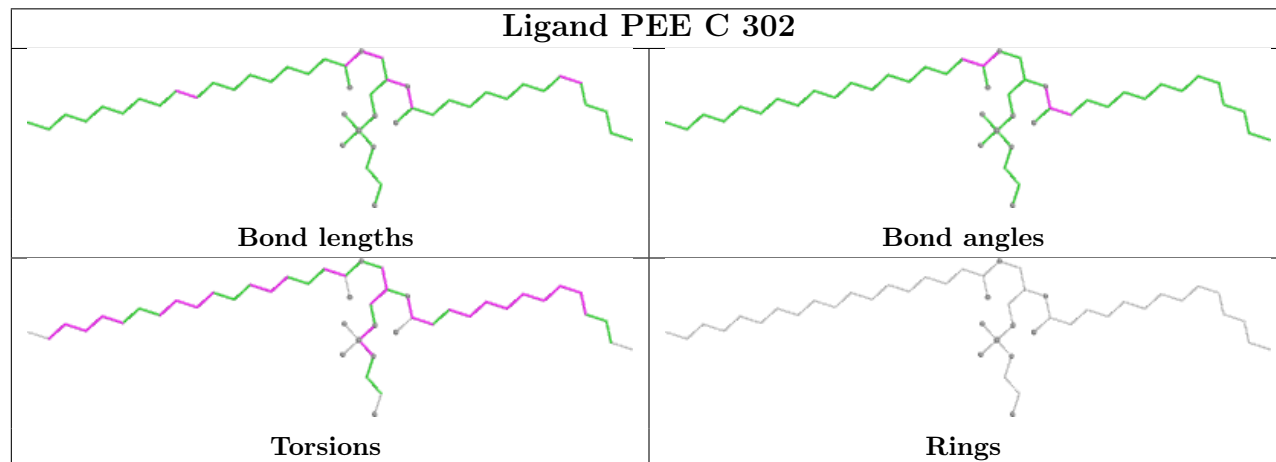
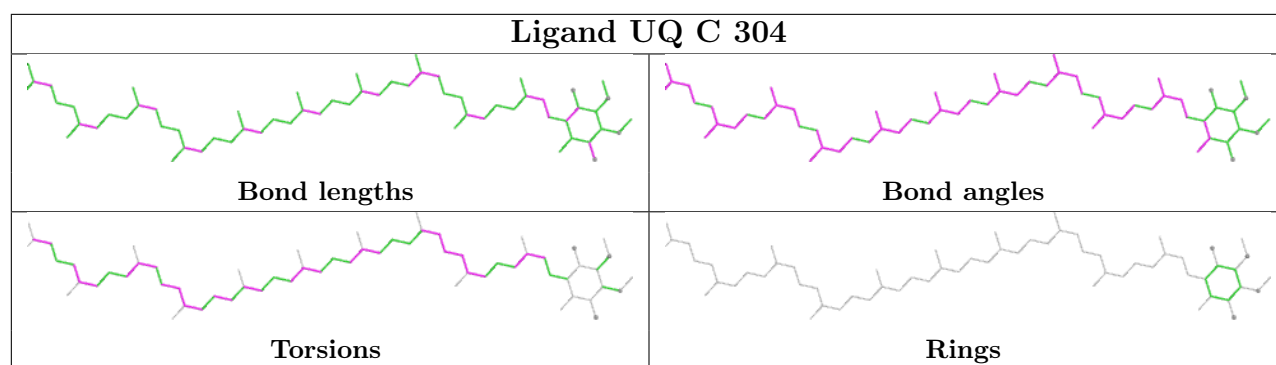
Ligand SF4 M 801

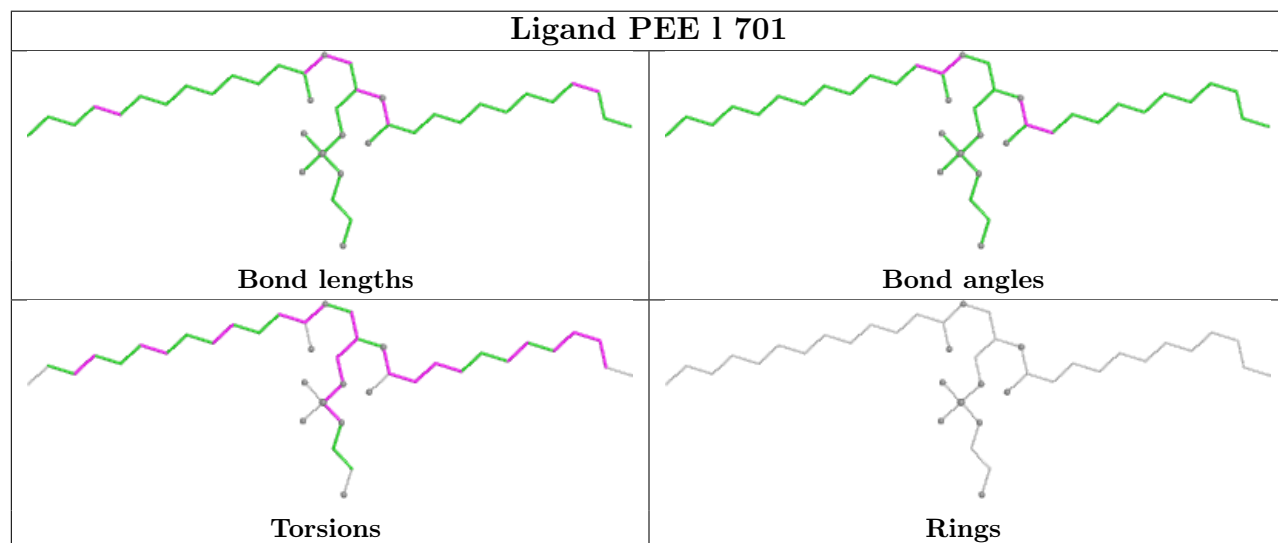
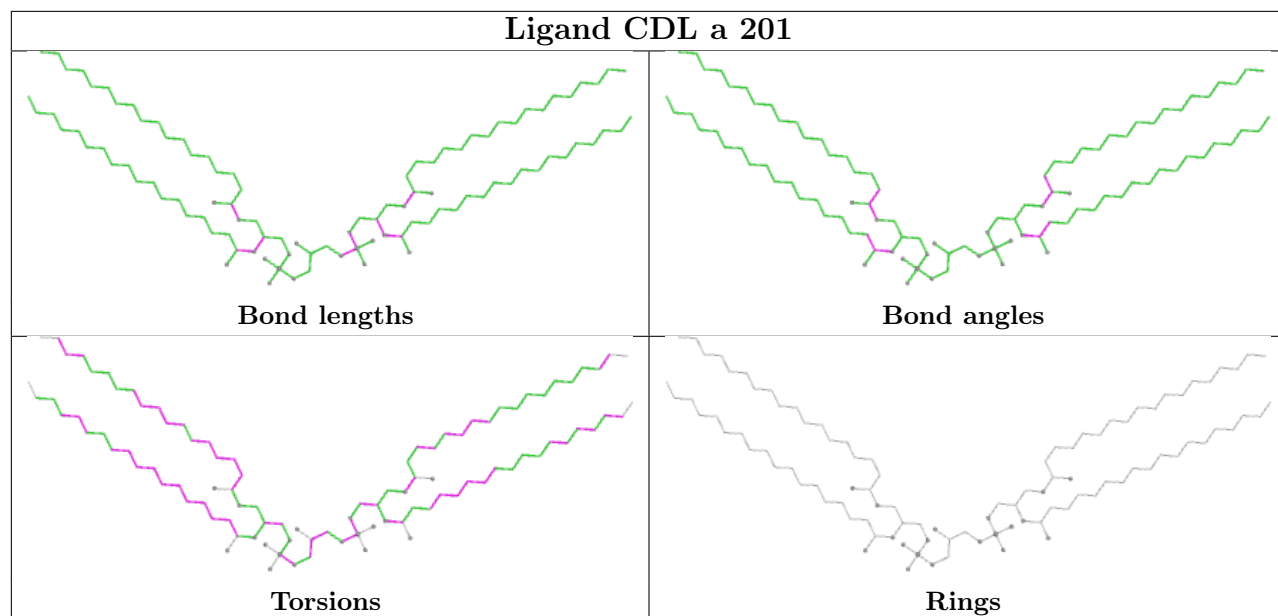


