



Full wwPDB EM Validation Report ⓘ

Aug 5, 2026 – 04:54 AM EDT

PDB ID : 8UD1 / pdb_00008ud1
EMDB ID : EMD-42143
Title : High resolution in-situ structure of complex I in respiratory supercomplex (composite)
Authors : Zheng, W.; Zhu, J.; Zhang, K.
Deposited on : 2023-09-27
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

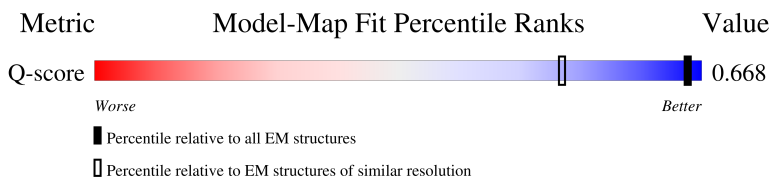
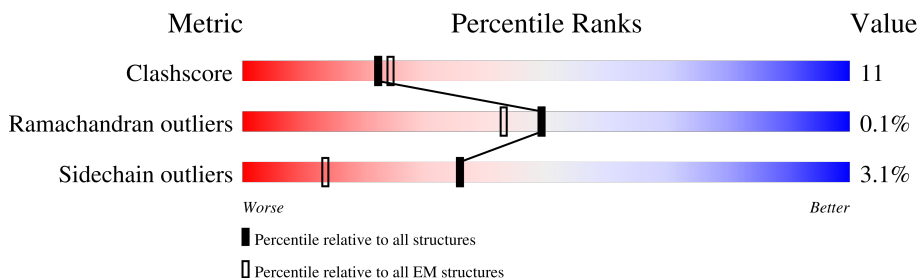
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 2.10 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	2317 (1.60 - 2.60)

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	1A	115	
2	1B	258	
3	1C	264	
4	1D	466	

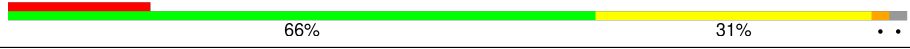
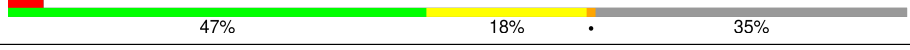
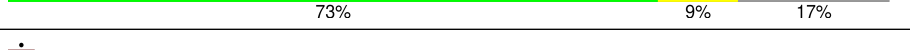
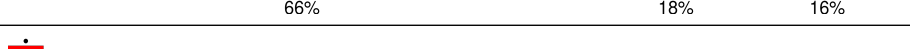
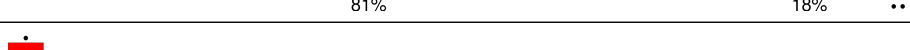
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Mol	Chain	Length	Quality of chain
5	1E	249	
6	1F	464	
7	1G	727	
8	1H	318	
9	1I	239	
10	1J	175	
11	1K	98	
12	1L	606	
13	1M	459	
14	1N	347	
15	1O	357	
16	1P	377	
17	1Q	175	
18	1R	123	
19	1S	99	
20	1T	156	
20	1U	156	
21	1V	116	
22	1W	128	
23	1X	172	
24	1Y	141	
25	1Z	144	
26	1a	70	
27	1b	84	
28	1c	76	

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Mol	Chain	Length	Quality of chain
29	1d	122	
30	1e	106	
31	1f	58	
32	1g	154	
33	1h	189	
34	1i	128	
35	1j	105	
36	1k	98	
37	1l	186	
38	1m	129	
39	1n	179	
40	1o	137	
41	1p	176	
42	1q	145	
43	1r	113	
44	1s	471	

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
46	SF4	1B	201	-	-	X	-

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 72881 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-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	115	Total	C	N	O	S	0	0
			916	616	134	159	7		

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	155	Total	C	N	O	S	0	0
			1242	791	226	211	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	209	Total	C	N	O	S	0	0
			1746	1128	299	317	2		

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	429	Total	C	N	O	S	0	0
			3452	2207	593	628	24		

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	214	Total	C	N	O	S	0	0
			1658	1058	278	312	10		

- Molecule 6 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	432	Total	C	N	O	S	0	0
			3325	2100	592	613	20		

- Molecule 7 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1G	699	Total	C	N	O	S	0	0
			5362	3360	933	1029	40		

- Molecule 8 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1H	318	Total	C	N	O	S	0	0
			2504	1673	385	425	21		

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	1I	176	Total	C	N	O	S	0	0
			1412	887	243	269	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	1J	174	Total	C	N	O	S	0	0
			1329	892	189	236	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	1K	98	Total	C	N	O	S	0	0
			750	494	113	129	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	1L	606	Total	C	N	O	S	0	0
			4818	3195	746	826	51		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	1M	459	Total	C	N	O	S	0	0
			3632	2411	572	610	39		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1N	347	Total	C	N	O	S	0	0
			2712	1783	420	463	46		

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	1O	320	Total	C	N	O	S	0	0
			2590	1649	440	491	10		

- Molecule 16 is a protein called NADH:ubiquinone oxidoreductase subunit A9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	1P	342	Total	C	N	O	S	0	0
			2751	1783	481	478	9		

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	1Q	129	Total	C	N	O	S	0	0
			1047	659	186	199	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1R	96	Total	C	N	O	S	0	0
			741	452	140	146	3		

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1S	87	Total	C	N	O	S	0	0
			700	440	131	127	2		

- Molecule 20 is a protein called NADH:ubiquinone oxidoreductase subunit AB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	1T	85	Total	C	N	O	S	0	0
			689	445	101	138	5		
20	1U	86	Total	C	N	O	S	0	0
			694	448	102	139	5		

- Molecule 21 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1V	115	Total	C	N	O	S	0	0
			927	599	157	168	3		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1W	115	Total	C	N	O	S	0	0
			971	619	179	168	5		

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1X	171	Total	C	N	O	S	0	0
			1398	887	250	251	10		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1Y	139	Total	C	N	O	S	0	0
			1016	648	173	189	6		

- Molecule 25 is a protein called NADH:ubiquinone oxidoreductase subunit A13.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1Z	141	Total	C	N	O	S	1	0
			1179	758	206	206	9		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1a	70	Total	C	N	O	S	0	0
			562	361	101	94	6		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1b	83	Total	C	N	O	S	0	0
			643	417	110	115	1		

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1c	49	Total	C	N	O		0	0
			417	276	71	70			

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	1d	120	Total	C	N	O	S	0	0
			993	646	172	169	6		

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	1e	99	Total	C	N	O	S	1	0
			827	525	155	141	6		

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	1f	57	Total	C	N	O	S	0	0
			487	316	89	80	2		

- Molecule 32 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1g	100	Total	C	N	O	S	0	0
			835	535	138	158	4		

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	1h	138	Total	C	N	O	S	0	0
			1151	754	195	199	3		

- Molecule 34 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	1i	127	Total	C	N	O	S	0	0
			1100	723	194	181	2		

- Molecule 35 is a protein called NADH:ubiquinone oxidoreductase subunit B2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	1j	71	Total	C	N	O	S	0	0
			601	394	99	107	1		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	1k	81	Total	C	N	O	S	0	0
			649	422	110	116	1		

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1l	156	Total	C	N	O	S	0	0
			1310	847	213	242	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	1m	128	Total	C	N	O		0	0
			1062	691	182	189			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	1n	172	Total	C	N	O	S	0	0
			1495	956	273	258	8		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	1o	122	Total	C	N	O	S	0	0
			1045	650	198	187	10		

- Molecule 41 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	1p	173	Total	C	N	O	S	0	0
			1449	908	263	270	8		

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	1q	145	Total	C	N	O	S	0	0
			1212	775	219	213	5		

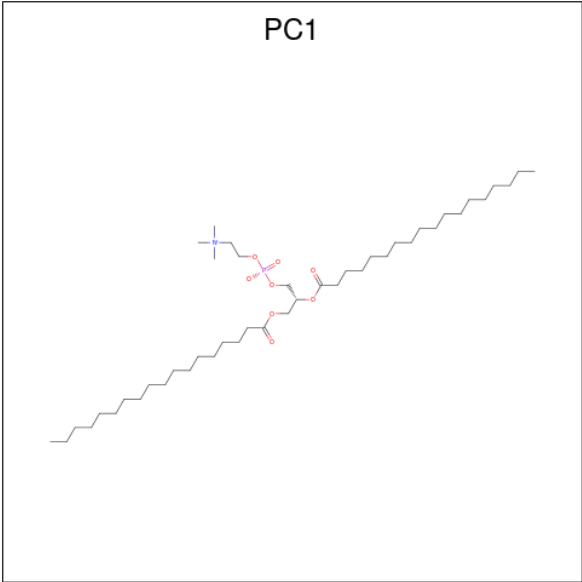
- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	1r	95	Total	C	N	O	S	0	0
			767	483	144	137	3		

- Molecule 44 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial.

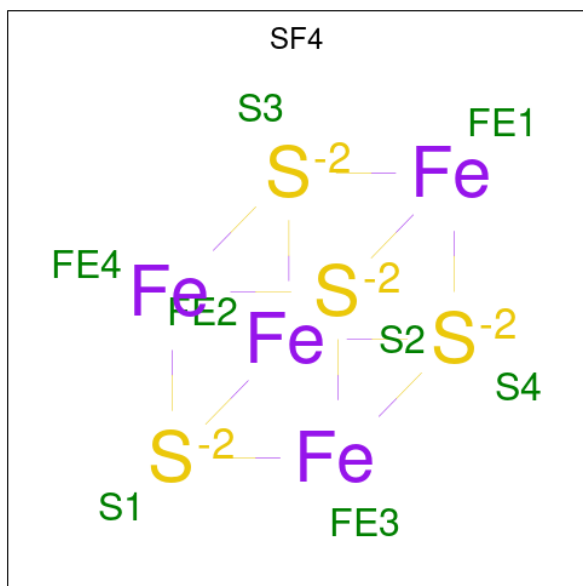
Mol	Chain	Residues	Atoms					AltConf	Trace
44	1s	45	Total	C	N	O	S	0	0
			382	238	70	73	1		

- Molecule 45 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).



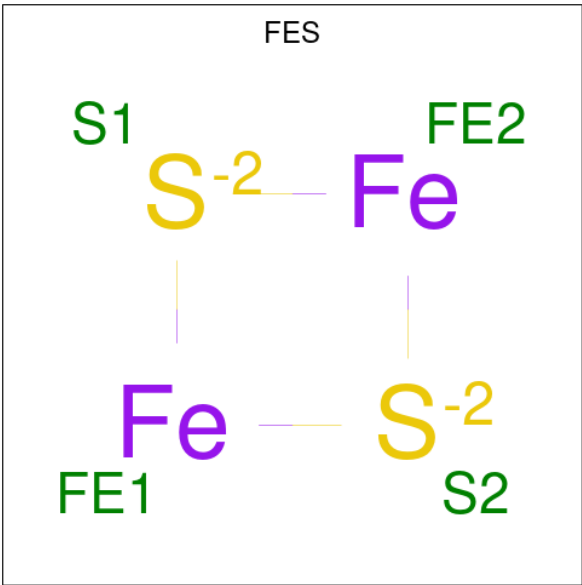
Mol	Chain	Residues	Atoms					AltConf
45	1A	1	Total	C	N	O	P	0
			35	25	1	8	1	
45	1H	1	Total	C	N	O	P	0
			54	44	1	8	1	
45	1H	1	Total	C	N	O	P	0
			48	38	1	8	1	
45	1I	1	Total	C	N	O	P	0
			44	34	1	8	1	
45	1M	1	Total	C	N	O	P	0
			35	25	1	8	1	
45	1M	1	Total	C	N	O	P	0
			44	34	1	8	1	
45	1P	1	Total	C	N	O	P	0
			33	23	1	8	1	
45	1P	1	Total	C	N	O	P	0
			46	36	1	8	1	
45	1d	1	Total	C	N	O	P	0
			39	29	1	8	1	
45	1f	1	Total	C	N	O	P	0
			46	36	1	8	1	
45	1h	1	Total	C	N	O	P	0
			47	37	1	8	1	
45	1m	1	Total	C	N	O	P	0
			46	36	1	8	1	
45	1q	1	Total	C	N	O	P	0
			48	38	1	8	1	
45	1q	1	Total	C	N	O	P	0
			49	39	1	8	1	

- Molecule 46 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



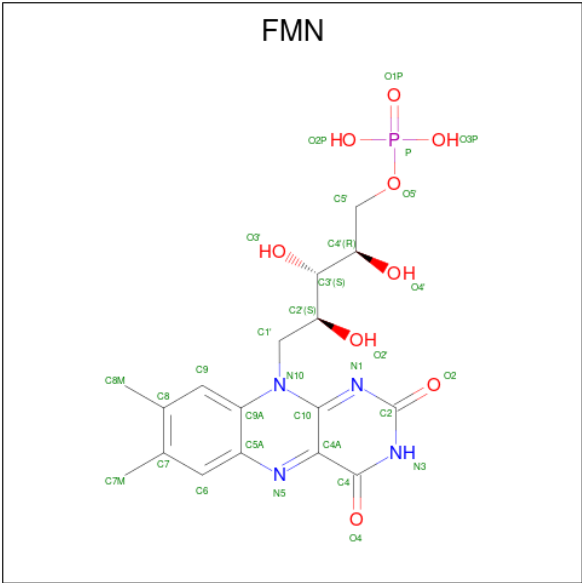
Mol	Chain	Residues	Atoms			AltConf
46	1B	1	Total	Fe	S	0
			8	4	4	
46	1F	1	Total	Fe	S	0
			8	4	4	
46	1G	1	Total	Fe	S	0
			8	4	4	
46	1G	1	Total	Fe	S	0
			8	4	4	
46	1I	1	Total	Fe	S	0
			8	4	4	
46	1I	1	Total	Fe	S	0
			8	4	4	

- Molecule 47 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			AltConf
47	1E	1	Total	Fe	S	0
			4	2	2	
47	1G	1	Total	Fe	S	0
			4	2	2	

- Molecule 48 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P).

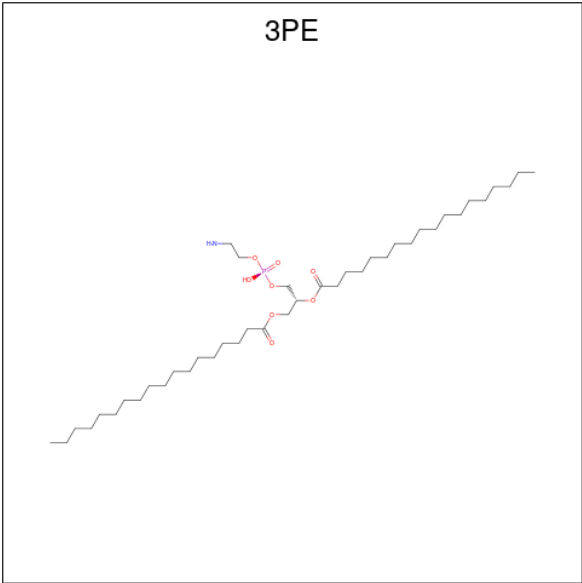


Mol	Chain	Residues	Atoms					AltConf
48	1F	1	Total	C	N	O	P	0
			31	17	4	9	1	

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

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

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



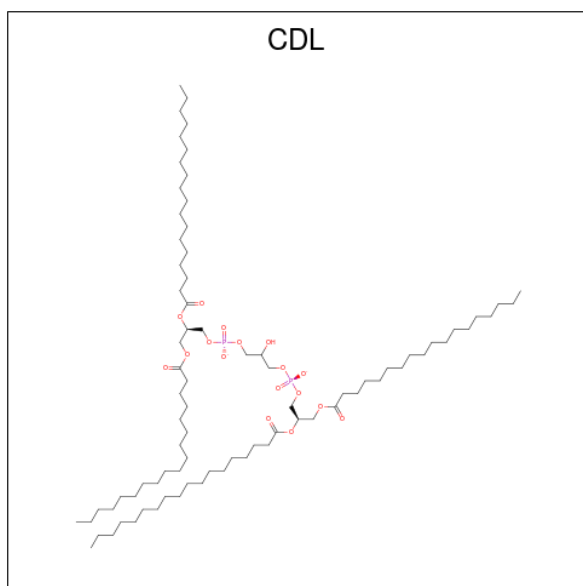
Mol	Chain	Residues	Atoms					AltConf
50	1J	1	Total	C	N	O	P	0
			44	34	1	8	1	
50	1L	1	Total	C	N	O	P	0
			46	36	1	8	1	
50	1L	1	Total	C	N	O	P	0
			45	35	1	8	1	
50	1L	1	Total	C	N	O	P	0
			41	31	1	8	1	
50	1L	1	Total	C	N	O	P	0
			42	32	1	8	1	
50	1M	1	Total	C	N	O	P	0
			45	35	1	8	1	
50	1M	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	1N	1	Total	C	N	O	P	0
			49	39	1	8	1	
50	1N	1	Total	C	N	O	P	0
			33	23	1	8	1	
50	1Y	1	Total	C	N	O	P	0
			31	21	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
50	1Y	1	Total	C	N	O	P	0
			40	30	1	8	1	
50	1Y	1	Total	C	N	O	P	0
			30	20	1	8	1	
50	1Y	1	Total	C	N	O	P	0
			27	17	1	8	1	
50	1b	1	Total	C	N	O	P	0
			47	37	1	8	1	
50	1d	1	Total	C	N	O	P	0
			48	38	1	8	1	
50	1j	1	Total	C	N	O	P	0
			44	34	1	8	1	
50	1m	1	Total	C	N	O	P	0
			50	40	1	8	1	
50	1m	1	Total	C	N	O	P	0
			41	31	1	8	1	

- Molecule 51 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



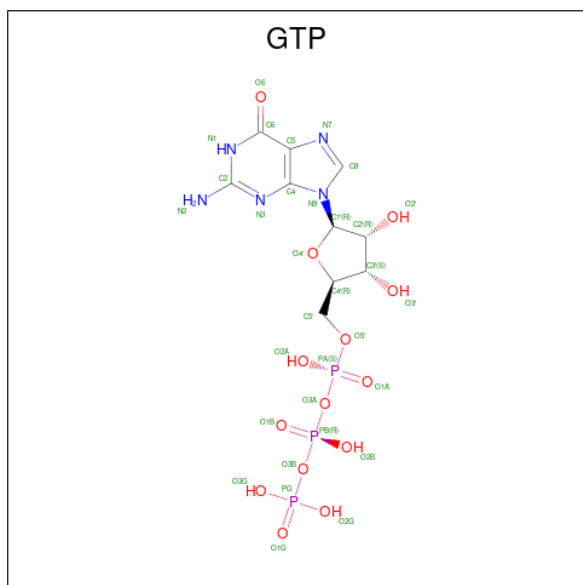
Mol	Chain	Residues	Atoms				AltConf
51	1L	1	Total	C	O	P	0
			87	68	17	2	
51	1N	1	Total	C	O	P	0
			62	43	17	2	
51	1X	1	Total	C	O	P	0
			86	67	17	2	

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Mol	Chain	Residues	Atoms				AltConf
51	1d	1	Total	C	O	P	0
			65	46	17	2	
51	1h	1	Total	C	O	P	0
			80	61	17	2	
51	1q	1	Total	C	O	P	0
			61	42	17	2	

- Molecule 52 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

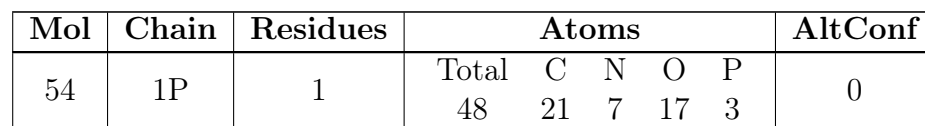


Mol	Chain	Residues	Atoms					AltConf
52	1O	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 54 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).

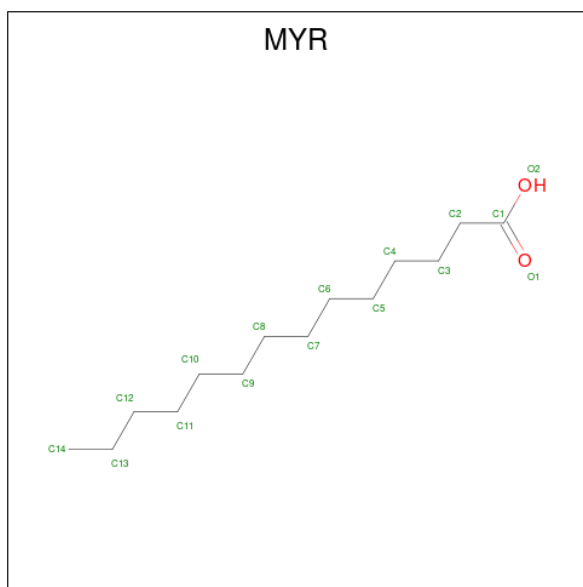


- | Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|-----------------|---------|
| 55 | 1R | 1 | Total Zn
1 1 | 0 |

- # EHZ
-
- The diagram illustrates the chemical structure of Ergosterol (EHZ), a steroid molecule. It features a four-ring steroid nucleus with several substituents: a hydroxyl group at C3, a double bond between C5 and C6, a side chain at C17 containing a double bond, a methyl group, and a phosphate ester group. The structure is labeled with atom numbers (e.g., C1, C2, ..., O10) and includes stereochemical indicators (wedges and dashes) to specify the three-dimensional arrangement of atoms.

Mol	Chain	Residues	Atoms						AltConf
56	1W	1	Total	C	N	O	P	S	0
			37	25	2	8	1	1	
56	1n	1	Total	C	N	O	P	S	0
			37	25	2	8	1	1	

- Molecule 57 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$).



Mol	Chain	Residues	Atoms			AltConf
57	1l	1	Total	C	O	0
			15	14	1	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms		AltConf
58	1A	23	Total	O	0
			23	23	
58	1B	68	Total	O	0
			68	68	
58	1C	131	Total	O	0
			131	131	
58	1D	213	Total	O	0
			213	213	
58	1E	50	Total	O	0
			50	50	
58	1F	105	Total	O	0
			105	105	
58	1G	365	Total	O	0
			365	365	

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Mol	Chain	Residues	Atoms		AltConf
58	1H	75	Total 75	O 75	0
58	1I	83	Total 83	O 83	0
58	1J	40	Total 40	O 40	0
58	1K	27	Total 27	O 27	0
58	1L	277	Total 277	O 277	0
58	1M	221	Total 221	O 221	0
58	1N	156	Total 156	O 156	0
58	1O	126	Total 126	O 126	0
58	1P	207	Total 207	O 207	0
58	1Q	110	Total 110	O 110	0
58	1R	71	Total 71	O 71	0
58	1S	58	Total 58	O 58	0
58	1T	24	Total 24	O 24	0
58	1U	37	Total 37	O 37	0
58	1V	36	Total 36	O 36	0
58	1W	64	Total 64	O 64	0
58	1X	150	Total 150	O 150	0
58	1Y	81	Total 81	O 81	0
58	1Z	92	Total 92	O 92	0
58	1a	34	Total 34	O 34	0
58	1b	42	Total 42	O 42	0

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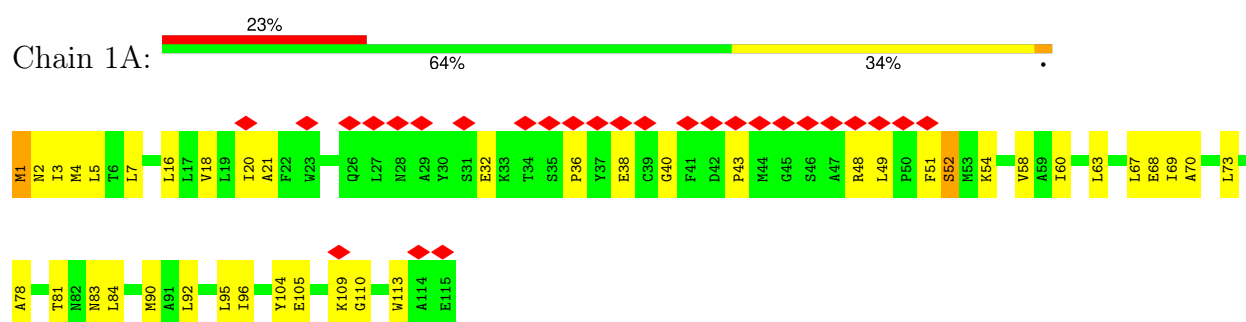
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
58	1c	26	Total 26	O 26	0
58	1d	93	Total 93	O 93	0
58	1e	105	Total 105	O 105	0
58	1f	38	Total 38	O 38	0
58	1g	80	Total 80	O 80	0
58	1h	128	Total 128	O 128	0
58	1i	46	Total 46	O 46	0
58	1j	32	Total 32	O 32	0
58	1k	37	Total 37	O 37	0
58	1l	111	Total 111	O 111	0
58	1m	105	Total 105	O 105	0
58	1n	129	Total 129	O 129	0
58	1o	84	Total 84	O 84	0
58	1p	153	Total 153	O 153	0
58	1q	64	Total 64	O 64	0
58	1r	47	Total 47	O 47	0
58	1s	21	Total 21	O 21	0

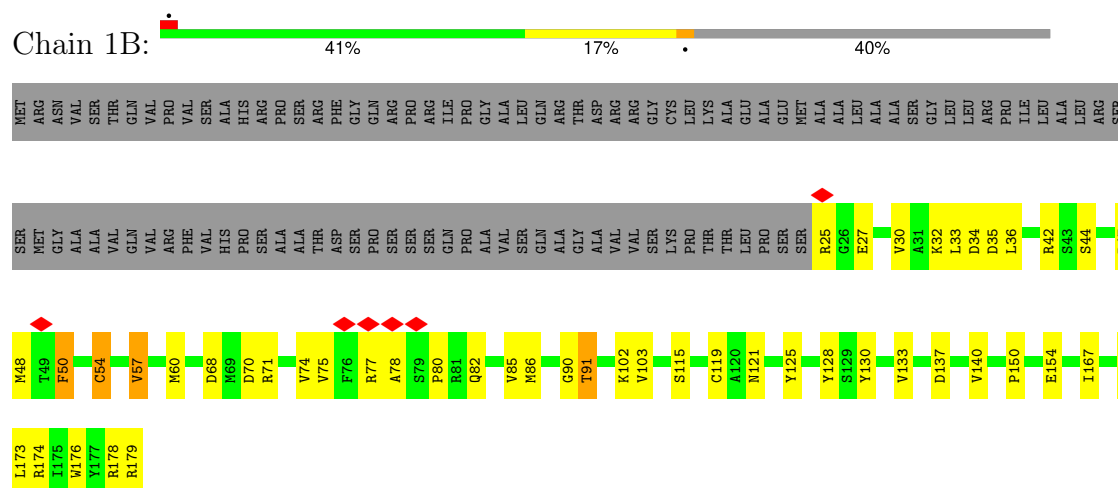
3 Residue-property plots

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

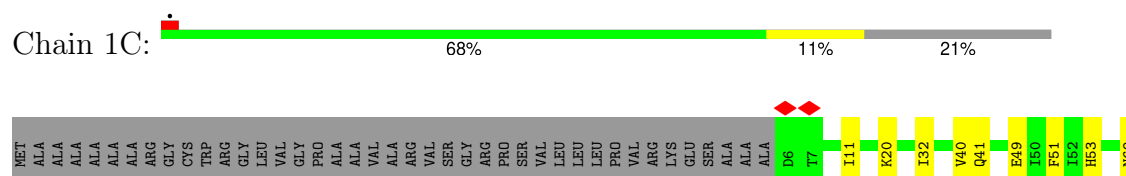
- Molecule 1: NADH-ubiquinone oxidoreductase chain 3

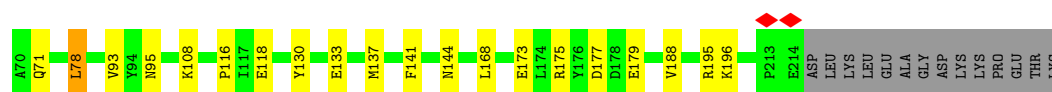


- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial

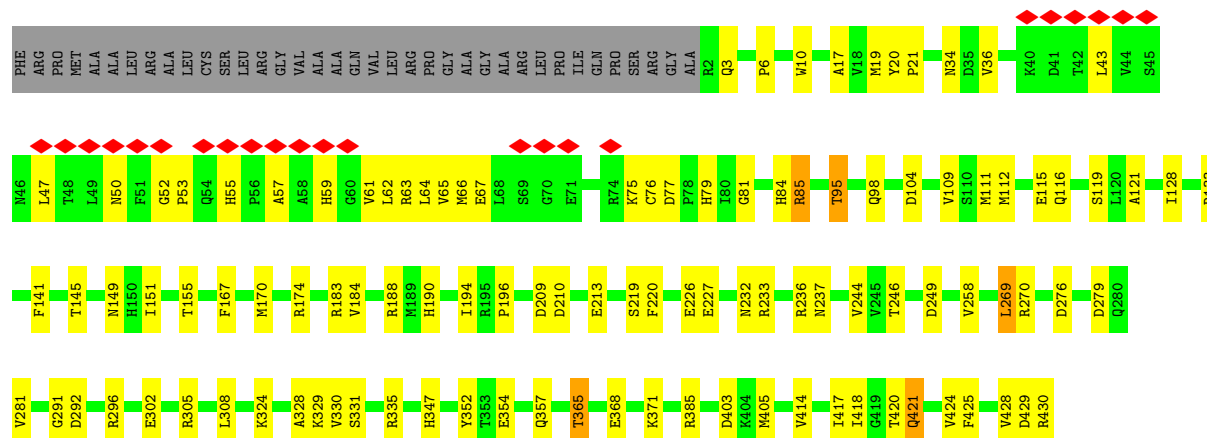


- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial

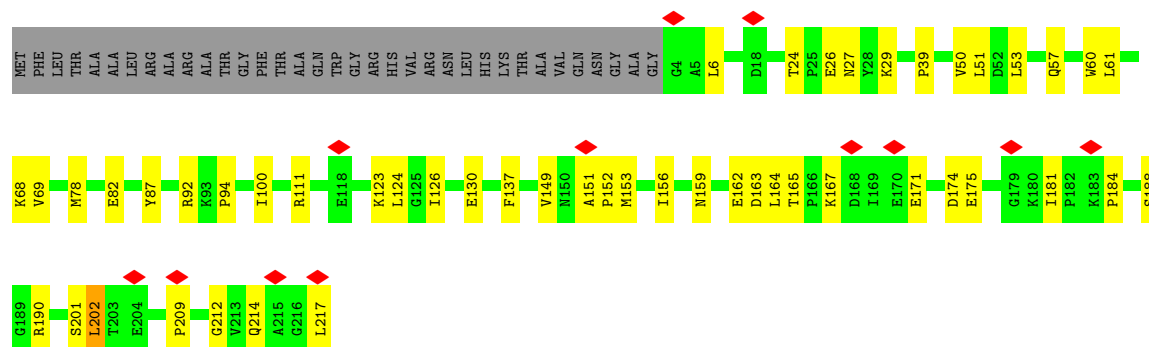




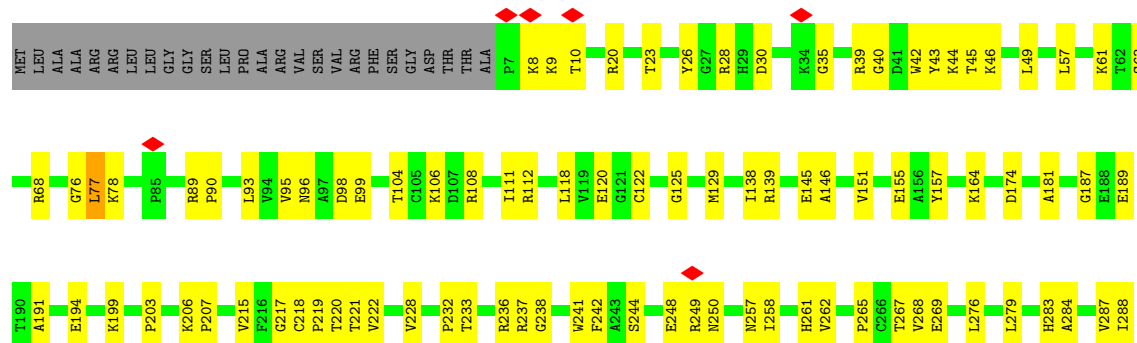
- Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial



- Molecule 5: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial

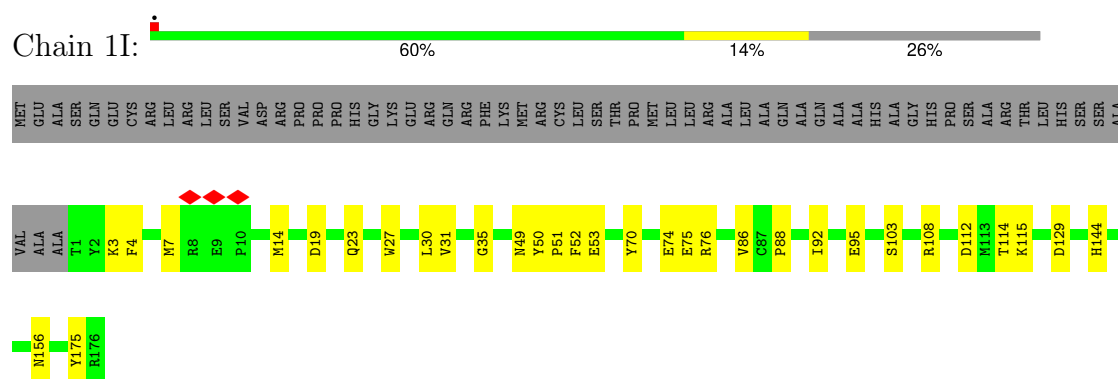


- Molecule 6: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial

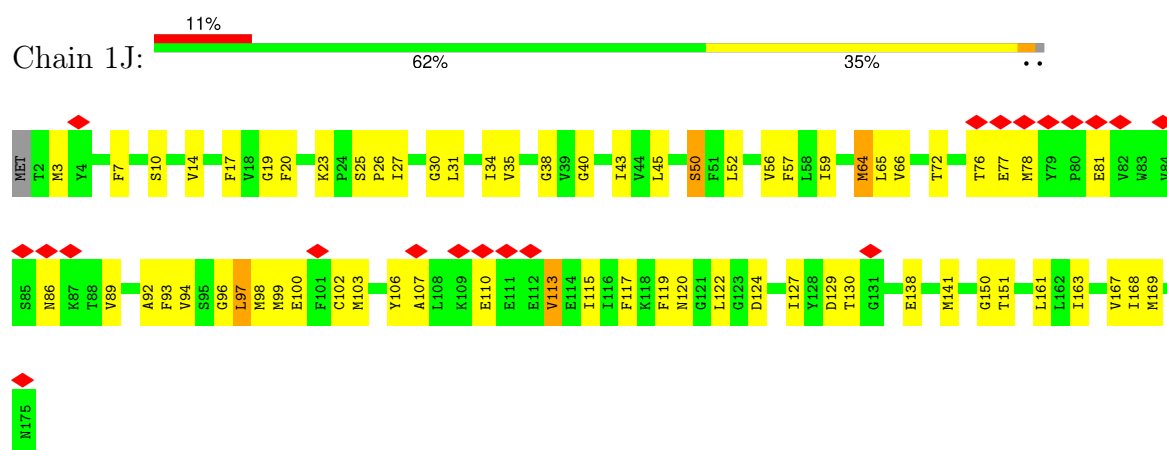




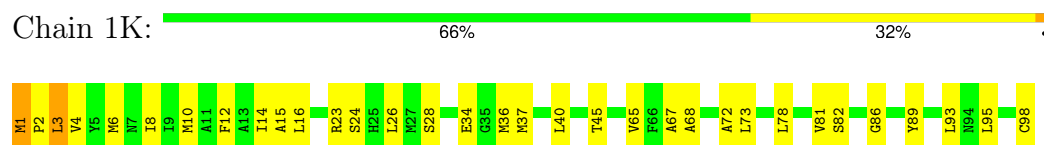
- Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial



- Molecule 10: NADH-ubiquinone oxidoreductase chain 6

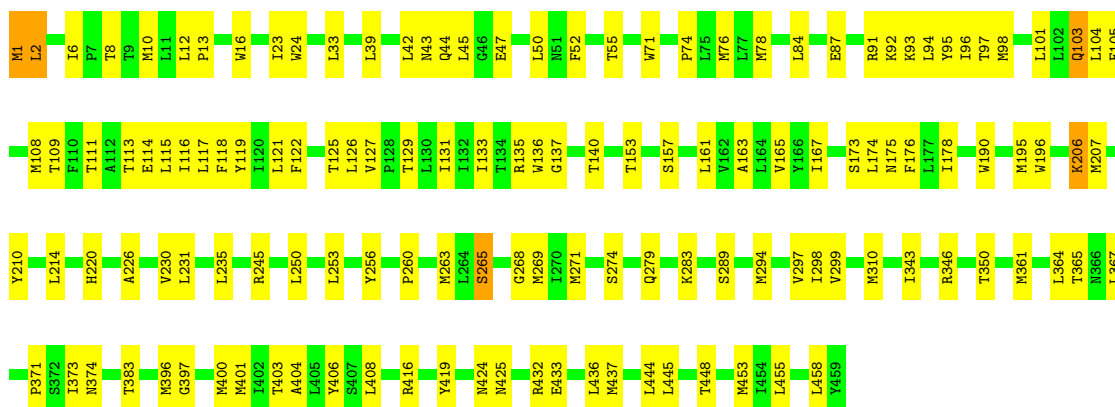
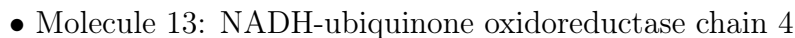


- Molecule 11: NADH-ubiquinone oxidoreductase chain 4L

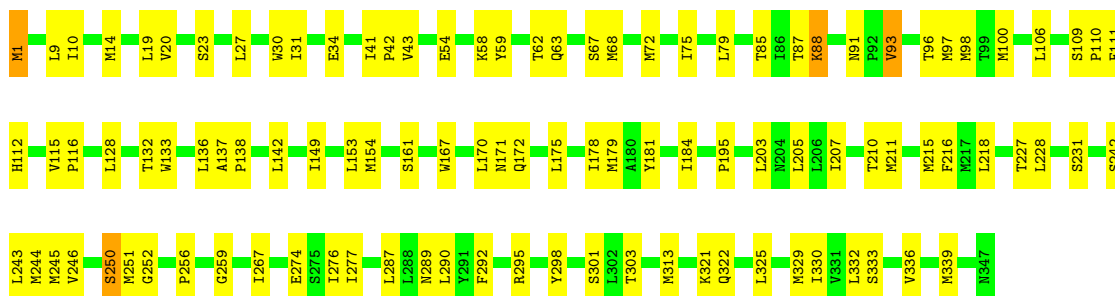


- Molecule 12: NADH-ubiquinone oxidoreductase chain 5

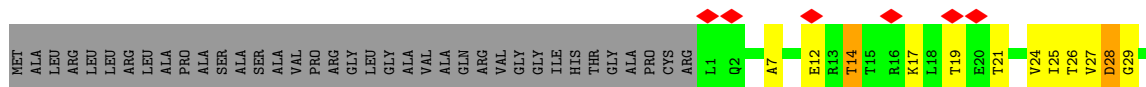


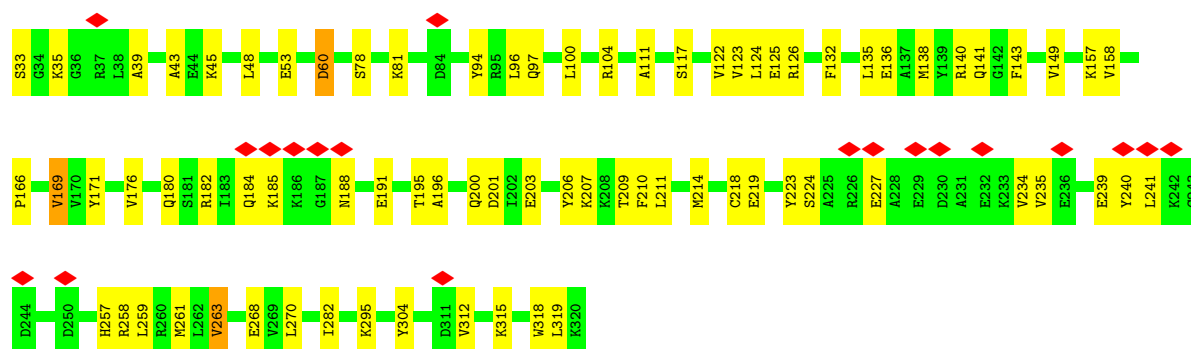


- Molecule 14: NADH-ubiquinone oxidoreductase chain 2

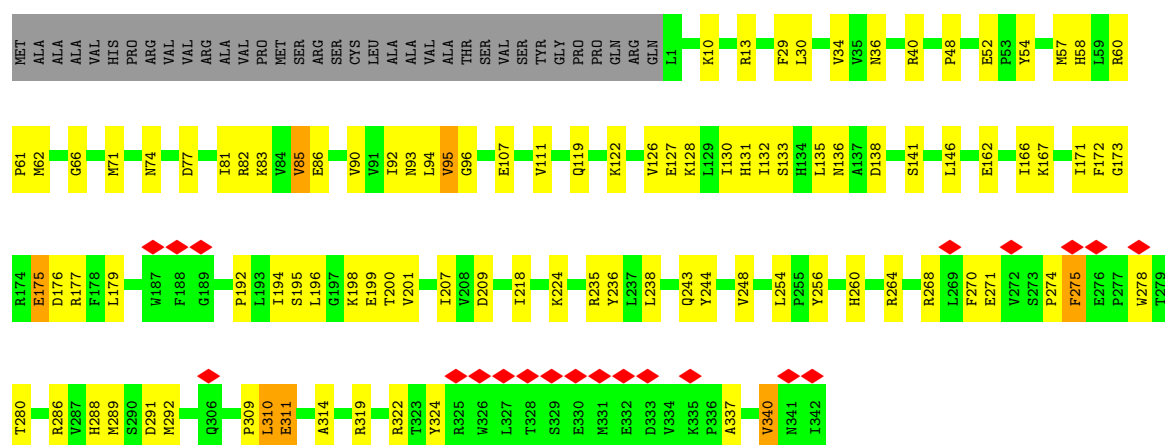


- Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

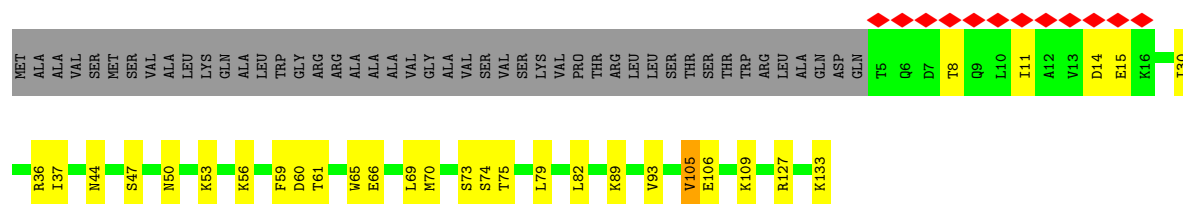




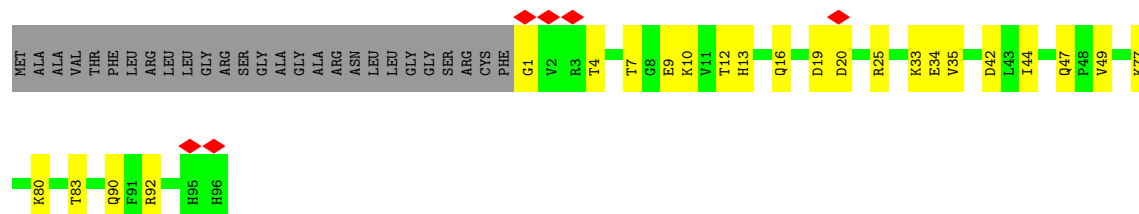
• Molecule 16: NADH:ubiquinone oxidoreductase subunit A9



• Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

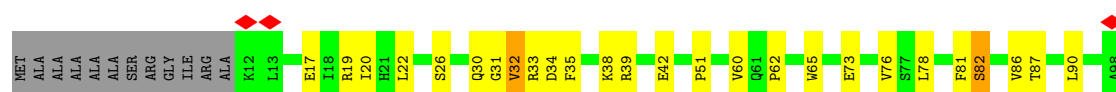


• Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial



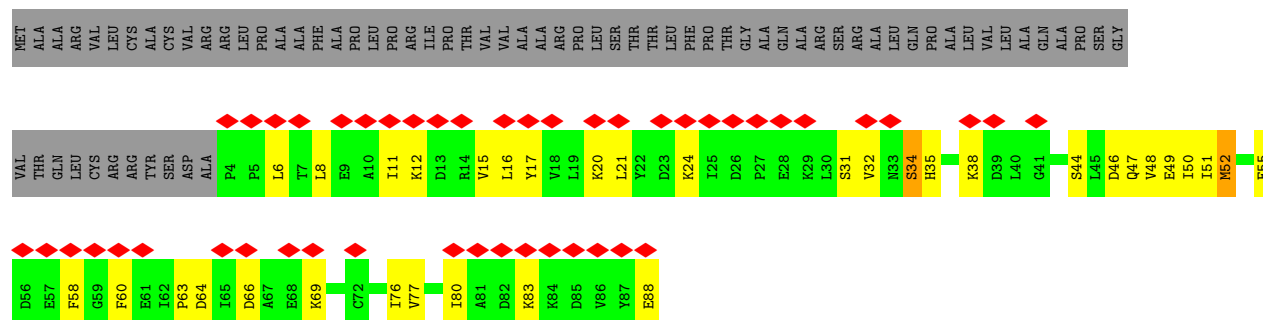
- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

Chain 1S: 

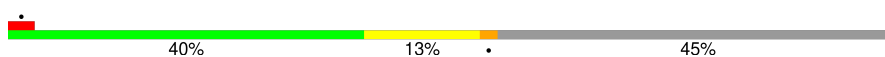


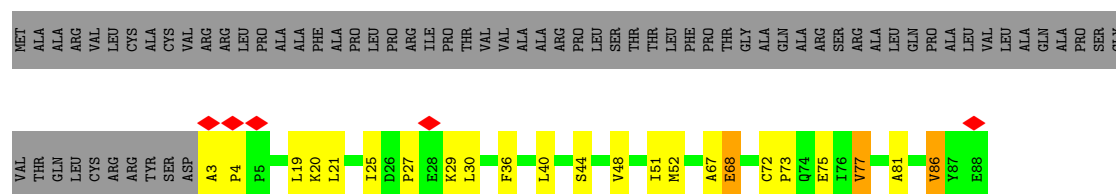
- Molecule 20: NADH:ubiquinone oxidoreductase subunit AB1

Chain 1T: 



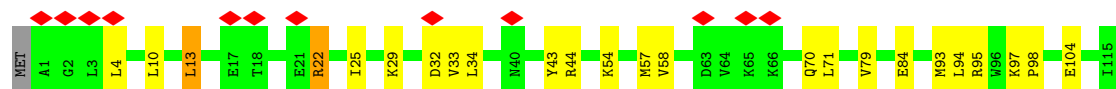
- Molecule 20: NADH:ubiquinone oxidoreductase subunit AB1

Chain 1U: 



- Molecule 21: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform X1

Chain 1V: 



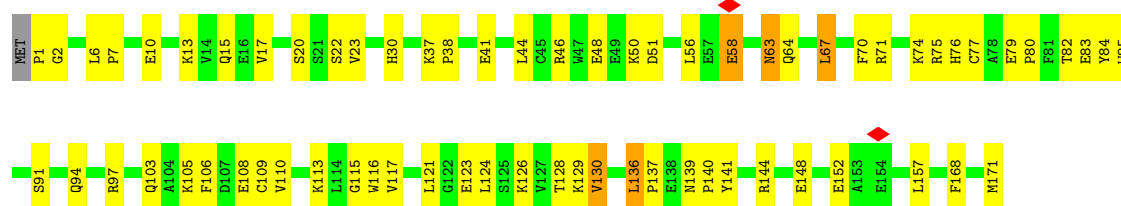
- Molecule 22: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6

