



Full wwPDB EM Validation Report ⓘ

Aug 4, 2026 – 10:02 AM EDT

PDB ID : 8UGE / pdb_00008uge
EMDB ID : EMD-42222
Title : In-situ complex III, state II
Authors : Zheng, W.; Zhang, K.; Zhu, J.
Deposited on : 2023-10-05
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

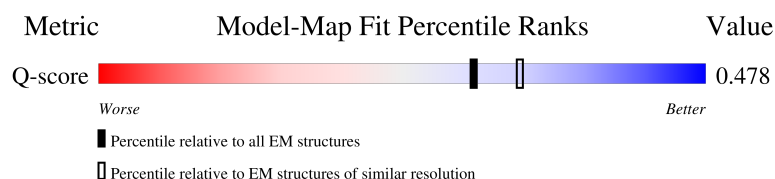
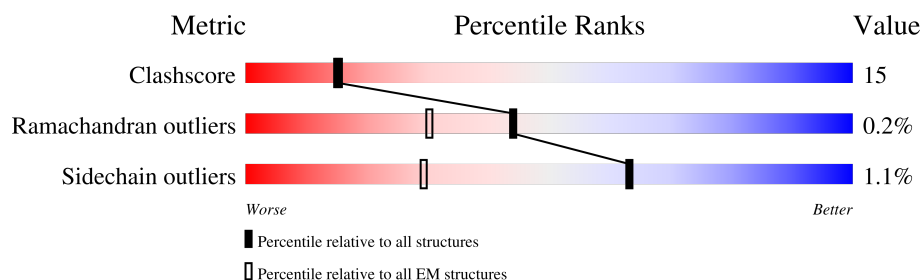
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	3A	480	
1	3N	480	
2	3B	453	
2	3O	453	

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Mol	Chain	Length	Quality of chain
3	3C	379	
3	3P	379	
4	3D	325	
4	3Q	325	
5	3E	274	
5	3I	274	
5	3R	274	
5	3V	274	
6	3F	111	
6	3S	111	
7	3G	82	
7	3T	82	
8	3H	91	
8	3U	91	
9	3J	64	
9	3W	64	
10	3X	56	
10	3Y	56	

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
15	HEC	3D	501	X	-	-	-
15	HEC	3Q	501	X	-	-	-

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 33534 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 Cytochrome b-c1 complex subunit 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	440	Total	C	N	O	S	0	0
			3411	2131	599	662	19		
1	3N	445	Total	C	N	O	S	1	0
			3424	2162	606	637	19		

- Molecule 2 is a protein called Cytochrome b-c1 complex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3B	418	Total	C	N	O	S	0	0
			3138	1965	555	610	8		
2	3O	417	Total	C	N	O	S	0	0
			3124	1960	554	602	8		

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3C	379	Total	C	N	O	S	0	0
			3025	2031	471	502	21		
3	3P	379	Total	C	N	O	S	0	0
			3024	2031	471	501	21		

- Molecule 4 is a protein called Cytochrome c1, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3D	237	Total	C	N	O	S	0	0
			1888	1205	325	342	16		
4	3Q	239	Total	C	N	O	S	0	0
			1904	1215	327	346	16		

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3E	196	Total	C	N	O	S	0	0
			1518	955	265	291	7		
5	3I	47	Total	C	N	O	S	0	0
			337	210	62	64	1		
5	3R	196	Total	C	N	O	S	0	0
			1518	955	265	291	7		
5	3V	31	Total	C	N	O	S	0	0
			223	137	45	40	1		

- Molecule 6 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	3F	98	Total	C	N	O	S	0	0
			868	557	152	157	2		
6	3S	98	Total	C	N	O	S	0	0
			868	557	152	157	2		

- Molecule 7 is a protein called Cytochrome b-c1 complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	3G	74	Total	C	N	O	S	0	0
			628	411	116	99	2		
7	3T	74	Total	C	N	O	S	0	0
			628	411	116	99	2		

- Molecule 8 is a protein called Cytochrome b-c1 complex subunit 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	3H	65	Total	C	N	O	S	0	0
			533	325	97	106	5		
8	3U	65	Total	C	N	O	S	0	0
			533	325	97	106	5		

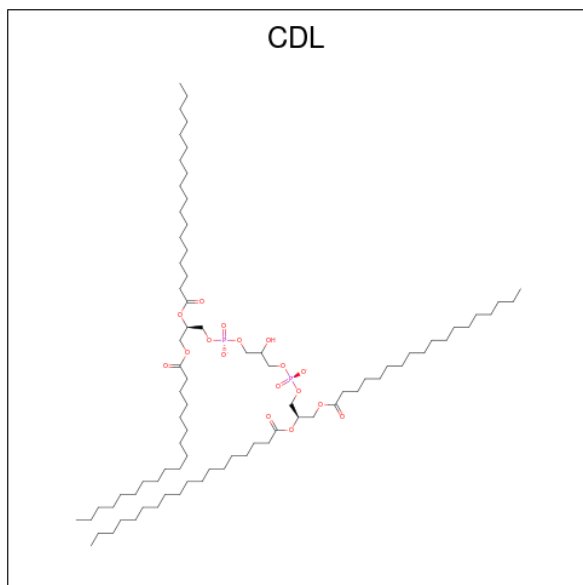
- Molecule 9 is a protein called Ubiquinol-cytochrome c reductase complex 7.2 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	3J	56	Total	C	N	O	0	0
			464	305	82	77		
9	3W	56	Total	C	N	O	0	0
			464	305	82	77		

- Molecule 10 is a protein called Cytochrome b-c1 complex subunit 10.

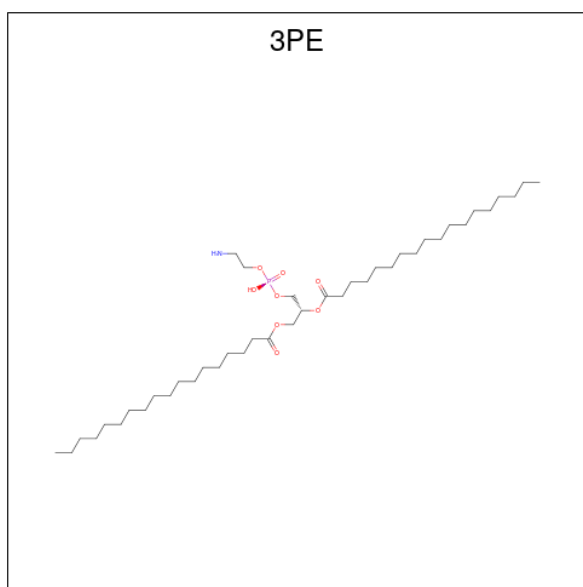
Mol	Chain	Residues	Atoms					AltConf	Trace
10	3X	52	Total	C	N	O	S	0	0
			429	286	75	66	2		
10	3Y	51	Total	C	N	O	S	0	0
			421	281	74	65	1		

- Molecule 11 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



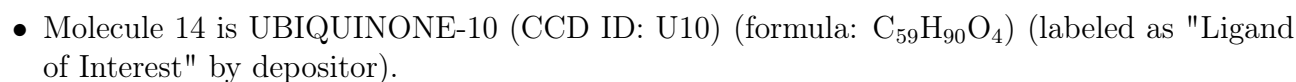
Mol	Chain	Residues	Atoms				AltConf
11	3A	1	Total	C	O	P	0
			58	39	17	2	
11	3C	1	Total	C	O	P	0
			52	33	17	2	
11	3G	1	Total	C	O	P	0
			56	37	17	2	
11	3P	1	Total	C	O	P	0
			56	37	17	2	
11	3P	1	Total	C	O	P	0
			43	24	17	2	
11	3Q	1	Total	C	O	P	0
			57	38	17	2	

- Molecule 12 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



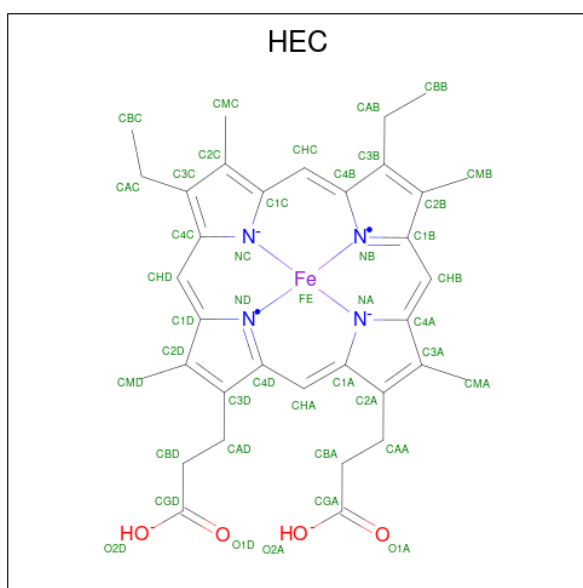
Mol	Chain	Residues	Atoms					AltConf
12	3A	1	Total	C	N	O	P	0
			27	17	1	8	1	
12	3A	1	Total	C	N	O	P	0
			32	22	1	8	1	
12	3C	1	Total	C	N	O	P	0
			35	25	1	8	1	
12	3C	1	Total	C	N	O	P	0
			34	24	1	8	1	
12	3D	1	Total	C	N	O	P	0
			33	23	1	8	1	
12	3G	1	Total	C	N	O	P	0
			29	19	1	8	1	
12	3N	1	Total	C	N	O	P	0
			33	23	1	8	1	
12	3N	1	Total	C	N	O	P	0
			25	15	1	8	1	
12	3P	1	Total	C	N	O	P	0
			33	23	1	8	1	
12	3Q	1	Total	C	N	O	P	0
			47	37	1	8	1	
12	3Y	1	Total	C	N	O	P	0
			30	20	1	8	1	

- Molecule 13 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



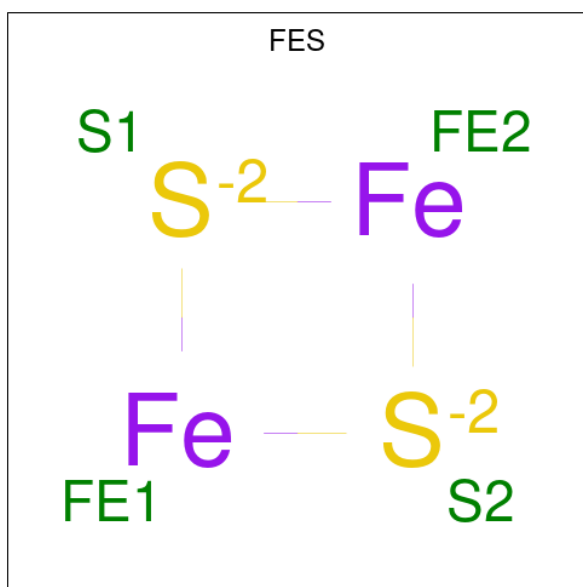
Mol	Chain	Residues	Atoms			AltConf
14	3C	1	Total 24	C 20	O 4	0
14	3C	1	Total 23	C 19	O 4	0
14	3P	1	Total 23	C 19	O 4	0
14	3P	1	Total 28	C 24	O 4	0

- Molecule 15 is HEME C (CCD ID: HEC) (formula: $\text{C}_{34}\text{H}_{36}\text{FeN}_4\text{O}_4$).



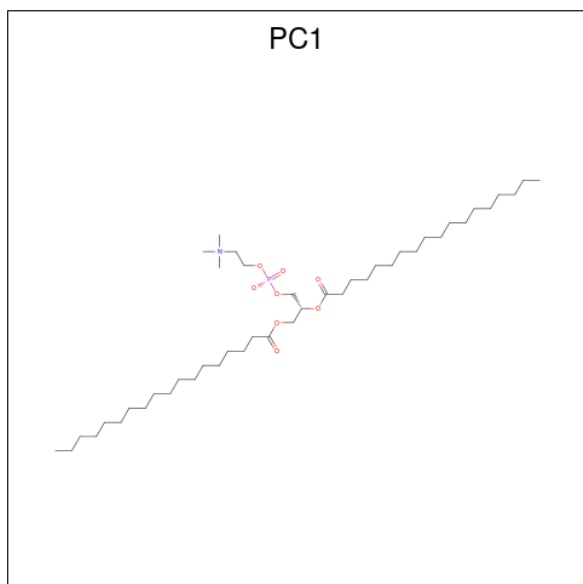
Mol	Chain	Residues	Atoms					AltConf
15	3D	1	Total 42	C 34	Fe 1	N 4	O 3	0
15	3Q	1	Total 43	C 34	Fe 1	N 4	O 4	0

- Molecule 16 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			AltConf
16	3E	1	Total	Fe	S	0
			4	2	2	
16	3R	1	Total	Fe	S	0
			4	2	2	

- Molecule 17 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
17	3E	1	Total	C	N	O	P	0
			47	37	1	8	1	

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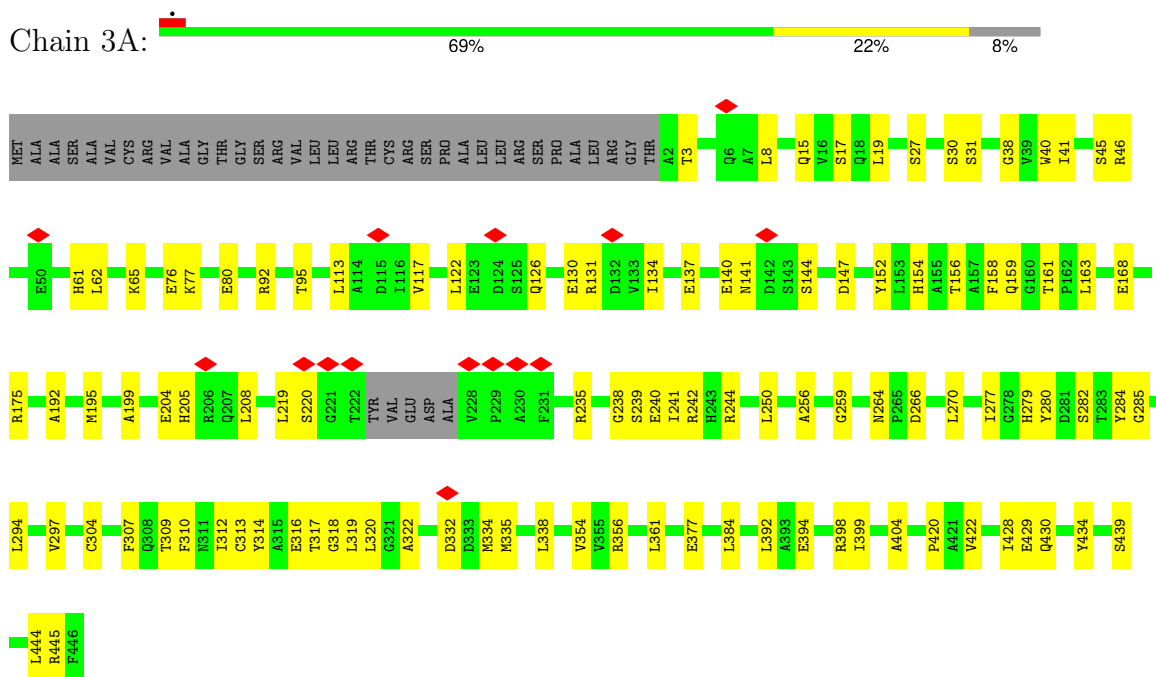
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Mol	Chain	Residues	Atoms					AltConf
17	3R	1	Total	C	N	O	P	0
			45	35	1	8	1	
17	3X	1	Total	C	N	O	P	0
			29	19	1	8	1	