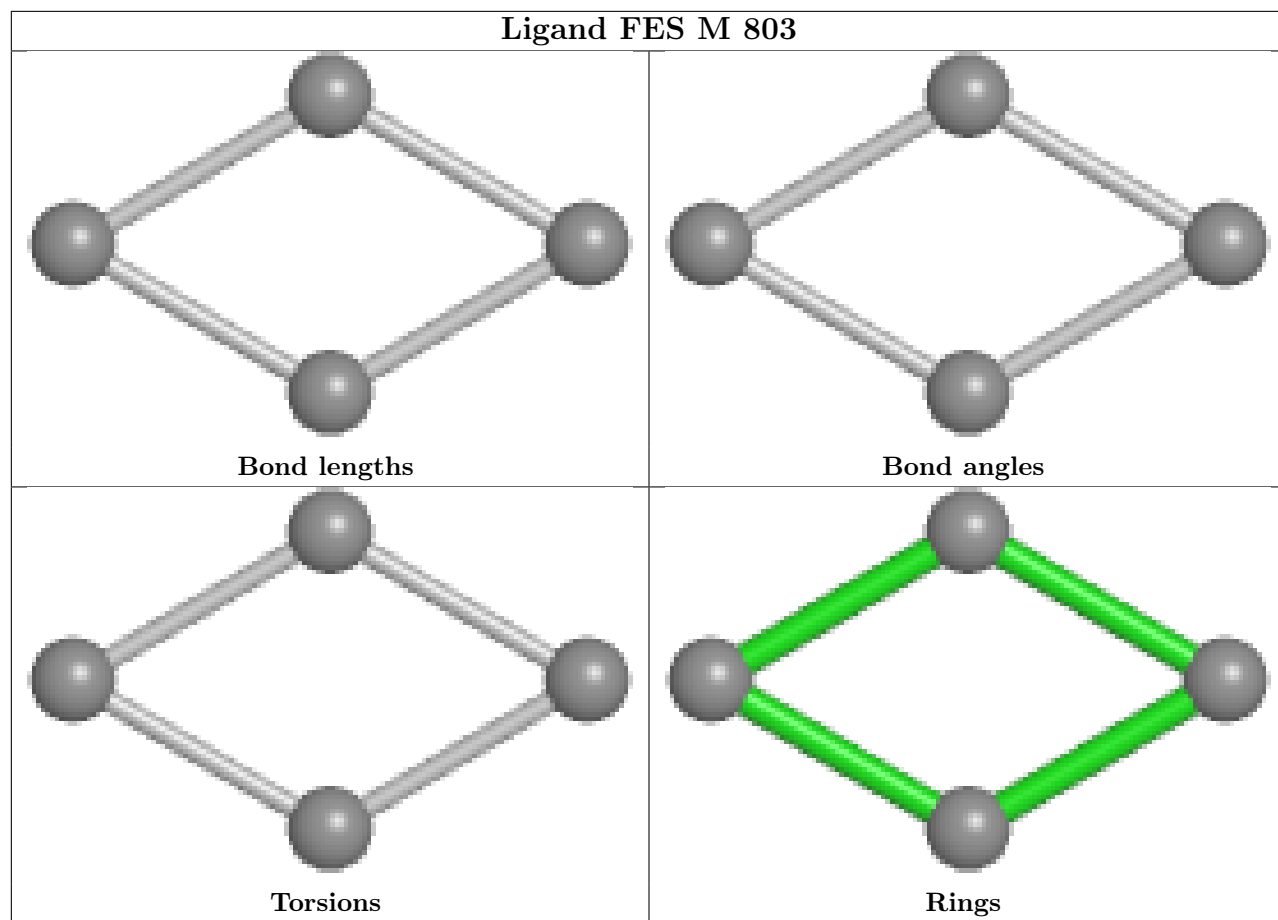
Ligand CDL n 101