Chain 1W: 



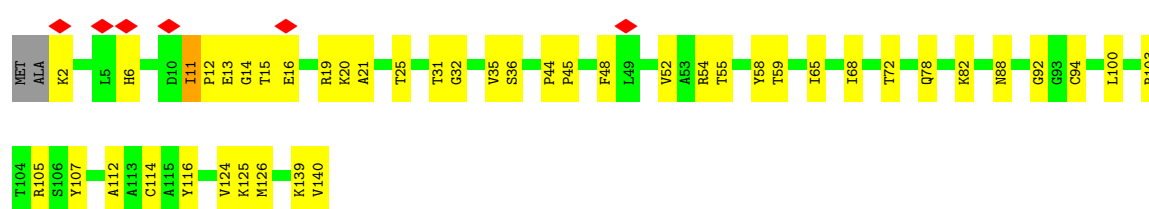
- Molecule 23: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

Chain 1X: 



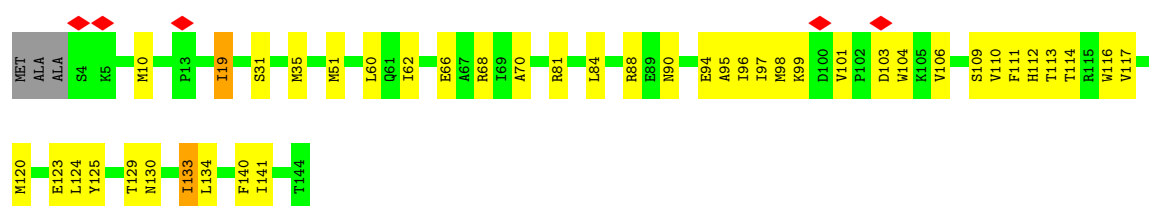
- Molecule 24: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

Chain 1Y: 



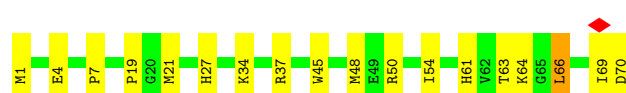
- Molecule 25: NADH:ubiquinone oxidoreductase subunit A13

Chain 1Z: 



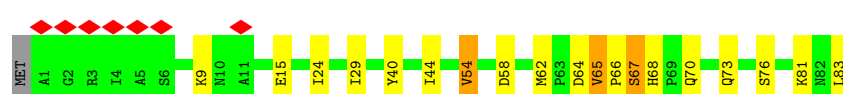
- Molecule 26: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1

Chain 1a: 

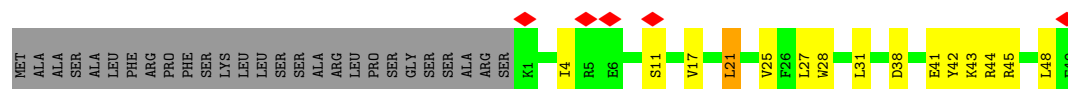


- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

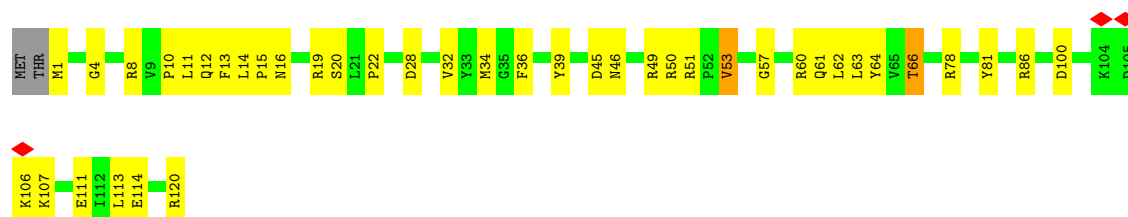
Chain 1b: 



- Molecule 28: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial



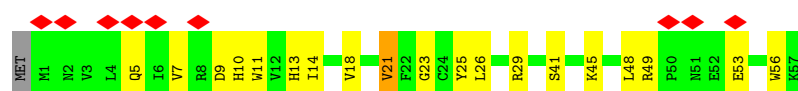
- Molecule 29: NADH dehydrogenase [ubiquinone] 1 subunit C2



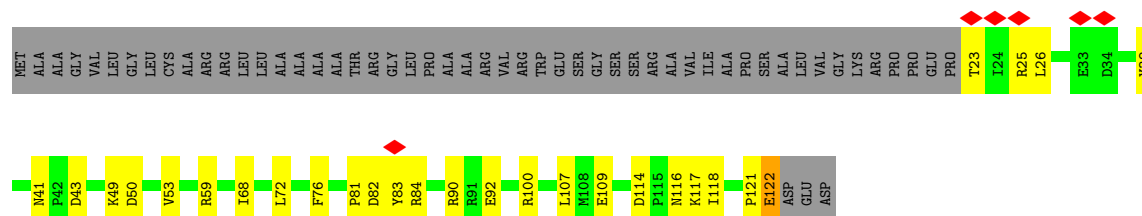
- Molecule 30: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5



- Molecule 31: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1

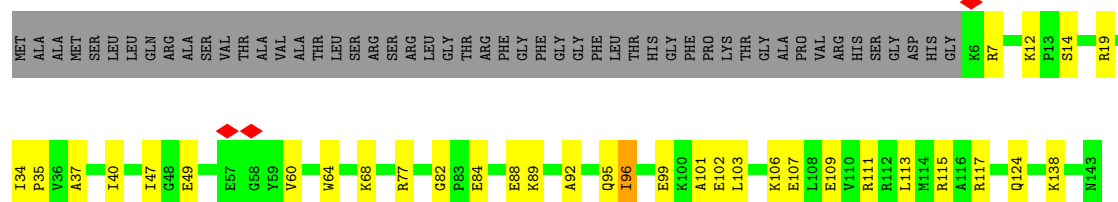


- Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



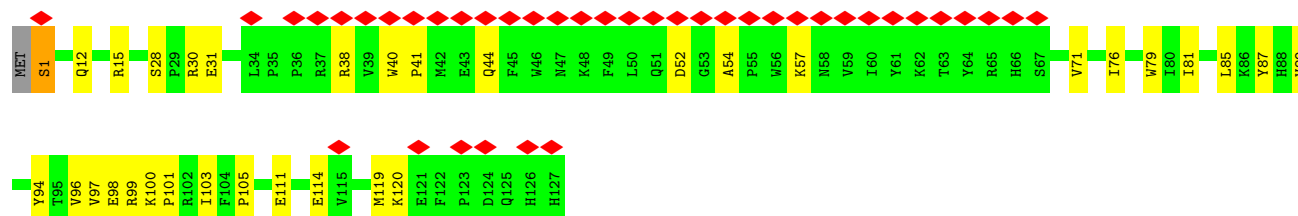
- Molecule 33: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial

Chain 1h: 

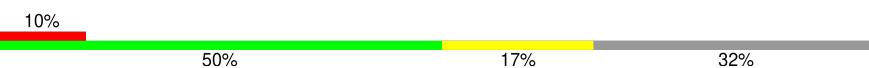


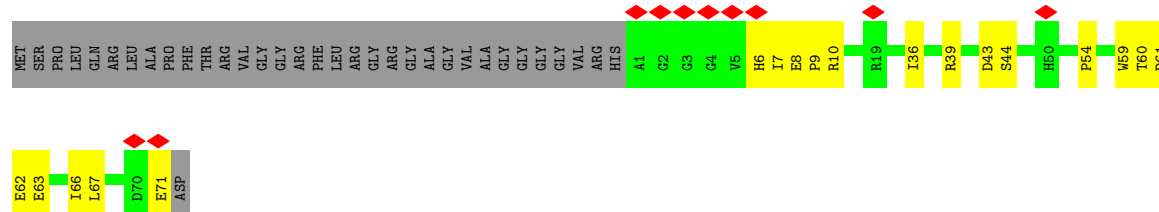
- Molecule 34: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6

Chain 1i: 



- Molecule 35: NADH:ubiquinone oxidoreductase subunit B2

Chain 1j: 



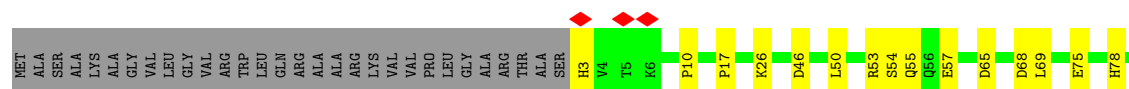
- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3

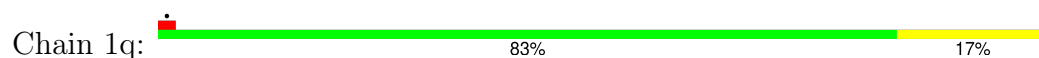
Chain 1k: 



- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

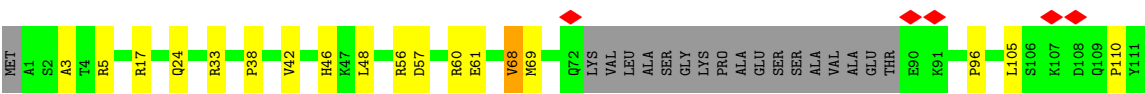
Chain 1l: 





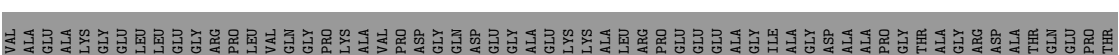
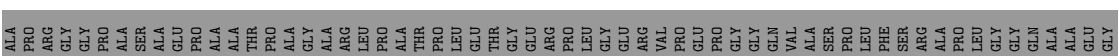
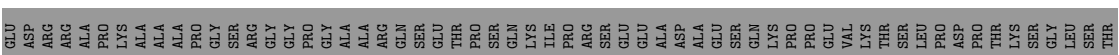
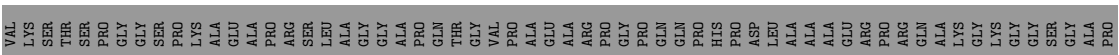
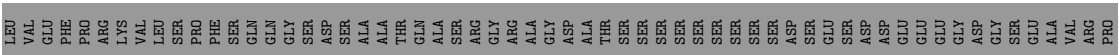
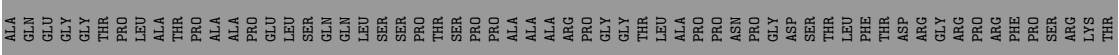
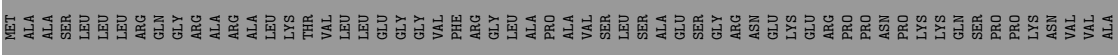


• Molecule 43: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7



L112

• Molecule 44: NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	113902	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.780	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	300.24, 300.24, 300.24	wwPDB
Map dimensions	720, 720, 720	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.417, 0.417, 0.417	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3PE, MG, FES, SAC, GTP, FME, SF4, FMN, EHZ, CDL, MYR, ZN, PC1, K, NDP, AYA

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	1A	0.17	0/930	0.47	0/1271
2	1B	0.16	0/1273	0.40	0/1722
3	1C	0.14	0/1797	0.34	0/2447
4	1D	0.30	2/3545 (0.1%)	0.58	4/4806 (0.1%)
5	1E	0.18	0/1698	0.43	0/2311
6	1F	0.16	0/3401	0.44	0/4595
7	1G	0.16	0/5451	0.41	0/7387
8	1H	0.17	0/2566	0.45	2/3509 (0.1%)
9	1I	0.13	0/1443	0.38	0/1952
10	1J	0.19	0/1364	0.52	0/1850
11	1K	0.20	0/751	0.41	0/1018
12	1L	0.16	0/4939	0.42	0/6718
13	1M	0.17	0/3713	0.39	0/5063
14	1N	0.17	0/2765	0.40	0/3758
15	1O	0.16	0/2650	0.43	0/3588
16	1P	0.21	1/2828 (0.0%)	0.44	2/3834 (0.1%)
17	1Q	0.13	0/1070	0.35	0/1446
18	1R	0.14	0/755	0.36	0/1018
19	1S	0.15	0/711	0.40	0/956
20	1T	0.20	0/701	0.39	0/946
20	1U	0.14	0/706	0.34	0/954
21	1V	0.13	0/946	0.33	0/1281
22	1W	0.15	0/995	0.34	0/1340
23	1X	0.22	0/1436	0.51	1/1938 (0.1%)
24	1Y	0.17	0/1037	0.36	0/1404
25	1Z	0.16	0/1210	0.40	0/1631
26	1a	0.17	0/577	0.36	0/777
27	1b	0.17	0/664	0.46	0/912
28	1c	0.15	0/430	0.39	0/581
29	1d	0.17	0/1024	0.41	0/1384
30	1e	0.17	0/847	0.43	0/1132
31	1f	0.15	0/499	0.38	0/673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	1g	0.15	0/858	0.43	0/1165
33	1h	0.15	0/1184	0.40	0/1603
34	1i	0.15	0/1131	0.43	2/1541 (0.1%)
35	1j	0.15	0/627	0.36	0/858
36	1k	0.12	0/668	0.32	0/903
37	1l	0.66	2/1365 (0.1%)	0.82	3/1867 (0.2%)
38	1m	0.13	0/1092	0.34	0/1481
39	1n	0.15	0/1549	0.38	0/2098
40	1o	0.15	0/1069	0.38	0/1430
41	1p	0.42	3/1481 (0.2%)	0.90	4/1997 (0.2%)
42	1q	0.12	0/1253	0.33	0/1704
43	1r	0.14	0/777	0.35	0/1051
44	1s	0.17	0/394	0.46	0/533
All	All	0.20	8/68170 (0.0%)	0.45	18/92433 (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
4	1D	0	1
8	1H	0	1
All	All	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	1l	17	PRO	CG-CD	-22.18	0.75	1.50
4	1D	21	PRO	CG-CD	-12.08	1.09	1.50
41	1p	19	PRO	CB-CG	-10.10	0.99	1.49
41	1p	19	PRO	CG-CD	-7.15	1.26	1.50
37	1l	17	PRO	N-CD	7.07	1.57	1.47
16	1P	309	PRO	CG-CD	-6.57	1.28	1.50
41	1p	19	PRO	N-CA	5.40	1.53	1.47
4	1D	21	PRO	N-CA	5.29	1.54	1.47

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	1l	17	PRO	N-CD-CG	-23.98	67.24	103.20
41	1p	19	PRO	CB-CG-CD	23.03	179.78	106.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	1D	21	PRO	N-CD-CG	-19.99	73.22	103.20
41	1p	19	PRO	N-CD-CG	-18.35	75.67	103.20
4	1D	21	PRO	CA-CB-CG	-17.70	70.87	104.50
41	1p	19	PRO	CA-CB-CG	-16.35	73.43	104.50
37	1l	17	PRO	CA-CB-CG	-13.60	78.66	104.50
4	1D	21	PRO	CB-CG-CD	12.37	145.67	106.10
37	1l	17	PRO	CB-CG-CD	11.89	144.14	106.10
16	1P	309	PRO	N-CD-CG	-11.06	86.61	103.20
16	1P	309	PRO	CA-CB-CG	-7.38	90.48	104.50
8	1H	91	MET	N-CA-C	-6.55	101.32	109.64
4	1D	21	PRO	CA-N-CD	-6.43	103.00	112.00
34	1i	30	ARG	CA-C-N	6.01	129.02	120.49
34	1i	30	ARG	C-N-CA	6.01	129.02	120.49
41	1p	19	PRO	CA-N-CD	-6.00	103.59	112.00
23	1X	109	CYS	CA-CB-SG	5.61	127.30	114.40
8	1H	124	ASN	CB-CA-C	-5.26	110.48	116.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	1D	421	GLN	Peptide
8	1H	91	MET	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	1A	916	0	950	40	0
2	1B	1242	0	1249	39	0
3	1C	1746	0	1697	24	0
4	1D	3452	0	3389	77	0
5	1E	1658	0	1662	36	0
6	1F	3325	0	3288	93	0
7	1G	5362	0	5388	101	0
8	1H	2504	0	2602	83	0
9	1I	1412	0	1366	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	1J	1329	0	1326	61	0
11	1K	750	0	798	37	0
12	1L	4818	0	4956	143	0
13	1M	3632	0	3836	108	0
14	1N	2712	0	2873	82	0
15	1O	2590	0	2555	58	0
16	1P	2751	0	2776	69	0
17	1Q	1047	0	1042	23	0
18	1R	741	0	704	15	0
19	1S	700	0	719	19	0
20	1T	689	0	687	27	0
20	1U	694	0	691	14	0
21	1V	927	0	972	16	0
22	1W	971	0	975	31	0
23	1X	1398	0	1378	60	0
24	1Y	1016	0	1020	33	0
25	1Z	1179	0	1173	43	0
26	1a	562	0	557	16	0
27	1b	643	0	645	14	0
28	1c	417	0	425	12	0
29	1d	993	0	990	41	0
30	1e	827	0	835	38	0
31	1f	487	0	498	14	0
32	1g	835	0	795	27	0
33	1h	1151	0	1164	30	0
34	1i	1100	0	1107	28	0
35	1j	601	0	546	15	0
36	1k	649	0	626	7	0
37	1l	1310	0	1204	25	0
38	1m	1062	0	1075	18	0
39	1n	1495	0	1434	29	0
40	1o	1045	0	1016	40	0
41	1p	1449	0	1416	36	0
42	1q	1212	0	1174	18	0
43	1r	767	0	792	16	0
44	1s	382	0	351	16	0
45	1A	35	0	44	1	0
45	1H	102	0	161	13	0
45	1I	44	0	62	6	0
45	1M	79	0	109	8	0
45	1P	79	0	106	3	0
45	1d	39	0	52	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	1f	46	0	69	3	0
45	1h	47	0	71	3	0
45	1m	46	0	65	4	0
45	1q	97	0	145	14	0
46	1B	8	0	0	2	0
46	1F	8	0	0	1	0
46	1G	16	0	0	0	0
46	1I	16	0	0	0	0
47	1E	4	0	0	0	0
47	1G	4	0	0	1	0
48	1F	31	0	19	0	0
49	1G	1	0	0	0	0
50	1J	44	0	62	7	0
50	1L	174	0	253	21	0
50	1M	96	0	146	15	0
50	1N	82	0	115	8	0
50	1Y	128	0	155	14	0
50	1b	47	0	71	4	0
50	1d	48	0	73	7	0
50	1j	44	0	65	3	0
50	1m	91	0	136	6	0
51	1L	87	0	124	6	0
51	1N	62	0	68	4	0
51	1X	86	0	125	10	0
51	1d	65	0	77	9	0
51	1h	80	0	104	12	0
51	1q	61	0	66	3	0
52	1O	32	0	12	2	0
53	1O	1	0	0	0	0
54	1P	48	0	26	2	0
55	1R	1	0	0	0	0
56	1W	37	0	0	2	0
56	1n	37	0	0	1	0
57	1l	15	0	27	0	0
58	1A	23	0	0	0	0
58	1B	68	0	0	2	0
58	1C	131	0	0	3	0
58	1D	213	0	0	6	0
58	1E	50	0	0	1	0
58	1F	105	0	0	7	0
58	1G	365	0	0	6	0
58	1H	75	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	1I	83	0	0	0	0
58	1J	40	0	0	0	0
58	1K	27	0	0	0	0
58	1L	277	0	0	13	0
58	1M	221	0	0	16	0
58	1N	156	0	0	5	0
58	1O	126	0	0	4	0
58	1P	207	0	0	7	0
58	1Q	110	0	0	2	0
58	1R	71	0	0	2	0
58	1S	58	0	0	4	0
58	1T	24	0	0	0	0
58	1U	37	0	0	0	0
58	1V	36	0	0	3	0
58	1W	64	0	0	3	0
58	1X	150	0	0	3	0
58	1Y	81	0	0	0	0
58	1Z	92	0	0	4	0
58	1a	34	0	0	1	0
58	1b	42	0	0	1	0
58	1c	26	0	0	4	0
58	1d	93	0	0	5	0
58	1e	105	0	0	3	0
58	1f	38	0	0	1	0
58	1g	80	0	0	5	0
58	1h	128	0	0	5	0
58	1i	46	0	0	2	0
58	1j	32	0	0	2	0
58	1k	37	0	0	2	0
58	1l	111	0	0	2	0
58	1m	105	0	0	3	0
58	1n	129	0	0	4	0
58	1o	84	0	0	4	0
58	1p	153	0	0	5	0
58	1q	64	0	0	0	0
58	1r	47	0	0	0	0
58	1s	21	0	0	0	0
All	All	72881	0	69330	1577	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 11.