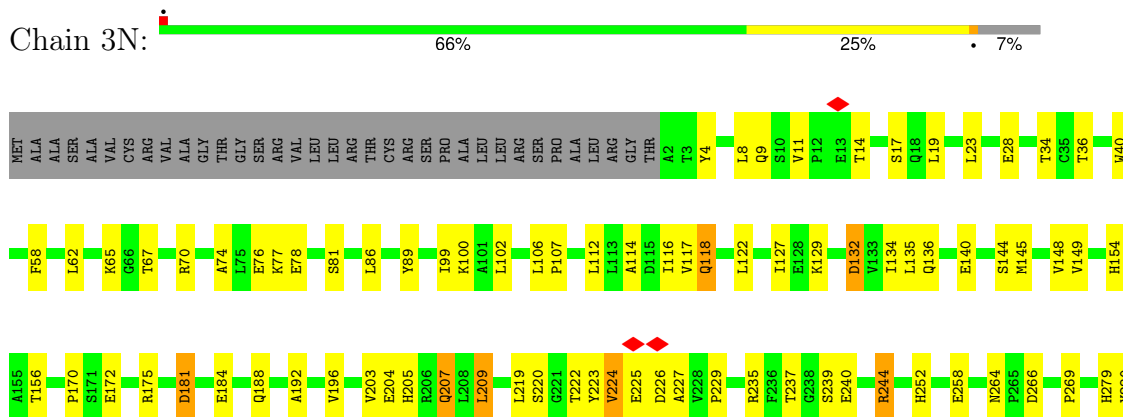
3 Residue-property plots

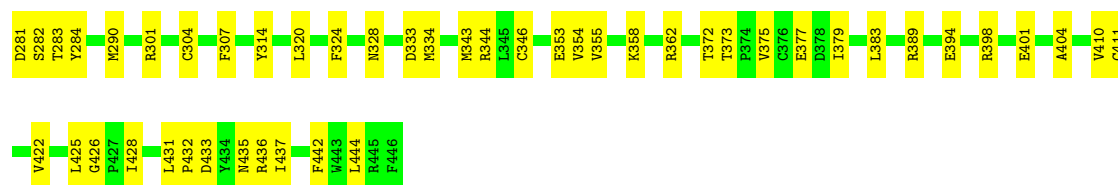
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Cytochrome b-c1 complex subunit 1, mitochondrial

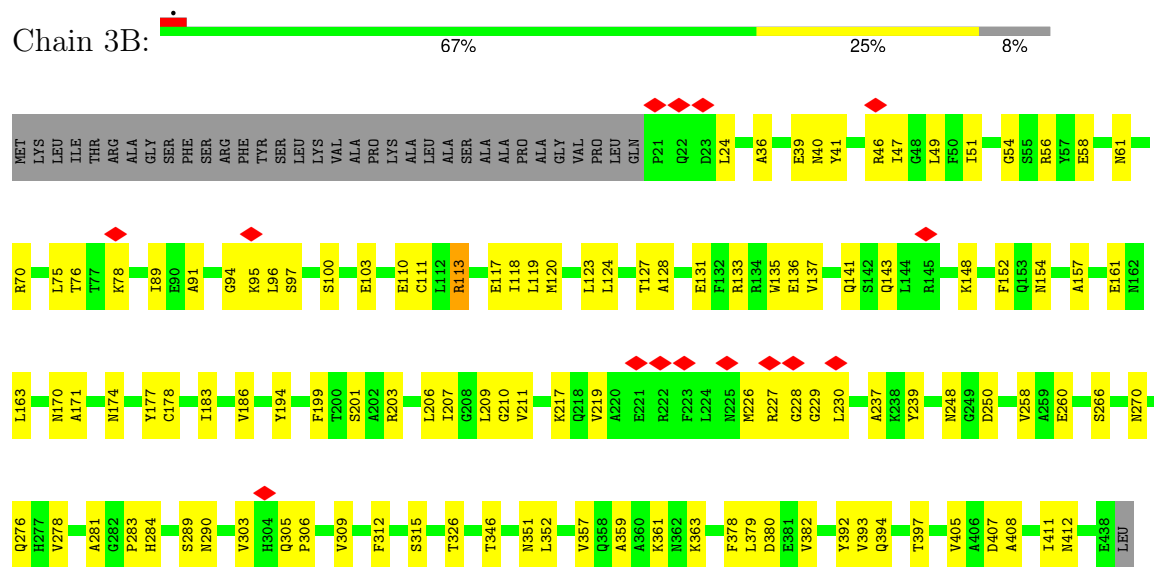


- Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial

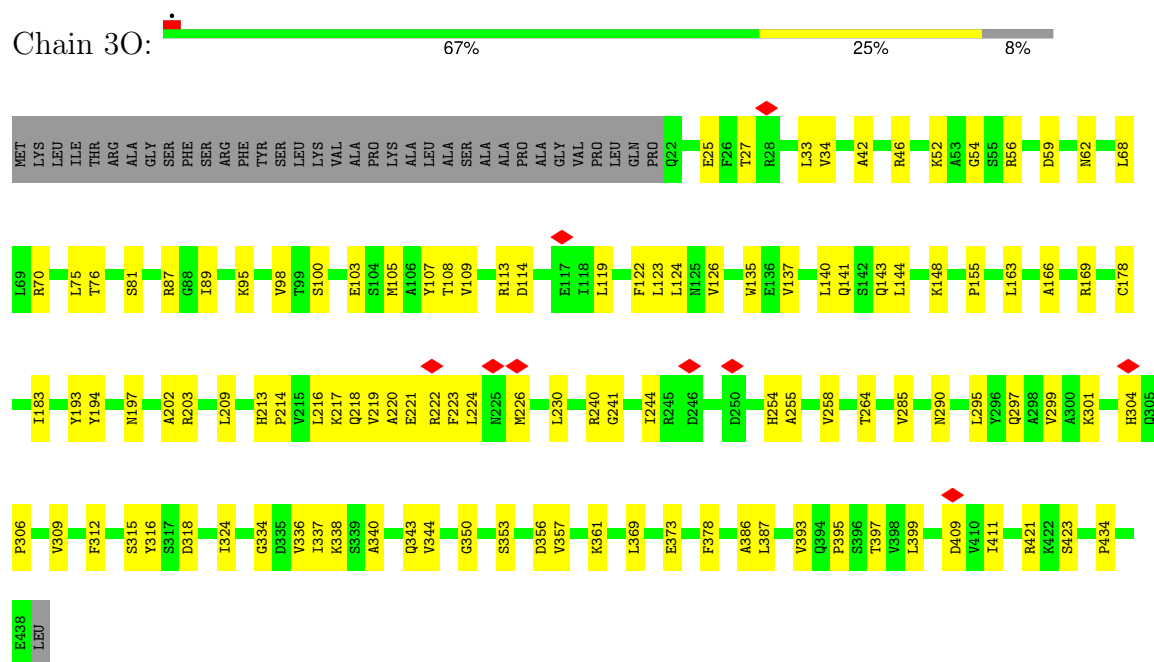




- Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial



- Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial

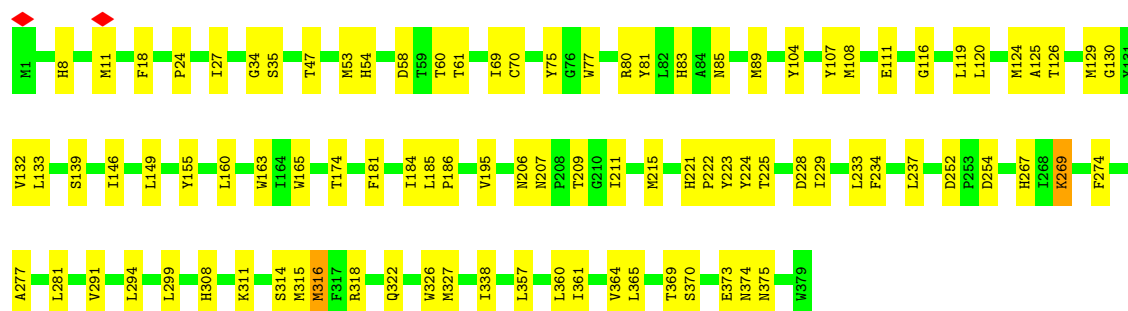
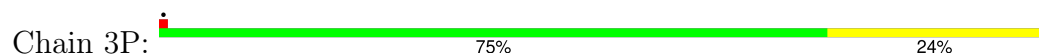


- Molecule 3: Cytochrome b

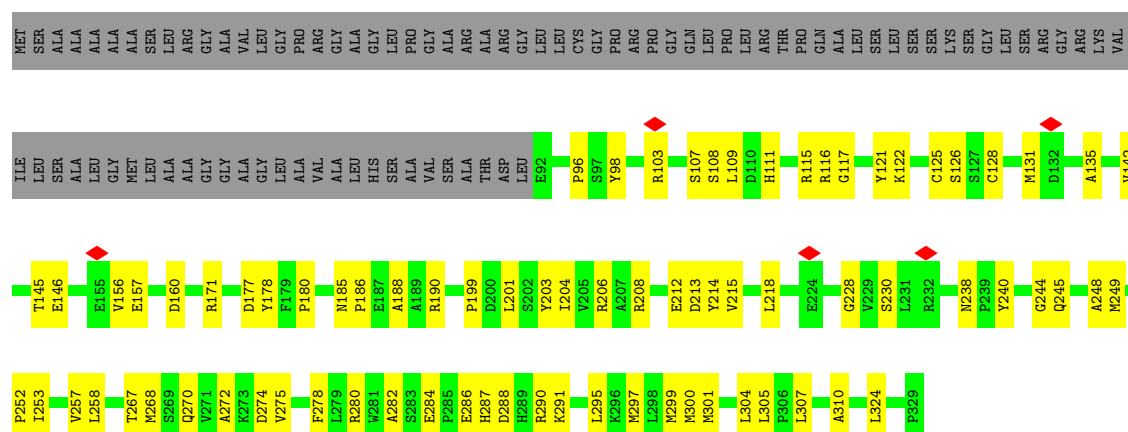




• Molecule 3: Cytochrome b



• Molecule 4: Cytochrome c1, heme protein, mitochondrial

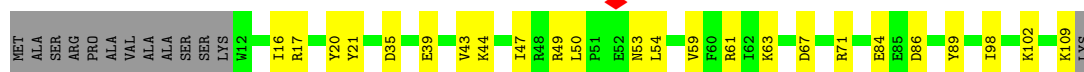


• Molecule 4: Cytochrome c1, heme protein, mitochondrial



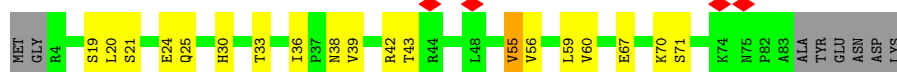


Chain 3S: 



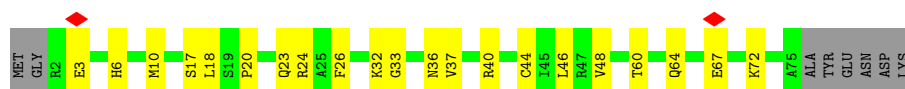
- Molecule 7: Cytochrome b-c1 complex subunit 8

Chain 3G: 



- Molecule 7: Cytochrome b-c1 complex subunit 8

Chain 3T: 



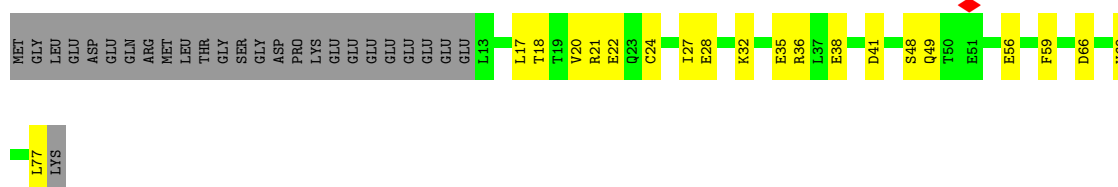
- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial

Chain 3H: 



- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial

Chain 3U: 



- Molecule 9: Ubiquinol-cytochrome c reductase complex 7.2 kDa protein

Chain 3J: 

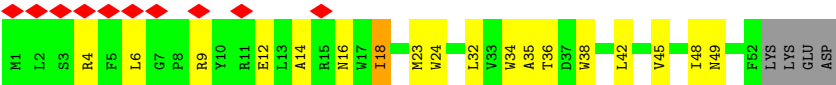


- Molecule 9: Ubiquinol-cytochrome c reductase complex 7.2 kDa protein

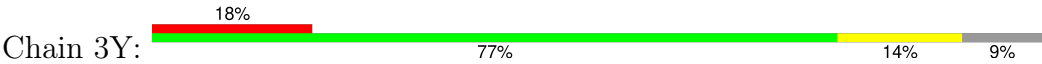
Chain 3W: 



• Molecule 10: Cytochrome b-c1 complex subunit 10



• Molecule 10: Cytochrome b-c1 complex subunit 10



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50000	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	0.599	Depositor
Minimum map value	-0.248	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	425.6, 425.6, 425.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEC, U10, PC1, FES, CDL, HEM, 3PE

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	3A	0.24	0/3481	0.36	0/4722
1	3N	0.25	0/3496	0.35	0/4723
2	3B	0.23	0/3190	0.34	0/4317
2	3O	0.23	0/3175	0.33	0/4292
3	3C	0.29	0/3123	0.38	0/4269
3	3P	0.28	0/3122	0.37	0/4269
4	3D	0.27	0/1946	0.41	0/2641
4	3Q	0.26	0/1962	0.39	0/2663
5	3E	0.22	0/1551	0.46	1/2098 (0.0%)
5	3I	0.41	0/342	0.60	0/465
5	3R	0.24	0/1551	0.56	0/2098
5	3V	0.19	0/225	0.35	0/303
6	3F	0.24	0/888	0.37	0/1193
6	3S	0.24	0/888	0.36	0/1193
7	3G	0.23	0/649	0.39	0/878
7	3T	0.25	0/649	0.45	0/878
8	3H	0.22	0/538	0.49	0/721
8	3U	0.23	0/539	0.45	0/724
9	3J	0.26	0/476	0.32	0/641
9	3W	0.24	0/476	0.37	0/641
10	3X	0.20	0/445	0.40	0/608
10	3Y	0.23	0/437	0.46	0/598
All	All	0.25	0/33149	0.39	1/44935 (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
5	3R	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	3E	224	PRO	CA-N-CD	-6.21	103.30	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	3R	148	ALA	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	3A	3411	0	3309	84	0
1	3N	3424	0	3350	92	0
2	3B	3138	0	3116	90	0
2	3O	3124	0	3108	76	0
3	3C	3025	0	3090	97	0
3	3P	3024	0	3090	77	0
4	3D	1888	0	1834	83	0
4	3Q	1904	0	1849	55	0
5	3E	1518	0	1498	82	0
5	3I	337	0	347	26	0
5	3R	1518	0	1498	112	0
5	3V	223	0	233	5	0
6	3F	868	0	857	33	0
6	3S	868	0	857	20	0
7	3G	628	0	634	19	0
7	3T	628	0	634	23	0
8	3H	533	0	512	16	0
8	3U	533	0	513	17	0
9	3J	464	0	467	28	0
9	3W	464	0	467	14	0
10	3X	429	0	430	20	0
10	3Y	421	0	418	7	0
11	3A	58	0	60	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	3C	52	0	48	5	0
11	3G	56	0	56	3	0
11	3P	99	0	86	12	0
11	3Q	57	0	58	13	0
12	3A	59	0	66	12	0
12	3C	69	0	86	5	0
12	3D	33	0	40	4	0
12	3G	29	0	32	1	0
12	3N	58	0	62	6	0
12	3P	33	0	40	3	0
12	3Q	47	0	71	8	0
12	3Y	30	0	34	0	0
13	3C	86	0	60	8	0
13	3P	86	0	60	5	0
14	3C	47	0	48	11	0
14	3P	51	0	54	5	0
15	3D	42	0	32	15	0
15	3Q	43	0	32	3	0
16	3E	4	0	0	1	0
16	3R	4	0	0	1	0
17	3E	47	0	68	7	0
17	3R	45	0	64	5	0
17	3X	29	0	32	5	0
All	All	33534	0	33300	991	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 15.