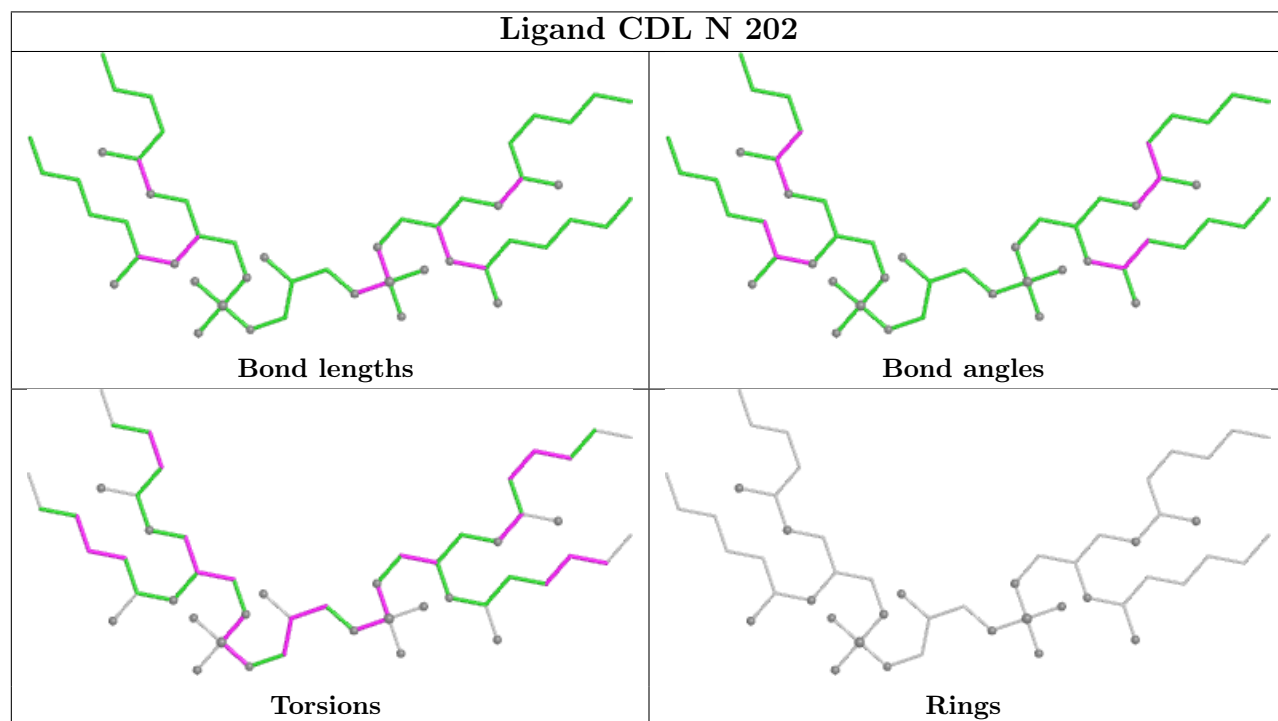
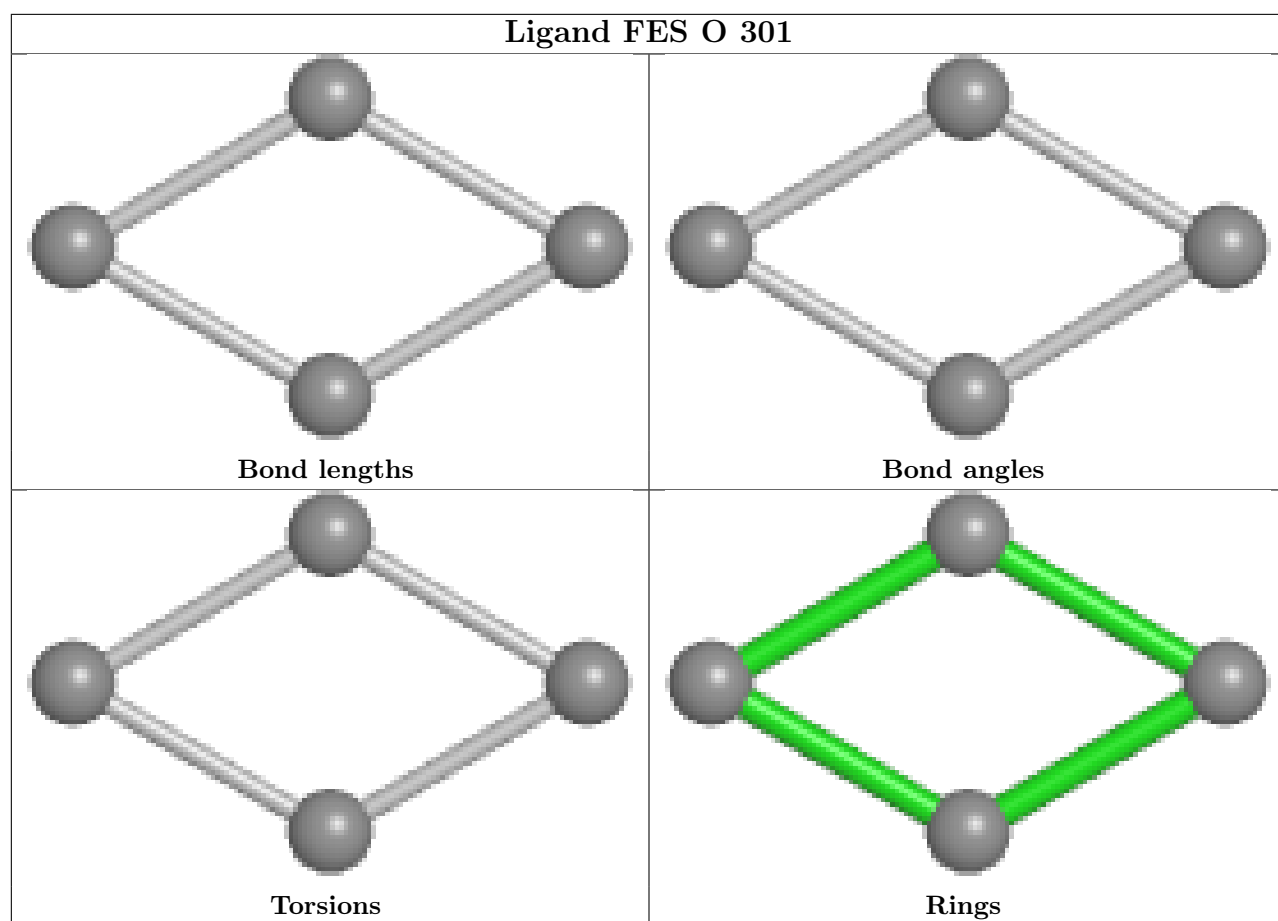