All (1577) 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)
23:1X:77:CYS:HB2	23:1X:80:PRO:HD2	1.50	0.93
12:1L:600:THR:HG22	12:1L:601:LEU:H	1.34	0.92
39:1n:130:GLU:HG3	39:1n:134:ARG:HH22	1.37	0.90
9:1I:14:MET:SD	27:1b:9:LYS:NZ	2.46	0.88
6:1F:215:VAL:HG12	6:1F:220:THR:HG21	1.60	0.84
13:1M:364:LEU:HA	13:1M:367:LEU:HD12	1.61	0.83
7:1G:110:GLN:HG3	7:1G:114:CYS:HA	1.60	0.82
6:1F:194:GLU:OE1	17:1Q:133:LYS:NZ	2.12	0.82
29:1d:63:LEU:HD23	51:1d:202:CDL:HA62	1.61	0.82
8:1H:146:LEU:HD11	8:1H:192:GLU:HG3	1.62	0.81
19:1S:26:SER:O	19:1S:33:ARG:NH2	2.14	0.80
8:1H:196:ALA:HB1	8:1H:197:PRO:HD2	1.64	0.78
7:1G:349:PHE:H	7:1G:509:PRO:HB2	1.48	0.78
22:1W:22:SER:HB3	22:1W:27:GLU:HB2	1.66	0.78
2:1B:44:SER:HB2	8:1H:54:LYS:HD3	1.66	0.77
9:1I:156:ASN:ND2	18:1R:34:GLU:OE1	2.18	0.77
33:1h:7:ARG:NH2	34:1i:31:GLU:O	2.17	0.77
6:1F:276:LEU:HD21	6:1F:297:VAL:HG11	1.67	0.76
12:1L:67:HIS:HE2	12:1L:70:THR:HG23	1.51	0.76
13:1M:76:MET:HE3	13:1M:230:VAL:HB	1.68	0.76
12:1L:60:GLU:HG2	12:1L:83:ASP:HA	1.68	0.76
12:1L:161:ARG:NH2	39:1n:87:GLY:O	2.19	0.75
51:1h:201:CDL:H562	34:1i:79:TRP:HB3	1.67	0.75
32:1g:122:GLU:OE2	41:1p:166:ARG:NH2	2.19	0.74
23:1X:139:ASN:ND2	58:1X:3401:HOH:O	2.20	0.74
32:1g:81:PRO:O	58:1g:201:HOH:O	2.05	0.74
22:1W:25:MET:HE1	22:1W:79:VAL:HG21	1.69	0.74
8:1H:32:GLN:OE1	8:1H:34:ARG:NH1	2.23	0.72
44:1s:34:ASP:HB3	44:1s:39:ARG:HH12	1.53	0.72
6:1F:189:GLU:OE2	6:1F:206:LYS:NZ	2.22	0.72
8:1H:88:PRO:HB3	8:1H:98:MET:HE3	1.71	0.72
12:1L:534:HIS:HB3	50:1L:701:3PE:H31	1.70	0.72
9:1I:53:GLU:OE2	42:1q:34:ARG:NH2	2.22	0.72
2:1B:42:ARG:NH1	45:1q:201:PC1:O12	2.21	0.71
39:1n:96:TYR:HB3	39:1n:178:MET:HB3	1.71	0.71
12:1L:562:LEU:HB3	50:1N:901:3PE:H3B2	1.71	0.71
13:1M:23:ILE:HD11	13:1M:93:LYS:HE2	1.70	0.71
20:1U:20:LYS:HD3	20:1U:27:PRO:HB3	1.70	0.71
5:1E:39:PRO:HB3	44:1s:66:PRO:HG2	1.72	0.71
14:1N:109:SER:O	14:1N:112:HIS:ND1	2.21	0.71
4:1D:66:MET:HE1	4:1D:414:VAL:HG21	1.72	0.70
13:1M:214:LEU:O	58:1M:601:HOH:O	2.08	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1F:233:THR:O	6:1F:237:ARG:HB2	1.90	0.70
22:1W:65:GLU:HG2	22:1W:66:MET:HE2	1.72	0.70
14:1N:142:LEU:HD22	14:1N:154:MET:HE1	1.74	0.70
5:1E:100:ILE:HG13	5:1E:156:ILE:HG12	1.74	0.70
10:1J:23:LYS:HE2	11:1K:23:ARG:HG3	1.72	0.70
12:1L:161:ARG:HA	39:1n:91:GLU:HG3	1.74	0.69
20:1U:72:CYS:HB3	20:1U:75:GLU:HG3	1.73	0.69
1:1A:70:ALA:HB2	10:1J:59:ILE:HG12	1.73	0.69
4:1D:95:THR:HG22	4:1D:98:GLN:H	1.56	0.69
20:1T:8:LEU:HD23	20:1T:88:GLU:HG3	1.75	0.69
50:1N:903:3PE:H242	50:1Y:803:3PE:H332	1.73	0.69
6:1F:237:ARG:NH1	58:1F:605:HOH:O	2.25	0.69
41:1p:9:TYR:O	58:1p:201:HOH:O	2.11	0.69
8:1H:85:MET:HE3	8:1H:108:MET:HB2	1.74	0.69
15:1O:24:VAL:HG13	15:1O:166:PRO:HA	1.74	0.69
23:1X:152:GLU:OE1	23:1X:152:GLU:N	2.24	0.69
34:1i:28:SER:HB2	34:1i:31:GLU:HG3	1.74	0.69
11:1K:73:LEU:HD21	14:1N:41:ILE:HG13	1.74	0.69
21:1V:95:ARG:NH1	58:1V:202:HOH:O	2.26	0.69
50:1L:701:3PE:H231	37:1L:88:ARG:HG2	1.74	0.68
6:1F:157:TYR:OH	6:1F:174:ASP:OD1	2.11	0.68
30:1e:29:PRO:HG3	33:1h:138:LYS:HB3	1.75	0.68
34:1i:38:ARG:HH21	34:1i:40:TRP:HA	1.59	0.68
18:1R:1:GLY:N	18:1R:42:ASP:OD1	2.27	0.68
30:1e:88:GLU:OE2	30:1e:88:GLU:N	2.27	0.68
8:1H:149:ILE:HG21	8:1H:185:TRP:HB2	1.74	0.68
4:1D:50:ASN:HB2	4:1D:65:VAL:HG22	1.75	0.68
4:1D:52:GLY:H	4:1D:53:PRO:HD3	1.59	0.68
4:1D:335:ARG:NH2	9:1I:129:ASP:OD2	2.27	0.68
24:1Y:11:ILE:O	24:1Y:20:LYS:NZ	2.27	0.68
7:1G:396:ARG:NH1	7:1G:416:THR:O	2.27	0.67
8:1H:102:VAL:HG21	8:1H:154:LEU:HD11	1.75	0.67
16:1P:128:LYS:HG2	16:1P:224:LYS:HE2	1.76	0.67
13:1M:135:ARG:NH1	58:1M:606:HOH:O	2.28	0.67
1:1A:21:ALA:HB1	8:1H:218:GLY:HA3	1.76	0.67
16:1P:243:GLN:NE2	58:1P:505:HOH:O	2.26	0.67
9:1I:27:TRP:HB3	9:1I:30:LEU:HD12	1.77	0.67
8:1H:189:THR:HG22	8:1H:270:PHE:HZ	1.59	0.67
16:1P:199:GLU:OE2	16:1P:200:THR:OG1	2.12	0.67
40:1o:14:LYS:NZ	58:1o:203:HOH:O	2.27	0.67
12:1L:6:SER:OG	58:1L:801:HOH:O	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1N:313:MET:HG2	15:1O:270:LEU:HD13	1.77	0.67
16:1P:177:ARG:NH2	58:1P:506:HOH:O	2.27	0.67
15:1O:188:ASN:HB3	15:1O:191:GLU:HB2	1.76	0.67
35:1j:62:GLU:OE2	58:1j:201:HOH:O	2.11	0.67
45:1M:504:PC1:H322	51:1h:201:CDL:H111	1.77	0.67
8:1H:99:ASN:ND2	58:1H:502:HOH:O	2.26	0.67
1:1A:36:PRO:HB2	1:1A:43:PRO:HG2	1.77	0.66
38:1m:51:ASN:O	58:1m:301:HOH:O	2.13	0.66
1:1A:60:ILE:HG21	10:1J:168:ILE:HG21	1.76	0.66
4:1D:3:GLN:NE2	13:1M:137:GLY:O	2.28	0.66
7:1G:114:CYS:O	7:1G:115:ASP:HB2	1.93	0.66
7:1G:324:ASP:HB3	7:1G:571:ALA:HB1	1.77	0.66
36:1k:71:LYS:NZ	58:1k:102:HOH:O	2.29	0.66
12:1L:8:THR:HB	12:1L:82:MET:HE3	1.77	0.66
12:1L:13:ILE:HG13	34:1i:81:ILE:HD11	1.76	0.66
12:1L:547:LYS:NZ	58:1L:816:HOH:O	2.28	0.66
16:1P:93:ASN:HD22	16:1P:131:HIS:HD2	1.43	0.66
16:1P:138:ASP:HB3	16:1P:141:SER:HB2	1.76	0.66
2:1B:25:ARG:HG2	2:1B:27:GLU:H	1.61	0.66
13:1M:367:LEU:HD23	13:1M:404:ALA:HA	1.76	0.66
3:1C:40:VAL:HG22	43:1r:69:MET:HB3	1.77	0.66
12:1L:331:MET:HE1	12:1L:468:ILE:HD12	1.76	0.66
20:1U:48:VAL:O	20:1U:52:MET:HG3	1.96	0.66
12:1L:358:LYS:NZ	58:1L:813:HOH:O	2.28	0.66
23:1X:148:GLU:O	30:1e:50:ARG:NH2	2.25	0.66
4:1D:226:GLU:OE1	4:1D:305:ARG:NH2	2.28	0.66
18:1R:16:GLN:OE1	18:1R:33:LYS:NZ	2.27	0.66
18:1R:47:GLN:NE2	58:1R:304:HOH:O	2.28	0.66
6:1F:95:VAL:HG11	6:1F:118:LEU:HD11	1.77	0.65
7:1G:533:THR:HA	7:1G:556:MET:HE1	1.77	0.65
51:1q:203:CDL:H172	51:1q:203:CDL:H331	1.77	0.65
5:1E:6:LEU:O	5:1E:92:ARG:NH2	2.29	0.65
4:1D:328:ALA:HB3	7:1G:126:ASP:HB2	1.78	0.65
25:1Z:120:MET:HE3	30:1e:68:ARG:HG3	1.78	0.65
38:1m:107:ASP:OD1	58:1m:302:HOH:O	2.15	0.65
17:1Q:8:THR:HB	22:1W:18:LYS:HB3	1.79	0.65
27:1b:66:PRO:HA	27:1b:73:GLN:HB2	1.77	0.65
42:1q:106:ARG:HB2	42:1q:109:ILE:HG13	1.78	0.65
44:1s:58:LEU:HD23	44:1s:61:PHE:HE1	1.60	0.65
12:1L:159:HIS:HB2	13:1M:416:ARG:HG2	1.79	0.65
3:1C:179:GLU:OE1	16:1P:40:ARG:NH2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1M:125:THR:OG1	58:1M:602:HOH:O	2.15	0.64
15:1O:27:VAL:HG21	15:1O:39:ALA:HB2	1.78	0.64
23:1X:10:GLU:HA	23:1X:13:LYS:HG3	1.80	0.64
4:1D:116:GLN:NE2	4:1D:276:ASP:OD2	2.28	0.64
11:1K:95:LEU:HD23	11:1K:95:LEU:H	1.62	0.64
13:1M:260:PRO:HG3	50:1m:202:3PE:H372	1.80	0.64
24:1Y:139:LYS:HG3	24:1Y:140:VAL:HG13	1.78	0.64
12:1L:545:SER:OG	13:1M:274:SER:O	2.16	0.64
24:1Y:16:GLU:OE1	24:1Y:19:ARG:NH1	2.31	0.64
12:1L:118:PHE:O	12:1L:122:VAL:HG23	1.98	0.64
16:1P:136:ASN:HD22	16:1P:292:MET:HG3	1.62	0.64
29:1d:107:LYS:NZ	58:1d:305:HOH:O	2.30	0.64
41:1p:166:ARG:NH1	58:1p:207:HOH:O	2.30	0.64
6:1F:112:ARG:HB3	6:1F:145:GLU:HG3	1.78	0.64
12:1L:561:ILE:HG23	45:1m:201:PC1:H291	1.78	0.64
2:1B:35:ASP:HB3	45:1q:202:PC1:H342	1.79	0.64
4:1D:227:GLU:OE1	43:1r:17:ARG:NH2	2.30	0.64
6:1F:294:LEU:HD11	6:1F:297:VAL:HG23	1.79	0.64
34:1i:41:PRO:HA	34:1i:44:GLN:HB2	1.79	0.64
14:1N:210:THR:HG23	14:1N:329:MET:HE3	1.80	0.64
20:1T:35:HIS:HD2	20:1T:38:LYS:H	1.46	0.63
20:1T:76:ILE:O	20:1T:80:ILE:HG12	1.98	0.63
23:1X:137:PRO:HB2	23:1X:140:PRO:HG3	1.78	0.63
25:1Z:90:ASN:ND2	25:1Z:123:GLU:O	2.32	0.63
37:1l:158:ILE:HD13	40:1o:99:LYS:HB3	1.80	0.63
40:1o:91:HIS:O	40:1o:95:VAL:HG23	1.98	0.63
7:1G:150:MET:HE2	7:1G:150:MET:HA	1.79	0.63
7:1G:477:ILE:HD11	7:1G:489:VAL:HG11	1.80	0.63
45:1H:402:PC1:H2I3	10:1J:35:VAL:HG13	1.80	0.63
10:1J:167:VAL:HG22	14:1N:42:PRO:HG2	1.81	0.63
51:1L:705:CDL:H142	13:1M:361:MET:HE1	1.79	0.63
14:1N:332:LEU:HD21	51:1d:202:CDL:H431	1.79	0.63
20:1T:12:LYS:HE2	20:1T:32:VAL:HG13	1.81	0.63
37:1l:98:TRP:HA	37:1l:101:MET:HE3	1.81	0.63
37:1l:55:GLN:NE2	37:1l:69:LEU:O	2.27	0.63
45:1q:201:PC1:H332	45:1q:202:PC1:H262	1.80	0.63
4:1D:385:ARG:NH2	58:1D:509:HOH:O	2.31	0.63
6:1F:262:VAL:HG11	6:1F:284:ALA:HB1	1.81	0.63
8:1H:91:MET:O	8:1H:93:TYR:N	2.32	0.63
13:1M:374:ASN:ND2	58:1M:613:HOH:O	2.31	0.63
6:1F:257:ASN:ND2	6:1F:267:THR:OG1	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1i:120:LYS:HD3	40:1o:39:VAL:HA	1.81	0.62
2:1B:34:ASP:HB3	2:1B:174:ARG:HH21	1.63	0.62
7:1G:615:THR:HG22	7:1G:618:GLN:H	1.63	0.62
13:1M:195:MET:HG3	50:1M:501:3PE:H221	1.81	0.62
17:1Q:14:ASP:OD1	17:1Q:15:GLU:N	2.32	0.62
38:1m:88:LEU:HD22	38:1m:92:PHE:HE2	1.64	0.62
3:1C:195:ARG:NH2	9:1I:92:ILE:O	2.32	0.62
12:1L:383:MET:HE2	35:1j:36:ILE:HD13	1.82	0.62
18:1R:20:ASP:O	18:1R:25:ARG:NH2	2.33	0.62
25:1Z:125:TYR:HB3	25:1Z:133:ILE:HG22	1.82	0.62
2:1B:178:ARG:NH1	58:1B:305:HOH:O	2.31	0.62
4:1D:188:ARG:NH1	58:1D:510:HOH:O	2.32	0.62
6:1F:367:GLU:OE1	7:1G:179:ASN:ND2	2.32	0.62
14:1N:87:THR:HG22	14:1N:88:LYS:H	1.63	0.62
21:1V:57:MET:HE2	21:1V:70:GLN:HG2	1.82	0.62
23:1X:7:PRO:HG2	25:1Z:84:LEU:HD13	1.82	0.62
23:1X:148:GLU:CD	23:1X:148:GLU:H	2.08	0.61
29:1d:49:ARG:NH1	58:1d:302:HOH:O	2.25	0.61
29:1d:106:LYS:HG3	41:1p:77:GLU:HB3	1.81	0.61
4:1D:50:ASN:HA	4:1D:65:VAL:HA	1.83	0.61
7:1G:199:ILE:HA	7:1G:202:ILE:HG12	1.82	0.61
8:1H:223:PHE:O	8:1H:227:GLU:HG2	2.01	0.61
10:1J:40:GLY:HA2	10:1J:43:ILE:HD12	1.82	0.61
12:1L:176:ARG:HB3	13:1M:401:MET:HG2	1.81	0.61
4:1D:34:ASN:HB3	15:1O:158:VAL:HG13	1.82	0.61
15:1O:25:ILE:HB	15:1O:123:VAL:HG12	1.81	0.61
42:1q:78:ASP:OD1	42:1q:80:SER:OG	2.14	0.61
50:1J:201:3PE:H3F2	11:1K:10:MET:HE1	1.82	0.61
13:1M:10:MET:HE2	13:1M:10:MET:HA	1.81	0.61
14:1N:172:GLN:HB2	14:1N:178:ILE:HG13	1.81	0.61
5:1E:100:ILE:HD11	5:1E:137:PHE:HD1	1.65	0.61
11:1K:26:LEU:HB3	11:1K:78:LEU:HD12	1.82	0.61
12:1L:147:VAL:HG13	12:1L:252:MET:HG3	1.82	0.61
20:1U:68:GLU:HG3	34:1i:1:SAC:H2A2	1.82	0.61
6:1F:306:LEU:HD22	6:1F:343:ILE:HD11	1.83	0.61
8:1H:292:SER:OG	45:1H:401:PC1:O32	2.18	0.61
12:1L:295:GLN:O	12:1L:425:ARG:NH1	2.34	0.61
6:1F:261:HIS:CD2	6:1F:338:ASP:H	2.19	0.61
7:1G:362:TYR:O	7:1G:494:HIS:NE2	2.29	0.61
12:1L:62:ILE:HG12	41:1p:114:GLN:HG2	1.82	0.61
16:1P:94:LEU:HD23	16:1P:132:ILE:HG13	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1q:75:TRP:H	45:1q:202:PC1:H131	1.66	0.61
7:1G:359:ARG:NH2	58:1G:924:HOH:O	2.34	0.61
50:1L:702:3PE:H262	51:1h:201:CDL:HB31	1.82	0.61
16:1P:244:TYR:HB2	16:1P:337:ALA:HB2	1.81	0.61
26:1a:70:ASP:O	58:1a:101:HOH:O	2.16	0.61
42:1q:60:ARG:HH22	42:1q:95:ASP:HA	1.65	0.61
14:1N:218:LEU:HB3	14:1N:244:MET:HE2	1.82	0.60
29:1d:15:PRO:HG2	29:1d:81:TYR:CZ	2.36	0.60
45:1d:203:PC1:O14	45:1d:203:PC1:H2	2.01	0.60
30:1e:88:GLU:HB3	30:1e:90:LYS:HE2	1.83	0.60
33:1h:37:ALA:HA	51:1h:201:CDL:H742	1.83	0.60
7:1G:194:GLU:HG2	7:1G:195:LEU:HG	1.83	0.60
10:1J:127:ILE:HA	25:1Z:120:MET:HE2	1.84	0.60
8:1H:65:THR:O	8:1H:124:ASN:ND2	2.35	0.60
14:1N:274:GLU:OE2	24:1Y:139:LYS:HE2	2.01	0.60
4:1D:112:MET:HA	4:1D:115:GLU:HG2	1.84	0.60
8:1H:187:ILE:HD11	45:1H:401:PC1:H271	1.83	0.60
50:1J:201:3PE:H221	50:1Y:804:3PE:H321	1.84	0.60
31:1f:56:TRP:HE1	33:1h:88:GLU:HG3	1.67	0.60
15:1O:224:SER:OG	15:1O:227:GLU:OE1	2.17	0.60
4:1D:65:VAL:HB	4:1D:77:ASP:HB3	1.83	0.60
14:1N:97:MET:HE3	14:1N:97:MET:HA	1.82	0.60
20:1T:49:GLU:OE1	22:1W:64:ARG:NH2	2.34	0.60
22:1W:88:MET:O	22:1W:92:GLU:HG3	2.01	0.60
22:1W:107:PHE:O	58:1W:301:HOH:O	2.17	0.60
8:1H:104:PHE:HE1	45:1H:402:PC1:H342	1.66	0.60
15:1O:60:ASP:N	15:1O:60:ASP:OD1	2.34	0.60
50:1M:503:3PE:H241	14:1N:242:SER:HB2	1.84	0.60
23:1X:41:GLU:OE1	23:1X:58:GLU:HB3	2.01	0.60
24:1Y:116:TYR:HB3	45:1m:201:PC1:H3E1	1.84	0.60
29:1d:46:ASN:HB3	29:1d:53:VAL:HA	1.83	0.60
38:1m:14:PRO:HG2	38:1m:17:LEU:HB2	1.83	0.60
2:1B:54:CYS:HB2	46:1B:201:SF4:S4	2.41	0.59
12:1L:600:THR:CG2	12:1L:601:LEU:H	2.13	0.59
21:1V:54:LYS:NZ	58:1V:204:HOH:O	2.35	0.59
32:1g:43:ASP:HA	58:1g:223:HOH:O	2.02	0.59
33:1h:84:GLU:O	33:1h:88:GLU:HG2	2.02	0.59
5:1E:209:PRO:HA	6:1F:40:GLY:HA2	1.84	0.59
12:1L:63:ILE:HG23	34:1i:96:VAL:HG22	1.84	0.59
1:1A:67:LEU:HD22	11:1K:65:VAL:HA	1.84	0.59
4:1D:258:VAL:HG12	4:1D:296:ARG:HG2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:1P:236:TYR:OH	16:1P:311:GLU:OE2	2.19	0.59
37:1l:157:GLU:N	40:1o:34:LYS:O	2.36	0.59
23:1X:129:LYS:NZ	27:1b:62:MET:O	2.35	0.59
6:1F:391:SER:OG	43:1r:48:LEU:HB3	2.03	0.59
12:1L:223:LYS:NZ	58:1L:826:HOH:O	2.35	0.59
15:1O:104:ARG:NH2	52:1O:401:GTP:N7	2.51	0.59
16:1P:10:LYS:NZ	22:1W:127:ASP:OD2	2.34	0.59
16:1P:179:LEU:HD11	16:1P:310:LEU:HD21	1.85	0.59
6:1F:9:LYS:NZ	58:1F:601:HOH:O	2.30	0.59
15:1O:96:LEU:O	15:1O:100:LEU:HG	2.02	0.59
37:1l:125:TYR:OH	40:1o:7:ARG:NH1	2.35	0.59
41:1p:6:LYS:NZ	58:1p:201:HOH:O	2.35	0.59
42:1q:75:TRP:HD1	45:1q:202:PC1:H132	1.67	0.59
8:1H:49:ILE:HD13	45:1q:202:PC1:H2F1	1.84	0.59
9:1L:35:GLY:HA3	45:1L:203:PC1:H331	1.83	0.59
10:1J:52:LEU:HD13	11:1K:45:THR:HG23	1.84	0.59
12:1L:419:THR:HA	12:1L:422:TYR:CE2	2.38	0.59
12:1L:544:MET:HE2	12:1L:549:ALA:HB2	1.85	0.59
14:1N:109:SER:HA	14:1N:112:HIS:HB3	1.84	0.59
16:1P:36:ASN:HA	16:1P:62:MET:HG2	1.84	0.59
17:1Q:37:ILE:HB	17:1Q:105:VAL:HB	1.85	0.59
4:1D:151:ILE:HG23	4:1D:170:MET:HB3	1.84	0.59
14:1N:1:FME:O	15:1O:258:ARG:NH2	2.36	0.59
16:1P:58:HIS:NE2	58:1P:511:HOH:O	2.31	0.59
1:1A:95:LEU:HD13	8:1H:302:MET:HG3	1.85	0.58
11:1K:40:LEU:HD22	14:1N:75:ILE:HD12	1.83	0.58
12:1L:402:SER:HB2	12:1L:404:THR:HG23	1.84	0.58
58:1L:831:HOH:O	40:1o:51:MET:SD	2.57	0.58
13:1M:163:ALA:HA	50:1M:501:3PE:H241	1.85	0.58
13:1M:403:THR:HA	13:1M:406:TYR:CE2	2.38	0.58
20:1T:46:ASP:OD1	22:1W:64:ARG:NH2	2.28	0.58
23:1X:15:GLN:OE1	23:1X:64:GLN:NE2	2.36	0.58
15:1O:94:TYR:OH	58:1O:501:HOH:O	2.17	0.58
29:1d:62:LEU:O	29:1d:66:THR:HG22	2.03	0.58
3:1C:133:GLU:OE1	4:1D:430:ARG:NH2	2.35	0.58
13:1M:98:MET:HE1	50:1M:503:3PE:H3D2	1.85	0.58
13:1M:343:ILE:HD11	38:1m:64:LEU:HD11	1.84	0.58
5:1E:217:LEU:HD23	6:1F:44:LYS:HD2	1.86	0.58
6:1F:355:LYS:HG3	6:1F:370:ASP:HA	1.85	0.58
12:1L:203:MET:HG2	41:1p:109:LEU:HD11	1.85	0.58
13:1M:126:LEU:HD21	13:1M:153:THR:HG21	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1b:66:PRO:O	27:1b:67:SER:HB2	2.03	0.58
38:1m:61:ASP:OD2	58:1m:303:HOH:O	2.16	0.58
19:1S:19:ARG:HB2	19:1S:65:TRP:HB2	1.86	0.58
33:1h:82:GLY:O	58:1h:301:HOH:O	2.16	0.58
4:1D:121:ALA:HA	4:1D:365:THR:HG21	1.84	0.58
10:1J:64:MET:HE1	11:1K:68:ALA:HA	1.86	0.58
12:1L:70:THR:HG22	12:1L:75:GLU:HG2	1.85	0.58
13:1M:6:ILE:HG12	51:1X:201:CDL:H652	1.86	0.58
29:1d:114:GLU:O	58:1d:301:HOH:O	2.17	0.58
1:1A:49:LEU:HD12	8:1H:126:LYS:HG3	1.83	0.58
10:1J:25:SER:HB2	10:1J:81:GLU:HB2	1.85	0.58
12:1L:9:LEU:O	12:1L:13:ILE:HG12	2.04	0.58
45:1f:101:PC1:H331	45:1f:101:PC1:H282	1.86	0.58
32:1g:49:LYS:O	58:1g:202:HOH:O	2.17	0.58
35:1j:59:TRP:O	40:1o:106:ARG:NH1	2.27	0.58
6:1F:89:ARG:NH1	6:1F:217:GLY:O	2.37	0.58
12:1L:364:LYS:NZ	36:1k:58:ASN:O	2.29	0.58
30:1e:36:GLU:HG3	30:1e:62:PHE:CZ	2.39	0.58
4:1D:52:GLY:N	4:1D:53:PRO:HD3	2.18	0.58
41:1p:18:ALA:O	58:1p:202:HOH:O	2.17	0.58
50:1L:702:3PE:H31	51:1h:201:CDL:HA62	1.85	0.57
13:1M:45:LEU:O	32:1g:84:ARG:NH1	2.37	0.57
40:1o:45:MET:HB3	40:1o:55:ARG:HD3	1.84	0.57
41:1p:80:ASP:O	41:1p:84:MET:HG3	2.04	0.57
44:1s:56:VAL:O	44:1s:59:SER:OG	2.21	0.57
8:1H:170:GLU:OE2	23:1X:97:ARG:NH2	2.34	0.57
10:1J:106:TYR:O	10:1J:110:GLU:HB2	2.04	0.57
50:1M:503:3PE:H2C2	50:1M:503:3PE:H3G2	1.86	0.57
19:1S:35:PHE:CD1	19:1S:39:ARG:HD3	2.40	0.57
20:1T:52:MET:HE1	22:1W:37:ARG:HA	1.85	0.57
1:1A:92:LEU:O	1:1A:96:ILE:HG12	2.04	0.57
16:1P:71:MET:HE2	16:1P:83:LYS:HE3	1.85	0.57
23:1X:110:VAL:O	23:1X:115:GLY:N	2.37	0.57
5:1E:39:PRO:HA	44:1s:65:GLN:HB3	1.84	0.57
20:1T:35:HIS:CD2	20:1T:38:LYS:H	2.22	0.57
34:1i:100:LYS:HG3	40:1o:49:GLN:HE22	1.70	0.57
6:1F:125:GLY:C	6:1F:129:MET:HE3	2.30	0.57
10:1J:138:GLU:HG3	30:1e:28:ILE:HG21	1.86	0.57
12:1L:600:THR:HG22	12:1L:601:LEU:N	2.14	0.57
23:1X:17:VAL:HG22	23:1X:67:LEU:HD13	1.87	0.57
42:1q:75:TRP:HB3	45:1q:201:PC1:O14	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:38:GLU:HB2	1:1A:43:PRO:HG3	1.87	0.57
13:1M:133:ILE:HD11	13:1M:231:LEU:HD11	1.87	0.57
13:1M:167:ILE:HD11	13:1M:195:MET:HE3	1.85	0.57
4:1D:133:ARG:HH12	25:1Z:10:MET:HE3	1.69	0.57
12:1L:172:ILE:HG21	13:1M:408:LEU:HD12	1.85	0.57
20:1U:44:SER:OG	56:1n:201:EHZ:O9	2.08	0.57
32:1g:82:ASP:O	58:1g:203:HOH:O	2.18	0.57
4:1D:269:LEU:HB2	4:1D:368:GLU:HB2	1.85	0.57
7:1G:283:MET:HB2	7:1G:560:ILE:HB	1.86	0.57
51:1L:705:CDL:H592	13:1M:445:LEU:HD22	1.87	0.57
16:1P:81:ILE:O	16:1P:85:VAL:HB	2.04	0.57
50:1d:201:3PE:H2G2	50:1d:201:3PE:H2C2	1.87	0.57
50:1j:101:3PE:H11	40:1o:77:LEU:HD21	1.86	0.57
12:1L:351:ASN:O	12:1L:351:ASN:ND2	2.34	0.57
21:1V:54:LYS:O	21:1V:58:VAL:HG23	2.05	0.57
23:1X:128:THR:HG22	27:1b:66:PRO:HG2	1.86	0.57
23:1X:144:ARG:NH2	30:1e:58:GLU:OE2	2.38	0.57
30:1e:67:LEU:O	58:1e:201:HOH:O	2.18	0.57
31:1f:41:SER:HB3	33:1h:88:GLU:OE1	2.05	0.57
4:1D:6:PRO:HB3	4:1D:10:TRP:CD1	2.39	0.56
6:1F:342:ASP:CG	6:1F:429:ARG:HH12	2.12	0.56
4:1D:66:MET:HE3	4:1D:76:CYS:SG	2.45	0.56
7:1G:139:ASP:OD2	7:1G:149:ILE:HA	2.05	0.56
20:1U:81:ALA:HA	20:1U:86:VAL:HG13	1.86	0.56
29:1d:45:ASP:OD1	29:1d:51:ARG:NH2	2.38	0.56
4:1D:291:GLY:O	4:1D:296:ARG:NH2	2.38	0.56
4:1D:324:LYS:HD3	4:1D:331:SER:HB3	1.88	0.56
7:1G:332:LYS:HG3	7:1G:343:LEU:HD13	1.88	0.56
45:1H:402:PC1:H332	45:1H:402:PC1:H2A2	1.86	0.56
29:1d:1:MET:SD	33:1h:111:ARG:HD3	2.45	0.56
45:1q:201:PC1:H341	45:1q:202:PC1:H282	1.87	0.56
12:1L:327:LEU:O	12:1L:331:MET:HG2	2.06	0.56
13:1M:114:GLU:OE2	13:1M:117:LEU:N	2.34	0.56
13:1M:196:TRP:HB2	13:1M:253:LEU:HD23	1.87	0.56
14:1N:289:ASN:HA	14:1N:292:PHE:CE2	2.41	0.56
23:1X:67:LEU:O	23:1X:71:ARG:HG3	2.06	0.56
5:1E:87:TYR:HB3	6:1F:181:ALA:O	2.06	0.56
8:1H:190:LEU:HD21	8:1H:273:ILE:HG21	1.87	0.56
20:1T:6:LEU:HD23	20:1T:6:LEU:H	1.71	0.56
35:1j:39:ARG:NE	35:1j:43:ASP:OD1	2.29	0.56
4:1D:385:ARG:NH1	58:1D:513:HOH:O	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1H:10:ILE:HG23	8:1H:83:LEU:HD22	1.88	0.56
12:1L:429:PHE:CZ	50:1L:704:3PE:H111	2.41	0.56
19:1S:22:LEU:HD13	19:1S:32:VAL:HG22	1.87	0.56
27:1b:68:HIS:CD2	27:1b:70:GLN:H	2.24	0.56
41:1p:45:THR:HG22	41:1p:49:GLU:OE2	2.05	0.56
1:1A:7:LEU:HD13	45:1H:402:PC1:H362	1.86	0.56
7:1G:418:ARG:HD2	44:1s:75:HIS:HA	1.87	0.56
10:1J:17:PHE:HA	10:1J:20:PHE:CE2	2.41	0.56
15:1O:14:THR:HA	15:1O:17:LYS:HE2	1.88	0.56
15:1O:28:ASP:OD2	15:1O:206:TYR:OH	2.18	0.56
18:1R:12:THR:HG22	18:1R:35:VAL:HG22	1.87	0.56
33:1h:64:TRP:CH2	45:1h:202:PC1:H121	2.41	0.56
16:1P:122:LYS:NZ	16:1P:162:GLU:OE1	2.36	0.56
19:1S:30:GLN:OE1	58:1S:102:HOH:O	2.18	0.56
21:1V:29:LYS:O	21:1V:33:VAL:HG23	2.06	0.56
6:1F:93:LEU:HD13	6:1F:129:MET:HE1	1.88	0.55
7:1G:262:TRP:HB2	7:1G:390:LEU:HD11	1.88	0.55
37:1l:54:SER:HA	37:1l:84:TYR:HB3	1.88	0.55
14:1N:96:THR:HG22	14:1N:100:MET:HE2	1.87	0.55
25:1Z:98:MET:HE2	30:1e:78:ILE:HA	1.88	0.55
37:1l:138:LEU:HB3	37:1l:141:GLU:HB2	1.89	0.55
6:1F:393:TRP:O	6:1F:397:LYS:HG2	2.05	0.55
7:1G:577:GLU:OE2	7:1G:579:ARG:NH1	2.39	0.55
39:1n:137:LYS:O	39:1n:141:GLU:HG3	2.06	0.55
6:1F:302:SER:HB2	6:1F:350:LEU:HD22	1.88	0.55
11:1K:37:MET:HG3	11:1K:67:ALA:CB	2.37	0.55
22:1W:37:ARG:NH2	58:1W:304:HOH:O	2.31	0.55
39:1n:13:GLN:O	39:1n:17:ARG:HG2	2.06	0.55
4:1D:354:GLU:OE2	4:1D:357:GLN:NE2	2.39	0.55
50:1M:503:3PE:H281	14:1N:246:VAL:HG21	1.88	0.55
14:1N:87:THR:HG22	14:1N:88:LYS:N	2.21	0.55
16:1P:74:ASN:HB3	16:1P:77:ASP:HB3	1.88	0.55
21:1V:22:ARG:HH11	21:1V:25:ILE:HD11	1.71	0.55
7:1G:21:GLU:OE1	7:1G:21:GLU:N	2.33	0.55
7:1G:534:ARG:NH1	7:1G:556:MET:O	2.38	0.55
45:1M:502:PC1:H331	45:1M:502:PC1:H231	1.89	0.55
21:1V:10:LEU:HD12	21:1V:13:LEU:HD12	1.87	0.55
39:1n:97:LYS:HG2	39:1n:177:PRO:HG3	1.89	0.55
14:1N:67:SER:OG	58:1N:1001:HOH:O	2.18	0.55
14:1N:136:LEU:HD23	14:1N:205:LEU:HD21	1.89	0.55
15:1O:295:LYS:HD2	15:1O:295:LYS:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:1P:136:ASN:HD21	16:1P:291:ASP:HA	1.71	0.55
3:1C:118:GLU:OE2	3:1C:144:ASN:ND2	2.40	0.55
15:1O:169:VAL:HG21	15:1O:214:MET:HB3	1.88	0.55
37:1I:134:PRO:HG2	40:1o:38:MET:HE2	1.89	0.55
40:1o:11:ASP:OD1	40:1o:13:SER:OG	2.23	0.55
1:1A:18:VAL:HG23	8:1H:222:MET:HE1	1.88	0.55
1:1A:58:VAL:HG21	8:1H:286:MET:HE1	1.89	0.55
5:1E:27:ASN:HD21	5:1E:57:GLN:HB2	1.72	0.55
16:1P:48:PRO:O	58:1P:501:HOH:O	2.18	0.55
16:1P:271:GLU:HG2	16:1P:280:THR:HG22	1.88	0.55
10:1J:103:MET:HE3	11:1K:6:MET:HE3	1.89	0.55
15:1O:141:GLN:NE2	15:1O:201:ASP:OD2	2.40	0.55
6:1F:96:ASN:ND2	6:1F:187:GLY:O	2.33	0.54
14:1N:10:ILE:O	14:1N:14:MET:HG2	2.06	0.54
20:1T:47:GLN:O	20:1T:50:ILE:HG13	2.07	0.54
24:1Y:72:THR:OG1	24:1Y:92:GLY:HA2	2.05	0.54
34:1i:101:PRO:HD2	41:1p:14:ARG:HH22	1.72	0.54
8:1H:88:PRO:HG2	8:1H:105:MET:HE2	1.89	0.54
12:1L:61:MET:HE2	34:1i:98:GLU:HG2	1.89	0.54
13:1M:101:LEU:HD22	51:1X:201:CDL:H471	1.88	0.54
50:1M:503:3PE:H2C1	50:1d:201:3PE:H3D1	1.90	0.54
28:1c:42:TYR:CZ	29:1d:22:PRO:HG3	2.43	0.54
34:1i:54:ALA:HB3	34:1i:57:LYS:HG3	1.88	0.54
6:1F:23:THR:OG1	6:1F:39:ARG:HD2	2.08	0.54
7:1G:155:GLN:HG2	7:1G:181:MET:HE2	1.89	0.54
13:1M:269:MET:HE1	13:1M:396:MET:HG3	1.88	0.54
34:1i:114:GLU:OE2	41:1p:15:ARG:NH1	2.40	0.54
6:1F:78:LYS:NZ	6:1F:222:VAL:O	2.40	0.54
7:1G:633:TYR:O	58:1G:901:HOH:O	2.18	0.54
13:1M:433:GLU:O	13:1M:437:MET:HG2	2.07	0.54
24:1Y:48:PHE:HA	50:1Y:804:3PE:H222	1.89	0.54
35:1j:67:LEU:HA	58:1j:201:HOH:O	2.06	0.54
4:1D:63:ARG:HB3	4:1D:79:HIS:HB2	1.89	0.54
5:1E:151:ALA:HB1	5:1E:152:PRO:HD2	1.88	0.54
6:1F:151:VAL:O	6:1F:155:GLU:HG3	2.07	0.54
50:1M:501:3PE:H341	14:1N:277:ILE:HG12	1.90	0.54
6:1F:28:ARG:HB3	44:1s:35:ASN:HA	1.89	0.54
12:1L:213:LEU:HB3	12:1L:273:VAL:HG11	1.88	0.54
2:1B:82:GLN:NE2	8:1H:215:TYR:O	2.40	0.54
8:1H:56:VAL:HG11	45:1P:402:PC1:H3G2	1.90	0.54
51:1L:705:CDL:H311	51:1L:705:CDL:HB31	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1N:30:TRP:O	14:1N:34:GLU:HG2	2.08	0.54
8:1H:24:GLU:HA	8:1H:271:LEU:HD13	1.90	0.54
8:1H:173:TRP:HB3	8:1H:175:ILE:HG22	1.89	0.54
16:1P:82:ARG:HE	16:1P:86:GLU:CG	2.21	0.54
23:1X:152:GLU:H	23:1X:152:GLU:CD	2.13	0.54
8:1H:274:ARG:O	58:1H:501:HOH:O	2.18	0.54
23:1X:37:LYS:HB3	23:1X:38:PRO:HD3	1.89	0.54
25:1Z:114:THR:O	58:1Z:201:HOH:O	2.19	0.54
30:1e:21:SER:OG	30:1e:36:GLU:OE1	2.20	0.54
32:1g:109:GLU:O	41:1p:141:ARG:NH1	2.37	0.54
3:1C:175:ARG:NH2	3:1C:177:ASP:OD2	2.41	0.54
7:1G:239:VAL:HG23	7:1G:253:ARG:HB2	1.89	0.54
13:1M:196:TRP:CD1	13:1M:250:LEU:HB3	2.43	0.54
12:1L:211:MET:HG3	50:1L:703:3PE:H361	1.90	0.53
12:1L:484:LEU:O	12:1L:488:MET:HG2	2.08	0.53
51:1d:202:CDL:H362	51:1d:202:CDL:H402	1.89	0.53
5:1E:53:LEU:HD13	44:1s:52:LEU:HD23	1.90	0.53
10:1J:120:ASN:HD22	30:1e:72:MET:HB3	1.73	0.53
23:1X:51:ASP:OD2	25:1Z:116:TRP:HB2	2.09	0.53
31:1f:5:GLN:O	31:1f:9:ASP:HB2	2.08	0.53
40:1o:21:MET:HE1	40:1o:101:PHE:HA	1.90	0.53
2:1B:90:GLY:HA2	46:1B:201:SF4:S2	2.48	0.53
10:1J:23:LYS:O	11:1K:23:ARG:NH1	2.41	0.53
12:1L:257:VAL:HG12	12:1L:314:MET:HE2	1.90	0.53
14:1N:58:LYS:O	14:1N:62:THR:HG23	2.08	0.53
12:1L:440:LEU:O	58:1L:802:HOH:O	2.19	0.53
15:1O:169:VAL:HG11	15:1O:214:MET:HG3	1.90	0.53
2:1B:68:ASP:O	2:1B:71:ARG:HG2	2.08	0.53
8:1H:179:TRP:O	8:1H:183:MET:HG3	2.08	0.53
13:1M:6:ILE:HD12	31:1f:23:GLY:HA2	1.91	0.53
4:1D:405:MET:HE2	4:1D:417:ILE:HG23	1.90	0.53
10:1J:127:ILE:HD13	11:1K:2:PRO:HG3	1.90	0.53
15:1O:210:PHE:HD2	15:1O:211:LEU:HD12	1.73	0.53
17:1Q:50:ASN:HA	17:1Q:53:LYS:HE2	1.90	0.53
33:1h:40:ILE:HG22	51:1h:201:CDL:OB9	2.08	0.53
7:1G:551:ASP:OD2	7:1G:679:ARG:NE	2.36	0.53
23:1X:123:GLU:HA	23:1X:126:LYS:HE3	1.91	0.53
29:1d:34:MET:HE1	51:1d:202:CDL:H442	1.90	0.53
33:1h:107:GLU:OE2	58:1h:302:HOH:O	2.19	0.53
1:1A:32:GLU:O	2:1B:102:LYS:NZ	2.41	0.53
7:1G:226:GLU:HG2	7:1G:253:ARG:HD3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:1H:402:PC1:H153	25:1Z:141:ILE:HA	1.91	0.53
23:1X:20:SER:HB2	26:1a:63:THR:HG23	1.91	0.53
32:1g:100:ARG:NH1	32:1g:107:LEU:O	2.42	0.53
33:1h:19:ARG:NH1	58:1h:314:HOH:O	2.40	0.53
39:1n:55:ASP:H	39:1n:58:LYS:HZ3	1.56	0.53
7:1G:252:PRO:HG3	7:1G:263:ILE:HG12	1.91	0.53
13:1M:92:LYS:O	13:1M:96:ILE:HG12	2.09	0.53
14:1N:321:LYS:NZ	58:1N:1006:HOH:O	2.30	0.53
16:1P:128:LYS:NZ	16:1P:218:ILE:O	2.35	0.53
30:1e:68:ARG:HB3	30:1e:71:THR:HB	1.91	0.53
31:1f:10:HIS:HB3	31:1f:13:HIS:HD2	1.74	0.53
8:1H:215:TYR:HD2	8:1H:219:PRO:HB2	1.74	0.53
51:1L:705:CDL:H671	13:1M:445:LEU:HB2	1.92	0.53
22:1W:37:ARG:O	22:1W:41:ARG:HG2	2.08	0.53
13:1M:271:MET:HA	13:1M:271:MET:HE2	1.90	0.52
14:1N:109:SER:HB2	14:1N:161:SER:HA	1.91	0.52
23:1X:124:LEU:HD21	25:1Z:70:ALA:HB2	1.90	0.52
26:1a:34:LYS:NZ	26:1a:61:HIS:O	2.43	0.52
37:1l:123:PRO:O	40:1o:8:TYR:OH	2.25	0.52
5:1E:159:ASN:HB3	5:1E:184:PRO:HB3	1.91	0.52
5:1E:171:GLU:O	5:1E:175:GLU:HG2	2.09	0.52
12:1L:500:LEU:HD12	50:1L:704:3PE:H362	1.91	0.52
15:1O:304:TYR:O	29:1d:50:ARG:HB3	2.09	0.52
21:1V:4:LEU:HD23	21:1V:4:LEU:H	1.75	0.52
25:1Z:113:THR:O	58:1Z:202:HOH:O	2.19	0.52
33:1h:95:GLN:O	33:1h:99:GLU:HG3	2.08	0.52
41:1p:61:TYR:O	58:1p:203:HOH:O	2.18	0.52
4:1D:115:GLU:HG3	4:1D:194:ILE:HB	1.90	0.52
13:1M:105:PHE:O	13:1M:109:THR:OG1	2.26	0.52
13:1M:265:SER:OG	13:1M:299:VAL:HG23	2.09	0.52
16:1P:92:ILE:HD11	16:1P:218:ILE:HD11	1.91	0.52
16:1P:310:LEU:HD22	16:1P:314:ALA:HB2	1.90	0.52
23:1X:144:ARG:NH1	30:1e:57:ILE:HD12	2.24	0.52
24:1Y:52:VAL:HG22	50:1Y:804:3PE:H262	1.90	0.52
35:1j:6:HIS:CD2	35:1j:7:ILE:HG12	2.44	0.52
2:1B:48:MET:HE2	2:1B:80:PRO:HG3	1.90	0.52
9:1I:31:VAL:HG12	45:1I:203:PC1:H321	1.90	0.52
16:1P:30:LEU:HA	16:1P:207:ILE:HD11	1.90	0.52
16:1P:82:ARG:HE	16:1P:86:GLU:HG2	1.75	0.52
3:1C:195:ARG:NH1	58:1C:313:HOH:O	2.41	0.52
10:1J:23:LYS:HD2	11:1K:28:SER:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1J:76:THR:OG1	10:1J:77:GLU:N	2.42	0.52
24:1Y:11:ILE:HD11	24:1Y:16:GLU:HB2	1.90	0.52
29:1d:64:TYR:CD1	51:1d:202:CDL:H331	2.45	0.52
30:1e:82:ARG:O	30:1e:86:ILE:HG12	2.09	0.52
33:1h:92:ALA:O	33:1h:96:ILE:HG23	2.10	0.52
1:1A:48:ARG:HE	10:1J:78:MET:HA	1.74	0.52
2:1B:154:GLU:OE2	58:1B:301:HOH:O	2.19	0.52
6:1F:191:ALA:HB2	6:1F:203:PRO:HG3	1.91	0.52
7:1G:194:GLU:HG3	7:1G:389:PRO:HB3	1.90	0.52
7:1G:569:LYS:HG3	7:1G:571:ALA:HB2	1.92	0.52
12:1L:440:LEU:HD11	36:1k:13:MET:HE3	1.92	0.52
16:1P:235:ARG:HB2	16:1P:340:VAL:O	2.10	0.52
20:1T:48:VAL:HG22	22:1W:37:ARG:HH21	1.75	0.52
23:1X:171:MET:HG3	51:1X:201:CDL:HA4	1.92	0.52
43:1r:105:LEU:HD13	43:1r:110:PRO:HB3	1.91	0.52
6:1F:244:SER:O	58:1F:601:HOH:O	2.18	0.52
34:1i:103:ILE:HB	40:1o:47:ASP:HB2	1.91	0.52
41:1p:38:LEU:HD12	41:1p:42:ARG:HH21	1.74	0.52
3:1C:32:ILE:HG23	21:1V:43:TYR:HB2	1.92	0.52
7:1G:144:PRO:HD2	7:1G:192:MET:HE1	1.90	0.52
12:1L:67:HIS:NE2	12:1L:70:THR:HG23	2.23	0.52
12:1L:249:SER:HB2	12:1L:336:LYS:HG3	1.91	0.52
12:1L:476:THR:HG22	12:1L:477:VAL:H	1.75	0.52
16:1P:52:GLU:HG3	16:1P:54:TYR:H	1.75	0.52
16:1P:146:LEU:HD11	16:1P:289:MET:HE1	1.92	0.52
35:1j:67:LEU:HB3	35:1j:71:GLU:HG3	1.92	0.52
12:1L:18:PRO:HG3	12:1L:39:THR:HG21	1.92	0.52
23:1X:82:THR:HA	23:1X:85:TRP:NE1	2.25	0.52
25:1Z:97:ILE:HG22	30:1e:81:GLN:HG3	1.92	0.52
28:1c:27:LEU:HD11	51:1d:202:CDL:H742	1.91	0.52
33:1h:49:GLU:CD	33:1h:68:LYS:HD3	2.34	0.52
1:1A:16:LEU:O	1:1A:20:ILE:HG13	2.10	0.52
6:1F:61:LYS:HG2	6:1F:76:GLY:HA3	1.91	0.52
8:1H:267:THR:O	8:1H:271:LEU:HG	2.09	0.52
2:1B:77:ARG:HG3	2:1B:78:ALA:H	1.73	0.51
2:1B:115:SER:OG	2:1B:121:ASN:OD1	2.20	0.51
3:1C:78:LEU:HB3	3:1C:130:TYR:HB3	1.92	0.51
6:1F:164:LYS:HB2	44:1s:63:MET:HE1	1.92	0.51
6:1F:261:HIS:HD2	6:1F:337:MET:HA	1.76	0.51
10:1J:167:VAL:HG13	14:1N:42:PRO:HG3	1.91	0.51
12:1L:124:PHE:CE1	12:1L:252:MET:HB2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1O:111:ALA:HB1	15:1O:122:VAL:HG21	1.91	0.51
2:1B:174:ARG:O	2:1B:178:ARG:HG3	2.09	0.51
4:1D:20:TYR:O	58:1D:501:HOH:O	2.19	0.51
7:1G:622:ARG:NH2	19:1S:73:GLU:OE2	2.36	0.51
4:1D:76:CYS:N	4:1D:403:ASP:OD1	2.40	0.51
12:1L:248:HIS:HA	12:1L:253:VAL:HG13	1.92	0.51
13:1M:119:TYR:CZ	13:1M:161:LEU:HB2	2.46	0.51
33:1h:77:ARG:NH1	45:1h:202:PC1:O14	2.36	0.51
6:1F:258:ILE:HD13	6:1F:284:ALA:HB2	1.92	0.51
6:1F:297:VAL:HA	6:1F:336:VAL:HA	1.93	0.51
6:1F:296:ALA:O	6:1F:297:VAL:HB	2.11	0.51
7:1G:117:GLN:O	7:1G:121:MET:HG2	2.11	0.51
7:1G:281:GLN:HB2	7:1G:293:TYR:CD1	2.46	0.51
8:1H:129:LEU:O	8:1H:133:LEU:HD23	2.11	0.51
13:1M:206:LYS:NZ	58:1M:604:HOH:O	2.26	0.51
45:1d:203:PC1:H221	45:1d:203:PC1:O11	2.11	0.51
33:1h:47:ILE:O	58:1h:303:HOH:O	2.19	0.51
3:1C:41:GLN:NE2	3:1C:49:GLU:OE1	2.37	0.51
5:1E:214:GLN:CD	6:1F:238:GLY:HA2	2.36	0.51
10:1J:129:ASP:HB3	30:1e:31[B]:ARG:CZ	2.41	0.51
12:1L:476:THR:HG22	12:1L:477:VAL:N	2.25	0.51
31:1f:18:VAL:HA	31:1f:21:VAL:HG13	1.93	0.51
37:1l:54:SER:OG	58:1l:301:HOH:O	2.19	0.51
12:1L:273:VAL:O	12:1L:277:THR:HG22	2.11	0.51
16:1P:96:GLY:O	54:1P:403:NDP:H8A	2.11	0.51
18:1R:49:VAL:HG22	18:1R:90:GLN:HB2	1.93	0.51
23:1X:129:LYS:HD3	27:1b:65:VAL:HB	1.91	0.51
33:1h:12:LYS:HA	39:1n:98:VAL:HG21	1.93	0.51
34:1i:71:VAL:O	34:1i:76:ILE:HG12	2.11	0.51
5:1E:29:LYS:HE2	44:1s:56:VAL:HG11	1.92	0.51
12:1L:359:MET:HB3	12:1L:430:ALA:HA	1.93	0.51
12:1L:536:LEU:HB3	12:1L:537:PRO:HD3	1.91	0.51
5:1E:126:ILE:HG13	5:1E:130:GLU:HG3	1.93	0.51
12:1L:187:ALA:HA	13:1M:383:THR:HG23	1.93	0.51
16:1P:192:PRO:HB3	16:1P:256:TYR:CZ	2.46	0.51
21:1V:71:LEU:HD13	21:1V:79:VAL:HG11	1.93	0.51
3:1C:71:GLN:NE2	58:1C:314:HOH:O	2.44	0.50
4:1D:183:ARG:NH1	4:1D:210:ASP:OD2	2.35	0.50
6:1F:30:ASP:HB3	6:1F:35:GLY:HA3	1.93	0.50
7:1G:412:PRO:HG3	7:1G:421:HIS:CE1	2.45	0.50
7:1G:564:ALA:HB3	7:1G:569:LYS:HD3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1L:702:3PE:H2B2	51:1h:201:CDL:H512	1.93	0.50
19:1S:42:GLU:OE2	58:1S:101:HOH:O	2.18	0.50
25:1Z:68:ARG:NH1	58:1Z:203:HOH:O	2.22	0.50
3:1C:93:VAL:HG22	3:1C:108:LYS:HG2	1.92	0.50
6:1F:363:THR:HG21	7:1G:97:LEU:HG	1.93	0.50
15:1O:136:GLU:O	15:1O:140:ARG:HG2	2.12	0.50
29:1d:4:GLY:HA3	33:1h:124:GLN:O	2.11	0.50
4:1D:329:LYS:NZ	7:1G:124:GLY:O	2.38	0.50
10:1J:86:ASN:HB3	10:1J:89:VAL:HG23	1.93	0.50
11:1K:15:ALA:HB3	11:1K:36:MET:HG3	1.93	0.50
12:1L:434:LYS:HD2	36:1k:51:ARG:O	2.11	0.50
24:1Y:21:ALA:O	24:1Y:25:THR:OG1	2.24	0.50
6:1F:364:PRO:HB2	6:1F:403:THR:HG22	1.93	0.50
7:1G:140:LYS:O	7:1G:148:THR:OG1	2.23	0.50
37:1l:53:ARG:HD3	37:1l:57:GLU:OE2	2.11	0.50
38:1m:2:PHE:CZ	39:1n:69:GLU:HG3	2.46	0.50
10:1J:38:GLY:HA2	10:1J:57:PHE:HE2	1.76	0.50
10:1J:102:CYS:SG	10:1J:103:MET:N	2.84	0.50
14:1N:250:SER:O	14:1N:259:GLY:HA3	2.12	0.50
17:1Q:11:ILE:HG21	22:1W:23:ARG:HA	1.93	0.50
19:1S:35:PHE:HD1	19:1S:39:ARG:HD3	1.77	0.50
23:1X:75:ARG:NH1	58:1X:3413:HOH:O	2.32	0.50
30:1e:16:TRP:CH2	30:1e:17:MET:HE2	2.46	0.50
8:1H:92:PRO:HG3	8:1H:255:TYR:HB3	1.92	0.50
12:1L:4:PHE:HD2	12:1L:61:MET:SD	2.35	0.50
12:1L:473:PRO:HG2	12:1L:475:MET:HE3	1.92	0.50
15:1O:318:TRP:CD1	15:1O:318:TRP:H	2.28	0.50
20:1T:66:ASP:HA	20:1T:69:LYS:HE3	1.94	0.50
4:1D:233:ARG:NH2	9:1I:23:GLN:O	2.44	0.50
7:1G:255:HIS:CE1	7:1G:257:ASP:HB2	2.47	0.50
11:1K:24:SER:HB3	11:1K:89:TYR:CD1	2.46	0.50
13:1M:364:LEU:HD23	13:1M:367:LEU:HD12	1.94	0.50
19:1S:62:PRO:HB2	19:1S:78:LEU:HB2	1.93	0.50
24:1Y:31:THR:O	24:1Y:35:VAL:HG13	2.11	0.50
25:1Z:129:THR:O	25:1Z:133:ILE:HG23	2.11	0.50
29:1d:8:ARG:NH1	58:1d:308:HOH:O	2.34	0.50
32:1g:83:TYR:CE1	32:1g:84:ARG:HD3	2.46	0.50
32:1g:109:GLU:HA	32:1g:109:GLU:OE2	2.11	0.50
38:1m:113:LYS:O	38:1m:117:GLU:HG2	2.11	0.50
4:1D:371:LYS:HE2	4:1D:424:VAL:HG23	1.94	0.50
6:1F:365:CYS:HB2	46:1F:502:SF4:S4	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1G:324:ASP:CB	7:1G:571:ALA:HB1	2.41	0.50
7:1G:333:ASP:OD2	7:1G:613:TYR:OH	2.26	0.50
20:1U:25:ILE:HG21	20:1U:30:LEU:HD13	1.94	0.50
1:1A:3:ILE:O	1:1A:7:LEU:HG	2.12	0.50
10:1J:45:LEU:HD23	10:1J:50:SER:HA	1.93	0.50
15:1O:78:SER:HB3	15:1O:81:LYS:HB2	1.94	0.50
9:1I:112:ASP:HB3	9:1I:115:LYS:HB2	1.94	0.49
10:1J:34:ILE:HG22	10:1J:65:LEU:HD13	1.93	0.49
11:1K:12:PHE:CG	14:1N:72:MET:HE3	2.47	0.49
50:1M:503:3PE:O14	50:1d:201:3PE:H12	2.12	0.49
27:1b:54:VAL:O	58:1b:301:HOH:O	2.20	0.49
28:1c:45:ARG:NH2	29:1d:16:ASN:OD1	2.41	0.49
39:1n:141:GLU:OE1	58:1n:302:HOH:O	2.19	0.49
5:1E:163:ASP:OD2	5:1E:188:SER:OG	2.24	0.49
12:1L:100:ILE:HG21	12:1L:246:LEU:HB2	1.93	0.49
12:1L:102:GLU:OE2	12:1L:456:ARG:NH2	2.45	0.49
12:1L:188:TRP:HZ2	50:1L:703:3PE:H121	1.77	0.49
12:1L:286:LEU:HG	12:1L:411:MET:SD	2.52	0.49
14:1N:20:VAL:HG11	14:1N:137:ALA:HB1	1.94	0.49
16:1P:319:ARG:HA	16:1P:322:ARG:HG3	1.94	0.49
25:1Z:110:VAL:CG2	30:1e:70:LYS:HB2	2.42	0.49
28:1c:28:TRP:NE1	29:1d:66:THR:HB	2.28	0.49
2:1B:173:LEU:HD21	45:1P:402:PC1:H231	1.94	0.49
8:1H:76:ILE:O	8:1H:80:SER:OG	2.26	0.49
13:1M:24:TRP:CZ3	13:1M:96:ILE:HD11	2.47	0.49
13:1M:71:TRP:CG	45:1M:504:PC1:H2C2	2.47	0.49
13:1M:115:LEU:HB2	13:1M:174:LEU:HB3	1.93	0.49
38:1m:2:PHE:CE1	39:1n:69:GLU:HG3	2.47	0.49
39:1n:7:ALA:N	58:1n:319:HOH:O	2.45	0.49
39:1n:94:GLU:OE2	39:1n:97:LYS:HE2	2.12	0.49
8:1H:279:ARG:NH2	58:1H:509:HOH:O	2.43	0.49
50:1J:201:3PE:H272	50:1J:201:3PE:H342	1.94	0.49
12:1L:23:ASN:ND2	58:1L:836:HOH:O	2.45	0.49
12:1L:407:TRP:CD2	37:1l:115:MET:HB3	2.47	0.49
15:1O:138:MET:HG2	15:1O:143:PHE:HD2	1.78	0.49
16:1P:66:GLY:HA3	17:1Q:69:LEU:HD13	1.93	0.49
16:1P:107:GLU:O	16:1P:111:VAL:HB	2.11	0.49
24:1Y:13:GLU:OE2	24:1Y:125:LYS:NZ	2.41	0.49
50:1Y:801:3PE:H231	50:1Y:801:3PE:H31	1.94	0.49
1:1A:2:ASN:HB3	8:1H:2:PHE:CZ	2.48	0.49
3:1C:40:VAL:HG23	43:1r:68:VAL:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1G:534:ARG:NH2	7:1G:541:CYS:O	2.43	0.49
8:1H:302:MET:SD	50:1b:201:3PE:H2D1	2.53	0.49
12:1L:109:HIS:O	58:1L:803:HOH:O	2.20	0.49
13:1M:207:MET:HE3	13:1M:298:ILE:HG13	1.95	0.49
21:1V:32:ASP:OD1	58:1V:201:HOH:O	2.20	0.49
24:1Y:16:GLU:HB3	24:1Y:19:ARG:HG3	1.94	0.49
33:1h:14:SER:OG	39:1n:110:GLU:OE2	2.28	0.49
4:1D:109:VAL:HG12	4:1D:149:ASN:HA	1.93	0.49
6:1F:279:LEU:HD12	6:1F:283:HIS:HD2	1.78	0.49
50:1N:903:3PE:H252	50:1N:903:3PE:H372	1.94	0.49
15:1O:43:ALA:HB2	15:1O:123:VAL:HG21	1.94	0.49
17:1Q:59:PHE:HE1	17:1Q:82:LEU:HD12	1.76	0.49
40:1o:114:ARG:NH1	58:1o:201:HOH:O	2.44	0.49
8:1H:55:LEU:HD13	8:1H:221:ALA:HB2	1.94	0.49
14:1N:59:TYR:O	14:1N:63:GLN:HG2	2.13	0.49
15:1O:35:LYS:HE3	15:1O:126:ARG:HG3	1.94	0.49
16:1P:136:ASN:HD21	16:1P:292:MET:H	1.60	0.49
22:1W:30:ARG:O	22:1W:34:GLU:HG3	2.12	0.49
23:1X:6:LEU:HB2	25:1Z:88[B]:ARG:HH21	1.77	0.49
30:1e:81:GLN:OE1	30:1e:84:LYS:HE3	2.12	0.49
34:1i:100:LYS:HG3	40:1o:49:GLN:NE2	2.26	0.49
35:1j:61:ASP:HB3	35:1j:66:ILE:HB	1.95	0.49
4:1D:62:LEU:HB2	4:1D:425:PHE:CZ	2.48	0.49
8:1H:302:MET:HE1	50:1b:201:3PE:H2F2	1.95	0.49
12:1L:36:VAL:HG21	12:1L:118:PHE:HB3	1.95	0.49
16:1P:177:ARG:NH1	58:1P:521:HOH:O	2.45	0.49
51:1q:203:CDL:HB22	43:1r:3:ALA:HA	1.94	0.49
1:1A:73:LEU:HD23	8:1H:151:LEU:HD12	1.94	0.49
7:1G:41:CYS:O	7:1G:161:ARG:NH2	2.44	0.49
17:1Q:89:LYS:O	17:1Q:93:VAL:HG13	2.12	0.49
25:1Z:10:MET:HE2	25:1Z:10:MET:HA	1.94	0.49
29:1d:60:ARG:NH1	51:1d:202:CDL:OA3	2.45	0.49
29:1d:86:ARG:HD2	33:1h:107:GLU:OE1	2.12	0.49
34:1i:99:ARG:O	58:1i:201:HOH:O	2.20	0.49
7:1G:243:ARG:HG2	7:1G:244:THR:HG23	1.94	0.49
12:1L:331:MET:SD	12:1L:465:GLY:HA2	2.53	0.49
13:1M:44:GLN:HB2	32:1g:83:TYR:HE2	1.78	0.49
13:1M:71:TRP:CE3	45:1M:504:PC1:H2B1	2.48	0.49
14:1N:1:FME:HE1	14:1N:9:LEU:HD12	1.94	0.49
20:1T:16:LEU:HG	20:1T:20:LYS:HE3	1.95	0.49
8:1H:87:VAL:HG22	8:1H:88:PRO:HD3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:1L:495:ILE:O	12:1L:499:MET:HG3	2.13	0.48
45:1M:504:PC1:H292	45:1M:504:PC1:H2D2	1.95	0.48
14:1N:97:MET:HE3	14:1N:100:MET:HE3	1.95	0.48
14:1N:252:GLY:HA3	14:1N:290:LEU:HD13	1.95	0.48
7:1G:333:ASP:O	7:1G:337:ARG:HG2	2.13	0.48
8:1H:9:LEU:HD12	26:1a:19:PRO:HB3	1.94	0.48
12:1L:249:SER:HA	12:1L:306:THR:HG21	1.95	0.48
13:1M:8:THR:HG21	13:1M:103:GLN:HG2	1.95	0.48
16:1P:268:ARG:HB2	16:1P:268:ARG:HH11	1.78	0.48
39:1n:131:SER:OG	58:1n:301:HOH:O	2.14	0.48
12:1L:529:TYR:HB3	12:1L:530:PRO:HD3	1.95	0.48
13:1M:263:MET:HG3	38:1m:101:TYR:HB2	1.95	0.48
14:1N:87:THR:HG22	14:1N:88:LYS:HG3	1.95	0.48
15:1O:132:PHE:O	15:1O:136:GLU:HG2	2.13	0.48
15:1O:319:LEU:HD13	28:1c:17:VAL:HG11	1.95	0.48
19:1S:20:ILE:HD11	19:1S:90:LEU:HD11	1.95	0.48
50:1b:201:3PE:H2E1	50:1b:201:3PE:H2A2	1.94	0.48
4:1D:155:THR:HB	4:1D:167:PHE:HA	1.96	0.48
7:1G:283:MET:HE3	7:1G:293:TYR:CE1	2.48	0.48
8:1H:70:MET:HA	8:1H:73:ILE:HB	1.94	0.48
16:1P:260:HIS:O	16:1P:264:ARG:HG3	2.13	0.48
25:1Z:98:MET:SD	25:1Z:101:VAL:HG21	2.54	0.48
27:1b:58:ASP:OD1	27:1b:58:ASP:N	2.43	0.48
29:1d:64:TYR:CE1	51:1d:202:CDL:H331	2.49	0.48
31:1f:53:GLU:N	31:1f:53:GLU:OE1	2.45	0.48
40:1o:14:LYS:HE2	40:1o:112:LYS:HD3	1.95	0.48
6:1F:361:GLN:OE1	17:1Q:133:LYS:HE2	2.12	0.48
7:1G:364:LEU:HD12	7:1G:491:ASN:HB3	1.94	0.48
13:1M:108:MET:HE1	51:1X:201:CDL:H271	1.94	0.48
20:1T:63:PRO:HD2	20:1T:66:ASP:OD2	2.12	0.48
23:1X:110:VAL:HB	23:1X:116:TRP:HB2	1.95	0.48
12:1L:398:ALA:O	12:1L:402:SER:OG	2.24	0.48
13:1M:346:ARG:O	13:1M:419:TYR:HA	2.13	0.48
23:1X:77:CYS:HB2	23:1X:80:PRO:CD	2.32	0.48
33:1h:109:GLU:HA	33:1h:109:GLU:OE1	2.13	0.48
1:1A:69:ILE:HD11	8:1H:144:VAL:HG13	1.95	0.48
6:1F:99:GLU:O	6:1F:139:ARG:NH1	2.45	0.48
8:1H:179:TRP:CD2	8:1H:180:PRO:HD3	2.48	0.48
23:1X:17:VAL:HG23	23:1X:63:ASN:HD22	1.78	0.48
29:1d:11:LEU:O	30:1e:8:ARG:NH1	2.46	0.48
7:1G:140:LYS:HG2	7:1G:150:MET:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1J:127:ILE:HA	25:1Z:120:MET:CE	2.42	0.48
13:1M:104:LEU:HG	13:1M:108:MET:HE2	1.94	0.48
13:1M:190:TRP:CG	24:1Y:126:MET:HG2	2.49	0.48
13:1M:425:ASN:ND2	38:1m:57:GLY:HA2	2.29	0.48
50:1N:903:3PE:H32	24:1Y:2:LYS:HE2	1.96	0.48
15:1O:43:ALA:HB2	15:1O:123:VAL:CG2	2.43	0.48
15:1O:157:LYS:NZ	58:1O:515:HOH:O	2.41	0.48
16:1P:119:GLN:NE2	58:1P:522:HOH:O	2.46	0.48
56:1W:201:EHZ:N2	56:1W:201:EHZ:O3	2.45	0.48
37:1l:140:LEU:HD12	40:1o:42:GLN:HE22	1.78	0.48
1:1A:49:LEU:HD13	4:1D:47:LEU:HD13	1.95	0.48
7:1G:285:ARG:NH2	7:1G:555:PRO:O	2.47	0.48
8:1H:313:SER:HB2	25:1Z:51:MET:HA	1.95	0.48
45:1H:402:PC1:H11	10:1J:50:SER:OG	2.14	0.48
17:1Q:66:GLU:OE2	58:1Q:201:HOH:O	2.19	0.48
40:1o:94:TYR:O	40:1o:98:MET:HG3	2.13	0.48
1:1A:68:GLU:HG2	10:1J:161:LEU:HD13	1.96	0.48
4:1D:352:TYR:HD1	9:1I:86:VAL:HG21	1.79	0.48
6:1F:26:TYR:OH	58:1F:602:HOH:O	2.20	0.48
10:1J:30:GLY:O	10:1J:34:ILE:HG23	2.14	0.48
12:1L:385:TYR:OH	35:1j:43:ASP:O	2.23	0.48
12:1L:566:THR:O	12:1L:570:GLN:HG2	2.14	0.48
24:1Y:140:VAL:O	33:1h:115:ARG:NH1	2.43	0.48
29:1d:34:MET:HE1	51:1d:202:CDL:C44	2.43	0.48
37:1l:10:PRO:HD3	38:1m:66:ARG:HG2	1.95	0.48
1:1A:105:GLU:O	1:1A:110:GLY:HA3	2.14	0.47
8:1H:189:THR:HG22	8:1H:270:PHE:CZ	2.45	0.47
12:1L:37:LYS:HD2	12:1L:102:GLU:HG3	1.95	0.47
12:1L:497:GLY:HA2	50:1L:704:3PE:H361	1.95	0.47
15:1O:176:VAL:HG21	15:1O:200:GLN:HE21	1.79	0.47
15:1O:180:GLN:NE2	15:1O:196:ALA:HB2	2.29	0.47
51:1X:201:CDL:H241	51:1X:201:CDL:H192	1.96	0.47
2:1B:36:LEU:HB2	45:1q:202:PC1:H381	1.96	0.47