All (991) 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)
9:3J:53:TRP:CE2	9:3J:57:LYS:HG2	1.79	1.18
5:3R:219:HIS:CE1	5:3R:239:HIS:ND1	2.18	1.11
4:3D:115:ARG:CD	9:3J:60:TYR:OH	2.02	1.07
4:3D:115:ARG:CZ	9:3J:60:TYR:CE1	2.39	1.05
9:3J:53:TRP:O	9:3J:57:LYS:HE3	1.57	1.04
5:3R:219:HIS:HE1	5:3R:239:HIS:ND1	1.57	1.00
14:3C:503:U10:H4M2	14:3C:503:U10:H3M2	1.47	0.92
4:3D:115:ARG:HD2	9:3J:60:TYR:OH	1.69	0.90
4:3D:115:ARG:CZ	9:3J:60:TYR:HE1	1.79	0.88
5:3E:242:HIS:HB2	5:3E:251:LYS:HB3	1.54	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3R:196:ARG:HD2	5:3R:249:ILE:HD13	1.53	0.88
2:3B:226:MET:HG3	2:3B:227:ARG:H	1.39	0.86
12:3D:502:3PE:H31	5:3E:131:ASN:HD22	1.42	0.85
9:3J:53:TRP:NE1	9:3J:57:LYS:HG2	1.79	0.84
2:3B:95:LYS:HB3	2:3B:110:GLU:H	1.43	0.83
2:3B:95:LYS:NZ	5:3I:71:ASN:O	2.12	0.82
4:3D:249:MET:SD	15:3D:501:HEC:FE	1.72	0.82
5:3R:204:ARG:NH2	5:3R:258:LEU:O	2.12	0.82
4:3D:115:ARG:HD3	9:3J:60:TYR:OH	1.79	0.81
7:3T:18:LEU:HB3	7:3T:23:GLN:HE21	1.46	0.81
5:3R:101:LYS:HD3	5:3R:103:SER:H	1.45	0.80
1:3N:184:GLU:OE2	1:3N:184:GLU:N	2.15	0.79
5:3I:32:ALA:C	5:3I:34:LEU:H	1.89	0.79
3:3C:264:THR:HG23	5:3R:223:VAL:HG22	1.65	0.79
3:3C:177:ARG:NH2	5:3R:140:MET:O	2.17	0.77
9:3J:53:TRP:NE1	9:3J:57:LYS:CG	2.37	0.76
12:3A:503:3PE:H32	3:3C:4:ILE:HD11	1.68	0.76
11:3Q:502:CDL:HA62	7:3T:33:GLY:HA3	1.66	0.76
3:3C:264:THR:OG1	5:3R:222:CYS:SG	2.43	0.74
4:3D:111:HIS:ND1	4:3D:142:VAL:O	2.21	0.74
11:3A:501:CDL:H132	12:3A:503:3PE:H381	1.70	0.73
2:3O:350:GLY:HA2	2:3O:411:ILE:HD13	1.70	0.73
3:3C:378:LYS:HZ1	6:3F:29:ARG:HD3	1.53	0.72
5:3R:156:LEU:HG	5:3R:176:VAL:HG22	1.70	0.72
6:3S:59:VAL:HG11	7:3T:10:MET:HG2	1.72	0.72
5:3E:153:GLU:O	5:3E:155:LYS:NZ	2.22	0.72
8:3H:50:GLU:OE1	8:3H:51:GLN:NE2	2.23	0.71
4:3D:249:MET:SD	15:3D:501:HEC:NB	2.63	0.71
3:3P:149:LEU:HD11	3:3P:281:LEU:HD22	1.71	0.71
1:3A:285:GLY:HA3	5:3I:70:LEU:HA	1.72	0.71
3:3P:314:SER:O	3:3P:318:ARG:NH1	2.22	0.71
1:3A:126:GLN:NE2	1:3A:130:GLU:OE1	2.23	0.71
3:3P:316:MET:HB2	12:3P:505:3PE:H112	1.73	0.71
2:3B:111:CYS:HB3	2:3B:119:LEU:HD22	1.73	0.70
1:3N:422:VAL:HG21	1:3N:437:ILE:HD13	1.74	0.70
3:3C:229:ILE:HD12	17:3E:302:PC1:H3A1	1.73	0.70
3:3C:316:MET:HG3	12:3C:506:3PE:H112	1.73	0.70
4:3D:267:THR:OG1	8:3H:40:ASP:OD1	2.10	0.70
4:3D:115:ARG:NH1	9:3J:60:TYR:CE1	2.60	0.70
4:3D:249:MET:SD	15:3D:501:HEC:NC	2.65	0.70
5:3R:264:GLU:HB2	5:3R:272:ILE:HG23	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3Q:232:SER:OG	7:3T:23:GLN:NE2	2.25	0.69
2:3O:306:PRO:HA	5:3V:52:ARG:HG3	1.74	0.69
10:3X:36:THR:HG21	17:3X:101:PC1:H332	1.75	0.69
3:3C:102:LEU:HD11	3:3C:304:MET:HE3	1.75	0.68
11:3Q:502:CDL:OA4	7:3T:36:ASN:ND2	2.26	0.68
11:3G:102:CDL:H532	11:3G:102:CDL:H722	1.74	0.68
5:3R:207:LYS:HD2	5:3R:210:TRP:HB3	1.75	0.68
1:3N:14:THR:HG21	1:3N:389:ARG:HB3	1.75	0.68
1:3A:17:SER:OG	1:3A:205:HIS:NE2	2.26	0.68
9:3J:53:TRP:O	9:3J:57:LYS:CE	2.39	0.68
1:3N:204:GLU:HG3	1:3N:207[A]:GLN:H	1.57	0.68
1:3N:145:MET:HG3	1:3N:425:LEU:HD23	1.75	0.68
10:3X:32:LEU:HD11	17:3X:101:PC1:H341	1.76	0.67
2:3B:141:GLN:HE22	2:3B:186:VAL:HB	1.59	0.67
4:3D:111:HIS:NE2	4:3D:288:ASP:OD2	2.28	0.67
5:3R:204:ARG:HH12	5:3R:257:ASN:HB3	1.58	0.67
5:3E:181:LYS:HA	5:3E:184:ILE:HD12	1.75	0.67
6:3F:121:LYS:NZ	10:3X:4:ARG:O	2.28	0.67
2:3B:227:ARG:HE	2:3B:229:GLY:HA3	1.58	0.66
5:3R:209:GLU:HB2	5:3R:210:TRP:HE3	1.61	0.66
2:3B:408:ALA:O	2:3B:412:ASN:ND2	2.29	0.66
5:3E:154:ILE:HB	5:3E:272:ILE:HG22	1.77	0.66
5:3R:107:SER:HB2	5:3R:111:LYS:HZ1	1.60	0.66
5:3E:229:GLY:HA2	5:3E:235:TYR:HD2	1.58	0.66
10:3Y:48:ILE:HD12	10:3Y:48:ILE:H	1.60	0.66
11:3Q:502:CDL:H311	7:3T:37:VAL:HG21	1.77	0.66
3:3C:33:PHE:HA	3:3C:36:LEU:HB2	1.77	0.66
3:3P:229:ILE:HG23	17:3R:302:PC1:H3C1	1.78	0.66
6:3F:84:GLN:OE1	7:3G:42:ARG:NH1	2.29	0.65
5:3R:214:ILE:HD12	5:3R:214:ILE:H	1.61	0.65
11:3P:506:CDL:H541	11:3P:506:CDL:HA61	1.78	0.65
10:3X:12:GLU:O	10:3X:16:ASN:ND2	2.28	0.65
2:3B:89:ILE:HD13	2:3B:119:LEU:HG	1.76	0.65
5:3I:32:ALA:C	5:3I:34:LEU:N	2.51	0.65
5:3I:64:LEU:HD11	5:3I:76:VAL:HG12	1.79	0.65
5:3V:53:GLU:N	5:3V:53:GLU:OE1	2.29	0.65
2:3B:346:THR:O	2:3B:351:ASN:ND2	2.29	0.65
3:3P:126:THR:HG21	13:3P:501:HEM:HBB2	1.78	0.65
12:3A:502:3PE:H32	17:3E:302:PC1:H31	1.79	0.65
6:3F:72:PHE:HE2	6:3F:76:ARG:HH21	1.45	0.65
3:3C:282:ARG:HD3	3:3C:343:VAL:HG22	1.77	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3R:169:TRP:CD1	5:3R:174:LEU:HB2	2.32	0.64
8:3U:56:GLU:OE1	8:3U:56:GLU:N	2.20	0.64
3:3C:149:LEU:HD21	3:3C:281:LEU:HD11	1.80	0.64
12:3A:503:3PE:O11	12:3A:503:3PE:N	2.31	0.63
8:3U:56:GLU:HA	8:3U:59:PHE:HB2	1.80	0.63
2:3B:201:SER:HB2	2:3B:228:GLY:HA2	1.81	0.63
2:3O:76:THR:HG23	2:3O:81:SER:HA	1.80	0.63
2:3O:240:ARG:O	2:3O:421:ARG:NH2	2.31	0.63
3:3C:38:GLY:HA3	14:3C:503:U10:H13	1.81	0.63
3:3C:379:TRP:HB3	6:3F:45:ARG:HH21	1.61	0.63
2:3O:226:MET:SD	2:3O:226:MET:N	2.71	0.63
4:3Q:223:LYS:NZ	11:3Q:502:CDL:OB4	2.26	0.63
5:3R:144:ALA:HA	5:3R:147:LEU:HB2	1.80	0.63
9:3W:10:TYR:HA	9:3W:14:PHE:HB2	1.81	0.63
5:3R:152:ILE:HD12	5:3R:169:TRP:HA	1.79	0.63
1:3A:304:CYS:HB3	1:3A:334:MET:HE3	1.80	0.63
5:3E:157:SER:HB2	5:3E:269:ASP:HB3	1.80	0.63
8:3U:32:LYS:HB2	8:3U:36:ARG:HH12	1.62	0.63
4:3D:109:LEU:HD11	4:3D:287:HIS:HB3	1.79	0.63
8:3H:76:GLU:OE2	8:3H:76:GLU:N	2.32	0.63
2:3O:56:ARG:HD2	2:3O:103:GLU:HG2	1.82	0.62
3:3P:125:ALA:O	3:3P:129:MET:HG3	1.98	0.62
5:3R:210:TRP:NE1	5:3R:269:ASP:OD1	2.27	0.62
5:3R:175:PHE:CE2	5:3R:215:GLY:HA2	2.34	0.62
11:3C:505:CDL:H122	11:3C:505:CDL:H321	1.82	0.62
6:3F:117:GLU:HG2	10:3X:4:ARG:HD3	1.81	0.62
9:3J:53:TRP:CE2	9:3J:57:LYS:CG	2.68	0.62
5:3E:267:SER:HB3	5:3E:270:LEU:HD12	1.81	0.62
4:3D:257:VAL:HG13	4:3D:258:LEU:HG	1.81	0.62
8:3H:75:THR:HG22	8:3H:77:GLU:H	1.64	0.62
4:3Q:28:ARG:NE	4:3Q:185:ASP:OD2	2.27	0.62
2:3O:100:SER:HB2	2:3O:105:MET:HG3	1.81	0.61
5:3E:125:VAL:HG21	17:3E:302:PC1:H362	1.81	0.61
2:3O:219:VAL:HG12	2:3O:222:ARG:HH22	1.65	0.61
5:3R:105:GLU:OE1	5:3R:105:GLU:N	2.25	0.61
1:3N:258:GLU:OE1	5:3R:101:LYS:NZ	2.34	0.61
3:3P:361:ILE:HA	3:3P:365:LEU:HB2	1.81	0.61
3:3P:129:MET:HE1	3:3P:181:PHE:HB3	1.82	0.61
11:3Q:502:CDL:OA3	7:3T:40:ARG:NH1	2.33	0.61
1:3A:131:ARG:HD3	1:3A:175:ARG:HA	1.82	0.61
5:3E:155:LYS:HZ1	5:3E:169:TRP:CD1	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3C:207:ASN:ND2	3:3C:211:ILE:O	2.34	0.61
2:3B:157:ALA:O	2:3B:161:GLU:HG2	2.00	0.61
3:3P:35:SER:OG	14:3P:503:U10:O5	2.15	0.61
4:3Q:120:ARG:NE	15:3Q:501:HEC:O1A	2.32	0.61
5:3R:101:LYS:HD3	5:3R:101:LYS:C	2.26	0.60
4:3D:295:LEU:O	4:3D:299:MET:HG2	2.01	0.60
1:3A:158:PHE:O	1:3A:161:THR:OG1	2.19	0.60
5:3R:182:LYS:HE2	5:3R:186:GLN:OE1	2.01	0.60
7:3T:60:THR:O	7:3T:64:GLN:HG2	2.02	0.60
1:3A:117:VAL:HG11	1:3A:195:MET:HE1	1.84	0.60
1:3A:61:HIS:CG	1:3A:134:ILE:HD11	2.37	0.60
4:3D:284:GLU:HG3	4:3D:286:GLU:HG2	1.83	0.60
5:3R:153:GLU:C	5:3R:154:ILE:HG13	2.26	0.60
3:3C:15:ASN:HA	3:3C:19:ILE:HB	1.82	0.60
3:3C:1:MET:SD	3:3C:1:MET:N	2.73	0.60
1:3N:280:TYR:HD1	1:3N:290:MET:HE1	1.67	0.60
2:3B:58:GLU:O	2:3B:174:ASN:ND2	2.35	0.60
2:3B:207:ILE:HD13	2:3B:382:VAL:HG12	1.83	0.60
2:3O:141:GLN:HA	2:3O:144:LEU:HD12	1.84	0.60
3:3P:360:LEU:HG	3:3P:365:LEU:HD23	1.83	0.60
3:3P:373:GLU:OE1	6:3S:20:TYR:OH	2.17	0.60
2:3B:47:ILE:HD11	2:3B:211:VAL:HG21	1.83	0.60
2:3B:248:ASN:ND2	2:3B:250:ASP:OD2	2.35	0.60
10:3X:45:VAL:O	10:3X:49:ASN:ND2	2.34	0.60
4:3Q:23:HIS:NE2	4:3Q:199:ASP:OD2	2.35	0.59
3:3C:51:LEU:HD13	13:3C:501:HEM:HBD1	1.84	0.59
1:3N:281:ASP:OD1	1:3N:282:SER:N	2.35	0.59
3:3C:32:ASN:ND2	11:3G:102:CDL:OB9	2.35	0.59
3:3C:221:HIS:O	3:3C:225:THR:OG1	2.18	0.59
3:3C:244:LEU:O	4:3D:290:ARG:NE	2.32	0.59
5:3E:225:ILE:HD11	4:3Q:144:ARG:HH12	1.67	0.59
5:3R:162:GLY:HA3	5:3R:180:THR:HG23	1.84	0.59
1:3A:147:ASP:OD2	5:3I:47:ARG:NH2	2.35	0.59
3:3P:149:LEU:HD22	3:3P:291:VAL:HG22	1.84	0.59
10:3X:38:TRP:HA	17:3X:101:PC1:H32	1.85	0.59
6:3F:45:ARG:NH1	6:3F:46:ASP:OD1	2.34	0.59
6:3S:16:ILE:HD12	6:3S:16:ILE:H	1.68	0.59
1:3A:76:GLU:OE2	2:3B:290:ASN:N	2.36	0.59
3:3P:314:SER:OG	3:3P:315:MET:N	2.34	0.59
5:3R:149:MET:SD	5:3R:150:SER:N	2.75	0.59
2:3O:89:ILE:HD13	2:3O:119:LEU:HD22	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:354:VAL:HG21	1:3A:404:ALA:HA	1.85	0.59
1:3N:192:ALA:HB2	1:3N:219:LEU:HB3	1.83	0.58
5:3R:184:ILE:HG12	5:3R:209:GLU:HG3	1.85	0.58
3:3C:34:GLY:HA3	13:3C:502:HEM:HBA2	1.86	0.58
2:3O:290:ASN:O	2:3O:297:GLN:NE2	2.36	0.58
2:3O:334:GLY:HA2	2:3O:434:PRO:HD3	1.84	0.58
3:3C:119:LEU:HD22	13:3C:502:HEM:HBB2	1.84	0.58
4:3D:230:SER:O	4:3D:230:SER:OG	2.22	0.58
6:3F:44:MET:HE1	6:3F:99:LYS:HB2	1.86	0.58
1:3A:279:HIS:CG	5:3I:35:PRO:HB3	2.38	0.58
11:3A:501:CDL:H321	11:3A:501:CDL:H131	1.86	0.58
2:3B:56:ARG:HD2	2:3B:103:GLU:HG2	1.85	0.58
5:3E:241:SER:HA	5:3E:249:ILE:HD11	1.85	0.58
5:3E:242:HIS:HD2	5:3E:251:LYS:HD2	1.69	0.58
4:3D:249:MET:SD	15:3D:501:HEC:NA	2.76	0.58
5:3E:161:GLU:HG3	5:3E:180:THR:HG22	1.85	0.58
1:3N:237:THR:HG22	7:3T:18:LEU:HD11	1.84	0.58
1:3N:304:CYS:HB3	1:3N:334:MET:SD	2.43	0.58
8:3U:32:LYS:HA	8:3U:35:GLU:HG2	1.85	0.58
3:3C:116:GLY:C	13:3C:502:HEM:HBC2	2.28	0.58
6:3F:24:TRP:CG	6:3F:25:LEU:H	2.21	0.58
5:3R:153:GLU:N	5:3R:153:GLU:OE2	2.37	0.58
3:3C:81:TYR:OH	4:3D:206:ARG:NH1	2.36	0.57
1:3A:144:SER:HB3	5:3I:47:ARG:CZ	2.34	0.57
3:3C:107:TYR:HB2	3:3C:305:PRO:HG3	1.86	0.57
5:3E:195:LEU:HD21	5:3E:248:ARG:HB3	1.87	0.57
1:3N:172:GLU:OE1	1:3N:175:ARG:NH2	2.36	0.57
