



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 07:18 AM UTC

PDB ID : 6ZKD / pdb_00006zkd
EMDB ID : EMD-11245
Title : Complex I during turnover, open1
Authors : Kampjut, D.; Sazanov, L.A.
Deposited on : 2020-06-30
Resolution : 2.70 Å(reported)
Based on initial model : 5LNK

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

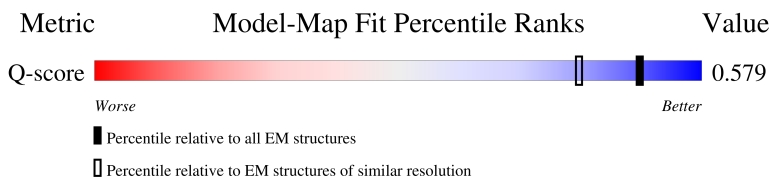
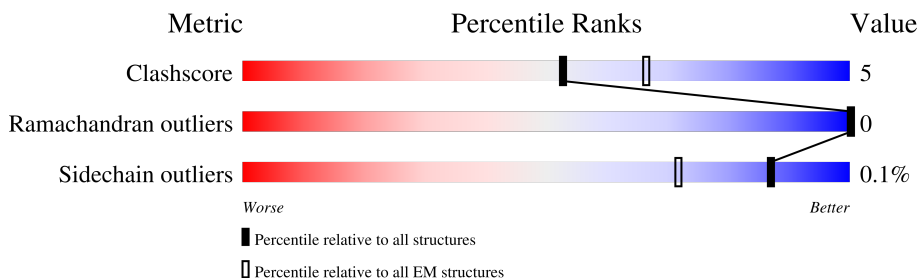
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.70 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	10327 (2.20 - 3.20)

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	1	464	
2	2	246	
3	3	727	
4	4	463	

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Mol	Chain	Length	Quality of chain
5	5	266	
6	6	223	
7	9	217	
8	A	115	
9	H	318	
10	J	175	
11	K	98	
12	L	606	
13	M	459	
14	N	347	
15	V	141	
16	W	189	
17	X	157	
17	j	157	
18	Y	172	
19	Z	175	
20	a	109	
21	b	124	
22	c	170	
23	d	380	
24	e	99	
25	f	116	
26	g	140	
27	h	114	
28	i	145	

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Mol	Chain	Length	Quality of chain
29	k	355	
30	l	106	
31	m	84	
32	n	98	
33	o	122	
34	p	130	
35	q	144	
36	r	128	
37	s	137	
38	t	179	
39	u	108	
40	v	186	
41	w	154	
42	x	76	
43	y	58	
44	z	70	

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
53	CDL	L	1003	X	-	-	-
53	CDL	V	204	X	-	-	-
53	CDL	Y	201	X	-	-	-
53	CDL	o	201	X	-	-	-

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 67450 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	1	430	Total	C	N	O	S	0	0
			3312	2086	593	613	20		

- Molecule 2 is a protein called Mitochondrial complex I, 24 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	213	Total	C	N	O	S	0	0
			1655	1058	278	309	10		

- Molecule 3 is a protein called NADH:ubiquinone oxidoreductase core subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	688	Total	C	N	O	S	0	0
			5275	3301	922	1011	41		

- Molecule 4 is a protein called Mitochondrial complex I, 49 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	421	Total	C	N	O	S	0	0
			3390	2165	581	619	25		

- Molecule 5 is a protein called NADH:ubiquinone oxidoreductase core subunit S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	208	Total	C	N	O	S	0	0
			1726	1112	296	315	3		

- Molecule 6 is a protein called Mitochondrial complex I, PSST subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	156	Total	C	N	O	S	0	0
			1247	795	225	213	14		

- Molecule 7 is a protein called Mitochondrial complex I, TYKY subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	9	176	Total	C	N	O	S	0	0
			1414	889	243	270	12		

- Molecule 8 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	110	Total	C	N	O	S	0	0
			880	593	128	153	6		

- Molecule 9 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	314	Total	C	N	O	S	0	0
			2498	1685	380	414	19		

- Molecule 10 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1294	870	185	226	13		

- Molecule 11 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	98	Total	C	N	O	S	0	0
			749	490	112	132	15		

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	606	Total	C	N	O	S	0	0
			4806	3187	746	829	44		

- Molecule 13 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	459	Total	C	N	O	S	0	0
			3647	2429	571	607	40		

- Molecule 14 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	347	Total	C	N	O	S	0	0
			2723	1808	416	459	40		

- Molecule 15 is a protein called Mitochondrial complex I, B14.7 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	V	140	Total	C	N	O	S	0	0
			1028	656	175	191	6		

- Molecule 16 is a protein called NADH:ubiquinone oxidoreductase subunit B5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	W	139	Total	C	N	O	S	0	0
			1155	761	194	198	2		

- Molecule 17 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	87	Total	C	N	O	S	0	0
			701	451	103	142	5		
17	j	82	Total	C	N	O	S	0	0
			660	425	98	132	5		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	171	Total	C	N	O	S	0	0
			1403	889	253	251	10		

- Molecule 19 is a protein called Mitochondrial complex I, PDSW subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Z	171	Total	C	N	O	S	0	0
			1441	905	266	262	8		

- Molecule 20 is a protein called Mitochondrial complex I, 10 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	a	44	Total	C	N	O	S	0	0
			371	233	66	71	1		

- Molecule 21 is a protein called Mitochondrial complex I, 13 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	95	Total	C	N	O	S	0	0
			737	451	139	144	3		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	c	126	Total	C	N	O	S	0	0
			1024	646	182	193	3		

- Molecule 23 is a protein called NADH:ubiquinone oxidoreductase subunit A9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	297	Total	C	N	O	S	0	0
			2372	1516	432	419	5		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	86	Total	C	N	O	S	0	0
			691	434	129	126	2		

- Molecule 25 is a protein called Mitochondrial complex I, B13 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	113	Total	C	N	O	S	0	0
			917	595	153	167	2		

- Molecule 26 is a protein called NADH:ubiquinone oxidoreductase subunit A6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	g	114	Total	C	N	O	S	0	0
			969	619	180	166	4		

- Molecule 27 is a protein called Mitochondrial complex I, B14.5a subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	h	96	Total	C	N	O	S	0	0
			769	480	146	140	3		

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	i	145	Total	C	N	O	S	0	0
			1209	778	216	210	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	320	Total	C	N	O	P S	0	0
			2596	1659	432	494	1 10		

- Molecule 30 is a protein called NADH:ubiquinone oxidoreductase subunit S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	105	Total	C	N	O	S	0	0
			874	551	164	153	6		

- Molecule 31 is a protein called NADH:ubiquinone oxidoreductase subunit A3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	m	80	Total	C	N	O	S	0	0
			626	411	103	110	2		

- Molecule 32 is a protein called NADH:ubiquinone oxidoreductase subunit B3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	n	79	Total	C	N	O	S	0	0
			634	415	106	111	2		

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	120	Total	C	N	O	S	0	0
			1004	652	175	172	5		

- Molecule 34 is a protein called NADH:ubiquinone oxidoreductase subunit B4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	p	128	Total	C	N	O	S	0	0
			1059	675	189	194	1		

- Molecule 35 is a protein called Mitochondrial complex I, B16.6 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	q	139	Total	C	N	O	S	0	0
			1142	733	200	200	9		

- Molecule 36 is a protein called Mitochondrial complex I, B17 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	99	Total	C	N	O	S	0	0
			846	554	149	142	1		

- Molecule 37 is a protein called NADH:ubiquinone oxidoreductase subunit B7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	s	122	Total	C	N	O	S	0	0
			1047	653	199	186	9		

- Molecule 38 is a protein called NADH:ubiquinone oxidoreductase subunit B9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	t	177	Total	C	N	O	S	0	0
			1520	973	279	262	6		

- Molecule 39 is a protein called NADH:ubiquinone oxidoreductase subunit B2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	65	Total	C	N	O	S	0	0
			563	372	93	97	1		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	155	Total	C	N	O	S	0	0
			1307	846	213	239	9		

- Molecule 41 is a protein called Mitochondrial complex I, ESSS subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	101	Total	C	N	O	S	0	0
			846	542	140	160	4		

- Molecule 42 is a protein called Mitochondrial complex I, KFYI subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	x	49	Total	C	N	O	0	0
			412	271	70	71		

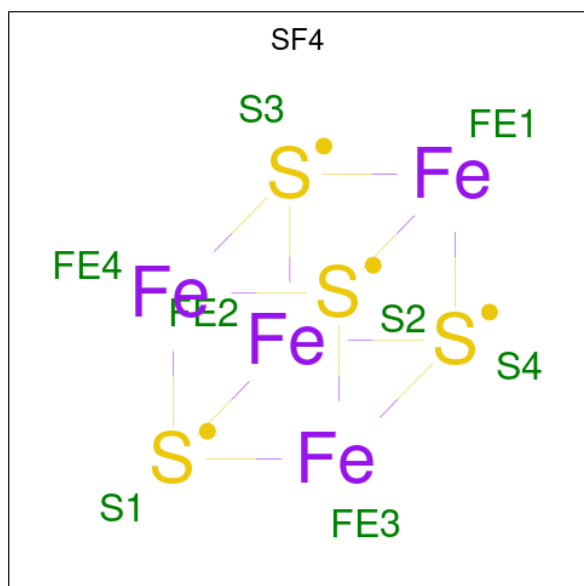
- Molecule 43 is a protein called Mitochondrial complex I, MNLL subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	y	50	Total	C	N	O	0	0
			436	287	77	72		

- Molecule 44 is a protein called Mitochondrial complex I, MWFE subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	70	Total	C	N	O	S	0	0
			576	369	106	96	5		

- Molecule 45 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
45	1	1	Total	Fe	S	0
			8	4	4	
45	3	1	Total	Fe	S	0
			8	4	4	
45	3	1	Total	Fe	S	0
			8	4	4	
45	6	1	Total	Fe	S	0
			8	4	4	

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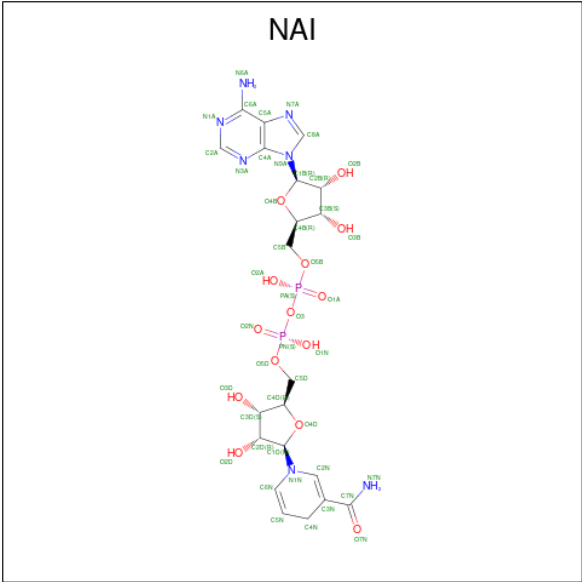
Mol	Chain	Residues	Atoms			AltConf
45	9	1	Total	Fe	S	0
			8	4	4	
45	9	1	Total	Fe	S	0
			8	4	4	

- Molecule 46 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



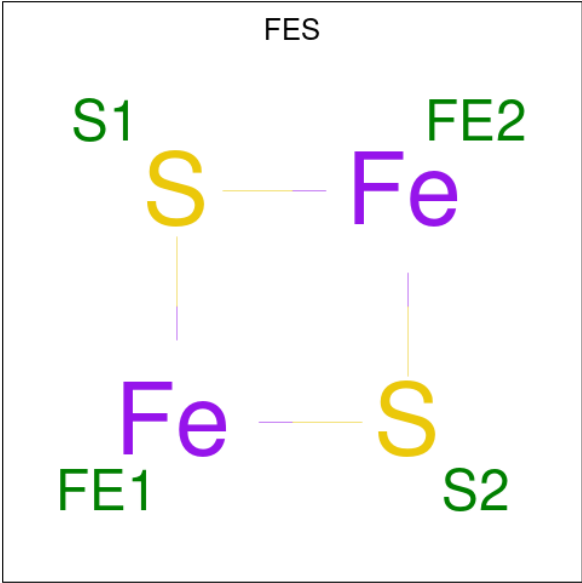
Mol	Chain	Residues	Atoms					AltConf
46	1	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 47 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					AltConf
47	1	1	Total	C	N	O	P	0
			44	21	7	14	2	

- Molecule 48 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).

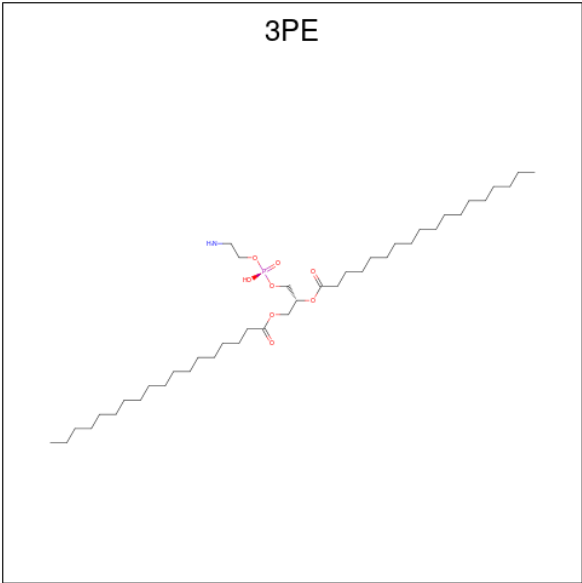


Mol	Chain	Residues	Atoms			AltConf
48	2	1	Total	Fe	S	0
			4	2	2	
48	3	1	Total	Fe	S	0
			4	2	2	

- Molecule 49 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
49	3	1	Total	K	0
			1	1	

- Molecule 50 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: C₄₁H₈₂NO₈P).



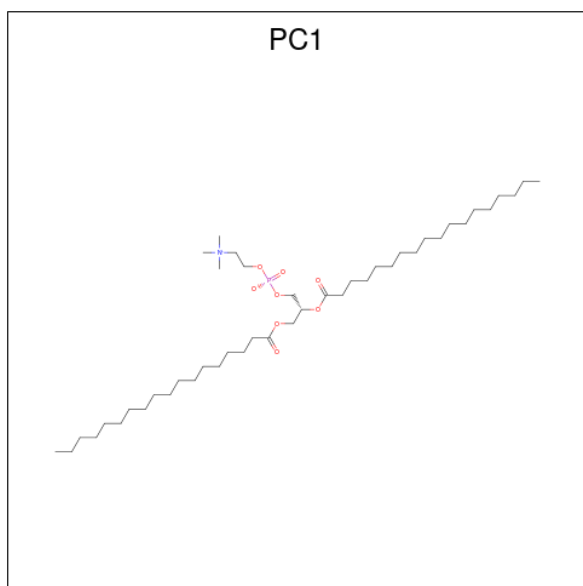
Mol	Chain	Residues	Atoms					AltConf
50	4	1	Total	C	N	O	P	0
			40	30	1	8	1	
50	A	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	H	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	K	1	Total	C	N	O	P	0
			40	30	1	8	1	
50	L	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	L	1	Total	C	N	O	P	0
			31	21	1	8	1	
50	M	1	Total	C	N	O	P	0
			44	34	1	8	1	
50	N	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	N	1	Total	C	N	O	P	0
			31	21	1	8	1	
50	V	1	Total	C	N	O	P	0
			35	25	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
50	V	1	Total	C	N	O	P	0
			37	27	1	8	1	
50	i	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	i	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	p	1	Total	C	O	P		0
			27	18	8	1		

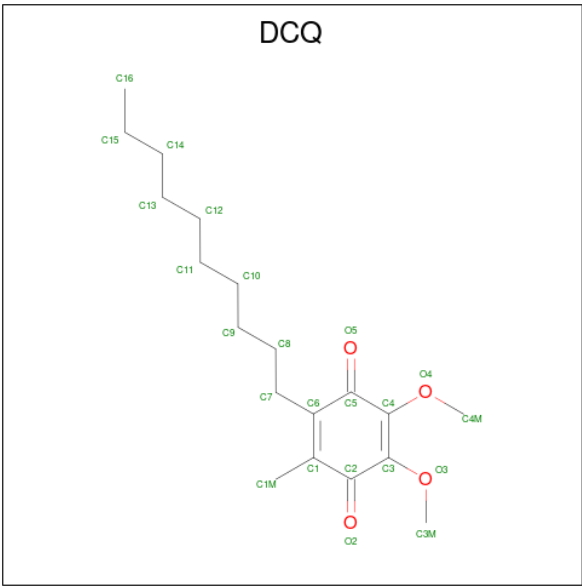
- Molecule 51 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).



Mol	Chain	Residues	Atoms					AltConf
51	9	1	Total	C	N	O	P	0
			54	44	1	8	1	
51	A	1	Total	C	N	O	P	0
			46	36	1	8	1	
51	A	1	Total	C	N	O	P	0
			37	27	1	8	1	
51	L	1	Total	C	N	O	P	0
			54	44	1	8	1	
51	M	1	Total	C	N	O	P	0
			54	44	1	8	1	
51	w	1	Total	C	N	O	P	0
			54	44	1	8	1	

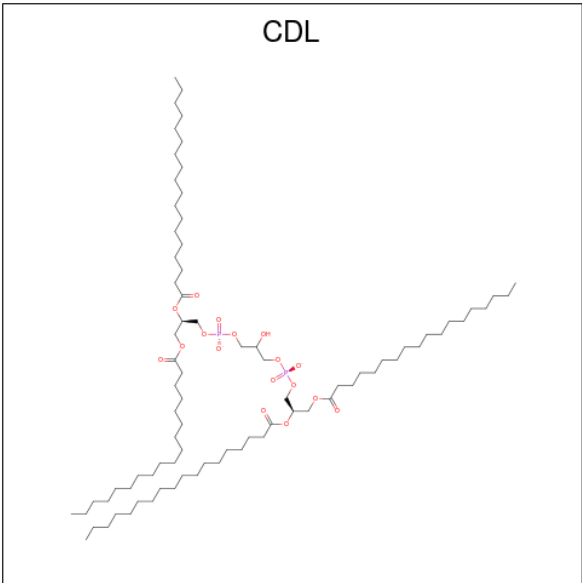
- Molecule 52 is 2-decyl-5,6-dimethoxy-3-methylcyclohexa-2,5-diene-1,4-dione (CCD ID:

DCQ) (formula: C₁₉H₃₀O₄).



Mol	Chain	Residues	Atoms			AltConf
52	H	1	Total	C	O	0
			23	19	4	

- Molecule 53 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



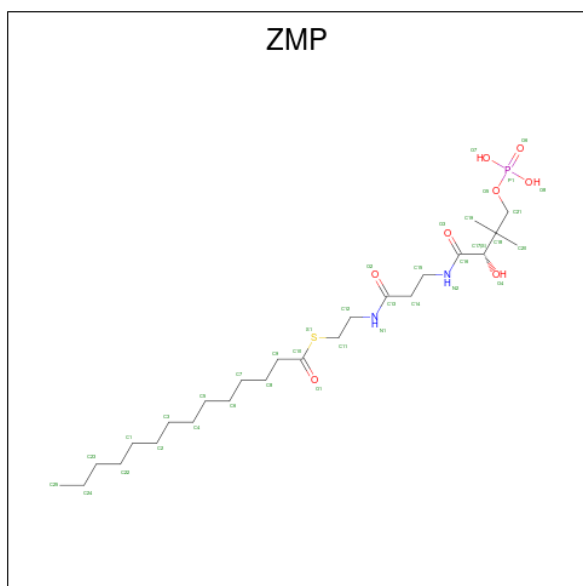
Mol	Chain	Residues	Atoms				AltConf
53	L	1	Total	C	O	P	0
			100	81	17	2	
53	V	1	Total	C	O	P	0
			94	75	17	2	

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Mol	Chain	Residues	Atoms				AltConf
53	V	1	Total	C	O	P	0
			85	66	17	2	
53	W	1	Total	C	O	P	0
			100	81	17	2	
53	Y	1	Total	C	O	P	0
			100	81	17	2	
53	o	1	Total	C	O	P	0
			75	56	17	2	
53	o	1	Total	C	O	P	0
			90	71	17	2	
53	z	1	Total	C	O	P	0
			58	39	17	2	

- Molecule 54 is S-[2-({N-[(2S)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl}amino)ethyl] tetradecanethioate (CCD ID: ZMP) (formula: C₂₅H₄₉N₂O₈PS).

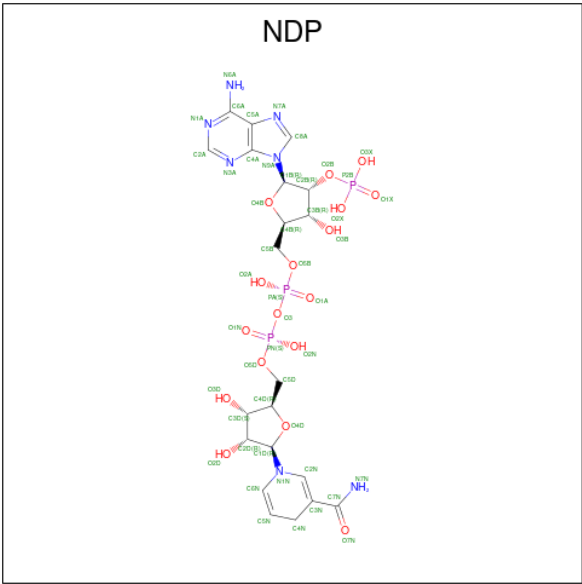


Mol	Chain	Residues	Atoms						AltConf
54	X	1	Total 31	C 20	N 2	O 7	P 1	S 1	0
54	g	1	Total 34	C 23	N 2	O 7	P 1	S 1	0

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

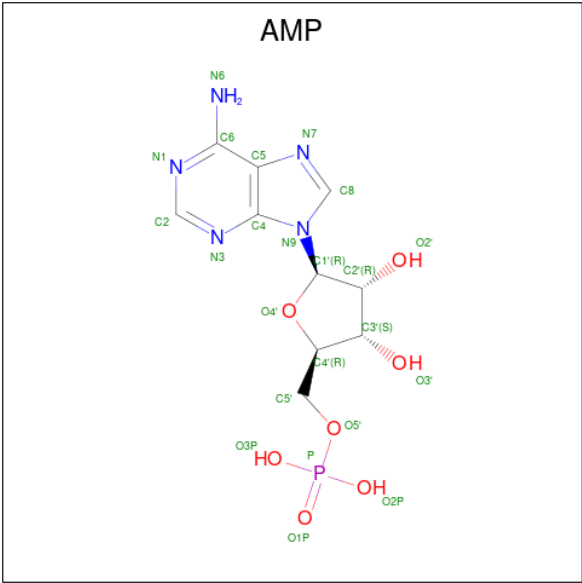
Mol	Chain	Residues	Atoms		AltConf
55	b	1	Total	Zn	0
			1	1	

- Molecule 56 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



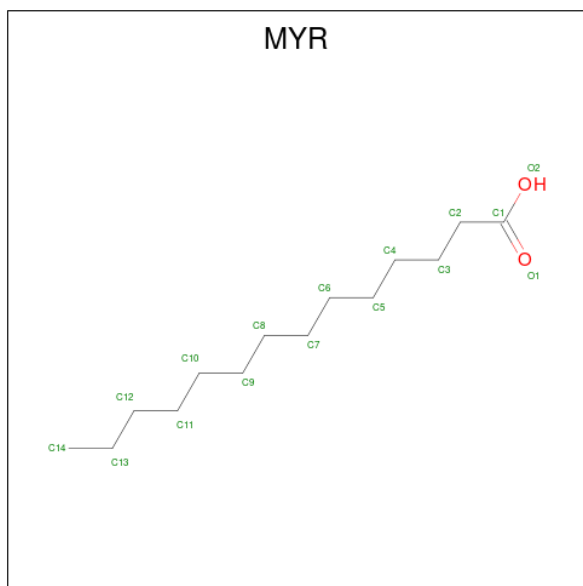
Mol	Chain	Residues	Atoms					AltConf
56	d	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 57 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms					AltConf
57	k	1	Total	C	N	O	P	0
			23	10	5	7	1	

- Molecule 58 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$).



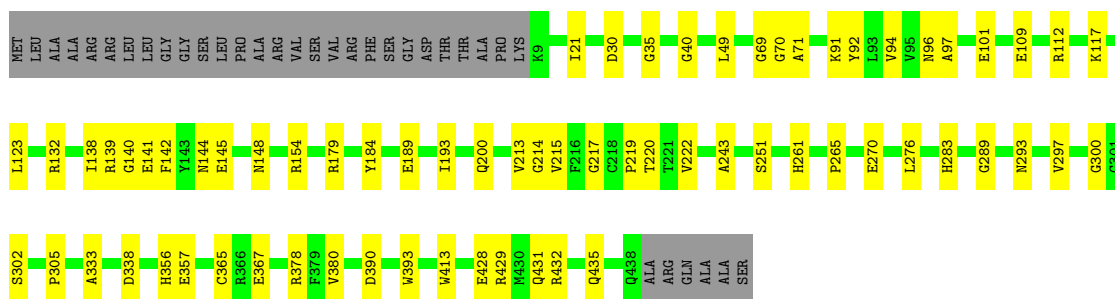
Mol	Chain	Residues	Atoms			AltConf
58	s	1	Total	C	O	0
			15	14	1	

3 Residue-property plots [i](#)

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

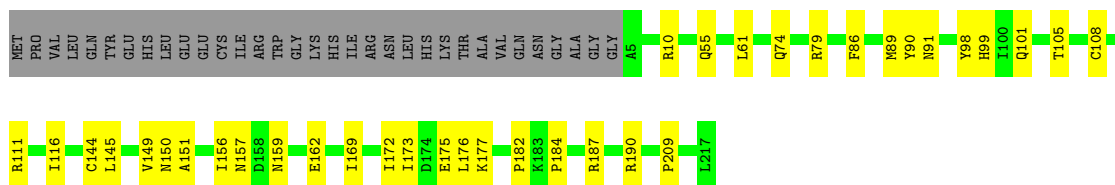
- Molecule 1: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial

Chain 1: 



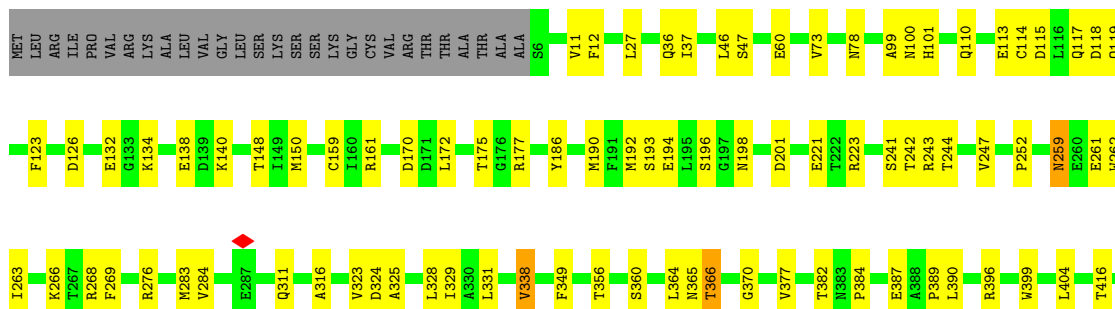
- Molecule 2: Mitochondrial complex I, 24 kDa subunit

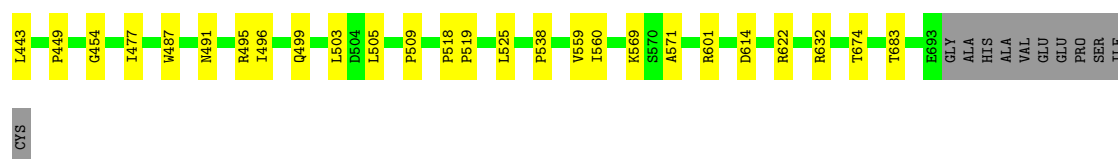
Chain 2: 



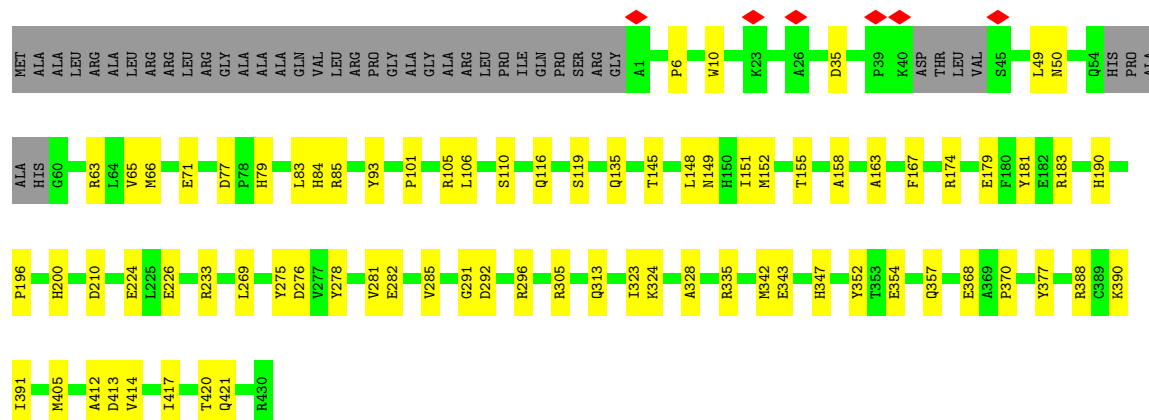
- Molecule 3: NADH:ubiquinone oxidoreductase core subunit S1

Chain 3: 

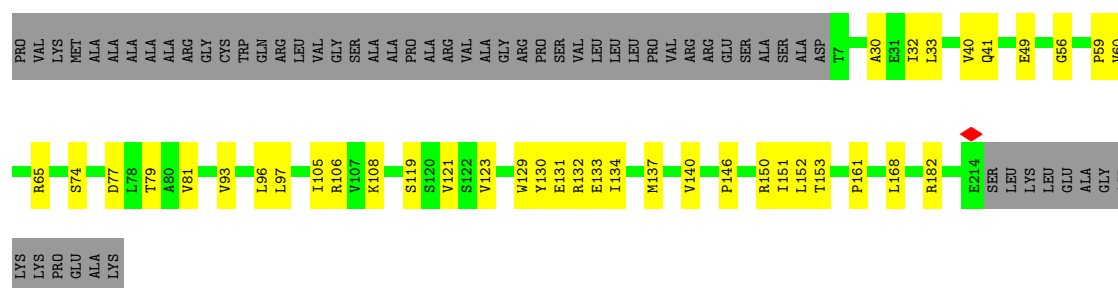




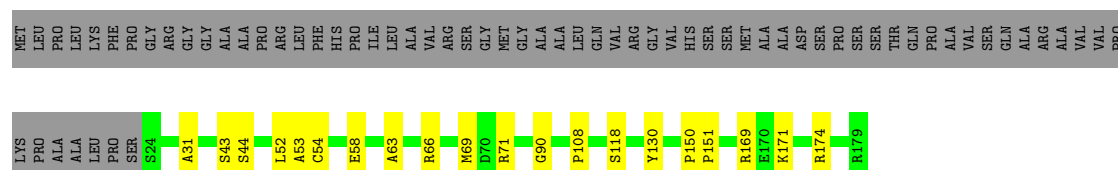
- Molecule 4: Mitochondrial complex I, 49 kDa subunit



- Molecule 5: NADH:ubiquinone oxidoreductase core subunit S3

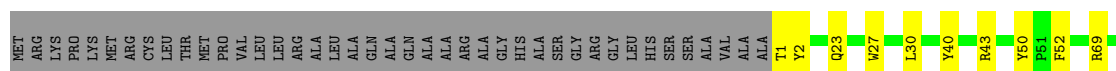


- Molecule 6: Mitochondrial complex I, PSST subunit

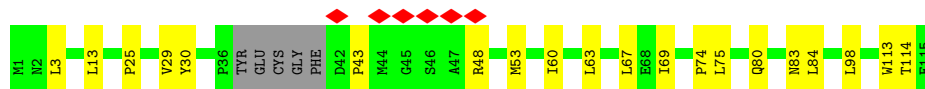
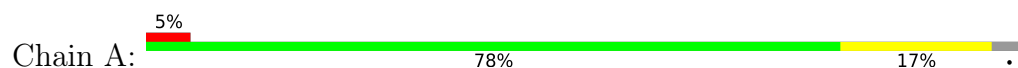


- Molecule 7: Mitochondrial complex I, TYKY subunit

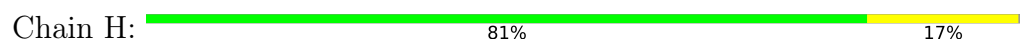




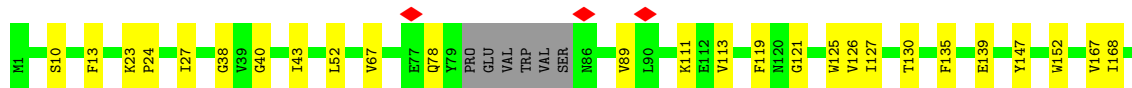
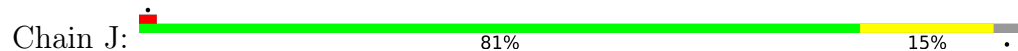
• Molecule 8: NADH-ubiquinone oxidoreductase chain 3