7:1G:244:THR:HB	17:1Q:73:SER:HB2	1.95	0.47
13:1M:135:ARG:HG2	50:1M:503:3PE:H352	1.96	0.47
24:1Y:54:ARG:HG3	50:1Y:802:3PE:HN1	1.79	0.47
25:1Z:98:MET:HB3	25:1Z:104:TRP:CD1	2.49	0.47
45:1f:101:PC1:H3B2	32:1g:76:PHE:HB2	1.97	0.47
51:1h:201:CDL:H582	34:1i:79:TRP:CD2	2.49	0.47
40:1o:30:PHE:CG	40:1o:33:ARG:HD3	2.49	0.47
41:1p:161:ARG:HG2	41:1p:165:GLU:OE1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:70:ASP:OD2	2:1B:75:VAL:HA	2.14	0.47
7:1G:534:ARG:HG3	7:1G:556:MET:HE2	1.96	0.47
10:1J:124:ASP:OD1	11:1K:4:VAL:HG12	2.14	0.47
12:1L:551:SER:HA	12:1L:555:LEU:HD12	1.95	0.47
14:1N:322:GLN:NE2	58:1N:1009:HOH:O	2.35	0.47
15:1O:240:TYR:OH	21:1V:84:GLU:OE1	2.32	0.47
24:1Y:112:ALA:HB2	45:1m:201:PC1:H242	1.96	0.47
25:1Z:112:HIS:CD2	30:1e:57:ILE:HG23	2.49	0.47
29:1d:11:LEU:HA	45:1d:203:PC1:H11	1.94	0.47
3:1C:20:LYS:HE2	3:1C:20:LYS:HB2	1.65	0.47
4:1D:17:ALA:HB1	11:1K:98:CYS:SG	2.54	0.47
10:1J:99:MET:HE1	50:1J:201:3PE:H3E2	1.96	0.47
40:1o:68:CYS:HB3	40:1o:79:CYS:SG	2.54	0.47
45:1q:202:PC1:H322	45:1q:202:PC1:H31	1.52	0.47
3:1C:41:GLN:HG2	3:1C:51:PHE:HE1	1.79	0.47
12:1L:257:VAL:O	12:1L:261:ILE:HG13	2.15	0.47
12:1L:297:ASP:HB3	12:1L:300:LYS:HB2	1.94	0.47
14:1N:109:SER:HB2	14:1N:161:SER:CA	2.45	0.47
20:1U:21:LEU:HD22	36:1k:46:ARG:HB3	1.97	0.47
40:1o:16:PRO:HB3	40:1o:104:GLU:HG2	1.97	0.47
4:1D:151:ILE:HG21	4:1D:174:ARG:HG3	1.96	0.47
8:1H:14:LEU:HD21	8:1H:83:LEU:HD21	1.97	0.47
8:1H:68:ILE:HA	8:1H:71:PHE:HB3	1.97	0.47
12:1L:116:ARG:NH1	58:1L:839:HOH:O	2.47	0.47
14:1N:243:LEU:HD22	14:1N:330:ILE:HG21	1.95	0.47
16:1P:286:ARG:O	16:1P:289:MET:HG2	2.14	0.47
28:1c:41:GLU:OE1	28:1c:44:ARG:NH1	2.48	0.47
29:1d:107:LYS:HG2	29:1d:111:GLU:OE2	2.14	0.47
30:1e:45:GLY:O	58:1e:202:HOH:O	2.20	0.47
37:1l:3:HIS:ND1	38:1m:60:GLU:OE1	2.48	0.47
5:1E:217:LEU:HD12	6:1F:236:ARG:HA	1.96	0.47
7:1G:254:MET:HA	7:1G:260:GLU:O	2.14	0.47
7:1G:358:LEU:HD12	7:1G:645:ALA:HB2	1.97	0.47
7:1G:478:ARG:NH2	58:1G:941:HOH:O	2.47	0.47
8:1H:124:ASN:C	8:1H:126:LYS:H	2.21	0.47
10:1J:107:ALA:HB2	11:1K:6:MET:HE1	1.95	0.47
12:1L:4:PHE:HZ	12:1L:87:VAL:HG11	1.78	0.47
12:1L:316:THR:HG23	12:1L:325:ALA:HB2	1.97	0.47
12:1L:363:TYR:CD1	12:1L:370:THR:HG21	2.50	0.47
13:1M:39:LEU:HD21	45:1M:504:PC1:H291	1.95	0.47
14:1N:128:LEU:HD13	51:1N:902:CDL:HA61	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1N:167:TRP:CZ2	50:1N:901:3PE:H2I1	2.49	0.47
16:1P:40:ARG:CZ	22:1W:110:THR:HG23	2.45	0.47
17:1Q:127:ARG:HE	44:1s:70:ARG:HH12	1.62	0.47
24:1Y:55:THR:O	24:1Y:59:THR:OG1	2.21	0.47
32:1g:118:ILE:HG23	41:1p:159:LYS:NZ	2.30	0.47
39:1n:134:ARG:HD2	39:1n:161:ASP:OD2	2.14	0.47
3:1C:11:ILE:HD11	43:1r:56:ARG:HA	1.96	0.47
5:1E:201:SER:HB2	6:1F:268:VAL:HG23	1.97	0.47
6:1F:95:VAL:HG21	6:1F:122:CYS:SG	2.55	0.47
7:1G:539:LYS:O	58:1G:902:HOH:O	2.20	0.47
7:1G:605:GLU:HG2	22:1W:119:LEU:HD22	1.96	0.47
9:1I:75:GLU:OE2	9:1I:151:LYS:NZ	2.48	0.47
11:1K:4:VAL:O	11:1K:8:ILE:HG12	2.14	0.47
12:1L:459:ILE:HG22	50:1j:101:3PE:H292	1.96	0.47
12:1L:591:PHE:CE1	14:1N:111:PHE:HA	2.50	0.47
19:1S:82:SER:O	19:1S:86:VAL:HG23	2.14	0.47
23:1X:23:VAL:HG22	23:1X:85:TRP:CD2	2.50	0.47
29:1d:11:LEU:HD11	30:1e:5:VAL:HA	1.96	0.47
30:1e:94:PRO:HD2	30:1e:97:HIS:HB2	1.97	0.47
37:1l:136:ASN:HA	37:1l:153:VAL:HB	1.96	0.47
8:1H:46:LEU:HD23	45:1q:201:PC1:H2C2	1.97	0.47
12:1L:298:ILE:O	12:1L:302:VAL:HG23	2.15	0.47
50:1L:703:3PE:H322	50:1L:703:3PE:H32	1.53	0.47
20:1T:17:TYR:O	20:1T:21:LEU:HG	2.15	0.47
25:1Z:130:ASN:O	25:1Z:134:LEU:HB2	2.15	0.47
29:1d:28:ASP:O	29:1d:32:VAL:HG23	2.15	0.47
8:1H:264:LEU:O	8:1H:268:ILE:HG12	2.15	0.47
26:1a:4:GLU:O	26:1a:7:PRO:HD2	2.15	0.47
40:1o:17:ASP:O	40:1o:21:MET:HG2	2.14	0.47
10:1J:7:PHE:CZ	11:1K:3:LEU:HD23	2.49	0.46
10:1J:96:GLY:O	10:1J:99:MET:HG3	2.15	0.46
12:1L:144:TRP:CZ2	12:1L:223:LYS:HG3	2.50	0.46
13:1M:207:MET:HE1	13:1M:297:VAL:HG12	1.96	0.46
23:1X:79:GLU:O	23:1X:83:GLU:HG3	2.15	0.46
39:1n:122:GLU:OE2	39:1n:122:GLU:HA	2.15	0.46
4:1D:246:THR:HG22	4:1D:249:ASP:H	1.80	0.46
6:1F:95:VAL:HG22	6:1F:228:VAL:HG21	1.97	0.46
7:1G:366:THR:O	7:1G:367:THR:OG1	2.32	0.46
7:1G:486:ASP:OD1	7:1G:486:ASP:N	2.44	0.46
50:1J:201:3PE:H2C2	12:1L:592:LEU:HD21	1.97	0.46
13:1M:165:VAL:HG21	14:1N:267:ILE:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:1f:48:LEU:HD13	31:1f:53:GLU:HA	1.97	0.46
31:1f:49:ARG:NH2	58:1f:205:HOH:O	2.49	0.46
4:1D:232:ASN:O	4:1D:236:ARG:HG3	2.16	0.46
12:1L:56:HIS:CD2	41:1p:27:ASN:HD21	2.34	0.46
13:1M:173:SER:HB2	33:1h:101:ALA:HB2	1.97	0.46
14:1N:321:LYS:NZ	51:1N:902:CDL:OA3	2.41	0.46
28:1c:43:LYS:HA	58:1c:116:HOH:O	2.14	0.46
45:1d:203:PC1:H132	45:1d:203:PC1:H111	1.76	0.46
1:1A:54:LYS:CD	1:1A:113:TRP:HA	2.45	0.46
3:1C:95:ASN:ND2	58:1C:307:HOH:O	2.31	0.46
7:1G:190:MET:SD	7:1G:190:MET:N	2.82	0.46
10:1J:107:ALA:HB1	11:1K:3:LEU:HD11	1.97	0.46
11:1K:34:GLU:OE1	11:1K:34:GLU:HA	2.15	0.46
13:1M:367:LEU:CD2	13:1M:404:ALA:HA	2.45	0.46
27:1b:15:GLU:OE2	50:1b:201:3PE:H31	2.16	0.46
8:1H:2:PHE:CE2	8:1H:6:ILE:HD11	2.50	0.46
10:1J:26:PRO:HB2	10:1J:72:THR:HG21	1.98	0.46
50:1L:702:3PE:H281	51:1h:201:CDL:HB62	1.98	0.46
13:1M:175:ASN:HD22	13:1M:178:ILE:H	1.63	0.46
23:1X:121:LEU:HB3	27:1b:81:LYS:HE2	1.98	0.46
29:1d:10:PRO:HA	45:1d:203:PC1:H241	1.97	0.46
6:1F:90:PRO:O	6:1F:218:CYS:HB3	2.16	0.46
7:1G:157:THR:HG22	7:1G:157:THR:O	2.15	0.46
10:1J:86:ASN:HD22	11:1K:23:ARG:NH2	2.14	0.46
12:1L:264:TYR:CD2	12:1L:265:PRO:HD3	2.51	0.46
15:1O:25:ILE:O	15:1O:123:VAL:HA	2.16	0.46
16:1P:195:SER:HB2	16:1P:199:GLU:OE1	2.14	0.46
17:1Q:127:ARG:NE	44:1s:70:ARG:HH12	2.14	0.46
20:1T:58:PHE:CE2	20:1T:80:ILE:HG13	2.50	0.46
30:1e:83:ASP:O	30:1e:87:LYS:HG2	2.15	0.46
1:1A:90:MET:HE2	10:1J:151:THR:HG23	1.98	0.46
5:1E:202:LEU:HD22	6:1F:23:THR:HA	1.97	0.46
8:1H:63:PRO:HG3	8:1H:214:GLU:HB3	1.96	0.46
13:1M:343:ILE:O	13:1M:346:ARG:NH1	2.42	0.46
31:1f:41:SER:O	31:1f:45:LYS:HE2	2.15	0.46
32:1g:23:THR:HB	32:1g:25:ARG:HH12	1.81	0.46
33:1h:34:ILE:HB	33:1h:35:PRO:HD3	1.98	0.46
35:1j:8:GLU:OE1	35:1j:9:PRO:HD2	2.15	0.46
42:1q:32:ASP:OD2	42:1q:58:ARG:NH2	2.48	0.46
1:1A:1:FME:HG2	1:1A:4:MET:HB2	1.97	0.46
8:1H:124:ASN:HB3	8:1H:125:SER:H	1.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1I:114:THR:HG21	9:1I:144:HIS:CE1	2.51	0.46
12:1L:397:GLU:HG2	12:1L:482:MET:HE1	1.98	0.46
12:1L:558:LEU:HD21	50:1m:203:3PE:H2H2	1.97	0.46
14:1N:106:LEU:HG	14:1N:138:PRO:HB2	1.98	0.46
25:1Z:19:ILE:O	25:1Z:19:ILE:HG13	2.14	0.46
32:1g:25:ARG:O	32:1g:26:LEU:HB3	2.15	0.46
34:1i:52:ASP:HB3	34:1i:57:LYS:HE3	1.96	0.46
41:1p:92:ARG:O	41:1p:96:LYS:NZ	2.43	0.46
42:1q:75:TRP:CD1	45:1q:202:PC1:H132	2.50	0.46
3:1C:173:GLU:HG3	3:1C:188:VAL:HA	1.98	0.46
7:1G:575:ASN:OD1	7:1G:579:ARG:HG3	2.16	0.46
11:1K:73:LEU:HD11	14:1N:41:ILE:HG21	1.97	0.46
14:1N:27:LEU:O	14:1N:31:ILE:HG12	2.16	0.46
18:1R:19:ASP:OD1	18:1R:19:ASP:N	2.42	0.46
23:1X:168:PHE:CE1	51:1X:201:CDL:H172	2.50	0.46
37:1l:68:ASP:OD2	58:1l:302:HOH:O	2.21	0.46
12:1L:571:MET:HE2	12:1L:571:MET:HB3	1.74	0.46
14:1N:211:MET:HG3	14:1N:333:SER:HB2	1.97	0.46
16:1P:209:ASP:N	16:1P:209:ASP:OD1	2.48	0.46
23:1X:105:LYS:HD3	23:1X:106:PHE:N	2.31	0.46
31:1f:7:VAL:O	31:1f:11:TRP:HB3	2.16	0.46
3:1C:69:ASN:O	43:1r:96:PRO:HD3	2.17	0.45
6:1F:68:ARG:O	6:1F:106:LYS:NZ	2.40	0.45
7:1G:643:GLN:O	7:1G:647:GLU:HG2	2.16	0.45
9:1I:151:LYS:HE3	18:1R:13:HIS:CE1	2.52	0.45
14:1N:54:GLU:OE2	14:1N:58:LYS:NZ	2.44	0.45
14:1N:203:LEU:O	14:1N:207:ILE:HG12	2.16	0.45
25:1Z:104:TRP:HH2	30:1e:74:ARG:HG3	1.80	0.45
41:1p:59:ARG:HA	41:1p:59:ARG:HD3	1.67	0.45
7:1G:601:ARG:NH2	7:1G:614:ASP:OD2	2.47	0.45
8:1H:149:ILE:HG12	8:1H:181:LEU:HD22	1.98	0.45
9:1I:4:PHE:HB3	9:1I:7:MET:HB2	1.99	0.45
16:1P:136:ASN:ND2	16:1P:292:MET:H	2.14	0.45
29:1d:39:TYR:CE2	50:1d:201:3PE:H2E2	2.51	0.45
41:1p:139:GLN:O	41:1p:143:SER:HB2	2.16	0.45
2:1B:32:LYS:HD2	2:1B:32:LYS:HA	1.71	0.45
7:1G:148:THR:OG1	7:1G:148:THR:O	2.33	0.45
10:1J:19:GLY:HA2	10:1J:93:PHE:HD2	1.80	0.45
12:1L:257:VAL:HG22	12:1L:329:ILE:HD11	1.98	0.45
12:1L:489:THR:O	12:1L:493:VAL:HG22	2.16	0.45
16:1P:274:PRO:HG2	16:1P:275:PHE:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1Q:59:PHE:CE2	17:1Q:79:LEU:HD13	2.52	0.45
22:1W:35:LEU:HD21	22:1W:86:GLY:HA3	1.98	0.45
26:1a:21:MET:HE3	26:1a:21:MET:HB3	1.90	0.45
37:1l:99:ASN:O	37:1l:103:LYS:HG3	2.16	0.45
7:1G:331:LEU:HD22	7:1G:525:LEU:HD22	1.99	0.45
12:1L:188:TRP:CZ2	50:1L:703:3PE:H121	2.51	0.45
14:1N:210:THR:HG22	14:1N:333:SER:HB3	1.98	0.45
16:1P:173:GLY:N	16:1P:176:ASP:HB3	2.31	0.45
23:1X:74:LYS:NZ	26:1a:66:LEU:O	2.37	0.45
32:1g:90:ARG:HA	32:1g:90:ARG:HD3	1.77	0.45
34:1i:87:TYR:CE1	41:1p:48:ARG:HG2	2.51	0.45
8:1H:102:VAL:HG22	8:1H:160:TYR:HD1	1.81	0.45
10:1J:113:VAL:HG22	10:1J:119:PHE:HB2	1.98	0.45
12:1L:115:ASN:OD1	58:1L:805:HOH:O	2.21	0.45
15:1O:97:GLN:HE21	15:1O:135:LEU:HB2	1.81	0.45
16:1P:135:LEU:HA	16:1P:167:LYS:HB3	1.97	0.45
19:1S:31:GLY:HA3	19:1S:81:PHE:O	2.17	0.45
30:1e:36:GLU:HG3	30:1e:62:PHE:CE2	2.51	0.45
34:1i:111:GLU:OE1	34:1i:111:GLU:N	2.46	0.45
6:1F:129:MET:SD	6:1F:221:THR:HB	2.57	0.45
10:1J:52:LEU:O	10:1J:56:VAL:HG23	2.17	0.45
13:1M:12:LEU:HB2	13:1M:13:PRO:HD3	1.98	0.45
15:1O:180:GLN:O	15:1O:184:GLN:HG2	2.16	0.45
26:1a:1:MET:O	26:1a:4:GLU:HG3	2.16	0.45
8:1H:152:SER:HA	8:1H:155:LEU:HD12	1.99	0.45
12:1L:54:PHE:CZ	12:1L:84:TYR:HB2	2.51	0.45
12:1L:203:MET:HE1	41:1p:124:CYS:HB2	1.98	0.45
13:1M:76:MET:HE1	58:1M:675:HOH:O	2.17	0.45
15:1O:257:HIS:O	15:1O:261:MET:HG2	2.17	0.45
16:1P:13:ARG:NH2	16:1P:61:PRO:O	2.48	0.45
16:1P:93:ASN:ND2	16:1P:131:HIS:HD2	2.13	0.45
33:1h:102:GLU:OE1	58:1h:304:HOH:O	2.20	0.45
41:1p:40:VAL:O	41:1p:44:VAL:HG13	2.16	0.45
42:1q:9:ARG:NH1	51:1q:203:CDL:OA2	2.49	0.45
43:1r:5:ARG:HD2	43:1r:5:ARG:HA	1.76	0.45
1:1A:96:ILE:HD11	27:1b:29:ILE:HD11	1.99	0.45
4:1D:43:LEU:O	58:1D:502:HOH:O	2.21	0.45
6:1F:45:THR:O	6:1F:49:LEU:HG	2.17	0.45
6:1F:324:GLN:NE2	58:1F:611:HOH:O	2.47	0.45
11:1K:82:SER:O	11:1K:86:GLY:N	2.47	0.45
12:1L:90:ILE:HG12	12:1L:129:MET:SD	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1M:97:THR:O	13:1M:101:LEU:HG	2.17	0.45
14:1N:128:LEU:O	14:1N:132:THR:OG1	2.24	0.45
15:1O:7:ALA:O	15:1O:12:GLU:HB2	2.16	0.45
15:1O:29:GLY:HA2	15:1O:171:TYR:CE1	2.52	0.45
15:1O:45:LYS:HD3	15:1O:235:VAL:HG21	1.98	0.45
16:1P:133:SER:OG	16:1P:167:LYS:HG2	2.16	0.45
25:1Z:104:TRP:CH2	30:1e:74:ARG:HG3	2.52	0.45
28:1c:48:LEU:HD22	58:1c:116:HOH:O	2.15	0.45
37:1l:26:LYS:NZ	37:1l:46:ASP:OD2	2.42	0.45
39:1n:117:TYR:HA	39:1n:120:LYS:NZ	2.31	0.45
41:1p:72:ASP:N	41:1p:75:GLU:OE2	2.47	0.45
1:1A:40:GLY:HA2	2:1B:103:VAL:HG13	1.99	0.45
2:1B:75:VAL:HG12	8:1H:25:ARG:NH2	2.32	0.45
5:1E:162:GLU:OE2	6:1F:108:ARG:NH1	2.48	0.45
6:1F:297:VAL:HG22	6:1F:336:VAL:HB	1.99	0.45
11:1K:81:VAL:HG11	11:1K:93:LEU:HD21	1.99	0.45
20:1U:51:ILE:HG21	20:1U:67:ALA:HB1	1.99	0.45
23:1X:141:TYR:O	58:1X:3402:HOH:O	2.20	0.45
29:1d:8:ARG:NH1	45:1d:203:PC1:H232	2.32	0.45
29:1d:113:LEU:HD22	32:1g:121:PRO:HG3	1.98	0.45
31:1f:25:TYR:CZ	31:1f:29:ARG:HD2	2.52	0.45
32:1g:50:ASP:HB3	32:1g:53:VAL:CG1	2.47	0.45
32:1g:114:ASP:OD2	32:1g:116:ASN:HB2	2.17	0.45
41:1p:26:PRO:HB2	41:1p:31:TYR:HE2	1.82	0.45
1:1A:104:TYR:CE2	10:1J:169:MET:HE2	2.52	0.45
8:1H:42:PRO:HG3	42:1q:28:PHE:CE1	2.52	0.45
30:1e:35:PHE:CE1	30:1e:61:ASP:HB3	2.51	0.45
32:1g:59:ARG:NH1	58:1g:215:HOH:O	2.50	0.45
43:1r:57:ASP:O	43:1r:61:GLU:HG3	2.17	0.45
5:1E:153:MET:HE2	5:1E:153:MET:HB2	1.85	0.44
6:1F:288:ILE:H	6:1F:288:ILE:HG13	1.60	0.44
7:1G:306:MET:HG3	7:1G:542:PHE:CG	2.52	0.44
7:1G:391:PHE:CE2	7:1G:395:ILE:HD11	2.52	0.44
9:1I:50:TYR:CD1	9:1I:51:PRO:HA	2.52	0.44
9:1I:52:PHE:CZ	42:1q:30:ALA:HA	2.51	0.44
12:1L:80:PHE:CZ	51:1h:201:CDL:H422	2.52	0.44
12:1L:210:ASN:ND2	50:1L:703:3PE:O22	2.50	0.44
13:1M:2:LEU:HD23	31:1f:26:LEU:HB3	1.99	0.44
23:1X:71:ARG:O	23:1X:75:ARG:HG2	2.16	0.44
23:1X:82:THR:HA	23:1X:85:TRP:CD1	2.52	0.44
24:1Y:94:CYS:HA	24:1Y:114:CYS:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1i:101:PRO:CD	41:1p:14:ARG:HH22	2.30	0.44
40:1o:111:LYS:NZ	58:1o:209:HOH:O	2.46	0.44
6:1F:262:VAL:CG1	6:1F:284:ALA:HB1	2.45	0.44
13:1M:231:LEU:HA	13:1M:235:LEU:HD12	1.99	0.44
32:1g:114:ASP:HB3	32:1g:117:LYS:HD3	1.99	0.44
1:1A:54:LYS:HD2	1:1A:113:TRP:HA	1.99	0.44
4:1D:244:VAL:HA	4:1D:291:GLY:O	2.18	0.44
8:1H:24:GLU:HB2	8:1H:271:LEU:HD22	1.99	0.44
8:1H:126:LYS:HD2	8:1H:126:LYS:HA	1.79	0.44
9:1I:19:ASP:HB3	45:1I:203:PC1:H131	1.99	0.44
58:1M:753:HOH:O	14:1N:276:ILE:HG22	2.17	0.44
14:1N:339:MET:O	45:1d:203:PC1:H3E2	2.17	0.44
15:1O:27:VAL:HB	58:1O:602:HOH:O	2.17	0.44
16:1P:171:ILE:O	58:1P:502:HOH:O	2.21	0.44
20:1T:16:LEU:O	20:1T:20:LYS:HG2	2.16	0.44
50:1Y:801:3PE:H231	50:1Y:801:3PE:O32	2.16	0.44
28:1c:21:LEU:O	28:1c:25:VAL:HG23	2.17	0.44
37:1I:57:GLU:OE1	37:1I:92:SER:HA	2.16	0.44
39:1n:21:ARG:HG2	39:1n:70:PHE:CZ	2.53	0.44
2:1B:71:ARG:NH2	9:1I:49:ASN:OD1	2.50	0.44
6:1F:20:ARG:NE	6:1F:269:GLU:O	2.48	0.44
6:1F:206:LYS:N	6:1F:207:PRO:HD2	2.32	0.44
6:1F:400:GLU:OE2	6:1F:413:TRP:NE1	2.34	0.44
9:1I:74:GLU:HB2	18:1R:44:ILE:HB	1.99	0.44
9:1I:175:TYR:CZ	43:1r:38:PRO:HG3	2.52	0.44
12:1L:10:THR:O	12:1L:14:ILE:HG22	2.16	0.44
12:1L:245:ALA:HB2	12:1L:340:PHE:HB3	1.99	0.44
23:1X:56:LEU:HD21	25:1Z:84:LEU:HD12	1.99	0.44
3:1C:116:PRO:HB3	3:1C:141:PHE:HD2	1.83	0.44
6:1F:394:GLU:OE1	58:1F:603:HOH:O	2.21	0.44
12:1L:358:LYS:HG3	39:1n:79:TYR:CE1	2.52	0.44
16:1P:57:MET:SD	16:1P:60:ARG:HD2	2.57	0.44
45:1H:402:PC1:H151	25:1Z:140:PHE:CZ	2.53	0.44
45:1M:502:PC1:H2	45:1M:502:PC1:H221	1.55	0.44
39:1n:131:SER:HA	39:1n:134:ARG:CZ	2.48	0.44
4:1D:270:ARG:HG3	4:1D:368:GLU:HB3	2.00	0.44
10:1J:94:VAL:O	10:1J:98:MET:HG2	2.17	0.44
10:1J:115:ILE:O	10:1J:117:PHE:N	2.48	0.44
12:1L:257:VAL:CG2	12:1L:329:ILE:HD11	2.48	0.44
12:1L:346:ILE:HD11	12:1L:431:PHE:CZ	2.53	0.44
13:1M:153:THR:O	13:1M:157:SER:OG	2.27	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:1P:82:ARG:O	16:1P:86:GLU:HG3	2.18	0.44
16:1P:194:ILE:HD13	16:1P:288:HIS:HB2	1.99	0.44
16:1P:200:THR:HB	16:1P:238:LEU:HB2	1.99	0.44
51:1X:201:CDL:H422	29:1d:36:PHE:CE2	2.52	0.44
29:1d:46:ASN:CB	29:1d:53:VAL:HA	2.47	0.44
51:1h:201:CDL:H511	51:1h:201:CDL:HB4	1.77	0.44
4:1D:119:SER:HA	4:1D:196:PRO:HG3	2.00	0.44
5:1E:24:THR:HG23	5:1E:27:ASN:H	1.83	0.44
8:1H:107:ALA:O	8:1H:111:LEU:HG	2.17	0.44
11:1K:1:FME:SD	14:1N:79:LEU:HD21	2.58	0.44
12:1L:562:LEU:HB2	12:1L:563:PRO:HD3	2.00	0.44
23:1X:70:PHE:HB3	26:1a:70:ASP:C	2.43	0.44
23:1X:97:ARG:HD2	25:1Z:60:LEU:HD13	1.99	0.44
24:1Y:14:GLY:O	24:1Y:78:GLN:HB3	2.18	0.44
25:1Z:95:ALA:O	25:1Z:99:LYS:HG2	2.17	0.44
34:1i:105:PRO:HG2	34:1i:119:MET:CG	2.48	0.44
4:1D:104:ASP:OD1	4:1D:111:MET:HB3	2.18	0.44
6:1F:125:GLY:O	6:1F:129:MET:HE3	2.17	0.44
6:1F:261:HIS:CD2	6:1F:337:MET:HA	2.53	0.44
8:1H:294:LEU:O	8:1H:298:LEU:HG	2.18	0.44
13:1M:42:LEU:HB3	13:1M:453:MET:HE3	2.00	0.44
18:1R:7:THR:HG23	18:1R:9:GLU:H	1.82	0.44
32:1g:92:GLU:OE1	41:1p:64:HIS:NE2	2.42	0.44
12:1L:89:PHE:CD2	12:1L:132:VAL:HG21	2.53	0.43
12:1L:201:ILE:HG21	12:1L:263:PHE:HE1	1.83	0.43
12:1L:496:MET:HE2	12:1L:496:MET:HB3	1.90	0.43
13:1M:129:THR:HG23	58:1M:788:HOH:O	2.18	0.43
14:1N:167:TRP:HZ2	50:1N:901:3PE:H2I1	1.83	0.43
14:1N:175:LEU:O	14:1N:179:MET:HG2	2.18	0.43
43:1r:42:VAL:HB	43:1r:46:HIS:CG	2.53	0.43
1:1A:83:ASN:ND2	45:1A:201:PC1:H112	2.33	0.43
2:1B:150:PRO:HD3	4:1D:190:HIS:CD2	2.54	0.43
4:1D:141:PHE:O	4:1D:145:THR:OG1	2.28	0.43
4:1D:425:PHE:HA	4:1D:428:VAL:HB	2.00	0.43
5:1E:78:MET:O	5:1E:82:GLU:HG3	2.18	0.43
7:1G:24:THR:HG23	7:1G:28:GLN:HB2	1.99	0.43
7:1G:39:ARG:HB2	47:1G:803:FES:S2	2.57	0.43
7:1G:168:GLY:O	58:1G:904:HOH:O	2.21	0.43
7:1G:344:CYS:HB3	7:1G:510:GLY:O	2.17	0.43
9:1I:151:LYS:HE3	18:1R:13:HIS:NE2	2.34	0.43
12:1L:93:ALA:O	12:1L:97:THR:HG22	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1M:95:TYR:HD1	13:1M:136:TRP:CD2	2.37	0.43
14:1N:68:MET:HA	14:1N:68:MET:HE2	2.00	0.43
24:1Y:44:PRO:HA	24:1Y:45:PRO:HD3	1.90	0.43
26:1a:69:ILE:HG23	26:1a:70:ASP:H	1.82	0.43
40:1o:65:LEU:HD12	40:1o:79:CYS:SG	2.58	0.43
1:1A:7:LEU:HD11	45:1H:402:PC1:H331	2.00	0.43
1:1A:58:VAL:HG21	8:1H:286:MET:CE	2.48	0.43
1:1A:63:LEU:HD23	11:1K:72:ALA:HB2	2.01	0.43
2:1B:137:ASP:HA	2:1B:140:VAL:O	2.18	0.43
4:1D:302:GLU:HG2	9:1I:3:LYS:HD2	2.00	0.43
6:1F:111:ILE:HG21	6:1F:138:ILE:HD12	2.00	0.43
7:1G:300:LEU:HB3	7:1G:606:ILE:HD12	2.00	0.43
7:1G:383:ASN:ND2	7:1G:413:VAL:HG21	2.34	0.43
8:1H:307:LEU:HB3	8:1H:308:PRO:HD3	2.00	0.43
14:1N:245:MET:HB2	14:1N:301:SER:OG	2.17	0.43
21:1V:34:LEU:O	21:1V:44:ARG:HD2	2.19	0.43
23:1X:157:LEU:HD23	23:1X:157:LEU:HA	1.85	0.43
50:1Y:804:3PE:H322	50:1Y:804:3PE:H32	1.67	0.43
28:1c:48:LEU:HD23	58:1c:114:HOH:O	2.18	0.43
6:1F:120:GLU:HG2	6:1F:232:PRO:CG	2.49	0.43
6:1F:237:ARG:HD3	6:1F:241:TRP:CE2	2.54	0.43
7:1G:11:VAL:HG11	7:1G:73:VAL:HB	1.99	0.43
7:1G:249:ARG:NH1	58:1G:933:HOH:O	2.44	0.43
19:1S:17:GLU:HB2	19:1S:51:PRO:HB2	2.01	0.43
37:1l:65:ASP:OD1	38:1m:43:LYS:NZ	2.50	0.43
6:1F:8:LYS:HE2	6:1F:8:LYS:HB2	1.92	0.43
7:1G:273:GLY:O	7:1G:549:HIS:NE2	2.47	0.43
7:1G:359:ARG:HG3	7:1G:362:TYR:OH	2.18	0.43
10:1J:92:ALA:HB2	50:1J:201:3PE:H252	2.01	0.43
50:1L:703:3PE:C31	50:1L:703:3PE:H272	2.48	0.43
15:1O:235:VAL:O	15:1O:239:GLU:HG3	2.18	0.43
15:1O:268:GLU:OE2	58:1O:502:HOH:O	2.22	0.43
35:1j:67:LEU:HD22	35:1j:71:GLU:HG3	2.01	0.43
40:1o:24:PHE:CZ	40:1o:111:LYS:HD2	2.52	0.43
4:1D:67:GLU:CD	4:1D:75:LYS:HG2	2.44	0.43
8:1H:45:LEU:HB3	45:1q:201:PC1:H2B2	2.01	0.43
14:1N:91:ASN:OD1	14:1N:93:VAL:HG13	2.18	0.43
14:1N:109:SER:HB2	14:1N:161:SER:N	2.33	0.43
14:1N:115:VAL:HB	14:1N:116:PRO:HD3	2.01	0.43
15:1O:259:LEU:O	15:1O:263:VAL:HB	2.18	0.43
23:1X:44:LEU:HD22	23:1X:130:VAL:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:1X:74:LYS:HB2	26:1a:70:ASP:OD1	2.18	0.43
25:1Z:140:PHE:HB2	26:1a:45:TRP:CD1	2.54	0.43
41:1p:140:ASP:O	41:1p:157:LYS:HE2	2.18	0.43
42:1q:2:GLU:O	42:1q:6:VAL:HG23	2.18	0.43
1:1A:48:ARG:HD2	10:1J:76:THR:O	2.19	0.43
6:1F:347:ILE:O	6:1F:351:ILE:HG12	2.19	0.43
7:1G:613:TYR:HB3	7:1G:618:GLN:HB3	2.00	0.43
8:1H:197:PRO:HB3	8:1H:278:PRO:O	2.19	0.43
10:1J:130:THR:HG21	25:1Z:124:LEU:HD12	2.00	0.43
12:1L:272:LEU:O	12:1L:276:MET:HG3	2.19	0.43
13:1M:207:MET:O	13:1M:294:MET:HG3	2.19	0.43
13:1M:432:ARG:HG2	58:1M:688:HOH:O	2.19	0.43
18:1R:77:LYS:HD3	18:1R:80:LYS:HE3	2.00	0.43
40:1o:46:ASN:ND2	58:1o:211:HOH:O	2.52	0.43
40:1o:110:ARG:O	40:1o:114:ARG:HG3	2.19	0.43
2:1B:176:TRP:HA	2:1B:179:ARG:HD2	1.99	0.43
6:1F:98:ASP:O	6:1F:139:ARG:HD2	2.19	0.43
7:1G:26:VAL:HB	7:1G:68:ALA:HA	2.00	0.43
12:1L:213:LEU:HD21	12:1L:266:LEU:HB3	1.99	0.43
14:1N:128:LEU:HD12	14:1N:216:PHE:HB3	1.99	0.43
16:1P:93:ASN:OD1	16:1P:95:VAL:HG13	2.18	0.43
19:1S:35:PHE:CZ	19:1S:90:LEU:HD12	2.53	0.43
19:1S:39:ARG:NH2	58:1S:105:HOH:O	2.49	0.43
22:1W:43:VAL:HG11	22:1W:60:ARG:HG3	2.01	0.43
24:1Y:65:ILE:HD11	24:1Y:100:LEU:HB2	2.01	0.43
25:1Z:111:PHE:CE2	25:1Z:117:VAL:HG11	2.53	0.43
40:1o:30:PHE:HB3	40:1o:33:ARG:HD3	2.00	0.43
40:1o:52:LEU:HA	40:1o:55:ARG:HG3	2.01	0.43
5:1E:26:GLU:OE2	58:1E:401:HOH:O	2.21	0.43
8:1H:173:TRP:CB	8:1H:175:ILE:HG22	2.49	0.43
9:1I:35:GLY:HA2	45:1I:203:PC1:H361	2.01	0.43
11:1K:40:LEU:HD21	14:1N:72:MET:HB2	1.99	0.43
13:1M:52:PHE:O	33:1h:89:LYS:NZ	2.43	0.43
13:1M:206:LYS:HE3	58:1M:639:HOH:O	2.19	0.43
15:1O:315:LYS:HD2	15:1O:315:LYS:HA	1.81	0.43
20:1T:24:LYS:HA	20:1T:24:LYS:HD3	1.81	0.43
22:1W:39:TRP:O	22:1W:43:VAL:HG23	2.19	0.43
23:1X:63:ASN:OD1	25:1Z:81:ARG:NH2	2.52	0.43
24:1Y:12:PRO:HG2	24:1Y:15:THR:OG1	2.19	0.43
26:1a:64:LYS:HD3	26:1a:64:LYS:HA	1.81	0.43
30:1e:90:LYS:HA	30:1e:90:LYS:HD3	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1D:417:ILE:O	4:1D:420:THR:HG22	2.19	0.43
10:1J:163:ILE:HD13	10:1J:163:ILE:HA	1.87	0.43
13:1M:176:PHE:CE1	13:1M:245:ARG:HB3	2.54	0.43
13:1M:397:GLY:O	13:1M:400:MET:HG2	2.18	0.43
20:1T:12:LYS:HD2	20:1T:77:VAL:HG21	2.00	0.43
20:1U:3:ALA:HA	20:1U:4:PRO:HD3	1.89	0.43
20:1U:36:PHE:HD1	20:1U:40:LEU:HD12	1.84	0.43
22:1W:92:GLU:HB2	22:1W:98:LYS:HD2	2.01	0.43
23:1X:48:GLU:OE1	23:1X:137:PRO:HD2	2.19	0.43
23:1X:136:LEU:HD23	23:1X:137:PRO:HD2	2.00	0.43
30:1e:49:ILE:O	30:1e:53:LYS:HD2	2.19	0.43
34:1i:85:LEU:HD23	34:1i:89:VAL:HG21	2.01	0.43
39:1n:91:GLU:HA	39:1n:94:GLU:OE1	2.19	0.43
6:1F:194:GLU:OE2	6:1F:199:LYS:NZ	2.35	0.42
9:1I:70:TYR:CE2	9:1I:76:ARG:HA	2.54	0.42
12:1L:142:ILE:HD11	13:1M:371:PRO:HB3	2.01	0.42
13:1M:436:LEU:HB2	58:1M:688:HOH:O	2.19	0.42
14:1N:325:LEU:HD12	51:1N:902:CDL:H351	2.01	0.42
23:1X:37:LYS:HA	23:1X:37:LYS:HD2	1.87	0.42
23:1X:171:MET:HE2	23:1X:171:MET:HB3	1.85	0.42
50:1Y:803:3PE:H2	50:1Y:803:3PE:H221	1.53	0.42
30:1e:73:LYS:HD2	30:1e:73:LYS:O	2.19	0.42
38:1m:89:GLY:C	50:1m:203:3PE:H2B1	2.43	0.42
1:1A:78:ALA:O	1:1A:81:THR:HG22	2.19	0.42
4:1D:405:MET:SD	4:1D:421:GLN:NE2	2.86	0.42
50:1L:701:3PE:H32	50:1L:701:3PE:H321	1.22	0.42
15:1O:223:TYR:CE2	15:1O:234:VAL:HG13	2.53	0.42
16:1P:132:ILE:HD13	16:1P:166:ILE:HB	2.01	0.42
23:1X:2:GLY:O	25:1Z:109:SER:N	2.34	0.42
24:1Y:54:ARG:HG3	50:1Y:802:3PE:N	2.33	0.42
27:1b:40:TYR:O	27:1b:44:ILE:HG13	2.18	0.42
30:1e:6:GLN:HG2	30:1e:13:LEU:HG	2.00	0.42
39:1n:117:TYR:HA	39:1n:120:LYS:HZ2	1.84	0.42
4:1D:279:ASP:OD1	4:1D:279:ASP:N	2.51	0.42
8:1H:65:THR:HA	16:1P:324:TYR:HB2	2.00	0.42
50:1L:702:3PE:H3B1	13:1M:448:THR:HG22	2.01	0.42
13:1M:279:GLN:NE2	58:1M:631:HOH:O	2.50	0.42
13:1M:424:ASN:HA	39:1n:101:TRP:CE2	2.54	0.42
14:1N:215:MET:HG3	14:1N:251:MET:SD	2.59	0.42
35:1j:54:PRO:HG3	40:1o:95:VAL:HG13	2.01	0.42
5:1E:190:ARG:NH2	6:1F:265:PRO:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:1L:218:LEU:HD22	50:1L:703:3PE:H2H1	2.01	0.42
14:1N:98:MET:HE2	14:1N:98:MET:HB2	1.89	0.42
23:1X:22:SER:OG	23:1X:94:GLN:NE2	2.48	0.42
2:1B:91:THR:HG21	4:1D:85:ARG:HG2	2.02	0.42
4:1D:292:ASP:OD1	4:1D:292:ASP:N	2.52	0.42
5:1E:165:THR:C	5:1E:167:LYS:H	2.27	0.42
6:1F:327:THR:OG1	6:1F:328:GLY:N	2.53	0.42
10:1J:141:MET:HA	10:1J:141:MET:HE2	2.01	0.42
12:1L:2:ASN:O	58:1L:801:HOH:O	2.21	0.42
12:1L:13:ILE:HG13	34:1i:81:ILE:CD1	2.46	0.42
12:1L:247:LEU:O	12:1L:252:MET:HB3	2.19	0.42
13:1M:43:ASN:HA	58:1M:729:HOH:O	2.20	0.42
17:1Q:36:ARG:NH2	17:1Q:106:GLU:OE1	2.47	0.42
29:1d:53:VAL:HG22	50:1d:201:3PE:HN2	1.84	0.42
30:1e:87:LYS:HB2	30:1e:88:GLU:OE2	2.18	0.42
39:1n:129:ARG:HG3	58:1n:322:HOH:O	2.20	0.42
7:1G:444:LYS:HE2	7:1G:445:GLU:HG3	2.00	0.42
7:1G:615:THR:HG23	7:1G:617:ASP:H	1.84	0.42
8:1H:81:LEU:O	8:1H:85:MET:HG3	2.19	0.42
8:1H:195:ARG:HD3	8:1H:231:ILE:HD11	2.00	0.42
12:1L:124:PHE:CZ	12:1L:252:MET:HB2	2.54	0.42
13:1M:91:ARG:HG2	50:1M:503:3PE:H332	2.01	0.42
50:1M:503:3PE:H2F2	14:1N:256:PRO:HG2	2.02	0.42
17:1Q:30:ILE:O	58:1Q:202:HOH:O	2.21	0.42
29:1d:57:GLY:O	29:1d:61:GLN:HG3	2.18	0.42
33:1h:77:ARG:NH1	45:1h:202:PC1:H122	2.35	0.42
5:1E:50:VAL:HG12	5:1E:69:VAL:HG22	2.00	0.42
6:1F:57:LEU:O	6:1F:61:LYS:HG3	2.19	0.42
6:1F:237:ARG:HD3	6:1F:241:TRP:CD2	2.54	0.42
7:1G:424:ASP:OD2	7:1G:660:PRO:HB3	2.20	0.42
9:1I:31:VAL:HG13	45:1I:203:PC1:H371	2.01	0.42
10:1J:19:GLY:HA2	10:1J:93:PHE:CD2	2.55	0.42
13:1M:44:GLN:HB2	32:1g:83:TYR:CE2	2.54	0.42
50:1M:503:3PE:H322	50:1M:503:3PE:H31	1.26	0.42
14:1N:170:LEU:O	14:1N:295:ARG:NH2	2.43	0.42
14:1N:287:LEU:HB3	50:1N:901:3PE:H291	2.01	0.42
15:1O:27:VAL:HG23	15:1O:35:LYS:HB3	2.02	0.42
19:1S:34:ASP:OD1	58:1S:102:HOH:O	2.22	0.42
29:1d:13:PHE:O	29:1d:78:ARG:NH1	2.52	0.42
40:1o:33:ARG:HA	40:1o:33:ARG:HD2	1.88	0.42
44:1s:38:TYR:CZ	44:1s:40:ASN:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:50:PHE:CE1	2:1B:103:VAL:HG21	2.55	0.42
4:1D:128:ILE:HD13	4:1D:330:VAL:HG11	2.01	0.42
6:1F:42:TRP:HD1	58:1F:661:HOH:O	2.02	0.42
7:1G:36:GLN:NE2	17:1Q:47:SER:O	2.52	0.42
7:1G:122:MET:HA	43:1r:60:ARG:HH22	1.84	0.42
8:1H:66:SER:HA	8:1H:122:ALA:O	2.20	0.42
10:1J:150:GLY:HA2	30:1e:16:TRP:CZ2	2.54	0.42
12:1L:267:MET:HE3	12:1L:267:MET:HB3	1.83	0.42
12:1L:338:MET:HE1	12:1L:372:ALA:O	2.20	0.42
19:1S:38:LYS:HE3	19:1S:38:LYS:HB2	1.63	0.42
20:1T:48:VAL:HG13	22:1W:37:ARG:HE	1.85	0.42
24:1Y:124:VAL:HA	50:1Y:803:3PE:H251	2.02	0.42
25:1Z:103:ASP:OD1	25:1Z:103:ASP:N	2.52	0.42
26:1a:34:LYS:HE2	26:1a:34:LYS:HB2	1.65	0.42
38:1m:13:LEU:HD12	38:1m:14:PRO:HD2	2.02	0.42
43:1r:105:LEU:HD23	43:1r:105:LEU:HA	1.89	0.42
3:1C:116:PRO:HD3	22:1W:20:ILE:HD13	2.02	0.42
4:1D:19:MET:HB2	14:1N:171:ASN:HA	2.02	0.42
5:1E:151:ALA:HB3	5:1E:163:ASP:HA	2.01	0.42
7:1G:102:PRO:HG3	7:1G:151:THR:OG1	2.19	0.42
15:1O:21:THR:HG22	15:1O:48:LEU:HD21	2.02	0.42
20:1T:11:ILE:O	20:1T:15:VAL:HG23	2.20	0.42
20:1U:29:LYS:HB3	20:1U:29:LYS:HE3	1.90	0.42
26:1a:37:ARG:HB3	26:1a:48:MET:SD	2.60	0.42
29:1d:100:ASP:CG	33:1h:117:ARG:HH22	2.27	0.42
32:1g:50:ASP:HB3	32:1g:53:VAL:HG12	2.01	0.42
39:1n:26:LEU:HD11	39:1n:39:PHE:HB3	2.02	0.42
40:1o:28:TYR:HD1	40:1o:28:TYR:HA	1.71	0.42
7:1G:427:LYS:HB2	7:1G:427:LYS:NZ	2.34	0.42
7:1G:514:ILE:HG23	7:1G:519:PRO:HD3	2.02	0.42
8:1H:115:SER:O	8:1H:119:SER:HB3	2.20	0.42
12:1L:137:LEU:HD23	12:1L:137:LEU:HA	1.89	0.42
12:1L:230:HIS:N	12:1L:231:PRO:HD3	2.35	0.42
15:1O:33:SER:N	52:1O:401:GTP:O3G	2.53	0.42
16:1P:270:PHE:CD2	16:1P:278:TRP:HB2	2.54	0.42
44:1s:71:GLN:OE1	44:1s:71:GLN:HA	2.20	0.42
1:1A:84:LEU:HD23	1:1A:84:LEU:HA	1.90	0.41
2:1B:173:LEU:HD23	2:1B:173:LEU:HA	1.91	0.41
5:1E:123:LYS:NZ	5:1E:174:ASP:OD1	2.48	0.41
5:1E:212:GLY:O	6:1F:237:ARG:HA	2.19	0.41
7:1G:61:LYS:HE2	7:1G:61:LYS:HB2	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1H:85:MET:HE1	8:1H:105:MET:O	2.20	0.41
8:1H:187:ILE:HG13	45:1H:401:PC1:H251	2.02	0.41
10:1J:103:MET:HE3	11:1K:6:MET:HG2	2.01	0.41
13:1M:76:MET:CE	13:1M:230:VAL:HB	2.44	0.41
13:1M:108:MET:HB3	13:1M:121:LEU:HD13	2.02	0.41
15:1O:97:GLN:NE2	15:1O:135:LEU:HB2	2.35	0.41
16:1P:29:PHE:CD1	16:1P:175:GLU:HG2	2.55	0.41
20:1T:48:VAL:HG22	22:1W:37:ARG:NH2	2.35	0.41
23:1X:1:PRO:HD3	58:1Z:233:HOH:O	2.20	0.41
50:1Y:802:3PE:H362	45:1m:201:PC1:H3B1	2.01	0.41
25:1Z:120:MET:HG2	25:1Z:123:GLU:OE1	2.21	0.41
44:1s:52:LEU:HD12	44:1s:52:LEU:HA	1.81	0.41
2:1B:57:VAL:HA	2:1B:60:MET:HG2	2.01	0.41
3:1C:53:HIS:NE2	21:1V:104:GLU:HB3	2.35	0.41
4:1D:237:ASN:O	8:1H:284:GLN:NE2	2.48	0.41
4:1D:329:LYS:HG2	4:1D:347:HIS:CD2	2.54	0.41
12:1L:345:SER:HB2	12:1L:450:LEU:HD11	2.02	0.41
12:1L:562:LEU:HD11	50:1m:202:3PE:H3I3	2.01	0.41
13:1M:16:TRP:HA	13:1M:93:LYS:HD3	2.02	0.41
50:1N:901:3PE:H341	50:1N:901:3PE:H271	2.03	0.41
15:1O:210:PHE:CD2	15:1O:211:LEU:HD12	2.54	0.41
17:1Q:56:LYS:HA	17:1Q:56:LYS:HD3	1.72	0.41
20:1T:44:SER:HB3	56:1W:201:EHZ:P1	2.60	0.41
22:1W:22:SER:OG	22:1W:80:ASP:OD1	2.37	0.41
24:1Y:2:LYS:O	24:1Y:6:HIS:N	2.44	0.41
24:1Y:82:LYS:O	24:1Y:88:ASN:ND2	2.53	0.41
30:1e:35:PHE:CD1	30:1e:61:ASP:HB3	2.54	0.41
32:1g:90:ARG:NH1	41:1p:9:TYR:OH	2.51	0.41
51:1h:201:CDL:HB62	51:1h:201:CDL:H712	1.66	0.41
34:1i:15:ARG:NH2	58:1i:204:HOH:O	2.37	0.41
39:1n:12:GLN:O	39:1n:16:LEU:HG	2.19	0.41
4:1D:308:LEU:HB3	25:1Z:19:ILE:HD11	2.02	0.41
5:1E:181:ILE:HD12	5:1E:181:ILE:HA	1.88	0.41
6:1F:43:TYR:CE2	6:1F:44:LYS:HG3	2.55	0.41
10:1J:119:PHE:CD1	11:1K:6:MET:HB2	2.56	0.41
13:1M:74:PRO:O	13:1M:78:MET:HG3	2.20	0.41
13:1M:113:THR:HG21	58:1M:634:HOH:O	2.20	0.41
13:1M:310:MET:HG2	13:1M:455:LEU:O	2.20	0.41
14:1N:149:ILE:HD11	14:1N:195:PRO:HG3	2.03	0.41
15:1O:219:GLU:HB2	15:1O:241:LEU:HD13	2.01	0.41
17:1Q:65:TRP:CE2	17:1Q:74:SER:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1Y:32:GLY:O	24:1Y:36:SER:OG	2.30	0.41
28:1c:38:ASP:CG	29:1d:19:ARG:HH12	2.28	0.41
37:1l:57:GLU:OE1	37:1l:93:PRO:HD3	2.20	0.41
2:1B:91:THR:HA	2:1B:119:CYS:HB3	2.02	0.41
7:1G:20:VAL:HG21	7:1G:73:VAL:HG21	2.03	0.41
7:1G:448:LYS:HD3	7:1G:487:TRP:CE3	2.55	0.41
12:1L:557:TRP:O	12:1L:561:ILE:HG12	2.20	0.41
13:1M:6:ILE:HD11	31:1f:26:LEU:HD12	2.02	0.41
13:1M:50:LEU:HD23	13:1M:50:LEU:HA	1.91	0.41
13:1M:84:LEU:HD22	13:1M:87:GLU:HG3	2.02	0.41
13:1M:373:ILE:HD11	13:1M:444:LEU:HD12	2.02	0.41
16:1P:275:PHE:CD1	45:1P:402:PC1:H221	2.55	0.41
17:1Q:60:ASP:OD1	17:1Q:60:ASP:N	2.48	0.41
18:1R:10:LYS:HB2	18:1R:10:LYS:HE3	1.74	0.41
23:1X:76:HIS:HB3	23:1X:113:LYS:HD3	2.03	0.41
29:1d:106:LYS:HD3	29:1d:106:LYS:HA	1.83	0.41
35:1j:60:THR:HG1	35:1j:63:GLU:HB3	1.85	0.41
2:1B:77:ARG:HA	2:1B:77:ARG:HD2	1.60	0.41
4:1D:81:GLY:N	4:1D:429:ASP:OD1	2.51	0.41
6:1F:138:ILE:HG21	6:1F:146:ALA:HB2	2.02	0.41
11:1K:16:LEU:HA	11:1K:36:MET:SD	2.60	0.41
12:1L:440:LEU:HD12	12:1L:440:LEU:HA	1.83	0.41
16:1P:248:VAL:O	16:1P:322:ARG:HD3	2.20	0.41
19:1S:30:GLN:HG2	19:1S:33:ARG:NH1	2.36	0.41
22:1W:91:GLU:OE1	22:1W:91:GLU:HA	2.19	0.41
22:1W:119:LEU:HD12	22:1W:119:LEU:HA	1.81	0.41
24:1Y:58:TYR:OH	50:1Y:802:3PE:H112	2.20	0.41
58:1d:301:HOH:O	41:1p:159:LYS:HD3	2.20	0.41
45:1f:101:PC1:H322	45:1f:101:PC1:H31	1.39	0.41
41:1p:158:GLN:HG2	41:1p:162:MET:SD	2.61	0.41
4:1D:59:HIS:CD2	4:1D:418:ILE:HG22	2.55	0.41
6:1F:391:SER:O	6:1F:395:ILE:HG12	2.20	0.41
7:1G:646:ASN:O	7:1G:650:LYS:HG3	2.21	0.41
9:1I:31:VAL:HG13	45:1I:203:PC1:H392	2.02	0.41
12:1L:184:LEU:HD21	50:1L:703:3PE:H372	2.01	0.41
12:1L:474:PRO:HD2	40:1o:66:LEU:HD11	2.03	0.41
12:1L:604:TYR:CE2	14:1N:153:LEU:HD13	2.56	0.41
13:1M:126:LEU:HD11	13:1M:153:THR:HG21	2.03	0.41
13:1M:210:TYR:CG	13:1M:268:GLY:HA3	2.55	0.41
50:1M:501:3PE:H332	58:1M:753:HOH:O	2.20	0.41
50:1M:503:3PE:H3A1	50:1M:503:3PE:H252	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1O:26:THR:HG22	15:1O:124:LEU:HB2	2.03	0.41
22:1W:28:ALA:HB1	22:1W:79:VAL:HG11	2.03	0.41
42:1q:12:GLN:O	42:1q:16:GLY:N	2.50	0.41
2:1B:33:LEU:HD23	2:1B:33:LEU:HA	1.88	0.41
2:1B:47:PRO:HD3	2:1B:74:VAL:HG13	2.03	0.41
4:1D:55:HIS:CD2	4:1D:57:ALA:HB3	2.54	0.41
4:1D:98:GLN:HE21	9:1I:88:PRO:HA	1.85	0.41
6:1F:248:GLU:O	6:1F:250:ASN:N	2.53	0.41
7:1G:148:THR:HB	7:1G:150:MET:HE3	2.02	0.41
45:1H:401:PC1:H3C1	27:1b:24:ILE:HD11	2.03	0.41
13:1M:71:TRP:CD1	45:1M:504:PC1:H2C2	2.56	0.41
14:1N:181:TYR:HA	14:1N:184:ILE:HD12	2.02	0.41
14:1N:228:LEU:O	14:1N:231:SER:OG	2.27	0.41
51:1X:201:CDL:H341	51:1X:201:CDL:H312	1.95	0.41
4:1D:269:LEU:HD12	4:1D:269:LEU:HA	1.96	0.41
6:1F:63:SER:HB2	6:1F:242:PHE:CD2	2.56	0.41
7:1G:575:ASN:HD21	7:1G:577:GLU:HG2	1.85	0.41
8:1H:9:LEU:O	8:1H:13:ILE:HD12	2.21	0.41
10:1J:98:MET:HE2	10:1J:98:MET:HA	2.01	0.41
13:1M:33:LEU:HD23	13:1M:33:LEU:HA	1.95	0.41
15:1O:53:GLU:HG3	15:1O:125:GLU:O	2.19	0.41
16:1P:172:PHE:CE1	16:1P:310:LEU:HD23	2.56	0.41
16:1P:196:LEU:HB3	16:1P:198:LYS:HG2	2.01	0.41
17:1Q:109:LYS:HE2	17:1Q:109:LYS:HB2	1.89	0.41
19:1S:90:LEU:HD23	19:1S:90:LEU:HA	1.73	0.41
20:1T:51:ILE:O	20:1T:55:GLU:HG3	2.20	0.41
20:1T:64:ASP:CG	22:1W:37:ARG:HH12	2.29	0.41
20:1U:73:PRO:O	20:1U:77:VAL:HG12	2.19	0.41
24:1Y:103:ARG:HD2	24:1Y:103:ARG:HA	1.84	0.41
24:1Y:105:ARG:HA	24:1Y:105:ARG:NE	2.36	0.41
32:1g:68:ILE:O	32:1g:72:LEU:HB2	2.21	0.41
1:1A:3:ILE:HG21	45:1H:402:PC1:H221	2.03	0.41
1:1A:21:ALA:HB1	8:1H:218:GLY:CA	2.48	0.41
3:1C:133:GLU:O	3:1C:137:MET:HG2	2.21	0.41
5:1E:111:ARG:HB2	5:1E:152:PRO:HD3	2.03	0.41
6:1F:28:ARG:HD2	44:1s:35:ASN:O	2.21	0.41
6:1F:298:ILE:O	6:1F:334:VAL:HA	2.21	0.41
7:1G:18:VAL:HG11	7:1G:33:VAL:HG13	2.03	0.41
9:1I:95:GLU:HB2	9:1I:108:ARG:HB3	2.03	0.41
10:1J:64:MET:HE3	11:1K:34:GLU:OE1	2.21	0.41
50:1J:201:3PE:H3B2	11:1K:14:ILE:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:1L:63:ILE:O	12:1L:79:SER:HA	2.20	0.41
12:1L:182:PHE:O	12:1L:186:MET:HG3	2.20	0.41
12:1L:603:ASN:O	58:1L:806:HOH:O	2.21	0.41
13:1M:260:PRO:HA	50:1m:202:3PE:H282	2.03	0.41
15:1O:182:ARG:HA	15:1O:185:LYS:HE2	2.03	0.41
15:1O:304:TYR:OH	50:1d:201:3PE:H112	2.21	0.41
20:1T:60:PHE:CE2	20:1T:83:LYS:HG2	2.56	0.41
51:1X:201:CDL:H422	29:1d:36:PHE:CZ	2.56	0.41
50:1Y:801:3PE:H352	50:1Y:802:3PE:H332	2.03	0.41
26:1a:50:ARG:O	26:1a:54:ILE:HG23	2.21	0.41
28:1c:31:LEU:HG	58:1c:103:HOH:O	2.21	0.41
36:1k:13:MET:O	36:1k:13:MET:HG3	2.20	0.41
40:1o:25:PRO:HD2	40:1o:28:TYR:CD2	2.56	0.41
42:1q:92:CYS:HB3	43:1r:33:ARG:HG3	2.03	0.41
42:1q:144:TYR:CZ	42:1q:145:LYS:HE3	2.56	0.41
45:1q:202:PC1:H322	45:1q:202:PC1:H221	2.03	0.41
4:1D:209:ASP:O	4:1D:213:GLU:HG2	2.21	0.41
4:1D:219:SER:OG	58:1D:503:HOH:O	2.22	0.41
5:1E:51:LEU:HD23	5:1E:51:LEU:HA	1.92	0.41
7:1G:9:ILE:HB	7:1G:75:LYS:HD2	2.03	0.41
7:1G:109:ASP:OD2	7:1G:214:ALA:HA	2.21	0.41
10:1J:10:SER:O	10:1J:14:VAL:HG23	2.21	0.41
12:1L:78:LEU:HD11	51:1L:705:CDL:H861	2.03	0.41
16:1P:95:VAL:HA	54:1P:403:NDP:O4B	2.21	0.41
21:1V:93:MET:SD	21:1V:98:PRO:HG2	2.61	0.41
23:1X:84:TYR:CE1	23:1X:103:GLN:HB2	2.56	0.41
25:1Z:62:ILE:O	25:1Z:66:GLU:HG3	2.21	0.41
37:1l:50:LEU:HD12	37:1l:78:HIS:HA	2.03	0.41
1:1A:51:PHE:O	1:1A:52:SER:HB3	2.21	0.40
1:1A:92:LEU:HD22	8:1H:302:MET:HG2	2.03	0.40
5:1E:214:GLN:O	5:1E:214:GLN:HG3	2.20	0.40
6:1F:77:LEU:HD12	6:1F:77:LEU:HA	1.84	0.40
7:1G:385:ARG:HB2	7:1G:415:LEU:HD23	2.02	0.40
10:1J:93:PHE:CE1	10:1J:97:LEU:HG	2.55	0.40
12:1L:36:VAL:HA	12:1L:39:THR:HG23	2.04	0.40
12:1L:545:SER:O	12:1L:549:ALA:HB3	2.21	0.40
14:1N:19:LEU:O	14:1N:23:SER:OG	2.26	0.40
22:1W:27:GLU:O	22:1W:31:ARG:HG3	2.21	0.40
23:1X:30:HIS:CE1	23:1X:110:VAL:HG21	2.56	0.40
23:1X:105:LYS:HA	23:1X:108:GLU:CG	2.51	0.40
24:1Y:107:TYR:H	50:1m:203:3PE:H122	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:1d:120:ARG:HD2	38:1m:115:ILE:HD13	2.03	0.40
33:1h:106:LYS:HB2	33:1h:106:LYS:HE3	1.94	0.40
34:1i:94:TYR:OH	41:1p:10:PRO:O	2.32	0.40
50:1j:101:3PE:H332	40:1o:76:PHE:HE2	1.86	0.40
41:1p:38:LEU:HD12	41:1p:42:ARG:NH2	2.35	0.40
2:1B:50:PHE:CD1	2:1B:86:MET:HE2	2.57	0.40
2:1B:154:GLU:HG2	9:1I:50:TYR:CE1	2.56	0.40
5:1E:60:TRP:CE2	5:1E:94:PRO:HG3	2.56	0.40
7:1G:41:CYS:HA	7:1G:156:CYS:HB2	2.03	0.40
13:1M:1:FME:SD	13:1M:111:THR:HG21	2.62	0.40
13:1M:118:PHE:O	13:1M:122:PHE:HB3	2.21	0.40
14:1N:85:THR:O	58:1N:1002:HOH:O	2.22	0.40
20:1T:31:SER:H	20:1T:34:SER:HB2	1.86	0.40
23:1X:46:ARG:HA	23:1X:46:ARG:HD2	1.79	0.40
25:1Z:125:TYR:HB3	25:1Z:133:ILE:CG2	2.49	0.40
30:1e:85:LEU:HB2	58:1e:208:HOH:O	2.21	0.40
32:1g:38:TYR:HA	32:1g:41:ASN:O	2.22	0.40
37:1l:75:GLU:OE2	38:1m:39:ARG:HD2	2.21	0.40
2:1B:167:ILE:HA	2:1B:170:GLU:HG3	2.03	0.40
6:1F:89:ARG:CZ	6:1F:219:PRO:HD3	2.51	0.40
6:1F:215:VAL:H	6:1F:220:THR:HG21	1.87	0.40
12:1L:67:HIS:ND1	50:1L:702:3PE:H121	2.37	0.40
12:1L:210:ASN:HB2	50:1L:703:3PE:H31	2.04	0.40
12:1L:442:LEU:HD23	35:1j:9:PRO:HB3	2.04	0.40
12:1L:591:PHE:HZ	58:1N:1038:HOH:O	2.03	0.40
12:1L:594:THR:HG21	14:1N:110:PRO:HB2	2.02	0.40
13:1M:127:VAL:O	13:1M:131:ILE:HG13	2.21	0.40
13:1M:220:HIS:O	13:1M:283:LYS:HE2	2.21	0.40
14:1N:133:TRP:HE3	51:1N:902:CDL:H201	1.86	0.40
16:1P:274:PRO:HG2	16:1P:275:PHE:CZ	2.56	0.40
20:1U:52:MET:HE1	39:1n:23:LEU:HB3	2.02	0.40
21:1V:97:LYS:N	21:1V:98:PRO:HD3	2.36	0.40
36:1k:38:ARG:NH1	58:1k:103:HOH:O	2.54	0.40
40:1o:74:PRO:HG3	41:1p:28:PRO:HD3	2.04	0.40
41:1p:57:LYS:H	41:1p:57:LYS:HG2	1.78	0.40
4:1D:64:LEU:HD11	4:1D:418:ILE:HD11	2.04	0.40
4:1D:183:ARG:HH12	4:1D:210:ASP:CG	2.25	0.40
6:1F:90:PRO:HD2	6:1F:218:CYS:SG	2.61	0.40
10:1J:3:MET:SD	25:1Z:134:LEU:HD13	2.62	0.40
10:1J:23:LYS:CD	11:1K:28:SER:HB3	2.51	0.40
12:1L:150:MET:SD	51:1L:705:CDL:H722	2.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:1R:25:ARG:O	58:1R:302:HOH:O	2.22	0.40
22:1W:65:GLU:OE1	58:1W:302:HOH:O	2.22	0.40
51:1X:201:CDL:H462	50:1d:201:3PE:H3D2	2.02	0.40
25:1Z:31:SER:O	25:1Z:35:MET:HG3	2.20	0.40
2:1B:128:TYR:O	3:1C:168:LEU:HG	2.22	0.40
2:1B:130:TYR:OH	4:1D:84:HIS:NE2	2.52	0.40
7:1G:18:VAL:HG23	7:1G:20:VAL:HG13	2.04	0.40
58:1L:993:HOH:O	35:1j:10:ARG:HB2	2.22	0.40
13:1M:76:MET:HG2	13:1M:226:ALA:HB1	2.04	0.40
13:1M:253:LEU:HD12	13:1M:256:TYR:CZ	2.56	0.40
58:1M:605:HOH:O	14:1N:274:GLU:HG3	2.21	0.40
14:1N:298:TYR:O	14:1N:303:THR:OG1	2.31	0.40
15:1O:203:GLU:O	15:1O:207:LYS:HD3	2.22	0.40
16:1P:270:PHE:HD2	16:1P:278:TRP:HB2	1.85	0.40
17:1Q:70:MET:SD	42:1q:126:PRO:HB2	2.62	0.40
40:1o:38:MET:HE1	40:1o:56:ASP:O	2.21	0.40
42:1q:1:MET:SD	42:1q:5:GLN:NE2	2.95	0.40
43:1r:33:ARG:HA	43:1r:33:ARG:HD2	1.92	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1A	113/115 (98%)	104 (92%)	7 (6%)	2 (2%)	6	3
2	1B	153/258 (59%)	142 (93%)	11 (7%)	0	100	100
3	1C	207/264 (78%)	205 (99%)	2 (1%)	0	100	100
4	1D	427/466 (92%)	409 (96%)	18 (4%)	0	100	100
5	1E	212/249 (85%)	197 (93%)	15 (7%)	0	100	100
6	1F	430/464 (93%)	411 (96%)	17 (4%)	2 (0%)	24	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	1G	697/727 (96%)	674 (97%)	20 (3%)	3 (0%)	30	28
8	1H	316/318 (99%)	302 (96%)	12 (4%)	2 (1%)	21	18
9	1I	174/239 (73%)	170 (98%)	4 (2%)	0	100	100
10	1J	172/175 (98%)	162 (94%)	9 (5%)	1 (1%)	21	18
11	1K	96/98 (98%)	95 (99%)	1 (1%)	0	100	100
12	1L	604/606 (100%)	579 (96%)	24 (4%)	1 (0%)	43	44
13	1M	457/459 (100%)	454 (99%)	3 (1%)	0	100	100
14	1N	345/347 (99%)	342 (99%)	3 (1%)	0	100	100
15	1O	318/357 (89%)	303 (95%)	15 (5%)	0	100	100
16	1P	340/377 (90%)	330 (97%)	10 (3%)	0	100	100
17	1Q	127/175 (73%)	124 (98%)	3 (2%)	0	100	100
18	1R	94/123 (76%)	92 (98%)	2 (2%)	0	100	100
19	1S	85/99 (86%)	82 (96%)	3 (4%)	0	100	100
20	1T	83/156 (53%)	81 (98%)	2 (2%)	0	100	100
20	1U	84/156 (54%)	83 (99%)	1 (1%)	0	100	100
21	1V	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
22	1W	113/128 (88%)	109 (96%)	4 (4%)	0	100	100
23	1X	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
24	1Y	137/141 (97%)	136 (99%)	1 (1%)	0	100	100
25	1Z	140/144 (97%)	138 (99%)	2 (1%)	0	100	100
26	1a	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
27	1b	81/84 (96%)	77 (95%)	3 (4%)	1 (1%)	10	7
28	1c	47/76 (62%)	45 (96%)	2 (4%)	0	100	100
29	1d	118/122 (97%)	117 (99%)	1 (1%)	0	100	100
30	1e	98/106 (92%)	95 (97%)	3 (3%)	0	100	100
31	1f	55/58 (95%)	55 (100%)	0	0	100	100
32	1g	98/154 (64%)	92 (94%)	6 (6%)	0	100	100
33	1h	136/189 (72%)	135 (99%)	1 (1%)	0	100	100
34	1i	125/128 (98%)	122 (98%)	3 (2%)	0	100	100
35	1j	69/105 (66%)	66 (96%)	3 (4%)	0	100	100
36	1k	79/98 (81%)	78 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	1l	154/186 (83%)	151 (98%)	3 (2%)	0	100	100
38	1m	126/129 (98%)	125 (99%)	1 (1%)	0	100	100
39	1n	170/179 (95%)	165 (97%)	5 (3%)	0	100	100
40	1o	120/137 (88%)	115 (96%)	5 (4%)	0	100	100
41	1p	171/176 (97%)	171 (100%)	0	0	100	100
42	1q	143/145 (99%)	143 (100%)	0	0	100	100
43	1r	91/113 (80%)	89 (98%)	2 (2%)	0	100	100
44	1s	43/471 (9%)	40 (93%)	3 (7%)	0	100	100
All	All	8198/9655 (85%)	7944 (97%)	242 (3%)	12 (0%)	49	50