2:3B:96:LEU:HB3	5:3I:70:LEU:HB3	1.86	0.57
2:3B:239:TYR:CD2	2:3B:260:GLU:HB2	2.39	0.57
5:3R:179:ARG:NH1	5:3R:183:GLU:OE1	2.37	0.57
6:3S:35:ASP:OD1	6:3S:89:TYR:OH	2.19	0.57
3:3C:50:PHE:HA	3:3C:53:MET:HE2	1.86	0.57
3:3C:360:LEU:HG	3:3C:365:LEU:HD23	1.86	0.57
11:3P:506:CDL:HB31	7:3T:40:ARG:HB3	1.87	0.57
1:3N:74:ALA:O	1:3N:78:GLU:HG2	2.04	0.57
5:3R:199:GLN:O	5:3R:248:ARG:NE	2.36	0.57
2:3B:394:GLN:O	2:3B:397:THR:OG1	2.22	0.57
4:3D:245:GLN:N	4:3D:245:GLN:OE1	2.38	0.57
1:3N:34:THR:OG1	2:3O:373:GLU:OE2	2.19	0.57
2:3B:133:ARG:HD2	2:3B:135:TRP:CZ2	2.38	0.57
4:3Q:37:CYS:HB2	15:3Q:501:HEC:CAB	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3O:357:VAL:HG12	2:3O:361:LYS:HD2	1.87	0.57
2:3B:97:SER:HA	5:3I:69:GLY:HA3	1.85	0.57
8:3U:18:THR:O	8:3U:22:GLU:HG2	2.05	0.57
3:3P:81:TYR:OH	4:3Q:118:ARG:NH2	2.34	0.56
1:3A:297:VAL:HG22	3:3C:1:MET:HG3	1.87	0.56
2:3B:361:LYS:NZ	2:3B:405:VAL:O	2.33	0.56
4:3D:249:MET:SD	15:3D:501:HEC:ND	2.79	0.56
3:3P:119:LEU:HD22	13:3P:502:HEM:HBB2	1.87	0.56
4:3Q:144:ARG:HD2	4:3Q:145:GLU:N	2.21	0.56
5:3R:231:PHE:H	5:3R:242:HIS:CE1	2.23	0.56
2:3B:117:GLU:HA	2:3B:120:MET:HE2	1.88	0.56
3:3C:237:LEU:HD13	4:3D:301:MET:HG2	1.86	0.56
4:3D:324:LEU:HD21	6:3F:75:LYS:HE3	1.86	0.56
2:3O:124:LEU:HD13	2:3O:223:PHE:HB2	1.87	0.56
1:3N:354:VAL:HG21	1:3N:404:ALA:HA	1.88	0.56
7:3T:18:LEU:HB3	7:3T:23:GLN:NE2	2.18	0.56
4:3D:252:PRO:HB3	15:3D:501:HEC:HHC	1.88	0.56
5:3E:235:TYR:HB2	5:3E:242:HIS:ND1	2.21	0.56
6:3F:90:GLU:H	6:3F:90:GLU:CD	2.12	0.56
5:3R:210:TRP:HE1	5:3R:269:ASP:CG	2.14	0.56
2:3B:226:MET:HG3	2:3B:227:ARG:N	2.17	0.56
4:3D:214:TYR:OH	15:3D:501:HEC:O2A	2.15	0.56
5:3E:191:GLU:OE2	5:3E:194:GLN:N	2.38	0.56
6:3F:79:ASP:OD2	6:3F:83:ARG:NH2	2.38	0.56
6:3F:85:GLN:HG2	7:3G:38:ASN:HD21	1.70	0.56
3:3P:322:GLN:HE22	12:3P:505:3PE:H111	1.69	0.56
4:3Q:225:HIS:CE1	7:3T:20:PRO:HB2	2.41	0.56
2:3B:54:GLY:O	2:3B:194:TYR:OH	2.24	0.56
2:3O:353:SER:OG	2:3O:356:ASP:OD1	2.21	0.56
1:3A:46:ARG:HH22	1:3A:316:GLU:CD	2.13	0.56
7:3T:24:ARG:HH12	7:3T:26:PHE:HD2	1.54	0.56
1:3A:144:SER:H	5:3I:47:ARG:NH1	2.04	0.56
4:3D:201:LEU:HA	4:3D:204:ILE:HB	1.87	0.56
7:3G:67:GLU:O	7:3G:71:SER:OG	2.19	0.56
1:3A:235:ARG:CZ	5:3E:92:ARG:HH22	2.19	0.55
5:3E:229:GLY:HA2	5:3E:235:TYR:CD2	2.40	0.55
1:3N:106:LEU:HD21	1:3N:203:VAL:HG23	1.88	0.55
10:3X:12:GLU:CD	10:3X:16:ASN:HD21	2.13	0.55
3:3C:361:ILE:HA	3:3C:365:LEU:HB2	1.88	0.55
1:3N:19:LEU:HD13	1:3N:23:LEU:HB3	1.87	0.55
3:3P:252:ASP:OD2	3:3P:269:LYS:NZ	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3Q:158:ILE:HG23	4:3Q:160:MET:H	1.70	0.55
5:3E:239:HIS:HB3	16:3E:301:FES:S2	2.45	0.55
8:3U:48:SER:OG	8:3U:49:GLN:OE1	2.24	0.55
3:3P:360:LEU:HD12	3:3P:364:VAL:HB	1.89	0.55
4:3D:108:SER:HB2	4:3D:288:ASP:OD1	2.07	0.55
7:3G:30:HIS:HB3	7:3G:33:THR:HB	1.89	0.55
3:3P:181:PHE:HA	3:3P:184:ILE:HG22	1.89	0.55
3:3C:319:PRO:HD2	6:3F:32:TYR:OH	2.07	0.55
1:3N:156:THR:HG1	1:3N:239:SER:HG	1.54	0.55
5:3R:156:LEU:HD13	5:3R:210:TRP:CD1	2.41	0.55
7:3T:3:GLU:N	7:3T:3:GLU:OE2	2.40	0.55
4:3D:300:MET:HE3	4:3D:304:LEU:HD22	1.88	0.55
1:3A:38:GLY:HA2	1:3A:113:LEU:HD21	1.89	0.54
4:3D:107:SER:O	4:3D:291:LYS:NZ	2.40	0.54
12:3D:502:3PE:H372	5:3E:128:ALA:HB1	1.89	0.54
5:3E:242:HIS:CD2	5:3E:251:LYS:HD2	2.42	0.54
1:3N:156:THR:OG1	1:3N:239:SER:OG	2.23	0.54
2:3O:68:LEU:HD21	2:3O:137:VAL:HG13	1.89	0.54
6:3S:21:TYR:OH	6:3S:86:ASP:OD2	2.20	0.54
8:3U:28:GLU:O	8:3U:32:LYS:NZ	2.40	0.54
1:3A:444:LEU:HD11	12:3A:502:3PE:H12	1.88	0.54
2:3B:148:LYS:HG3	2:3B:177:TYR:HB3	1.88	0.54
5:3E:239:HIS:O	5:3E:241:SER:OG	2.24	0.54
5:3R:102:SER:O	5:3R:106:SER:OG	2.13	0.54
10:3X:14:ALA:O	10:3X:18:ILE:HG12	2.08	0.54
9:3J:23:LEU:O	9:3J:27:VAL:HG23	2.08	0.54
9:3J:52:LEU:HD13	9:3J:55:HIS:HE1	1.73	0.54
3:3P:215:MET:HB2	7:3T:10:MET:SD	2.48	0.54
4:3Q:83:ARG:NH1	4:3Q:89:ASP:OD2	2.41	0.54
1:3A:30:SER:OG	1:3A:31:SER:N	2.35	0.54
12:3Q:503:3PE:H2H1	5:3R:133:VAL:HG13	1.88	0.54
5:3R:117:ILE:O	5:3R:121:THR:HG22	2.08	0.54
8:3U:28:GLU:OE1	8:3U:28:GLU:N	2.41	0.54
9:3W:33:ARG:HD3	10:3X:48:ILE:HA	1.90	0.54
2:3B:46:ARG:HG2	2:3B:379:LEU:HD22	1.88	0.54
3:3C:97:HIS:NE2	13:3C:502:HEM:O1A	2.36	0.54
7:3G:39:VAL:O	7:3G:43:THR:HG22	2.07	0.54
3:3P:207:ASN:ND2	3:3P:211:ILE:O	2.39	0.54
3:3P:209:THR:HA	3:3P:316:MET:HE3	1.90	0.54
3:3P:369:THR:O	3:3P:373:GLU:HG2	2.07	0.54
5:3R:156:LEU:HB3	5:3R:210:TRP:NE1	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3E:225:ILE:HG13	5:3E:235:TYR:CZ	2.43	0.54
4:3Q:156:GLN:HG2	8:3U:59:PHE:HZ	1.73	0.54
4:3Q:222:MET:SD	5:3R:121:THR:HG21	2.47	0.54
1:3A:219:LEU:HG	1:3A:220:SER:H	1.72	0.54
7:3G:67:GLU:OE1	7:3G:70:LYS:NZ	2.31	0.54
3:3P:229:ILE:HG21	17:3R:302:PC1:H362	1.90	0.54
4:3Q:74:PRO:HA	4:3Q:79:GLU:O	2.08	0.54
2:3B:305:GLN:HG3	2:3B:306:PRO:HD2	1.88	0.54
1:3N:269:PRO:HB2	1:3N:410:VAL:HG11	1.90	0.54
4:3D:249:MET:HG3	15:3D:501:HEC:C4C	2.38	0.53
6:3F:120:ALA:O	10:3X:9:ARG:NH1	2.41	0.53
2:3B:133:ARG:HB2	2:3B:136:GLU:HG3	1.91	0.53
1:3N:301:ARG:NH2	1:3N:333:ASP:OD2	2.40	0.53
1:3N:394:GLU:O	1:3N:398:ARG:HG3	2.07	0.53
3:3P:221:HIS:O	3:3P:225:THR:OG1	2.16	0.53
10:3Y:14:ALA:O	10:3Y:18:ILE:HG12	2.07	0.53
3:3C:128:PHE:CD1	14:3C:504:U10:H4M1	2.43	0.53
4:3D:128:CYS:SG	15:3D:501:HEC:HBC3	2.49	0.53
11:3P:506:CDL:OB4	7:3T:40:ARG:NE	2.36	0.53
1:3N:36:THR:HG21	1:3N:373:THR:HA	1.91	0.53
2:3B:283:PRO:HD3	5:3I:57:GLY:HA2	1.90	0.53
2:3O:209:LEU:HD11	2:3O:378:PHE:HD2	1.73	0.53
5:3R:179:ARG:HH22	5:3R:246:SER:HA	1.74	0.53
5:3R:217:CYS:SG	5:3R:218:THR:N	2.82	0.53
4:3D:96:PRO:HG3	8:3H:91:ASP:HB3	1.91	0.53
2:3O:166:ALA:HB2	2:3O:244:ILE:HG12	1.91	0.53
3:3P:375:ASN:O	6:3S:17:ARG:NH1	2.38	0.53
4:3Q:113:LEU:HA	4:3Q:116:ILE:HB	1.91	0.53
4:3D:115:ARG:NE	9:3J:60:TYR:CE1	2.76	0.53
4:3D:157:GLU:N	4:3D:157:GLU:OE1	2.42	0.53
1:3N:132:ASP:HA	1:3N:135:LEU:HD12	1.91	0.53
4:3D:307:LEU:HB3	5:3E:121:THR:OG1	2.09	0.53
1:3N:279:HIS:ND1	1:3N:284:TYR:OH	2.41	0.53
3:3P:75:TYR:HE1	4:3Q:200:HIS:HE1	1.56	0.53
3:3C:185:LEU:HD23	3:3C:188:ILE:HD12	1.91	0.52
1:3N:76:GLU:OE2	2:3O:290:ASN:N	2.42	0.52
8:3H:47:GLU:CD	8:3H:47:GLU:H	2.17	0.52
2:3O:42:ALA:O	2:3O:113:ARG:NH1	2.38	0.52
3:3P:277:ALA:HB1	3:3P:294:LEU:HD11	1.91	0.52
5:3E:200:HIS:HB3	5:3E:203:GLU:HG2	1.90	0.52
5:3E:212:ILE:HG22	5:3E:261:PRO:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3O:34:VAL:HG21	2:3O:386:ALA:HB1	1.91	0.52
5:3R:176:VAL:HG23	5:3R:212:ILE:CG2	2.40	0.52
2:3B:163:LEU:HD21	2:3B:258:VAL:HG21	1.90	0.52
2:3B:266:SER:O	2:3B:270:ASN:ND2	2.42	0.52
7:3G:21:SER:HB2	7:3G:24:GLU:HG3	1.91	0.52
1:3N:436:ARG:HD3	3:3P:222:PRO:HD3	1.90	0.52
3:3P:35:SER:OG	3:3P:228:ASP:OD2	2.28	0.52
6:3S:53:ASN:OD1	6:3S:54:LEU:N	2.43	0.52
3:3P:111:GLU:HA	3:3P:111:GLU:OE1	2.09	0.52
3:3P:237:LEU:HB2	4:3Q:212:MET:HE2	1.91	0.52
6:3S:67:ASP:OD2	6:3S:71:ARG:NH1	2.42	0.52
1:3N:19:LEU:H	1:3N:19:LEU:HD12	1.74	0.52
3:3C:207:ASN:HD22	3:3C:213:SER:HB3	1.74	0.52
1:3N:433:ASP:CG	3:3P:223:TYR:HH	2.13	0.52
3:3P:8:HIS:HB3	3:3P:11:MET:HB2	1.92	0.52
5:3R:151:LYS:NZ	5:3R:274:GLY:OXT	2.42	0.52
4:3D:171:ARG:NH2	4:3D:177:ASP:OD2	2.30	0.52
5:3E:199:GLN:HG2	5:3E:204:ARG:HE	1.75	0.52
2:3O:304:HIS:HA	5:3V:52:ARG:HH22	1.75	0.52
4:3Q:173:ASP:HB3	4:3Q:175:THR:HG23	1.92	0.52
1:3A:80:GLU:HG2	2:3B:284:HIS:HB2	1.91	0.52
1:3A:280:TYR:HB3	1:3A:307:PHE:CE1	2.45	0.52
1:3A:282:SER:O	2:3B:143:GLN:NE2	2.43	0.52
2:3O:369:LEU:HD11	2:3O:399:LEU:HD11	1.92	0.52
4:3Q:47:ALA:HA	4:3Q:90:TYR:HA	1.91	0.52
4:3D:253:ILE:HG22	4:3D:268:MET:HG3	1.92	0.51
5:3E:212:ILE:HG21	5:3E:263:TYR:HB3	1.92	0.51
9:3W:18:SER:HB3	10:3X:24:TRP:CE2	2.45	0.51
8:3H:77:GLU:O	8:3H:78:ASP:N	2.43	0.51
2:3B:357:VAL:HG12	2:3B:361:LYS:HD2	1.91	0.51
4:3Q:72:ASP:HB3	4:3Q:81:PHE:CE1	2.45	0.51
2:3B:24:LEU:HD11	2:3B:36:ALA:HB1	1.93	0.51
5:3R:176:VAL:HG23	5:3R:212:ILE:HG22	1.93	0.51
3:3C:53:MET:HE1	5:3E:140:MET:HG3	1.92	0.51
5:3E:219:HIS:O	5:3E:219:HIS:ND1	2.43	0.51
4:3Q:208:MET:HA	12:3Q:503:3PE:H341	1.92	0.51
5:3R:222:CYS:HB3	5:3R:236:CYS:SG	2.51	0.51
1:3A:204:GLU:OE1	1:3A:204:GLU:N	2.42	0.51
4:3D:186:PRO:O	4:3D:190:ARG:HG3	2.11	0.51
5:3E:214:ILE:HG22	5:3E:259:GLU:HB3	1.93	0.51
6:3F:51:GLU:N	6:3F:51:GLU:OE1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:3H:59:ARG:NE	8:3H:59:ARG:HA	2.26	0.51
2:3O:107:TYR:HB3	2:3O:123:LEU:HD11	1.91	0.51
9:3W:18:SER:OG	10:3X:23:MET:HE1	2.11	0.51
12:3C:507:3PE:H2B2	5:3R:130:LYS:HA	1.92	0.51
5:3E:134:SER:O	5:3E:138:SER:OG	2.21	0.51
2:3O:70:ARG:O	2:3O:98:VAL:HG21	2.11	0.51
1:3A:62:LEU:HD23	1:3A:122:LEU:HA	1.92	0.51
4:3D:125:CYS:HB3	15:3D:501:HEC:C3B	2.41	0.51
9:3J:34:ARG:HG2	10:3Y:48:ILE:HG23	1.92	0.51
4:3Q:9:SER:HB2	4:3Q:15:ARG:HH12	1.75	0.51
5:3R:255:PRO:HB2	5:3R:256:LEU:HD23	1.93	0.51
1:3N:235:ARG:CZ	5:3R:92:ARG:HH22	2.24	0.50
3:3C:346:PRO:HG3	7:3G:67:GLU:HB3	1.93	0.50
4:3D:156:VAL:HG21	4:3D:180:PRO:HG2	1.92	0.50
3:3P:234:PHE:HB3	11:3Q:502:CDL:H762	1.93	0.50
3:3P:326:TRP:HZ2	12:3P:505:3PE:H31	1.76	0.50
12:3Q:503:3PE:H3A1	12:3Q:503:3PE:H362	1.94	0.50
5:3R:101:LYS:HD2	5:3R:104:LYS:H	1.75	0.50
8:3H:91:ASP:HA	8:3H:94:VAL:HG12	1.94	0.50
1:3N:181:ASP:OD1	1:3N:181:ASP:N	2.42	0.50
1:3A:280:TYR:HB3	1:3A:307:PHE:HE1	1.77	0.50
3:3C:373:GLU:OE2	6:3F:32:TYR:CZ	2.65	0.50
12:3C:507:3PE:H291	5:3R:133:VAL:HB	1.93	0.50
5:3E:119:ALA:HB2	9:3J:21:PHE:CE1	2.47	0.50
5:3E:217:CYS:SG	5:3E:221:GLY:HA2	2.51	0.50
4:3Q:164:ILE:HG13	4:3Q:164:ILE:O	2.12	0.50