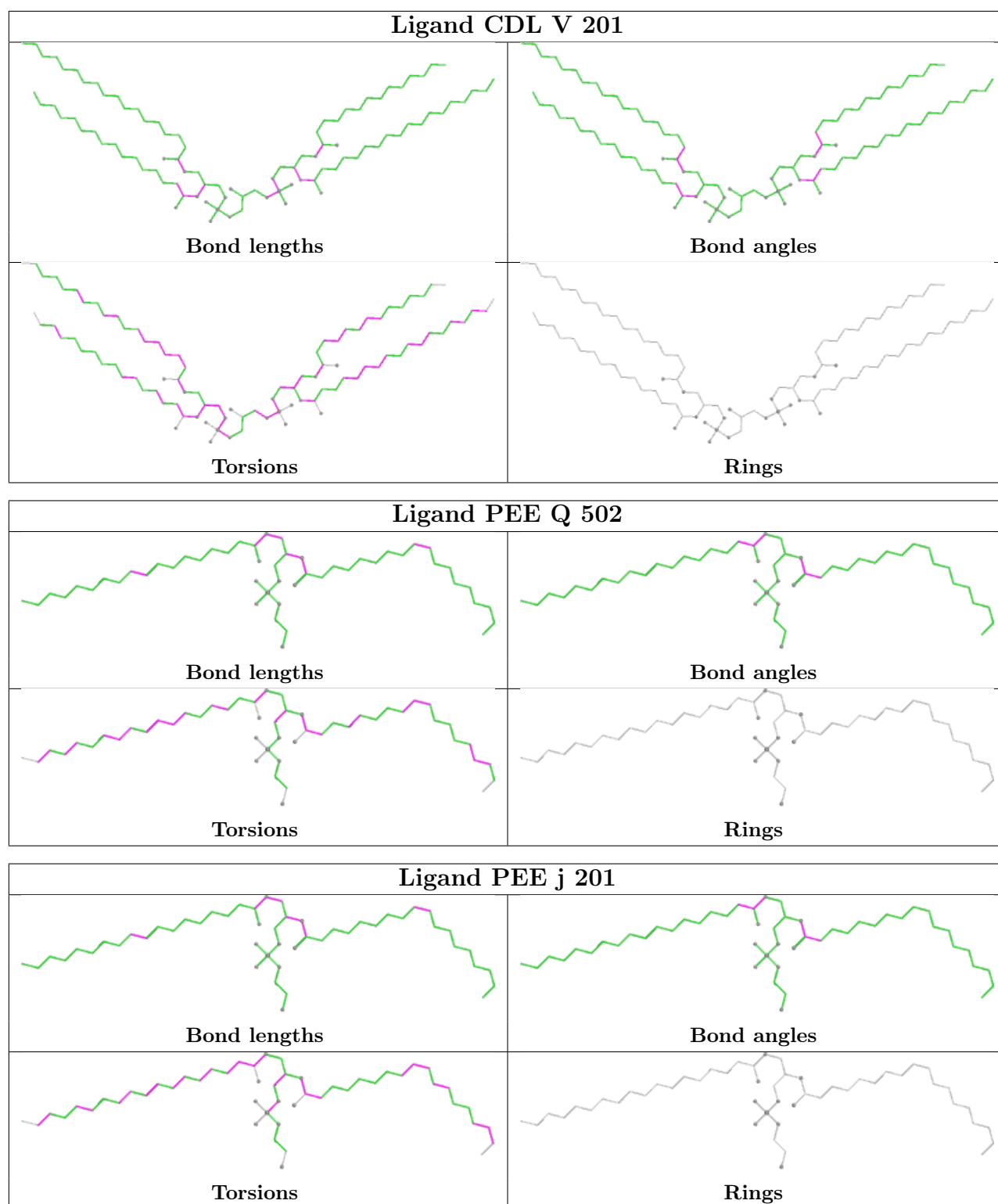
Ligand PLX g 201	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand PLX a 202	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand PLX r 502	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand UQ J 402	
 Bond lengths	 Bond angles
 Torsions	 Rings











5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

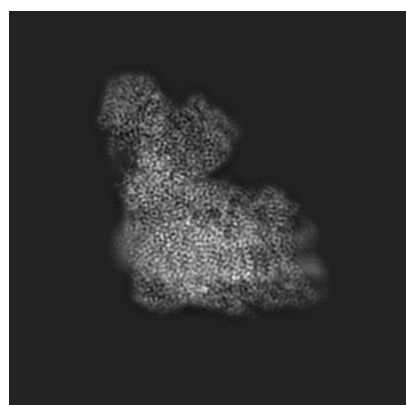
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32230. These allow visual inspection of the internal detail of the map and identification of artifacts.

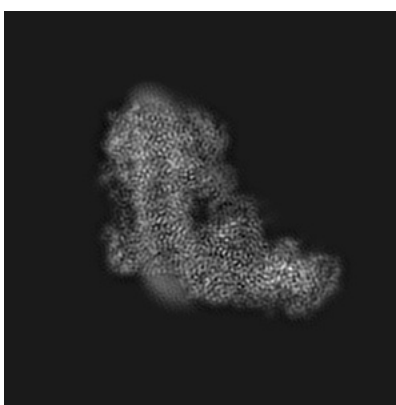
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

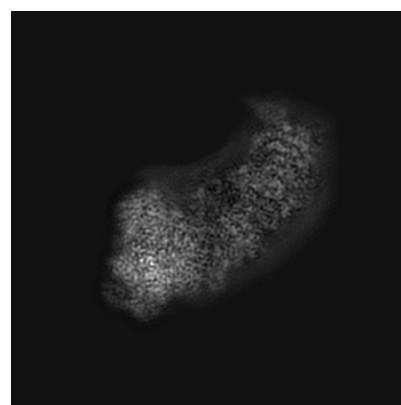
6.1.1 Primary map



X



Y

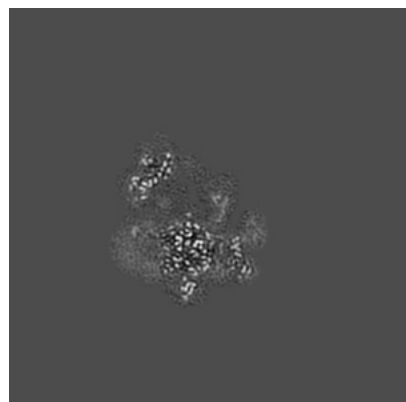


Z

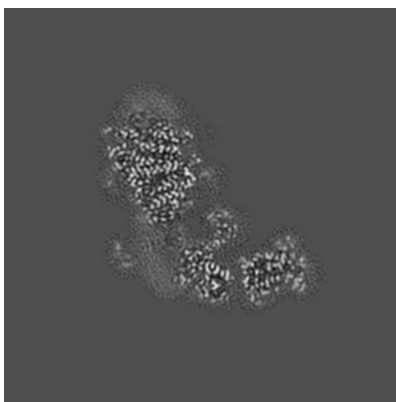
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

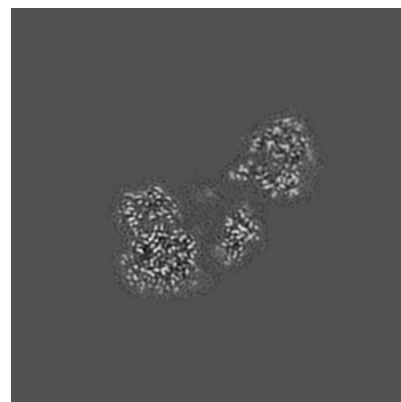
6.2.1 Primary map



X Index: 165



Y Index: 165



Z Index: 165

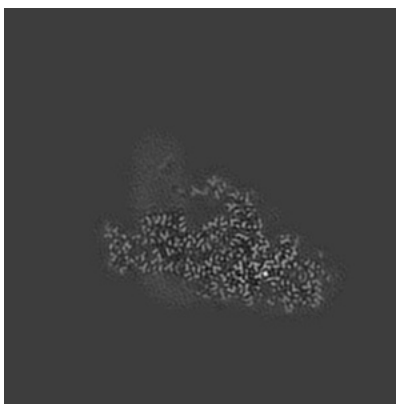
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