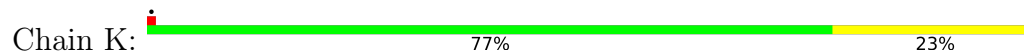
• Molecule 9: NADH-ubiquinone oxidoreductase chain 1



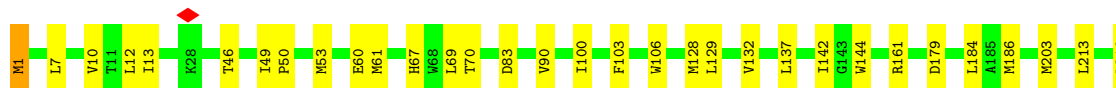
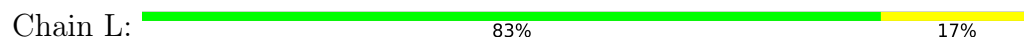
• Molecule 10: NADH-ubiquinone oxidoreductase chain 6

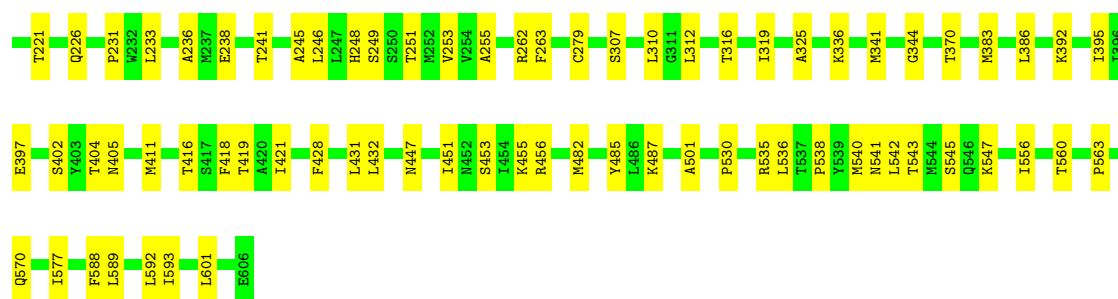


• Molecule 11: NADH-ubiquinone oxidoreductase chain 4L

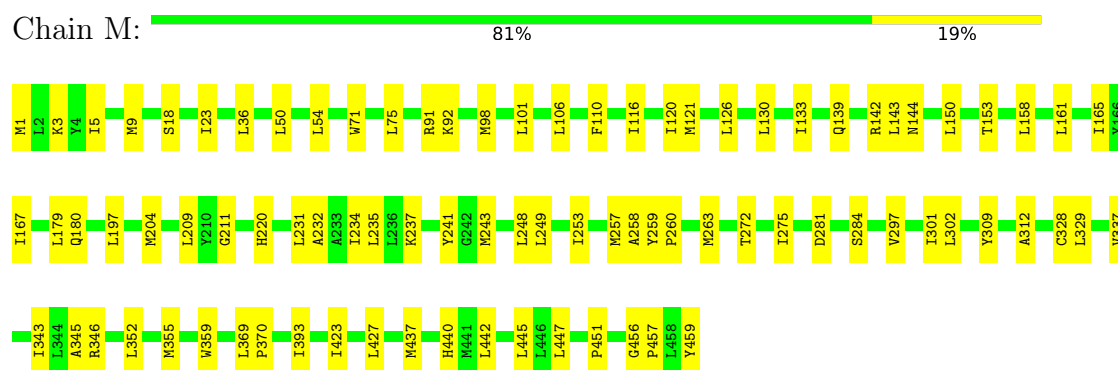


• Molecule 12: NADH-ubiquinone oxidoreductase chain 5

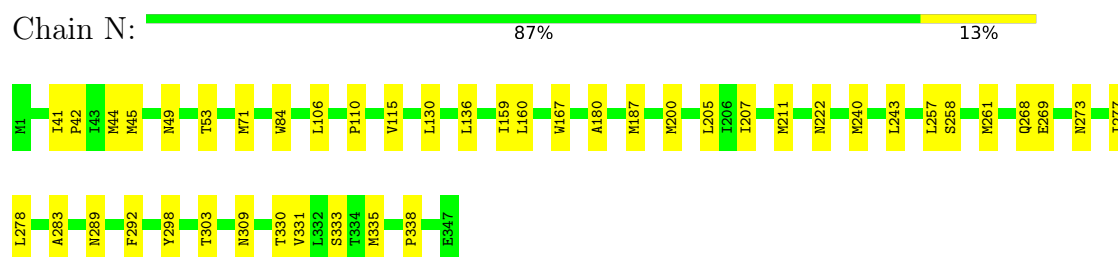




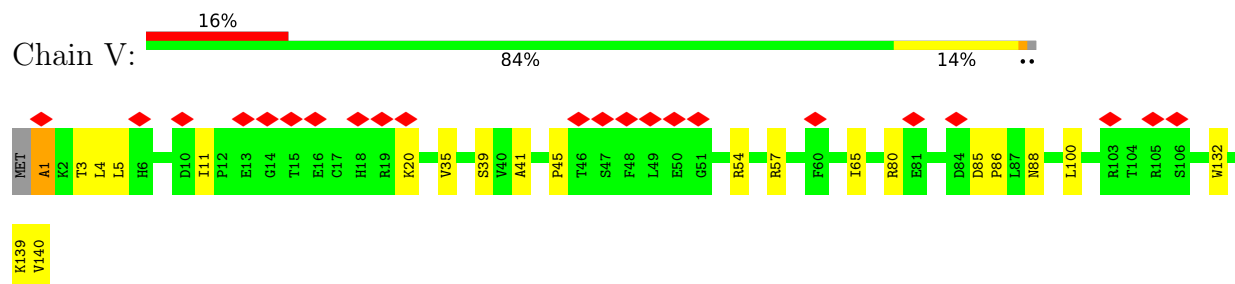
- Molecule 13: NADH-ubiquinone oxidoreductase chain 4



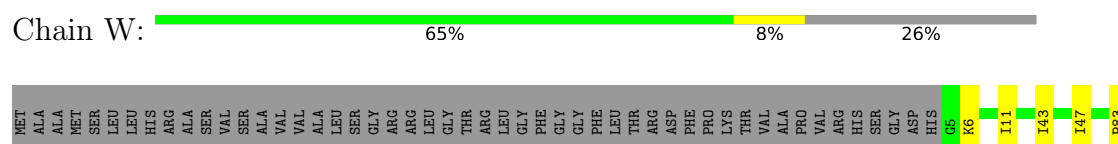
- Molecule 14: NADH-ubiquinone oxidoreductase chain 2

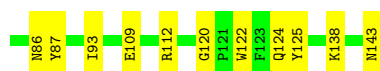


- Molecule 15: Mitochondrial complex I, B14.7 subunit

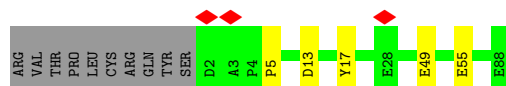


- Molecule 16: NADH:ubiquinone oxidoreductase subunit B5

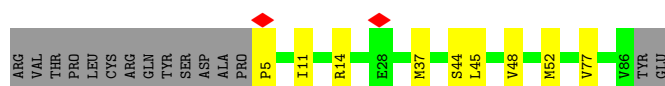




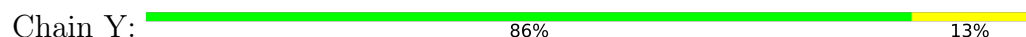
- Molecule 17: Acyl carrier protein



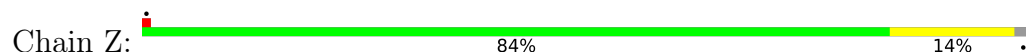
- Molecule 17: Acyl carrier protein



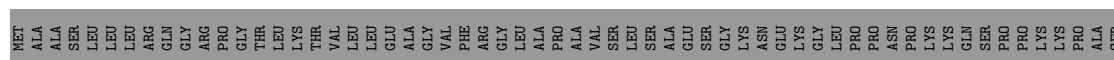
- Molecule 18: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



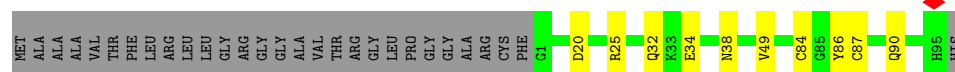
- Molecule 19: Mitochondrial complex I, PDSW subunit



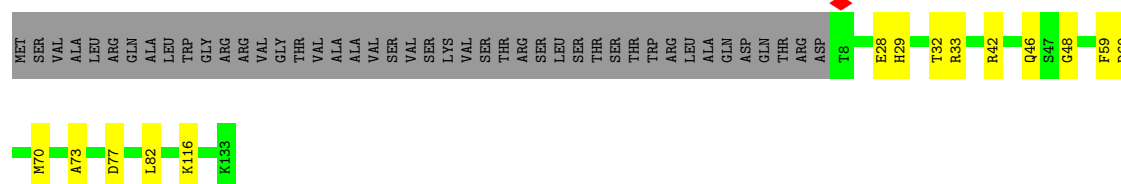
- Molecule 20: Mitochondrial complex I, 10 kDa subunit



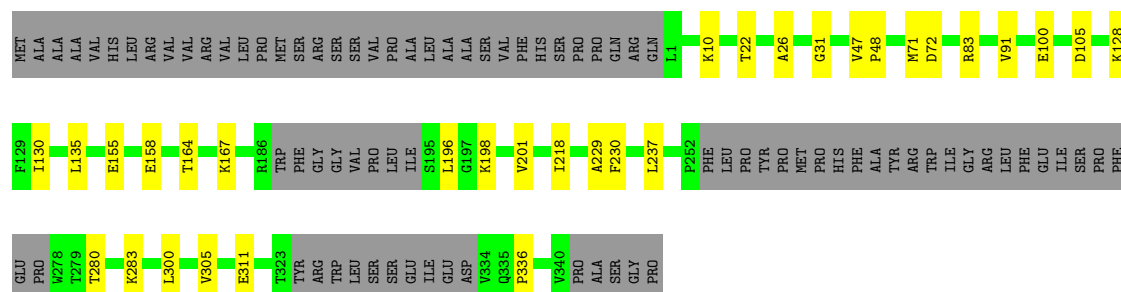
- Molecule 21: Mitochondrial complex I, 13 kDa subunit



- Molecule 22: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial



- Molecule 23: NADH:ubiquinone oxidoreductase subunit A9



- Molecule 24: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

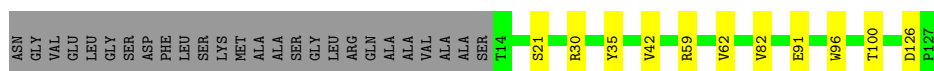


- Molecule 25: Mitochondrial complex I, B13 subunit

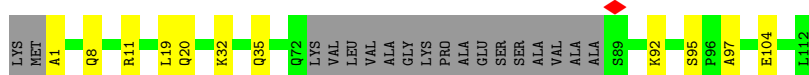


- Molecule 26: NADH:ubiquinone oxidoreductase subunit A6

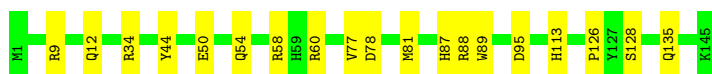
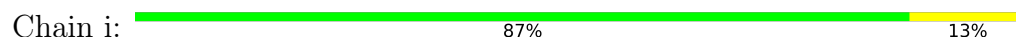




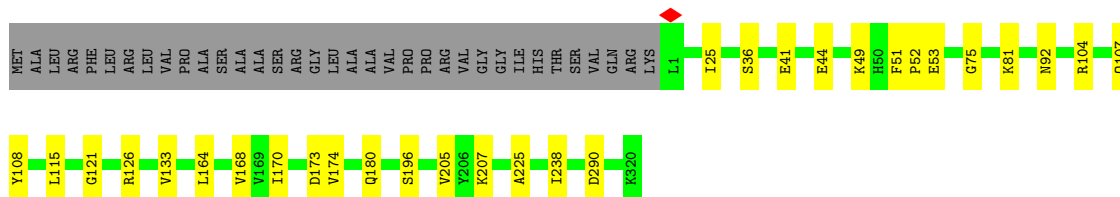
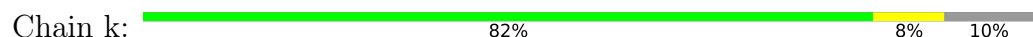
- Molecule 27: Mitochondrial complex I, B14.5a subunit



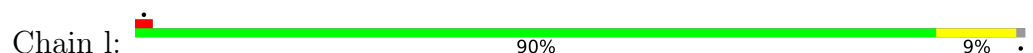
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12



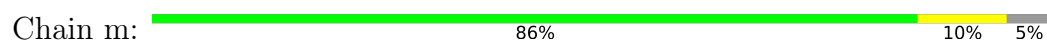
- Molecule 29: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial



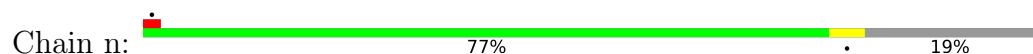
- Molecule 30: NADH:ubiquinone oxidoreductase subunit S5



- Molecule 31: NADH:ubiquinone oxidoreductase subunit A3

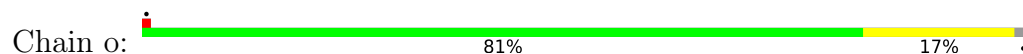


- Molecule 32: NADH:ubiquinone oxidoreductase subunit B3





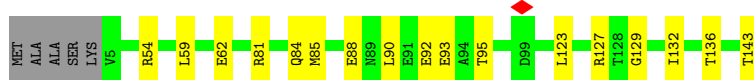
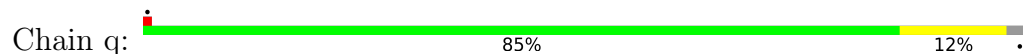
- Molecule 33: NADH dehydrogenase [ubiquinone] 1 subunit C2



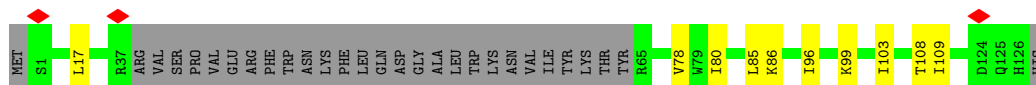
- Molecule 34: NADH:ubiquinone oxidoreductase subunit B4



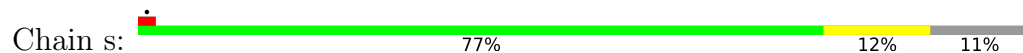
- Molecule 35: Mitochondrial complex I, B16.6 subunit



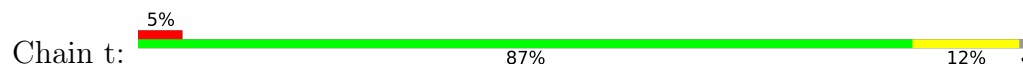
- Molecule 36: Mitochondrial complex I, B17 subunit



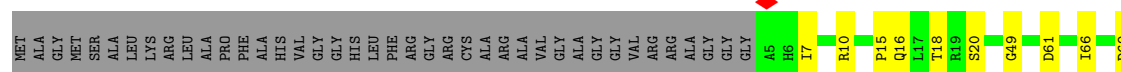
- Molecule 37: NADH:ubiquinone oxidoreductase subunit B7



- Molecule 38: NADH:ubiquinone oxidoreductase subunit B9

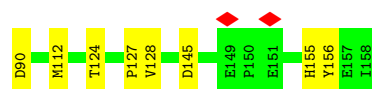
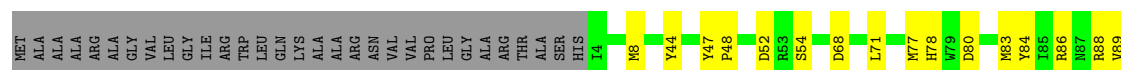


- Molecule 39: NADH:ubiquinone oxidoreductase subunit B2

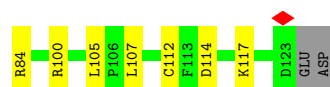
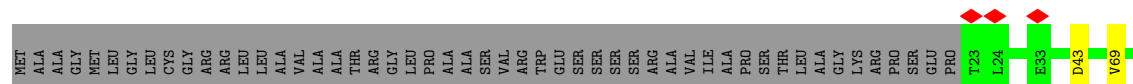


ASP
GLU
ASP

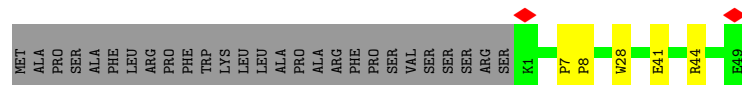
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial



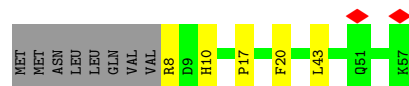
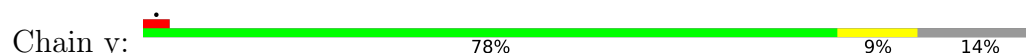
- Molecule 41: Mitochondrial complex I, ESSS subunit



- Molecule 42: Mitochondrial complex I, KFYI subunit



- Molecule 43: Mitochondrial complex I, MNLL subunit



- Molecule 44: Mitochondrial complex I, MWFE subunit





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81780	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 ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.370	Depositor
Minimum map value	-0.140	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	170.821, 196.285, 286.47	wwPDB
Map dimensions	270, 185, 161	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, FME, FES, SF4, CDL, 2MR, AMP, DCQ, PC1, NAI, K, MYR, NDP, 3PE, AYA, ZN, SEP, ZMP

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	1	0.33	0/3386	0.58	0/4575
2	2	0.32	0/1695	0.58	0/2306
3	3	0.34	0/5362	0.57	3/7266 (0.0%)
4	4	0.36	0/3463	0.57	0/4687
5	5	0.36	0/1776	0.56	0/2417
6	6	0.40	0/1278	0.56	0/1728
7	9	0.41	0/1445	0.58	0/1956
8	A	0.31	0/902	0.64	0/1234
9	H	0.37	0/2572	0.65	2/3517 (0.1%)
10	J	0.31	0/1324	0.63	0/1790
11	K	0.36	0/749	0.62	0/1014
12	L	0.29	0/4924	0.57	0/6698
13	M	0.34	0/3731	0.59	0/5085
14	N	0.35	0/2787	0.58	0/3795
15	V	0.19	0/1041	0.45	0/1412
16	W	0.26	0/1188	0.49	0/1607
17	X	0.19	0/713	0.43	0/963
17	j	0.22	0/670	0.48	0/902
18	Y	0.28	0/1440	0.53	0/1942
19	Z	0.25	0/1475	0.48	0/1989
20	a	0.23	0/383	0.40	0/518
21	b	0.29	0/749	0.46	0/1009
22	c	0.33	0/1047	0.48	0/1415
23	d	0.29	0/2424	0.50	0/3276
24	e	0.25	0/702	0.50	0/945
25	f	0.26	0/937	0.51	0/1271
26	g	0.28	0/993	0.53	0/1336
27	h	0.32	0/779	0.53	0/1053
28	i	0.30	0/1250	0.47	0/1698
29	k	0.25	0/2646	0.45	0/3579
30	l	0.28	0/896	0.51	0/1200

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	m	0.25	0/647	0.50	0/890
32	n	0.18	0/653	0.39	0/882
33	o	0.25	0/1035	0.48	0/1398
34	p	0.22	0/1085	0.47	0/1467
35	q	0.26	0/1171	0.49	0/1579
36	r	0.23	0/874	0.49	0/1188
37	s	0.20	0/1072	0.48	0/1436
38	t	0.22	0/1573	0.52	0/2130
39	u	0.19	0/590	0.45	0/810
40	v	0.22	0/1361	0.46	0/1861
41	w	0.25	0/872	0.53	0/1185
42	x	0.21	0/425	0.41	0/576
43	y	0.25	0/449	0.54	0/605
44	z	0.35	0/591	0.57	0/795
All	All	0.30	0/67125	0.54	5/90985 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	3	0	1
4	4	0	1
8	A	0	1
All	All	0	3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	H	90	PRO	CA-C-N	-7.08	114.73	122.59
9	H	90	PRO	C-N-CA	-7.08	114.73	122.59
3	3	338	VAL	N-CA-C	-6.92	105.60	112.17
3	3	366	THR	CA-C-N	6.42	133.79	121.54
3	3	366	THR	C-N-CA	6.42	133.79	121.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	259	ASN	Peptide
4	4	275	TYR	Peptide
8	A	113	TRP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	3312	0	3269	45	0
2	2	1655	0	1668	24	0
3	3	5275	0	5300	72	0
4	4	3390	0	3333	54	0
5	5	1726	0	1676	22	0
6	6	1247	0	1259	16	0
7	9	1414	0	1371	29	0
8	A	880	0	920	19	0
9	H	2498	0	2609	45	0
10	J	1294	0	1317	24	0
11	K	749	0	793	22	0
12	L	4806	0	4945	73	0
13	M	3647	0	3849	62	0
14	N	2723	0	2930	33	0
15	V	1028	0	1036	16	0
16	W	1155	0	1177	13	0
17	X	701	0	692	6	0
17	j	660	0	663	5	0
18	Y	1403	0	1392	17	0
19	Z	1441	0	1419	19	0
20	a	371	0	344	5	0
21	b	737	0	710	7	0
22	c	1024	0	1023	12	0
23	d	2372	0	2407	18	0
24	e	691	0	706	8	0
25	f	917	0	958	6	0
26	g	969	0	980	8	0
27	h	769	0	780	8	0
28	i	1209	0	1182	13	0
29	k	2596	0	2559	17	0
30	l	874	0	869	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	m	626	0	635	6	0
32	n	634	0	616	3	0
33	o	1004	0	995	16	0
34	p	1059	0	1062	10	0
35	q	1142	0	1137	16	0
36	r	846	0	864	9	0
37	s	1047	0	1015	14	0
38	t	1520	0	1477	21	0
39	u	563	0	509	7	0
40	v	1307	0	1207	21	0
41	w	846	0	792	9	0
42	x	412	0	411	3	0
43	y	436	0	437	4	0
44	z	576	0	570	5	0
45	1	8	0	0	1	0
45	3	16	0	0	0	0
45	6	8	0	0	1	0
45	9	16	0	0	0	0
46	1	31	0	19	1	0
47	1	44	0	27	6	0
48	2	4	0	0	1	0
48	3	4	0	0	0	0
49	3	1	0	0	0	0
50	4	40	0	54	1	0
50	A	51	0	82	2	0
50	H	51	0	82	2	0
50	K	40	0	54	4	0
50	L	82	0	118	2	0
50	M	44	0	65	3	0
50	N	82	0	118	1	0
50	V	72	0	92	5	0
50	i	102	0	164	2	0
50	p	27	0	27	0	0
51	9	54	0	88	4	0
51	A	83	0	117	3	0
51	L	54	0	88	7	0
51	M	54	0	88	5	0
51	w	54	0	88	7	0
52	H	23	0	30	2	0
53	L	100	0	156	6	0
53	V	179	0	261	4	0
53	W	100	0	156	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	Y	100	0	156	9	0
53	o	165	0	230	10	0
53	z	58	0	60	0	0
54	X	31	0	34	1	0
54	g	34	0	40	1	0
55	b	1	0	0	0	0
56	d	48	0	26	0	0
57	k	23	0	12	0	0
58	s	15	0	27	0	0
All	All	67450	0	68422	720	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 5.