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	1G	115	ASP
8	1H	196	ALA
10	1J	66	VAL
27	1b	67	SER
8	1H	208	VAL
6	1F	249	ARG
7	1G	538	PRO
12	1L	72	GLN
1	1A	52	SER
1	1A	109	LYS
6	1F	297	VAL
7	1G	186	TYR

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	1A	99/99 (100%)	98 (99%)	1 (1%)	68	76
2	1B	131/212 (62%)	123 (94%)	8 (6%)	17	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1C	191/228 (84%)	189 (99%)	2 (1%)	68	76
4	1D	371/396 (94%)	362 (98%)	9 (2%)	43	49
5	1E	183/207 (88%)	177 (97%)	6 (3%)	33	37
6	1F	346/368 (94%)	338 (98%)	8 (2%)	44	51
7	1G	588/610 (96%)	571 (97%)	17 (3%)	37	42
8	1H	274/274 (100%)	266 (97%)	8 (3%)	37	42
9	1I	151/201 (75%)	150 (99%)	1 (1%)	76	83
10	1J	140/141 (99%)	132 (94%)	8 (6%)	18	17
11	1K	84/84 (100%)	83 (99%)	1 (1%)	63	72
12	1L	539/539 (100%)	527 (98%)	12 (2%)	45	53
13	1M	408/408 (100%)	395 (97%)	13 (3%)	34	38
14	1N	310/310 (100%)	304 (98%)	6 (2%)	50	58
15	1O	283/307 (92%)	270 (95%)	13 (5%)	24	25
16	1P	296/323 (92%)	282 (95%)	14 (5%)	23	24
17	1Q	117/152 (77%)	113 (97%)	4 (3%)	32	35
18	1R	79/97 (81%)	76 (96%)	3 (4%)	29	32
19	1S	77/82 (94%)	72 (94%)	5 (6%)	15	13
20	1T	79/133 (59%)	77 (98%)	2 (2%)	42	48
20	1U	79/133 (59%)	75 (95%)	4 (5%)	21	21
21	1V	100/101 (99%)	97 (97%)	3 (3%)	36	41
22	1W	107/112 (96%)	106 (99%)	1 (1%)	70	78
23	1X	153/154 (99%)	145 (95%)	8 (5%)	21	20
24	1Y	101/102 (99%)	99 (98%)	2 (2%)	48	56
25	1Z	124/124 (100%)	119 (96%)	5 (4%)	28	29
26	1a	58/58 (100%)	56 (97%)	2 (3%)	32	35
27	1b	69/70 (99%)	64 (93%)	5 (7%)	13	11
28	1c	45/66 (68%)	42 (93%)	3 (7%)	15	12
29	1d	107/109 (98%)	102 (95%)	5 (5%)	23	24
30	1e	88/94 (94%)	84 (96%)	4 (4%)	24	25
31	1f	54/55 (98%)	52 (96%)	2 (4%)	30	33
32	1g	92/129 (71%)	91 (99%)	1 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	1h	121/158 (77%)	117 (97%)	4 (3%)	33	37
34	1i	119/120 (99%)	117 (98%)	2 (2%)	53	62
35	1j	62/84 (74%)	61 (98%)	1 (2%)	55	64
36	1k	63/76 (83%)	60 (95%)	3 (5%)	23	23
37	1l	141/161 (88%)	141 (100%)	0	100	100
38	1m	113/114 (99%)	108 (96%)	5 (4%)	25	26
39	1n	156/160 (98%)	156 (100%)	0	100	100
40	1o	110/120 (92%)	104 (94%)	6 (6%)	19	18
41	1p	154/156 (99%)	149 (97%)	5 (3%)	34	38
42	1q	131/131 (100%)	130 (99%)	1 (1%)	73	81
43	1r	85/98 (87%)	82 (96%)	3 (4%)	32	35
44	1s	44/351 (12%)	39 (89%)	5 (11%)	5	3
All	All	7222/8207 (88%)	7001 (97%)	221 (3%)	36	39

All (221) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1A	5	LEU
2	1B	30	VAL
2	1B	50	PHE
2	1B	54	CYS
2	1B	57	VAL
2	1B	85	VAL
2	1B	91	THR
2	1B	125	TYR
2	1B	133	VAL
3	1C	78	LEU
3	1C	196	LYS
4	1D	36	VAL
4	1D	61	VAL
4	1D	85	ARG
4	1D	95	THR
4	1D	184	VAL
4	1D	220	PHE
4	1D	269	LEU
4	1D	281	VAL
4	1D	365	THR
5	1E	61	LEU

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Mol	Chain	Res	Type
5	1E	68	LYS
5	1E	124	LEU
5	1E	149	VAL
5	1E	164	LEU
5	1E	202	LEU
6	1F	10	THR
6	1F	46	LYS
6	1F	77	LEU
6	1F	104	THR
6	1F	287	VAL
6	1F	334	VAL
6	1F	336	VAL
6	1F	428	GLU
7	1G	151	THR
7	1G	172	LEU
7	1G	209	THR
7	1G	216	THR
7	1G	315	VAL
7	1G	342	SER
7	1G	348	VAL
7	1G	371	VAL
7	1G	376	VAL
7	1G	403	ASP
7	1G	503	LEU
7	1G	531	CYS
7	1G	585	VAL
7	1G	613	TYR
7	1G	615	THR
7	1G	659	ASP
7	1G	704	CYS
8	1H	58	LYS
8	1H	73	ILE
8	1H	87	VAL
8	1H	102	VAL
8	1H	116	ILE
8	1H	119	SER
8	1H	163	SER
8	1H	177	THR
9	1I	103	SER
10	1J	27	ILE
10	1J	31	LEU
10	1J	50	SER

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Mol	Chain	Res	Type
10	1J	64	MET
10	1J	97	LEU
10	1J	100	GLU
10	1J	113	VAL
10	1J	122	LEU
11	1K	3	LEU
12	1L	39	THR
12	1L	132	VAL
12	1L	147	VAL
12	1L	257	VAL
12	1L	277	THR
12	1L	278	LEU
12	1L	343	SER
12	1L	507	THR
12	1L	514	LYS
12	1L	543	SER
12	1L	544	MET
12	1L	548	SER
13	1M	2	LEU
13	1M	47	GLU
13	1M	55	THR
13	1M	94	LEU
13	1M	103	GLN
13	1M	116	ILE
13	1M	140	THR
13	1M	206	LYS
13	1M	265	SER
13	1M	289	SER
13	1M	350	THR
13	1M	365	THR
13	1M	458	LEU
14	1N	43	VAL
14	1N	88	LYS
14	1N	93	VAL
14	1N	227	THR
14	1N	250	SER
14	1N	336	VAL
15	1O	14	THR
15	1O	19	THR
15	1O	28	ASP
15	1O	60	ASP
15	1O	117	SER

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Mol	Chain	Res	Type
15	1O	149	VAL
15	1O	169	VAL
15	1O	195	THR
15	1O	209	THR
15	1O	218	CYS
15	1O	263	VAL
15	1O	282	ILE
15	1O	312	VAL
16	1P	34	VAL
16	1P	85	VAL
16	1P	90	VAL
16	1P	95	VAL
16	1P	126	VAL
16	1P	127	GLU
16	1P	130	ILE
16	1P	175	GLU
16	1P	201	VAL
16	1P	254	LEU
16	1P	275	PHE
16	1P	310	LEU
16	1P	311	GLU
16	1P	340	VAL
17	1Q	44	ASN
17	1Q	61	THR
17	1Q	75	THR
17	1Q	105	VAL
18	1R	4	THR
18	1R	83	THR
18	1R	92	ARG
19	1S	32	VAL
19	1S	60	VAL
19	1S	76	VAL
19	1S	82	SER
19	1S	87	THR
20	1T	34	SER
20	1T	52	MET
20	1U	19	LEU
20	1U	68	GLU
20	1U	77	VAL
20	1U	86	VAL
21	1V	13	LEU
21	1V	22	ARG

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Mol	Chain	Res	Type
21	1V	94	LEU
22	1W	22	SER
23	1X	50	LYS
23	1X	58	GLU
23	1X	63	ASN
23	1X	67	LEU
23	1X	91	SER
23	1X	117	VAL
23	1X	130	VAL
23	1X	136	LEU
24	1Y	11	ILE
24	1Y	68	ILE
25	1Z	19	ILE
25	1Z	94	GLU
25	1Z	96	ILE
25	1Z	106	VAL
25	1Z	133	ILE
26	1a	27	HIS
26	1a	66	LEU
27	1b	54	VAL
27	1b	64	ASP
27	1b	65	VAL
27	1b	76	SER
27	1b	83	LEU
28	1c	4	ILE
28	1c	11	SER
28	1c	21	LEU
29	1d	12	GLN
29	1d	14	LEU
29	1d	20	SER
29	1d	53	VAL
29	1d	66	THR
30	1e	9	LEU
30	1e	18	THR
30	1e	52	GLU
30	1e	83	ASP
31	1f	14	ILE
31	1f	21	VAL
32	1g	122	GLU
33	1h	60	VAL
33	1h	96	ILE
33	1h	103	LEU

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Mol	Chain	Res	Type
33	1h	113	LEU
34	1i	12	GLN
34	1i	97	VAL
35	1j	44	SER
36	1k	19	LYS
36	1k	63	VAL
36	1k	79	VAL
38	1m	8	SER
38	1m	39	ARG
38	1m	58	VAL
38	1m	68	THR
38	1m	87	LEU
40	1o	9	LEU
40	1o	19	LEU
40	1o	28	TYR
40	1o	30	PHE
40	1o	53	GLN
40	1o	66	LEU
41	1p	44	VAL
41	1p	46	LEU
41	1p	49	GLU
41	1p	53	GLN
41	1p	119	SER
42	1q	125	VAL
43	1r	24	GLN
43	1r	68	VAL
43	1r	112	LEU
44	1s	35	ASN
44	1s	41	LEU
44	1s	47	SER
44	1s	52	LEU
44	1s	61	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
3	1C	144	ASN
4	1D	157	HIS
6	1F	257	ASN
6	1F	261	HIS
6	1F	324	GLN
6	1F	326	GLN

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Mol	Chain	Res	Type
7	1G	141	ASN
7	1G	313	ASN
7	1G	392	ASN
7	1G	475	GLN
7	1G	517	ASN
8	1H	47	GLN
8	1H	99	ASN
8	1H	287	HIS
8	1H	304	HIS
10	1J	120	ASN
12	1L	175	ASN
12	1L	210	ASN
12	1L	270	ASN
12	1L	309	GLN
12	1L	354	GLN
12	1L	447	ASN
12	1L	518	GLN
13	1M	331	ASN
14	1N	134	GLN
14	1N	144	GLN
14	1N	268	GLN
15	1O	147	GLN
15	1O	180	GLN
15	1O	204	ASN
16	1P	44	GLN
16	1P	87	HIS
16	1P	131	HIS
16	1P	136	ASN
18	1R	90	GLN
20	1T	35	HIS
23	1X	64	GLN
23	1X	94	GLN
25	1Z	8	GLN
27	1b	51	ASN
27	1b	68	HIS
27	1b	70	GLN
28	1c	9	HIS
30	1e	6	GLN
35	1j	24	GLN
38	1m	54	ASN
39	1n	50	HIS
39	1n	168	HIS

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Mol	Chain	Res	Type
40	1o	42	GLN
40	1o	46	ASN
40	1o	81	HIS
40	1o	116	GLN
41	1p	27	ASN
41	1p	53	GLN
42	1q	31	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 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	$\# Z > 2$
13	FME	1M	1	13	8,9,10	0.54	0	8,9,11	1.00	1 (12%)
12	FME	1L	1	12	8,9,10	0.55	0	8,9,11	1.42	2 (25%)
14	FME	1N	1	14	8,9,10	0.53	0	8,9,11	0.95	1 (12%)
8	FME	1H	1	8	8,9,10	0.56	0	8,9,11	1.00	1 (12%)
1	FME	1A	1	1	8,9,10	0.55	0	8,9,11	0.90	1 (12%)
11	FME	1K	1	11	8,9,10	0.55	0	8,9,11	0.97	1 (12%)
34	SAC	1i	1	34	7,8,9	0.58	0	7,9,11	0.89	1 (14%)
43	AYA	1r	1	43	6,7,8	0.67	0	6,8,10	0.79	0

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
13	FME	1M	1	13	-	1/7/9/11	-
12	FME	1L	1	12	-	3/7/9/11	-
14	FME	1N	1	14	-	2/7/9/11	-
8	FME	1H	1	8	-	1/7/9/11	-
1	FME	1A	1	1	-	2/7/9/11	-
11	FME	1K	1	11	-	0/7/9/11	-
34	SAC	1i	1	34	-	0/7/8/10	-
43	AYA	1r	1	43	-	1/5/6/8	-

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	1L	1	FME	CA-N-CN	2.76	127.06	122.82
8	1H	1	FME	O-C-CA	-2.64	117.97	124.77
12	1L	1	FME	O-C-CA	-2.64	117.98	124.77
11	1K	1	FME	O-C-CA	-2.61	118.06	124.77
13	1M	1	FME	O-C-CA	-2.58	118.13	124.77
14	1N	1	FME	O-C-CA	-2.45	118.47	124.77
1	1A	1	FME	O-C-CA	-2.31	118.83	124.77
34	1i	1	SAC	O-C-CA	-2.31	118.84	124.77

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	1L	1	FME	CB-CA-N-CN
12	1L	1	FME	O-C-CA-CB
43	1r	1	AYA	O-C-CA-CB
8	1H	1	FME	CA-CB-CG-SD
1	1A	1	FME	N-CA-CB-CG
12	1L	1	FME	N-CA-CB-CG
1	1A	1	FME	C-CA-CB-CG
13	1M	1	FME	C-CA-CB-CG
14	1N	1	FME	CB-CG-SD-CE
14	1N	1	FME	CB-CA-N-CN

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	1M	1	FME	1	0
14	1N	1	FME	2	0
1	1A	1	FME	1	0
11	1K	1	FME	1	0
34	1i	1	SAC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 55 ligands modelled in this entry, 3 are monoatomic - leaving 52 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	$\# Z > 2$
45	PC1	1d	203	-	38,38,53	0.35	0	44,46,61	0.86	2 (4%)
51	CDL	1L	705	-	86,86,99	0.29	0	92,98,111	0.37	0
45	PC1	1M	504	-	43,43,53	0.33	0	49,51,61	0.35	0
50	3PE	1Y	801	-	30,30,50	0.33	0	33,35,55	0.80	1 (3%)
45	PC1	1q	201	-	47,47,53	0.29	0	53,55,61	0.36	0
50	3PE	1Y	804	-	26,26,50	0.36	0	29,31,55	0.42	0
46	SF4	1G	801	7	0,12,12	-	-	-	-	-
54	NDP	1P	403	-	51,52,52	0.51	0	71,80,80	0.78	2 (2%)
50	3PE	1b	201	-	46,46,50	0.28	0	49,51,55	0.41	0
48	FMN	1F	501	-	33,33,33	0.60	0	48,50,50	0.68	1 (2%)
45	PC1	1q	202	-	48,48,53	0.29	0	54,56,61	0.60	1 (1%)
56	EHZ	1n	201	-	31,36,37	0.19	0	36,44,47	1.17	1 (2%)
50	3PE	1L	701	-	45,45,50	0.31	0	48,50,55	0.44	0
46	SF4	1I	201	9	0,12,12	-	-	-	-	-
47	FES	1E	301	5	0,4,4	-	-	-	-	-
45	PC1	1H	402	-	47,47,53	0.29	0	53,55,61	0.41	0
45	PC1	1M	502	-	34,34,53	0.33	0	40,42,61	0.60	1 (2%)
51	CDL	1d	202	-	64,64,99	0.33	0	70,76,111	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	3PE	1Y	803	-	29,29,50	0.35	0	32,34,55	0.61	1 (3%)
51	CDL	1X	201	-	85,85,99	0.29	0	91,97,111	0.41	0
50	3PE	1L	704	-	41,41,50	0.29	0	44,46,55	0.40	0
56	EHZ	1W	201	-	31,36,37	0.18	0	36,44,47	1.11	1 (2%)
46	SF4	1F	502	6	0,12,12	-	-	-		
46	SF4	1B	201	2	0,12,12	-	-	-		
50	3PE	1L	703	-	40,40,50	0.30	0	43,45,55	0.45	0
46	SF4	1G	802	7	0,12,12	-	-	-		
50	3PE	1M	501	-	44,44,50	0.29	0	47,49,55	0.40	0
50	3PE	1M	503	-	50,50,50	0.27	0	53,55,55	0.38	0
46	SF4	1I	202	9	0,12,12	-	-	-		
52	GTP	1O	401	53,15	33,34,34	0.60	0	50,54,54	0.62	0
45	PC1	1m	201	38	45,45,53	0.28	0	51,53,61	0.44	0
50	3PE	1d	201	-	47,47,50	0.30	0	50,52,55	0.39	0
51	CDL	1q	203	-	60,60,99	0.34	0	66,72,111	0.45	0
50	3PE	1L	702	-	44,44,50	0.29	0	47,49,55	0.47	0
45	PC1	1I	203	-	43,43,53	0.29	0	49,51,61	0.35	0
50	3PE	1N	903	-	32,32,50	0.33	0	35,37,55	0.45	0
50	3PE	1Y	802	-	39,39,50	0.30	0	42,44,55	0.41	0
45	PC1	1h	202	-	46,46,53	0.29	0	52,54,61	0.41	0
45	PC1	1f	101	-	45,45,53	0.30	0	51,53,61	0.38	0
45	PC1	1H	401	-	53,53,53	0.27	0	59,61,61	0.36	0
50	3PE	1j	101	-	43,43,50	0.29	0	46,48,55	0.47	0
51	CDL	1N	902	-	61,61,99	0.31	0	67,73,111	0.57	1 (1%)
50	3PE	1J	201	-	43,43,50	0.29	0	46,48,55	0.37	0
50	3PE	1m	202	-	49,49,50	0.27	0	52,54,55	0.39	0
51	CDL	1h	201	-	79,79,99	0.31	0	85,91,111	0.38	0
45	PC1	1P	402	-	45,45,53	0.29	0	51,53,61	0.34	0
50	3PE	1N	901	-	48,48,50	0.29	0	51,53,55	0.43	0
50	3PE	1m	203	-	40,40,50	0.29	0	43,45,55	0.64	1 (2%)
47	FES	1G	803	7	0,4,4	-	-	-		
57	MYR	1l	201	-	13,14,15	0.32	0	12,13,15	0.30	0
45	PC1	1P	401	-	32,32,53	0.33	0	38,40,61	0.45	0
45	PC1	1A	201	-	34,34,53	0.33	0	40,42,61	0.40	0

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
45	PC1	1d	203	-	-	19/42/42/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
51	CDL	1L	705	-	-	15/97/97/110	-
45	PC1	1M	504	-	-	12/47/47/57	-
50	3PE	1Y	801	-	-	7/34/34/54	-
45	PC1	1q	201	-	-	10/51/51/57	-
50	3PE	1Y	804	-	-	5/30/30/54	-
46	SF4	1G	801	7	-	-	0/6/5/5
54	NDP	1P	403	-	-	5/34/77/77	0/5/5/5
50	3PE	1b	201	-	-	9/50/50/54	-
48	FMN	1F	501	-	-	1/18/18/18	0/3/3/3
45	PC1	1q	202	-	-	10/52/52/57	-
56	EHZ	1n	201	-	-	4/42/44/45	-
50	3PE	1L	701	-	-	8/49/49/54	-
46	SF4	1I	201	9	-	-	0/6/5/5
47	FES	1E	301	5	-	-	0/1/1/1
45	PC1	1H	402	-	-	12/51/51/57	-
45	PC1	1M	502	-	-	9/38/38/57	-
51	CDL	1d	202	-	-	14/75/75/110	-
50	3PE	1Y	803	-	-	10/33/33/54	-
51	CDL	1X	201	-	-	19/96/96/110	-
50	3PE	1L	704	-	-	1/45/45/54	-
56	EHZ	1W	201	-	-	11/42/44/45	-
50	3PE	1M	501	-	-	6/48/48/54	-
46	SF4	1B	201	2	-	-	0/6/5/5
50	3PE	1L	703	-	-	8/44/44/54	-
46	SF4	1F	502	6	-	-	0/6/5/5
46	SF4	1G	802	7	-	-	0/6/5/5
50	3PE	1M	503	-	-	10/54/54/54	-
52	GTP	1O	401	53,15	-	6/22/38/38	0/3/3/3
46	SF4	1I	202	9	-	-	0/6/5/5
45	PC1	1m	201	38	-	9/49/49/57	-
50	3PE	1d	201	-	-	15/51/51/54	-
51	CDL	1q	203	-	-	4/71/71/110	-
50	3PE	1L	702	-	-	8/48/48/54	-
45	PC1	1I	203	-	-	1/47/47/57	-
50	3PE	1N	903	-	-	7/36/36/54	-
50	3PE	1Y	802	-	-	7/43/43/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	PC1	1h	202	-	-	13/50/50/57	-
45	PC1	1f	101	-	-	9/49/49/57	-
45	PC1	1H	401	-	-	11/57/57/57	-
50	3PE	1j	101	-	-	4/47/47/54	-
51	CDL	1N	902	-	-	8/71/71/110	-
50	3PE	1J	201	-	-	8/47/47/54	-
50	3PE	1m	202	-	-	8/53/53/54	-
51	CDL	1h	201	-	-	11/90/90/110	-
45	PC1	1P	402	-	-	4/49/49/57	-
50	3PE	1N	901	-	-	7/52/52/54	-
50	3PE	1m	203	-	-	11/44/44/54	-
47	FES	1G	803	7	-	-	0/1/1/1
57	MYR	1l	201	-	-	0/12/12/13	-
45	PC1	1P	401	-	-	4/36/36/57	-
45	PC1	1A	201	-	-	3/38/38/57	-

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	1n	201	EHZ	C10-S1-C9	6.33	120.55	101.84
56	1W	201	EHZ	C10-S1-C9	5.95	119.43	101.84
45	1d	203	PC1	O21-C21-C22	4.30	120.79	111.48
54	1P	403	NDP	P2B-O2B-C2B	-4.17	112.28	123.43
50	1Y	801	3PE	O21-C21-C22	3.18	118.36	111.48
51	1N	902	CDL	OB6-CB5-C51	3.14	116.69	111.09
50	1m	203	3PE	O21-C21-C22	2.91	117.77	111.48
45	1q	202	PC1	O21-C21-C22	2.84	117.62	111.48
54	1P	403	NDP	O4D-C1D-C2D	-2.65	100.94	106.62
45	1M	502	PC1	O21-C21-C22	2.35	116.56	111.48
50	1Y	803	3PE	O21-C21-C22	2.12	116.07	111.48
48	1F	501	FMN	C4-N3-C2	-2.10	121.91	125.64
45	1d	203	PC1	O21-C2-C1	2.06	115.75	108.34

There are no chirality outliers.