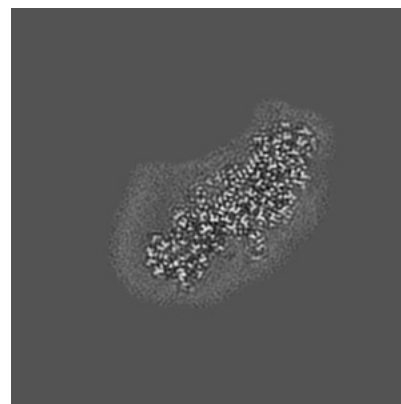
6.3.1 Primary map



X Index: 115



Y Index: 120

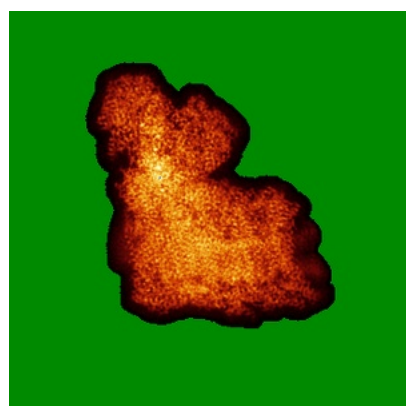


Z Index: 137

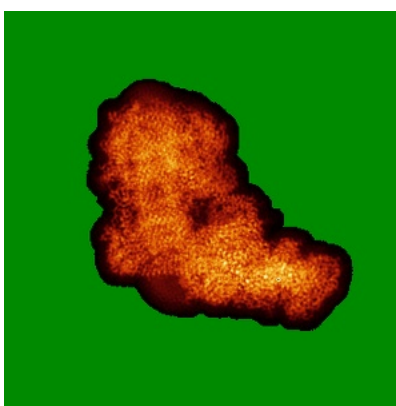
The images above show the largest variance slices of the map in three orthogonal directions.

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

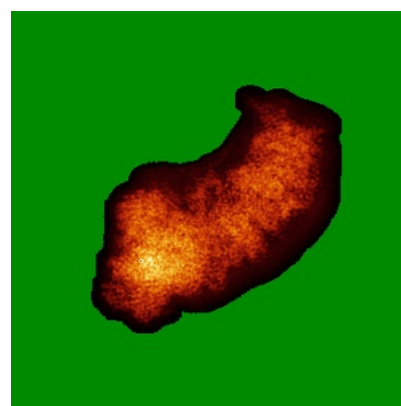
6.4.1 Primary map



X



Y

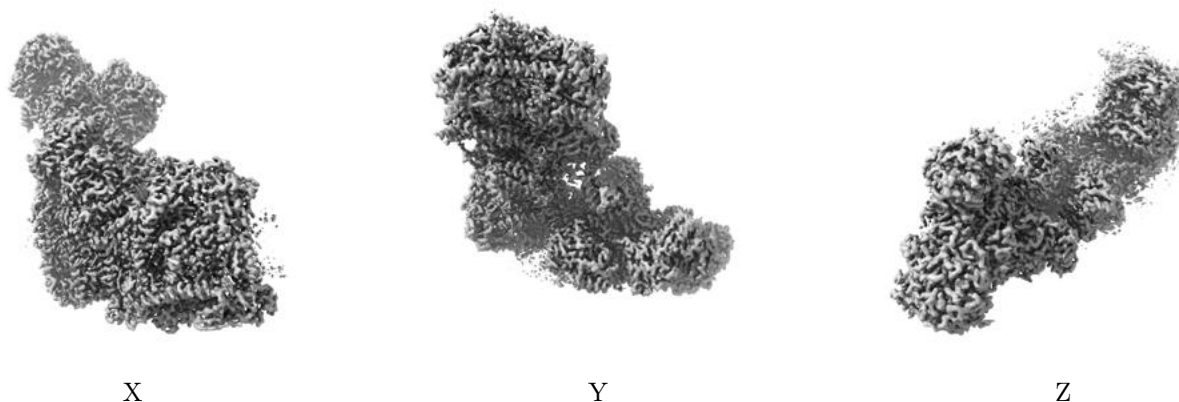


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0205. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

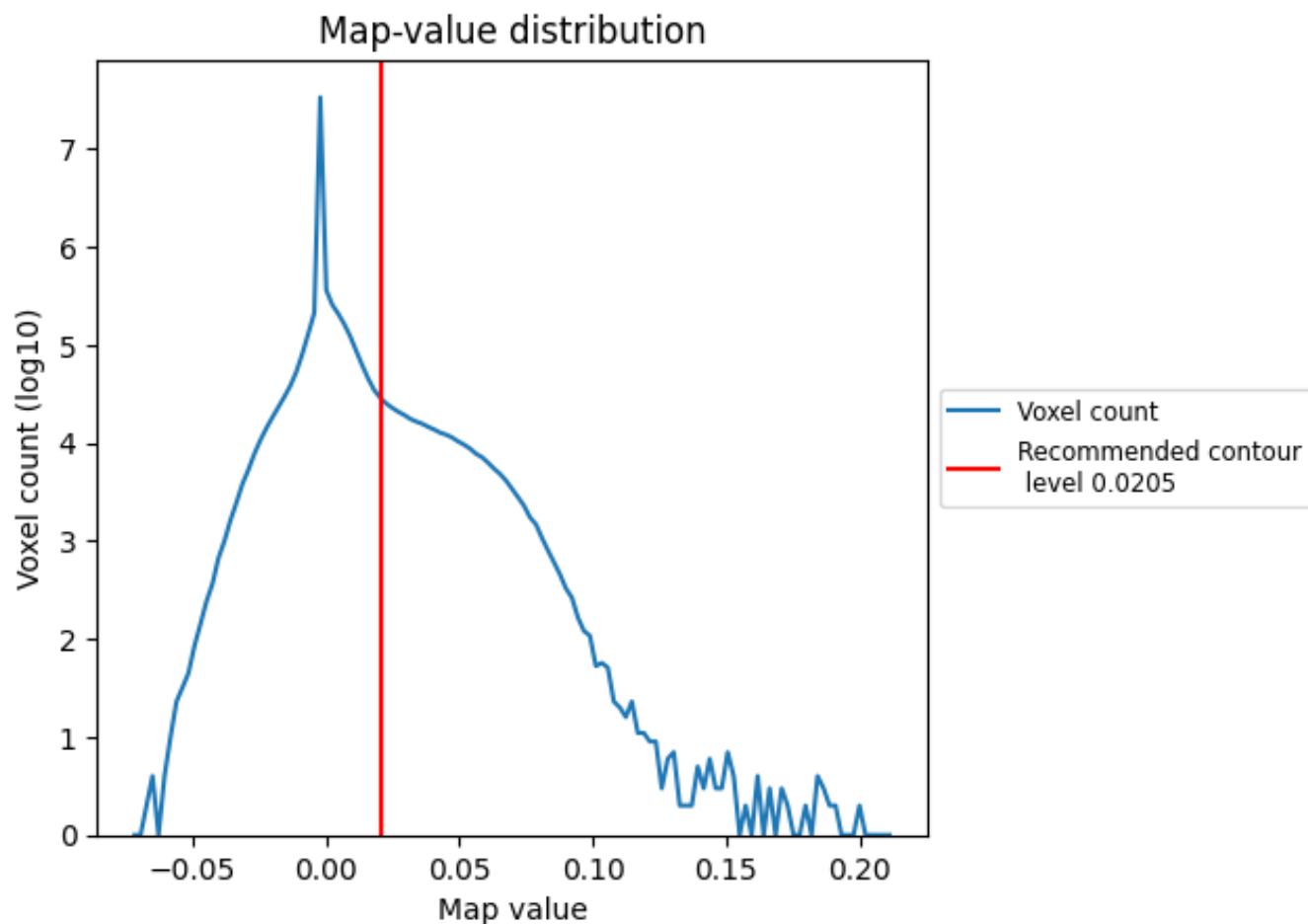
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