4:3D:145:THR:OG1	4:3D:146:GLU:OE1	2.30	0.50
7:3G:20:LEU:HB3	7:3G:25:GLN:NE2	2.26	0.50
2:3B:36:ALA:O	2:3B:207:ILE:HA	2.12	0.50
2:3B:41:TYR:HA	2:3B:113:ARG:HH12	1.76	0.50
4:3D:117:GLY:HA3	4:3D:278:PHE:HB2	1.94	0.50
2:3O:155:PRO:HB2	2:3O:254:HIS:CE1	2.46	0.50
3:3P:165:TRP:O	3:3P:174:THR:OG1	2.29	0.50
3:3C:337:TRP:NE1	3:3C:341:GLN:HE21	2.10	0.50
11:3C:505:CDL:OB3	7:3G:42:ARG:NH1	2.44	0.50
5:3E:196:ARG:NH1	5:3E:255:PRO:O	2.45	0.50
4:3D:109:LEU:HD12	4:3D:109:LEU:H	1.75	0.50
5:3E:125:VAL:HG11	17:3E:302:PC1:H381	1.93	0.50
1:3N:375:VAL:O	1:3N:379:ILE:HG13	2.12	0.50
4:3Q:207:LYS:NZ	12:3Q:503:3PE:O12	2.35	0.50
1:3A:140:GLU:HG2	5:3I:50:LEU:HD23	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3E:164:ASN:HB3	5:3E:177:ARG:HB2	1.93	0.49
1:3N:196:VAL:HG21	1:3N:383:LEU:HB3	1.94	0.49
5:3R:217:CYS:SG	5:3R:243:TYR:OH	2.69	0.49
11:3A:501:CDL:H151	12:3A:502:3PE:H242	1.93	0.49
1:3N:240:GLU:HG2	7:3T:17:SER:HB2	1.92	0.49
4:3Q:32:VAL:HG11	4:3Q:186:VAL:HB	1.94	0.49
1:3A:322:ALA:HB3	1:3A:338:LEU:HD21	1.94	0.49
4:3Q:42:SER:OG	4:3Q:112:ASP:OD2	2.30	0.49
5:3R:219:HIS:CE1	5:3R:220:LEU:HD12	2.47	0.49
2:3B:123:LEU:O	2:3B:127:THR:HG23	2.12	0.49
2:3B:312:PHE:HA	5:3I:61:GLY:HA2	1.95	0.49
4:3D:310:ALA:HB2	12:3G:101:3PE:H342	1.94	0.49
2:3O:27:THR:HG21	2:3O:217:LYS:HZ2	1.77	0.49
2:3O:312:PHE:HA	5:3V:61:GLY:HA2	1.94	0.49
5:3R:92:ARG:HB3	5:3R:97:LEU:HD13	1.94	0.49
2:3B:276:GLN:HG2	2:3B:281:ALA:HB2	1.93	0.49
3:3C:154:PRO:HG3	3:3C:288:LEU:HD11	1.94	0.49
2:3O:52:LYS:HB3	2:3O:203:ARG:HB2	1.94	0.49
2:3O:214:PRO:O	2:3O:218:GLN:HG2	2.12	0.49
3:3P:124:MET:HB3	3:3P:274:PHE:HE1	1.77	0.49
12:3Q:503:3PE:H232	12:3Q:503:3PE:H332	1.95	0.49
1:3N:244:ARG:HB2	1:3N:428:ILE:HD11	1.95	0.49
2:3O:148:LYS:HE3	2:3O:178:CYS:O	2.13	0.49
2:3O:264:THR:HB	2:3O:315:SER:HB2	1.95	0.49
1:3N:372:THR:OG1	2:3O:373:GLU:OE2	2.20	0.49
2:3B:36:ALA:HB3	2:3B:207:ILE:HG23	1.94	0.49
5:3R:159:ILE:HD13	5:3R:163:LYS:H	1.77	0.49
3:3C:245:PHE:O	4:3D:290:ARG:NH2	2.46	0.49
5:3R:187:GLU:HG3	5:3R:248:ARG:HH22	1.78	0.49
1:3A:156:THR:OG1	1:3A:239:SER:HB2	2.13	0.49
3:3C:35:SER:HB3	14:3C:503:U10:H1M1	1.95	0.49
4:3D:199:PRO:HG2	15:3D:501:HEC:HAA1	1.95	0.49
9:3J:43:ILE:O	9:3J:47:ILE:HG13	2.13	0.49
11:3P:507:CDL:H312	11:3P:507:CDL:H121	1.94	0.49
1:3A:141:ASN:ND2	1:3A:168:GLU:OE2	2.45	0.48
1:3A:154:HIS:NE2	1:3A:314:TYR:OH	2.35	0.48
2:3B:393:VAL:HG22	2:3B:397:THR:OG1	2.12	0.48
5:3R:183:GLU:HB3	5:3R:187:GLU:HB2	1.95	0.48
1:3A:356:ARG:HG3	2:3B:91:ALA:HA	1.94	0.48
12:3N:501:3PE:O12	12:3N:501:3PE:N	2.34	0.48
5:3R:179:ARG:HD2	5:3R:184:ILE:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:3T:67:GLU:N	7:3T:67:GLU:OE1	2.44	0.48
9:3W:46:ILE:HG22	9:3W:47:ASN:ND2	2.28	0.48
3:3C:10:LEU:HD21	3:3P:195:VAL:HG13	1.95	0.48
3:3C:44:GLN:O	3:3C:83:HIS:HE1	1.96	0.48
1:3N:145:MET:HA	1:3N:148:VAL:HG22	1.95	0.48
3:3P:186:PRO:HG2	13:3P:501:HEM:HMC3	1.95	0.48
2:3B:113:ARG:NH2	2:3B:210:GLY:O	2.46	0.48
3:3C:78:VAL:O	3:3C:82:LEU:HB2	2.13	0.48
8:3U:24:CYS:O	8:3U:27:ILE:HG22	2.13	0.48
13:3C:501:HEM:O1D	13:3C:501:HEM:HHA	2.13	0.48
5:3E:174:LEU:HD22	5:3E:214:ILE:HG13	1.95	0.48
2:3O:220:ALA:HA	2:3O:224:LEU:HD23	1.96	0.48
4:3Q:27:ARG:NH2	4:3Q:60:GLU:OE1	2.47	0.48
12:3A:503:3PE:H2	12:3A:503:3PE:H221	1.50	0.48
3:3C:248:ASP:OD1	3:3C:256:TYR:OH	2.29	0.48
3:3C:370:SER:HA	3:3C:373:GLU:HB2	1.96	0.48
5:3E:204:ARG:HG3	5:3E:205:VAL:HG23	1.95	0.48
6:3F:57:GLU:OE1	6:3F:60:ARG:NH1	2.46	0.48
1:3A:384:LEU:HD23	1:3A:384:LEU:HA	1.70	0.48
2:3B:227:ARG:HD2	2:3B:229:GLY:H	1.79	0.48
8:3U:49:GLN:H	8:3U:49:GLN:CD	2.22	0.48
1:3A:192:ALA:H	1:3A:220:SER:HB3	1.79	0.48
4:3D:116:ARG:NE	4:3D:274:ASP:OD2	2.41	0.48
4:3D:284:GLU:HG2	4:3D:287:HIS:HB2	1.95	0.48
5:3R:209:GLU:HB2	5:3R:210:TRP:CE3	2.46	0.48
5:3R:213:LEU:HD13	5:3R:258:LEU:HB3	1.94	0.48
8:3U:20:VAL:HG12	8:3U:69:VAL:HG22	1.95	0.48
1:3A:27:SER:HB3	1:3A:208:LEU:HD22	1.96	0.48
2:3B:137:VAL:O	2:3B:141:GLN:HG2	2.14	0.48
3:3C:197:LEU:HD11	14:3C:503:U10:H111	1.95	0.48
4:3D:115:ARG:HD2	9:3J:60:TYR:CZ	2.49	0.48
5:3E:191:GLU:OE1	5:3E:193:SER:N	2.45	0.48
6:3F:44:MET:HB2	6:3F:47:ASP:OD1	2.14	0.48
3:3P:116:GLY:C	13:3P:502:HEM:HBC2	2.38	0.48
8:3U:38:GLU:HA	8:3U:41:ASP:OD1	2.13	0.48
1:3A:445:ARG:NH1	11:3A:501:CDL:OB3	2.46	0.48
2:3B:135:TRP:CG	6:3S:49:ARG:HD3	2.49	0.48
5:3R:131:ASN:O	5:3R:131:ASN:ND2	2.39	0.48
8:3U:17:LEU:HD11	8:3U:21:ARG:CZ	2.44	0.48
17:3X:101:PC1:H31	17:3X:101:PC1:H112	1.95	0.48
2:3B:135:TRP:CD2	6:3S:49:ARG:HD3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3D:125:CYS:HB3	15:3D:501:HEC:CAB	2.43	0.47
5:3E:196:ARG:HB2	5:3E:253:PRO:HA	1.96	0.47
5:3R:161:GLU:HG2	5:3R:180:THR:HA	1.94	0.47
2:3B:96:LEU:O	5:3I:70:LEU:N	2.47	0.47
3:3C:24:PRO:HB2	3:3C:27:ILE:HG12	1.96	0.47
3:3P:357:LEU:O	3:3P:361:ILE:HG13	2.14	0.47
1:3A:15:GLN:HB2	1:3A:205:HIS:ND1	2.30	0.47
2:3B:120:MET:HE3	2:3B:219:VAL:HG11	1.96	0.47
8:3H:54:LYS:HE2	8:3H:54:LYS:HA	1.96	0.47
12:3N:502:3PE:H242	17:3R:302:PC1:H241	1.97	0.47
2:3O:255:ALA:HB3	2:3O:337:ILE:HD11	1.95	0.47
3:3P:277:ALA:HB1	3:3P:294:LEU:CD1	2.44	0.47
5:3R:162:GLY:N	5:3R:178:HIS:O	2.41	0.47
1:3A:279:HIS:ND1	1:3A:284:TYR:OH	2.38	0.47
11:3C:505:CDL:H112	11:3C:505:CDL:HA4	1.47	0.47
5:3E:140:MET:HE2	3:3P:163:TRP:CZ2	2.49	0.47
1:3N:224:VAL:HG13	1:3N:225:GLU:N	2.28	0.47
5:3R:176:VAL:HA	5:3R:212:ILE:HG22	1.95	0.47
1:3A:163:LEU:HD23	1:3A:163:LEU:HA	1.73	0.47
3:3C:71:ARG:NH2	4:3D:282:ALA:O	2.46	0.47
4:3D:98:TYR:O	4:3D:103:ARG:NH1	2.47	0.47
4:3Q:235:LEU:HD21	6:3S:63:LYS:HE3	1.95	0.47
1:3A:238:GLY:O	7:3G:21:SER:OG	2.28	0.47
3:3C:53:MET:HE1	5:3E:140:MET:CG	2.44	0.47
12:3Q:503:3PE:H231	12:3Q:503:3PE:H272	1.97	0.47
5:3R:159:ILE:HD12	5:3R:161:GLU:N	2.29	0.47
3:3C:185:LEU:HD23	3:3C:185:LEU:HA	1.74	0.47
1:3N:58:PHE:HE2	1:3N:127:ILE:HG23	1.79	0.47
2:3O:122:PHE:O	2:3O:126:VAL:HG23	2.14	0.47
2:3O:395:PRO:O	2:3O:399:LEU:HG	2.15	0.47
3:3P:47:THR:HG1	3:3P:83:HIS:HD1	1.62	0.47
4:3Q:20:SER:HB2	4:3Q:199:ASP:OD1	2.14	0.47
5:3R:249:ILE:HG22	5:3R:254:ALA:HB1	1.95	0.47
1:3A:312:ILE:O	1:3A:319:LEU:N	2.46	0.47
4:3D:287:HIS:O	4:3D:291:LYS:HG2	2.14	0.47
12:3N:501:3PE:O21	11:3P:507:CDL:H512	2.15	0.47
5:3R:214:ILE:HG22	5:3R:215:GLY:H	1.79	0.47
10:3Y:46:PRO:O	10:3Y:49:ASN:ND2	2.48	0.47
3:3C:240:LEU:HD21	12:3D:502:3PE:H251	1.97	0.47
5:3E:163:LYS:HD3	5:3E:164:ASN:H	1.80	0.47
9:3J:34:ARG:HG3	10:3Y:48:ILE:HA	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3N:144:SER:HA	5:3V:47:ARG:NH1	2.30	0.47
1:3N:280:TYR:CD1	1:3N:290:MET:HE1	2.47	0.47
2:3O:393:VAL:HG13	2:3O:397:THR:HB	1.95	0.47
5:3R:103:SER:O	5:3R:107:SER:HB3	2.15	0.47
3:3C:85:ASN:HB3	3:3C:242:LEU:HD23	1.97	0.47
1:3N:224:VAL:HG13	1:3N:225:GLU:H	1.80	0.47
1:3A:250:LEU:HD12	5:3I:44:ASP:HB2	1.98	0.46
4:3D:240:TYR:OH	8:3H:91:ASP:OD2	2.25	0.46
1:3N:435:ASN:ND2	3:3P:223:TYR:OH	2.48	0.46
11:3Q:502:CDL:HA62	7:3T:33:GLY:CA	2.42	0.46
5:3R:249:ILE:O	5:3R:249:ILE:HD12	2.15	0.46
2:3B:227:ARG:HD2	2:3B:227:ARG:C	2.41	0.46
3:3C:337:TRP:HE1	3:3C:341:GLN:HE21	1.62	0.46
4:3D:131:MET:HE1	4:3D:278:PHE:CE2	2.51	0.46
5:3E:162:GLY:H	5:3E:178:HIS:HB3	1.80	0.46
5:3E:165:MET:HA	5:3E:165:MET:HE2	1.97	0.46
6:3F:24:TRP:CG	6:3F:25:LEU:N	2.83	0.46
6:3S:44:LYS:HA	6:3S:47:ILE:HD12	1.96	0.46
1:3A:294:LEU:HD12	1:3A:307:PHE:CE2	2.49	0.46
3:3C:3:ASN:HB2	3:3C:6:LYS:HG2	1.97	0.46
3:3C:113:TRP:NE1	3:3C:301:LEU:O	2.28	0.46
3:3C:128:PHE:O	3:3C:132:VAL:HG23	2.15	0.46
1:3N:184:GLU:O	1:3N:188:GLN:HB2	2.14	0.46
2:3O:25:GLU:HB2	2:3O:213:HIS:ND1	2.30	0.46
2:3B:239:TYR:CE2	2:3B:260:GLU:HB2	2.50	0.46
5:3E:159:ILE:HD11	5:3E:163:LYS:C	2.40	0.46
5:3E:164:ASN:OD1	5:3E:164:ASN:N	2.47	0.46
5:3E:182:LYS:HE2	5:3E:182:LYS:HB2	1.56	0.46
1:3A:242:ARG:HB3	1:3A:428:ILE:HD11	1.98	0.46
1:3A:444:LEU:HA	9:3J:18:THR:HG21	1.98	0.46
2:3B:178:CYS:SG	2:3B:183:ILE:HG12	2.56	0.46
17:3E:302:PC1:H111	17:3E:302:PC1:H11	1.98	0.46
6:3F:24:TRP:CD1	6:3F:25:LEU:H	2.33	0.46
5:3R:205:VAL:HG22	5:3R:207:LYS:H	1.80	0.46
11:3A:501:CDL:H351	3:3C:225:THR:HG21	1.96	0.46
4:3D:228:GLY:HA3	8:3H:78:ASP:N	2.30	0.46
5:3E:199:GLN:O	5:3E:248:ARG:NH1	2.49	0.46
7:3G:67:GLU:OE1	7:3G:67:GLU:HA	2.15	0.46
2:3O:409:ASP:N	2:3O:409:ASP:OD1	2.48	0.46
7:3T:72:LYS:HE2	8:3U:56:GLU:OE2	2.16	0.46
1:3A:279:HIS:ND1	5:3I:35:PRO:HB3	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3C:231:GLY:HA2	11:3G:102:CDL:H711	1.97	0.46
5:3E:120:THR:HA	5:3E:123:VAL:HG12	1.97	0.46
4:3Q:32:VAL:HG22	4:3Q:169:LEU:HD21	1.97	0.46
5:3R:206:LYS:HE3	5:3R:263:TYR:HE1	1.80	0.46
4:3Q:71:GLN:OE1	4:3Q:82:MET:HE2	2.16	0.46
4:3Q:160:MET:HE2	4:3Q:163:PRO:HG3	1.98	0.46
1:3A:259:GLY:N	1:3A:318:GLY:O	2.37	0.46
1:3A:439:SER:O	12:3A:502:3PE:N	2.48	0.46
5:3R:159:ILE:HD13	5:3R:163:LYS:N	2.31	0.46
1:3A:40:TRP:CZ2	1:3A:377:GLU:HA	2.50	0.46
2:3B:124:LEU:O	2:3B:128:ALA:HB3	2.16	0.46
4:3D:212:GLU:HA	4:3D:215:VAL:HG12	1.98	0.46
5:3E:236:CYS:O	5:3E:241:SER:OG	2.30	0.46
5:3E:249:ILE:HD12	5:3E:249:ILE:HA	1.79	0.46
7:3G:56:VAL:O	7:3G:60:VAL:HG23	2.16	0.46
2:3O:202:ALA:HB3	2:3O:230:LEU:HA	1.97	0.46
5:3R:184:ILE:HD12	5:3R:184:ILE:H	1.80	0.46
1:3A:264:ASN:O	1:3A:266:ASP:N	2.49	0.45
4:3D:108:SER:N	9:3J:48:ASN:OD1	2.48	0.45
2:3O:169:ARG:HG3	2:3O:240:ARG:HB3	1.98	0.45
5:3R:241:SER:HB3	5:3R:254:ALA:HB2	1.99	0.45
4:3D:115:ARG:NH2	9:3J:60:TYR:HE1	2.10	0.45
4:3D:280:ARG:O	4:3D:280:ARG:HD3	2.16	0.45
1:3N:431:LEU:HD12	1:3N:432:PRO:HD2	1.98	0.45