All (363) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
45	1H	401	PC1	C11-O13-P-O14
45	1H	402	PC1	C11-O13-P-O11
45	1H	402	PC1	C1-O11-P-O14
45	1H	402	PC1	C1-O11-P-O13
45	1H	402	PC1	C12-C11-O13-P
45	1H	402	PC1	O13-C11-C12-N
45	1I	203	PC1	C1-O11-P-O14
45	1M	502	PC1	C1-O11-P-O14
45	1M	502	PC1	O22-C21-O21-C2
45	1M	502	PC1	C22-C21-O21-C2
45	1M	504	PC1	C11-O13-P-O12
45	1M	504	PC1	C11-O13-P-O11
45	1d	203	PC1	C11-O13-P-O12
45	1d	203	PC1	C11-O13-P-O11
45	1d	203	PC1	C12-C11-O13-P
45	1d	203	PC1	O13-C11-C12-N
45	1d	203	PC1	C2-C1-O11-P
45	1d	203	PC1	O22-C21-O21-C2
45	1d	203	PC1	C22-C21-O21-C2
45	1d	203	PC1	O32-C31-O31-C3
45	1d	203	PC1	C32-C31-O31-C3
45	1f	101	PC1	C1-O11-P-O14
45	1f	101	PC1	O32-C31-O31-C3
45	1f	101	PC1	C32-C31-O31-C3
45	1h	202	PC1	C11-O13-P-O14
45	1h	202	PC1	O13-C11-C12-N
45	1h	202	PC1	O21-C2-C3-O31
45	1m	201	PC1	C11-O13-P-O11
45	1m	201	PC1	O32-C31-O31-C3
45	1m	201	PC1	C32-C31-O31-C3
45	1q	202	PC1	O22-C21-O21-C2
45	1q	202	PC1	C22-C21-O21-C2
45	1q	202	PC1	O32-C31-O31-C3
45	1q	202	PC1	C32-C31-O31-C3
50	1L	701	3PE	O32-C31-O31-C3
50	1L	701	3PE	C32-C31-O31-C3
50	1L	703	3PE	C1-O11-P-O12
50	1L	703	3PE	C1-O11-P-O13
50	1L	703	3PE	C2-C1-O11-P
50	1L	703	3PE	O32-C31-O31-C3
50	1L	703	3PE	C32-C31-O31-C3
50	1M	503	3PE	O32-C31-O31-C3
50	1M	503	3PE	C32-C31-O31-C3

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Mol	Chain	Res	Type	Atoms
50	1N	903	3PE	C1-O11-P-O14
50	1N	903	3PE	O21-C2-C3-O31
50	1Y	801	3PE	O22-C21-O21-C2
50	1Y	801	3PE	C22-C21-O21-C2
50	1Y	802	3PE	C2-C1-O11-P
50	1Y	803	3PE	C1-O11-P-O12
50	1Y	803	3PE	C1-O11-P-O13
50	1Y	803	3PE	C2-C1-O11-P
50	1Y	803	3PE	C12-C11-O13-P
50	1Y	803	3PE	O22-C21-O21-C2
50	1Y	803	3PE	C22-C21-O21-C2
50	1Y	804	3PE	C11-O13-P-O14
50	1Y	804	3PE	O32-C31-O31-C3
50	1Y	804	3PE	C32-C31-O31-C3
50	1b	201	3PE	C11-O13-P-O12
50	1d	201	3PE	C1-O11-P-O13
50	1d	201	3PE	C1-O11-P-O14
50	1d	201	3PE	C2-C1-O11-P
50	1j	101	3PE	O22-C21-O21-C2
50	1j	101	3PE	C22-C21-O21-C2
50	1m	203	3PE	C1-O11-P-O13
50	1m	203	3PE	C1-O11-P-O14
50	1m	203	3PE	C11-O13-P-O11
50	1m	203	3PE	C11-O13-P-O12
50	1m	203	3PE	O22-C21-O21-C2
50	1m	203	3PE	C22-C21-O21-C2
51	1X	201	CDL	C1-CA2-OA2-PA1
51	1X	201	CDL	CA2-OA2-PA1-OA4
51	1X	201	CDL	CA2-OA2-PA1-OA5
51	1h	201	CDL	OB5-CB3-CB4-OB6
51	1h	201	CDL	OB7-CB5-OB6-CB4
51	1h	201	CDL	C51-CB5-OB6-CB4
51	1h	201	CDL	OB9-CB7-OB8-CB6
51	1h	201	CDL	C71-CB7-OB8-CB6
51	1q	203	CDL	CA3-OA5-PA1-OA3
52	1O	401	GTP	PB-O3A-PA-O5'
52	1O	401	GTP	C5'-O5'-PA-O3A
52	1O	401	GTP	C5'-O5'-PA-O2A
54	1P	403	NDP	C5D-O5D-PN-O3
54	1P	403	NDP	C5D-O5D-PN-O1N
56	1W	201	EHZ	N2-C15-C16-C17
56	1W	201	EHZ	N2-C15-C16-O5

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Mol	Chain	Res	Type	Atoms
56	1W	201	EHZ	O4-C15-C16-C17
56	1W	201	EHZ	O4-C15-C16-O5
56	1W	201	EHZ	C13-C12-N1-C11
56	1n	201	EHZ	C13-C12-N1-C11
51	1N	902	CDL	OB7-CB5-OB6-CB4
51	1N	902	CDL	C51-CB5-OB6-CB4
45	1f	101	PC1	C2-C1-O11-P
56	1W	201	EHZ	O3-C12-N1-C11
56	1n	201	EHZ	O3-C12-N1-C11
51	1L	705	CDL	CA2-C1-CB2-OB2
45	1d	203	PC1	C11-C12-N-C13
45	1q	202	PC1	C11-C12-N-C14
51	1d	202	CDL	O1-C1-CA2-OA2
52	1O	401	GTP	O4'-C4'-C5'-O5'
52	1O	401	GTP	C3'-C4'-C5'-O5'
45	1q	202	PC1	C11-C12-N-C13
45	1H	401	PC1	C31-C32-C33-C34
45	1H	402	PC1	C2-C1-O11-P
51	1X	201	CDL	CA7-C31-C32-C33
45	1d	203	PC1	C11-C12-N-C15
51	1L	705	CDL	O1-C1-CB2-OB2
51	1h	201	CDL	O1-C1-CB2-OB2
50	1L	702	3PE	C2-C1-O11-P
50	1Y	801	3PE	C2-C1-O11-P
50	1Y	802	3PE	O21-C2-C3-O31
45	1d	203	PC1	C11-C12-N-C14
51	1d	202	CDL	C32-C33-C34-C35
45	1h	202	PC1	C33-C34-C35-C36
45	1H	401	PC1	C38-C39-C3A-C3B
51	1X	201	CDL	C19-C20-C21-C22
50	1d	201	3PE	C23-C24-C25-C26
51	1X	201	CDL	C14-C15-C16-C17
50	1m	202	3PE	C2B-C2C-C2D-C2E
45	1q	202	PC1	C11-C12-N-C15
45	1P	402	PC1	C38-C39-C3A-C3B
50	1M	503	3PE	C3B-C3C-C3D-C3E
45	1M	502	PC1	C32-C33-C34-C35
45	1q	202	PC1	C2A-C2B-C2C-C2D
45	1M	504	PC1	C32-C33-C34-C35
50	1M	503	3PE	C33-C34-C35-C36
50	1M	501	3PE	C34-C35-C36-C37
56	1n	201	EHZ	C12-C13-C14-N2

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Mol	Chain	Res	Type	Atoms
51	1L	705	CDL	C12-C13-C14-C15
45	1A	201	PC1	C33-C34-C35-C36
45	1P	402	PC1	C32-C33-C34-C35
50	1J	201	3PE	C34-C35-C36-C37
50	1N	901	3PE	O21-C2-C3-O31
51	1N	902	CDL	OA6-CA4-CA6-OA8
45	1q	201	PC1	C32-C33-C34-C35
45	1M	502	PC1	C2-C1-O11-P
51	1L	705	CDL	CB4-CB3-OB5-PB2
50	1m	203	3PE	C27-C28-C29-C2A
45	1M	504	PC1	C2A-C2B-C2C-C2D
50	1Y	802	3PE	O11-C1-C2-C3
51	1d	202	CDL	OA5-CA3-CA4-CA6
51	1h	201	CDL	OB5-CB3-CB4-CB6
51	1X	201	CDL	C58-C59-C60-C61
51	1X	201	CDL	C61-C62-C63-C64
51	1d	202	CDL	C34-C35-C36-C37
45	1h	202	PC1	C1-C2-C3-O31
50	1L	702	3PE	C1-C2-C3-O31
50	1m	203	3PE	C1-C2-C3-O31
51	1X	201	CDL	CB3-CB4-CB6-OB8
51	1d	202	CDL	CA3-CA4-CA6-OA8
50	1d	201	3PE	C26-C27-C28-C29
54	1P	403	NDP	O4D-C1D-N1N-C6N
50	1L	702	3PE	C33-C34-C35-C36
45	1P	401	PC1	O21-C2-C3-O31
50	1N	901	3PE	C28-C29-C2A-C2B
45	1h	202	PC1	C2-C1-O11-P
48	1F	501	FMN	C4'-C5'-O5'-P
51	1X	201	CDL	C12-C11-CA5-OA6
51	1L	705	CDL	C53-C54-C55-C56
45	1d	203	PC1	O11-C1-C2-C3
51	1d	202	CDL	OB5-CB3-CB4-CB6
50	1J	201	3PE	C3A-C3B-C3C-C3D
50	1d	201	3PE	C39-C3A-C3B-C3C
45	1q	201	PC1	C24-C25-C26-C27
50	1L	702	3PE	C3A-C3B-C3C-C3D
50	1N	901	3PE	C2B-C2C-C2D-C2E
51	1h	201	CDL	C34-C35-C36-C37
45	1q	201	PC1	C1-C2-C3-O31
50	1N	901	3PE	C1-C2-C3-O31
50	1N	903	3PE	C1-C2-C3-O31

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Mol	Chain	Res	Type	Atoms
50	1Y	802	3PE	C1-C2-C3-O31
50	1M	501	3PE	C37-C38-C39-C3A
50	1M	501	3PE	C21-C22-C23-C24
51	1d	202	CDL	OB5-CB3-CB4-OB6
50	1b	201	3PE	O21-C21-C22-C23
50	1N	903	3PE	C2-C1-O11-P
51	1X	201	CDL	C1-CB2-OB2-PB2
45	1H	402	PC1	C21-C22-C23-C24
45	1q	201	PC1	O21-C2-C3-O31
50	1L	702	3PE	O21-C2-C3-O31
51	1d	202	CDL	OA6-CA4-CA6-OA8
50	1d	201	3PE	C31-C32-C33-C34
50	1d	201	3PE	O21-C21-C22-C23
45	1M	504	PC1	O11-C1-C2-C3
50	1N	901	3PE	C2D-C2E-C2F-C2G
51	1X	201	CDL	C31-C32-C33-C34
50	1N	903	3PE	C35-C36-C37-C38
50	1M	503	3PE	C38-C39-C3A-C3B
45	1M	504	PC1	O11-C1-C2-O21
45	1d	203	PC1	O11-C1-C2-O21
50	1L	701	3PE	O11-C1-C2-O21
45	1P	401	PC1	C1-C2-C3-O31
45	1d	203	PC1	C1-C2-C3-O31
51	1N	902	CDL	CA3-CA4-CA6-OA8
45	1M	502	PC1	C12-C11-O13-P
45	1h	202	PC1	C12-C11-O13-P
45	1q	201	PC1	C12-C11-O13-P
50	1J	201	3PE	C12-C11-O13-P
50	1L	704	3PE	C12-C11-O13-P
50	1Y	804	3PE	C12-C11-O13-P
50	1j	101	3PE	C12-C11-O13-P
50	1m	202	3PE	C12-C11-O13-P
56	1W	201	EHZ	C15-C16-C17-C19
45	1d	203	PC1	C32-C33-C34-C35
51	1d	202	CDL	C71-C72-C73-C74
45	1H	401	PC1	C2B-C2C-C2D-C2E
45	1H	401	PC1	C22-C23-C24-C25
45	1A	201	PC1	O13-C11-C12-N
45	1f	101	PC1	O13-C11-C12-N
45	1m	201	PC1	O13-C11-C12-N
45	1q	201	PC1	O13-C11-C12-N
50	1L	701	3PE	C28-C29-C2A-C2B

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Mol	Chain	Res	Type	Atoms
50	1Y	802	3PE	C2D-C2E-C2F-C2G
50	1M	501	3PE	C35-C36-C37-C38
56	1W	201	EHZ	C15-C16-C17-C20
45	1m	201	PC1	C22-C23-C24-C25
50	1m	202	3PE	C26-C27-C28-C29
51	1X	201	CDL	C55-C56-C57-C58
50	1Y	804	3PE	C2-C1-O11-P
52	1O	401	GTP	C4'-C5'-O5'-PA
51	1L	705	CDL	C37-C38-C39-C40
45	1q	201	PC1	C35-C36-C37-C38
51	1L	705	CDL	C54-C55-C56-C57
50	1N	903	3PE	O11-C1-C2-O21
50	1Y	802	3PE	O11-C1-C2-O21
51	1N	902	CDL	C32-C31-CA7-OA8
51	1X	201	CDL	OB6-CB4-CB6-OB8
50	1Y	803	3PE	C1-C2-C3-O31
45	1H	402	PC1	C11-O13-P-O14
45	1H	402	PC1	C1-O11-P-O12
45	1M	502	PC1	C1-O11-P-O12
45	1M	502	PC1	C1-O11-P-O13
45	1d	203	PC1	C1-O11-P-O14
45	1f	101	PC1	C1-O11-P-O13
45	1h	202	PC1	C11-O13-P-O11
45	1m	201	PC1	C11-O13-P-O14
45	1q	202	PC1	C11-O13-P-O11
50	1J	201	3PE	C11-O13-P-O14
50	1M	501	3PE	C1-O11-P-O14
50	1N	901	3PE	C11-O13-P-O14
50	1b	201	3PE	C11-O13-P-O11
50	1b	201	3PE	C11-O13-P-O14
50	1d	201	3PE	C1-O11-P-O12
51	1N	902	CDL	CA3-OA5-PA1-OA3
54	1P	403	NDP	C5D-O5D-PN-O2N
45	1m	201	PC1	C23-C24-C25-C26
50	1M	501	3PE	C23-C24-C25-C26
45	1M	504	PC1	C2-C1-O11-P
50	1m	203	3PE	C2-C1-O11-P
50	1d	201	3PE	C36-C37-C38-C39
51	1X	201	CDL	C24-C25-C26-C27
50	1b	201	3PE	C2A-C2B-C2C-C2D
45	1H	402	PC1	O21-C21-C22-C23
51	1d	202	CDL	OA5-CA3-CA4-OA6

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Mol	Chain	Res	Type	Atoms
51	1q	203	CDL	C13-C14-C15-C16
50	1L	701	3PE	C27-C28-C29-C2A
45	1f	101	PC1	C31-C32-C33-C34
51	1L	705	CDL	CA4-CA3-OA5-PA1
45	1H	401	PC1	O21-C2-C3-O31
50	1m	203	3PE	O21-C2-C3-O31
50	1d	201	3PE	C32-C33-C34-C35
50	1L	701	3PE	C26-C27-C28-C29
50	1m	202	3PE	C24-C25-C26-C27
50	1j	101	3PE	C32-C33-C34-C35
45	1q	201	PC1	C22-C23-C24-C25
51	1X	201	CDL	C36-C37-C38-C39
50	1J	201	3PE	C28-C29-C2A-C2B
51	1X	201	CDL	C35-C36-C37-C38
50	1J	201	3PE	C23-C24-C25-C26
50	1Y	801	3PE	C21-C22-C23-C24
56	1n	201	EHZ	S1-C10-C11-N1
50	1M	503	3PE	C27-C28-C29-C2A
45	1m	201	PC1	O21-C21-C22-C23
45	1P	402	PC1	C37-C38-C39-C3A
51	1d	202	CDL	C37-C38-C39-C40
45	1f	101	PC1	C32-C33-C34-C35
50	1m	202	3PE	C39-C3A-C3B-C3C
50	1d	201	3PE	C2C-C2D-C2E-C2F
51	1L	705	CDL	C79-C80-C81-C82
51	1h	201	CDL	C38-C39-C40-C41
50	1M	503	3PE	C2D-C2E-C2F-C2G
50	1M	503	3PE	C3-C2-O21-C21
50	1b	201	3PE	C37-C38-C39-C3A
50	1J	201	3PE	O11-C1-C2-O21
50	1N	901	3PE	O11-C1-C2-O21
45	1A	201	PC1	C2-C1-O11-P
50	1L	701	3PE	O11-C1-C2-C3
50	1d	201	3PE	O11-C1-C2-C3
45	1H	401	PC1	C32-C33-C34-C35
54	1P	403	NDP	C2N-C3N-C7N-N7N
50	1L	702	3PE	C36-C37-C38-C39
50	1Y	802	3PE	C23-C24-C25-C26
45	1M	504	PC1	C21-C22-C23-C24
51	1q	203	CDL	C15-C16-C17-C18
45	1H	401	PC1	C1-C2-C3-O31
51	1L	705	CDL	C82-C83-C84-C85

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Mol	Chain	Res	Type	Atoms
50	1d	201	3PE	O11-C1-C2-O21
45	1h	202	PC1	C2C-C2D-C2E-C2F
56	1W	201	EHZ	C12-C13-C14-N2
45	1m	201	PC1	C26-C27-C28-C29
45	1h	202	PC1	C36-C37-C38-C39
50	1m	202	3PE	C27-C28-C29-C2A
51	1L	705	CDL	CB6-CB4-OB6-CB5
45	1P	401	PC1	O11-C1-C2-O21
56	1W	201	EHZ	C21-C1-C2-C3
45	1h	202	PC1	C22-C23-C24-C25
50	1L	703	3PE	C34-C35-C36-C37
45	1f	101	PC1	C37-C38-C39-C3A
56	1W	201	EHZ	C15-C16-C17-C18
45	1d	203	PC1	O21-C2-C3-O31
51	1L	705	CDL	OB6-CB4-CB6-OB8
50	1b	201	3PE	C2B-C2C-C2D-C2E
50	1L	702	3PE	C32-C33-C34-C35
45	1P	401	PC1	O11-C1-C2-C3
50	1N	903	3PE	O11-C1-C2-C3
50	1m	203	3PE	C26-C27-C28-C29
51	1X	201	CDL	C12-C11-CA5-OA7
50	1b	201	3PE	O22-C21-C22-C23
45	1H	402	PC1	C25-C26-C27-C28
51	1h	201	CDL	C72-C73-C74-C75
50	1Y	801	3PE	O21-C21-C22-C23
51	1q	203	CDL	CA5-C11-C12-C13
51	1d	202	CDL	C44-C45-C46-C47
51	1d	202	CDL	C72-C73-C74-C75
50	1Y	803	3PE	O21-C21-C22-C23
45	1q	202	PC1	C34-C35-C36-C37
50	1L	702	3PE	C39-C3A-C3B-C3C
51	1L	705	CDL	C74-C75-C76-C77
50	1L	703	3PE	C28-C29-C2A-C2B
51	1X	201	CDL	C63-C64-C65-C66
50	1Y	803	3PE	C32-C33-C34-C35
45	1M	502	PC1	O11-C1-C2-C3
50	1L	703	3PE	C1-C2-O21-C21
45	1H	402	PC1	C2B-C2C-C2D-C2E
45	1M	504	PC1	C28-C29-C2A-C2B
45	1h	202	PC1	C11-C12-N-C13
50	1b	201	3PE	C36-C37-C38-C39
51	1d	202	CDL	CB4-CB3-OB5-PB2

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Mol	Chain	Res	Type	Atoms
45	1d	203	PC1	C33-C34-C35-C36
50	1d	201	3PE	O22-C21-C22-C23
51	1h	201	CDL	C75-C76-C77-C78
50	1Y	801	3PE	C23-C24-C25-C26
45	1h	202	PC1	C11-C12-N-C15
50	1Y	801	3PE	O22-C21-C22-C23
45	1q	201	PC1	C23-C24-C25-C26
45	1M	504	PC1	C2D-C2E-C2F-C2G
45	1H	401	PC1	C34-C35-C36-C37
50	1L	701	3PE	C39-C3A-C3B-C3C
51	1N	902	CDL	C34-C35-C36-C37
50	1m	202	3PE	C3C-C3D-C3E-C3F
45	1M	504	PC1	O22-C21-C22-C23
50	1Y	803	3PE	O22-C21-C22-C23
45	1P	402	PC1	C35-C36-C37-C38
50	1m	202	3PE	C37-C38-C39-C3A
51	1L	705	CDL	C52-C51-CB5-OB6
45	1H	401	PC1	O31-C31-C32-C33
45	1M	504	PC1	O21-C21-C22-C23
50	1J	201	3PE	O11-C1-C2-C3
51	1L	705	CDL	C16-C17-C18-C19
50	1M	503	3PE	O31-C31-C32-C33
45	1q	201	PC1	C3D-C3E-C3F-C3G
45	1H	401	PC1	C39-C3A-C3B-C3C
50	1M	503	3PE	O32-C31-C32-C33
51	1N	902	CDL	C32-C33-C34-C35

There are no ring outliers.

44 monomers are involved in 191 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	1d	203	PC1	7	0
51	1L	705	CDL	6	0
45	1M	504	PC1	6	0
50	1Y	801	3PE	3	0
45	1q	201	PC1	6	0
50	1Y	804	3PE	4	0
54	1P	403	NDP	2	0
50	1b	201	3PE	4	0
45	1q	202	PC1	10	0
56	1n	201	EHZ	1	0
50	1L	701	3PE	3	0

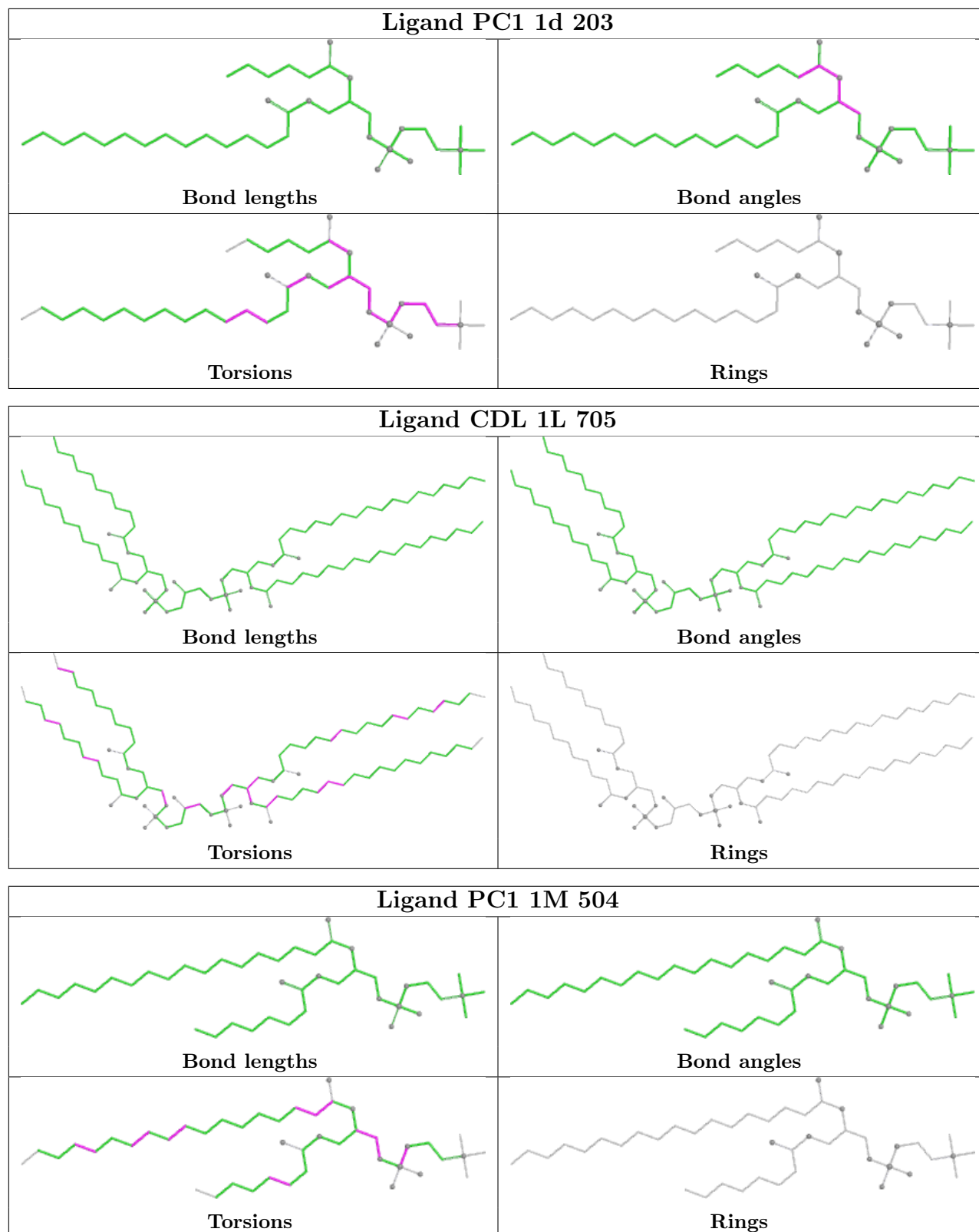
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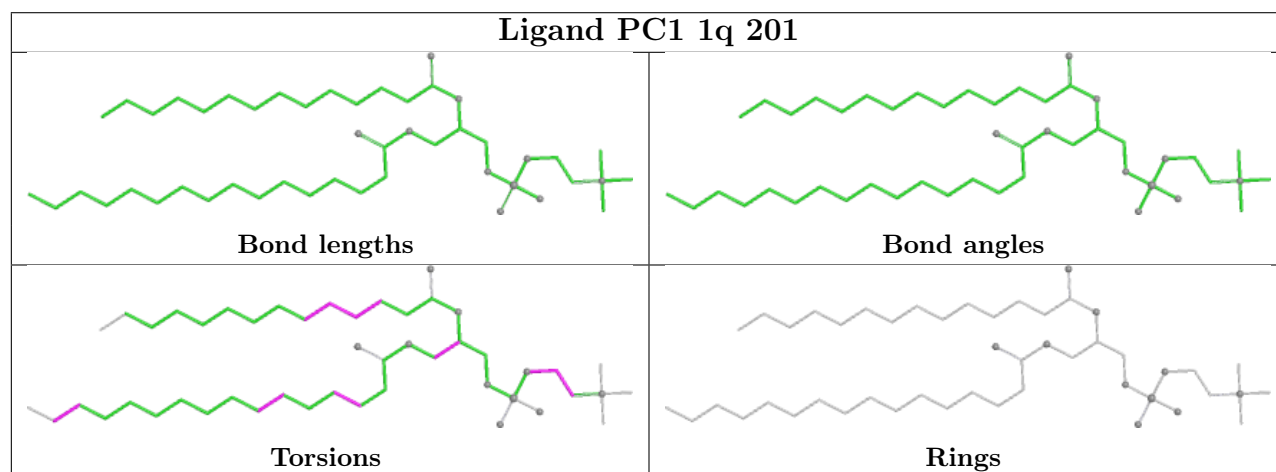
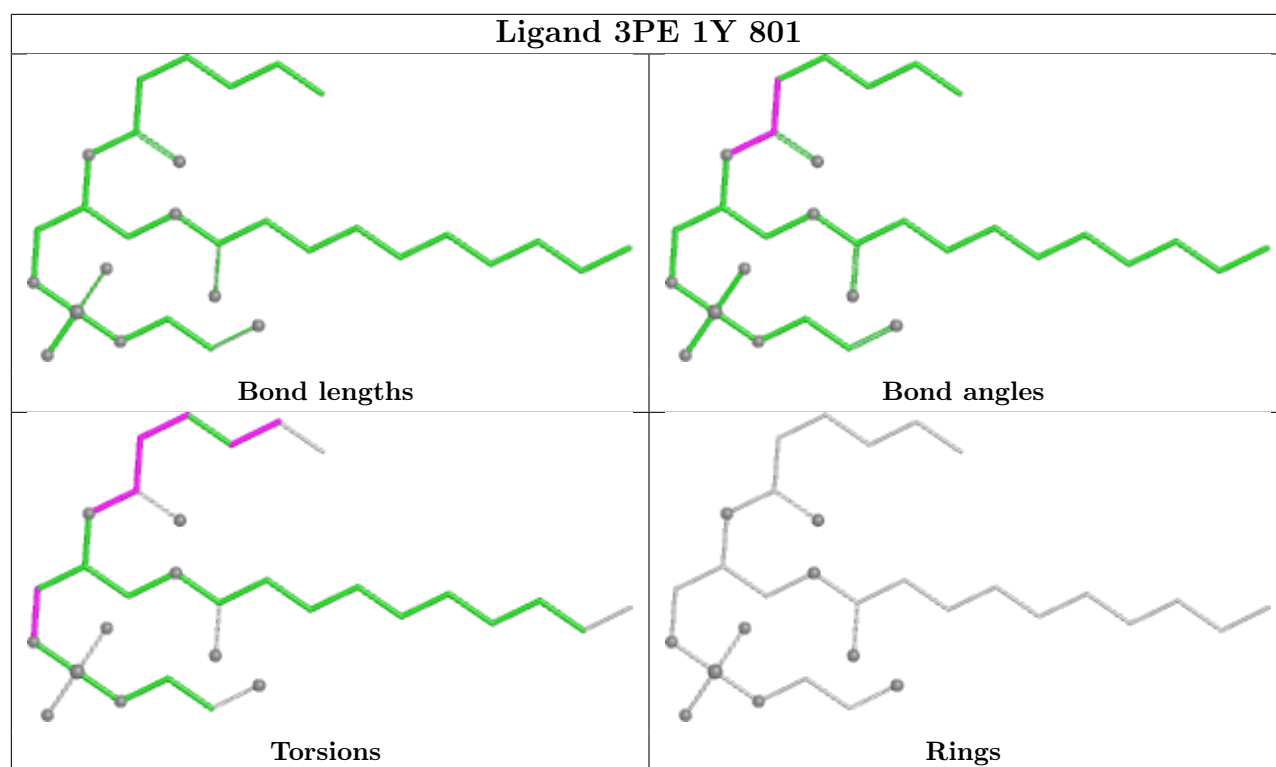
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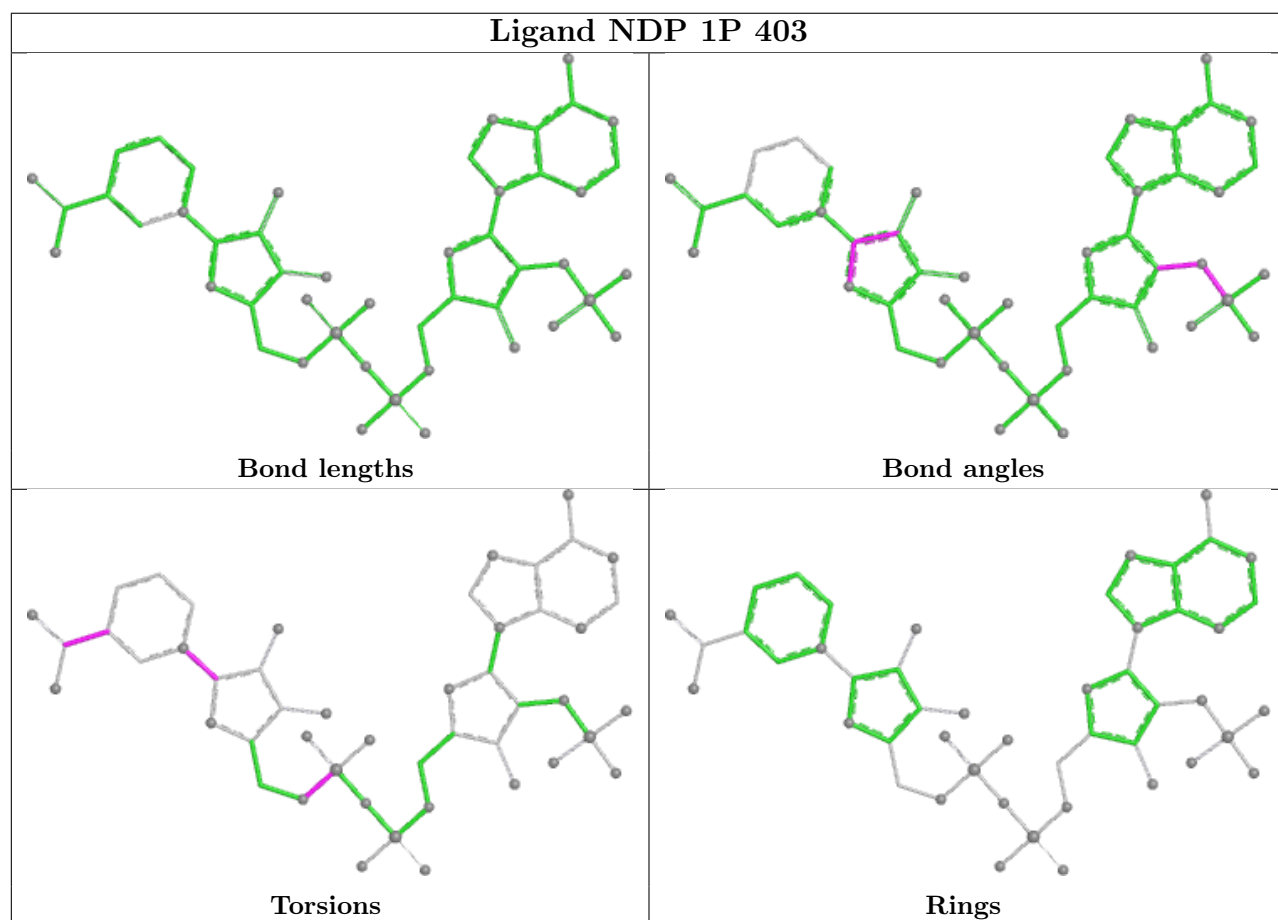
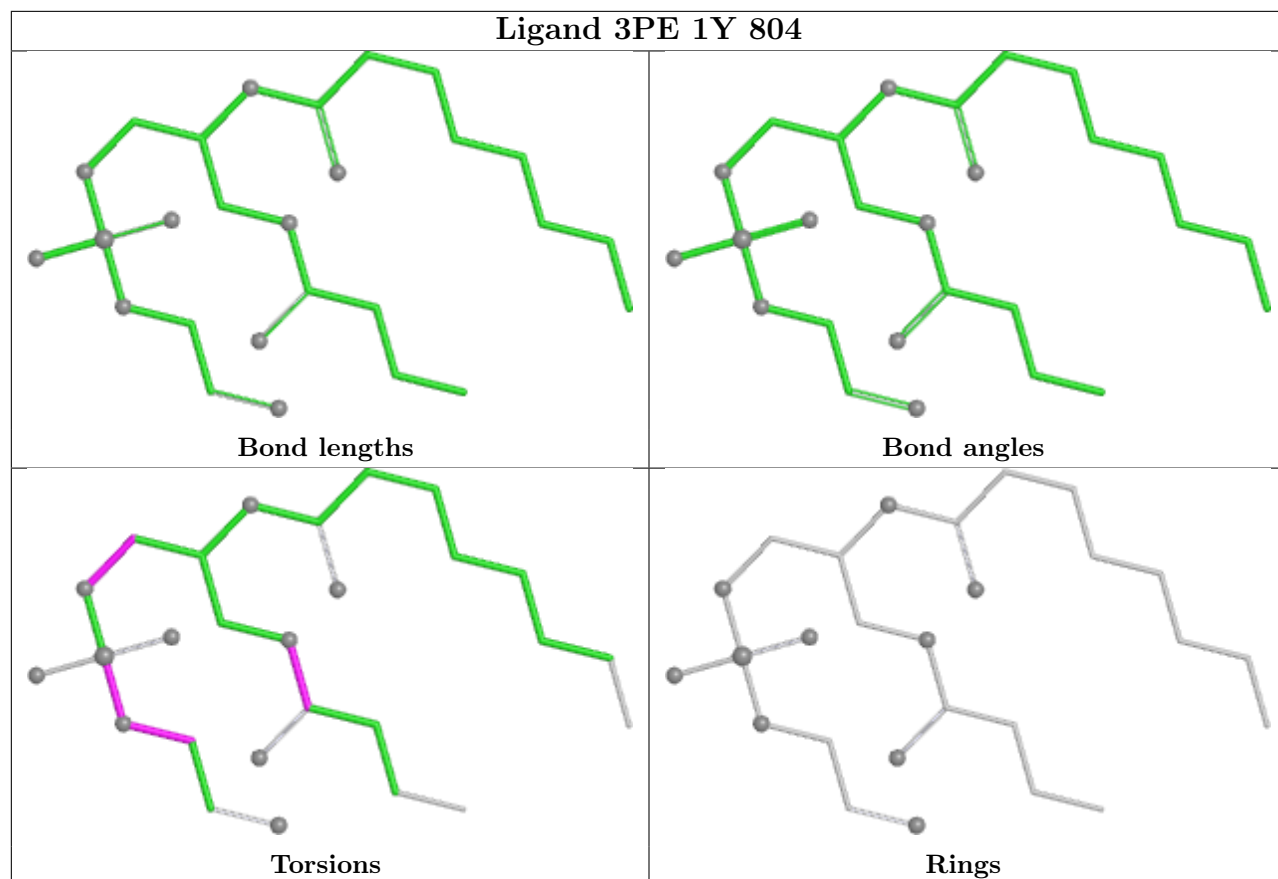
Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	1H	402	PC1	9	0
45	1M	502	PC1	2	0
51	1d	202	CDL	9	0
50	1Y	803	3PE	3	0
51	1X	201	CDL	10	0
50	1L	704	3PE	3	0
56	1W	201	EHZ	2	0
46	1F	502	SF4	1	0
46	1B	201	SF4	2	0
50	1L	703	3PE	9	0
50	1M	501	3PE	4	0
50	1M	503	3PE	11	0
52	1O	401	GTP	2	0
45	1m	201	PC1	4	0
50	1d	201	3PE	7	0
51	1q	203	CDL	3	0
50	1L	702	3PE	6	0
45	1I	203	PC1	6	0
50	1N	903	3PE	3	0
50	1Y	802	3PE	5	0
45	1h	202	PC1	3	0
45	1f	101	PC1	3	0
45	1H	401	PC1	4	0
50	1j	101	3PE	3	0
51	1N	902	CDL	4	0
50	1J	201	3PE	7	0
50	1m	202	3PE	3	0
51	1h	201	CDL	12	0
45	1P	402	PC1	3	0
50	1N	901	3PE	5	0
50	1m	203	3PE	3	0
47	1G	803	FES	1	0
45	1A	201	PC1	1	0

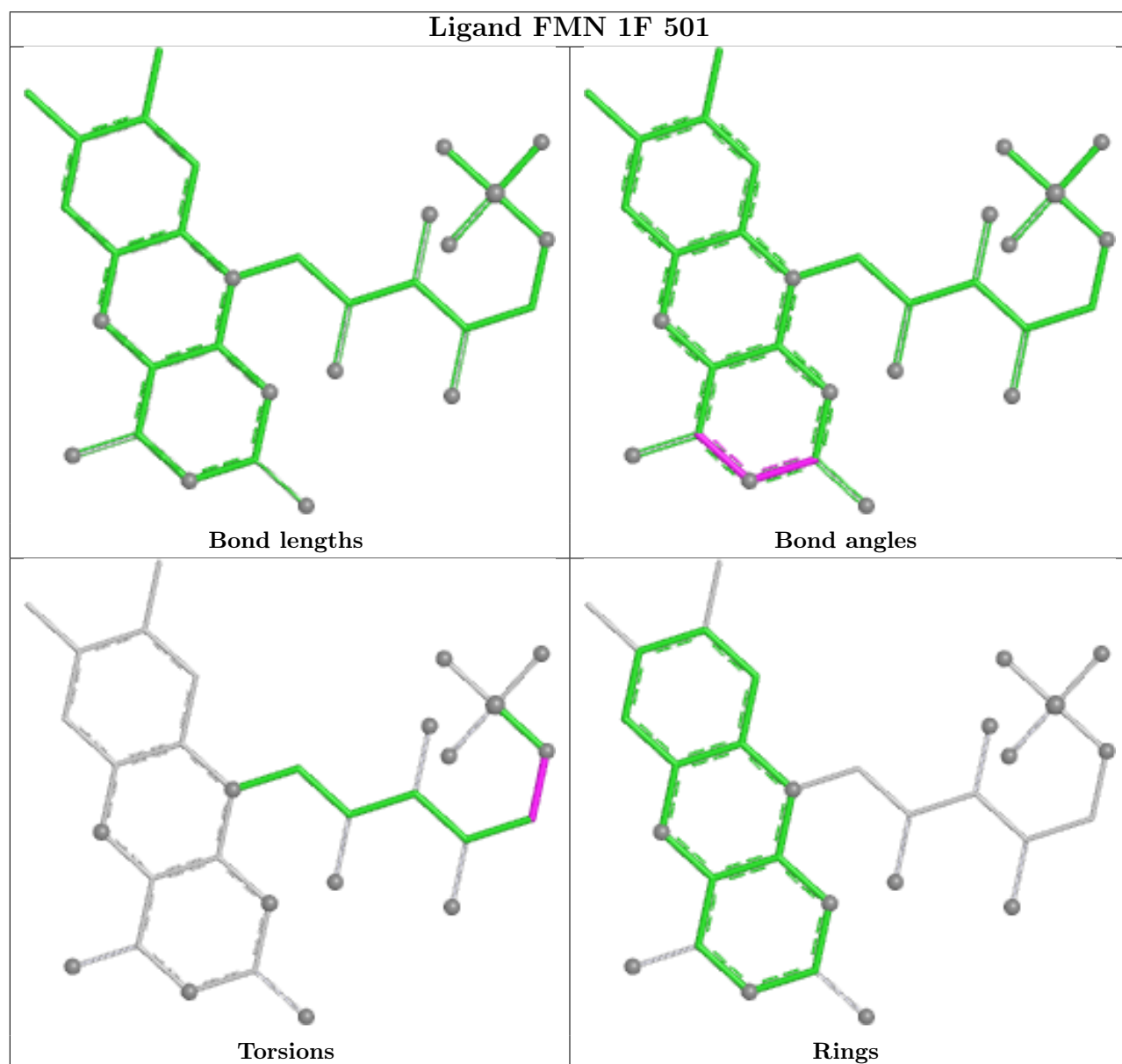
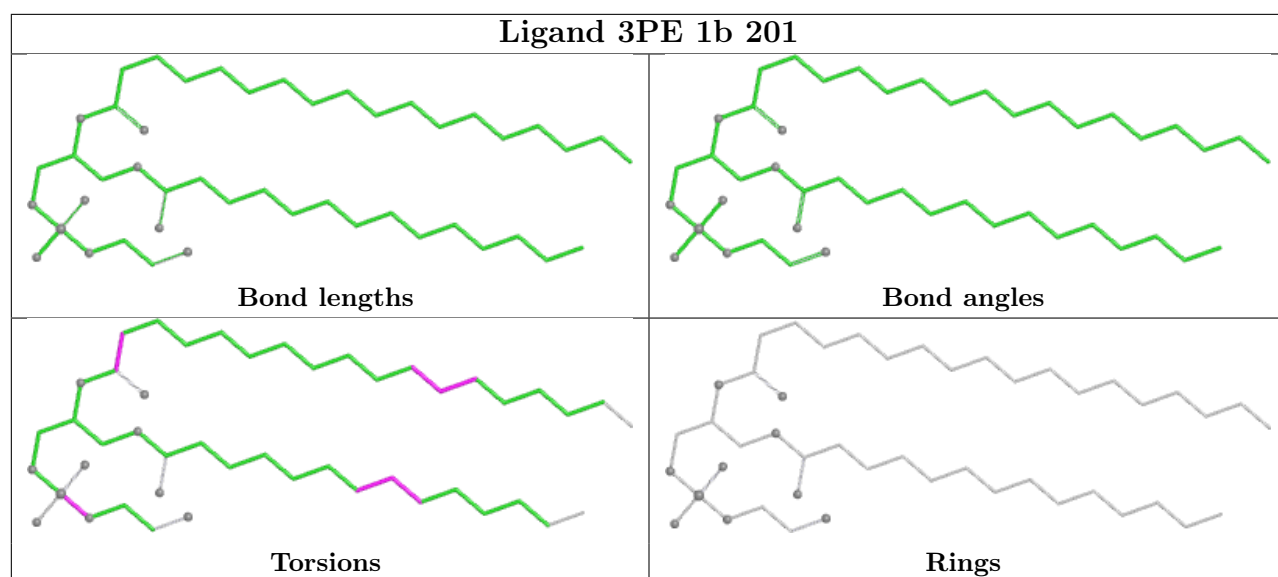
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

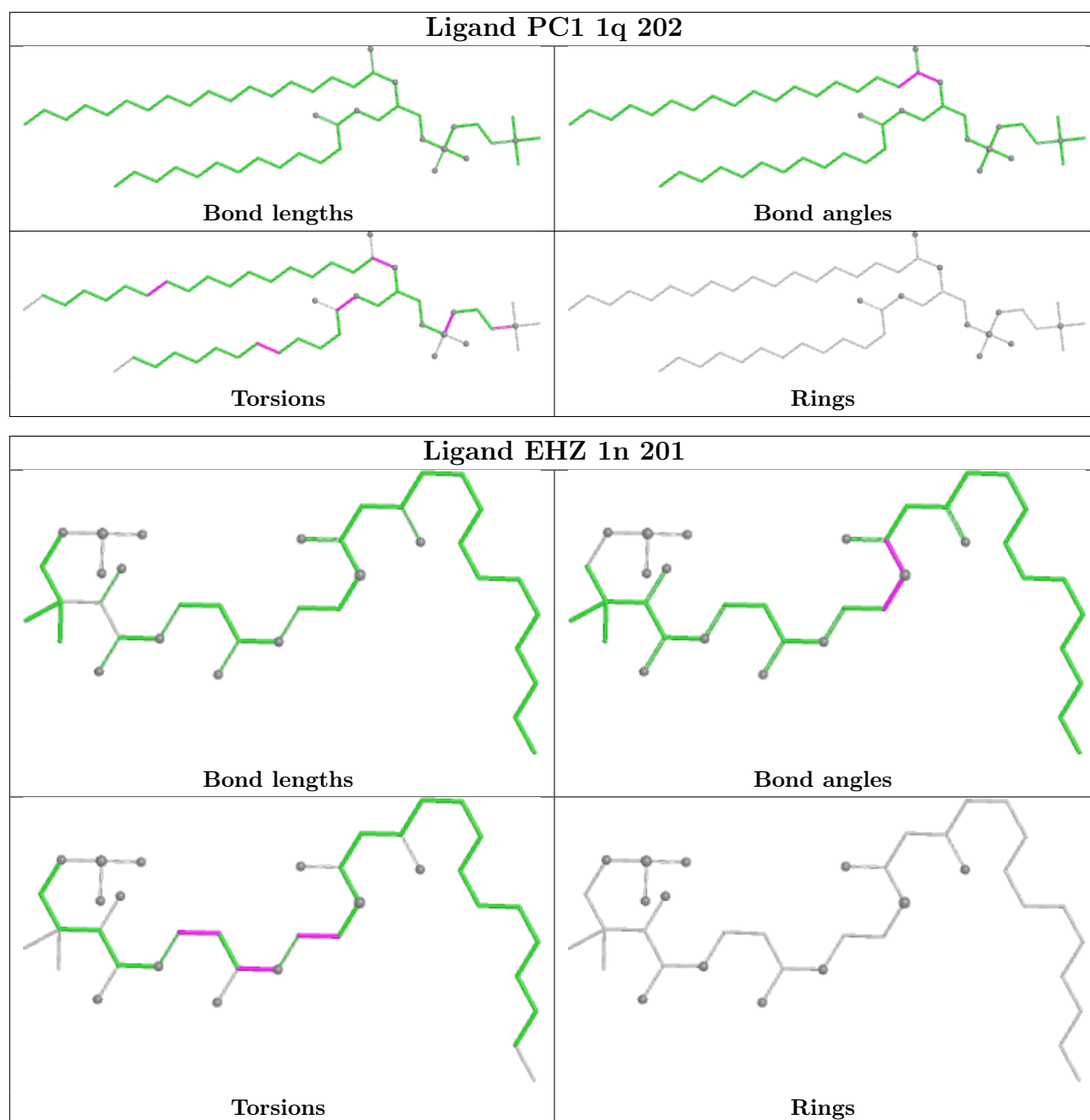
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

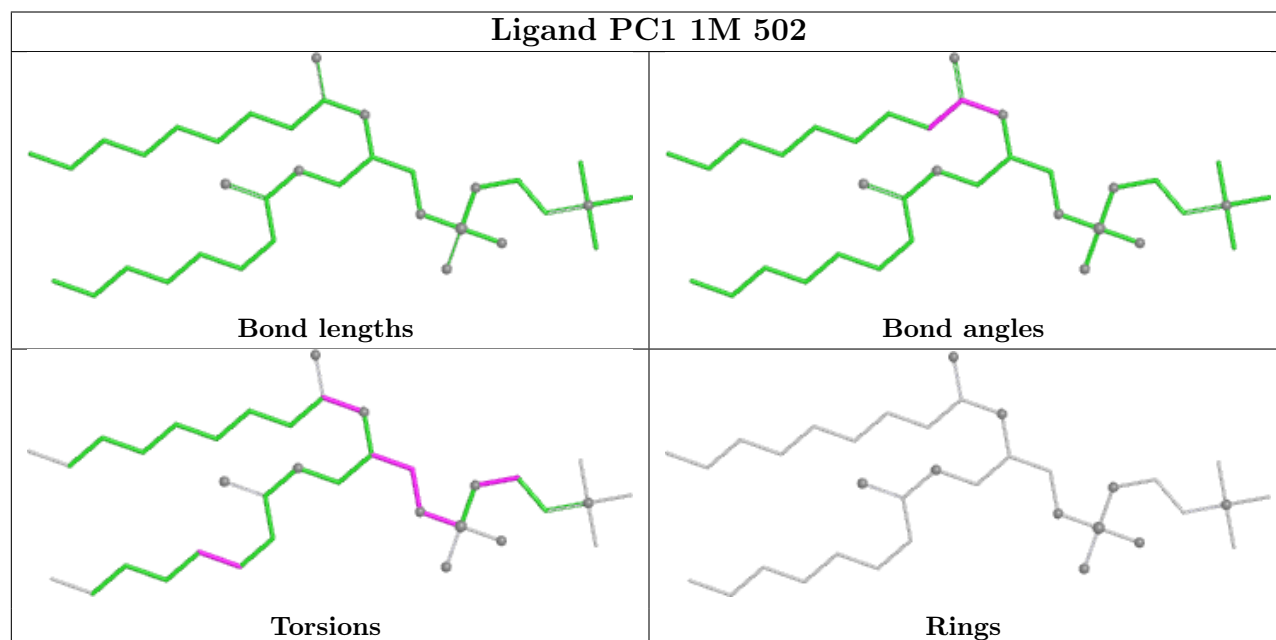
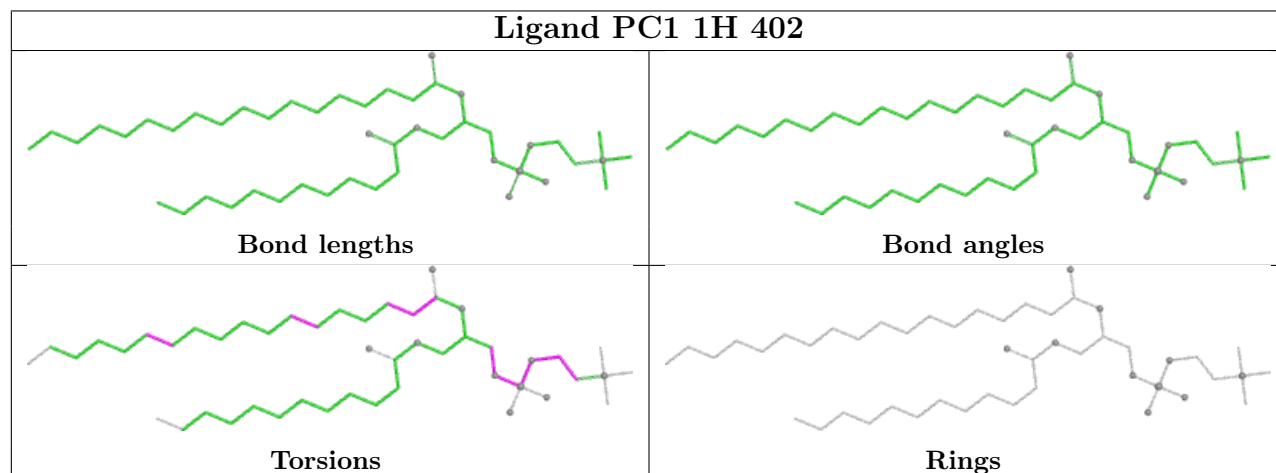
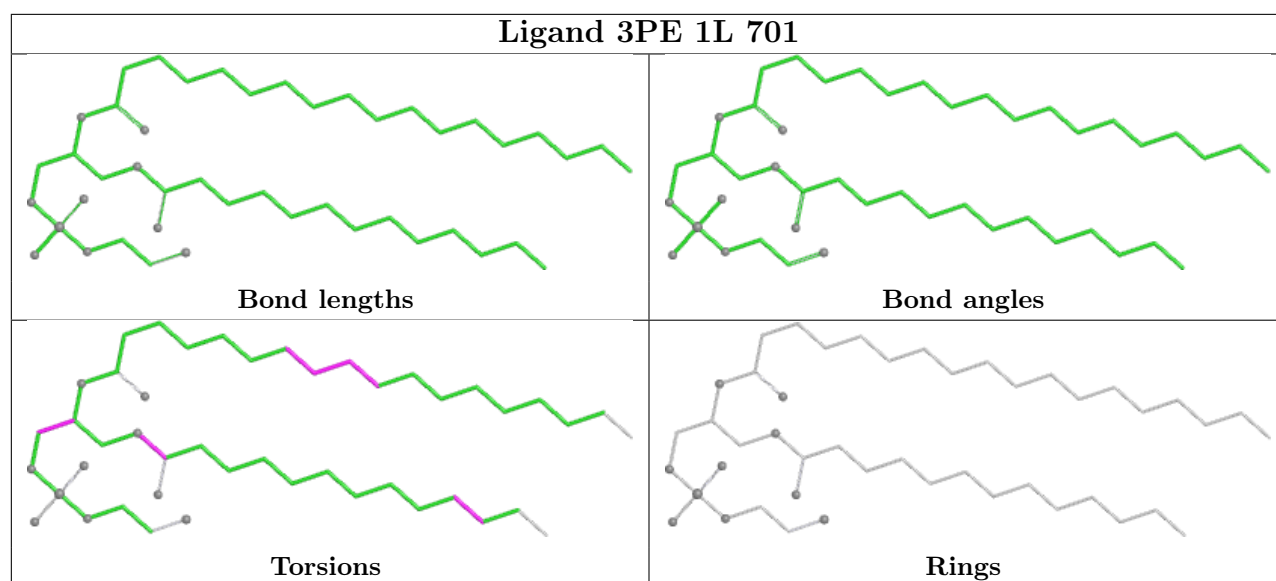