All (720) 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)
37:s:57:TYR:HH	40:v:155:HIS:HD1	1.32	0.74
4:4:152:MET:HE2	4:4:174:ARG:HH12	1.58	0.69
9:H:97:ASN:H	35:q:143:THR:HG22	1.58	0.68
44:z:34:ARG:NH2	44:z:61:TYR:O	2.28	0.66
31:m:83:LEU:HD13	35:q:54:ARG:HD3	1.78	0.65
53:L:1003:CDL:H562	53:L:1003:CDL:H631	1.78	0.65
4:4:50:ASN:HD21	4:4:63:ARG:HH21	1.44	0.65
1:1:132:ARG:NH2	20:a:64:PRO:O	2.30	0.64
14:N:243:LEU:HD22	14:N:330:THR:HG21	1.79	0.64
18:Y:165:ARG:NH1	33:o:87:ASP:OD1	2.30	0.64
6:6:171:LYS:HG2	6:6:174:ARG:HH11	1.63	0.64
7:9:43:ARG:HG2	27:h:11:ARG:HD2	1.80	0.64
3:3:118:ASP:OD2	22:c:46:GLN:NE2	2.32	0.63
4:4:405:MET:SD	4:4:421:GLN:NE2	2.70	0.63
13:M:158:LEU:HD23	14:N:283:ALA:HB1	1.81	0.63
9:H:141:SER:HB3	9:H:289:LEU:HD22	1.80	0.62
29:k:51:PHE:HB3	29:k:107:GLN:HE21	1.64	0.62
30:l:104:ARG:NH1	35:q:84:GLN:OE1	2.32	0.62
4:4:269:LEU:HB2	4:4:368:GLU:HB2	1.81	0.62
7:9:164:GLU:HG3	28:i:88:ARG:HG3	1.82	0.61
12:L:370:THR:HG23	12:L:431:LEU:HD13	1.82	0.61
24:e:40:TYR:O	24:e:43:LEU:HB3	2.00	0.61
1:1:101:GLU:HB2	47:1:503:NAI:H42N	1.81	0.61
1:1:139:ARG:NH2	2:2:144:CYS:O	2.28	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:98:TYR:HA	2:2:157:ASN:HD21	1.65	0.60
3:3:632:ARG:HH12	24:e:59:ASP:H	1.46	0.60
14:N:45:MET:HE3	14:N:53:THR:HG22	1.83	0.60
28:i:34:ARG:NH2	28:i:58:ARG:O	2.33	0.60
29:k:81:LYS:HD2	29:k:92:ASN:HD22	1.66	0.60
34:p:47:GLN:HA	34:p:50:TYR:HB3	1.83	0.60
17:j:37:MET:HE1	17:j:44:SER:HA	1.83	0.59
3:3:126:ASP:HB2	4:4:328:ALA:HB3	1.83	0.59
15:V:39:SER:OG	15:V:54:ARG:NH2	2.35	0.59
6:6:44:SER:O	9:H:54:LYS:NZ	2.36	0.59
6:6:108:PRO:HB2	9:H:58:LYS:HD2	1.82	0.59
34:p:39:ARG:NH2	38:t:3:LEU:O	2.35	0.59
16:W:124:GLN:HB2	33:o:4:GLY:HA3	1.83	0.59
17:j:48:VAL:HG12	17:j:52:MET:HE2	1.85	0.59
39:u:18:THR:HG22	39:u:20:SER:H	1.68	0.59
9:H:10:ILE:HA	9:H:13:ILE:HD12	1.84	0.59
12:L:249:SER:HB2	12:L:336:LYS:HG3	1.84	0.59
2:2:74:GLN:O	20:a:74:ARG:NH2	2.36	0.59
2:2:150:ASN:HB3	2:2:162:GLU:HB3	1.83	0.59
14:N:106:LEU:HD22	14:N:187:MET:HE2	1.85	0.59
3:3:194:GLU:HG3	3:3:389:PRO:HB3	1.84	0.58
12:L:103:PHE:HB2	12:L:341:MET:HE3	1.85	0.58
11:K:23:ARG:HG2	50:K:101:3PE:H11	1.85	0.58
13:M:456:GLY:O	41:w:84:ARG:NH2	2.37	0.58
35:q:81:ARG:NH1	35:q:85:MET:SD	2.76	0.58
24:e:23:CYS:SG	24:e:24:GLN:N	2.77	0.58
18:Y:29:HIS:HB3	18:Y:119:PRO:HD2	1.86	0.57
3:3:601:ARG:NH2	3:3:614:ASP:OD1	2.37	0.57
4:4:200:HIS:NE2	7:9:124:GLU:OE1	2.37	0.57
28:i:60:ARG:HH22	28:i:95:ASP:HA	1.68	0.57
36:r:103:ILE:HB	37:s:47:ASP:HB3	1.86	0.57
1:1:365:CYS:HB2	45:1:501:SF4:S3	2.44	0.57
13:M:101:LEU:HD21	53:o:202:CDL:H841	1.85	0.57
3:3:396:ARG:NH1	3:3:416:THR:O	2.38	0.57
9:H:312:SER:HB3	35:q:54:ARG:HH21	1.69	0.57
12:L:570:GLN:OE1	14:N:167:TRP:NE1	2.37	0.57
2:2:175:GLU:HG3	2:2:182:PRO:HG3	1.87	0.57
3:3:382:THR:HG23	3:3:384:PRO:HD3	1.87	0.57
4:4:335:ARG:NH2	7:9:129:ASP:OD1	2.38	0.57
13:M:50:LEU:HA	16:W:86:ASN:HD21	1.70	0.57
22:c:33:ARG:NH1	22:c:77:ASP:OD1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:233:ARG:NH2	7:9:23:GLN:O	2.38	0.57
29:k:52:PRO:O	29:k:107:GLN:NE2	2.38	0.57
12:L:128:MET:HG2	12:L:251:THR:HG22	1.86	0.56
4:4:84:HIS:NE2	6:6:130:TYR:OH	2.36	0.56
20:a:57:ASP:OD1	20:a:60:LYS:NZ	2.38	0.56
3:3:261:GLU:OE1	22:c:42:ARG:NH2	2.39	0.56
7:9:92:ILE:HG12	7:9:111:ILE:HG12	1.86	0.56
39:u:61:ASP:HB3	39:u:66:ILE:HB	1.88	0.56
41:w:100:ARG:HB2	41:w:105:LEU:HB2	1.87	0.56
12:L:221:THR:HG23	12:L:226:GLN:HB2	1.86	0.56
51:9:401:PC1:H261	9:H:180:PRO:HB3	1.88	0.56
12:L:90:VAL:HG22	12:L:129:LEU:HD22	1.88	0.56
16:W:43:ILE:HG12	16:W:47:ILE:HD12	1.87	0.56
4:4:49:LEU:HD22	8:A:43:PRO:HB2	1.88	0.55
12:L:485:TYR:OH	37:s:1:GLY:N	2.38	0.55
14:N:338:PRO:HG3	53:Y:201:CDL:H792	1.87	0.55
3:3:148:THR:HG23	3:3:150:MET:HE3	1.88	0.55
5:5:129:TRP:O	5:5:132:ARG:HB3	2.05	0.55
10:J:126:VAL:HG23	10:J:127:ILE:HG23	1.87	0.55
4:4:158:ALA:HB1	4:4:163:ALA:HB3	1.88	0.55
1:1:428:GLU:HA	1:1:431:GLN:HG2	1.89	0.55
14:N:211:MET:HG2	14:N:333:SER:HB2	1.88	0.55
3:3:364:LEU:HD12	3:3:491:ASN:HB3	1.89	0.55
18:Y:66:ALA:O	18:Y:69:PHE:HB3	2.07	0.55
29:k:173:ASP:OD1	29:k:207:LYS:NZ	2.40	0.55
29:k:174:VAL:HG22	29:k:225:ALA:HB2	1.88	0.55
23:d:167:LYS:HB2	23:d:229:ALA:HA	1.89	0.55
6:6:118:SER:N	45:6:300:SF4:S4	2.80	0.55
8:A:80:GLN:NE2	9:H:315:PRO:O	2.40	0.55
19:Z:68:ARG:NH1	43:y:43:LEU:O	2.40	0.55
38:t:169:ILE:O	38:t:172:ARG:NH1	2.40	0.54
4:4:66:MET:HE1	4:4:414:VAL:HG11	1.90	0.54
11:K:46:LEU:O	11:K:50:ASN:HB2	2.07	0.54
24:e:17:GLU:OE2	24:e:19:ARG:NH1	2.40	0.54
3:3:190:MET:HG2	3:3:192:MET:HG2	1.90	0.54
22:c:42:ARG:NH1	22:c:46:GLN:O	2.39	0.54
2:2:105:THR:OG1	48:2:300:FES:S2	2.65	0.54
13:M:5:ILE:HG22	13:M:9:MET:HE2	1.90	0.54
9:H:26:LYS:HB3	44:z:5:VAL:HG12	1.90	0.54
31:m:78:GLU:OE1	31:m:82:ARG:NH1	2.41	0.54
4:4:35:ASP:O	14:N:49:ASN:ND2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:t:27:GLU:OE2	38:t:33:ARG:NH1	2.41	0.54
2:2:55:GLN:NE2	2:2:91:ASN:OD1	2.41	0.54
1:1:270:GLU:OE1	1:1:283:HIS:NE2	2.41	0.54
3:3:252:PRO:HG3	3:3:263:ILE:HG12	1.90	0.54
13:M:36:LEU:HB2	41:w:69:VAL:HG22	1.90	0.54
37:s:102:GLU:OE2	37:s:105:ARG:NH2	2.37	0.54
13:M:54:LEU:HD23	16:W:93:ILE:HG23	1.90	0.53
25:f:37:ILE:O	25:f:44:ARG:NH1	2.41	0.53
51:A:401:PC1:H3D1	9:H:53:ILE:HG12	1.91	0.53
19:Z:3:SER:OG	19:Z:6:LYS:NZ	2.41	0.53
19:Z:67:PHE:HD1	43:y:43:LEU:HD21	1.72	0.53
3:3:221:GLU:OE2	3:3:243:ARG:NH1	2.42	0.53
8:A:25:PRO:HB2	9:H:60:PRO:HD3	1.91	0.53
15:V:139:LYS:HG3	15:V:140:VAL:HG13	1.91	0.53
25:f:49:GLN:HE22	27:h:92:LYS:HA	1.73	0.53
4:4:101:PRO:O	4:4:105:ARG:NH1	2.40	0.53
12:L:231:PRO:HB3	12:L:530:PRO:HG3	1.91	0.53
8:A:53:MET:HE2	10:J:172:THR:HB	1.91	0.53
9:H:149:ILE:HG21	9:H:185:TRP:HB2	1.90	0.53
13:M:23:ILE:HD11	13:M:92:LYS:HD2	1.91	0.53
6:6:31:ALA:HA	6:6:174:ARG:HH21	1.74	0.53
24:e:19:ARG:HB2	24:e:65:TRP:HB2	1.90	0.53
1:1:140:GLY:O	1:1:179:ARG:NH2	2.42	0.53
51:L:1002:PC1:H2A2	53:L:1003:CDL:H821	1.91	0.53
5:5:74:SER:HB3	5:5:97:LEU:HB3	1.91	0.53
3:3:201:ASP:OD2	3:3:268:ARG:NH2	2.37	0.52
33:o:45:ASP:OD2	33:o:51:ARG:NH2	2.41	0.52
1:1:142:PHE:HB3	1:1:145:GLU:HB2	1.91	0.52
4:4:282:GLU:HB3	4:4:313:GLN:HE22	1.73	0.52
36:r:85:LEU:HD22	36:r:96:ILE:HD11	1.91	0.52
3:3:27:LEU:HA	3:3:37:ILE:HD12	1.91	0.52
3:3:262:TRP:HB2	3:3:390:LEU:HD21	1.91	0.52
5:5:121:VAL:HG21	5:5:146:PRO:HD3	1.92	0.52
7:9:108:ARG:NH1	22:c:70:MET:O	2.34	0.52
9:H:64:ALA:O	9:H:124:ASN:ND2	2.43	0.52
13:M:18:SER:HB2	13:M:23:ILE:HG22	1.91	0.52
12:L:69:LEU:HD13	13:M:451:PRO:HG2	1.90	0.52
9:H:24:GLU:OE2	9:H:274:ARG:NH1	2.42	0.52
9:H:237:PHE:O	9:H:241:LEU:HB2	2.10	0.52
13:M:243:MET:HB3	13:M:301:ILE:HG21	1.90	0.52
18:Y:48:GLU:OE1	31:m:57:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:t:107:HIS:NE2	41:w:43:ASP:OD1	2.38	0.52
3:3:198:ASN:OD1	3:3:268:ARG:NH2	2.42	0.52
4:4:352:TYR:HD1	7:9:86:VAL:HG21	1.75	0.52
14:N:115:VAL:HG12	14:N:180:ALA:HB1	1.91	0.52
18:Y:35:CYS:O	18:Y:39:ASN:ND2	2.43	0.52
18:Y:43:MET:HE3	18:Y:47:TRP:HZ3	1.74	0.52
8:A:30:TYR:OH	9:H:57:ILE:O	2.28	0.52
13:M:260:PRO:HG2	50:M:501:3PE:H342	1.92	0.52
19:Z:41:ASP:OD1	36:r:86:LYS:NZ	2.41	0.52
10:J:167:VAL:HG22	14:N:42:PRO:HG2	1.92	0.52
15:V:1:AYA:HA	15:V:4:LEU:HD23	1.92	0.52
3:3:349:PHE:H	3:3:509:PRO:HB2	1.75	0.51
4:4:354:GLU:OE2	4:4:357:GLN:NE2	2.43	0.51
7:9:69:ARG:NH1	7:9:73:GLY:O	2.41	0.51
23:d:48:PRO:HA	23:d:71:MET:O	2.10	0.51
1:1:213:VAL:HG13	1:1:217:GLY:HA2	1.92	0.51
4:4:413:ASP:OD1	9:H:281:ARG:NH2	2.43	0.51
8:A:114:THR:HB	9:H:286:MET:HG3	1.91	0.51
15:V:65:ILE:HD11	15:V:100:LEU:HD23	1.92	0.51
37:s:30:PHE:HB3	37:s:33:ARG:HB2	1.93	0.51
4:4:343:GLU:O	4:4:347:HIS:ND1	2.34	0.51
13:M:232:ALA:O	13:M:237:LYS:NZ	2.43	0.51
19:Z:159:LYS:NZ	33:o:112:VAL:O	2.44	0.51
41:w:114:ASP:HB3	41:w:117:LYS:HG2	1.90	0.51
3:3:382:THR:HB	3:3:454:GLY:HA3	1.92	0.51
5:5:41:GLN:NE2	5:5:49:GLU:OE1	2.40	0.51
5:5:96:LEU:HB2	5:5:105:ILE:HG22	1.92	0.51
12:L:601:LEU:O	15:V:1:AYA:N	2.42	0.51
13:M:204:MET:HE1	13:M:302:LEU:HD11	1.92	0.51
15:V:11:ILE:HB	15:V:20:LYS:HD3	1.92	0.51
19:Z:119:SER:HB3	37:s:55:ARG:HH22	1.76	0.51
3:3:99:ALA:O	3:3:134:LYS:NZ	2.38	0.51
8:A:48:ARG:NH1	11:K:86:GLY:O	2.44	0.51
13:M:133:ILE:HD11	13:M:231:LEU:HD11	1.92	0.51
13:M:328:CYS:HB3	13:M:437:MET:HE1	1.93	0.51
12:L:316:THR:HA	12:L:319:ILE:HG12	1.93	0.51
17:X:13:ASP:OD2	32:n:12:LYS:NZ	2.43	0.51
7:9:108:ARG:NH2	28:i:128:SER:OG	2.44	0.51
19:Z:141:ARG:HG3	41:w:112:CYS:HB2	1.92	0.51
53:o:201:CDL:H132	53:o:201:CDL:H522	1.93	0.51
5:5:49:GLU:HG2	5:5:106:ARG:HD2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:283:MET:HB2	3:3:560:ILE:HB	1.92	0.50
5:5:33:LEU:HD13	5:5:60:VAL:HG22	1.92	0.50
29:k:25:ILE:HG12	29:k:168:VAL:HB	1.93	0.50
34:p:47:GLN:HG3	38:t:165:LEU:HD13	1.92	0.50
23:d:100:GLU:HB2	23:d:105:ASP:HA	1.93	0.50
3:3:276:ARG:HA	28:i:135:GLN:HB2	1.93	0.50
3:3:324:ASP:HB3	3:3:571:ALA:HB1	1.93	0.50
4:4:145:THR:OG1	4:4:181:TYR:OH	2.27	0.50
12:L:161:ARG:HA	38:t:91:GLU:HG3	1.92	0.50
23:d:10:LYS:NZ	26:g:126:ASP:OD2	2.44	0.50
23:d:72:ASP:O	23:d:83:ARG:NH2	2.44	0.50
1:1:243:ALA:HA	1:1:251:SER:HB3	1.94	0.50
3:3:140:LYS:HB2	3:3:148:THR:HG21	1.92	0.50
8:A:3:LEU:HD23	50:H:502:3PE:H231	1.93	0.50
37:s:110:ARG:NH1	39:u:69:ASP:OD2	2.45	0.50
1:1:378:ARG:NE	3:3:132:GLU:OE2	2.44	0.50
4:4:145:THR:HA	4:4:148:LEU:HD12	1.94	0.50
4:4:155:THR:HB	4:4:167:PHE:HA	1.92	0.50
8:A:67:LEU:HD22	11:K:65:VAL:HA	1.93	0.50
12:L:536:LEU:HG	12:L:540:MET:HE2	1.94	0.50
1:1:71:ALA:HB2	47:1:503:NAI:H4D	1.94	0.50
12:L:142:ILE:HG12	13:M:370:PRO:HB2	1.93	0.50
3:3:46:LEU:O	22:c:116:LYS:NZ	2.37	0.50
13:M:459:TYR:H	41:w:84:ARG:HH22	1.59	0.50
29:k:104:ARG:NH1	29:k:126:ARG:O	2.44	0.50
33:o:45:ASP:OD1	33:o:49:ARG:NH2	2.44	0.50
2:2:149:VAL:O	2:2:190:ARG:NH2	2.40	0.50
4:4:71:GLU:OE2	9:H:134:ARG:NH1	2.37	0.50
12:L:128:MET:HE1	12:L:255:ALA:HB2	1.94	0.50
13:M:98:MET:HE1	53:o:202:CDL:H822	1.94	0.50
51:M:502:PC1:H252	14:N:277:ILE:HG12	1.93	0.50
21:b:32:GLN:HE22	21:b:34:GLU:HB2	1.76	0.50
38:t:29:ARG:HD2	38:t:75:HIS:HD2	1.77	0.50
2:2:79:ARG:NH2	3:3:170:ASP:OD1	2.45	0.49
3:3:223:ARG:O	3:3:241:SER:HA	2.12	0.49
3:3:632:ARG:NH1	24:e:57:CYS:SG	2.84	0.49
3:3:329:ILE:HD13	3:3:505:LEU:HD22	1.94	0.49
4:4:226:GLU:OE1	4:4:305:ARG:NH2	2.36	0.49
12:L:543:THR:HG23	40:v:83:MET:HE1	1.93	0.49
50:V:201:3PE:H291	50:V:201:3PE:H342	1.94	0.49
18:Y:48:GLU:OE1	18:Y:134:ARG:NH2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:70:MET:HE1	10:J:27:ILE:HG22	1.94	0.49
14:N:207:ILE:HG22	14:N:211:MET:HE2	1.95	0.49
53:o:201:CDL:H191	53:o:201:CDL:H762	1.94	0.49
2:2:159:ASN:HB3	2:2:184:PRO:HB3	1.95	0.49
4:4:200:HIS:O	4:4:324:LYS:NZ	2.37	0.49
5:5:77:ASP:OD2	5:5:79:THR:OG1	2.31	0.49
9:H:21:THR:HG21	52:H:501:DCQ:H8	1.93	0.49
13:M:91:ARG:NH2	29:k:290:ASP:OD2	2.46	0.49
50:N:401:3PE:H392	50:N:401:3PE:H2D2	1.93	0.49
53:W:201:CDL:H381	51:w:801:PC1:H251	1.95	0.49
53:Y:201:CDL:H571	53:Y:201:CDL:H152	1.95	0.49
23:d:130:ILE:HG12	23:d:164:THR:HB	1.94	0.49
34:p:66:ARG:HH21	40:v:8:MET:HB3	1.78	0.49
8:A:60:ILE:HG21	10:J:168:ILE:HG21	1.94	0.49
12:L:161:ARG:NH2	38:t:90:TYR:O	2.38	0.49
51:L:1002:PC1:H262	53:W:201:CDL:H621	1.95	0.49
13:M:126:LEU:HD21	13:M:153:THR:HG21	1.95	0.49
13:M:272:THR:HA	13:M:275:ILE:HD12	1.93	0.49
14:N:331:VAL:HG13	14:N:335:MET:HE3	1.95	0.49
19:Z:15:ARG:HB3	36:r:109:ILE:HD12	1.95	0.49
14:N:200:MET:HG3	14:N:269:GLU:HG3	1.93	0.49
33:o:66:THR:OG1	42:x:28:TRP:NE1	2.46	0.49
7:9:52:PHE:HE1	28:i:77:VAL:HG21	1.78	0.49
12:L:50:PRO:HA	12:L:53:MET:HG2	1.94	0.49
12:L:161:ARG:NE	12:L:238:GLU:OE2	2.46	0.49
25:f:71:LEU:HD13	25:f:79:VAL:HG11	1.95	0.49
37:s:6:ARG:HH12	37:s:105:ARG:HD2	1.78	0.49
8:A:74:PRO:HG2	10:J:147:TYR:HE2	1.77	0.48
11:K:56:ALA:O	11:K:59:MET:HB3	2.13	0.48
51:M:502:PC1:H251	51:M:502:PC1:H372	1.95	0.48
1:1:356:HIS:O	3:3:177:ARG:NH2	2.41	0.48
7:9:27:TRP:HB3	7:9:30:LEU:HD12	1.95	0.48
10:J:40:GLY:HA2	10:J:43:ILE:HD12	1.94	0.48
19:Z:119:SER:OG	19:Z:123:ASN:ND2	2.47	0.48
4:4:285:VAL:H	7:9:2:TYR:HA	1.79	0.48
12:L:547:LYS:NZ	40:v:44:TYR:OH	2.46	0.48
3:3:569:LYS:HG3	3:3:571:ALA:HB2	1.94	0.48
4:4:292:ASP:OD1	4:4:292:ASP:N	2.44	0.48
14:N:258:SER:O	14:N:261:MET:HB3	2.14	0.48
28:i:78:ASP:HB3	28:i:81:MET:HG3	1.94	0.48
1:1:69:GLY:O	47:1:503:NAI:H2N	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:A:403:3PE:H3D2	9:H:302:MET:HE1	1.95	0.48
13:M:369:LEU:HD12	13:M:370:PRO:HD2	1.96	0.48
26:g:91:GLU:HG2	26:g:96:TRP:HE3	1.79	0.48
15:V:54:ARG:HG2	15:V:57:ARG:HH22	1.78	0.48
23:d:300:LEU:HB3	23:d:305:VAL:HB	1.95	0.48
3:3:11:VAL:HG11	3:3:73:VAL:HB	1.94	0.48
3:3:622:ARG:NH2	24:e:73:GLU:OE2	2.47	0.48
8:A:83:ASN:ND2	51:A:402:PC1:O14	2.40	0.48
16:W:109:GLU:OE2	16:W:112:ARG:NH2	2.39	0.48
1:1:289:GLY:HA3	1:1:293:ASN:HD22	1.78	0.48
3:3:119:GLN:HB2	3:3:123:PHE:HD2	1.78	0.48
12:L:10:VAL:HG21	36:r:78:VAL:HG22	1.94	0.48
12:L:487:LYS:HE3	39:u:49:GLY:HA2	1.96	0.48
53:V:203:CDL:H561	53:V:204:CDL:H201	1.95	0.48
27:h:11:ARG:NH2	27:h:20:GLN:OE1	2.47	0.48
12:L:556:ILE:O	12:L:560:THR:N	2.46	0.48
16:W:83:PRO:O	16:W:87:TYR:HB2	2.14	0.48
29:k:133:VAL:HG12	29:k:205:VAL:HG12	1.94	0.48
10:J:111:LYS:HA	10:J:121:GLY:HA3	1.96	0.48
11:K:21:MET:HE1	50:K:101:3PE:H331	1.95	0.48
11:K:21:MET:HG2	12:L:589:LEU:HD23	1.96	0.48
12:L:542:LEU:HB2	40:v:83:MET:HE3	1.96	0.48
13:M:130:LEU:HD22	13:M:150:LEU:HD13	1.96	0.48
6:6:169:ARG:NH2	7:9:142:GLU:OE2	2.42	0.47
8:A:63:LEU:HB2	10:J:67:VAL:HG21	1.96	0.47
12:L:203:MET:HB2	19:Z:113:GLN:HG3	1.96	0.47
12:L:428:PHE:HA	12:L:432:LEU:HD12	1.96	0.47
23:d:311:GLU:HG2	23:d:336:PRO:HB3	1.96	0.47
37:s:4:LEU:HD11	40:v:124:THR:HA	1.95	0.47
1:1:21:ILE:O	1:1:117:LYS:NZ	2.36	0.47
3:3:377:VAL:HG23	3:3:404:LEU:HD11	1.94	0.47
53:L:1003:CDL:H391	53:L:1003:CDL:H171	1.96	0.47
19:Z:5:ASP:HB3	19:Z:8:VAL:HG12	1.96	0.47
30:l:96:HIS:HA	30:l:101:GLU:HG2	1.96	0.47
4:4:93:TYR:HE2	5:5:168:LEU:HB2	1.79	0.47
8:A:75:LEU:HD12	9:H:151:LEU:HD21	1.94	0.47
9:H:20:LEU:HD13	44:z:12:MET:HE1	1.96	0.47
12:L:1:FME:HG3	12:L:61:MET:HE1	1.96	0.47
18:Y:118:ARG:NH2	35:q:62:GLU:OE2	2.46	0.47
20:a:70:ARG:NH1	20:a:75:HIS:O	2.47	0.47
14:N:277:ILE:HD13	50:V:202:3PE:H372	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Y:97:ARG:HD3	35:q:59:LEU:HD13	1.95	0.47
19:Z:3:SER:OG	19:Z:4:TRP:N	2.46	0.47
29:k:108:TYR:OH	29:k:164:LEU:O	2.20	0.47
1:1:184:TYR:HB3	1:1:357:GLU:HB3	1.96	0.47
11:K:53:PHE:HE2	14:N:84:TRP:HE1	1.63	0.47
28:i:54:GLN:HB3	28:i:58:ARG:HB2	1.96	0.47
29:k:115:LEU:HD13	29:k:121:GLY:HA2	1.97	0.47
4:4:412:ALA:HB3	9:H:281:ARG:HG3	1.97	0.47
1:1:144:ASN:O	1:1:148:ASN:HB2	2.14	0.47
3:3:193:SER:H	3:3:196:SER:HB3	1.79	0.47
5:5:93:VAL:HG22	5:5:108:LYS:HG2	1.97	0.47
5:5:137:MET:HA	5:5:161:PRO:HD2	1.96	0.47
5:5:151:ILE:HG23	5:5:152:LEU:HG	1.97	0.47
12:L:593:ILE:HD12	15:V:41:ALA:HB2	1.97	0.47
13:M:179:LEU:HD13	13:M:249:LEU:HD11	1.97	0.47
17:X:49:GLU:OE2	38:t:19:TYR:OH	2.33	0.47
33:o:34:ILE:HG22	33:o:68:PHE:HB3	1.96	0.47
50:A:403:3PE:H381	9:H:295:PRO:HB3	1.97	0.47
12:L:541:ASN:O	12:L:545:SER:N	2.47	0.47
14:N:309:ASN:ND2	29:k:75:GLY:O	2.44	0.47
2:2:111:ARG:HD3	2:2:151:ALA:HB3	1.97	0.47
3:3:47:SER:O	3:3:161:ARG:NH1	2.41	0.47
51:L:1002:PC1:H3A1	36:r:80:ILE:HG23	1.96	0.47
13:M:343:ILE:O	13:M:346:ARG:NH1	2.47	0.47
1:1:96:ASN:ND2	46:1:502:FMN:O4'	2.45	0.47
4:4:179:GLU:OE2	6:6:66:ARG:NH1	2.39	0.47
12:L:453:SER:HA	12:L:456:ARG:HH21	1.80	0.47
50:M:501:3PE:H2A2	50:M:501:3PE:H371	1.96	0.47
53:Y:201:CDL:H432	33:o:27:THR:HG21	1.97	0.47
39:u:7:ILE:HG23	39:u:16:GLN:HB3	1.95	0.47
1:1:30:ASP:HB3	1:1:35:GLY:HA3	1.97	0.46
12:L:245:ALA:O	12:L:249:SER:OG	2.27	0.46
51:L:1002:PC1:H271	51:w:801:PC1:H281	1.98	0.46
17:X:55:GLU:OE1	38:t:24:ARG:NH2	2.48	0.46
3:3:443:LEU:HD13	3:3:477:ILE:HD11	1.96	0.46
13:M:9:MET:HB3	53:Y:201:CDL:H232	1.96	0.46
16:W:138:LYS:HB2	16:W:143:ASN:HD21	1.80	0.46
18:Y:165:ARG:HH12	33:o:90:MET:HE1	1.79	0.46
7:9:94:ILE:HA	7:9:108:ARG:O	2.15	0.46
11:K:14:VAL:HG22	50:K:101:3PE:H2B2	1.96	0.46
13:M:197:LEU:HD23	51:M:502:PC1:H3B2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:91:LYS:HG2	1:1:219:PRO:HB2	1.97	0.46
1:1:94:VAL:O	1:1:222:VAL:HA	2.16	0.46
13:M:457:PRO:O	41:w:84:ARG:NH1	2.49	0.46
18:Y:89:ASP:OD2	44:z:34:ARG:NH1	2.48	0.46
19:Z:140:ASP:O	19:Z:161:ARG:NH1	2.47	0.46
1:1:40:GLY:HA2	2:2:209:PRO:HA	1.97	0.46
1:1:70:GLY:HA3	47:1:503:NAI:H1D	1.96	0.46
2:2:173:ILE:HG22	2:2:177:LYS:HE2	1.98	0.46
53:L:1003:CDL:H182	13:M:442:LEU:HD22	1.97	0.46
39:u:10:ARG:HD2	39:u:15:PRO:HA	1.97	0.46
3:3:356:THR:HG21	3:3:503:LEU:HD22	1.97	0.46
4:4:377:TYR:HB3	4:4:390:LYS:HB3	1.97	0.46
5:5:56:GLY:HA2	5:5:59:PRO:HD2	1.96	0.46
14:N:298:TYR:O	14:N:303:THR:OG1	2.31	0.46
1:1:305:PRO:HG3	1:1:413:TRP:HB3	1.98	0.46
5:5:182:ARG:HD2	26:g:100:THR:HA	1.97	0.46
12:L:279:CYS:SG	12:L:405:ASN:ND2	2.89	0.46
3:3:325:ALA:HA	3:3:328:LEU:HD12	1.97	0.46
4:4:190:HIS:CD2	6:6:150:PRO:HD3	2.51	0.46
13:M:427:LEU:HD21	34:p:56:ARG:HH12	1.81	0.46
25:f:5:LYS:NZ	25:f:68:GLU:OE2	2.47	0.46
1:1:92:TYR:O	1:1:220:THR:HA	2.15	0.46
4:4:224:GLU:OE2	7:9:40:TYR:OH	2.31	0.46
40:v:52:ASP:OD1	40:v:78:HIS:NE2	2.35	0.46
3:3:60:GLU:HG2	3:3:78:ASN:HB3	1.98	0.46
3:3:324:ASP:N	3:3:324:ASP:OD1	2.48	0.46
4:4:291:GLY:O	4:4:296:ARG:NH1	2.49	0.46
11:K:63:LEU:HD13	14:N:71:MET:HE3	1.97	0.46
14:N:257:LEU:HD11	53:o:202:CDL:H873	1.98	0.46
6:6:58:GLU:HG2	6:6:151:PRO:O	2.16	0.45
41:w:100:ARG:HG3	41:w:107:LEU:HD23	1.98	0.45
3:3:499:GLN:HE21	3:3:503:LEU:HD11	1.81	0.45
3:3:518:PRO:HB2	3:3:538:PRO:HD3	1.98	0.45
4:4:63:ARG:HB3	4:4:79:HIS:HB2	1.99	0.45
12:L:451:ILE:O	12:L:455:LYS:HB2	2.17	0.45
13:M:258:ALA:HB1	13:M:302:LEU:HB3	1.98	0.45
3:3:110:GLN:NE2	3:3:113:GLU:O	2.49	0.45
4:4:110:SER:OG	4:4:149:ASN:ND2	2.50	0.45
4:4:388:ARG:HG2	5:5:81:VAL:HG22	1.97	0.45
7:9:105:ARG:NH2	21:b:86:TYR:O	2.49	0.45
9:H:162:LEU:HD21	9:H:237:PHE:HE1	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:113:VAL:HG12	10:J:119:PHE:HB2	1.99	0.45
40:v:54:SER:HA	40:v:84:TYR:HB3	1.98	0.45
12:L:12:LEU:HB3	53:W:201:CDL:H662	1.97	0.45
12:L:392:LYS:HA	12:L:395:ILE:HD12	1.96	0.45
2:2:99:HIS:CE1	2:2:101:GLN:HE21	2.34	0.45
3:3:242:THR:HG22	3:3:247:VAL:HA	1.97	0.45
12:L:100:ILE:HG21	12:L:246:LEU:HB2	1.97	0.45
12:L:421:ILE:HG12	12:L:501:ALA:HB2	1.99	0.45
13:M:9:MET:HE1	53:Y:201:CDL:H162	1.98	0.45
13:M:75:LEU:HD23	13:M:440:HIS:CE1	2.51	0.45
16:W:11:ILE:HG12	38:t:103:LEU:HD11	1.99	0.45
33:o:52:PRO:HG2	33:o:56:ALA:HB2	1.98	0.45
3:3:382:THR:OG1	3:3:387:GLU:OE1	2.31	0.45
12:L:137:LEU:HB3	12:L:186:MET:HG2	1.99	0.45
13:M:231:LEU:HA	13:M:235:LEU:HB2	1.99	0.45
11:K:67:ALA:O	11:K:70:GLU:HB3	2.16	0.45
12:L:392:LYS:O	12:L:395:ILE:HB	2.17	0.45
22:c:28:GLU:O	22:c:32:THR:OG1	2.23	0.45
50:i:501:3PE:H362	50:i:502:3PE:H221	1.98	0.45
34:p:107:ASP:OD1	34:p:110:ARG:NH2	2.50	0.45
4:4:149:ASN:HD22	4:4:370:PRO:HB2	1.82	0.45
5:5:134:ILE:HG22	5:5:140:VAL:HB	1.99	0.45
7:9:151:LYS:HE2	7:9:155:LEU:HD11	1.98	0.45
11:K:73:LEU:HD11	14:N:41:ILE:HG13	1.99	0.45
53:L:1003:CDL:H632	13:M:445:LEU:HD22	1.98	0.45
3:3:114:CYS:HB3	3:3:117:GLN:HB2	1.98	0.45
5:5:150:ARG:NH1	5:5:153:THR:OG1	2.49	0.45
28:i:50:GLU:HG3	28:i:89:TRP:HZ2	1.80	0.45
33:o:46:ASN:ND2	33:o:61:GLN:HE21	2.15	0.45
43:y:8:ARG:HG3	43:y:10:HIS:H	1.82	0.45
2:2:156:ILE:HD13	2:2:176:LEU:HD11	1.98	0.45
3:3:175:THR:HG21	3:3:186:TYR:HB2	1.99	0.45
7:9:132:VAL:HG21	7:9:165:ILE:HG21	1.98	0.45
50:K:101:3PE:H3C2	12:L:592:LEU:HD21	1.99	0.45
13:M:423:ILE:HG12	34:p:58:VAL:HG22	1.98	0.45
51:M:502:PC1:H3E1	51:M:502:PC1:H3B1	1.86	0.45
34:p:51:ASN:HD22	38:t:165:LEU:HD22	1.82	0.45
38:t:29:ARG:HD2	38:t:75:HIS:CD2	2.52	0.45
38:t:134:ARG:HA	38:t:137:LYS:HE3	1.99	0.45
1:1:380:VAL:O	1:1:429:ARG:NH1	2.46	0.44
3:3:366:THR:HG22	3:3:370:GLY:HA3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:417:ILE:HA	4:4:420:THR:HG22	1.98	0.44
6:6:71:ARG:NH2	7:9:50:TYR:O	2.50	0.44
9:H:126:LYS:HD3	10:J:78:GLN:HE21	1.82	0.44
10:J:130:THR:HG21	35:q:123:LEU:HD12	1.98	0.44
13:M:106:LEU:HD13	13:M:234:ILE:HG21	1.98	0.44
33:o:43:LEU:HB3	53:o:202:CDL:H321	1.99	0.44
10:J:10:SER:O	10:J:13:PHE:HB3	2.17	0.44
13:M:211:GLY:HA3	50:M:501:3PE:H3G2	1.99	0.44
16:W:125:TYR:HB2	30:l:48:SER:HB3	1.98	0.44
17:X:13:ASP:O	17:X:17:TYR:HB2	2.17	0.44
28:i:44:TYR:OH	28:i:113:HIS:N	2.39	0.44
35:q:92:GLU:HA	35:q:95:THR:HG22	1.98	0.44
50:4:501:3PE:H3A1	12:L:563:PRO:HA	1.98	0.44
7:9:92:ILE:HA	7:9:110:ASP:O	2.17	0.44
8:A:67:LEU:HB3	11:K:65:VAL:HG13	2.00	0.44
12:L:538:PRO:HA	50:L:1001:3PE:H271	1.99	0.44
14:N:44:MET:HE2	14:N:130:LEU:HD12	1.99	0.44
21:b:84:CYS:CB	21:b:87:CYS:SG	3.05	0.44
34:p:62:PRO:O	34:p:66:ARG:HB2	2.16	0.44
3:3:311:GLN:HA	3:3:338:VAL:HG12	2.00	0.44
8:A:69:ILE:HD11	9:H:144:VAL:HG13	1.99	0.44
12:L:312:LEU:HD21	12:L:392:LYS:HG3	1.99	0.44
13:M:165:ILE:HG21	14:N:268:GLN:HA	1.99	0.44
53:W:201:CDL:H402	51:w:801:PC1:H272	1.99	0.44
21:b:49:VAL:HG22	21:b:90:GLN:HG3	1.98	0.44
40:v:71:LEU:HD21	40:v:77:MET:HG2	1.98	0.44
1:1:154:ARG:HA	20:a:58:LEU:HD21	1.99	0.44
4:4:65:VAL:HB	4:4:77:ASP:HB3	1.99	0.44
4:4:106:LEU:HD13	4:4:391:ILE:HG21	1.98	0.44
14:N:222:ASN:HD21	14:N:240:MET:HB3	1.83	0.44
23:d:135:LEU:HA	23:d:167:LYS:HB3	2.00	0.44
4:4:323:ILE:HD12	4:4:324:LYS:HG3	2.00	0.44
12:L:144:TRP:NE1	12:L:179:ASP:OD1	2.46	0.44
12:L:184:LEU:HD13	13:M:393:ILE:HG21	1.99	0.44
12:L:383:MET:HB3	12:L:386:LEU:HD12	2.00	0.44
23:d:155:GLU:HA	23:d:158:GLU:HG2	2.00	0.44
1:1:141:GLU:HG2	2:2:145:LEU:HD22	1.99	0.44
4:4:278:TYR:HA	4:4:281:VAL:HG22	1.99	0.44
10:J:125:TRP:HB2	35:q:136:THR:HG21	2.00	0.44
51:L:1002:PC1:H32	51:w:801:PC1:H142	2.00	0.44
22:c:29:HIS:HD2	22:c:33:ARG:HH11	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:d:128:LYS:NZ	23:d:218:ILE:O	2.36	0.44
23:d:280:THR:HG23	23:d:283:LYS:H	1.83	0.44
29:k:49:LYS:HE3	29:k:51:PHE:HE1	1.83	0.44
35:q:88:GLU:OE1	35:q:127:ARG:NH2	2.51	0.44
1:l:109:GLU:OE2	1:l:112:ARG:NH2	2.51	0.44
11:K:55:LEU:HD13	30:l:16:TRP:HE3	1.82	0.44
12:L:13:ILE:HD11	53:W:201:CDL:H622	2.00	0.44
12:L:589:LEU:HD11	50:V:201:3PE:H232	1.99	0.44
13:M:116:ILE:HD11	13:M:161:LEU:HD12	1.99	0.44
13:M:447:LEU:HD11	51:w:801:PC1:H3F1	1.99	0.44
15:V:35:VAL:HG21	53:V:203:CDL:H721	1.99	0.44
53:Y:201:CDL:H671	53:Y:201:CDL:H141	1.99	0.44
26:g:42:VAL:HG11	26:g:59:ARG:HG3	1.99	0.44
3:3:101:HIS:HD2	4:4:342:MET:HE2	1.83	0.44
3:3:323:VAL:HG11	3:3:525:LEU:HD13	2.00	0.44
5:5:65:ARG:NH1	5:5:123:VAL:O	2.50	0.44
10:J:43:ILE:HG22	11:K:46:LEU:HD21	2.00	0.44
13:M:143:LEU:HD11	14:N:303:THR:HG21	2.00	0.44
40:v:68:ASP:HA	40:v:86:ARG:HH21	1.83	0.44
50:H:502:3PE:H2G1	10:J:38:GLY:HA3	1.99	0.43
51:L:1002:PC1:H372	51:L:1002:PC1:H341	1.80	0.43
16:W:120:GLY:O	16:W:124:GLN:NE2	2.51	0.43
23:d:196:LEU:HD21	23:d:198:LYS:HE2	2.00	0.43
24:e:17:GLU:HG2	24:e:67:ARG:HB3	1.99	0.43
17:j:11:ILE:HG22	17:j:77:VAL:HG23	2.00	0.43
38:t:137:LYS:HA	38:t:140:GLN:HG2	2.00	0.43
10:J:10:SER:OG	11:K:7:ASN:ND2	2.51	0.43
10:J:52:LEU:HD13	11:K:45:THR:HG23	2.00	0.43
23:d:26:ALA:HB3	23:d:47:VAL:HG13	2.00	0.43
23:d:167:LYS:O	23:d:230:PHE:N	2.46	0.43
26:g:21:SER:OG	26:g:30:ARG:NH1	2.51	0.43
30:l:64:GLU:HG3	30:l:70:LYS:HD2	2.00	0.43
43:y:17:PRO:O	43:y:20:PHE:HB3	2.18	0.43
1:l:300:GLY:HA2	1:l:333:ALA:H	1.83	0.43
3:3:244:THR:HB	22:c:73:ALA:HB2	2.01	0.43
3:3:449:PRO:O	3:3:487:TRP:NE1	2.35	0.43
4:4:149:ASN:ND2	4:4:370:PRO:HB2	2.33	0.43
7:9:132:VAL:HG11	7:9:169:ILE:HD11	2.01	0.43
12:L:83:ASP:OD2	12:L:262:ARG:NH1	2.50	0.43
12:L:137:LEU:HD21	12:L:263:PHE:HZ	1.83	0.43
12:L:233:LEU:HD23	12:L:307:SER:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:L:1002:PC1:H372	53:W:201:CDL:H512	2.00	0.43
15:V:80:ARG:NH1	15:V:88:ASN:OD1	2.51	0.43
53:Y:201:CDL:H852	53:Y:201:CDL:H822	1.88	0.43
25:f:34:LEU:HD12	25:f:37:ILE:HD12	2.00	0.43
8:A:84:LEU:HD11	31:m:45:ASN:HD22	1.83	0.43
9:H:293:PHE:O	9:H:297:THR:OG1	2.31	0.43
16:W:138:LYS:HA	30:l:27:ARG:HB3	2.00	0.43
18:Y:82:THR:HA	18:Y:85:TRP:CD1	2.54	0.43
19:Z:81:VAL:HG23	19:Z:82:LEU:HD22	2.00	0.43
53:o:201:CDL:H142	53:o:201:CDL:H171	1.88	0.43
12:L:67:HIS:NE2	12:L:70:THR:OG1	2.44	0.43
31:m:80:LEU:HD12	31:m:83:LEU:HD11	2.00	0.43
34:p:17:LEU:HD11	38:t:71:TRP:CG	2.54	0.43
3:3:159:CYS:HB3	3:3:172:LEU:HD13	2.00	0.43
1:1:390:ASP:O	1:1:393:TRP:HB3	2.18	0.43
4:4:183:ARG:NH1	4:4:210:ASP:OD2	2.40	0.43
14:N:160:LEU:HD21	53:V:203:CDL:H191	2.00	0.43
19:Z:26:PRO:HB2	19:Z:31:TYR:HE2	1.83	0.43
42:x:41:GLU:OE2	42:x:44:ARG:NH2	2.40	0.43
3:3:269:PHE:HB3	3:3:683:THR:HG21	1.99	0.43
51:9:401:PC1:H351	9:H:187:ILE:HD12	2.01	0.43
8:A:13:LEU:HD22	9:H:10:ILE:HD12	2.01	0.43
13:M:301:ILE:HA	13:M:309:TYR:HE1	1.84	0.43
18:Y:6:LEU:HD12	35:q:90:LEU:HD22	2.01	0.43
21:b:84:CYS:HB3	21:b:87:CYS:SG	2.58	0.43
36:r:17:LEU:HD11	38:t:162:LEU:HD22	2.01	0.43
6:6:43:SER:HB2	9:H:40:VAL:HG22	2.00	0.43
7:9:114:THR:HG21	7:9:144:HIS:CD2	2.53	0.43
9:H:169:GLN:NE2	9:H:241:LEU:O	2.52	0.43
12:L:129:LEU:HA	12:L:132:VAL:HG22	2.00	0.43
12:L:253:VAL:HB	12:L:310:LEU:HD11	2.00	0.43
23:d:26:ALA:HA	23:d:31:GLY:HA3	2.00	0.43
38:t:153:LEU:HD11	38:t:165:LEU:HD12	2.01	0.43
6:6:52:LEU:HB2	6:6:90:GLY:HA3	2.01	0.43
11:K:79:VAL:O	11:K:83:ASN:N	2.52	0.43
13:M:259:TYR:O	13:M:263:MET:HG2	2.19	0.43
14:N:289:ASN:HA	14:N:292:PHE:CE1	2.54	0.43
53:o:202:CDL:H851	53:o:202:CDL:H821	1.66	0.43
1:1:140:GLY:C	2:2:89:MET:HE1	2.44	0.42
3:3:495:ARG:HG3	3:3:496:ILE:HG12	2.01	0.42
7:9:145:GLU:HB2	28:i:126:PRO:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A:402:PC1:H292	10:J:152:TRP:HZ3	1.84	0.42
10:J:24:PRO:HB3	10:J:89:VAL:HG11	2.01	0.42
12:L:416:THR:O	12:L:419:THR:OG1	2.36	0.42
13:M:220:HIS:NE2	13:M:231:LEU:HB3	2.34	0.42
22:c:60:ASP:N	22:c:60:ASP:OD1	2.52	0.42
6:6:71:ARG:HA	9:H:37:PRO:HA	2.01	0.42
9:H:216:ALA:HB3	9:H:219:PRO:HD2	2.01	0.42
9:H:318:THR:HG21	10:J:135:PHE:HB3	2.01	0.42
12:L:60:GLU:HG2	12:L:83:ASP:HA	2.01	0.42
14:N:335:MET:O	33:o:33:TYR:OH	2.35	0.42
53:Y:201:CDL:H632	53:Y:201:CDL:H601	1.87	0.42
53:Y:201:CDL:H641	53:Y:201:CDL:H872	2.00	0.42
29:k:180:GLN:NE2	29:k:196:SER:OG	2.41	0.42
3:3:115:ASP:O	3:3:119:GLN:HG2	2.20	0.42
14:N:110:PRO:HD3	14:N:160:LEU:HD23	2.00	0.42
15:V:5:LEU:HD23	50:V:202:3PE:H231	2.01	0.42
33:o:43:LEU:HD22	33:o:53:VAL:HG12	2.02	0.42
37:s:106:ARG:NH1	39:u:61:ASP:OD1	2.52	0.42
1:1:214:GLY:HA3	1:1:220:THR:HB	2.01	0.42
54:X:101:ZMP:H6	38:t:69:GLU:HG2	2.01	0.42
23:d:22:THR:HB	23:d:91:VAL:HG22	2.01	0.42
53:o:201:CDL:H731	53:o:201:CDL:H761	1.90	0.42
1:1:261:HIS:ND1	1:1:338:ASP:OD1	2.52	0.42
1:1:432:ARG:HA	1:1:435:GLN:HG3	2.01	0.42
3:3:331:LEU:HD22	3:3:525:LEU:HG	2.02	0.42
5:5:32:ILE:HG23	25:f:43:TYR:HB2	2.02	0.42
9:H:49:ILE:HG23	50:i:501:3PE:H2G1	2.01	0.42
13:M:329:LEU:HB3	13:M:359:TRP:CZ2	2.54	0.42
17:j:5:PRO:HD3	17:j:14:ARG:HH22	1.84	0.42
32:n:21:TRP:HB3	32:n:49:ALA:HB3	2.01	0.42
37:s:35:GLU:HA	40:v:156:TYR:HA	2.02	0.42
4:4:296:ARG:HH21	4:4:420:THR:HG21	1.85	0.42
9:H:202:GLU:OE2	9:H:279:ARG:NH1	2.52	0.42
12:L:397:GLU:HB3	12:L:482:MET:HE1	2.02	0.42
16:W:122:TRP:CD1	33:o:2:MET:HG2	2.54	0.42
29:k:53:GLU:HG3	29:k:104:ARG:HH12	1.84	0.42
3:3:12:PHE:HB2	3:3:78:ASN:HA	2.01	0.42
4:4:116:GLN:NE2	4:4:276:ASP:OD2	2.51	0.42
4:4:151:ILE:O	4:4:155:THR:OG1	2.30	0.42
7:9:1:THR:N	27:h:104:GLU:O	2.40	0.42
8:A:98:LEU:HD22	9:H:298:LEU:HD21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:7:LEU:HD22	12:L:46:THR:HG23	2.01	0.42
12:L:411:MET:HG3	40:v:112:MET:HE1	2.01	0.42
13:M:204:MET:O	13:M:209:LEU:N	2.43	0.42
19:Z:81:VAL:HA	19:Z:84:MET:HG2	2.01	0.42
1:1:367:GLU:OE1	3:3:100:ASN:ND2	2.44	0.42
2:2:61:LEU:HD12	2:2:90:TYR:HB3	2.02	0.42
2:2:108:CYS:HA	2:2:151:ALA:HB1	2.02	0.42
13:M:180:GLN:HA	13:M:248:LEU:HD21	2.01	0.42
17:X:55:GLU:OE2	38:t:20:LYS:NZ	2.43	0.42
18:Y:44:LEU:HD22	18:Y:130:VAL:HB	2.01	0.42
29:k:170:ILE:HD11	29:k:238:ILE:HD11	2.02	0.42
2:2:172:ILE:HD11	2:2:187:ARG:HE	1.84	0.42
12:L:418:PHE:HD1	12:L:421:ILE:HD12	1.85	0.42
13:M:120:ILE:HG22	13:M:121:MET:HE2	2.01	0.42
10:J:24:PRO:HA	10:J:89:VAL:HG21	2.01	0.42
18:Y:100:ARG:NH1	18:Y:103:GLN:OE1	2.52	0.42
29:k:41:GLU:HA	29:k:44:GLU:HG2	2.02	0.42
40:v:145:ASP:OD1	40:v:145:ASP:N	2.53	0.42
2:2:116:ILE:HG23	2:2:169:ILE:HG21	2.02	0.41
5:5:119:SER:OG	5:5:131:GLU:OE2	2.28	0.41
9:H:152:SER:HA	9:H:155:LEU:HD12	2.01	0.41
13:M:1:FME:O1	13:M:3:LYS:NZ	2.52	0.41
37:s:97:ARG:HB3	40:v:128:VAL:HB	2.01	0.41
3:3:266:LYS:NZ	3:3:674:THR:OG1	2.48	0.41
3:3:399:TRP:HA	3:3:404:LEU:HB3	2.02	0.41
52:H:501:DCQ:H13A	52:H:501:DCQ:H10	1.83	0.41
10:J:23:LYS:HE2	11:K:23:ARG:HG3	2.01	0.41
13:M:110:PHE:O	13:M:241:TYR:OH	2.34	0.41
27:h:95:SER:OG	27:h:97:ALA:O	2.33	0.41
40:v:80:ASP:HB3	40:v:83:MET:HB3	2.00	0.41
4:4:6:PRO:HB3	4:4:10:TRP:CD1	2.55	0.41
7:9:77:CYS:O	7:9:105:ARG:NH1	2.53	0.41
53:L:1003:CDL:H351	53:L:1003:CDL:H161	2.02	0.41
15:V:45:PRO:HG2	50:V:201:3PE:H31	2.01	0.41
18:Y:17:VAL:O	44:z:50:ARG:NH2	2.54	0.41
30:l:91:TYR:OH	35:q:92:GLU:OE1	2.29	0.41
1:1:49:LEU:HD11	1:1:123:LEU:HD21	2.01	0.41
1:1:193:ILE:HG23	1:1:215:VAL:HA	2.02	0.41
3:3:36:GLN:HE22	22:c:48:GLY:HA2	1.85	0.41
4:4:135:GLN:HB3	4:4:276:ASP:HB3	2.02	0.41
5:5:130:TYR:O	5:5:133:GLU:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:9:69:ARG:NH2	21:b:38:ASN:O	2.52	0.41
11:K:20:LEU:HD13	12:L:588:PHE:HD1	1.86	0.41
12:L:236:ALA:HB1	12:L:248:HIS:CE1	2.55	0.41
18:Y:17:VAL:HG12	18:Y:19:VAL:HG22	2.03	0.41
35:q:129:GLY:HA2	35:q:132:ILE:HD12	2.01	0.41
40:v:88:ARG:HB3	40:v:89:VAL:H	1.74	0.41
42:x:7:PRO:HA	42:x:8:PRO:HD3	1.97	0.41
12:L:49:ILE:HG12	19:Z:32:LEU:HD13	2.01	0.41
14:N:159:ILE:HG21	14:N:278:LEU:HD11	2.01	0.41
1:1:97:ALA:HB3	1:1:138:ILE:HA	2.02	0.41
1:1:276:LEU:HD21	1:1:297:VAL:HG11	2.02	0.41
32:n:48:GLU:OE2	38:t:33:ARG:NH2	2.44	0.41
4:4:233:ARG:NH1	51:9:401:PC1:O12	2.54	0.41
12:L:402:SER:OG	12:L:404:THR:OG1	2.30	0.41
12:L:577:ILE:HD13	53:V:203:CDL:H121	2.03	0.41
31:m:68:HIS:N	31:m:71:ASP:OD2	2.54	0.41
6:6:63:ALA:HB2	6:6:69:MET:HE3	2.03	0.41
12:L:7:LEU:HD13	12:L:49:ILE:HD13	2.03	0.41
12:L:213:LEU:HD23	12:L:216:LEU:HD12	2.03	0.41
12:L:241:THR:HG21	12:L:344:GLY:HA3	2.02	0.41
12:L:316:THR:HG23	12:L:325:ALA:HB2	2.03	0.41
12:L:535:ARG:NH1	40:v:90:ASP:O	2.54	0.41
13:M:139:GLN:O	13:M:142:ARG:NH1	2.53	0.41
13:M:352:LEU:HB3	13:M:355:MET:HB3	2.03	0.41
27:h:8:GLN:NE2	27:h:20:GLN:HG3	2.35	0.41
1:1:189:GLU:OE2	47:1:503:NAI:O2B	2.29	0.41
3:3:243:ARG:HD2	3:3:244:THR:HG23	2.03	0.41
9:H:165:LEU:HD21	9:H:241:LEU:HA	2.02	0.41
9:H:311:LEU:O	35:q:54:ARG:NH2	2.53	0.41
51:M:502:PC1:H222	15:V:132:TRP:CD2	2.56	0.41
14:N:273:ASN:HA	15:V:139:LYS:HG2	2.03	0.41
27:h:11:ARG:HG2	27:h:19:LEU:HD12	2.03	0.41
27:h:32:LYS:O	27:h:35:GLN:NE2	2.45	0.41
37:s:33:ARG:NH1	37:s:103:ARG:HH22	2.18	0.41
13:M:116:ILE:HD12	13:M:116:ILE:HA	1.96	0.41
14:N:136:LEU:HD23	14:N:205:LEU:HD21	2.02	0.41
19:Z:115:ARG:HA	36:r:99:LYS:HA	2.02	0.41
30:l:74:ARG:NH2	35:q:93:GLU:OE2	2.54	0.41
51:w:801:PC1:H2B1	51:w:801:PC1:H282	1.97	0.41
1:1:265:PRO:O	2:2:190:ARG:NH1	2.49	0.40
4:4:119:SER:HA	4:4:196:PRO:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:9:145:GLU:HA	7:9:148:LEU:HD13	2.03	0.40
51:9:401:PC1:H252	9:H:296:LEU:HD13	2.01	0.40
10:J:139:GLU:HG3	11:K:49:LEU:HD21	2.02	0.40
53:o:202:CDL:H842	53:o:202:CDL:H671	2.02	0.40
40:v:47:TYR:OH	40:v:77:MET:O	2.23	0.40
1:1:101:GLU:OE2	1:1:302:SER:N	2.54	0.40
1:1:200:GLN:HG2	2:2:86:PHE:HB2	2.03	0.40
47:1:503:NAI:H6N	47:1:503:NAI:H2D	1.87	0.40
2:2:10:ARG:NH2	3:3:138:GLU:OE2	2.54	0.40
3:3:360:SER:O	3:3:365:ASN:ND2	2.37	0.40
5:5:30:ALA:HB2	5:5:40:VAL:HG21	2.03	0.40
50:L:1001:3PE:H221	40:v:88:ARG:HG2	2.02	0.40
15:V:85:ASP:HA	15:V:86:PRO:HD3	1.95	0.40
21:b:20:ASP:O	21:b:25:ARG:NH2	2.41	0.40
26:g:30:ARG:HB3	26:g:82:VAL:HG11	2.03	0.40
26:g:35:TYR:CG	17:j:45:LEU:HD22	2.56	0.40
40:v:47:TYR:HA	40:v:48:PRO:HD3	1.93	0.40
3:3:284:VAL:HG12	3:3:559:VAL:HG22	2.04	0.40
4:4:83:LEU:HD11	6:6:53:ALA:HB2	2.03	0.40
12:L:106:TRP:CD1	12:L:447:ASN:HD22	2.39	0.40
13:M:253:ILE:HG12	13:M:257:MET:HG2	2.03	0.40
26:g:62:VAL:HG22	54:g:201:ZMP:H1A	2.04	0.40
28:i:9:ARG:HA	28:i:12:GLN:HG2	2.02	0.40
13:M:297:VAL:HG13	13:M:312:ALA:HB1	2.03	0.40
16:W:6:LYS:HE2	17:X:5:PRO:HG3	2.03	0.40
22:c:59:PHE:HE2	22:c:82:LEU:HD23	1.87	0.40
23:d:201:VAL:HG22	23:d:237:LEU:HD23	2.03	0.40
3:3:259:ASN:O	3:3:262:TRP:N	2.53	0.40
3:3:316:ALA:HB3	3:3:519:PRO:HG3	2.04	0.40
7:9:164:GLU:OE2	28:i:87:HIS:ND1	2.43	0.40
9:H:189:THR:HG22	9:H:234:MET:HE3	2.03	0.40
11:K:38:LEU:O	11:K:42:ILE:HG12	2.21	0.40
13:M:71:TRP:CG	51:w:801:PC1:H3C2	2.56	0.40
13:M:167:ILE:HD13	13:M:249:LEU:HD13	2.02	0.40
13:M:281:ASP:HB3	13:M:284:SER:HB2	2.03	0.40
13:M:337:VAL:HG11	13:M:345:ALA:HB2	2.03	0.40
15:V:1:AYA:HM2	15:V:3:THR:HG22	2.04	0.40
19:Z:18:ALA:N	36:r:108:THR:O	2.46	0.40
33:o:13:PHE:O	33:o:78:ARG:NH1	2.54	0.40
37:s:3:HIS:CE1	40:v:127:PRO:HD3	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1	428/464 (92%)	405 (95%)	23 (5%)	0	100	100
2	2	211/246 (86%)	196 (93%)	15 (7%)	0	100	100
3	3	686/727 (94%)	660 (96%)	26 (4%)	0	100	100
4	4	414/463 (89%)	397 (96%)	17 (4%)	0	100	100
5	5	206/266 (77%)	199 (97%)	7 (3%)	0	100	100
6	6	154/223 (69%)	150 (97%)	4 (3%)	0	100	100
7	9	174/217 (80%)	167 (96%)	7 (4%)	0	100	100
8	A	106/115 (92%)	94 (89%)	12 (11%)	0	100	100
9	H	310/318 (98%)	304 (98%)	6 (2%)	0	100	100
10	J	165/175 (94%)	159 (96%)	6 (4%)	0	100	100
11	K	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
12	L	604/606 (100%)	578 (96%)	26 (4%)	0	100	100
13	M	457/459 (100%)	452 (99%)	5 (1%)	0	100	100
14	N	345/347 (99%)	336 (97%)	9 (3%)	0	100	100
15	V	138/141 (98%)	135 (98%)	3 (2%)	0	100	100
16	W	137/189 (72%)	136 (99%)	1 (1%)	0	100	100
17	X	85/157 (54%)	82 (96%)	3 (4%)	0	100	100
17	j	80/157 (51%)	78 (98%)	2 (2%)	0	100	100
18	Y	169/172 (98%)	164 (97%)	5 (3%)	0	100	100
19	Z	169/175 (97%)	166 (98%)	3 (2%)	0	100	100
20	a	42/109 (38%)	41 (98%)	1 (2%)	0	100	100
21	b	93/124 (75%)	92 (99%)	1 (1%)	0	100	100
22	c	124/170 (73%)	121 (98%)	3 (2%)	0	100	100
23	d	289/380 (76%)	285 (99%)	4 (1%)	0	100	100
24	e	84/99 (85%)	81 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	f	111/116 (96%)	110 (99%)	1 (1%)	0	100	100
26	g	112/140 (80%)	108 (96%)	4 (4%)	0	100	100
27	h	92/114 (81%)	87 (95%)	5 (5%)	0	100	100
28	i	143/145 (99%)	142 (99%)	1 (1%)	0	100	100
29	k	317/355 (89%)	302 (95%)	15 (5%)	0	100	100
30	l	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
31	m	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
32	n	77/98 (79%)	75 (97%)	2 (3%)	0	100	100
33	o	118/122 (97%)	116 (98%)	2 (2%)	0	100	100
34	p	126/130 (97%)	122 (97%)	4 (3%)	0	100	100
35	q	137/144 (95%)	134 (98%)	3 (2%)	0	100	100
36	r	95/128 (74%)	89 (94%)	6 (6%)	0	100	100
37	s	120/137 (88%)	113 (94%)	7 (6%)	0	100	100
38	t	175/179 (98%)	172 (98%)	3 (2%)	0	100	100
39	u	63/108 (58%)	60 (95%)	3 (5%)	0	100	100
40	v	153/186 (82%)	145 (95%)	8 (5%)	0	100	100
41	w	99/154 (64%)	94 (95%)	5 (5%)	0	100	100
42	x	47/76 (62%)	46 (98%)	1 (2%)	0	100	100
43	y	48/58 (83%)	47 (98%)	1 (2%)	0	100	100
44	z	68/70 (97%)	68 (100%)	0	0	100	100
All	All	8048/9247 (87%)	7775 (97%)	273 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	1	344/368 (94%)	344 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	2	183/210 (87%)	183 (100%)	0	100	100
3	3	578/608 (95%)	578 (100%)	0	100	100
4	4	363/391 (93%)	363 (100%)	0	100	100
5	5	189/230 (82%)	189 (100%)	0	100	100
6	6	132/181 (73%)	131 (99%)	1 (1%)	73	88
7	9	151/179 (84%)	150 (99%)	1 (1%)	76	90
8	A	99/103 (96%)	98 (99%)	1 (1%)	68	86
9	H	274/278 (99%)	274 (100%)	0	100	100
10	J	138/144 (96%)	138 (100%)	0	100	100
11	K	86/86 (100%)	86 (100%)	0	100	100
12	L	538/538 (100%)	538 (100%)	0	100	100
13	M	411/411 (100%)	410 (100%)	1 (0%)	87	95
14	N	315/315 (100%)	315 (100%)	0	100	100
15	V	101/102 (99%)	101 (100%)	0	100	100
16	W	122/160 (76%)	122 (100%)	0	100	100
17	X	80/141 (57%)	80 (100%)	0	100	100
17	j	76/141 (54%)	76 (100%)	0	100	100
18	Y	154/155 (99%)	154 (100%)	0	100	100
19	Z	155/157 (99%)	155 (100%)	0	100	100
20	a	43/93 (46%)	43 (100%)	0	100	100
21	b	79/97 (81%)	79 (100%)	0	100	100
22	c	113/150 (75%)	113 (100%)	0	100	100
23	d	255/326 (78%)	255 (100%)	0	100	100
24	e	76/82 (93%)	76 (100%)	0	100	100
25	f	101/102 (99%)	101 (100%)	0	100	100
26	g	107/124 (86%)	107 (100%)	0	100	100
27	h	84/96 (88%)	84 (100%)	0	100	100
28	i	131/131 (100%)	131 (100%)	0	100	100
29	k	283/309 (92%)	283 (100%)	0	100	100
30	l	94/95 (99%)	94 (100%)	0	100	100
31	m	69/72 (96%)	69 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	n	61/76 (80%)	61 (100%)	0	100	100
33	o	107/109 (98%)	107 (100%)	0	100	100
34	p	114/116 (98%)	114 (100%)	0	100	100
35	q	119/122 (98%)	119 (100%)	0	100	100
36	r	95/122 (78%)	95 (100%)	0	100	100
37	s	110/120 (92%)	110 (100%)	0	100	100
38	t	159/161 (99%)	159 (100%)	0	100	100
39	u	59/84 (70%)	59 (100%)	0	100	100
40	v	140/160 (88%)	140 (100%)	0	100	100
41	w	92/130 (71%)	92 (100%)	0	100	100
42	x	44/67 (66%)	44 (100%)	0	100	100
43	y	46/54 (85%)	46 (100%)	0	100	100
44	z	59/59 (100%)	59 (100%)	0	100	100
All	All	7129/7955 (90%)	7125 (100%)	4 (0%)	87	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	6	54	CYS
7	9	78	ILE
8	A	29	VAL
13	M	144	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	148	ASN
1	1	150	GLN
1	1	293	ASN
1	1	402	HIS
2	2	99	HIS
2	2	101	GLN
2	2	121	GLN
2	2	155	GLN
2	2	157	ASN
3	3	237	ASN