12:3A:502:3PE:C3	17:3E:302:PC1:H31	2.45	0.45
4:3D:160:ASP:HB2	4:3D:171:ARG:HE	1.82	0.45
6:3F:59:ILE:HA	6:3F:62:LEU:HD12	1.99	0.45
3:3P:58:ASP:HB3	3:3P:61:THR:HG22	1.97	0.45
3:3P:254:ASP:OD2	3:3P:267:HIS:NE2	2.50	0.45
1:3A:61:HIS:CD2	1:3A:134:ILE:HD11	2.51	0.45
2:3B:76:THR:HG21	2:3B:133:ARG:NH2	2.31	0.45
2:3B:309:VAL:HG23	2:3B:326:THR:HG22	1.97	0.45
2:3O:137:VAL:O	2:3O:141:GLN:HG2	2.16	0.45
2:3B:94:GLY:HA3	2:3B:119:LEU:HD21	1.99	0.45
3:3C:186:PRO:HG2	13:3C:501:HEM:HMC3	1.98	0.45
3:3C:277:ALA:HB1	3:3C:294:LEU:CD1	2.46	0.45
5:3E:154:ILE:HA	5:3E:271:VAL:O	2.17	0.45
1:3N:77:LYS:HE3	1:3N:77:LYS:HB2	1.63	0.45
1:3N:114:ALA:O	1:3N:118:GLN:HB2	2.15	0.45
2:3O:193:TYR:O	2:3O:197:ASN:HB2	2.16	0.45
2:3O:299:VAL:HG11	2:3O:336:VAL:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3P:18:PHE:CE1	14:3P:503:U10:H72	2.51	0.45
6:3S:35:ASP:OD2	6:3S:61:ARG:NH1	2.49	0.45
6:3S:43:VAL:O	6:3S:47:ILE:HD12	2.16	0.45
6:3S:84:GLU:OE1	6:3S:84:GLU:N	2.40	0.45
2:3B:131:GLU:OE1	2:3B:133:ARG:NH1	2.49	0.45
2:3B:278:VAL:HG11	2:3B:352:LEU:HD11	1.98	0.45
5:3E:268:ASP:O	5:3E:270:LEU:HG	2.16	0.45
1:3N:283:THR:HA	2:3O:143:GLN:NE2	2.32	0.45
11:3P:506:CDL:H312	11:3Q:502:CDL:H731	1.99	0.45
4:3Q:130:LEU:HA	4:3Q:150:ASN:HD21	1.80	0.45
5:3R:132:ALA:O	5:3R:135:GLN:HB2	2.17	0.45
5:3R:164:ASN:HD22	5:3R:175:PHE:HB3	1.82	0.45
3:3C:277:ALA:HB1	3:3C:294:LEU:HD11	1.99	0.45
4:3D:208:ARG:HA	4:3D:208:ARG:HD3	1.65	0.45
8:3H:63:GLU:OE2	8:3H:63:GLU:HA	2.16	0.45
1:3N:209:LEU:HD23	1:3N:209:LEU:HA	1.70	0.45
1:3N:220:SER:OG	1:3N:222:THR:HG22	2.17	0.45
5:3R:219:HIS:ND1	5:3R:239:HIS:ND1	2.59	0.45
2:3B:303:VAL:HG22	2:3B:305:GLN:H	1.82	0.45
2:3B:359:ALA:O	2:3B:363:LYS:HG3	2.16	0.45
3:3C:302:ILE:O	3:3C:305:PRO:HD2	2.17	0.45
3:3C:329:VAL:HG22	12:3C:506:3PE:H2E1	1.99	0.45
12:3C:507:3PE:H281	10:3X:35:ALA:HB1	1.97	0.45
5:3E:179:ARG:NH1	5:3E:208:PRO:O	2.50	0.45
5:3E:233:GLY:H	5:3E:245:ALA:HA	1.82	0.45
1:3N:343:MET:HE1	1:3N:442:PHE:HA	1.99	0.45
2:3O:124:LEU:HB3	2:3O:223:PHE:HD2	1.81	0.45
4:3Q:79:GLU:O	4:3Q:80:MET:HE2	2.17	0.45
5:3R:92:ARG:HG2	5:3R:96:VAL:O	2.17	0.45
10:3X:18:ILE:HD13	10:3X:18:ILE:HA	1.83	0.45
1:3A:394:GLU:OE2	1:3A:398:ARG:NH1	2.44	0.45
2:3B:40:ASN:HD21	2:3B:209:LEU:HD21	1.81	0.45
2:3O:241:GLY:HA2	2:3O:423:SER:OG	2.17	0.45
5:3R:187:GLU:CD	5:3R:248:ARG:HH12	2.25	0.45
1:3N:40:TRP:CZ2	1:3N:377:GLU:HA	2.52	0.45
3:3P:54:HIS:HB2	3:3P:69:ILE:HG12	1.98	0.45
5:3R:249:ILE:H	5:3R:249:ILE:HG13	1.54	0.45
5:3E:176:VAL:HG12	5:3E:212:ILE:CD1	2.47	0.44
1:3N:77:LYS:O	1:3N:81:SER:OG	2.24	0.44
1:3N:149:VAL:HG21	1:3N:252:HIS:CB	2.47	0.44
5:3R:242:HIS:CB	5:3R:251:LYS:HB3	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:361:LEU:HD23	1:3A:399:ILE:HG12	1.99	0.44
3:3C:132:VAL:O	3:3C:139:SER:OG	2.32	0.44
3:3C:374:ASN:HB3	3:3C:379:TRP:O	2.17	0.44
5:3I:70:LEU:HD23	5:3I:71:ASN:HB3	1.98	0.44
4:3Q:37:CYS:SG	4:3Q:41:HIS:HB2	2.57	0.44
10:3X:6:LEU:HD12	10:3X:6:LEU:HA	1.79	0.44
1:3A:156:THR:HB	1:3A:241:ILE:HG13	1.99	0.44
1:3A:335:MET:HE2	1:3A:335:MET:HB2	1.84	0.44
6:3F:114:LYS:HE3	6:3F:114:LYS:HB2	1.77	0.44
5:3I:62:ARG:HB2	5:3I:77:ARG:HH12	1.82	0.44
1:3N:34:THR:HA	1:3N:102:LEU:HA	1.99	0.44
12:3N:502:3PE:H322	17:3R:302:PC1:H351	1.98	0.44
5:3R:207:LYS:HD3	5:3R:265:PHE:CE2	2.52	0.44
1:3A:159:GLN:O	1:3A:235:ARG:NH2	2.47	0.44
11:3A:501:CDL:HB61	12:3A:503:3PE:H242	2.00	0.44
9:3J:53:TRP:CD2	9:3J:57:LYS:HG2	2.44	0.44
1:3N:17:SER:OG	1:3N:205:HIS:NE2	2.46	0.44
1:3N:148:VAL:HG12	5:3R:80:HIS:ND1	2.32	0.44
14:3P:504:U10:O5	14:3P:504:U10:H4M2	2.17	0.44
4:3Q:33:TYR:HD1	4:3Q:37:CYS:HG	1.64	0.44
11:3Q:502:CDL:HB61	11:3Q:502:CDL:H711	1.81	0.44
2:3B:203:ARG:HD2	2:3B:230:LEU:O	2.17	0.44
3:3C:35:SER:HB3	14:3C:503:U10:H71	1.98	0.44
1:3N:344:ARG:HH12	1:3N:353:GLU:CD	2.26	0.44
3:3P:24:PRO:O	3:3P:224:TYR:OH	2.23	0.44
3:3P:70:CYS:SG	3:3P:80:ARG:NH1	2.90	0.44
3:3P:108:MET:HE2	3:3P:308:HIS:ND1	2.33	0.44
11:3P:506:CDL:HA32	11:3Q:502:CDL:HB4	2.00	0.44
4:3Q:160:MET:HE1	15:3Q:501:HEC:NB	2.33	0.44
2:3B:70:ARG:HD3	2:3B:100:SER:OG	2.18	0.44
3:3C:176:THR:OG1	3:3P:53:MET:O	2.36	0.44
5:3E:192:VAL:HB	5:3E:198:PRO:HB3	2.00	0.44
1:3N:346:CYS:SG	1:3N:411:CYS:HB3	2.57	0.44
2:3O:95:LYS:O	2:3O:109:VAL:HA	2.18	0.44
3:3P:160:LEU:HD23	3:3P:160:LEU:HA	1.83	0.44
3:3P:185:LEU:HD23	3:3P:185:LEU:HA	1.74	0.44
4:3Q:27:ARG:HH22	4:3Q:60:GLU:CD	2.24	0.44
4:3Q:210:MET:HE3	9:3W:35:PHE:CE1	2.53	0.44
1:3A:62:LEU:HD12	1:3A:130:GLU:HG2	2.00	0.44
5:3E:262:THR:O	5:3E:262:THR:OG1	2.30	0.44
1:3N:148:VAL:HG12	5:3R:80:HIS:CG	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3N:264:ASN:O	1:3N:266:ASP:N	2.51	0.44
2:3O:338:LYS:HB2	2:3O:338:LYS:HE3	1.76	0.44
3:3P:120:LEU:O	3:3P:124:MET:HG3	2.18	0.44
4:3Q:208:MET:O	4:3Q:212:MET:HG2	2.17	0.44
3:3C:141:TRP:CD1	3:3C:265:PRO:HD3	2.53	0.44
6:3F:33:TYR:HE1	6:3F:39:ASN:HB3	1.83	0.44
4:3Q:126:TYR:CZ	4:3Q:130:LEU:HD12	2.52	0.44
3:3P:75:TYR:CG	5:3R:135:GLN:OE1	2.71	0.44
1:3A:277:ILE:HB	1:3A:309:THR:HG21	1.99	0.43
2:3B:49:LEU:HD13	2:3B:206:LEU:HD13	2.00	0.43
3:3C:39:ILE:HG23	17:3E:302:PC1:H3F1	2.00	0.43
4:3D:272:ALA:O	4:3D:275:VAL:HG12	2.18	0.43
6:3F:30:LYS:NZ	6:3F:96:GLU:OE1	2.43	0.43
14:3P:504:U10:C13	14:3P:504:U10:H101	2.48	0.43
1:3A:317:THR:OG1	1:3A:318:GLY:N	2.50	0.43
3:3C:201:HIS:CD2	14:3C:503:U10:H4M1	2.53	0.43
14:3C:504:U10:H121	14:3C:504:U10:H101	1.81	0.43
5:3E:187:GLU:HG2	5:3E:246:SER:HB3	1.99	0.43
1:3N:188:GLN:HE22	1:3N:227:ALA:HB3	1.83	0.43
5:3R:222:CYS:HB2	16:3R:301:FES:S2	2.59	0.43
9:3W:8:ARG:HD2	9:3W:8:ARG:N	2.33	0.43
2:3B:407:ASP:N	2:3B:407:ASP:OD1	2.49	0.43
5:3R:141:SER:OG	5:3R:142:ALA:N	2.49	0.43
7:3T:32:LYS:HE3	7:3T:32:LYS:HB2	1.85	0.43
7:3T:44:CYS:O	7:3T:48:VAL:HG12	2.18	0.43
1:3A:141:ASN:HA	5:3I:47:ARG:NH1	2.33	0.43
3:3C:97:HIS:CE1	3:3C:100:ARG:HH22	2.37	0.43
6:3F:94:LYS:H	6:3F:94:LYS:HG2	1.57	0.43
1:3N:170:PRO:C	1:3N:172:GLU:H	2.26	0.43
1:3N:398:ARG:O	1:3N:401:GLU:HG2	2.18	0.43
2:3O:301:LYS:HB2	2:3O:301:LYS:HE2	1.83	0.43
11:3P:506:CDL:H121	11:3Q:502:CDL:H521	1.99	0.43
5:3R:169:TRP:HD1	5:3R:174:LEU:HB2	1.82	0.43
5:3R:192:VAL:HG13	5:3R:193:SER:H	1.83	0.43
1:3A:41:ILE:HB	1:3A:95:THR:HB	2.00	0.43
1:3A:240:GLU:HA	1:3A:422:VAL:O	2.18	0.43
1:3A:244:ARG:CZ	1:3A:429:GLU:HB2	2.49	0.43
1:3A:420:PRO:O	1:3A:434:TYR:OH	2.31	0.43
2:3B:39:GLU:CD	2:3B:113:ARG:HH22	2.25	0.43
4:3D:115:ARG:NH2	9:3J:60:TYR:CE1	2.84	0.43
4:3D:122:LYS:O	4:3D:126:SER:OG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3I:57:GLY:O	5:3I:58:GLN:C	2.61	0.43
3:3P:107:TYR:HE2	3:3P:308:HIS:HB2	1.82	0.43
3:3P:130:GLY:HA2	3:3P:133:LEU:HD23	2.00	0.43
1:3A:19:LEU:HD23	1:3A:19:LEU:HA	1.82	0.43
1:3A:27:SER:HA	1:3A:199:ALA:O	2.18	0.43
2:3B:408:ALA:O	2:3B:411:ILE:HG22	2.18	0.43
5:3E:155:LYS:HZ3	5:3E:273:VAL:HG22	1.83	0.43
5:3E:242:HIS:O	5:3E:250:ARG:N	2.41	0.43
8:3H:52:ILE:HD13	8:3H:52:ILE:HA	1.85	0.43
5:3R:196:ARG:HH11	5:3R:249:ILE:HD13	1.82	0.43
9:3W:42:ILE:O	9:3W:46:ILE:HG13	2.18	0.43
1:3A:137:GLU:HA	1:3A:140:GLU:HG3	2.01	0.43
1:3A:239:SER:HB3	7:3G:19:SER:O	2.19	0.43
1:3A:430:GLN:O	1:3A:430:GLN:HG3	2.18	0.43
12:3A:502:3PE:H32	12:3A:502:3PE:H322	1.43	0.43
3:3C:133:LEU:HD21	3:3C:179:PHE:HA	2.01	0.43
1:3N:426:GLY:O	1:3N:428:ILE:HG13	2.18	0.43
2:3B:148:LYS:HE3	2:3B:152:PHE:HE2	1.83	0.43
8:3H:47:GLU:OE2	8:3H:47:GLU:N	2.47	0.43
2:3O:54:GLY:O	2:3O:194:TYR:OH	2.36	0.43
3:3P:104:TYR:O	3:3P:206:ASN:ND2	2.52	0.43
5:3R:235:TYR:CD1	5:3R:242:HIS:HD2	2.37	0.43
1:3A:240:GLU:HG2	7:3G:19:SER:HB3	1.99	0.43
2:3B:171:ALA:HB3	2:3B:237:ALA:HB2	2.00	0.43
3:3C:373:GLU:OE2	6:3F:32:TYR:OH	2.37	0.43
4:3D:121:TYR:HA	4:3D:125:CYS:SG	2.59	0.43
4:3D:249:MET:HG3	15:3D:501:HEC:NC	2.33	0.43
1:3N:106:LEU:CD2	1:3N:203:VAL:HG23	2.48	0.43
1:3N:328:ASN:OD1	1:3N:328:ASN:N	2.50	0.43
2:3B:217:LYS:HE3	2:3B:217:LYS:HB3	1.79	0.43
2:3B:315:SER:O	2:3B:315:SER:OG	2.31	0.43
3:3C:51:LEU:HD23	3:3C:51:LEU:HA	1.78	0.43
3:3C:71:ARG:HE	4:3D:203:TYR:HE1	1.67	0.43
5:3E:150:SER:O	5:3E:170:ARG:NH2	2.52	0.43
7:3G:55:VAL:O	7:3G:59:LEU:HG	2.19	0.43
12:3N:502:3PE:H2	12:3N:502:3PE:H221	1.52	0.43
1:3A:256:ALA:HB2	1:3A:310:PHE:CZ	2.53	0.42
11:3C:505:CDL:OB3	7:3G:42:ARG:HD2	2.19	0.42
4:3D:115:ARG:CD	9:3J:60:TYR:CZ	2.99	0.42
4:3D:135:ALA:HB2	4:3D:178:TYR:CD2	2.53	0.42
7:3G:67:GLU:HA	7:3G:70:LYS:NZ	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3O:87:ARG:HD3	2:3O:87:ARG:HA	1.78	0.42
3:3P:24:PRO:HB2	3:3P:27:ILE:HG23	2.00	0.42
3:3P:338:ILE:HD13	3:3P:338:ILE:HA	1.83	0.42
4:3Q:120:ARG:HD3	4:3Q:120:ARG:HA	1.67	0.42
6:3S:39:GLU:OE1	6:3S:39:GLU:N	2.48	0.42
2:3B:51:ILE:HG21	2:3B:199:PHE:CD1	2.54	0.42
8:3H:64:LEU:O	8:3H:68:ARG:HG3	2.18	0.42
3:3P:327:MET:HE3	3:3P:327:MET:HB2	1.88	0.42
1:3A:313:CYS:HA	1:3A:318:GLY:HA3	2.00	0.42
2:3B:124:LEU:HD13	2:3B:124:LEU:HA	1.84	0.42
2:3B:227:ARG:CD	2:3B:229:GLY:H	2.32	0.42
3:3C:112:THR:HG22	3:3C:199:PHE:HB3	2.01	0.42
6:3F:83:ARG:HG3	6:3F:85:GLN:HB2	2.01	0.42
1:3N:136:GLN:O	1:3N:140:GLU:HG3	2.19	0.42
4:3Q:180:SER:OG	8:3U:77:LEU:HD11	2.19	0.42
1:3A:294:LEU:HD12	1:3A:307:PHE:CZ	2.54	0.42
3:3C:180:ALA:O	3:3C:184:ILE:HG22	2.20	0.42
1:3N:86:LEU:HD13	1:3N:99:ILE:HG13	2.02	0.42
1:3N:154:HIS:NE2	1:3N:314:TYR:OH	2.52	0.42
3:3P:373:GLU:OE1	6:3S:20:TYR:CZ	2.72	0.42
10:3X:38:TRP:CD1	17:3X:101:PC1:H32	2.54	0.42
1:3N:149:VAL:HG21	1:3N:252:HIS:HB2	2.00	0.42
4:3Q:200:HIS:NE2	12:3Q:503:3PE:O14	2.44	0.42