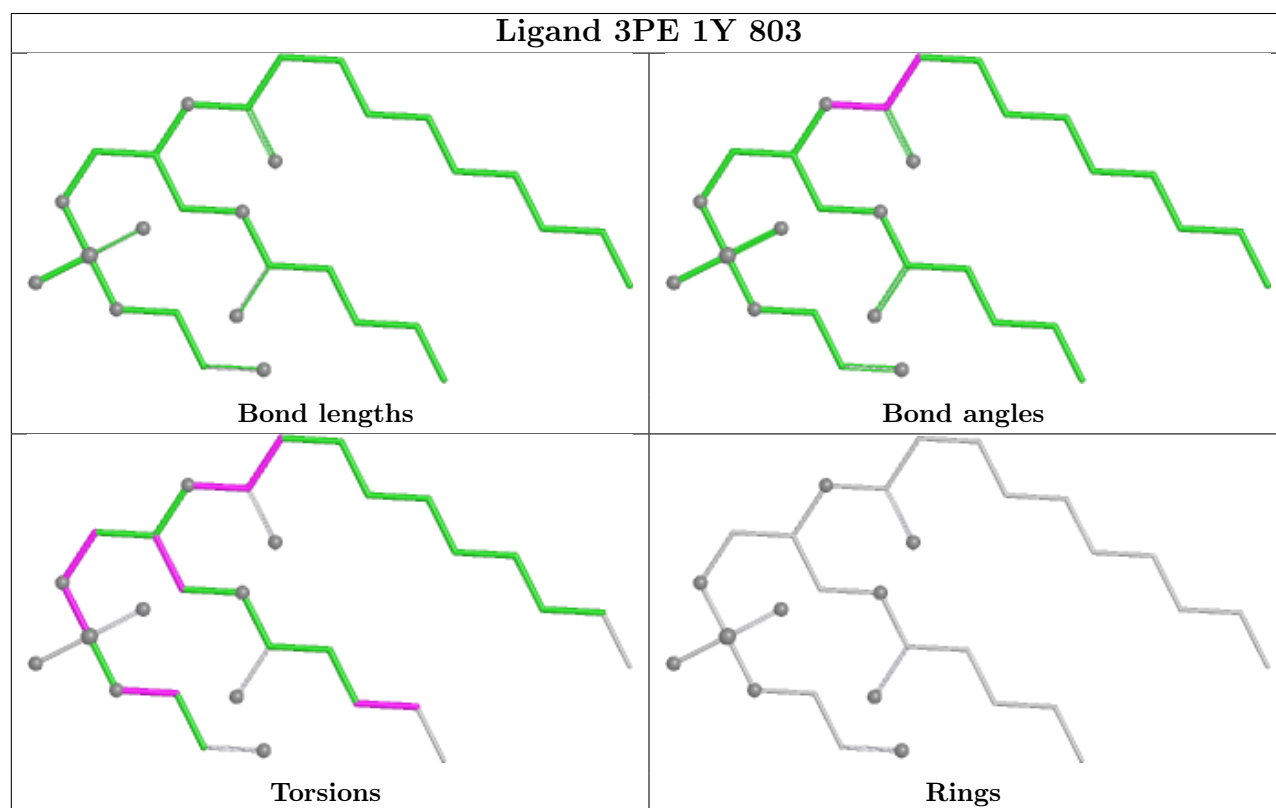
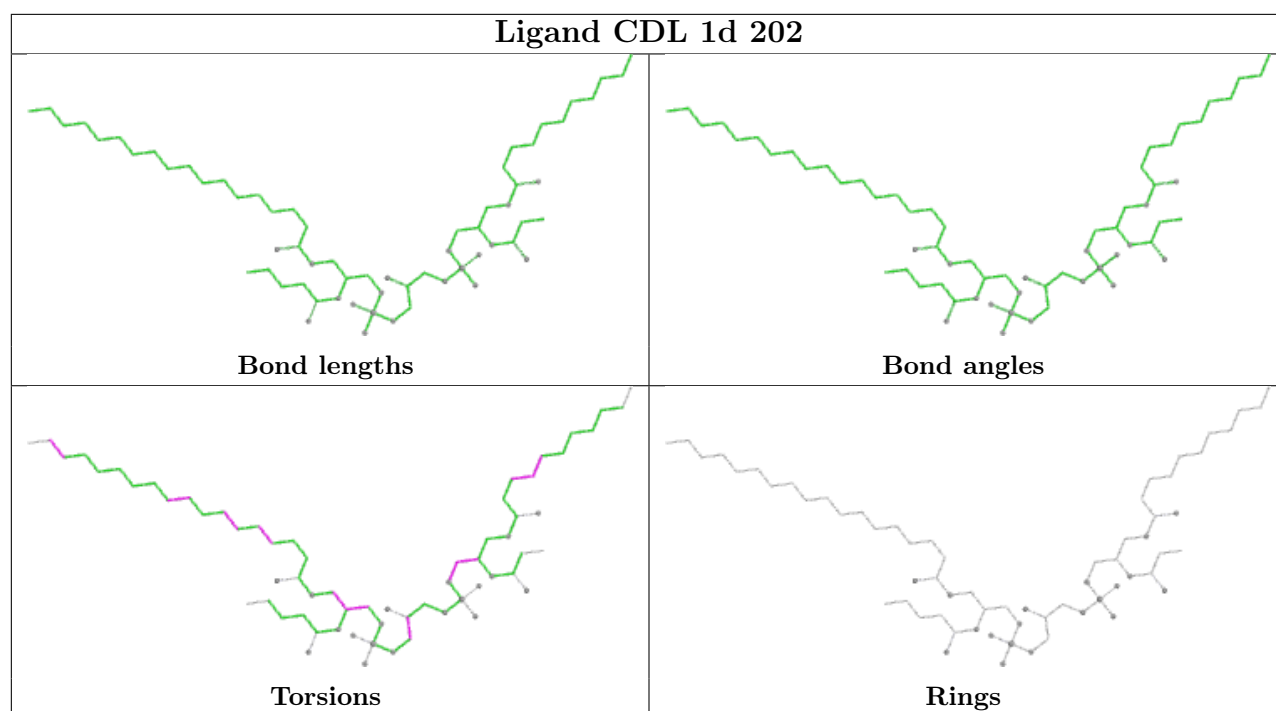


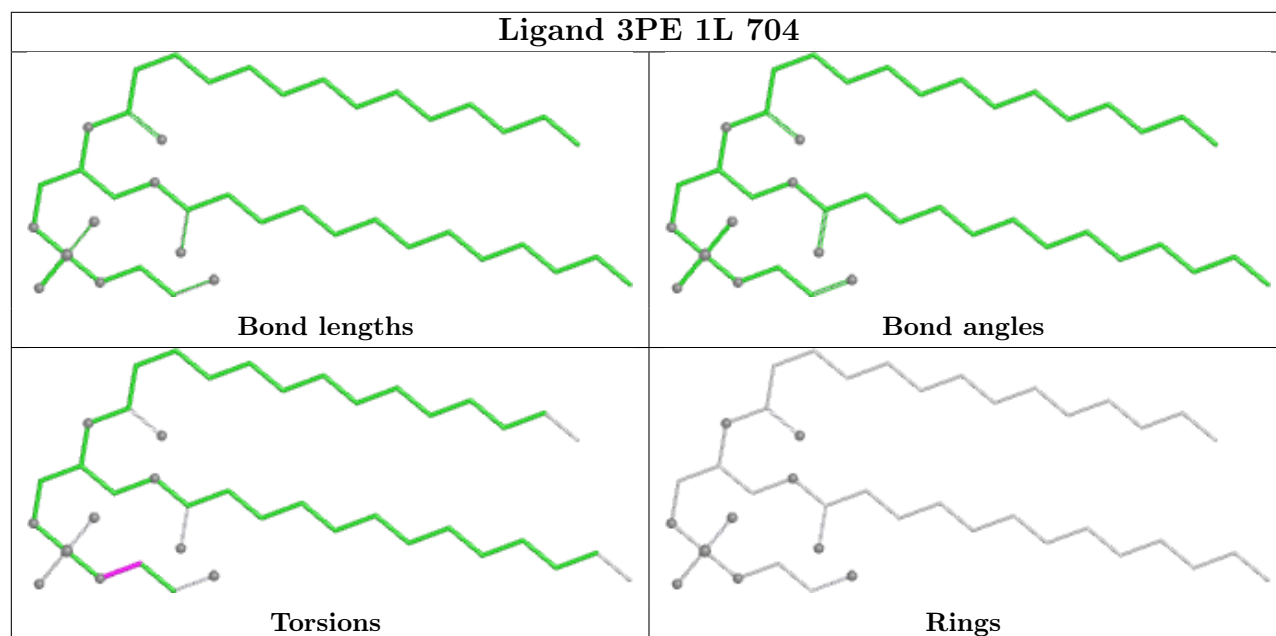
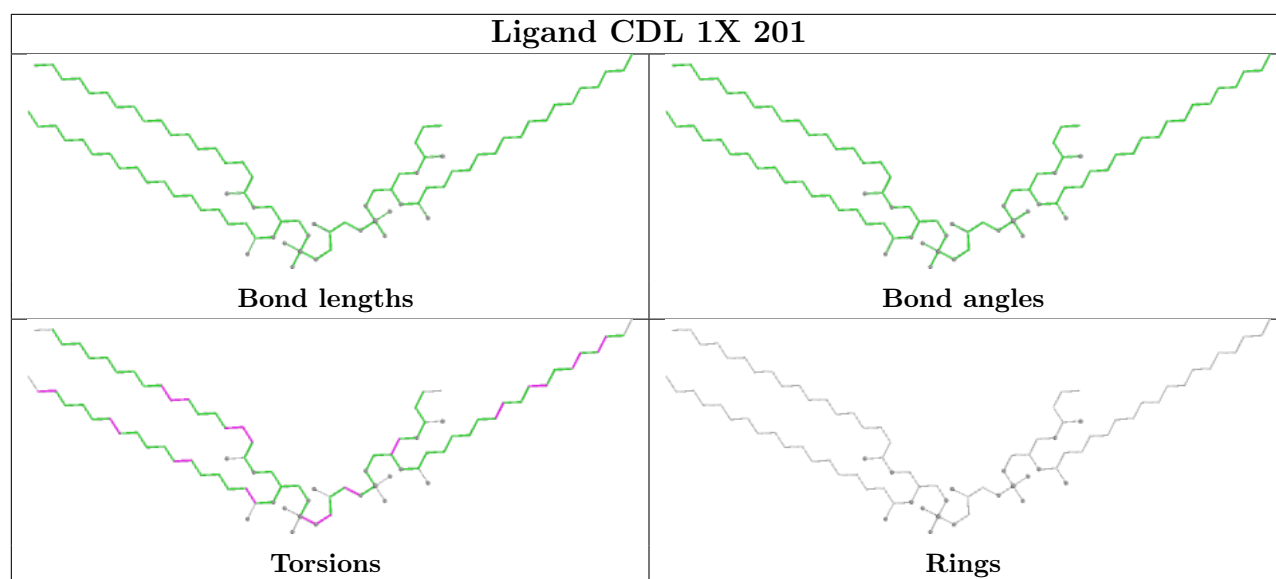


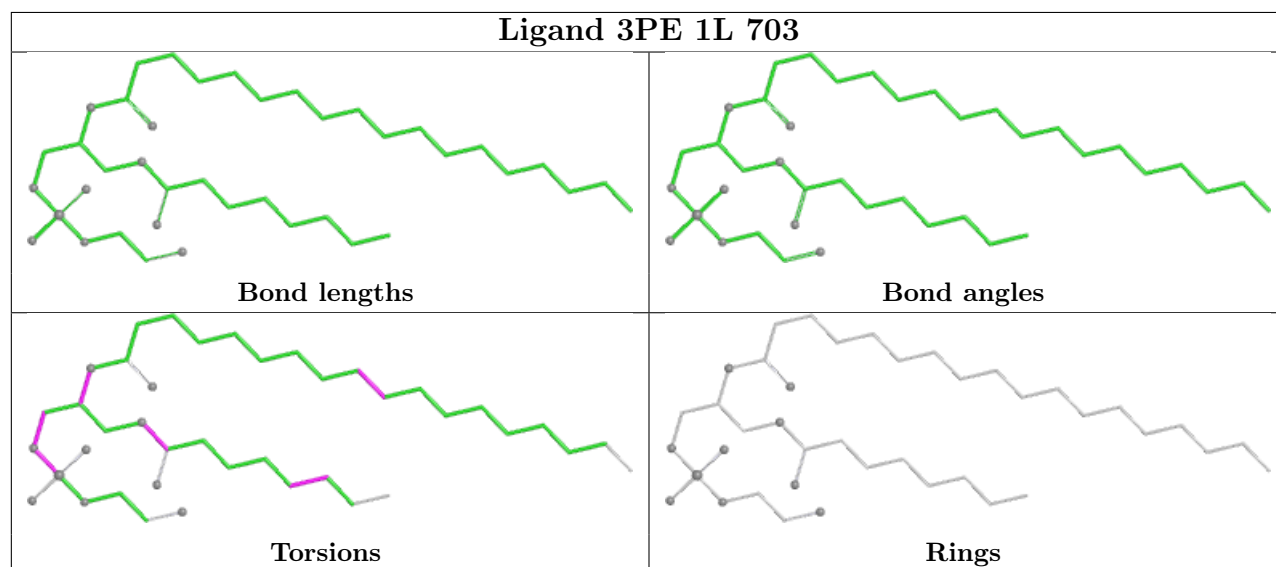
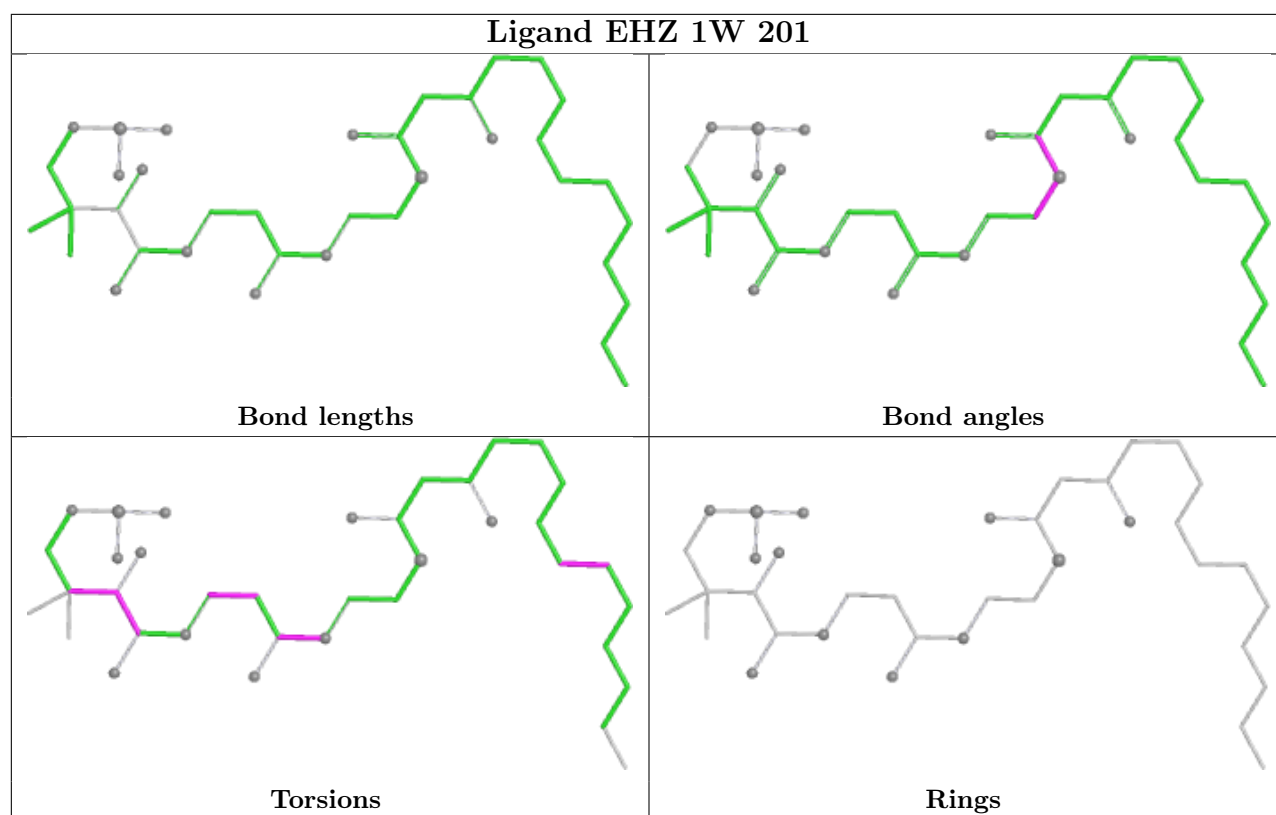


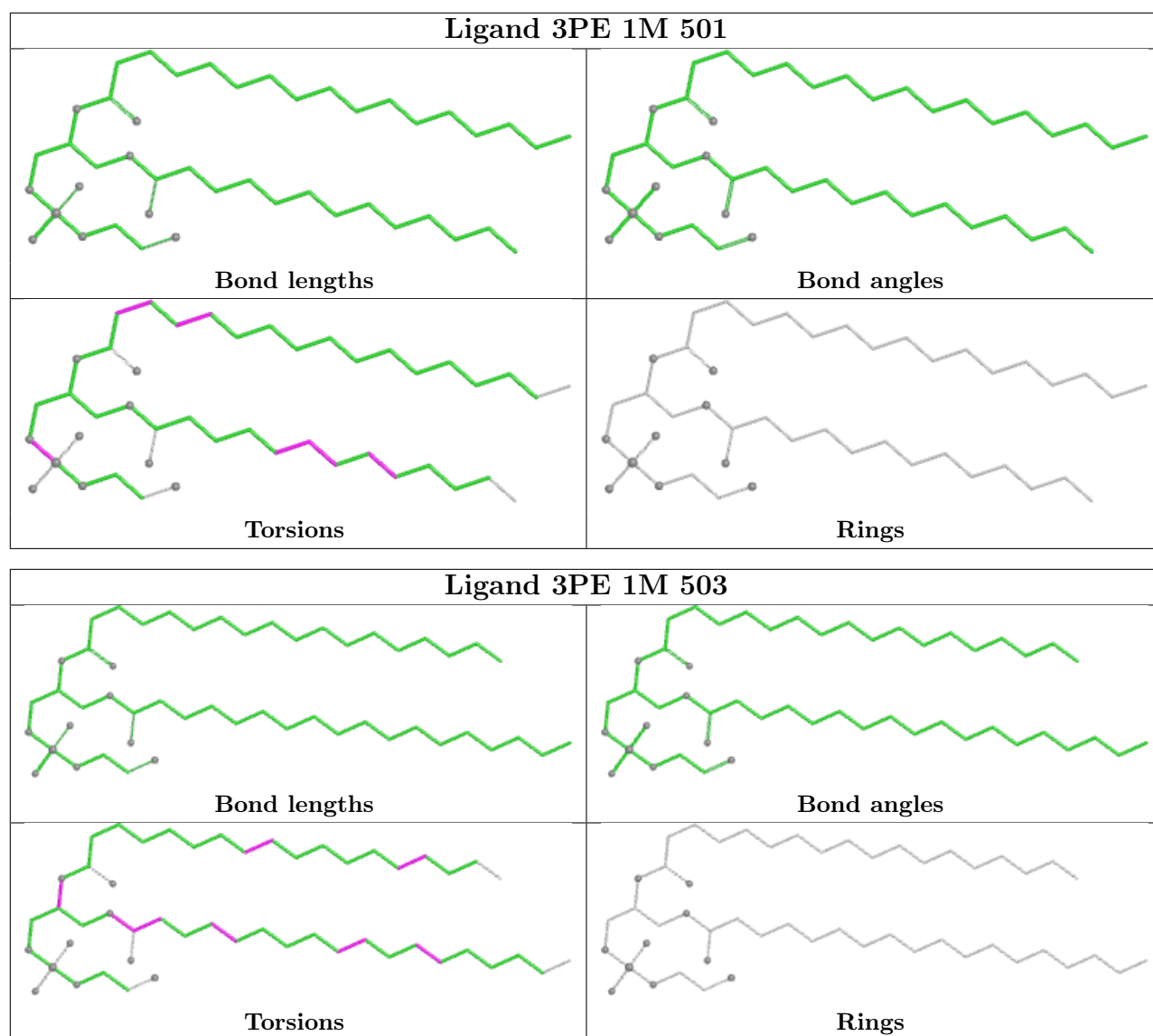


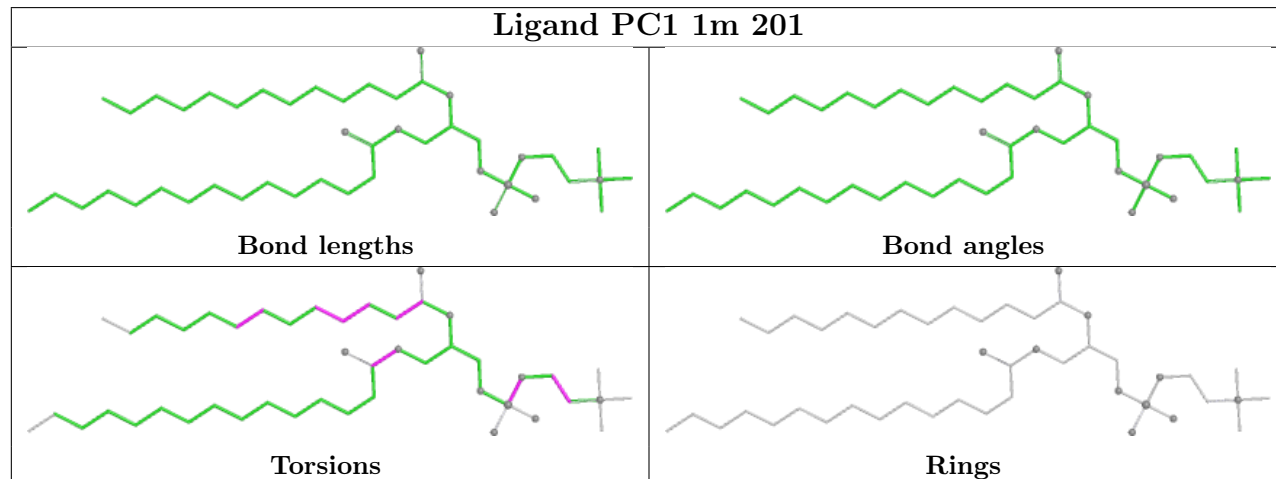
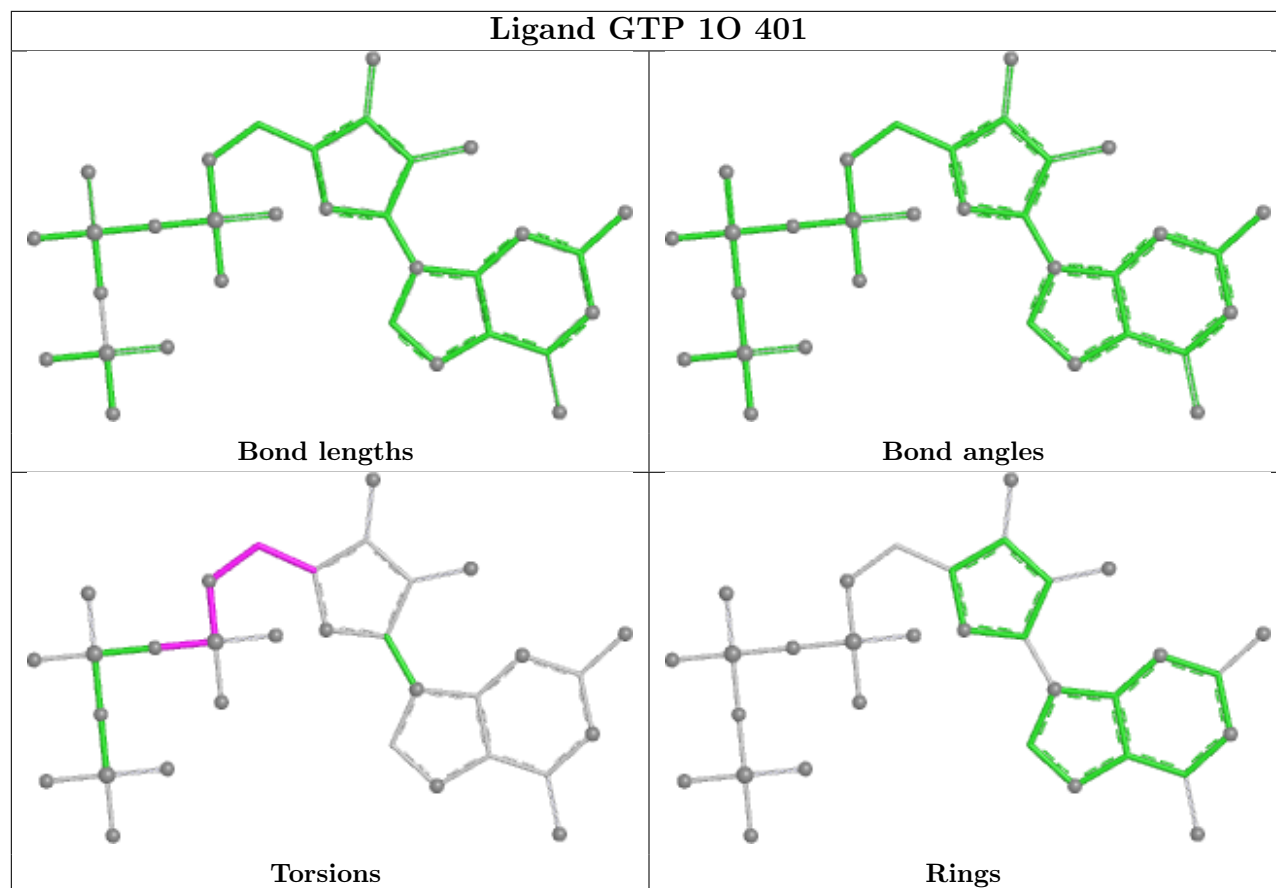


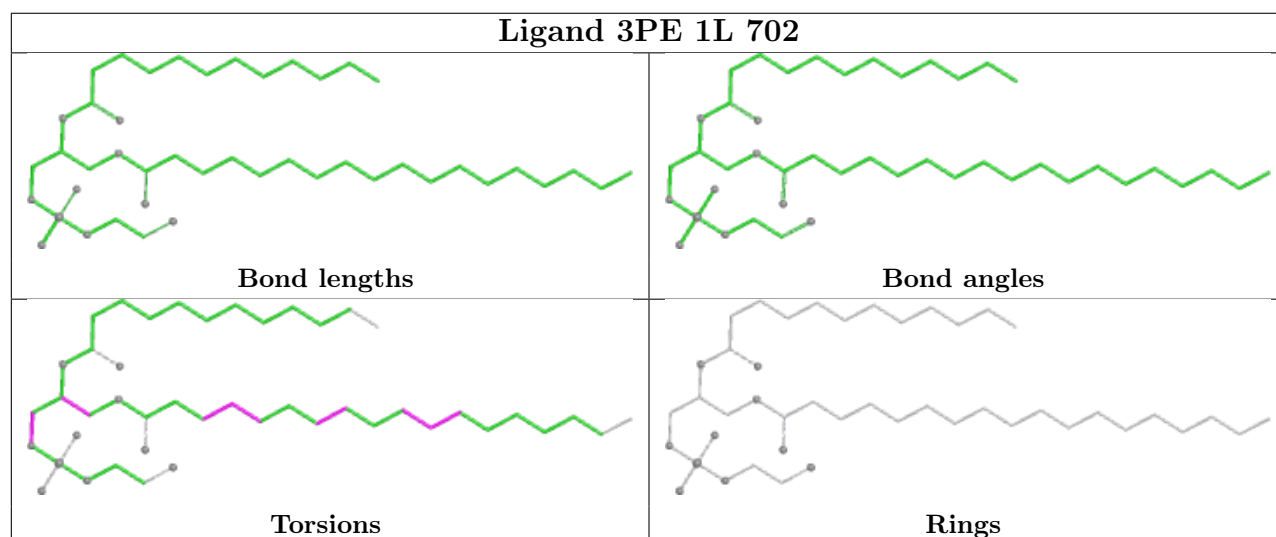
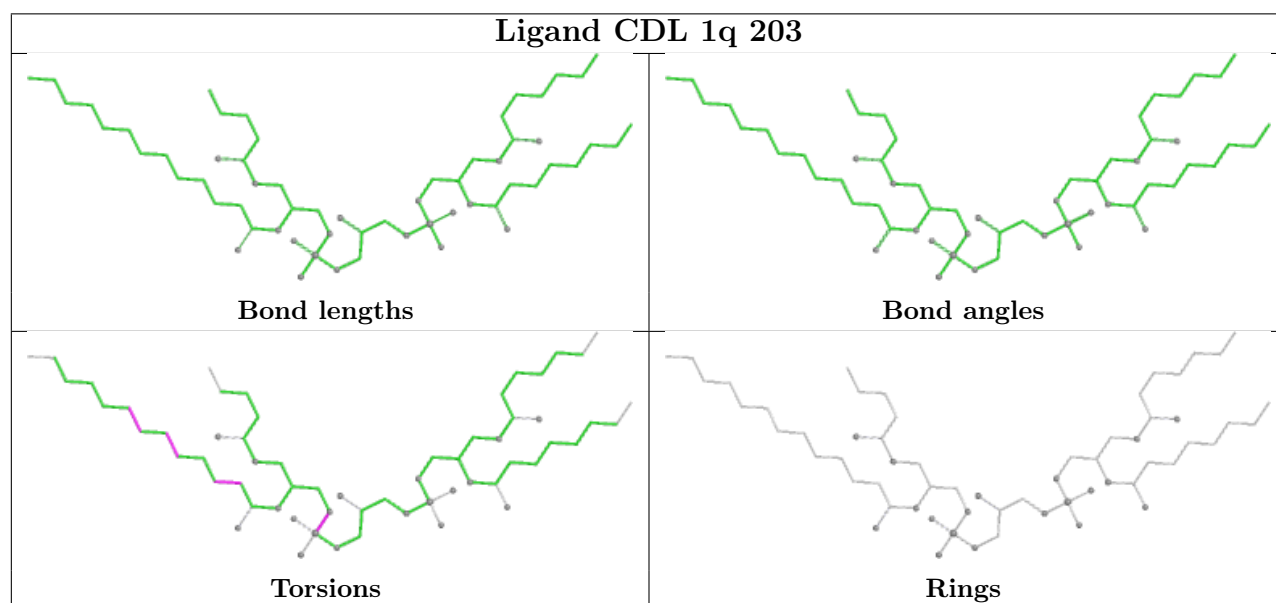
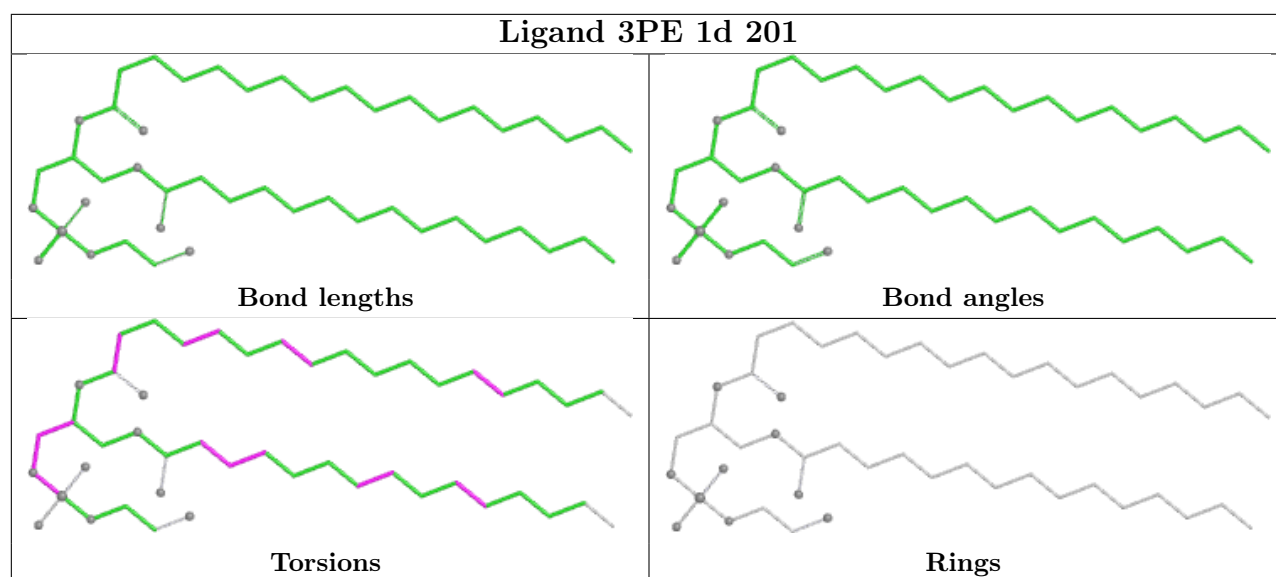


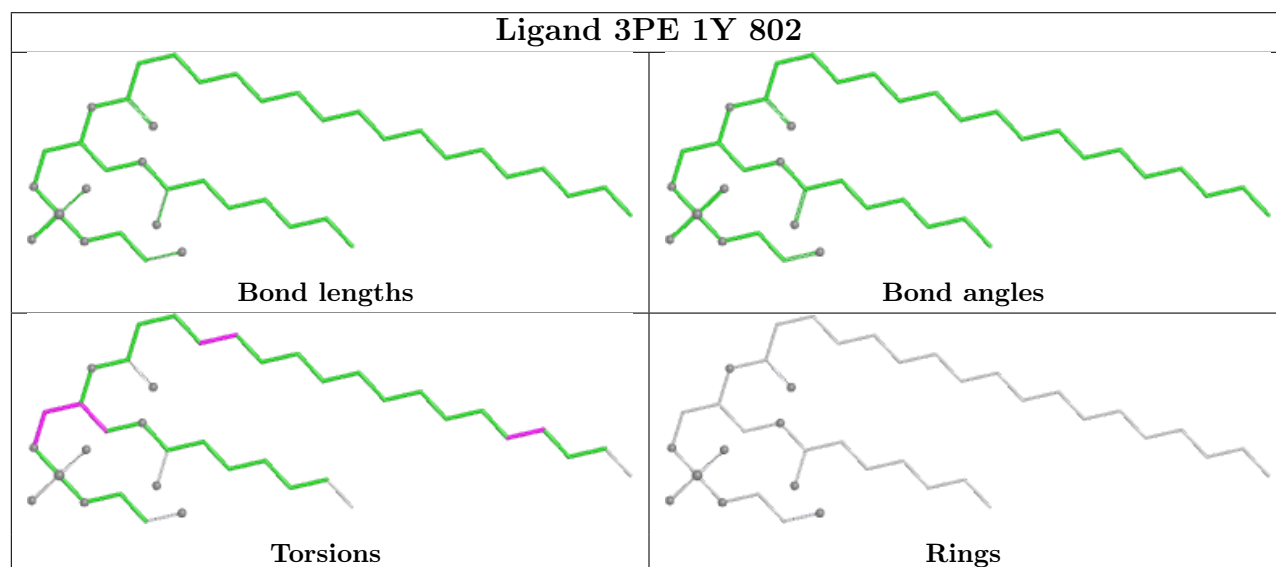
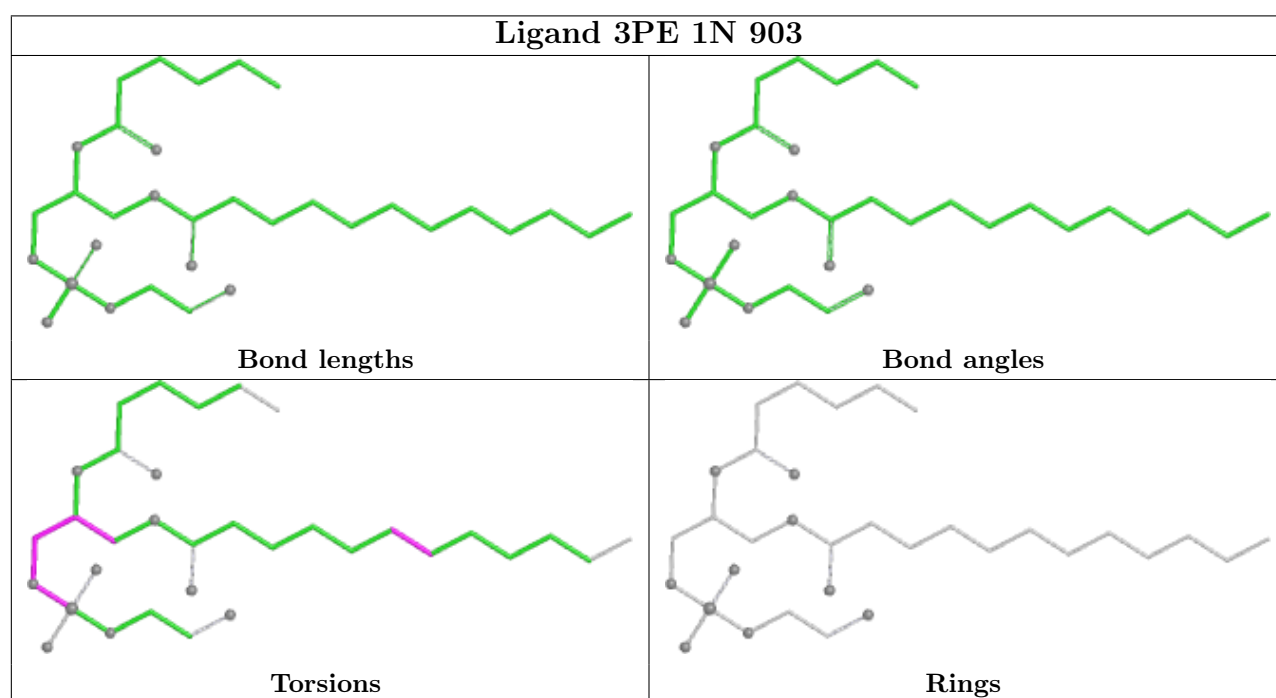
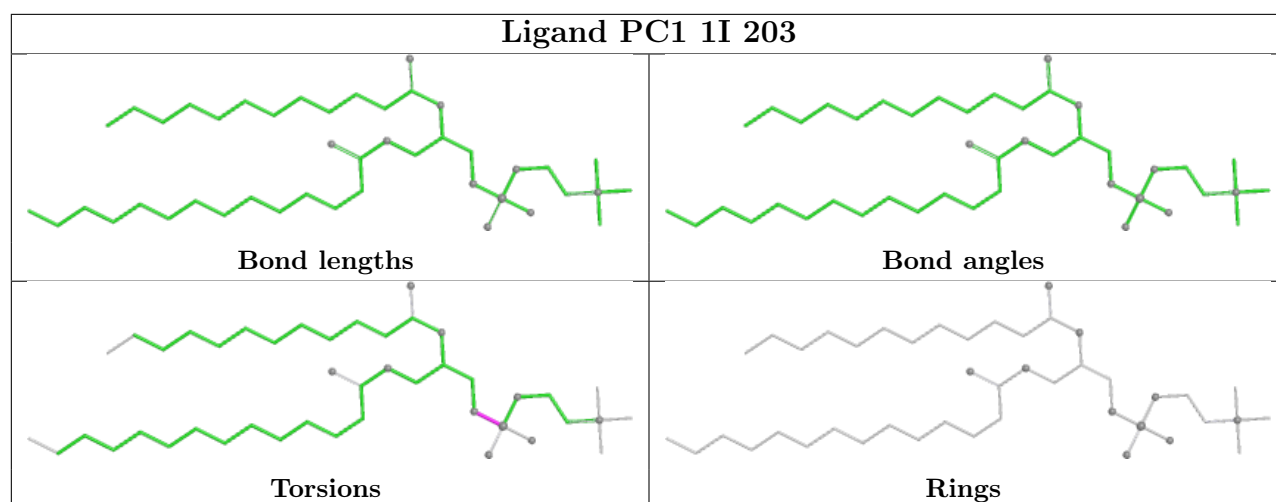


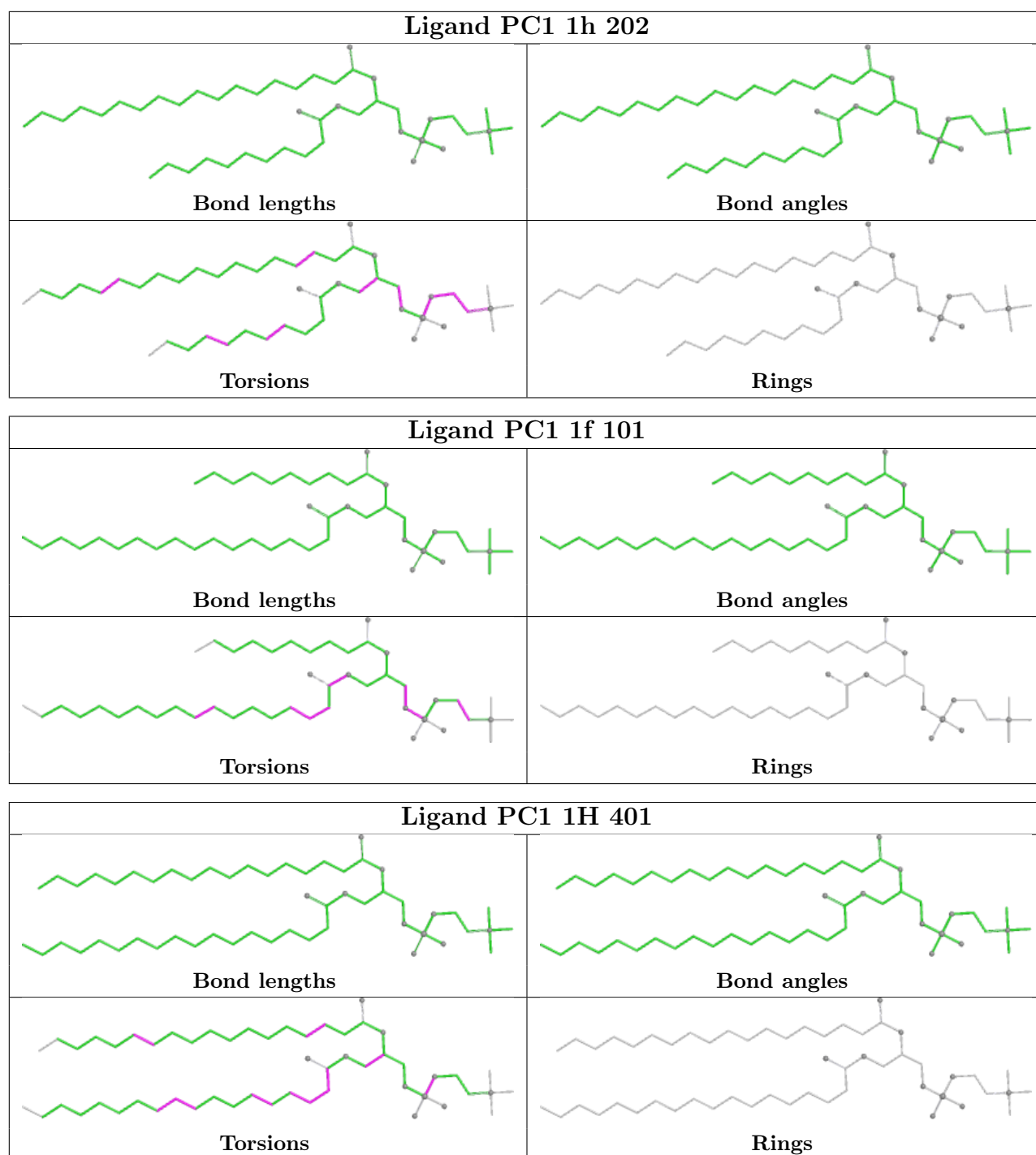


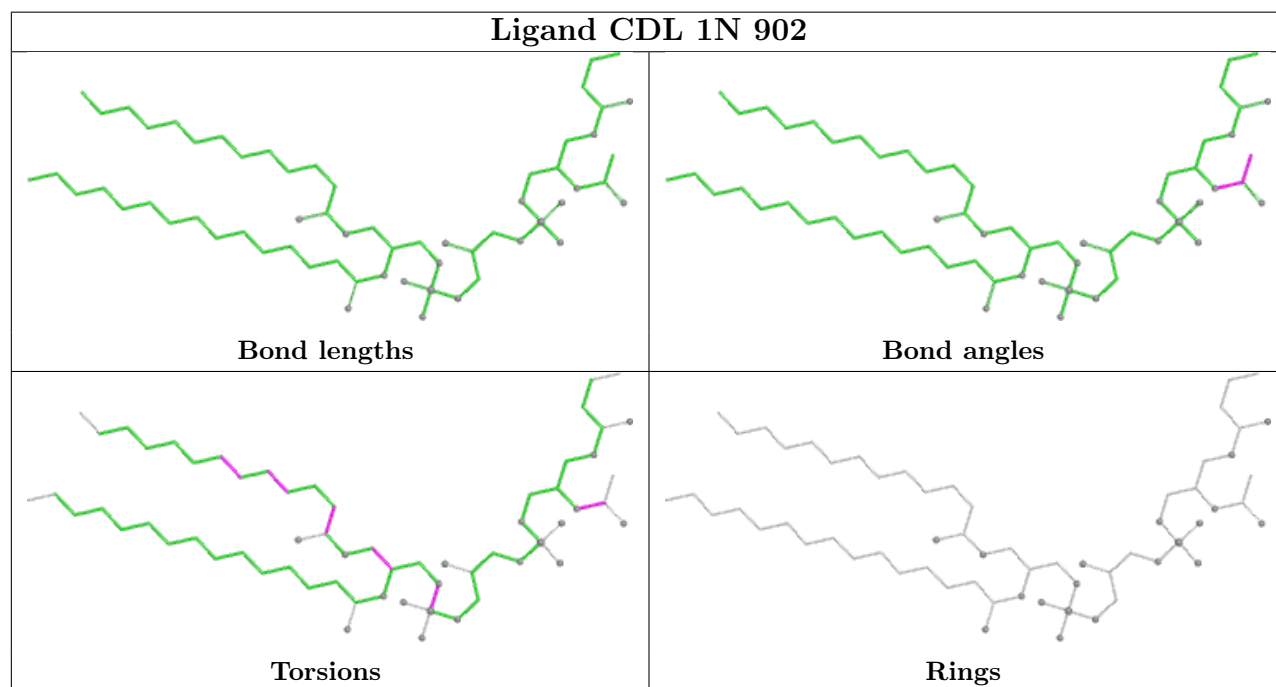
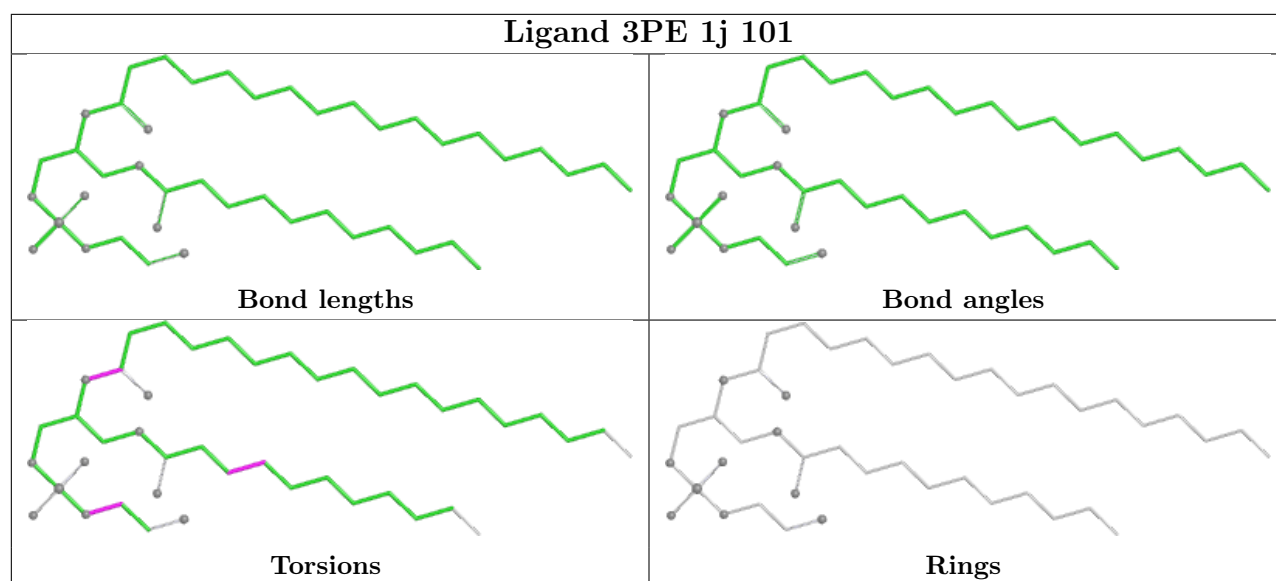