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Mol	Chain	Res	Type
3	3	535	GLN
4	4	149	ASN
4	4	150	HIS
4	4	252	ASN
4	4	409	HIS
5	5	19	HIS
5	5	102	ASN
5	5	144	ASN
5	5	160	HIS
9	H	317	GLN
10	J	78	GLN
10	J	86	ASN
12	L	269	ASN
12	L	323	HIS
12	L	354	GLN
12	L	405	ASN
12	L	434	GLN
12	L	442	ASN
12	L	446	ASN
12	L	471	ASN
13	M	81	GLN
13	M	138	ASN
13	M	144	ASN
13	M	169	ASN
13	M	192	ASN
13	M	333	ASN
13	M	338	HIS
13	M	374	ASN
13	M	390	ASN
14	N	48	HIS
14	N	134	GLN
14	N	235	ASN
15	V	7	GLN
15	V	18	HIS
18	Y	29	HIS
18	Y	63	ASN
18	Y	142	HIS
19	Z	106	GLN
19	Z	123	ASN
19	Z	143	HIS
20	a	40	ASN
21	b	32	GLN

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Mol	Chain	Res	Type
21	b	36	ASN
23	d	36	ASN
23	d	148	ASN
23	d	184	ASN
23	d	321	HIS
25	f	49	GLN
25	f	52	ASN
26	g	25	ASN
26	g	125	HIS
27	h	28	GLN
28	i	31	ASN
28	i	69	ASN
29	k	97	GLN
29	k	107	GLN
29	k	141	GLN
29	k	180	GLN
29	k	204	ASN
29	k	251	GLN
30	l	100	GLN
33	o	12	GLN
33	o	61	GLN
34	p	125	ASN
35	q	111	HIS
37	s	3	HIS
37	s	46	ASN
37	s	81	HIS
38	t	50	HIS
39	u	50	HIS
40	v	87	ASN
41	w	57	ASN
42	x	9	HIS
42	x	34	GLN
42	x	46	ASN
43	y	10	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

7 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
27	AYA	h	1	27	6,7,8	1.25	1 (16%)	6,8,10	1.02	1 (16%)
29	SEP	k	36	29	8,9,10	1.62	1 (12%)	7,12,14	1.06	1 (14%)
12	FME	L	1	12	8,9,10	0.96	0	8,9,11	1.05	1 (12%)
15	AYA	V	1	15	6,7,8	1.22	1 (16%)	6,8,10	1.71	2 (33%)
13	FME	M	1	13	8,9,10	1.00	0	8,9,11	0.99	0
11	FME	K	1	11	8,9,10	0.99	0	8,9,11	0.88	0
4	2MR	4	85	4	10,12,13	2.40	3 (30%)	5,13,15	1.74	2 (40%)

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
27	AYA	h	1	27	-	0/5/6/8	-
29	SEP	k	36	29	-	5/6/8/10	-
12	FME	L	1	12	-	2/7/9/11	-
15	AYA	V	1	15	-	2/5/6/8	-
13	FME	M	1	13	-	2/7/9/11	-
11	FME	K	1	11	-	3/7/9/11	-
4	2MR	4	85	4	-	1/10/13/15	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	4	85	2MR	CZ-NH2	4.79	1.43	1.33
4	4	85	2MR	CZ-NE	4.53	1.43	1.34
29	k	36	SEP	P-O1P	3.53	1.61	1.50
4	4	85	2MR	CQ1-NH1	-2.55	1.41	1.46
27	h	1	AYA	CA-N	-2.45	1.43	1.46
15	V	1	AYA	CA-N	-2.15	1.44	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	V	1	AYA	CA-N-CT	2.90	125.24	121.50
4	4	85	2MR	NE-CZ-NH2	-2.74	116.97	119.48
15	V	1	AYA	CB-CA-N	2.40	112.39	109.68
12	L	1	FME	C-CA-N	2.23	113.81	109.50
27	h	1	AYA	CB-CA-N	2.20	112.17	109.68
4	4	85	2MR	CD-NE-CZ	-2.10	119.42	123.36
29	k	36	SEP	OG-CB-CA	2.08	110.17	108.14

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	K	1	FME	O1-CN-N-CA
29	k	36	SEP	N-CA-CB-OG
29	k	36	SEP	CB-OG-P-O2P
29	k	36	SEP	CB-OG-P-O3P
4	4	85	2MR	O-C-CA-CB
12	L	1	FME	CA-CB-CG-SD
15	V	1	AYA	OT-CT-N-CA
15	V	1	AYA	CM-CT-N-CA
11	K	1	FME	CA-CB-CG-SD
13	M	1	FME	C-CA-CB-CG
12	L	1	FME	N-CA-CB-CG
29	k	36	SEP	CB-OG-P-O1P
11	K	1	FME	CB-CA-N-CN
13	M	1	FME	CB-CA-N-CN
29	k	36	SEP	CA-CB-OG-P

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	L	1	FME	1	0
15	V	1	AYA	3	0
13	M	1	FME	1	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 46 ligands modelled in this entry, 2 are monoatomic - leaving 44 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
50	3PE	A	403	-	50,50,50	0.31	0	53,55,55	0.36	0
50	3PE	p	201	-	26,26,50	0.49	0	29,31,55	0.52	1 (3%)
50	3PE	i	502	-	50,50,50	0.30	0	53,55,55	0.31	0
45	SF4	9	403	7	0,12,12	-	-	-		
50	3PE	H	502	-	50,50,50	0.31	0	53,55,55	0.48	1 (1%)
45	SF4	3	801	3	0,12,12	-	-	-		
47	NAI	1	503	-	47,48,48	0.38	0	64,73,73	1.82	4 (6%)
50	3PE	4	501	-	39,39,50	0.33	0	42,44,55	0.36	0
53	CDL	Y	201	-	99,99,99	0.26	0	105,111,111	0.33	0
51	PC1	M	502	-	53,53,53	0.30	0	59,61,61	0.36	0
45	SF4	1	501	1	0,12,12	-	-	-		
53	CDL	o	201	-	74,74,99	0.30	0	80,86,111	0.47	1 (1%)
45	SF4	3	802	3	0,12,12	-	-	-		
50	3PE	L	1004	-	30,30,50	0.41	0	33,35,55	0.79	1 (3%)
51	PC1	w	801	-	53,53,53	0.30	0	59,61,61	0.39	0
53	CDL	z	101	-	57,57,99	0.34	0	63,69,111	0.34	0
57	AMP	k	501	-	25,25,25	1.41	4 (16%)	37,38,38	1.97	7 (18%)
50	3PE	K	101	-	39,39,50	0.34	0	42,44,55	0.40	0
48	FES	3	803	3	0,4,4	-	-	-		
53	CDL	W	201	-	99,99,99	0.27	0	105,111,111	0.31	0
54	ZMP	X	101	17	25,30,36	0.73	1 (4%)	29,37,45	1.06	2 (6%)
53	CDL	o	202	-	89,89,99	0.31	0	95,101,111	0.41	0
51	PC1	L	1002	-	53,53,53	0.30	0	59,61,61	0.62	2 (3%)
58	MYR	s	201	37	13,14,15	0.16	0	12,13,15	0.13	0
50	3PE	N	402	-	30,30,50	0.38	0	33,35,55	0.35	0
50	3PE	V	201	-	34,34,50	0.36	0	37,39,55	0.35	0
48	FES	2	300	2	0,4,4	-	-	-		
51	PC1	9	401	-	53,53,53	0.32	0	59,61,61	0.52	1 (1%)
45	SF4	9	402	7	0,12,12	-	-	-		
53	CDL	V	204	-	84,84,99	0.28	0	90,96,111	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
53	CDL	L	1003	-	99,99,99	0.25	0	105,111,111	0.32	0
50	3PE	L	1001	-	50,50,50	0.30	0	53,55,55	0.36	0
53	CDL	V	203	-	93,93,99	0.25	0	99,105,111	0.25	0
50	3PE	i	501	-	50,50,50	0.30	0	53,55,55	0.34	0
52	DCQ	H	501	-	23,23,23	0.18	0	27,29,29	0.51	0
45	SF4	6	300	6	0,12,12	-	-	-		
51	PC1	A	402	-	36,36,53	0.36	0	42,44,61	0.61	1 (2%)
54	ZMP	g	201	-	28,33,36	0.79	1 (3%)	32,40,45	1.34	4 (12%)
50	3PE	V	202	-	36,36,50	0.34	0	39,41,55	0.33	0
51	PC1	A	401	-	45,45,53	0.32	0	51,53,61	0.31	0
46	FMN	1	502	-	33,33,33	1.09	3 (9%)	48,50,50	1.39	7 (14%)
50	3PE	M	501	-	43,43,50	0.32	0	46,48,55	0.43	0
56	NDP	d	401	-	51,52,52	0.44	0	71,80,80	0.40	0
50	3PE	N	401	-	50,50,50	0.31	0	53,55,55	0.57	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
50	3PE	A	403	-	-	17/54/54/54	-
50	3PE	p	201	-	-	5/27/27/54	-
50	3PE	i	502	-	-	9/54/54/54	-
45	SF4	9	403	7	-	-	0/6/5/5
50	3PE	H	502	-	-	19/54/54/54	-
47	NAI	1	503	-	-	5/29/72/72	0/5/5/5
45	SF4	3	801	3	-	-	0/6/5/5
50	3PE	4	501	-	-	7/43/43/54	-
53	CDL	Y	201	-	1/1/9/9	26/110/110/110	-
51	PC1	M	502	-	-	22/57/57/57	-
45	SF4	1	501	1	-	-	0/6/5/5
53	CDL	o	201	-	2/2/9/9	22/85/85/110	-
45	SF4	3	802	3	-	-	0/6/5/5
50	3PE	L	1004	-	-	7/34/34/54	-
51	PC1	w	801	-	-	9/57/57/57	-
53	CDL	z	101	-	-	22/68/68/110	-
57	AMP	k	501	-	-	6/10/26/26	0/3/3/3
50	3PE	K	101	-	-	7/43/43/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	CDL	W	201	-	-	28/110/110/110	-
48	FES	3	803	3	-	-	0/1/1/1
54	ZMP	X	101	17	-	13/35/37/43	-
53	CDL	o	202	-	-	40/100/100/110	-
51	PC1	L	1002	-	-	20/57/57/57	-
58	MYR	s	201	37	-	2/12/12/13	-
50	3PE	N	402	-	-	1/34/34/54	-
50	3PE	V	201	-	-	2/38/38/54	-
51	PC1	9	401	-	-	16/57/57/57	-
48	FES	2	300	2	-	-	0/1/1/1
45	SF4	9	402	7	-	-	0/6/5/5
53	CDL	V	204	-	1/1/9/9	27/95/95/110	-
53	CDL	L	1003	-	1/1/9/9	32/110/110/110	-
50	3PE	L	1001	-	-	10/54/54/54	-
53	CDL	V	203	-	-	32/104/104/110	-
50	3PE	i	501	-	-	10/54/54/54	-
52	DCQ	H	501	-	-	3/14/38/38	0/1/1/1
51	PC1	A	402	-	-	5/40/40/57	-
45	SF4	6	300	6	-	-	0/6/5/5
54	ZMP	g	201	-	-	3/38/40/43	-
50	3PE	V	202	-	-	14/40/40/54	-
51	PC1	A	401	-	-	17/49/49/57	-
46	FMN	1	502	-	-	9/18/18/18	0/3/3/3
50	3PE	M	501	-	-	13/47/47/54	-
56	NDP	d	401	-	-	5/34/77/77	0/5/5/5
50	3PE	N	401	-	-	13/54/54/54	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	k	501	AMP	C5-C4	4.75	1.47	1.39
54	g	201	ZMP	C10-S1	-3.20	1.68	1.76
46	1	502	FMN	C4A-N5	2.83	1.36	1.30
57	k	501	AMP	C5-C6	2.62	1.48	1.41
57	k	501	AMP	C5-N7	-2.48	1.34	1.39
54	X	101	ZMP	C9-C10	2.31	1.53	1.50
57	k	501	AMP	C8-N7	2.15	1.35	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	1	502	FMN	C4A-C10	-2.07	1.38	1.44
46	1	502	FMN	C10-N1	2.07	1.37	1.33