3:3C:26:ASN:HA	6:3F:82:MET:HB2	2.00	0.42
3:3C:348:ILE:HG22	3:3C:352:GLN:OE1	2.18	0.42
2:3O:216:LEU:HD12	2:3O:216:LEU:HA	1.89	0.42
3:3P:146:ILE:O	3:3P:149:LEU:HB2	2.19	0.42
4:3Q:216:LEU:HD23	4:3Q:216:LEU:HA	1.87	0.42
1:3A:65:LYS:HA	1:3A:65:LYS:HD3	1.73	0.42
1:3A:130:GLU:O	1:3A:134:ILE:HD13	2.20	0.42
3:3C:77:TRP:CZ3	4:3D:290:ARG:HG3	2.55	0.42
3:3C:177:ARG:HH21	5:3R:140:MET:HG3	1.85	0.42
13:3C:502:HEM:HBA1	14:3C:503:U10:C2	2.49	0.42
5:3E:95:GLU:OE1	5:3E:95:GLU:N	2.42	0.42
5:3E:194:GLN:HE22	5:3E:250:ARG:HA	1.83	0.42
5:3I:35:PRO:O	5:3I:36:ALA:C	2.62	0.42
3:3P:132:VAL:HA	3:3P:139:SER:OG	2.20	0.42
5:3R:251:LYS:HZ2	5:3R:251:LYS:HG3	1.69	0.42
9:3W:32:GLU:OE2	10:3X:34:TRP:NE1	2.45	0.42
5:3E:231:PHE:CD1	5:3E:231:PHE:N	2.87	0.42
5:3E:231:PHE:N	5:3E:231:PHE:HD1	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3E:239:HIS:O	5:3E:241:SER:N	2.53	0.42
5:3R:131:ASN:O	5:3R:135:GLN:HG2	2.20	0.42
1:3A:76:GLU:CD	2:3B:289:SER:H	2.28	0.42
2:3B:378:PHE:O	2:3B:382:VAL:HG23	2.20	0.42
6:3F:45:ARG:CZ	6:3F:100:PHE:HE1	2.32	0.42
1:3N:100:LYS:HB3	1:3N:100:LYS:HZ2	1.84	0.42
2:3O:217:LYS:O	2:3O:221:GLU:HG3	2.19	0.42
3:3P:18:PHE:HE1	14:3P:503:U10:H72	1.85	0.42
3:3P:89:MET:HE2	3:3P:89:MET:HB2	1.74	0.42
5:3R:150:SER:HB2	5:3R:169:TRP:CE3	2.54	0.42
1:3A:161:THR:HG21	1:3A:235:ARG:H	1.85	0.42
3:3C:218:ILE:HD12	3:3C:223:TYR:CD2	2.55	0.42
3:3C:274:PHE:HB3	14:3C:504:U10:H3M3	2.02	0.42
1:3N:67:THR:OG1	1:3N:70:ARG:N	2.51	0.42
1:3N:129:LYS:NZ	1:3N:129:LYS:HB3	2.34	0.42
1:3N:223:TYR:CD2	1:3N:229:PRO:HD2	2.55	0.42
3:3C:330:ALA:O	3:3C:334:THR:OG1	2.34	0.41
4:3D:218:LEU:HD21	15:3D:501:HEC:HBA1	2.02	0.41
4:3D:244:GLY:C	4:3D:245:GLN:OE1	2.63	0.41
5:3E:187:GLU:HB3	5:3E:201:ASP:HB2	2.02	0.41
5:3E:224:PRO:HA	5:3E:236:CYS:HA	2.02	0.41
1:3N:40:TRP:NE1	1:3N:89:TYR:OH	2.45	0.41
2:3O:340:ALA:O	2:3O:343:GLN:HB3	2.20	0.41
3:3P:370:SER:O	3:3P:373:GLU:HB2	2.19	0.41
11:3P:506:CDL:H111	11:3Q:502:CDL:H132	2.02	0.41
4:3Q:211:MET:HG3	4:3Q:215:LEU:HD12	2.02	0.41
5:3R:170:ARG:HD2	5:3R:172:LYS:NZ	2.35	0.41
5:3R:250:ARG:O	5:3R:250:ARG:HG2	2.19	0.41
2:3B:61:ASN:OD1	2:3B:61:ASN:N	2.53	0.41
5:3E:176:VAL:HG12	5:3E:212:ILE:HD13	2.02	0.41
5:3I:32:ALA:O	5:3I:34:LEU:N	2.52	0.41
1:3N:76:GLU:HG3	2:3O:285:VAL:HG21	2.01	0.41
1:3N:307:PHE:HB2	1:3N:324:PHE:HB3	2.02	0.41
1:3N:334:MET:HE2	1:3N:334:MET:HB3	1.81	0.41
2:3O:46:ARG:HH21	2:3O:108:THR:HG21	1.84	0.41
2:3O:209:LEU:HD23	2:3O:209:LEU:HA	1.88	0.41
5:3R:183:GLU:OE2	5:3R:245:ALA:HB3	2.20	0.41
11:3A:501:CDL:H511	11:3A:501:CDL:H141	2.02	0.41
12:3A:502:3PE:H2	12:3A:502:3PE:H222	1.47	0.41
11:3C:505:CDL:OB5	11:3C:505:CDL:O1	2.35	0.41
1:3N:145:MET:SD	1:3N:252:HIS:CD2	3.14	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:3P:506:CDL:CA6	11:3P:506:CDL:H522	2.50	0.41
5:3R:150:SER:HB3	5:3R:170:ARG:HG3	2.02	0.41
5:3R:156:LEU:HD22	5:3R:210:TRP:CG	2.55	0.41
5:3R:230:ASP:N	5:3R:242:HIS:NE2	2.62	0.41
1:3A:45:SER:OG	1:3A:92:ARG:HG2	2.20	0.41
1:3N:122:LEU:HD23	1:3N:122:LEU:HA	1.89	0.41
2:3O:318:ASP:OD1	2:3O:318:ASP:N	2.43	0.41
3:3P:77:TRP:CD2	4:3Q:197:GLU:HG3	2.56	0.41
4:3Q:166:ASN:C	4:3Q:167:GLU:HG3	2.46	0.41
5:3R:101:LYS:HD2	5:3R:104:LYS:N	2.34	0.41
5:3R:234:TYR:N	5:3R:243:TYR:O	2.53	0.41
1:3A:332:ASP:H	1:3A:430:GLN:HG2	1.85	0.41
3:3C:213:SER:O	3:3C:217:LYS:HG2	2.21	0.41
4:3D:185:ASN:OD1	4:3D:188:ALA:N	2.39	0.41
1:3N:62:LEU:HA	1:3N:65:LYS:HG2	2.03	0.41
2:3O:25:GLU:OE1	2:3O:25:GLU:N	2.48	0.41
2:3O:137:VAL:HG12	2:3O:141:GLN:HE21	1.85	0.41
4:3Q:195:GLU:OE2	4:3Q:201:ARG:NE	2.53	0.41
5:3R:104:LYS:HD2	5:3R:104:LYS:HA	1.71	0.41
14:3C:504:U10:O2	14:3C:504:U10:C3M	2.68	0.41
4:3D:297:MET:HA	12:3D:502:3PE:H321	2.03	0.41
5:3E:225:ILE:HD11	4:3Q:144:ARG:NH1	2.36	0.41
5:3I:47:ARG:O	5:3I:49:PHE:CE2	2.74	0.41
1:3N:343:MET:HB3	1:3N:343:MET:HE3	1.89	0.41
3:3P:58:ASP:OD1	3:3P:60:THR:HG22	2.21	0.41
5:3R:218:THR:HG23	5:3R:258:LEU:HD22	2.02	0.41
2:3B:117:GLU:CD	2:3B:118:ILE:HG13	2.45	0.41
2:3B:170:ASN:OD1	2:3B:170:ASN:N	2.54	0.41
3:3C:137:GLN:HB3	3:3C:265:PRO:HG3	2.02	0.41
4:3D:305:LEU:HD23	4:3D:305:LEU:HA	1.83	0.41
5:3E:249:ILE:HG12	5:3E:254:ALA:HB3	2.02	0.41
2:3O:33:LEU:HD23	2:3O:33:LEU:HA	1.82	0.41
2:3O:59:ASP:N	2:3O:62:ASN:OD1	2.54	0.41
3:3P:299:LEU:HD12	3:3P:299:LEU:HA	1.89	0.41
6:3S:109:LYS:H	6:3S:109:LYS:HG3	1.75	0.41
2:3B:380:ASP:OD1	2:3B:380:ASP:N	2.51	0.41
3:3C:282:ARG:HD3	3:3C:343:VAL:CG2	2.46	0.41
5:3E:207:LYS:HA	5:3E:207:LYS:HD2	1.82	0.41
5:3I:55:LEU:HA	5:3I:58:GLN:OE1	2.20	0.41
9:3J:17:ARG:HB2	9:3J:20:THR:OG1	2.20	0.41
1:3N:358:LYS:O	1:3N:362:ARG:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:3Q:503:3PE:H12	5:3R:131:ASN:ND2	2.36	0.41
6:3S:98:ILE:O	6:3S:102:LYS:HG2	2.21	0.41
9:3W:5:LEU:HD23	9:3W:5:LEU:HA	1.88	0.41
1:3A:77:LYS:HB2	1:3A:77:LYS:HE3	1.67	0.41
2:3B:24:LEU:HD23	2:3B:392:TYR:CD2	2.56	0.41
3:3C:42:ILE:HD13	3:3C:42:ILE:HA	1.91	0.41
3:3C:81:TYR:O	3:3C:85:ASN:ND2	2.37	0.41
4:3D:218:LEU:HD12	4:3D:238:ASN:OD1	2.21	0.41
5:3E:231:PHE:HB3	5:3E:250:ARG:NH1	2.36	0.41
6:3F:61:ARG:HD3	2:3O:135:TRP:CE2	2.56	0.41
6:3F:90:GLU:CD	6:3F:90:GLU:N	2.78	0.41
7:3G:36:ILE:HA	7:3G:36:ILE:HD13	1.80	0.41
1:3N:4:TYR:H	2:3O:114:ASP:CG	2.29	0.41
1:3N:106:LEU:HB3	1:3N:107:PRO:HD3	2.03	0.41
3:3P:311:LYS:H	3:3P:374:ASN:HD21	1.69	0.41
11:3P:506:CDL:HA32	11:3Q:502:CDL:OB7	2.20	0.41
4:3Q:68:VAL:HG21	4:3Q:92:PRO:HG2	2.03	0.41
5:3R:97:LEU:HD12	5:3R:97:LEU:HA	1.91	0.41
7:3T:46:LEU:HD23	7:3T:46:LEU:HA	1.76	0.41
10:3X:42:LEU:HD23	10:3X:42:LEU:HA	1.88	0.41
10:3Y:23:MET:HE3	10:3Y:23:MET:HB2	1.78	0.41
2:3B:78:LYS:HE2	2:3B:78:LYS:HB2	1.59	0.41
3:3C:246:SER:O	3:3C:246:SER:OG	2.21	0.41
3:3C:304:MET:HE2	3:3C:304:MET:HB2	1.96	0.41
4:3D:96:PRO:O	4:3D:213:ASP:HB3	2.20	0.41
4:3D:111:HIS:CE1	4:3D:142:VAL:HG23	2.57	0.41
1:3N:258:GLU:CD	5:3R:101:LYS:HZ1	2.27	0.41
1:3N:444:LEU:HD13	12:3N:502:3PE:H122	2.03	0.41
2:3O:163:LEU:HD11	2:3O:258:VAL:HG22	2.02	0.41
5:3R:82:ASP:OD1	5:3R:82:ASP:N	2.54	0.41
9:3W:29:LEU:CD1	10:3X:34:TRP:HB2	2.51	0.41
1:3A:270:LEU:HD22	1:3A:320:LEU:HD21	2.03	0.40
2:3B:154:ASN:ND2	5:3I:78:TYR:OH	2.36	0.40
3:3C:191:ALA:O	3:3C:195:VAL:HG23	2.21	0.40
6:3F:99:LYS:HD3	6:3F:99:LYS:HA	1.75	0.40
1:3N:225:GLU:HG2	1:3N:226:ASP:N	2.35	0.40
1:3N:240:GLU:HA	1:3N:422:VAL:O	2.21	0.40
2:3O:219:VAL:HA	2:3O:222:ARG:NH1	2.37	0.40
2:3O:324:ILE:HD11	2:3O:344:VAL:HG21	2.03	0.40
3:3P:34:GLY:C	13:3P:502:HEM:HMA3	2.46	0.40
5:3R:200:HIS:O	5:3R:204:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:8:LEU:HD22	1:3A:392:LEU:HB3	2.03	0.40
2:3B:199:PHE:O	2:3B:226:MET:HG2	2.21	0.40
4:3D:270:GLN:O	4:3D:274:ASP:OD1	2.39	0.40
5:3E:127:TYR:CE1	9:3J:33:GLU:HG3	2.56	0.40
2:3O:295:LEU:HD13	2:3O:309:VAL:HG22	2.03	0.40
3:3P:81:TYR:O	3:3P:85:ASN:ND2	2.48	0.40
3:3P:233:LEU:HD12	3:3P:233:LEU:HA	1.80	0.40
6:3S:50:LEU:HD23	6:3S:50:LEU:HA	1.91	0.40
10:3Y:32:LEU:HA	10:3Y:32:LEU:HD12	1.80	0.40
2:3B:75:LEU:HD23	2:3B:75:LEU:HA	1.89	0.40
2:3B:96:LEU:HD12	2:3B:96:LEU:HA	1.83	0.40
2:3B:227:ARG:HD2	2:3B:227:ARG:O	2.21	0.40
5:3E:194:GLN:HE22	5:3E:250:ARG:HE	1.68	0.40
1:3N:355:VAL:HA	1:3N:358:LYS:HD3	2.03	0.40
2:3O:75:LEU:HD11	2:3O:140:LEU:HD12	2.04	0.40
2:3O:217:LYS:HE2	2:3O:217:LYS:HB2	1.60	0.40
11:3P:506:CDL:H522	11:3P:506:CDL:HA4	2.04	0.40
4:3Q:8:PRO:HG3	8:3U:66:ASP:HB3	2.04	0.40
4:3Q:130:LEU:O	4:3Q:150:ASN:ND2	2.54	0.40
5:3R:158:ASP:OD1	5:3R:159:ILE:HG23	2.21	0.40
9:3W:43:TYR:C	9:3W:43:TYR:CD1	3.00	0.40
3:3C:207:ASN:ND2	3:3C:213:SER:HB3	2.34	0.40
4:3D:248:ALA:HB3	15:3D:501:HEC:HBD2	2.04	0.40
4:3D:307:LEU:HD21	5:3E:120:THR:HG22	2.02	0.40
1:3N:223:TYR:CE2	1:3N:229:PRO:HD2	2.56	0.40
2:3O:98:VAL:HG12	2:3O:107:TYR:CD2	2.57	0.40
4:3Q:57:THR:HG22	4:3Q:60:GLU:HB2	2.04	0.40
5:3R:151:LYS:HE3	5:3R:272:ILE:HD11	2.02	0.40
5:3R:244:ASP:OD2	5:3R:250:ARG:HB2	2.22	0.40
1:3A:152:TYR:O	1:3A:156:THR:HG22	2.21	0.40
3:3C:17:ALA:HA	3:3C:201:HIS:CE1	2.57	0.40
3:3C:210:GLY:O	3:3C:313:ARG:HD2	2.22	0.40
5:3E:159:ILE:HD11	5:3E:163:LYS:O	2.21	0.40
5:3E:225:ILE:N	5:3E:235:TYR:O	2.52	0.40
2:3O:264:THR:HG22	2:3O:316:TYR:O	2.20	0.40
2:3O:387:LEU:HD23	2:3O:387:LEU:HA	1.75	0.40
17:3R:302:PC1:H281	9:3W:24:ILE:HG21	2.04	0.40
9:3W:5:LEU:O	9:3W:9:LEU:HD12	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3A	436/480 (91%)	410 (94%)	26 (6%)	0	100	100
1	3N	444/480 (92%)	412 (93%)	30 (7%)	2 (0%)	24	57
2	3B	414/453 (91%)	398 (96%)	16 (4%)	0	100	100
2	3O	413/453 (91%)	394 (95%)	19 (5%)	0	100	100
3	3C	377/379 (100%)	366 (97%)	10 (3%)	1 (0%)	36	67
3	3P	377/379 (100%)	359 (95%)	17 (4%)	1 (0%)	36	67
4	3D	235/325 (72%)	217 (92%)	18 (8%)	0	100	100
4	3Q	237/325 (73%)	219 (92%)	18 (8%)	0	100	100
5	3E	194/274 (71%)	172 (89%)	22 (11%)	0	100	100
5	3I	45/274 (16%)	37 (82%)	7 (16%)	1 (2%)	5	30
5	3R	194/274 (71%)	158 (81%)	32 (16%)	4 (2%)	5	31
5	3V	29/274 (11%)	28 (97%)	1 (3%)	0	100	100
6	3F	96/111 (86%)	95 (99%)	1 (1%)	0	100	100
6	3S	96/111 (86%)	96 (100%)	0	0	100	100
7	3G	72/82 (88%)	71 (99%)	1 (1%)	0	100	100
7	3T	72/82 (88%)	72 (100%)	0	0	100	100
8	3H	61/91 (67%)	55 (90%)	6 (10%)	0	100	100
8	3U	63/91 (69%)	58 (92%)	5 (8%)	0	100	100
9	3J	54/64 (84%)	51 (94%)	3 (6%)	0	100	100
9	3W	54/64 (84%)	52 (96%)	2 (4%)	0	100	100
10	3X	50/56 (89%)	47 (94%)	3 (6%)	0	100	100
10	3Y	49/56 (88%)	44 (90%)	5 (10%)	0	100	100
All	All	4062/5178 (78%)	3811 (94%)	242 (6%)	9 (0%)	44	74