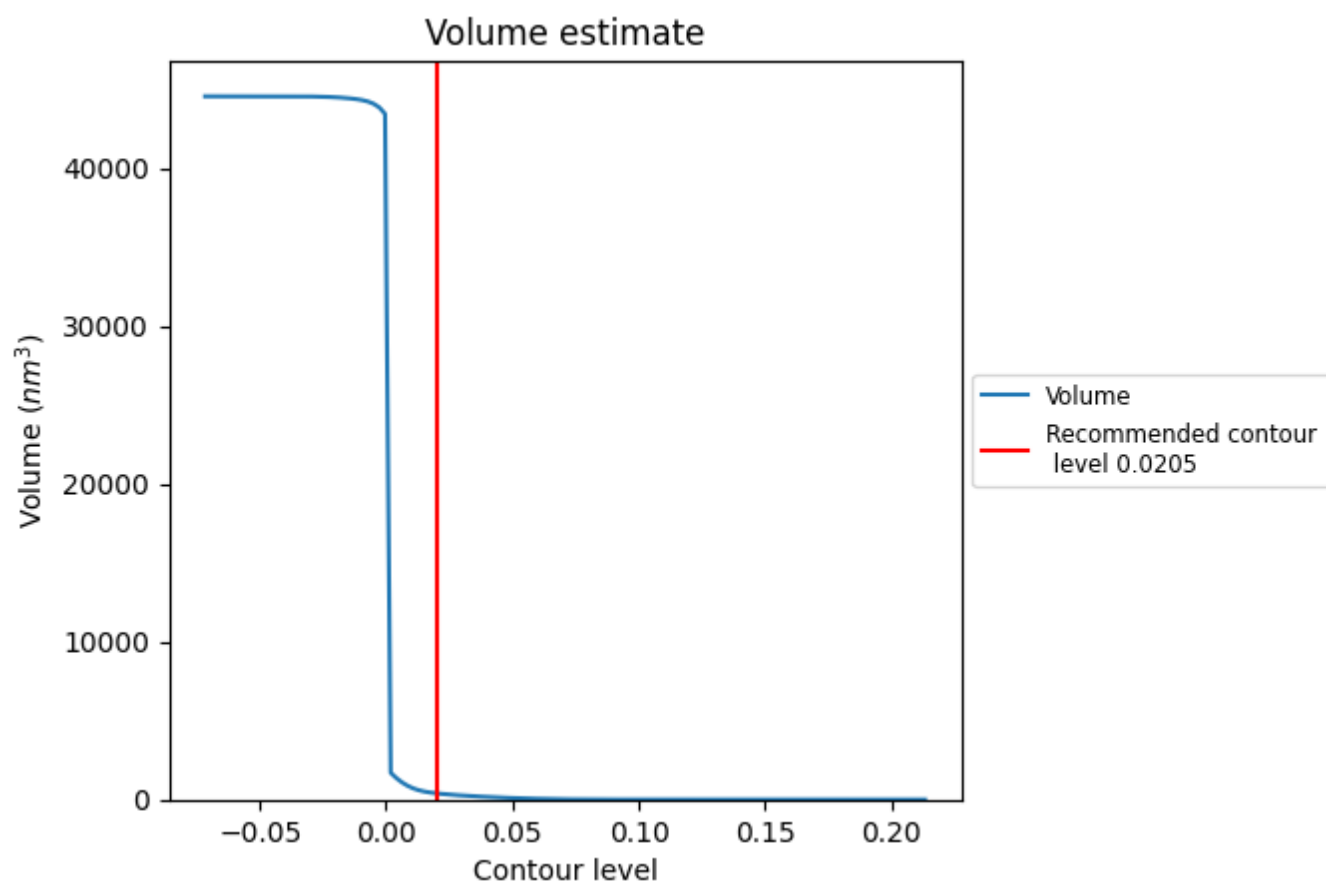
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