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	1	503	NAI	O5B-PA-O1A	-9.52	71.19	108.94
47	1	503	NAI	O2A-PA-O1A	-8.67	72.13	112.44
57	k	501	AMP	C5-C4-N3	-6.47	117.81	126.72
47	1	503	NAI	O3-PA-O1A	-5.71	93.52	110.70
57	k	501	AMP	N3-C4-N9	5.39	136.33	127.17
57	k	501	AMP	C2-N3-C4	3.98	121.54	111.83
46	1	502	FMN	C4-N3-C2	-3.75	118.97	125.64
57	k	501	AMP	N3-C2-N1	-3.30	123.58	128.58
54	g	201	ZMP	C15-C14-C13	-3.19	107.08	112.39
46	1	502	FMN	C4A-C10-N10	3.17	121.03	116.48
54	g	201	ZMP	C14-C15-N2	-3.17	105.25	112.00
57	k	501	AMP	C4-C5-N7	-2.98	107.17	110.58
46	1	502	FMN	O4-C4-C4A	-2.90	118.89	126.53
54	X	101	ZMP	O1-C10-C9	-2.82	120.72	123.98
46	1	502	FMN	C4A-C4-N3	2.81	120.40	113.25
54	g	201	ZMP	O1-C10-C9	-2.71	120.86	123.98
50	H	502	3PE	O31-C3-C2	2.56	115.78	108.40
47	1	503	NAI	O2A-PA-O5B	2.56	119.17	107.57
46	1	502	FMN	C4A-C10-N1	-2.51	118.43	124.59
50	L	1004	3PE	C2-O21-C21	2.48	123.73	117.80
51	L	1002	PC1	C2-O21-C21	2.43	123.61	117.80
57	k	501	AMP	C4-N9-C8	2.36	108.22	105.74
57	k	501	AMP	C5-N7-C8	2.32	107.10	103.45
51	A	402	PC1	C2-O21-C21	2.31	123.32	117.80
50	N	401	3PE	O21-C2-C1	2.30	116.59	108.34
46	1	502	FMN	C10-C4A-N5	-2.26	120.20	124.81
50	p	201	3PE	O12-P-O14	2.12	119.11	110.83
50	N	401	3PE	C2-O21-C21	2.12	122.87	117.80
46	1	502	FMN	C4-C4A-C10	2.12	120.57	116.93
53	o	201	CDL	CB4-OB6-CB5	2.09	122.79	117.80
51	9	401	PC1	C2-O21-C21	2.08	122.78	117.80
54	g	201	ZMP	C20-C18-C17	2.08	112.31	108.77
51	L	1002	PC1	O21-C2-C1	2.03	115.61	108.34
54	X	101	ZMP	C14-C15-N2	-2.00	107.73	112.00

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
53	L	1003	CDL	CB4
53	V	204	CDL	CB4
53	Y	201	CDL	CB4
53	o	201	CDL	CA4
53	o	201	CDL	CB4

All (498) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	1	502	FMN	N10-C1'-C2'-O2'
46	1	502	FMN	N10-C1'-C2'-C3'
46	1	502	FMN	C5'-O5'-P-O2P
46	1	502	FMN	C5'-O5'-P-O3P
47	1	503	NAI	C5B-O5B-PA-O1A
50	4	501	3PE	C1-O11-P-O12
50	4	501	3PE	C1-O11-P-O13
50	4	501	3PE	C1-O11-P-O14
50	A	403	3PE	C1-O11-P-O12
50	A	403	3PE	C1-O11-P-O13
50	A	403	3PE	C11-O13-P-O12
50	H	502	3PE	C1-O11-P-O12
50	H	502	3PE	C11-O13-P-O11
50	H	502	3PE	C11-O13-P-O12
50	H	502	3PE	C11-O13-P-O14
50	H	502	3PE	O13-C11-C12-N
50	K	101	3PE	C1-O11-P-O13
50	K	101	3PE	O13-C11-C12-N
50	L	1001	3PE	C11-O13-P-O14
50	L	1001	3PE	O13-C11-C12-N
50	L	1004	3PE	C1-O11-P-O13
50	L	1004	3PE	C2-C1-O11-P
50	M	501	3PE	C1-O11-P-O12
50	M	501	3PE	C1-O11-P-O13
50	M	501	3PE	C1-O11-P-O14
50	M	501	3PE	C11-O13-P-O11
50	M	501	3PE	C11-O13-P-O12
50	N	401	3PE	O13-C11-C12-N
50	N	402	3PE	C11-O13-P-O14
50	V	202	3PE	C11-O13-P-O11
50	V	202	3PE	C11-O13-P-O12
50	V	202	3PE	C11-O13-P-O14
50	V	202	3PE	O13-C11-C12-N
50	i	501	3PE	C11-O13-P-O11

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Mol	Chain	Res	Type	Atoms
50	i	501	3PE	C11-O13-P-O12
50	i	502	3PE	C1-O11-P-O12
51	9	401	PC1	C11-O13-P-O14
51	9	401	PC1	C11-O13-P-O11
51	9	401	PC1	O13-C11-C12-N
51	A	401	PC1	C11-O13-P-O12
51	A	401	PC1	C11-O13-P-O11
51	L	1002	PC1	C1-O11-P-O12
51	M	502	PC1	C11-O13-P-O14
51	M	502	PC1	C11-O13-P-O11
51	M	502	PC1	C1-O11-P-O12
51	w	801	PC1	C11-O13-P-O14
53	L	1003	CDL	CA3-OA5-PA1-OA2
53	L	1003	CDL	CA3-OA5-PA1-OA3
53	L	1003	CDL	CA3-OA5-PA1-OA4
53	V	203	CDL	CA2-OA2-PA1-OA3
53	V	203	CDL	CA2-OA2-PA1-OA4
53	V	203	CDL	CA3-OA5-PA1-OA3
53	V	203	CDL	CB2-OB2-PB2-OB4
53	V	204	CDL	O1-C1-CB2-OB2
53	V	204	CDL	CA2-OA2-PA1-OA3
53	V	204	CDL	CA2-OA2-PA1-OA4
53	V	204	CDL	CA2-OA2-PA1-OA5
53	V	204	CDL	CB2-OB2-PB2-OB3
53	V	204	CDL	CB3-OB5-PB2-OB2
53	V	204	CDL	CB3-OB5-PB2-OB3
53	W	201	CDL	CA2-OA2-PA1-OA4
53	W	201	CDL	CA2-OA2-PA1-OA5
53	W	201	CDL	CA3-OA5-PA1-OA2
53	Y	201	CDL	CB3-OB5-PB2-OB3
53	o	201	CDL	O1-C1-CB2-OB2
53	o	201	CDL	CA2-OA2-PA1-OA3
53	o	201	CDL	CB2-OB2-PB2-OB3
53	o	201	CDL	CB2-OB2-PB2-OB5
53	o	201	CDL	CB3-OB5-PB2-OB2
53	o	201	CDL	CB3-OB5-PB2-OB3
53	o	202	CDL	O1-C1-CB2-OB2
53	o	202	CDL	CA3-OA5-PA1-OA2
53	o	202	CDL	CB2-OB2-PB2-OB3
53	o	202	CDL	CB2-OB2-PB2-OB5
53	o	202	CDL	CB3-OB5-PB2-OB3
53	z	101	CDL	CA2-C1-CB2-OB2

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Mol	Chain	Res	Type	Atoms
53	z	101	CDL	CA2-OA2-PA1-OA3
53	z	101	CDL	CA2-OA2-PA1-OA5
53	z	101	CDL	CB3-OB5-PB2-OB2
53	z	101	CDL	CB3-OB5-PB2-OB3
53	z	101	CDL	CB3-OB5-PB2-OB4
54	X	101	ZMP	O4-C17-C18-C21
54	X	101	ZMP	C16-C17-C18-C21
54	X	101	ZMP	O4-C17-C18-C19
54	X	101	ZMP	C16-C17-C18-C20
54	X	101	ZMP	C17-C16-N2-C15
54	g	201	ZMP	S1-C11-C12-N1
54	g	201	ZMP	C12-C11-S1-C10
56	d	401	NDP	C5B-O5B-PA-O1A
57	k	501	AMP	C5'-O5'-P-O1P
57	k	501	AMP	C5'-O5'-P-O2P
57	k	501	AMP	C5'-O5'-P-O3P
58	s	201	MYR	C1-C2-C3-C4
53	V	203	CDL	O1-C1-CB2-OB2
53	Y	201	CDL	O1-C1-CB2-OB2
53	z	101	CDL	O1-C1-CB2-OB2
54	X	101	ZMP	O3-C16-N2-C15
57	k	501	AMP	C3'-C4'-C5'-O5'
53	o	202	CDL	C1-CA2-OA2-PA1
53	V	203	CDL	CA2-C1-CB2-OB2
57	k	501	AMP	O4'-C4'-C5'-O5'
53	L	1003	CDL	CB7-C71-C72-C73
51	A	401	PC1	C11-C12-N-C14
51	M	502	PC1	C11-C12-N-C14
51	M	502	PC1	C11-C12-N-C15
51	L	1002	PC1	C21-C22-C23-C24
51	A	401	PC1	C31-C32-C33-C34
53	z	101	CDL	O1-C1-CA2-OA2
53	W	201	CDL	CA5-C11-C12-C13
50	H	502	3PE	C33-C34-C35-C36
53	V	204	CDL	CA2-C1-CB2-OB2
53	o	201	CDL	CA2-C1-CB2-OB2
51	A	401	PC1	C11-C12-N-C15
53	W	201	CDL	O1-C1-CA2-OA2
50	V	202	3PE	C2-C1-O11-P
53	o	202	CDL	C82-C83-C84-C85
53	V	203	CDL	CA7-C31-C32-C33
53	L	1003	CDL	C21-C22-C23-C24

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Mol	Chain	Res	Type	Atoms
53	W	201	CDL	C35-C36-C37-C38
50	K	101	3PE	C34-C35-C36-C37
50	N	401	3PE	C32-C33-C34-C35
53	Y	201	CDL	C81-C82-C83-C84
50	V	201	3PE	C31-C32-C33-C34
53	V	203	CDL	C52-C53-C54-C55
54	X	101	ZMP	C6-C7-C8-C9
51	9	401	PC1	C3C-C3D-C3E-C3F
51	A	401	PC1	C3B-C3C-C3D-C3E
51	L	1002	PC1	C38-C39-C3A-C3B
53	Y	201	CDL	C15-C16-C17-C18
53	Y	201	CDL	C63-C64-C65-C66
53	L	1003	CDL	C22-C23-C24-C25
53	L	1003	CDL	C41-C42-C43-C44
53	L	1003	CDL	C77-C78-C79-C80
53	V	203	CDL	C79-C80-C81-C82
53	V	203	CDL	C40-C41-C42-C43
51	w	801	PC1	C39-C3A-C3B-C3C
51	L	1002	PC1	C33-C34-C35-C36
53	L	1003	CDL	C56-C57-C58-C59
51	w	801	PC1	C2D-C2E-C2F-C2G
53	W	201	CDL	CB5-C51-C52-C53
50	A	403	3PE	C2D-C2E-C2F-C2G
51	L	1002	PC1	C37-C38-C39-C3A
53	V	204	CDL	C71-C72-C73-C74
53	L	1003	CDL	C82-C83-C84-C85
53	W	201	CDL	CA7-C31-C32-C33
57	k	501	AMP	C4'-C5'-O5'-P
51	M	502	PC1	C25-C26-C27-C28
53	Y	201	CDL	C11-C12-C13-C14
50	A	403	3PE	C22-C23-C24-C25
51	M	502	PC1	C3A-C3B-C3C-C3D
50	i	501	3PE	C36-C37-C38-C39
53	L	1003	CDL	C17-C18-C19-C20
51	9	401	PC1	C3B-C3C-C3D-C3E
50	N	401	3PE	C21-C22-C23-C24
53	V	203	CDL	C31-C32-C33-C34
53	o	201	CDL	C32-C33-C34-C35
53	V	204	CDL	C12-C13-C14-C15
50	L	1001	3PE	C37-C38-C39-C3A
53	V	204	CDL	C34-C35-C36-C37
51	9	401	PC1	C22-C21-O21-C2

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Mol	Chain	Res	Type	Atoms
51	M	502	PC1	C31-C32-C33-C34
50	M	501	3PE	C23-C24-C25-C26
53	L	1003	CDL	C32-C33-C34-C35
51	A	401	PC1	C11-C12-N-C13
51	M	502	PC1	C11-C12-N-C13
50	A	403	3PE	C3A-C3B-C3C-C3D
53	Y	201	CDL	C57-C58-C59-C60
51	L	1002	PC1	C2-C1-O11-P
51	M	502	PC1	C3B-C3C-C3D-C3E
52	H	501	DCQ	C11-C12-C13-C14
53	W	201	CDL	CB2-C1-CA2-OA2
53	o	202	CDL	CA2-C1-CB2-OB2
53	z	101	CDL	CB2-C1-CA2-OA2
53	o	202	CDL	C64-C65-C66-C67
50	M	501	3PE	C33-C34-C35-C36
50	i	501	3PE	C23-C24-C25-C26
53	o	202	CDL	C51-C52-C53-C54
50	H	502	3PE	O11-C1-C2-C3
51	L	1002	PC1	O11-C1-C2-C3
51	M	502	PC1	O11-C1-C2-C3
53	L	1003	CDL	OB5-CB3-CB4-CB6
56	d	401	NDP	O4B-C4B-C5B-O5B
53	V	204	CDL	C51-C52-C53-C54
53	V	204	CDL	C52-C53-C54-C55
53	Y	201	CDL	CB5-C51-C52-C53
53	o	201	CDL	CB7-C71-C72-C73
50	K	101	3PE	C24-C25-C26-C27
51	L	1002	PC1	C28-C29-C2A-C2B
50	4	501	3PE	C1-C2-C3-O31
53	Y	201	CDL	CA3-CA4-CA6-OA8
53	z	101	CDL	CA3-CA4-CA6-OA8
53	o	202	CDL	C81-C82-C83-C84
47	1	503	NAI	C2D-C1D-N1N-C2N
47	1	503	NAI	C2D-C1D-N1N-C6N
53	L	1003	CDL	CB5-C51-C52-C53
46	1	502	FMN	C5'-O5'-P-O1P
53	o	202	CDL	C78-C79-C80-C81
53	V	203	CDL	OB6-CB4-CB6-OB8
53	V	204	CDL	OA6-CA4-CA6-OA8
53	W	201	CDL	OA6-CA4-CA6-OA8
53	L	1003	CDL	O1-C1-CB2-OB2
50	p	201	3PE	C22-C23-C24-C25

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Mol	Chain	Res	Type	Atoms
51	L	1002	PC1	C3F-C3G-C3H-C3I
53	W	201	CDL	C31-C32-C33-C34
54	X	101	ZMP	O4-C17-C18-C20
50	A	403	3PE	C21-C22-C23-C24
53	o	201	CDL	C31-C32-C33-C34
50	H	502	3PE	C2-C1-O11-P
50	M	501	3PE	C2-C1-O11-P
53	V	204	CDL	C1-CA2-OA2-PA1
53	V	204	CDL	C1-CB2-OB2-PB2
53	o	202	CDL	CB7-C71-C72-C73
51	A	401	PC1	C23-C24-C25-C26
53	V	203	CDL	OA5-CA3-CA4-CA6
53	V	204	CDL	C11-C12-C13-C14
50	V	201	3PE	C32-C33-C34-C35
50	V	202	3PE	C33-C34-C35-C36
51	w	801	PC1	C3A-C3B-C3C-C3D
51	9	401	PC1	O22-C21-O21-C2
50	N	401	3PE	C1-C2-C3-O31
53	V	203	CDL	CB3-CB4-CB6-OB8
53	z	101	CDL	CB3-CB4-CB6-OB8
53	Y	201	CDL	C37-C38-C39-C40
53	Y	201	CDL	C52-C53-C54-C55
50	N	401	3PE	O11-C1-C2-O21
51	M	502	PC1	O11-C1-C2-O21
50	N	401	3PE	C24-C25-C26-C27
53	o	202	CDL	CA4-CA3-OA5-PA1
51	M	502	PC1	C27-C28-C29-C2A
51	9	401	PC1	C22-C23-C24-C25
54	g	201	ZMP	C3-C4-C5-C6
53	V	204	CDL	OB6-CB4-CB6-OB8
53	W	201	CDL	C72-C73-C74-C75
50	L	1001	3PE	C24-C25-C26-C27
51	A	401	PC1	C21-C22-C23-C24
53	V	204	CDL	C78-C79-C80-C81
51	L	1002	PC1	C39-C3A-C3B-C3C
51	w	801	PC1	C31-C32-C33-C34
46	1	502	FMN	C2'-C3'-C4'-O4'
50	i	501	3PE	C32-C33-C34-C35
53	Y	201	CDL	C82-C83-C84-C85
53	Y	201	CDL	CA2-C1-CB2-OB2
50	i	501	3PE	C3C-C3D-C3E-C3F
53	o	202	CDL	C72-C73-C74-C75

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Mol	Chain	Res	Type	Atoms
50	H	502	3PE	C36-C37-C38-C39
53	o	202	CDL	C73-C74-C75-C76
50	H	502	3PE	O11-C1-C2-O21
50	L	1004	3PE	O11-C1-C2-O21
50	i	501	3PE	O11-C1-C2-O21
51	A	402	PC1	O11-C1-C2-O21
53	V	203	CDL	OA5-CA3-CA4-OA6
53	W	201	CDL	OB5-CB3-CB4-OB6
53	V	204	CDL	CB3-CB4-CB6-OB8
53	W	201	CDL	CA3-CA4-CA6-OA8
53	o	202	CDL	C83-C84-C85-C86
50	A	403	3PE	C12-C11-O13-P
54	X	101	ZMP	C16-C17-C18-C19
50	4	501	3PE	O21-C2-C3-O31
53	V	203	CDL	OA6-CA4-CA6-OA8
53	Y	201	CDL	OA6-CA4-CA6-OA8
53	z	101	CDL	OA6-CA4-CA6-OA8
51	M	502	PC1	C2C-C2D-C2E-C2F
51	9	401	PC1	C2C-C2D-C2E-C2F
51	L	1002	PC1	O13-C11-C12-N
51	w	801	PC1	O13-C11-C12-N
56	d	401	NDP	PN-O3-PA-O2A
53	o	202	CDL	C19-C20-C21-C22
54	X	101	ZMP	O3-C16-C17-O4
53	o	201	CDL	CA7-C31-C32-C33
50	M	501	3PE	C3B-C3C-C3D-C3E
53	Y	201	CDL	C14-C15-C16-C17
46	1	502	FMN	C4'-C5'-O5'-P
51	9	401	PC1	C2-C1-O11-P
51	M	502	PC1	C2-C1-O11-P
53	L	1003	CDL	CA4-CA3-OA5-PA1
53	z	101	CDL	C1-CB2-OB2-PB2
53	W	201	CDL	C79-C80-C81-C82
56	d	401	NDP	O4D-C1D-N1N-C6N
53	o	202	CDL	OA6-CA4-CA6-OA8
53	z	101	CDL	OB6-CB4-CB6-OB8
53	L	1003	CDL	CA2-C1-CB2-OB2
50	N	401	3PE	C23-C24-C25-C26
50	H	502	3PE	C32-C31-O31-C3
53	o	202	CDL	C53-C54-C55-C56
51	L	1002	PC1	C3A-C3B-C3C-C3D
50	L	1001	3PE	C3B-C3C-C3D-C3E

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Mol	Chain	Res	Type	Atoms
50	A	403	3PE	O13-C11-C12-N
50	H	502	3PE	C1-O11-P-O13
50	H	502	3PE	C1-O11-P-O14
50	K	101	3PE	C1-O11-P-O14
50	L	1004	3PE	C1-O11-P-O14
50	M	501	3PE	C11-O13-P-O14
50	N	401	3PE	C11-O13-P-O14
50	V	202	3PE	C1-O11-P-O12
50	V	202	3PE	C1-O11-P-O13
50	V	202	3PE	C1-O11-P-O14
50	i	502	3PE	C11-O13-P-O14
51	9	401	PC1	C11-O13-P-O12
51	A	401	PC1	C11-O13-P-O14
51	A	401	PC1	C1-O11-P-O12
51	A	401	PC1	C1-O11-P-O14
51	A	401	PC1	C1-O11-P-O13
51	M	502	PC1	C1-O11-P-O14
51	M	502	PC1	C1-O11-P-O13
51	w	801	PC1	C1-O11-P-O14
53	L	1003	CDL	CA2-OA2-PA1-OA3
53	L	1003	CDL	CA2-OA2-PA1-OA4
53	L	1003	CDL	CA2-OA2-PA1-OA5
53	L	1003	CDL	CB2-OB2-PB2-OB3
53	V	203	CDL	CA2-OA2-PA1-OA5
53	V	203	CDL	CA3-OA5-PA1-OA2
53	V	203	CDL	CA3-OA5-PA1-OA4
53	V	203	CDL	CB3-OB5-PB2-OB2
53	V	203	CDL	CB3-OB5-PB2-OB3
53	V	203	CDL	CB3-OB5-PB2-OB4
53	V	204	CDL	CB3-OB5-PB2-OB4
53	W	201	CDL	CA3-OA5-PA1-OA3
53	W	201	CDL	CB2-OB2-PB2-OB5
53	Y	201	CDL	CA2-OA2-PA1-OA3
53	Y	201	CDL	CA2-OA2-PA1-OA4
53	Y	201	CDL	CA2-OA2-PA1-OA5
53	o	201	CDL	CA2-OA2-PA1-OA4
53	o	201	CDL	CA2-OA2-PA1-OA5
53	o	201	CDL	CB3-OB5-PB2-OB4
53	o	202	CDL	CA2-OA2-PA1-OA3
53	o	202	CDL	CA2-OA2-PA1-OA4
53	o	202	CDL	CA2-OA2-PA1-OA5
53	o	202	CDL	CA3-OA5-PA1-OA3

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Mol	Chain	Res	Type	Atoms
53	o	202	CDL	CB2-OB2-PB2-OB4
53	z	101	CDL	CA3-OA5-PA1-OA2
53	z	101	CDL	CA3-OA5-PA1-OA3
53	z	101	CDL	CA3-OA5-PA1-OA4
53	V	203	CDL	CA4-CA3-OA5-PA1
53	W	201	CDL	C1-CA2-OA2-PA1
51	M	502	PC1	C2B-C2C-C2D-C2E
47	1	503	NAI	O4D-C1D-N1N-C2N
53	V	203	CDL	C38-C39-C40-C41
51	w	801	PC1	C3E-C3F-C3G-C3H
53	L	1003	CDL	C78-C79-C80-C81
53	o	202	CDL	CB5-C51-C52-C53
51	L	1002	PC1	C36-C37-C38-C39
53	V	204	CDL	C77-C78-C79-C80
51	M	502	PC1	O31-C31-C32-C33
50	V	202	3PE	O11-C1-C2-O21
53	L	1003	CDL	OB5-CB3-CB4-OB6
47	1	503	NAI	O4D-C1D-N1N-C6N
53	o	202	CDL	CB4-CB3-OB5-PB2
50	N	401	3PE	O21-C2-C3-O31
50	M	501	3PE	C38-C39-C3A-C3B
52	H	501	DCQ	C11-C10-C9-C8
50	N	401	3PE	C31-C32-C33-C34
53	V	204	CDL	CA3-CA4-CA6-OA8
51	A	402	PC1	O21-C21-C22-C23
53	o	202	CDL	C31-C32-C33-C34
50	L	1001	3PE	C38-C39-C3A-C3B
51	M	502	PC1	C39-C3A-C3B-C3C
53	o	202	CDL	C1-CB2-OB2-PB2
53	V	203	CDL	C37-C38-C39-C40
53	o	201	CDL	OA5-CA3-CA4-OA6
58	s	201	MYR	C11-C10-C9-C8
50	H	502	3PE	O32-C31-O31-C3
53	L	1003	CDL	C80-C81-C82-C83
53	o	202	CDL	C56-C57-C58-C59
53	W	201	CDL	C16-C17-C18-C19
53	o	202	CDL	CA3-CA4-CA6-OA8
54	X	101	ZMP	C3-C4-C5-C6
51	9	401	PC1	C3F-C3G-C3H-C3I
51	9	401	PC1	C2D-C2E-C2F-C2G
50	L	1004	3PE	C1-C2-O21-C21
51	9	401	PC1	C3-C2-O21-C21

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Mol	Chain	Res	Type	Atoms
51	L	1002	PC1	C1-C2-O21-C21
53	o	202	CDL	C80-C81-C82-C83
51	L	1002	PC1	C2A-C2B-C2C-C2D
53	o	201	CDL	C72-C73-C74-C75
53	o	201	CDL	C15-C16-C17-C18
53	o	201	CDL	CA5-C11-C12-C13
50	H	502	3PE	C28-C29-C2A-C2B
50	A	403	3PE	C2-C1-O11-P
53	z	101	CDL	CB4-CB3-OB5-PB2
53	Y	201	CDL	C59-C60-C61-C62
50	H	502	3PE	C26-C27-C28-C29
53	W	201	CDL	C53-C54-C55-C56
53	V	203	CDL	C11-C12-C13-C14
50	L	1001	3PE	C39-C3A-C3B-C3C
53	o	202	CDL	C84-C85-C86-C87
56	d	401	NDP	C2B-O2B-P2B-O1X
50	i	501	3PE	C38-C39-C3A-C3B
53	L	1003	CDL	C37-C38-C39-C40
51	9	401	PC1	C2B-C2C-C2D-C2E
50	i	502	3PE	C36-C37-C38-C39
54	X	101	ZMP	C4-C5-C6-C7
50	4	501	3PE	C25-C26-C27-C28
46	1	502	FMN	O3'-C3'-C4'-O4'
53	L	1003	CDL	C1-CA2-OA2-PA1
51	L	1002	PC1	C27-C28-C29-C2A
46	1	502	FMN	O3'-C3'-C4'-C5'
53	W	201	CDL	C14-C15-C16-C17
53	Y	201	CDL	C32-C33-C34-C35
53	V	203	CDL	C80-C81-C82-C83
53	o	202	CDL	C54-C55-C56-C57
53	o	201	CDL	C71-C72-C73-C74
53	V	203	CDL	C19-C20-C21-C22
53	L	1003	CDL	C60-C61-C62-C63
51	L	1002	PC1	O31-C31-C32-C33
50	A	403	3PE	C38-C39-C3A-C3B
51	M	502	PC1	O21-C21-C22-C23
53	L	1003	CDL	C39-C40-C41-C42
53	W	201	CDL	OB5-CB3-CB4-CB6
53	o	201	CDL	OA5-CA3-CA4-CA6
51	A	402	PC1	O31-C31-C32-C33
50	A	403	3PE	C34-C35-C36-C37
53	o	202	CDL	C52-C53-C54-C55

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Mol	Chain	Res	Type	Atoms
50	i	501	3PE	C3D-C3E-C3F-C3G
50	K	101	3PE	O31-C31-C32-C33
50	N	401	3PE	C3-C2-O21-C21
53	z	101	CDL	C52-C53-C54-C55
53	W	201	CDL	C81-C82-C83-C84
50	A	403	3PE	O11-C1-C2-O21
53	o	202	CDL	OA5-CA3-CA4-OA6
53	z	101	CDL	OA5-CA3-CA4-OA6
50	L	1001	3PE	C34-C35-C36-C37
50	H	502	3PE	C12-C11-O13-P
53	Y	201	CDL	C18-C19-C20-C21
50	i	502	3PE	C3A-C3B-C3C-C3D
50	A	403	3PE	O21-C2-C3-O31
51	A	401	PC1	C3F-C3G-C3H-C3I
50	A	403	3PE	O11-C1-C2-C3
50	V	202	3PE	O11-C1-C2-C3
53	V	203	CDL	OB5-CB3-CB4-CB6
50	A	403	3PE	C2E-C2F-C2G-C2H
51	L	1002	PC1	C3C-C3D-C3E-C3F
50	4	501	3PE	C31-C32-C33-C34
51	L	1002	PC1	C34-C35-C36-C37
51	M	502	PC1	C34-C35-C36-C37
50	L	1001	3PE	C23-C24-C25-C26
51	A	402	PC1	O13-C11-C12-N
53	L	1003	CDL	CA7-C31-C32-C33
50	i	502	3PE	O21-C21-C22-C23
50	V	202	3PE	C25-C26-C27-C28
53	L	1003	CDL	C38-C39-C40-C41
53	o	202	CDL	C71-C72-C73-C74
50	i	502	3PE	C2A-C2B-C2C-C2D
53	z	101	CDL	C52-C51-CB5-OB6
51	A	402	PC1	C22-C23-C24-C25
50	p	201	3PE	C21-C22-C23-C24
51	L	1002	PC1	O11-C1-C2-O21
50	p	201	3PE	C26-C27-C28-C29
53	o	202	CDL	C34-C35-C36-C37
53	Y	201	CDL	CB7-C71-C72-C73
50	i	502	3PE	O31-C31-C32-C33
53	V	203	CDL	C71-C72-C73-C74
50	H	502	3PE	C24-C25-C26-C27
53	Y	201	CDL	C12-C13-C14-C15
53	V	204	CDL	C52-C51-CB5-OB6

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Mol	Chain	Res	Type	Atoms
51	A	401	PC1	C22-C23-C24-C25
51	A	401	PC1	C24-C25-C26-C27
50	L	1004	3PE	O21-C21-C22-C23
50	V	202	3PE	O31-C31-C32-C33
50	A	403	3PE	C35-C36-C37-C38
50	H	502	3PE	C31-C32-C33-C34
53	W	201	CDL	C12-C11-CA5-OA6
53	V	204	CDL	C32-C31-CA7-OA8
50	M	501	3PE	O21-C21-C22-C23
53	Y	201	CDL	C12-C11-CA5-OA6
53	o	202	CDL	CB3-CB4-OB6-CB5
53	Y	201	CDL	C80-C81-C82-C83
53	W	201	CDL	C58-C59-C60-C61
50	p	201	3PE	O21-C21-C22-C23
50	i	502	3PE	O22-C21-C22-C23
50	K	101	3PE	C2-C1-O11-P
53	L	1003	CDL	C58-C59-C60-C61
51	A	401	PC1	C3E-C3F-C3G-C3H
50	N	401	3PE	C2C-C2D-C2E-C2F
53	W	201	CDL	C64-C65-C66-C67
53	o	201	CDL	C72-C71-CB7-OB8
50	V	202	3PE	O32-C31-C32-C33
50	N	401	3PE	C3E-C3F-C3G-C3H
51	w	801	PC1	C27-C28-C29-C2A
53	V	204	CDL	C32-C31-CA7-OA9
53	z	101	CDL	C52-C51-CB5-OB7
53	V	204	CDL	C52-C51-CB5-OB7
50	M	501	3PE	O22-C21-C22-C23
53	o	202	CDL	C12-C13-C14-C15
50	L	1004	3PE	O22-C21-C22-C23
53	L	1003	CDL	C52-C51-CB5-OB6
53	W	201	CDL	C22-C23-C24-C25
54	X	101	ZMP	N2-C16-C17-O4
50	i	502	3PE	O32-C31-C32-C33
53	o	201	CDL	C33-C34-C35-C36
53	V	203	CDL	CB5-C51-C52-C53
52	H	501	DCQ	C10-C11-C12-C13
50	i	501	3PE	O11-C1-C2-C3
51	9	401	PC1	C34-C35-C36-C37
53	W	201	CDL	C12-C11-CA5-OA7
50	L	1001	3PE	O21-C21-C22-C23
53	V	203	CDL	C72-C71-CB7-OB8

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Mol	Chain	Res	Type	Atoms
50	p	201	3PE	O22-C21-C22-C23
53	Y	201	CDL	C12-C11-CA5-OA7

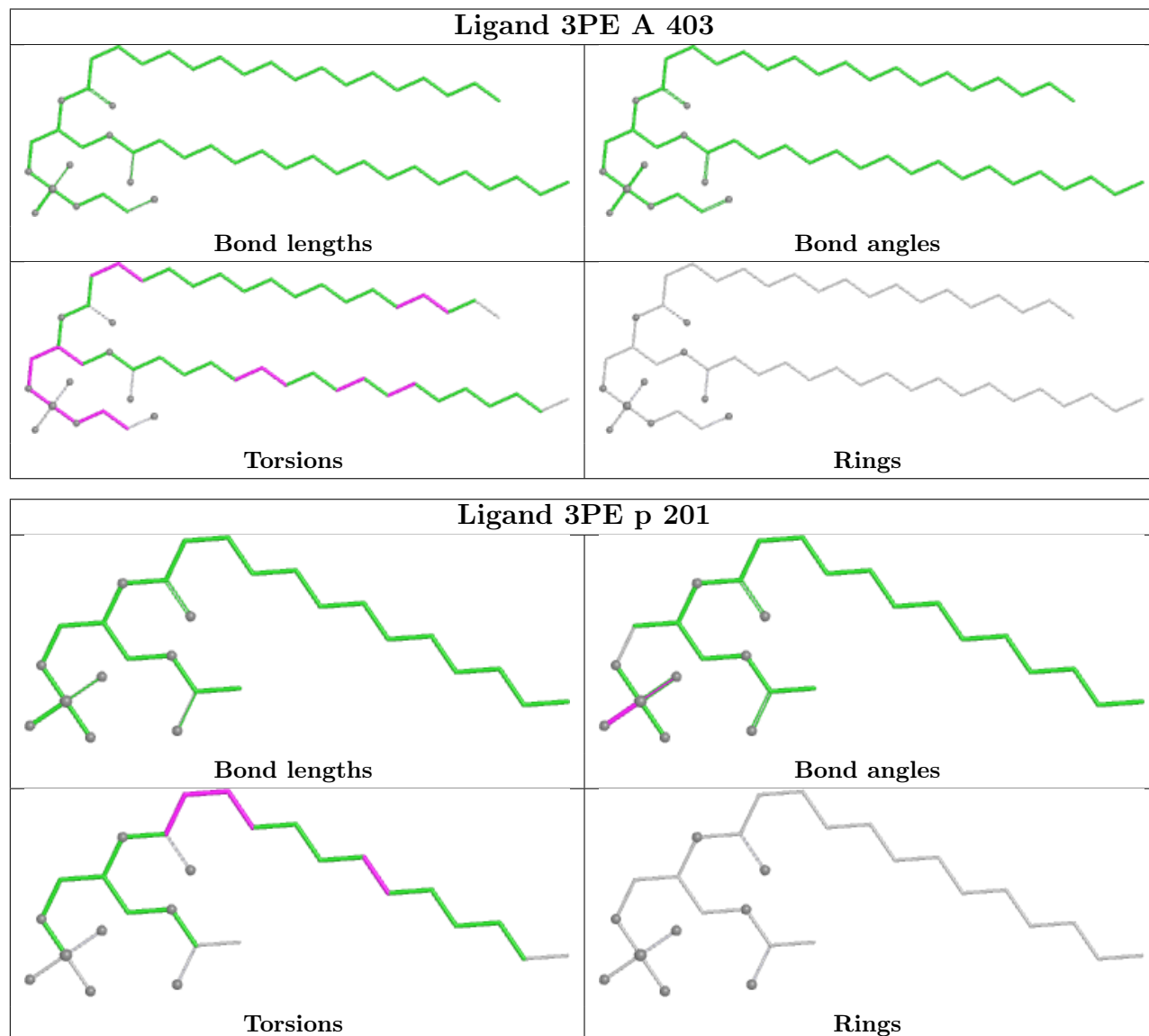
There are no ring outliers.