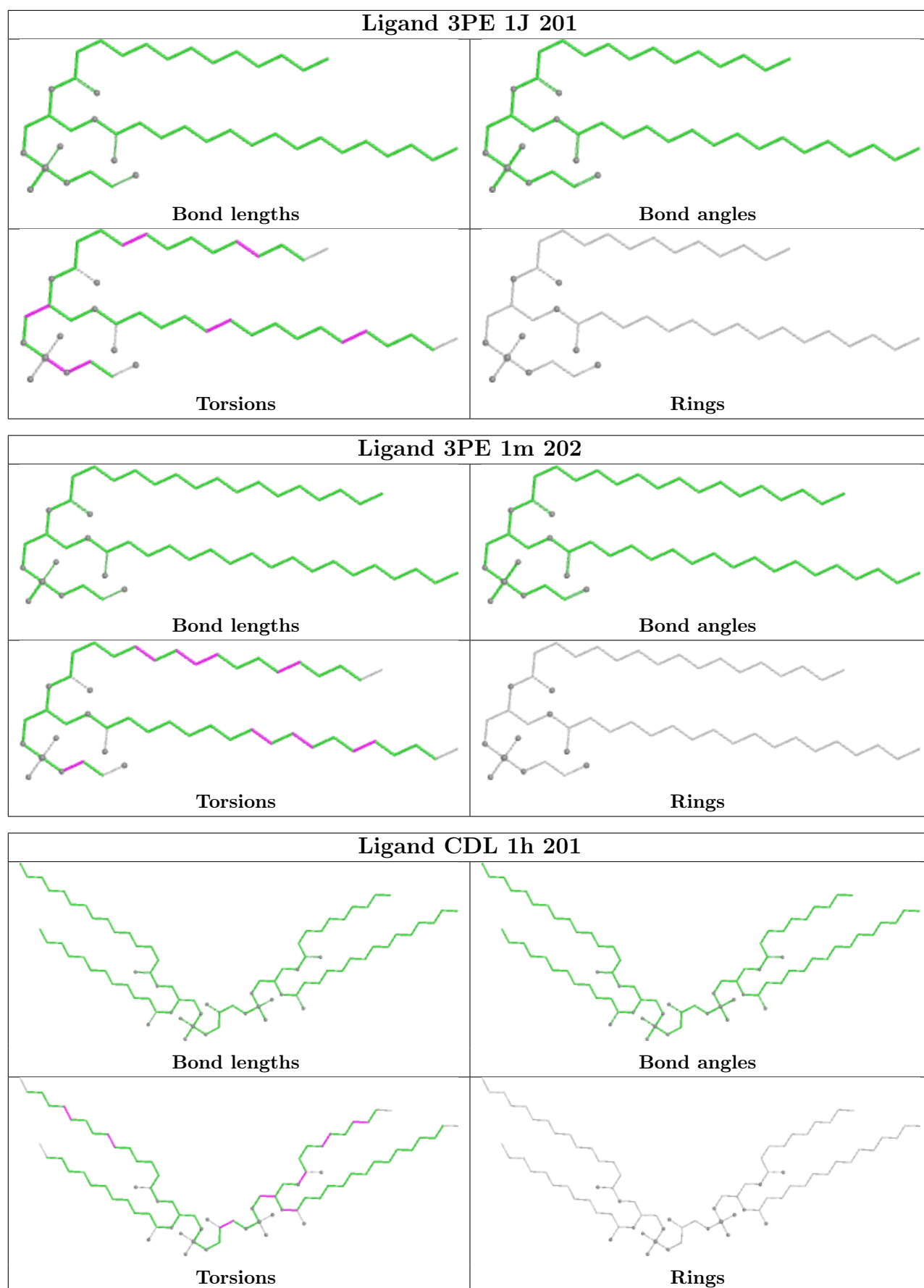


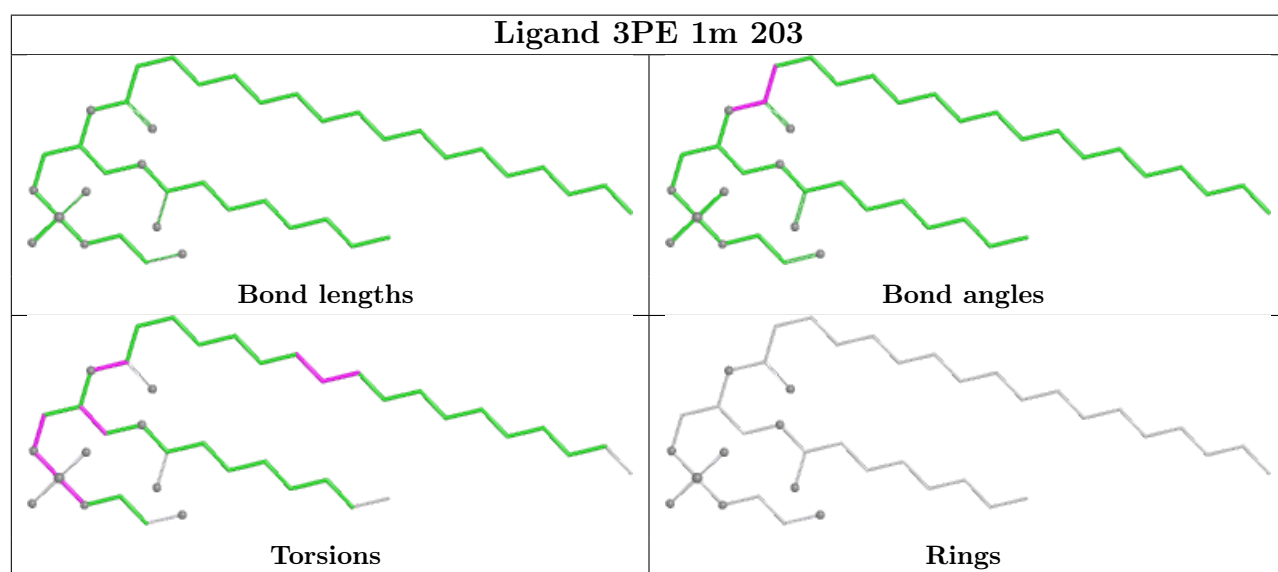
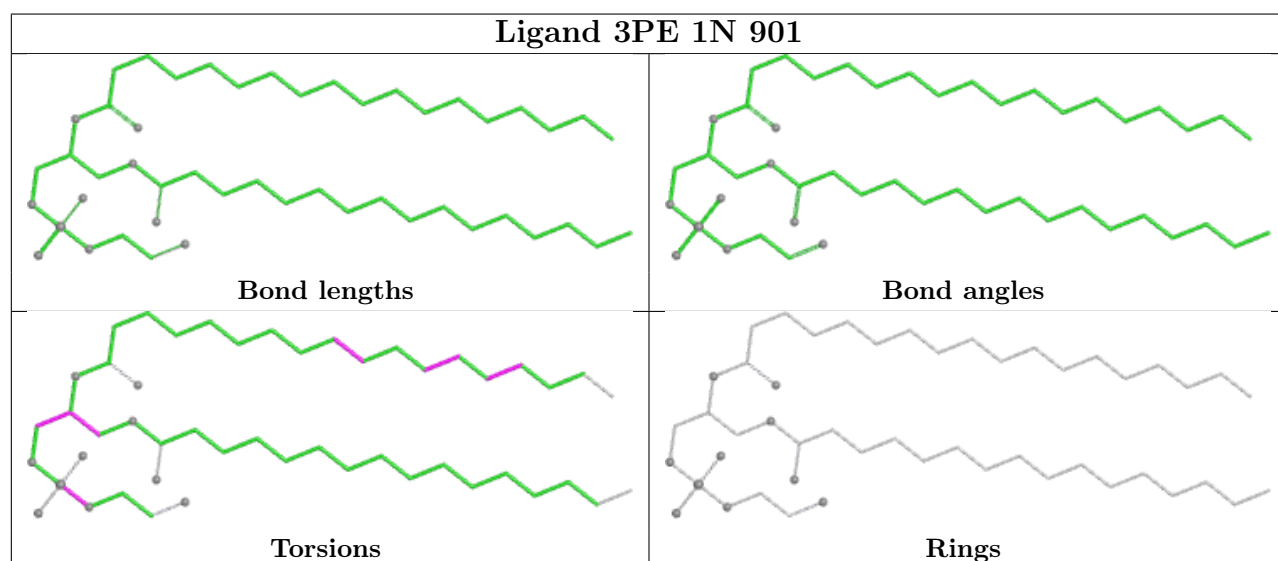
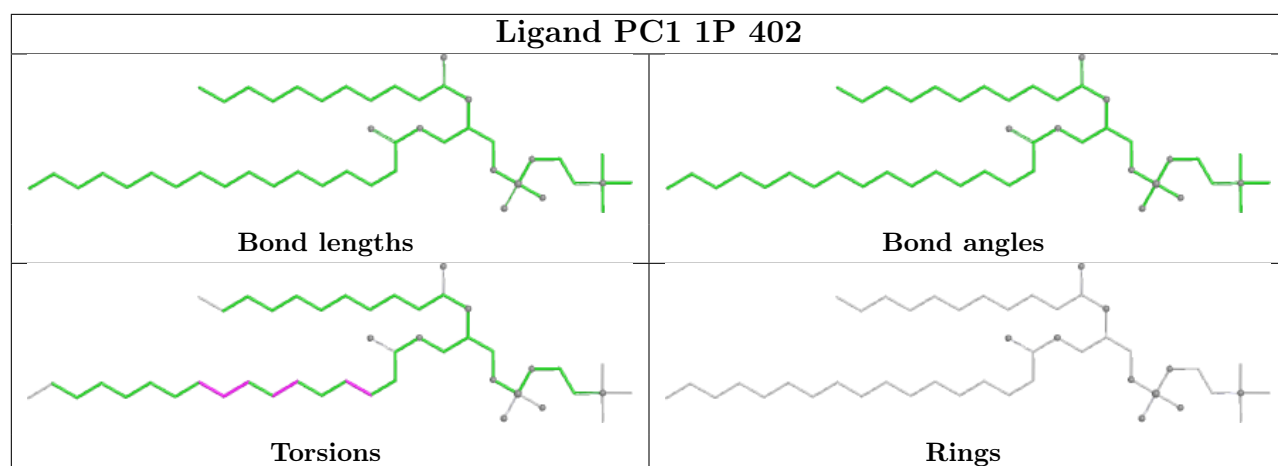


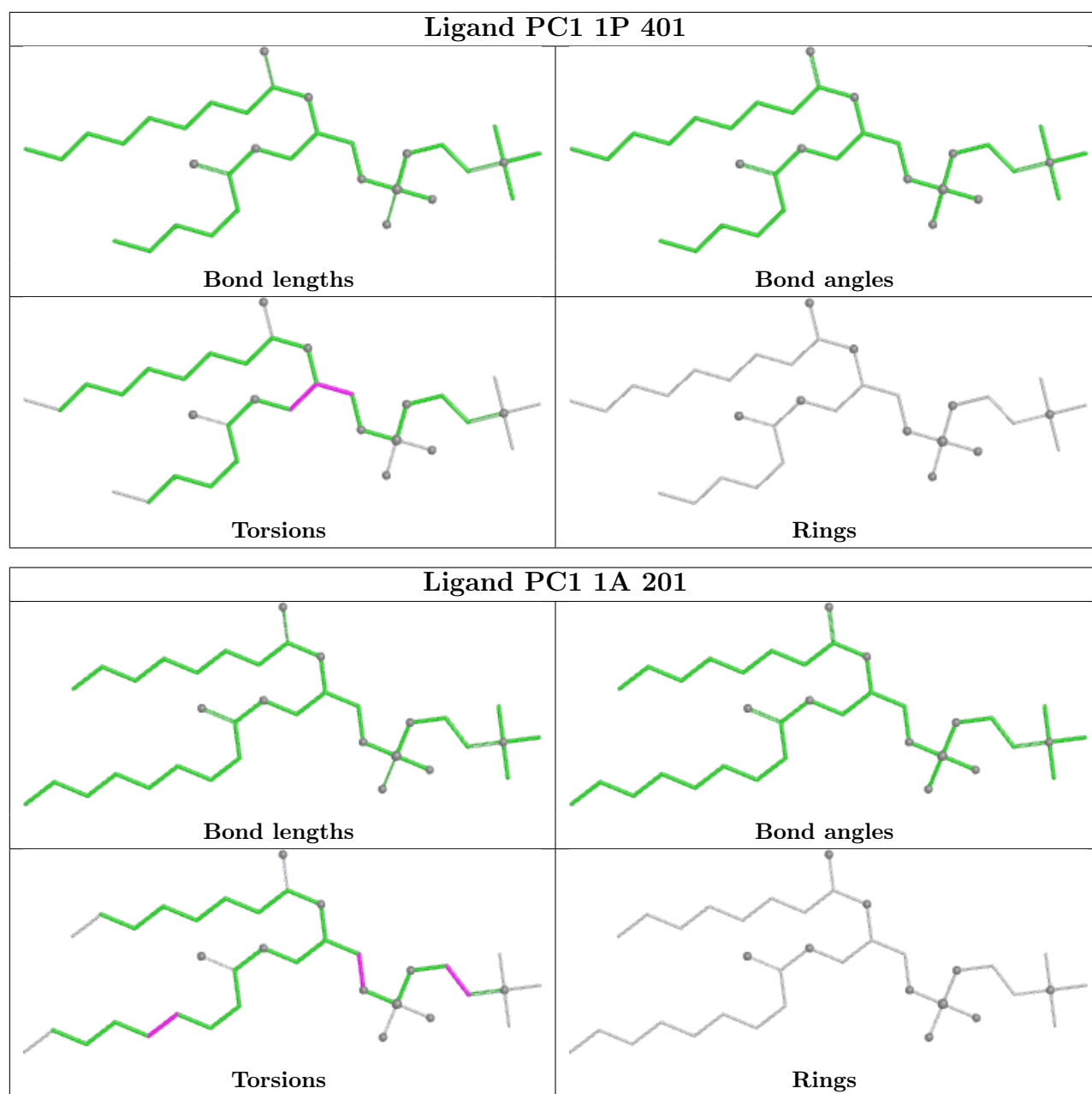












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

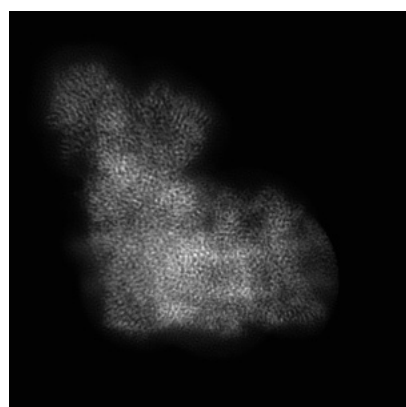
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42143. These allow visual inspection of the internal detail of the map and identification of artifacts.

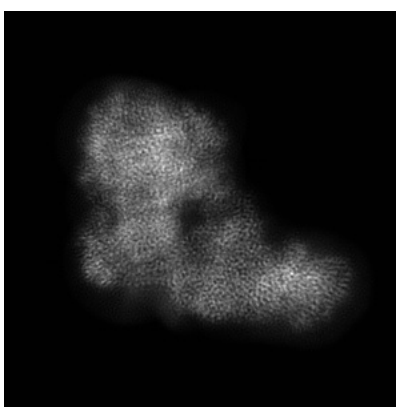
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

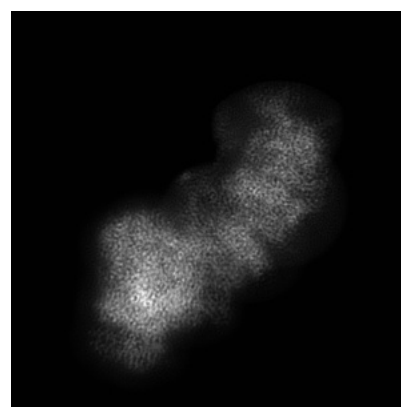
6.1.1 Primary map



X



Y

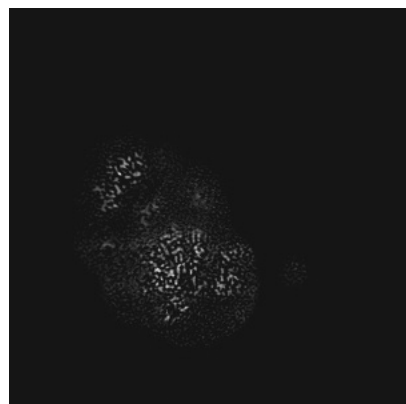


Z

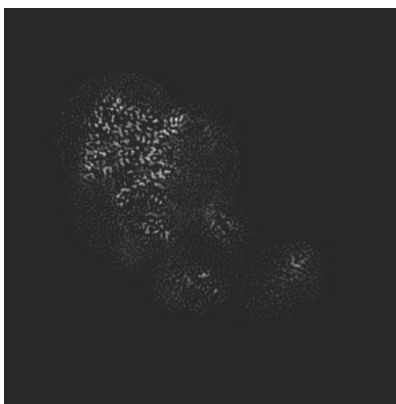
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

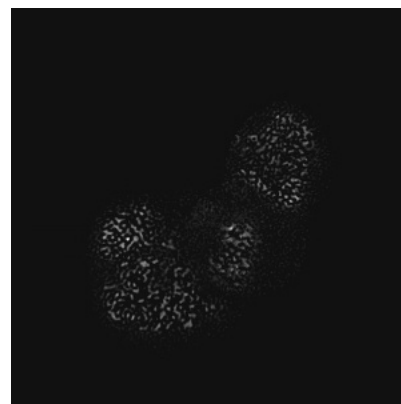
6.2.1 Primary map



X Index: 360



Y Index: 360

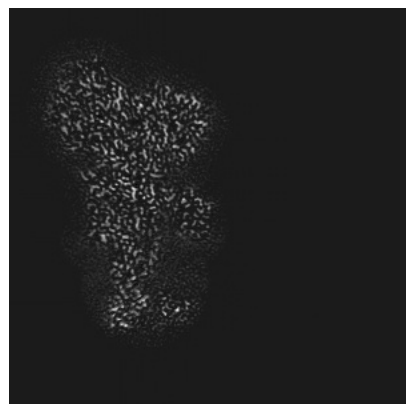


Z Index: 360

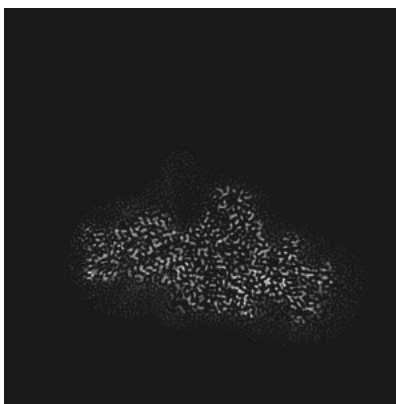
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

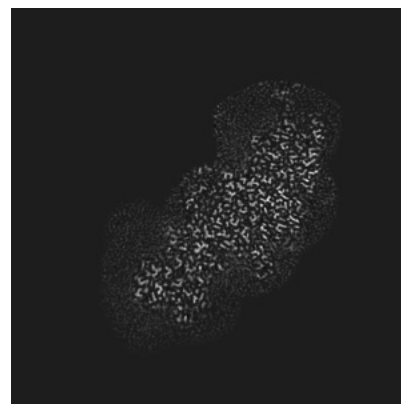
6.3.1 Primary map



X Index: 239



Y Index: 196

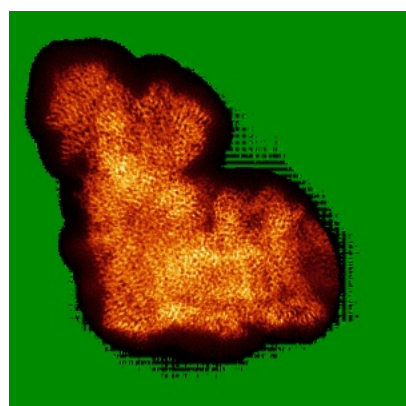


Z Index: 275

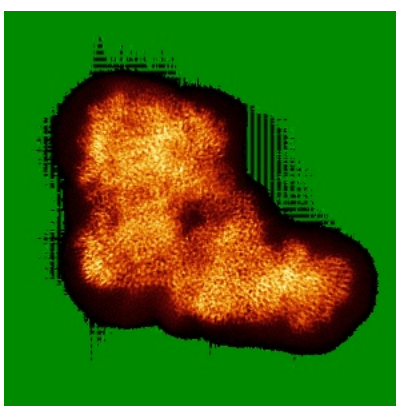
The images above show the largest variance slices of the map in three orthogonal directions.

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

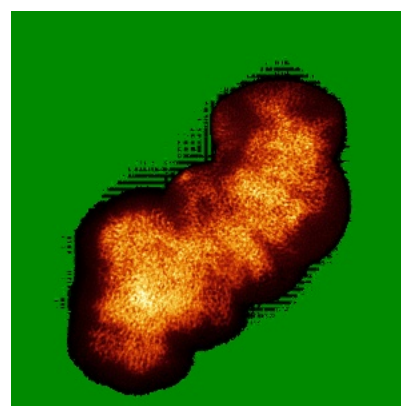
6.4.1 Primary map



X



Y

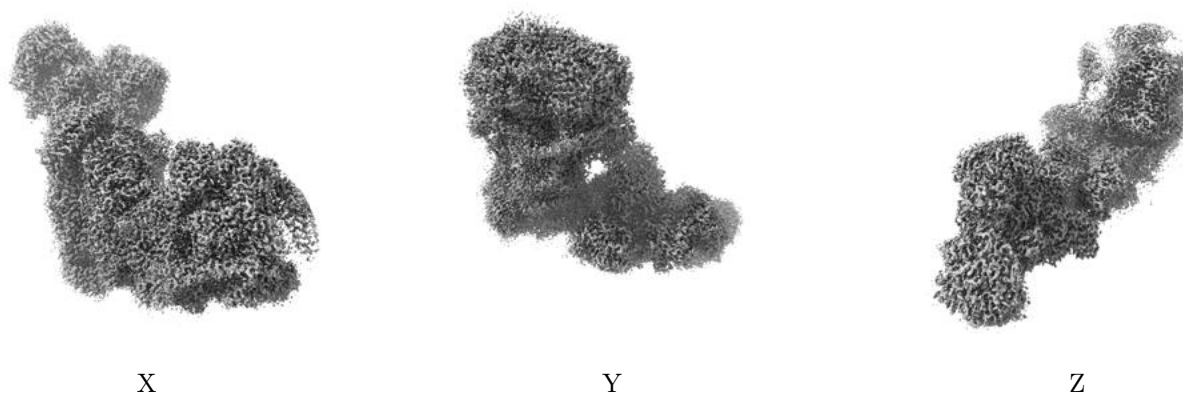


Z

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

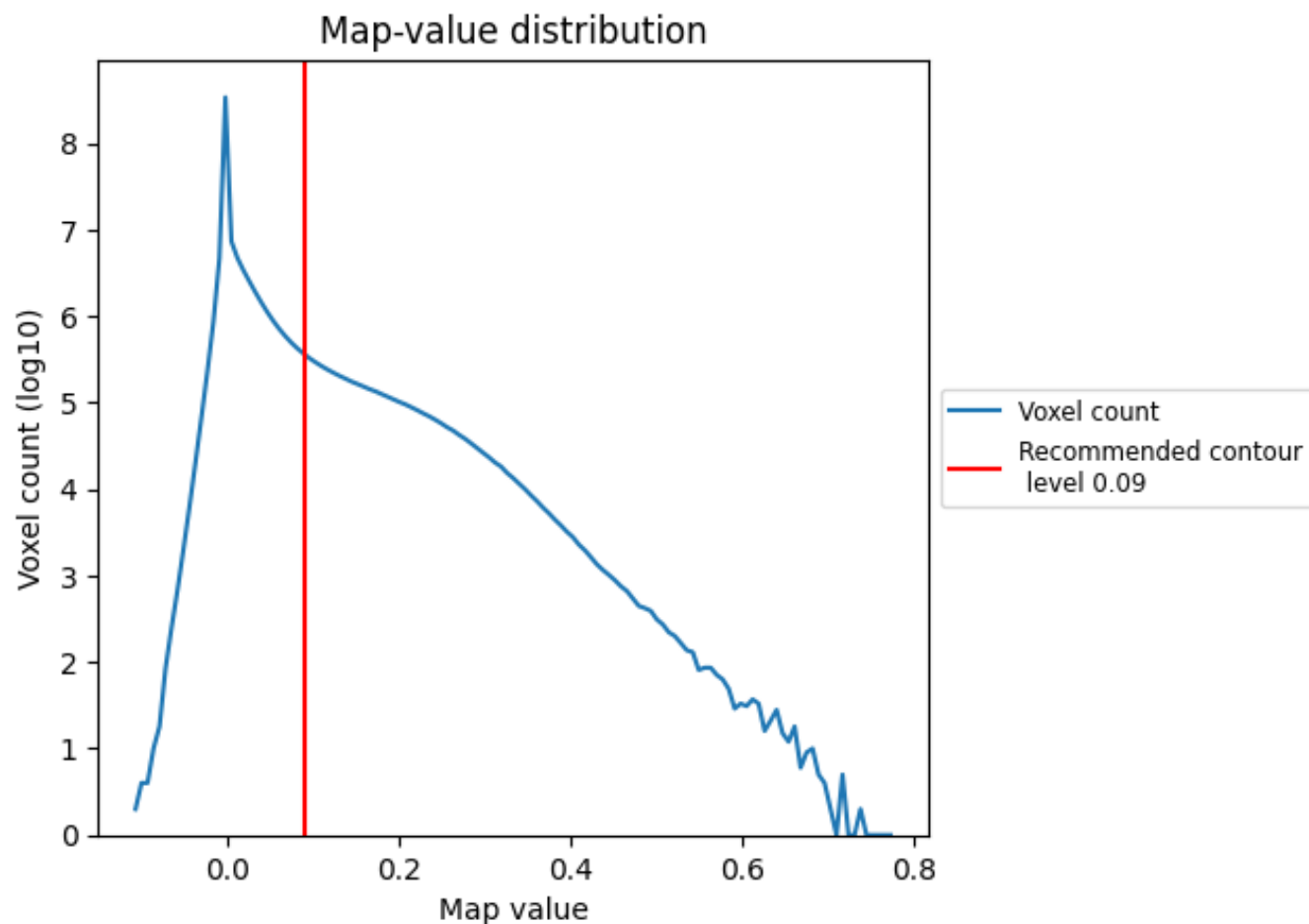
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

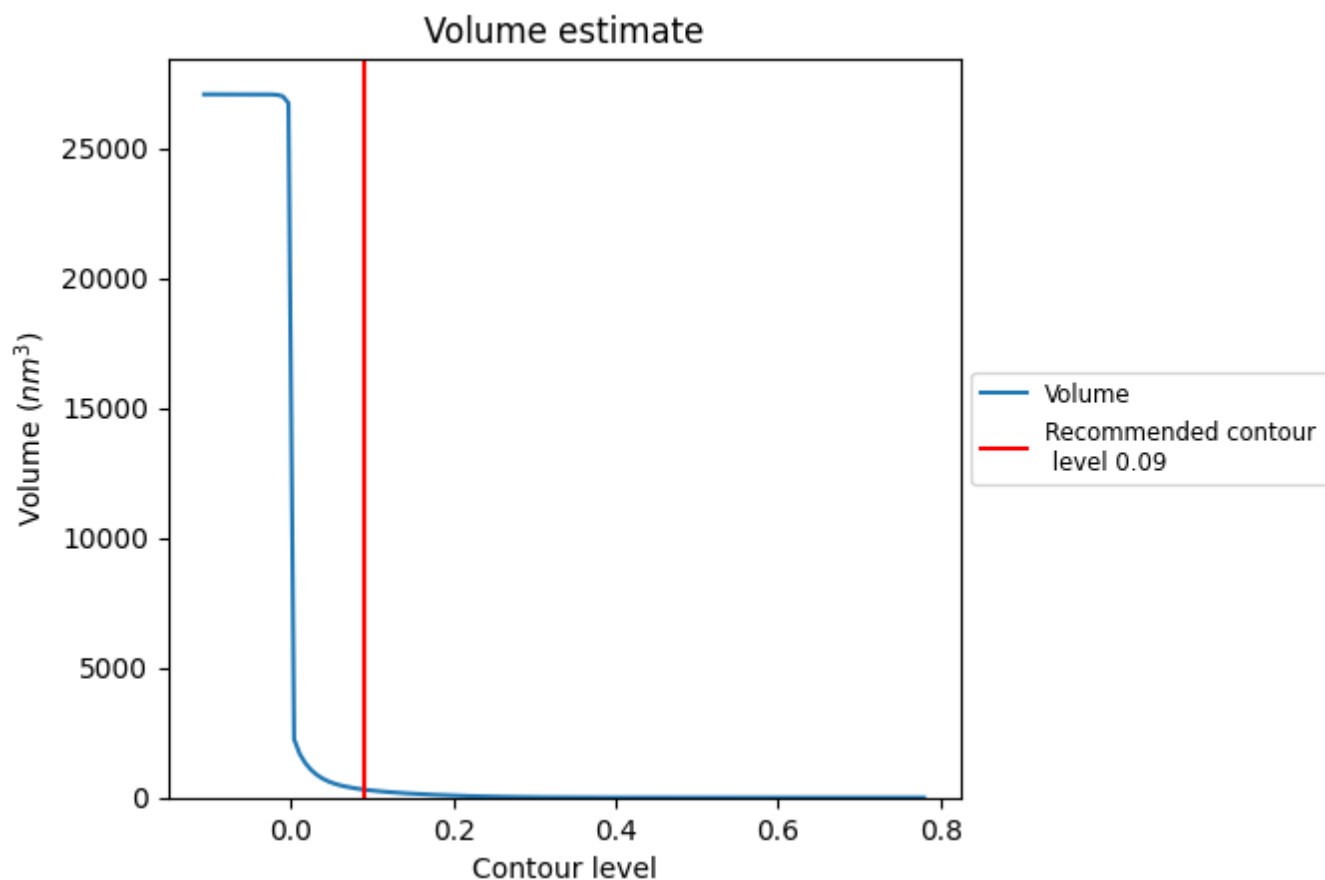
This section contains the results of statistical analysis of the map.

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.

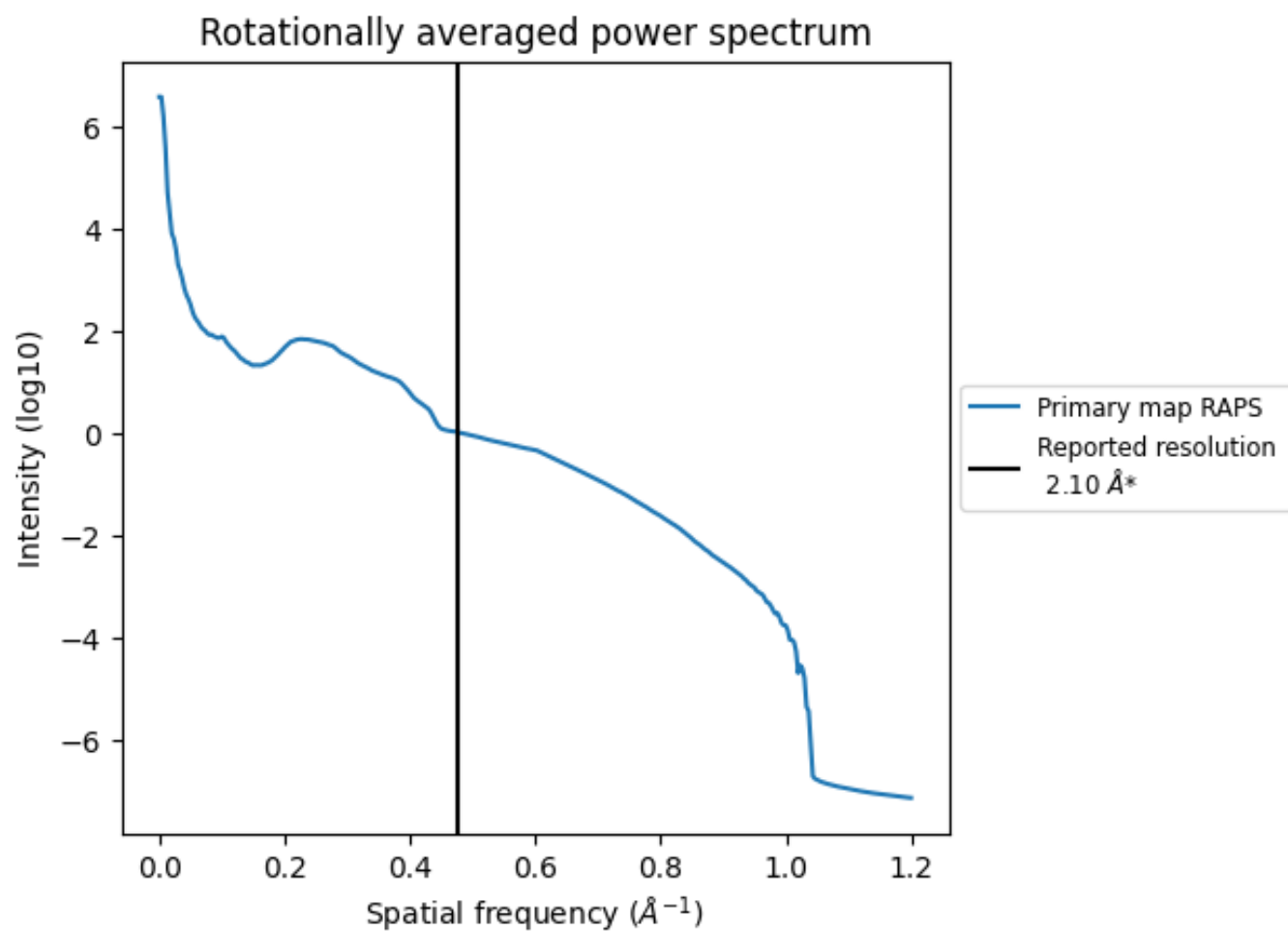
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 306 nm³; this corresponds to an approximate mass of 277 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.476 Å⁻¹

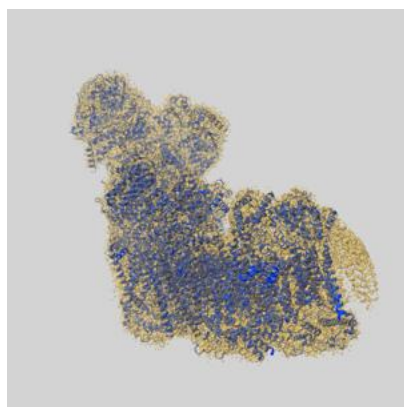
8 Fourier-Shell correlation

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

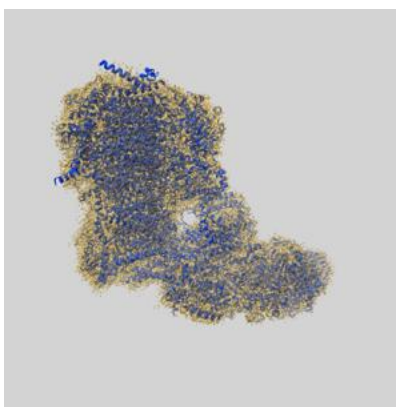
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42143 and PDB model 8UD1. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

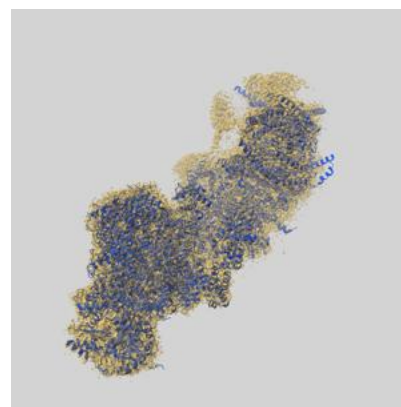
9.1 Map-model overlay [i](#)



X



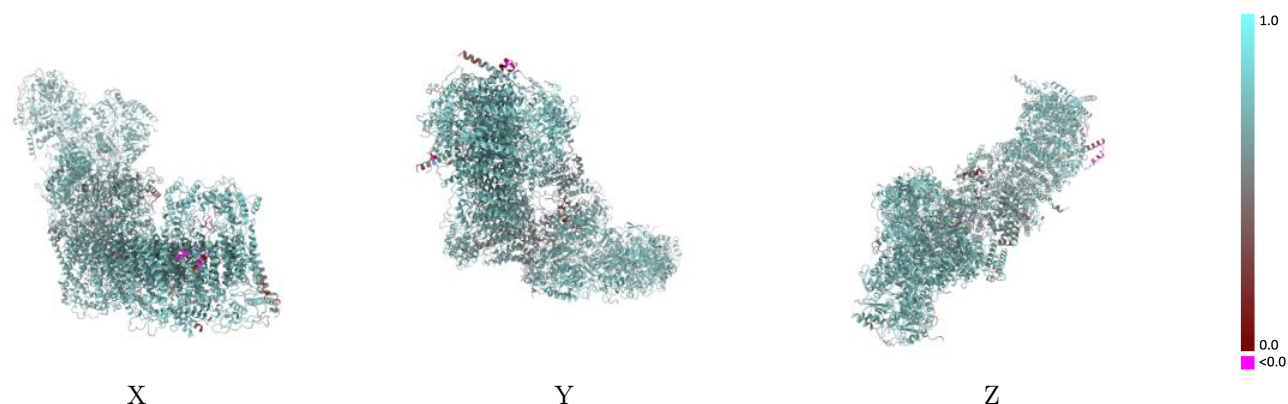
Y



Z

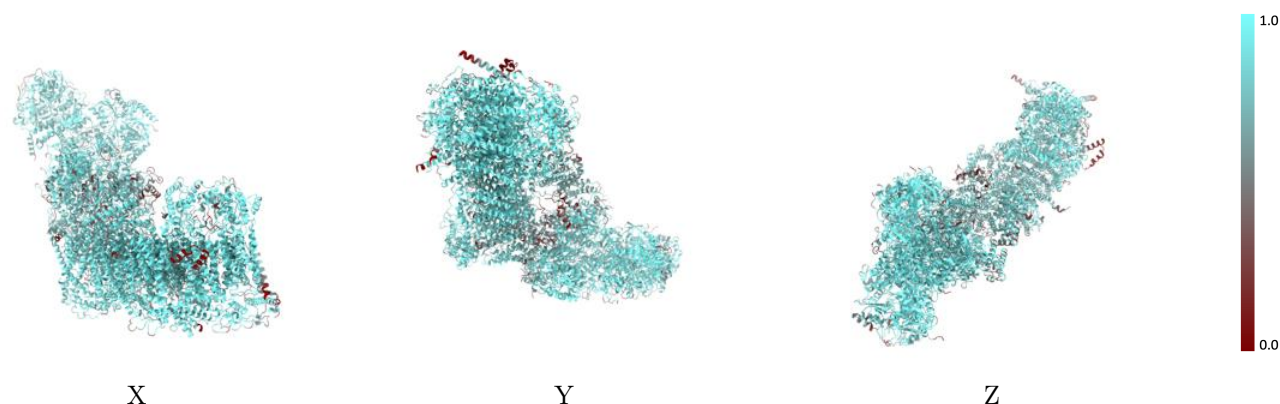
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



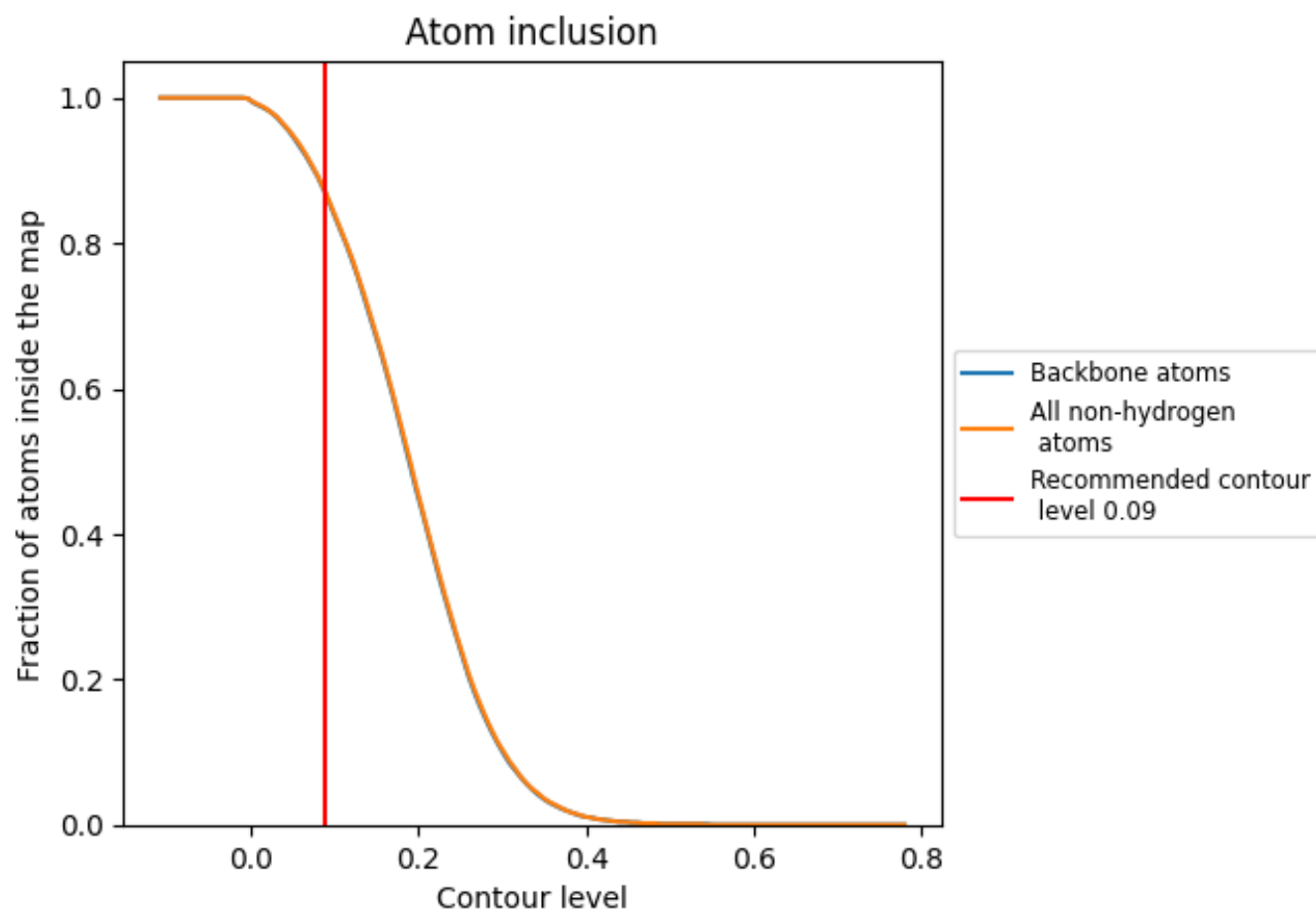
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 87% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8690	 0.6680
1A	 0.6800	 0.5560
1B	 0.9100	 0.6920
1C	 0.9390	 0.7190
1D	 0.9040	 0.6960
1E	 0.8070	 0.6470
1F	 0.8770	 0.6610
1G	 0.9120	 0.6940
1H	 0.8900	 0.6440
1I	 0.9440	 0.7130
1J	 0.7800	 0.5940
1K	 0.9810	 0.6960
1L	 0.9420	 0.7040
1M	 0.9680	 0.7160
1N	 0.9560	 0.7100
1O	 0.7960	 0.6070
1P	 0.8300	 0.6610
1Q	 0.8620	 0.6700
1R	 0.8550	 0.6740
1S	 0.8900	 0.6630
1T	 0.4110	 0.4370
1U	 0.8180	 0.6790
1V	 0.7500	 0.6390
1W	 0.8620	 0.6740
1X	 0.8840	 0.6560
1Y	 0.7820	 0.6530
1Z	 0.8900	 0.6660
1a	 0.9490	 0.6700
1b	 0.8150	 0.6250
1c	 0.7540	 0.6260
1d	 0.8920	 0.6680
1e	 0.9350	 0.6860
1f	 0.7600	 0.6210
1g	 0.8670	 0.6700
1h	 0.8950	 0.6980



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Chain	Atom inclusion	Q-score
1i	 0.6200	 0.5180
1j	 0.7660	 0.6100
1k	 0.7470	 0.6050
1l	 0.8930	 0.6980
1m	 0.8570	 0.6690
1n	 0.8850	 0.6960
1o	 0.8210	 0.6400
1p	 0.8770	 0.6690
1q	 0.8420	 0.6840
1r	 0.8530	 0.6840
1s	 0.7440	 0.6140