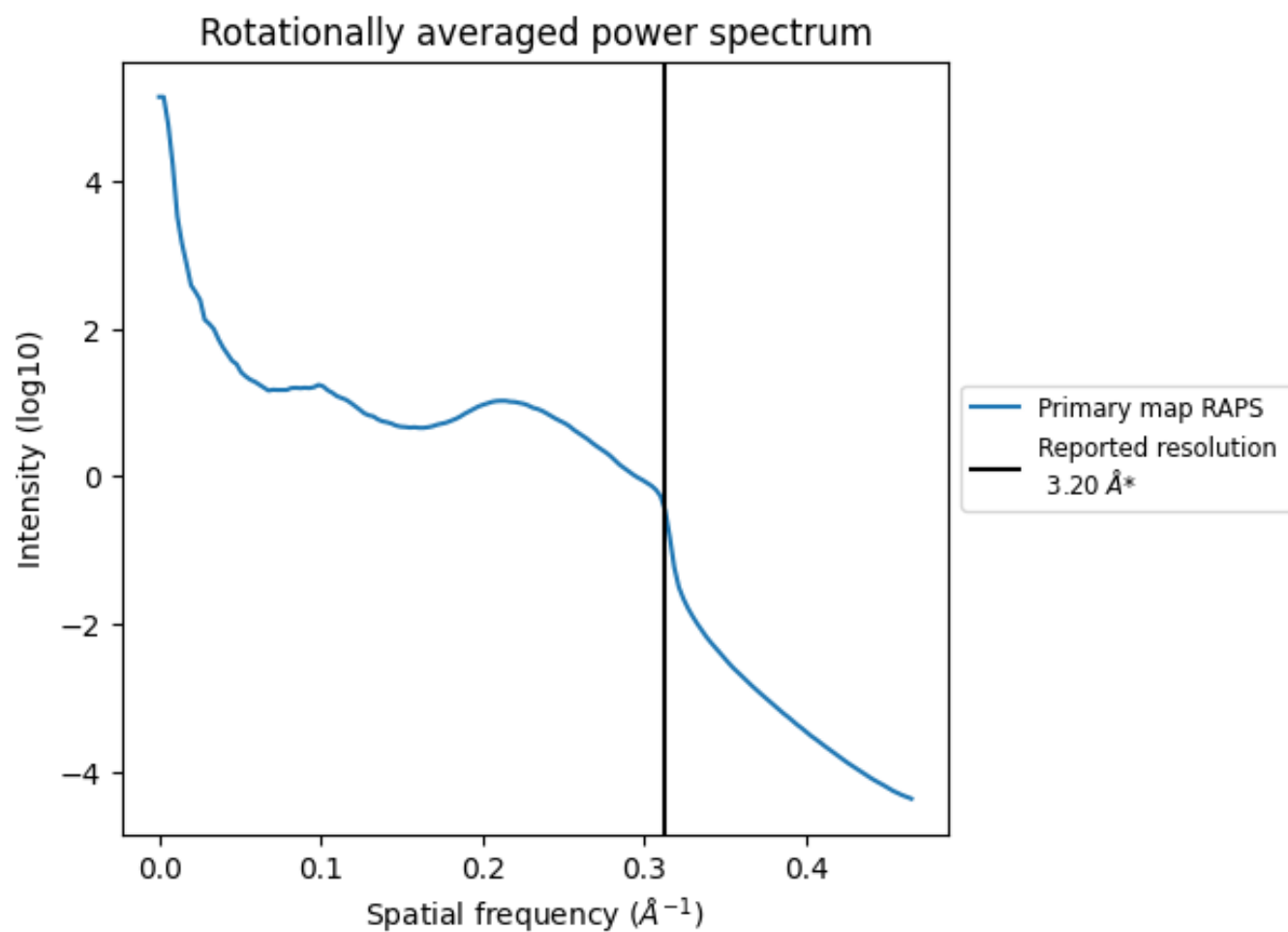
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 385 nm^3 ; this corresponds to an approximate mass of 348 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 0.312 Å⁻¹

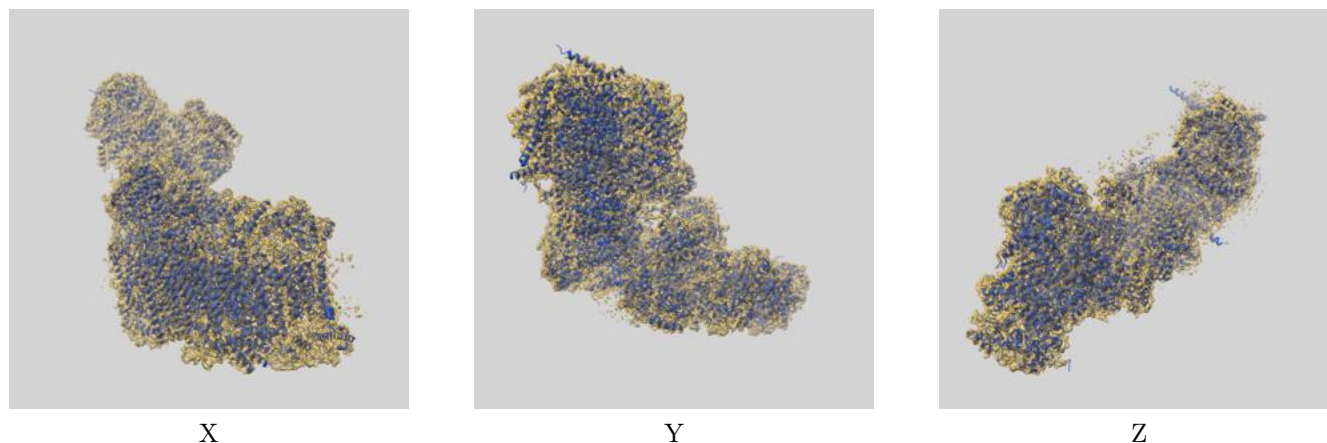
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

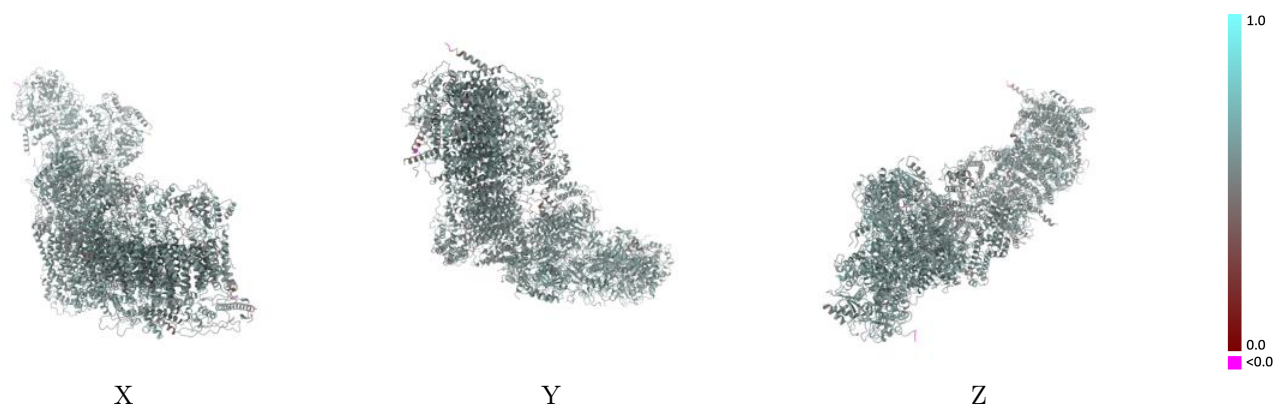
This section contains information regarding the fit between EMDB map EMD-32230 and PDB model 7VZV. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