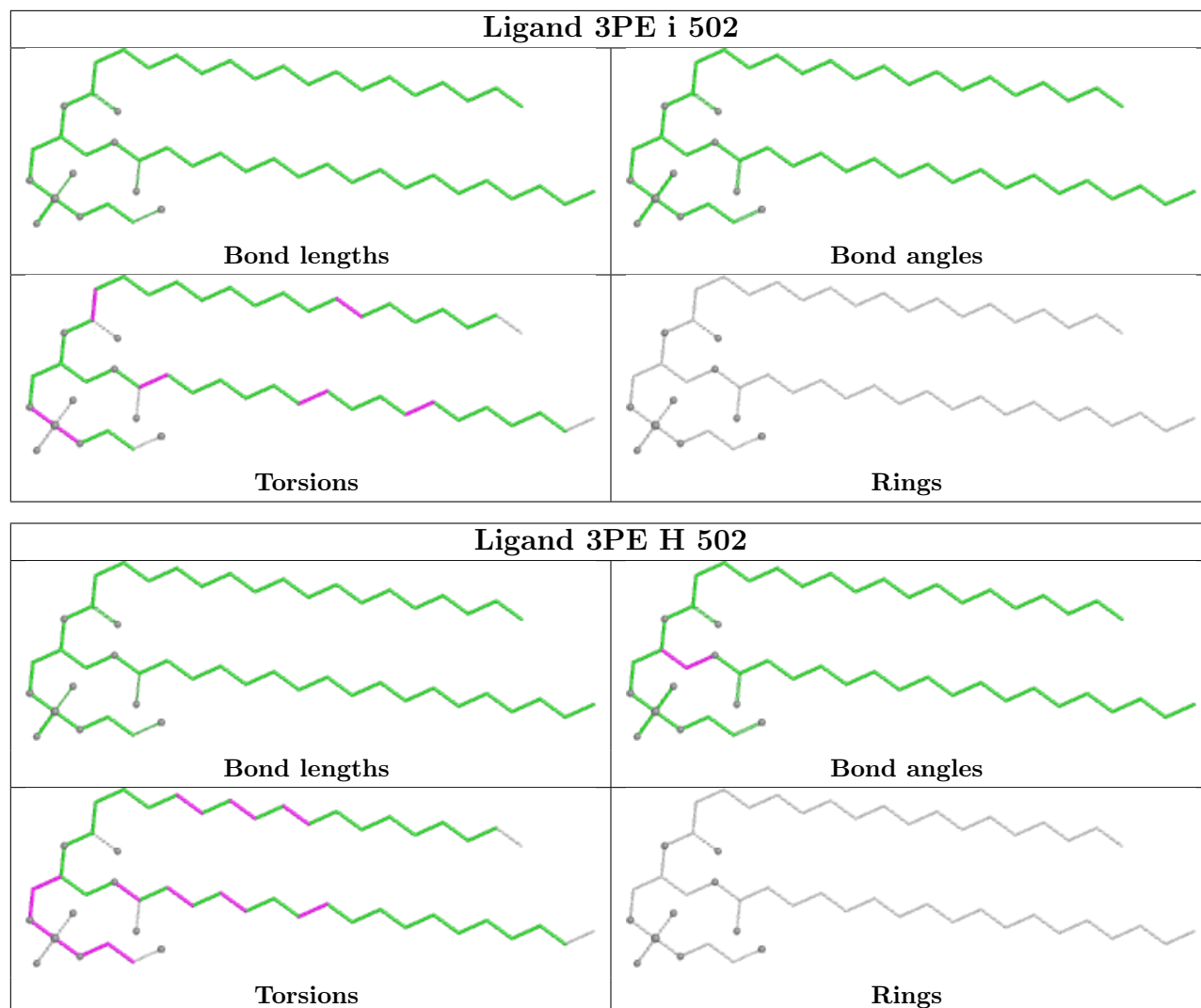
32 monomers are involved in 90 short contacts:

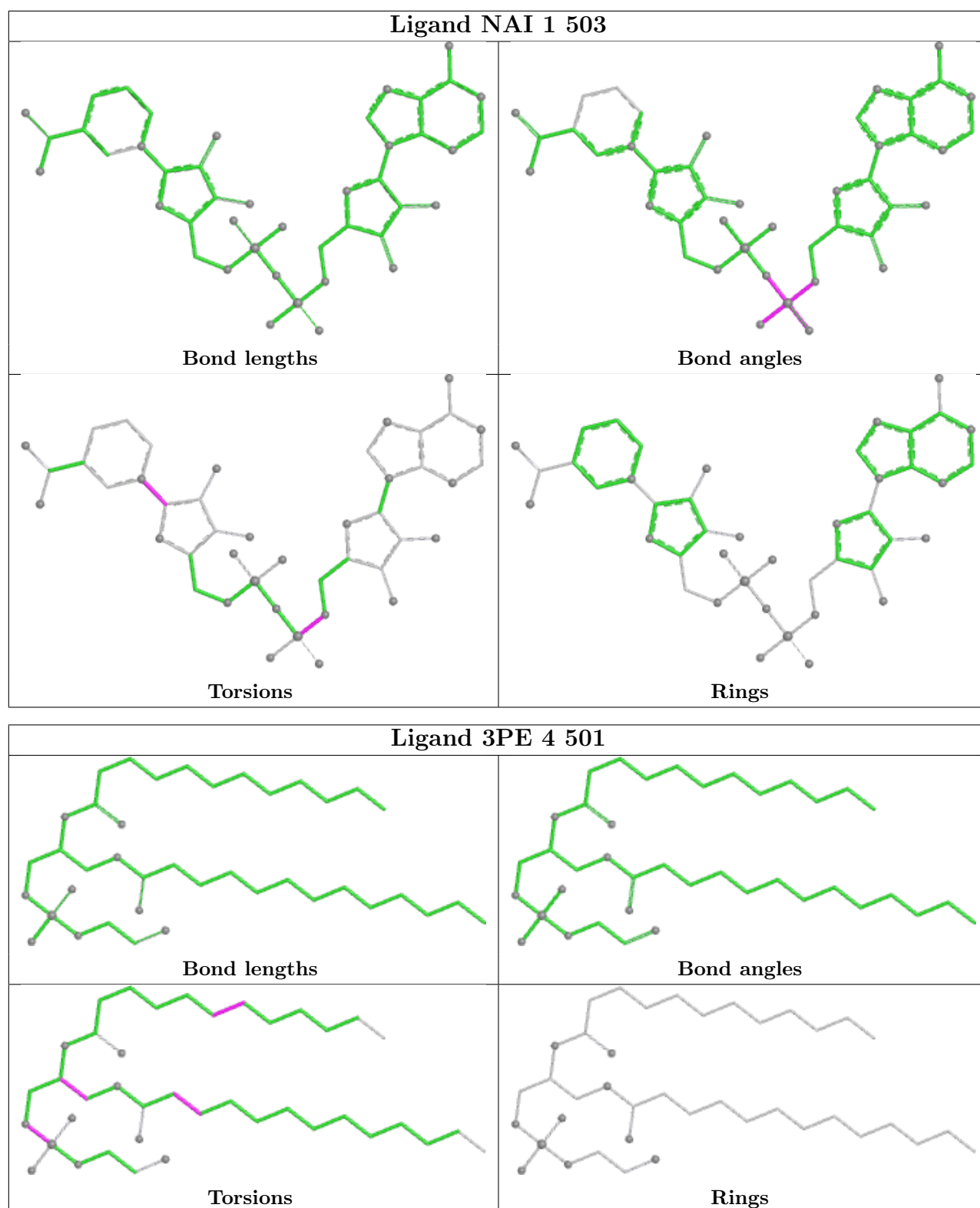
Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	A	403	3PE	2	0
50	i	502	3PE	1	0
50	H	502	3PE	2	0
47	1	503	NAI	6	0
50	4	501	3PE	1	0
53	Y	201	CDL	9	0
51	M	502	PC1	5	0
45	1	501	SF4	1	0
53	o	201	CDL	4	0
51	w	801	PC1	7	0
50	K	101	3PE	4	0
53	W	201	CDL	6	0
54	X	101	ZMP	1	0
53	o	202	CDL	6	0
51	L	1002	PC1	7	0
50	V	201	3PE	3	0
48	2	300	FES	1	0
51	9	401	PC1	4	0
53	V	204	CDL	1	0
53	L	1003	CDL	6	0
50	L	1001	3PE	2	0
53	V	203	CDL	4	0
50	i	501	3PE	2	0
52	H	501	DCQ	2	0
45	6	300	SF4	1	0
51	A	402	PC1	2	0
54	g	201	ZMP	1	0
50	V	202	3PE	2	0
51	A	401	PC1	1	0
46	1	502	FMN	1	0
50	M	501	3PE	3	0
50	N	401	3PE	1	0

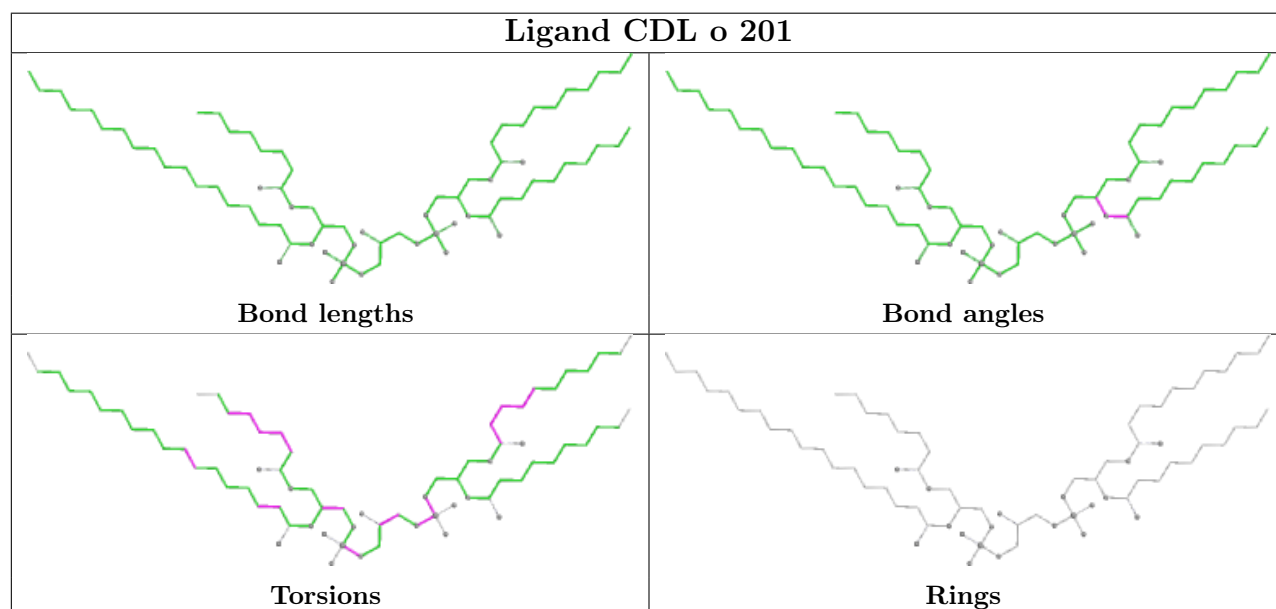
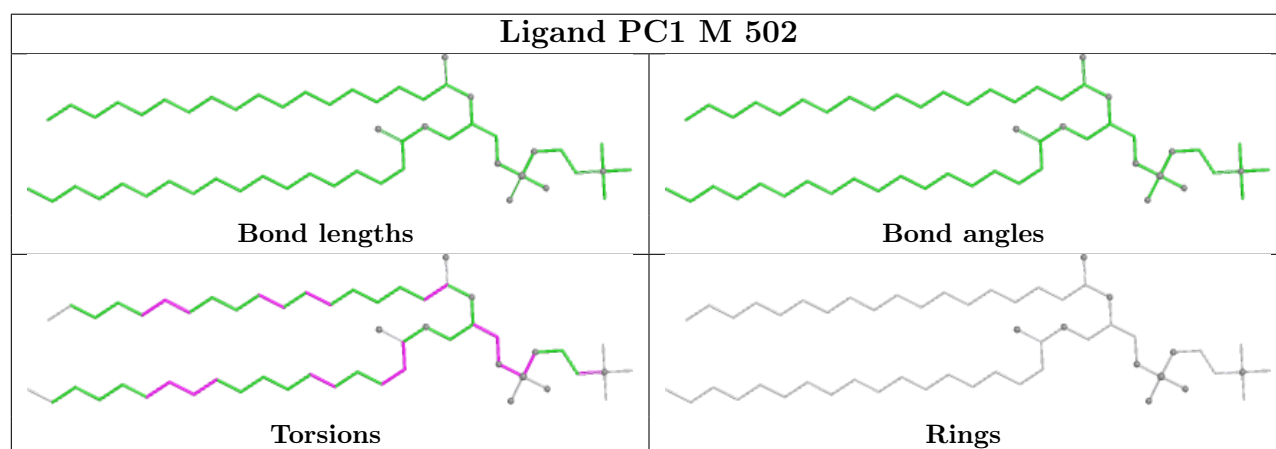
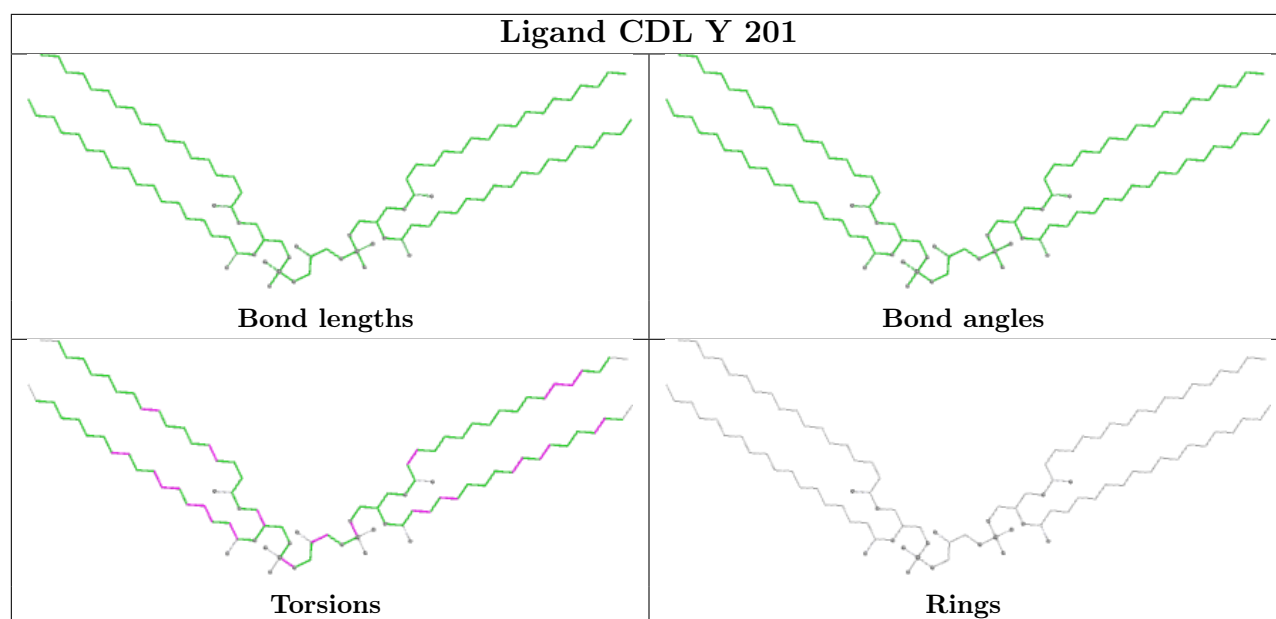
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

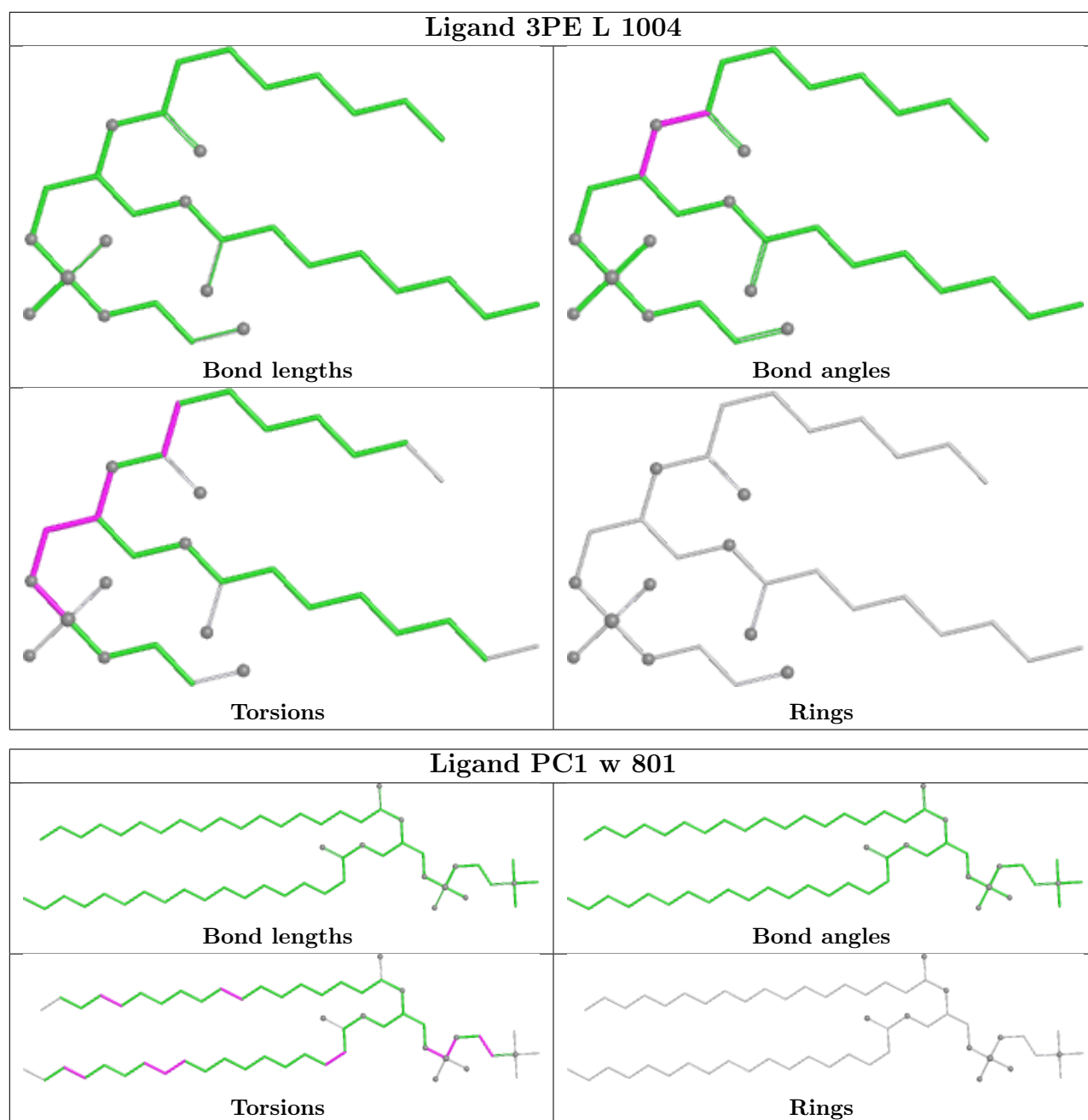
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.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

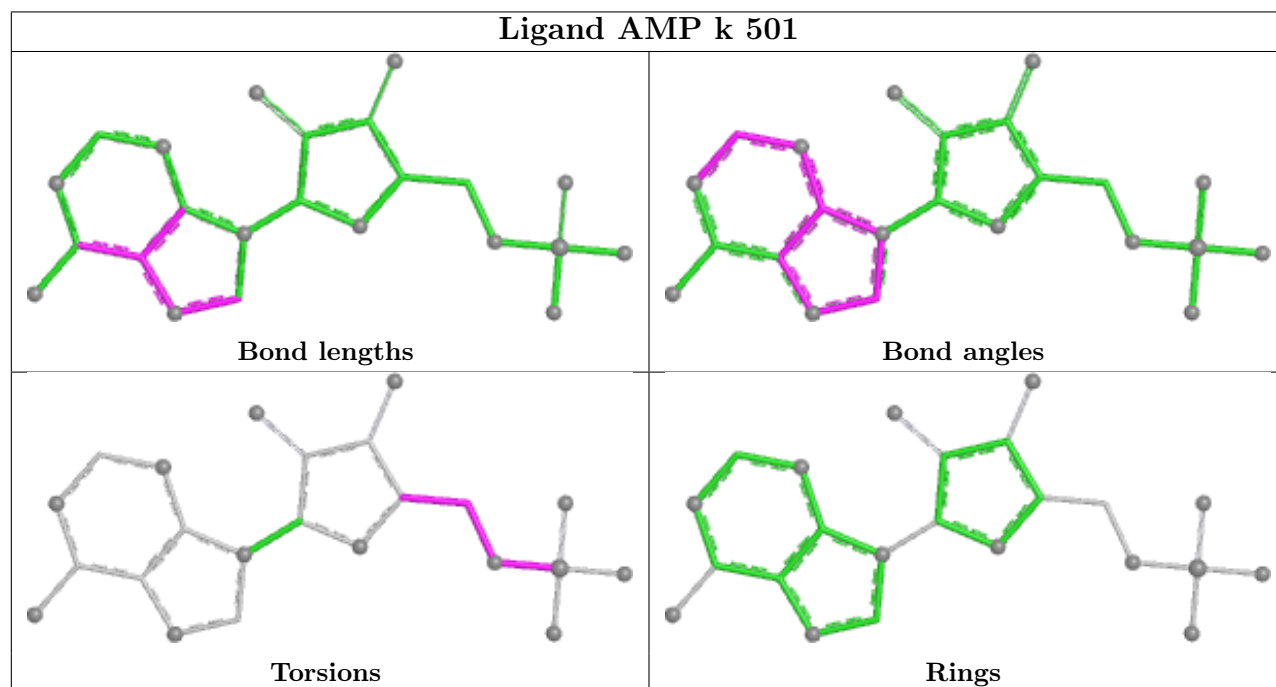
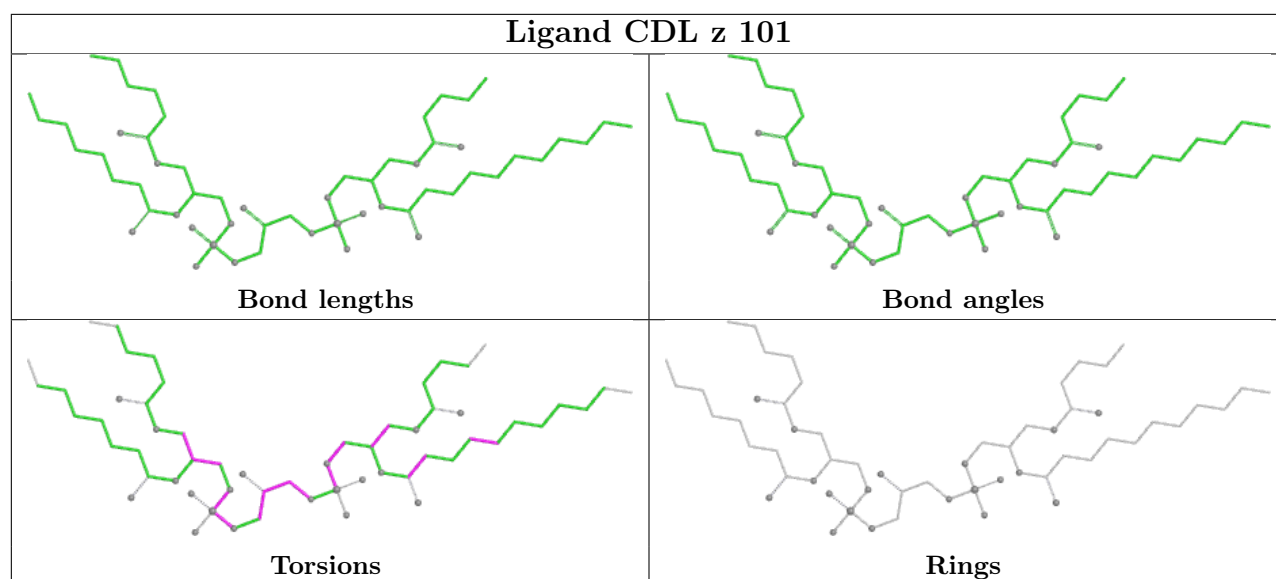