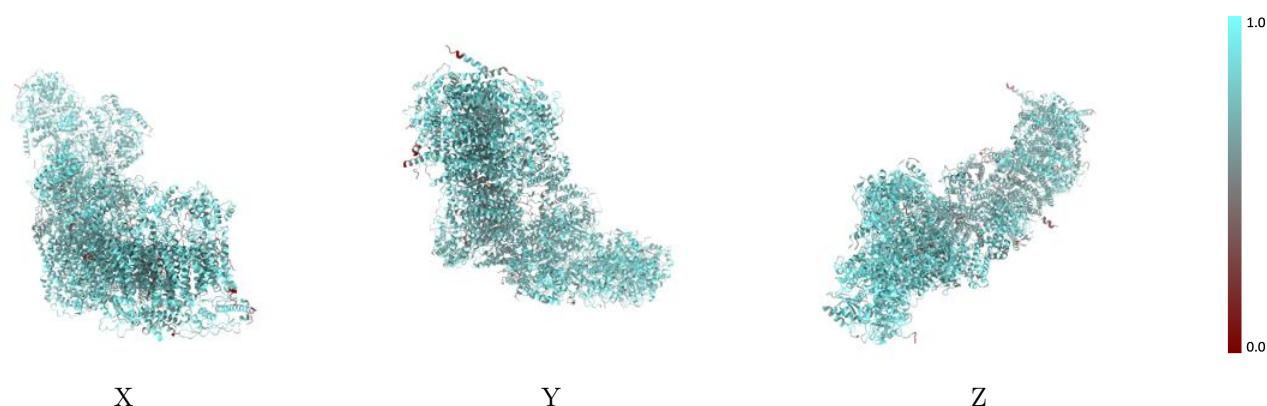
The images above show the 3D surface view of the map at the recommended contour level 0.0205 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



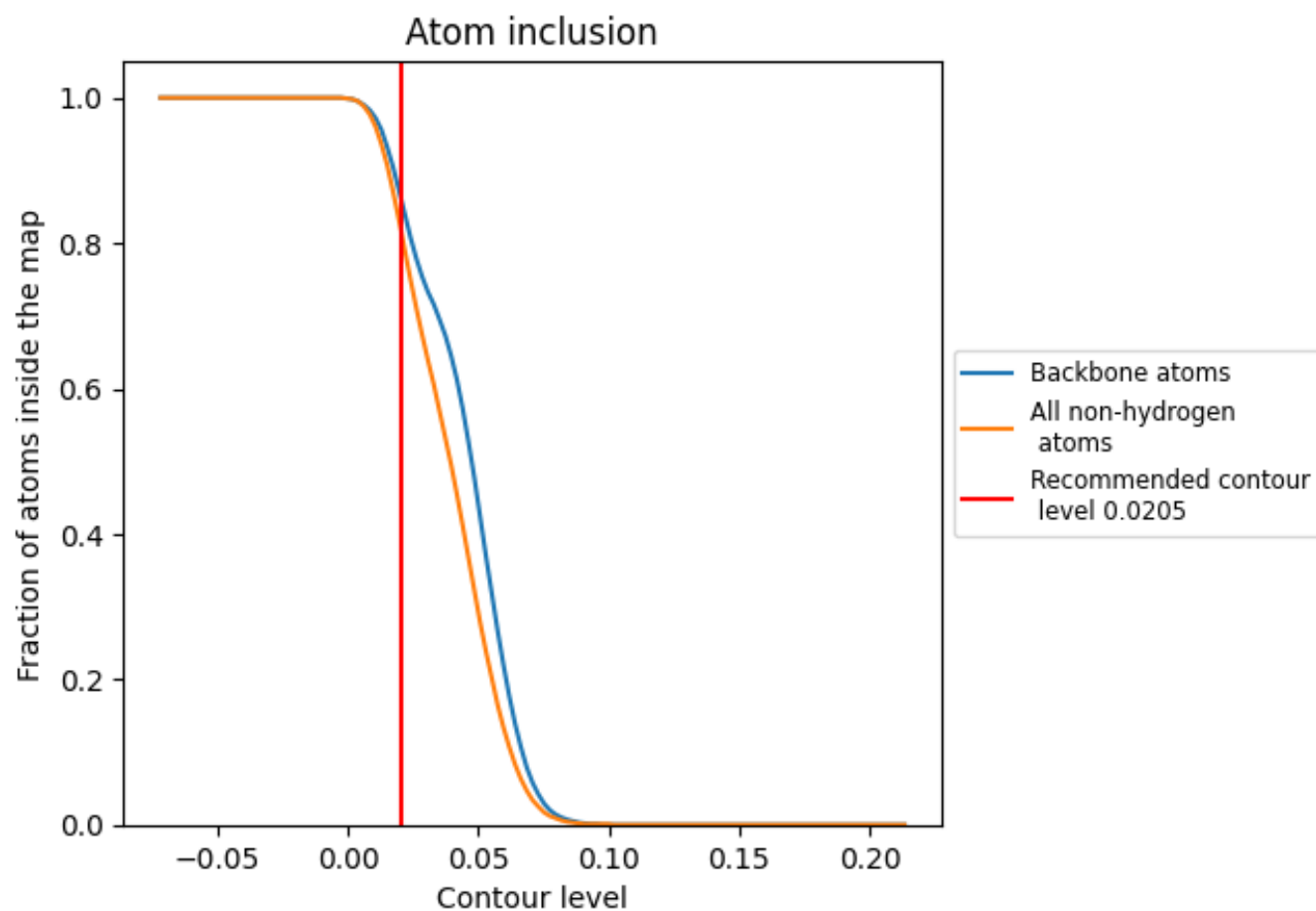
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0205).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 82% 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 (0.0205) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8170	 0.5580
A	 0.8460	 0.5570
B	 0.9000	 0.5810
C	 0.8390	 0.5790
E	 0.8220	 0.5650
F	 0.7810	 0.5300
G	 0.6590	 0.4720
H	 0.8360	 0.5540
I	 0.7430	 0.5470
J	 0.8390	 0.5670
K	 0.8030	 0.5490
L	 0.8410	 0.5720
M	 0.8550	 0.5680
N	 0.7080	 0.5520
O	 0.8260	 0.5510
P	 0.8890	 0.5900
Q	 0.8690	 0.5790
S	 0.8390	 0.5640
T	 0.7980	 0.5680
U	 0.8140	 0.5510
V	 0.6960	 0.5410
W	 0.8350	 0.5540
X	 0.7800	 0.5290
Y	 0.7590	 0.5190
Z	 0.6910	 0.5110
a	 0.8050	 0.5620
b	 0.7570	 0.5330
c	 0.8140	 0.5570
d	 0.7750	 0.5320
e	 0.7730	 0.5420
f	 0.6760	 0.5090
g	 0.8330	 0.5610
h	 0.8120	 0.5440
i	 0.8500	 0.5700
j	 0.7690	 0.5660



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
k	 0.8520	 0.5660
l	 0.8030	 0.5570
m	 0.7380	 0.5380
n	 0.7230	 0.5380
o	 0.8060	 0.5510
p	 0.8220	 0.5530
r	 0.8350	 0.5710
s	 0.8440	 0.5680
u	 0.8270	 0.5560
v	 0.7890	 0.5250
w	 0.8090	 0.5450