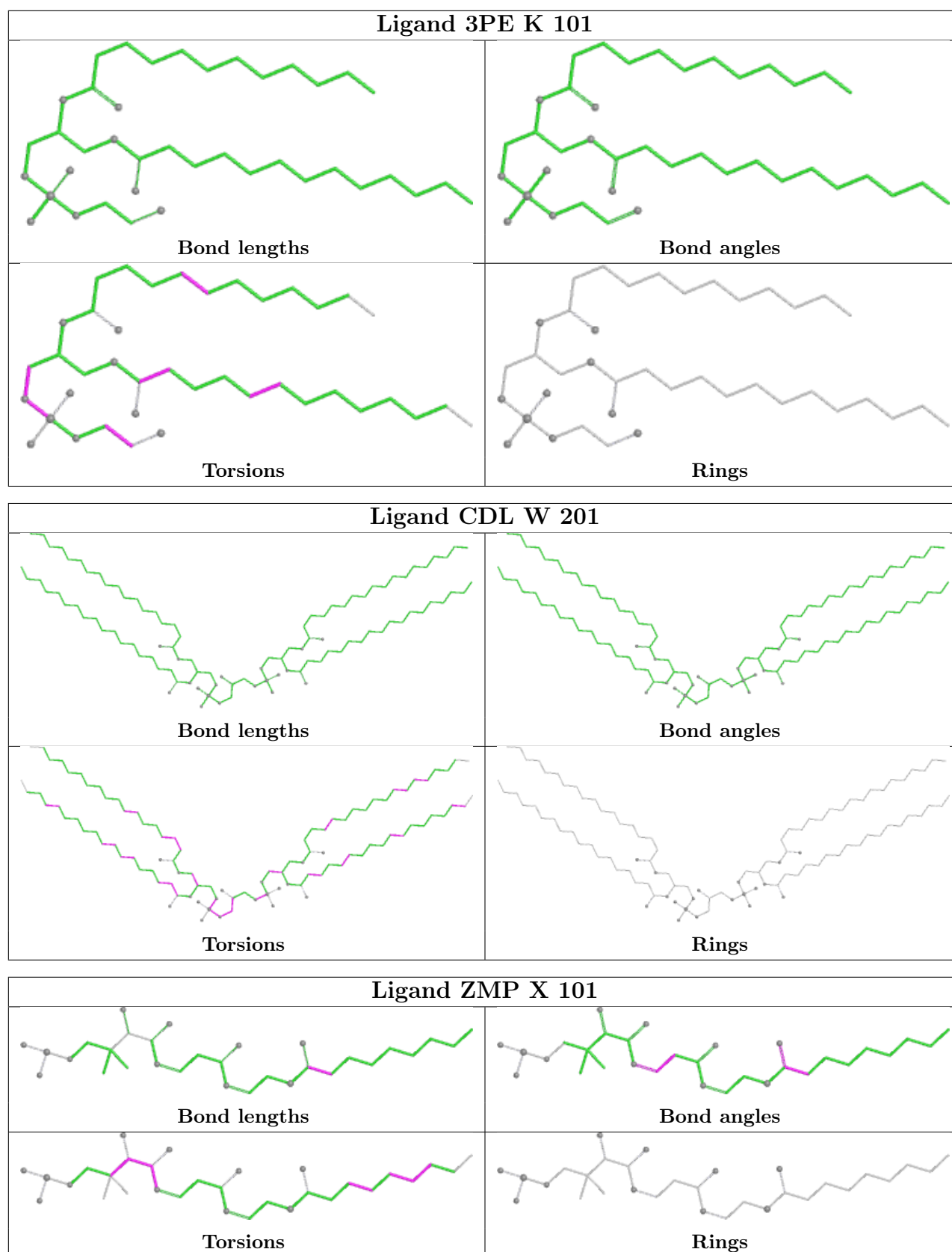


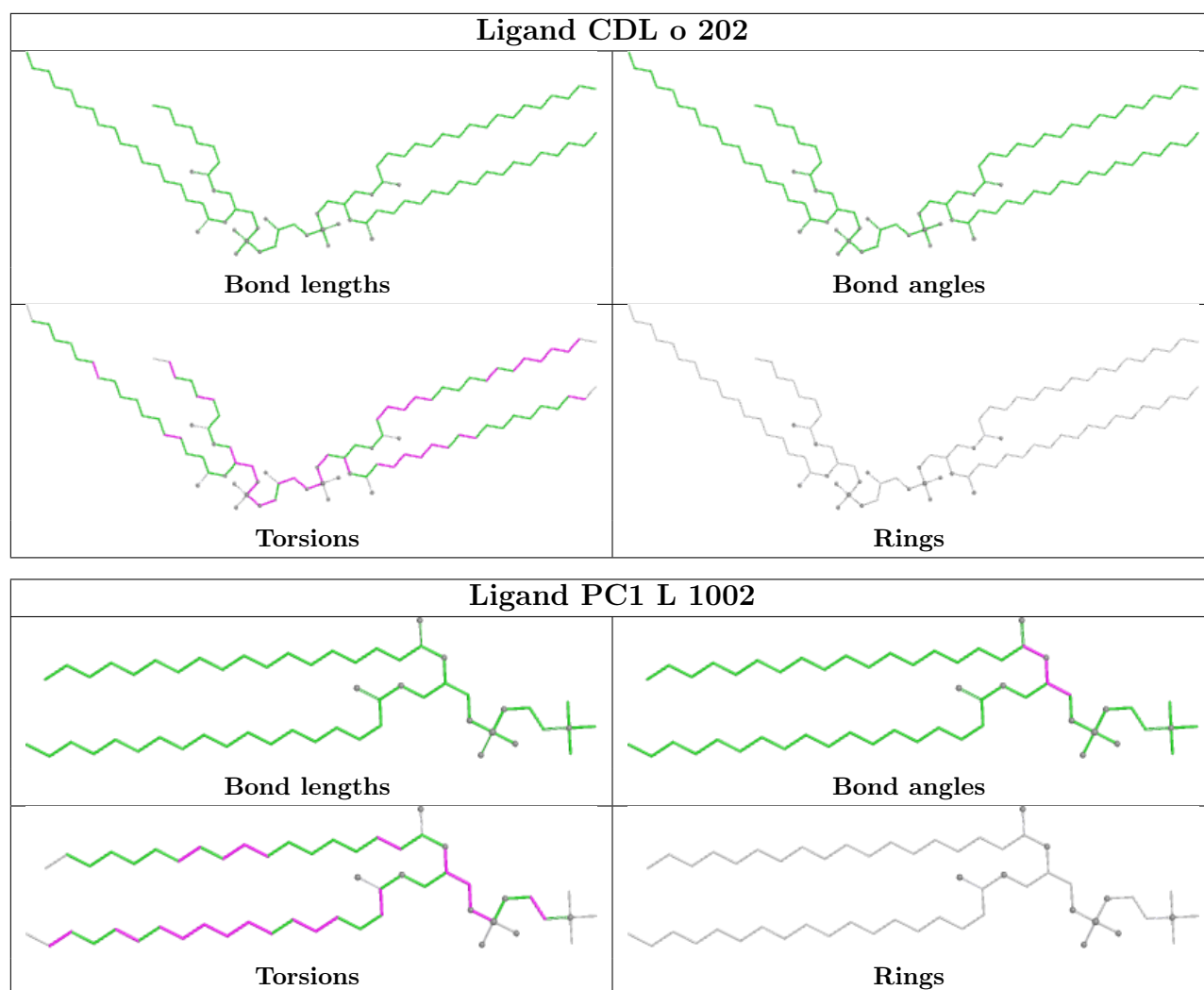


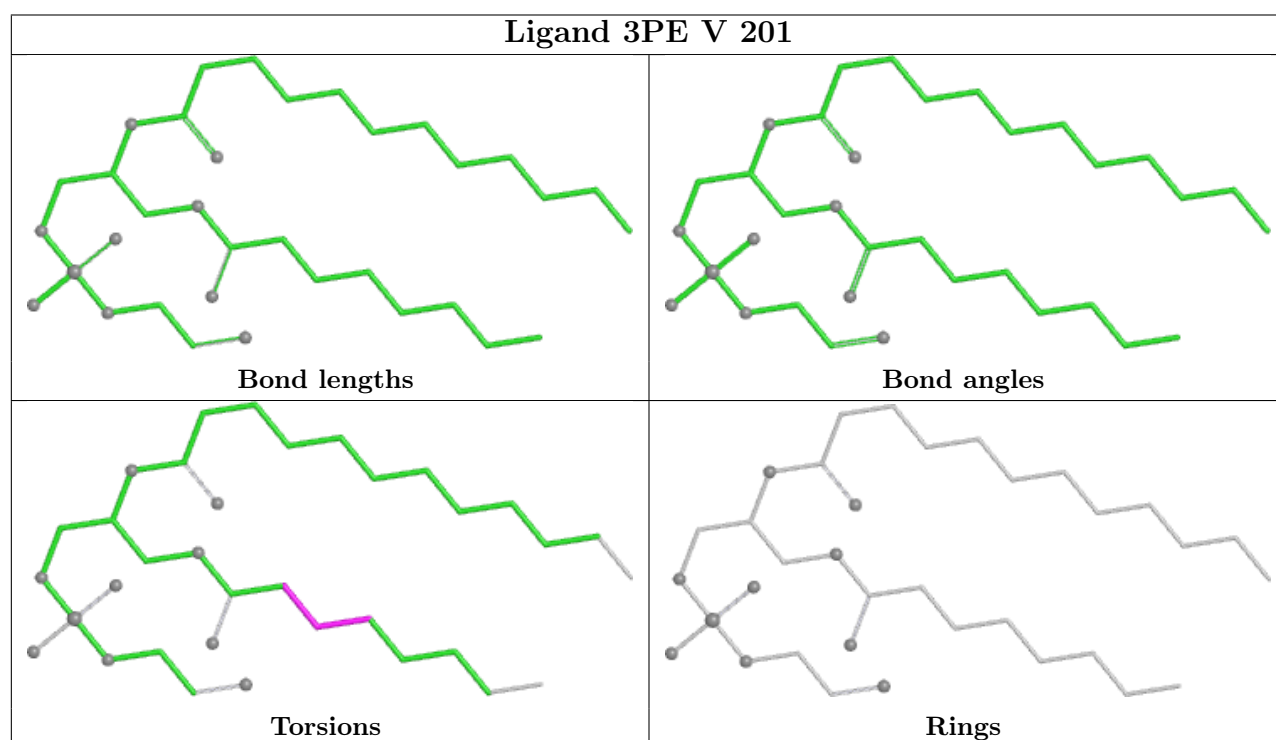
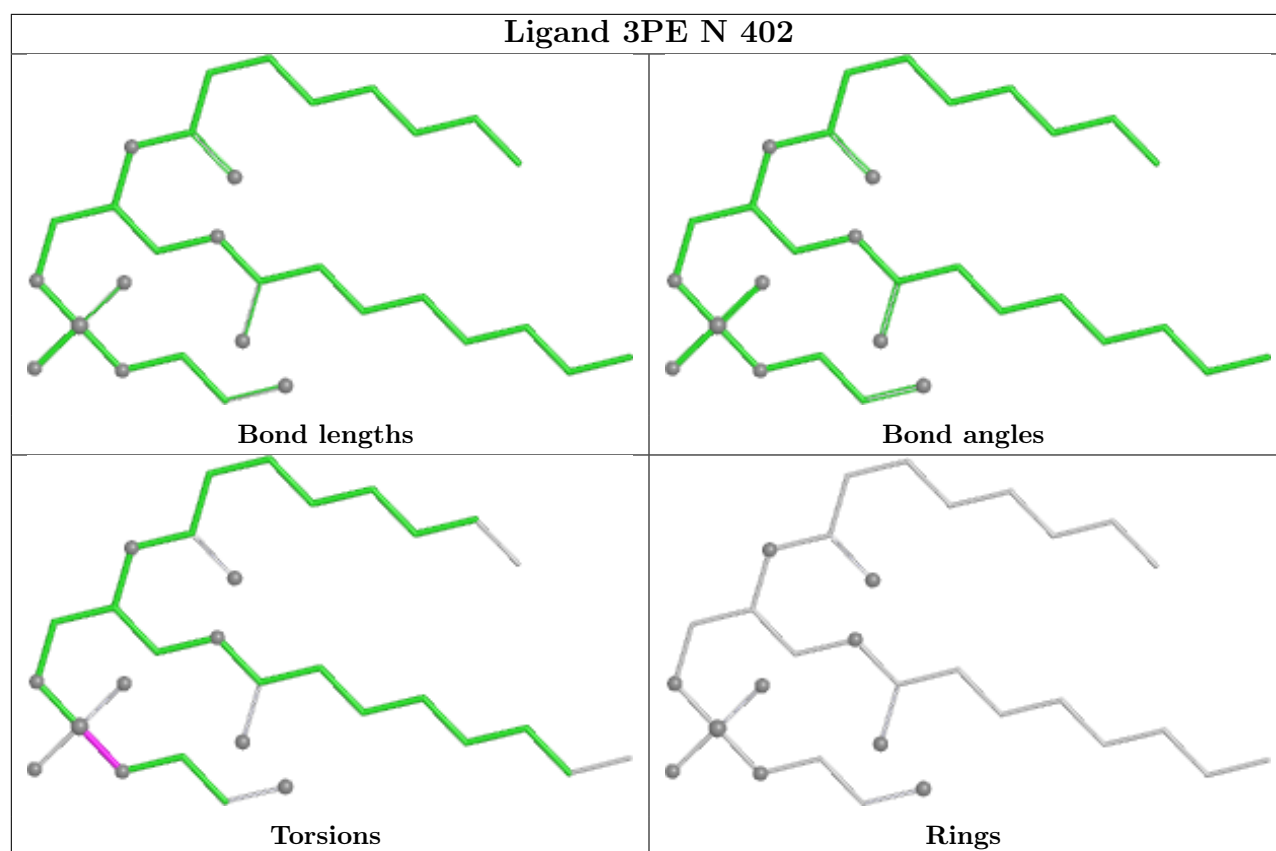


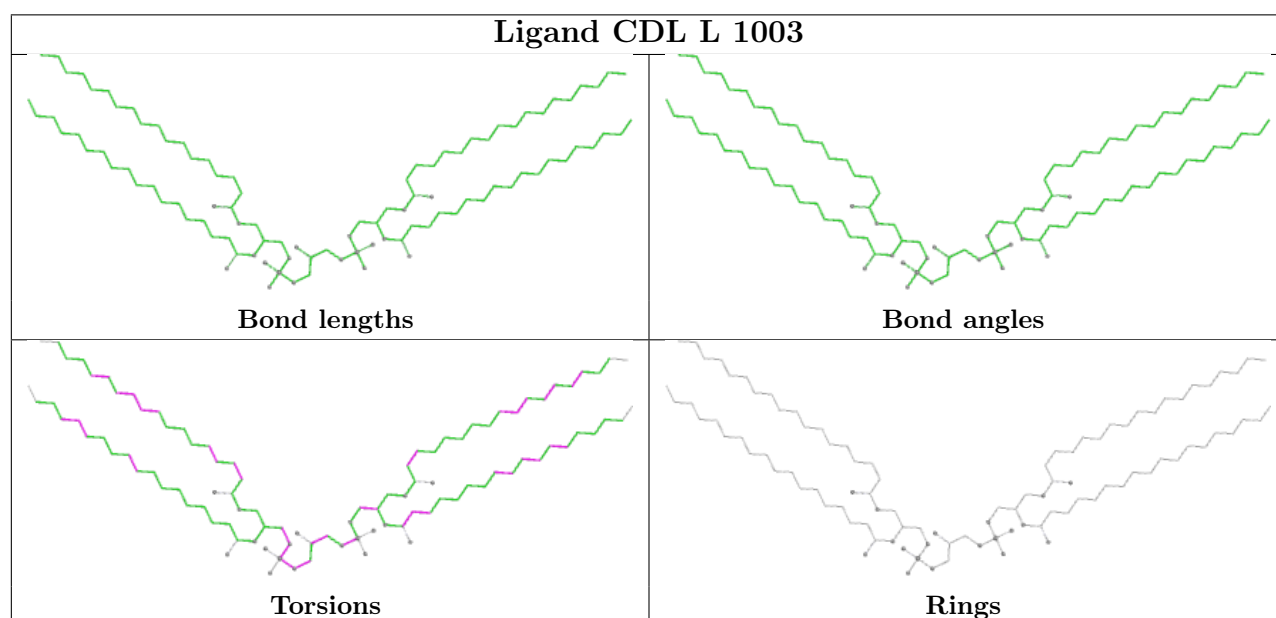
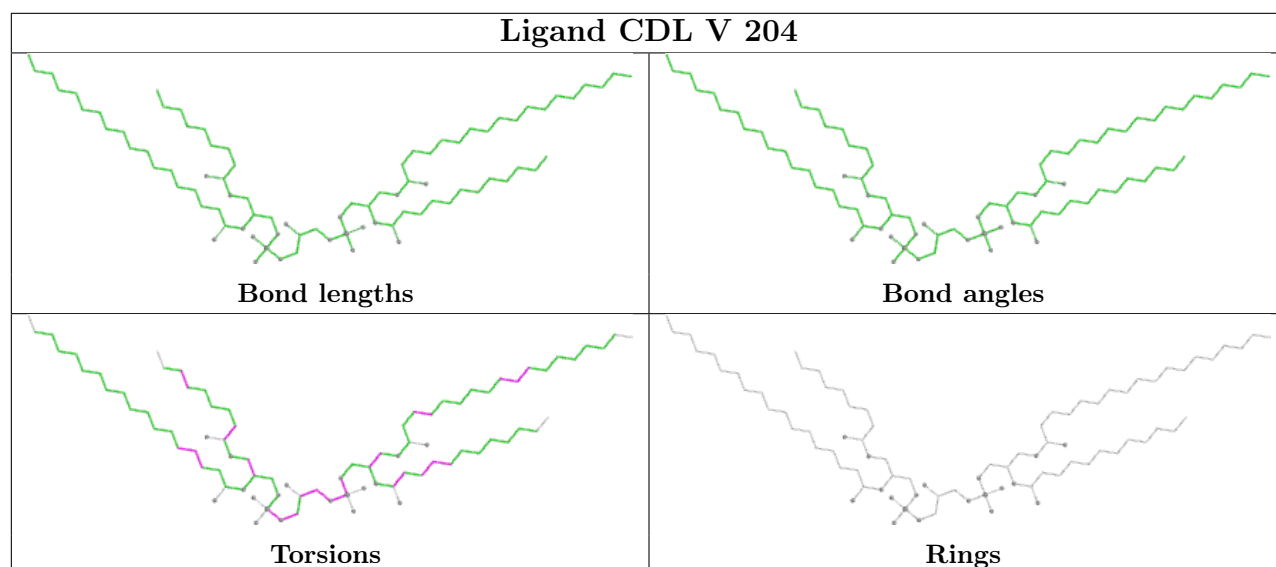
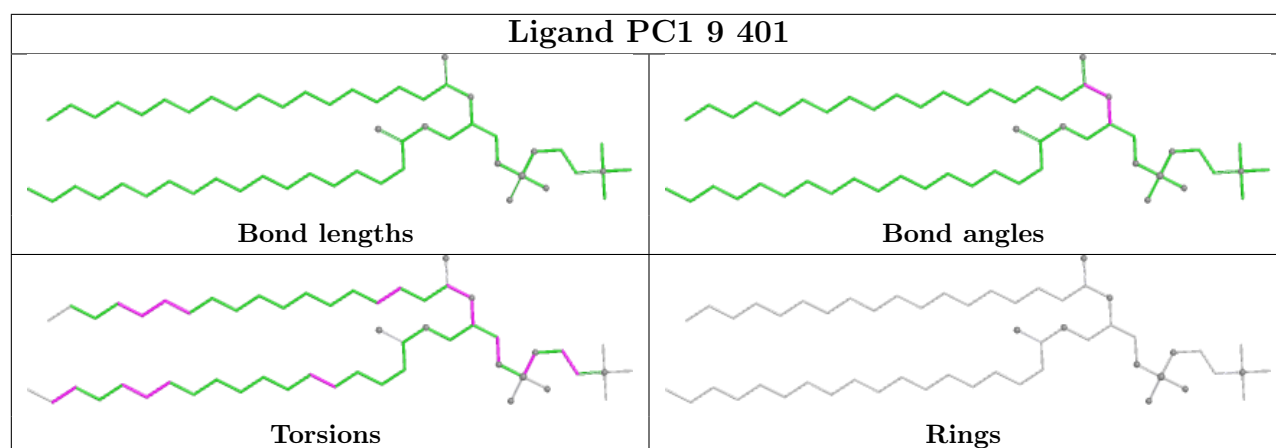


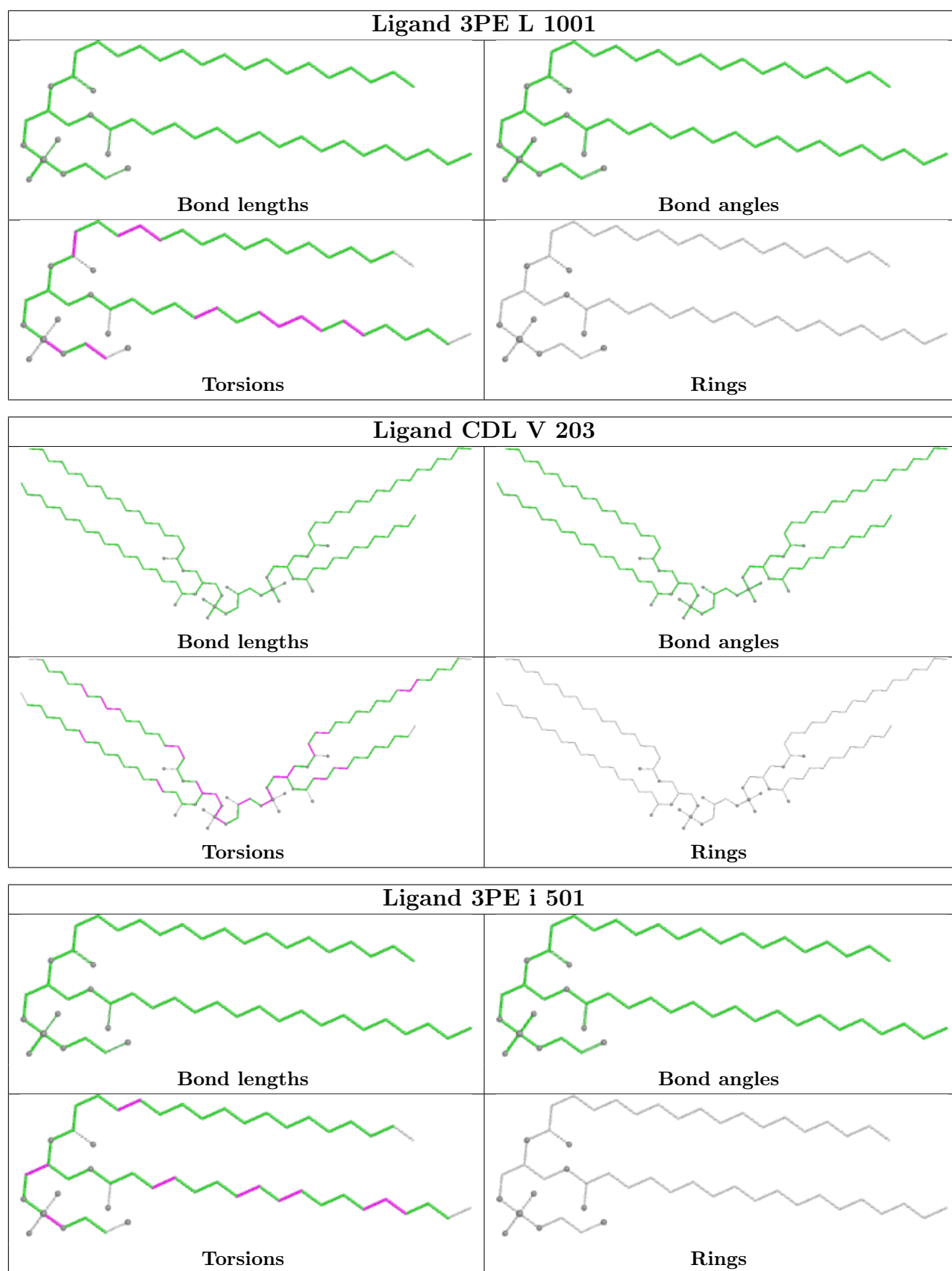


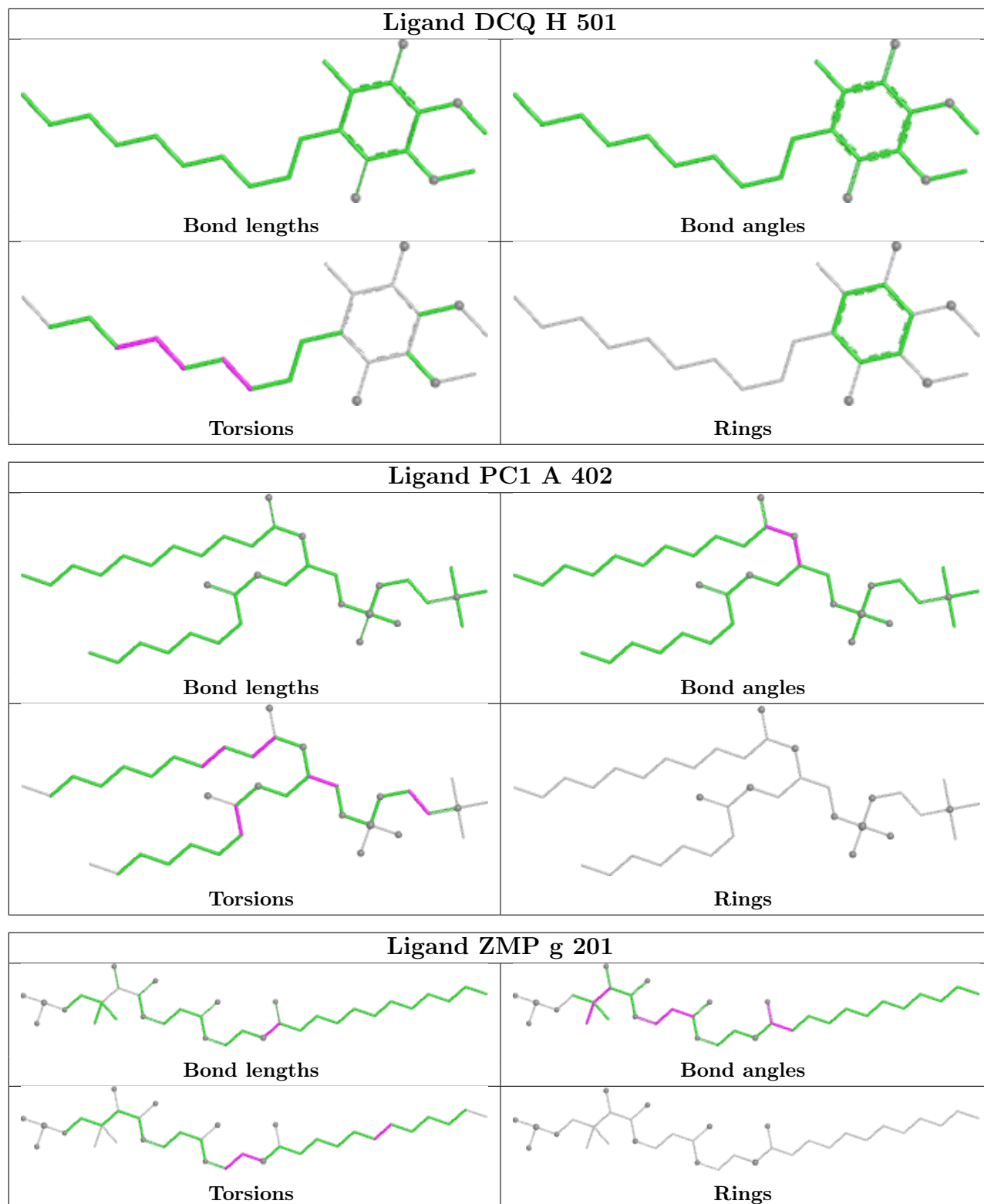


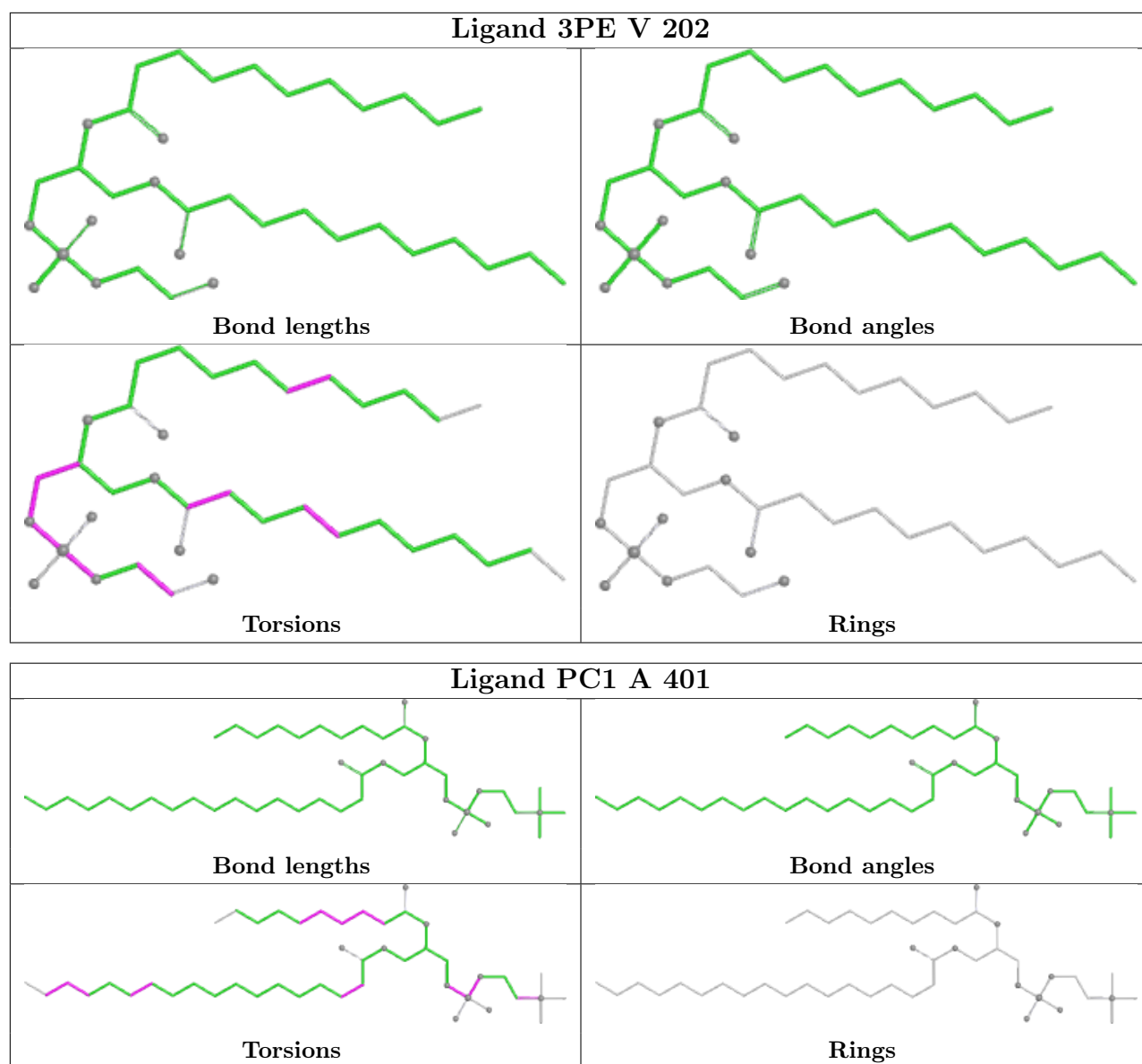


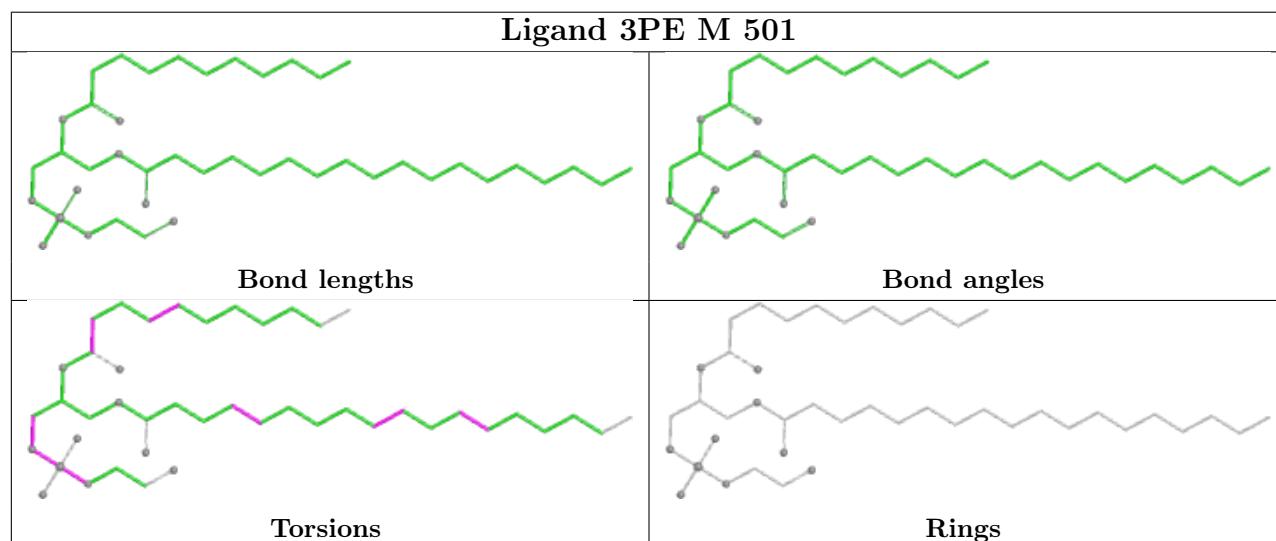
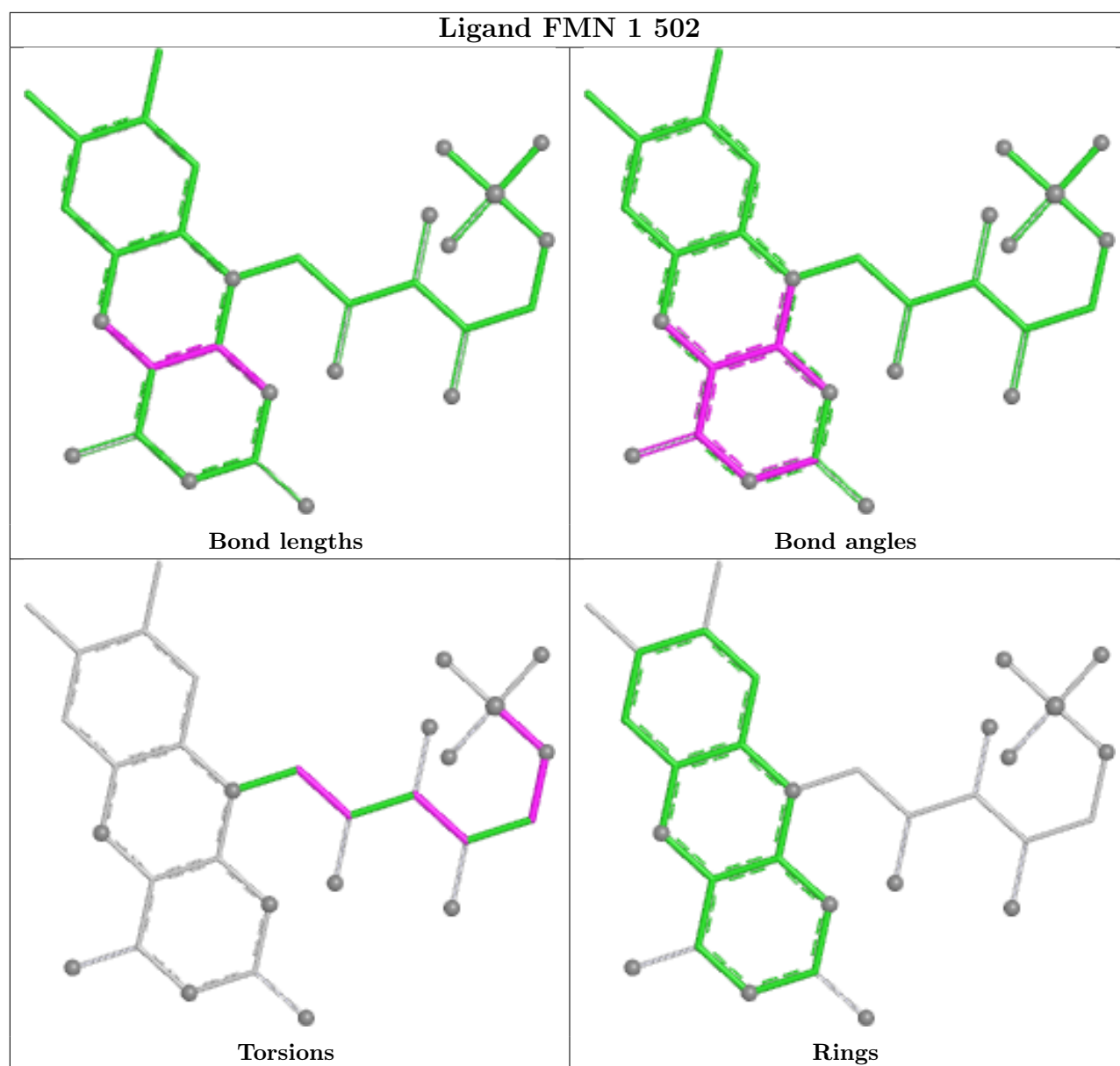


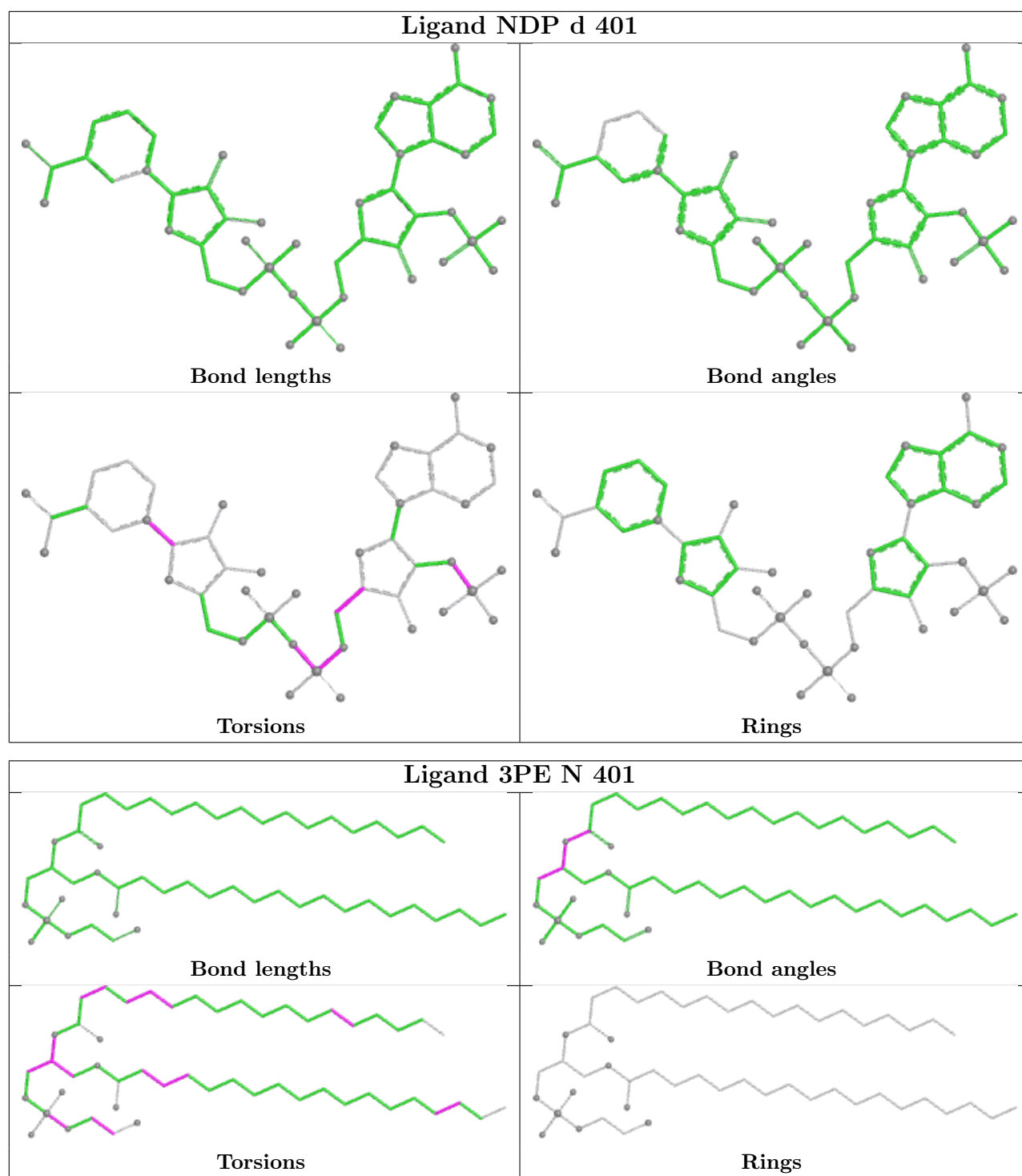












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

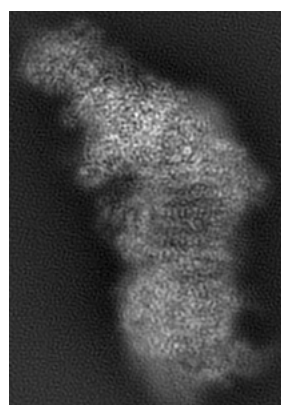
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11245. These allow visual inspection of the internal detail of the map and identification of artifacts.

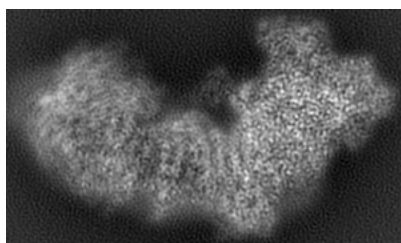
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

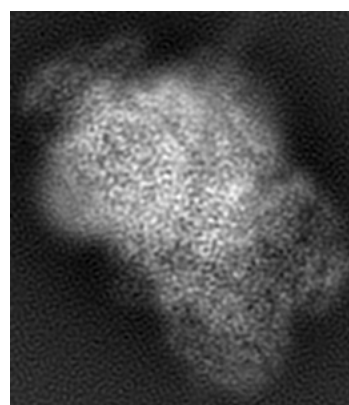
6.1.1 Primary map



X



Y

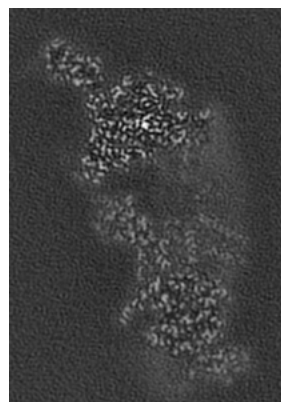


Z

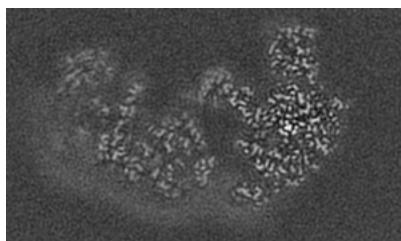
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

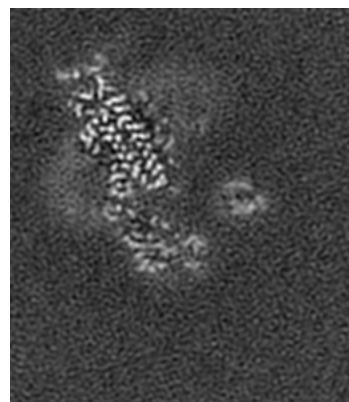
6.2.1 Primary map



X Index: 80



Y Index: 92

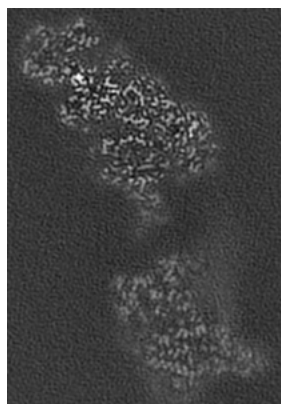


Z Index: 135

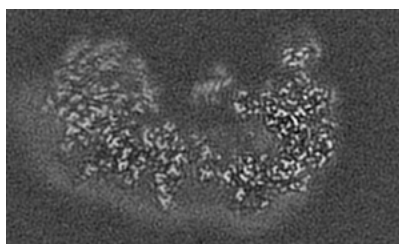
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

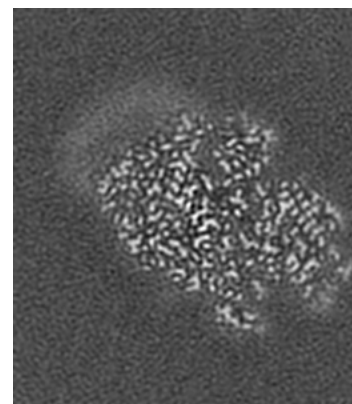
6.3.1 Primary map



X Index: 99



Y Index: 102

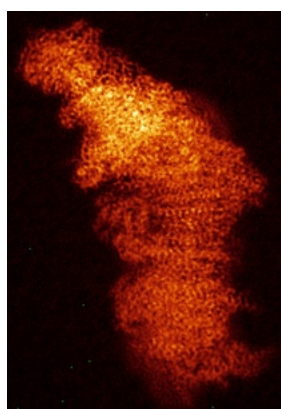


Z Index: 196

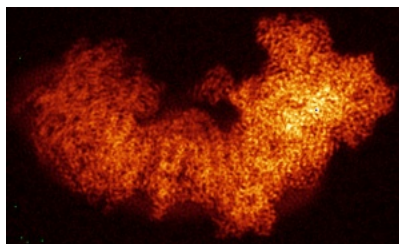
The images above show the largest variance slices of the map in three orthogonal directions.

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

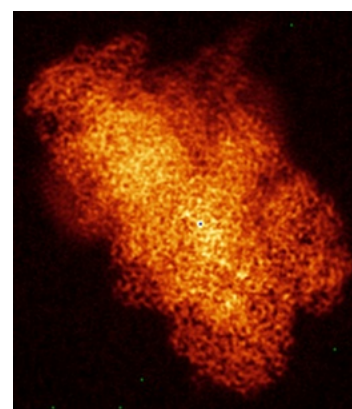
6.4.1 Primary map



X



Y

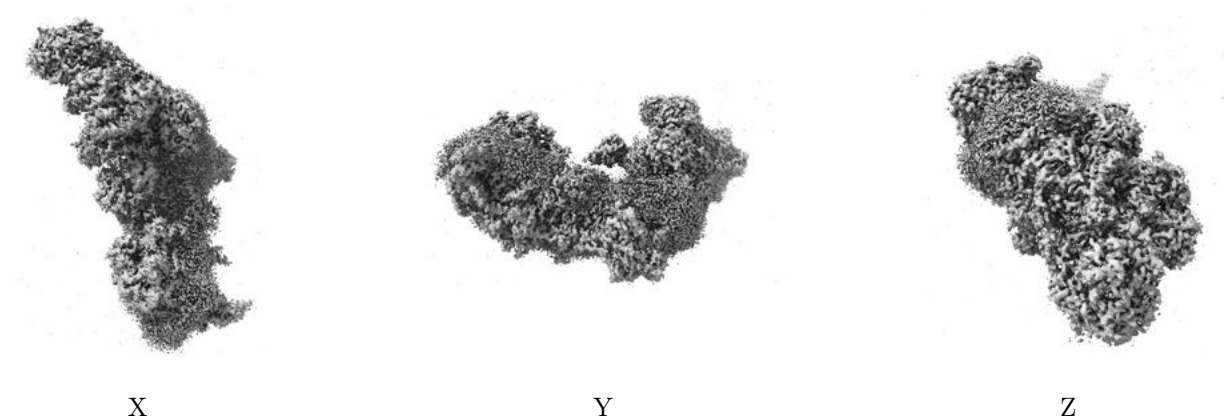


Z

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 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

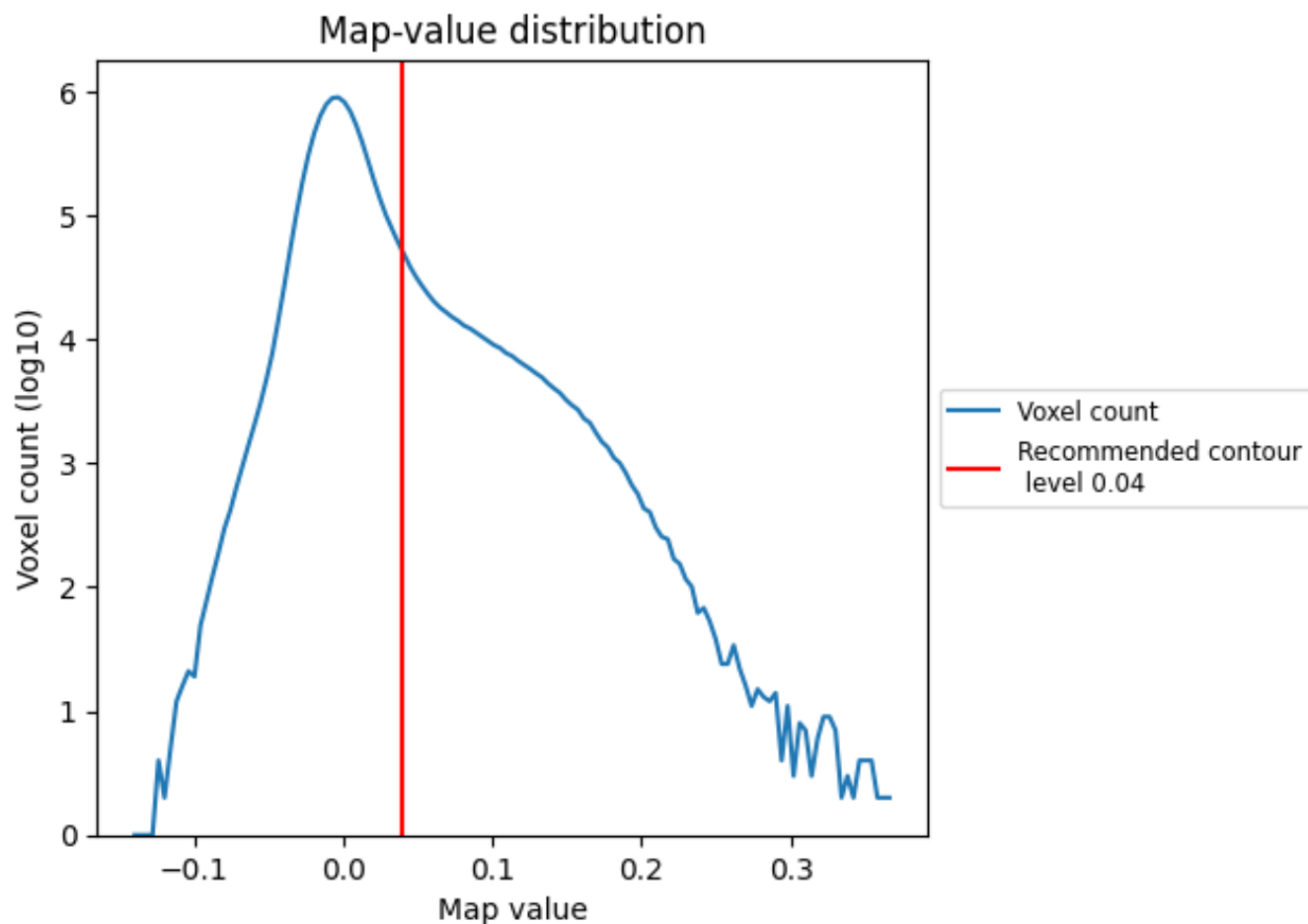
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

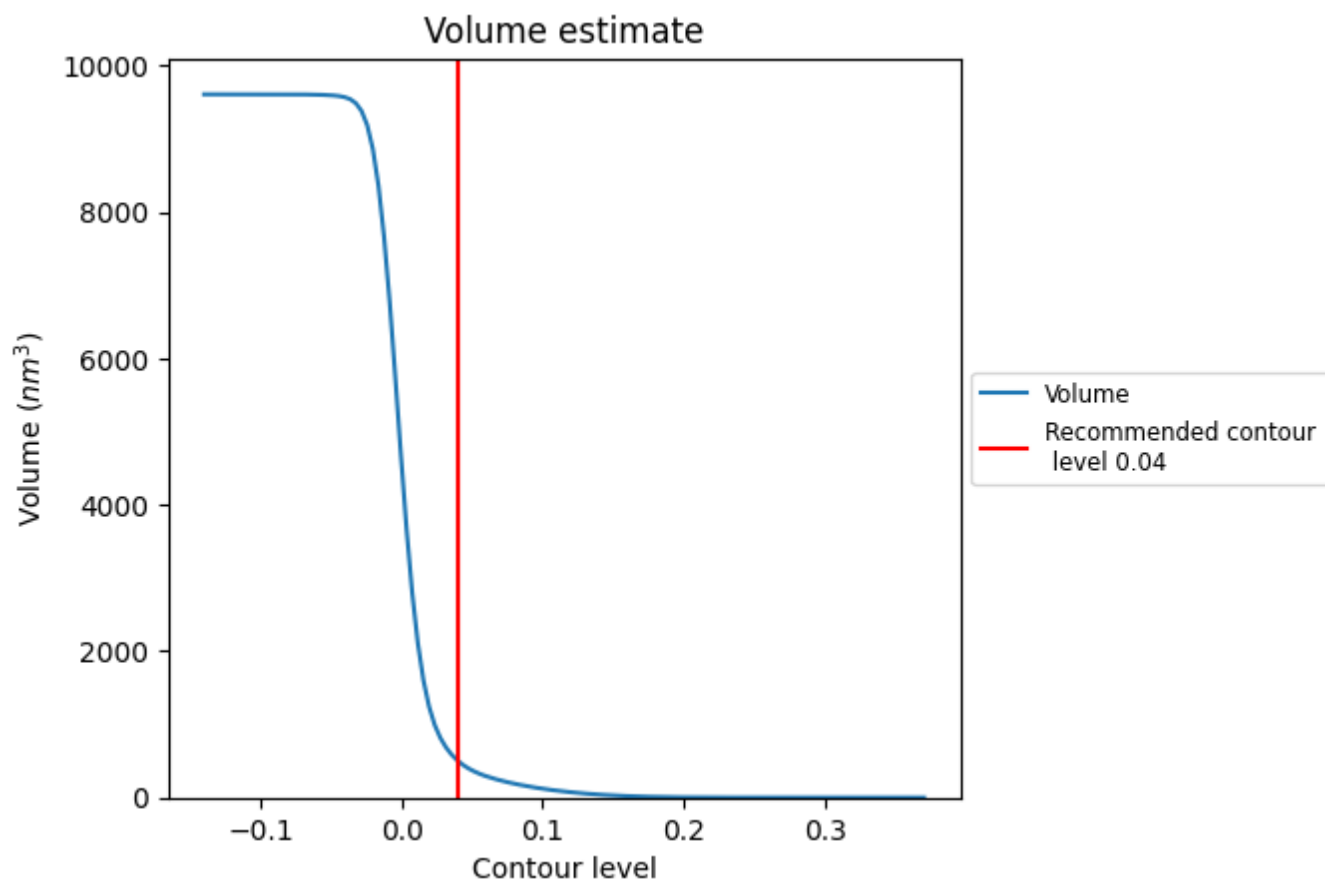
This section contains the results of statistical analysis of the map.

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 500 nm³; this corresponds to an approximate mass of 452 kDa.

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

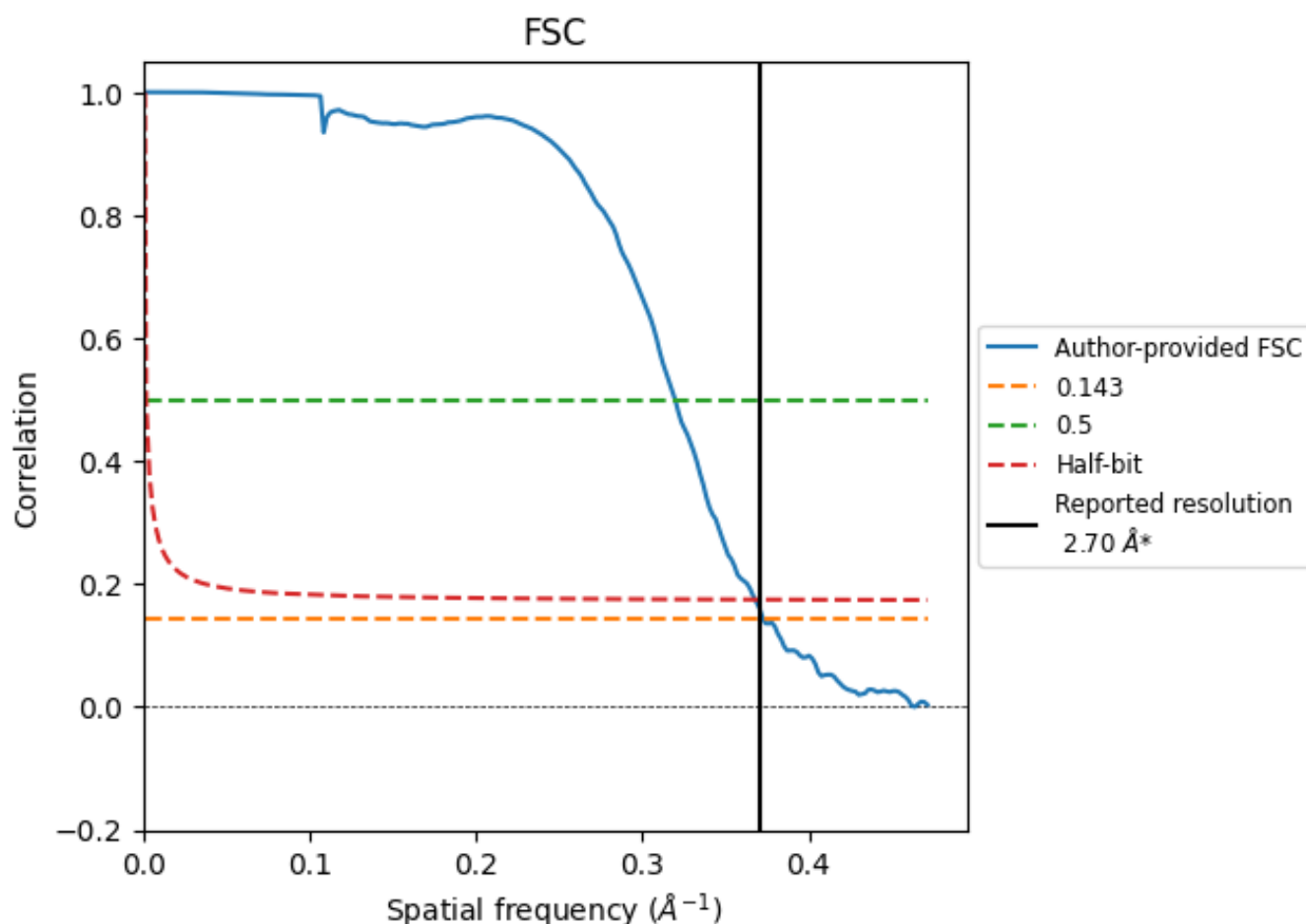
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

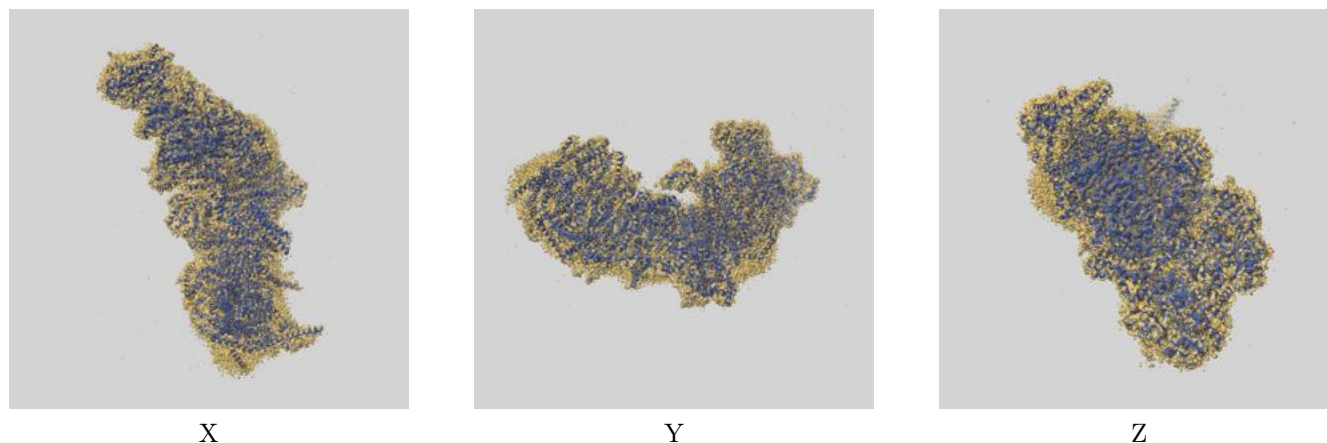
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.68	3.13	2.72
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

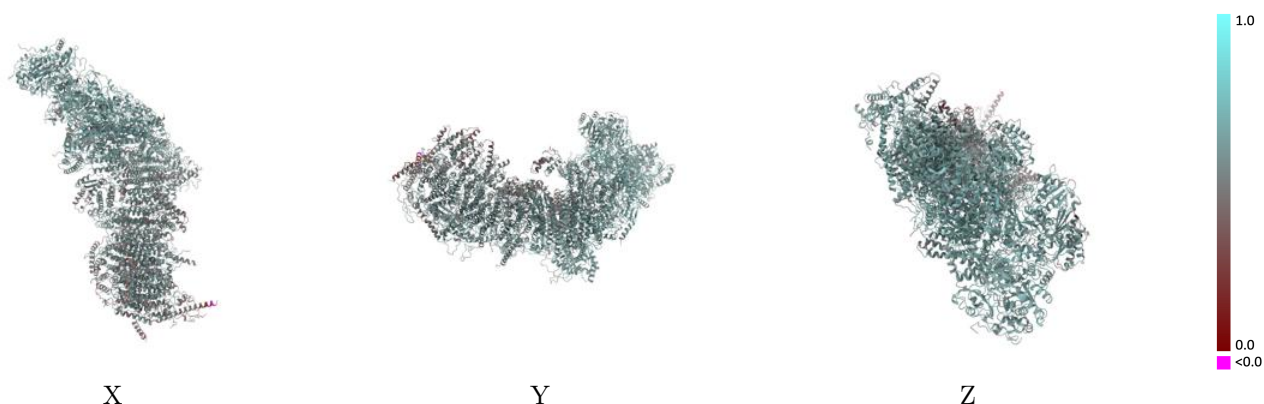
This section contains information regarding the fit between EMDB map EMD-11245 and PDB model 6ZKD. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



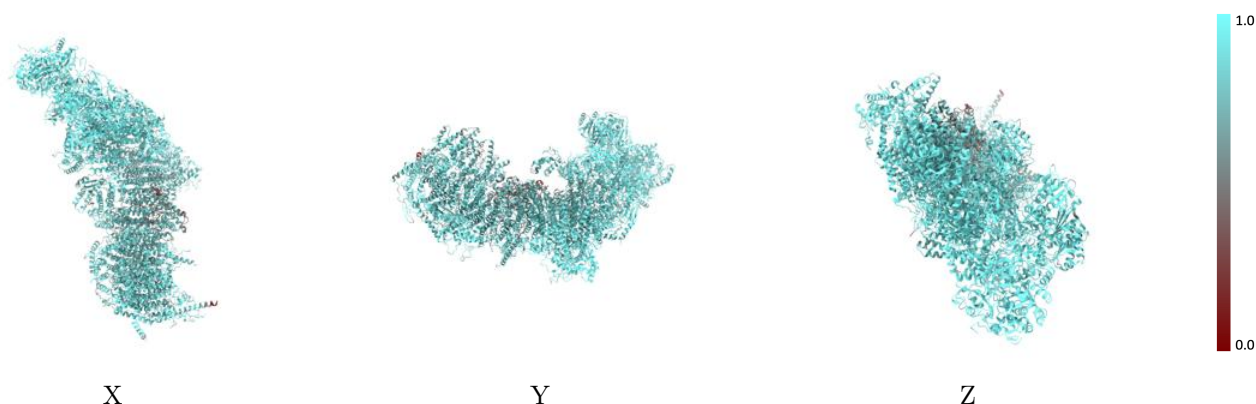
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



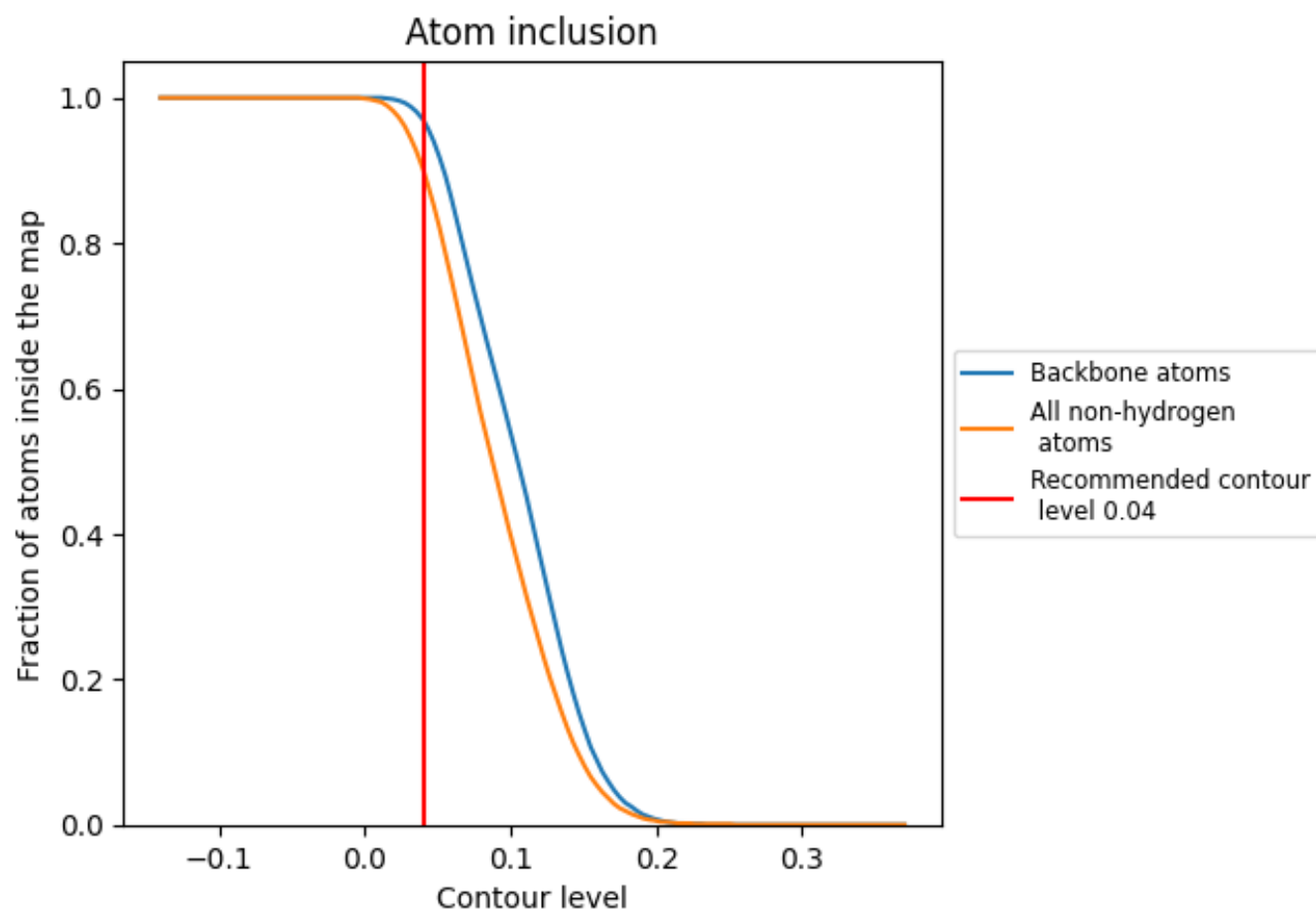
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 90% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9020	 0.5790
1	 0.9630	 0.6050
2	 0.9360	 0.5960
3	 0.9470	 0.6130
4	 0.9370	 0.6240
5	 0.9610	 0.6370
6	 0.9640	 0.6290
9	 0.9650	 0.6400
A	 0.8230	 0.5560
H	 0.9360	 0.6110
J	 0.8600	 0.5580
K	 0.9070	 0.5940
L	 0.8720	 0.5570
M	 0.9380	 0.6060
N	 0.9450	 0.6120
V	 0.5810	 0.4830
W	 0.8970	 0.5820
X	 0.7990	 0.4760
Y	 0.9050	 0.5780
Z	 0.8950	 0.5510
a	 0.9610	 0.6000
b	 0.9420	 0.6210
c	 0.9330	 0.6220
d	 0.9300	 0.5910
e	 0.9020	 0.5590
f	 0.9050	 0.5860
g	 0.9190	 0.6030
h	 0.9380	 0.6140
i	 0.9280	 0.6170
j	 0.7970	 0.4740
k	 0.8720	 0.5490
l	 0.9010	 0.5600
m	 0.9230	 0.5800
n	 0.7830	 0.4420
o	 0.8810	 0.5750



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Chain	Atom inclusion	Q-score
p	 0.8220	 0.5130
q	 0.9460	 0.5930
r	 0.8560	 0.5050
s	 0.8020	 0.4510
t	 0.8290	 0.4980
u	 0.8290	 0.4680
v	 0.8620	 0.5110
w	 0.8560	 0.5480
x	 0.8590	 0.5380
y	 0.8700	 0.5460
z	 0.9440	 0.6020