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	3N	118	GLN
5	3R	94	ALA
5	3R	154	ILE
1	3N	224	VAL
3	3P	155	TYR
5	3R	161	GLU
5	3I	59	ALA
5	3R	196	ARG
3	3C	155	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	3A	367/397 (92%)	366 (100%)	1 (0%)	86	83
1	3N	372/397 (94%)	357 (96%)	15 (4%)	28	54
2	3B	328/355 (92%)	327 (100%)	1 (0%)	86	83
2	3O	327/355 (92%)	326 (100%)	1 (0%)	86	83
3	3C	332/332 (100%)	329 (99%)	3 (1%)	70	76
3	3P	332/332 (100%)	330 (99%)	2 (1%)	78	79
4	3D	202/258 (78%)	202 (100%)	0	100	100
4	3Q	204/258 (79%)	202 (99%)	2 (1%)	68	75
5	3E	166/225 (74%)	166 (100%)	0	100	100
5	3I	36/225 (16%)	32 (89%)	4 (11%)	6	25
5	3R	166/225 (74%)	163 (98%)	3 (2%)	51	69
5	3V	24/225 (11%)	23 (96%)	1 (4%)	26	52
6	3F	90/99 (91%)	89 (99%)	1 (1%)	65	74
6	3S	90/99 (91%)	90 (100%)	0	100	100
7	3G	67/73 (92%)	66 (98%)	1 (2%)	57	71
7	3T	67/73 (92%)	66 (98%)	1 (2%)	57	71
8	3H	62/85 (73%)	61 (98%)	1 (2%)	55	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	3U	62/85 (73%)	62 (100%)	0	100	100
9	3J	46/52 (88%)	46 (100%)	0	100	100
9	3W	46/52 (88%)	45 (98%)	1 (2%)	45	65
10	3X	42/46 (91%)	41 (98%)	1 (2%)	43	64
10	3Y	41/46 (89%)	40 (98%)	1 (2%)	43	64
All	All	3469/4294 (81%)	3429 (99%)	40 (1%)	63	73

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	3A	3	THR
2	3B	113	ARG
3	3C	18	PHE
3	3C	300	ILE
3	3C	343	VAL
6	3F	91	GLN
7	3G	55	VAL
8	3H	38	LEU
5	3I	34	LEU
5	3I	37	THR
5	3I	53	GLU
5	3I	58	GLN
1	3N	8	LEU
1	3N	9	GLN
1	3N	11	VAL
1	3N	28	GLU
1	3N	112	LEU
1	3N	116	ILE
1	3N	117	VAL
1	3N	132	ASP
1	3N	134	ILE
1	3N	181	ASP
1	3N	207[A]	GLN
1	3N	207[B]	GLN
1	3N	209	LEU
1	3N	244	ARG
1	3N	320	LEU
2	3O	183	ILE
3	3P	269	LYS
3	3P	316	MET

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Mol	Chain	Res	Type
4	3Q	75	ASN
4	3Q	231	LYS
5	3R	140	MET
5	3R	165	MET
5	3R	169	TRP
7	3T	6	HIS
5	3V	68	VAL
9	3W	9	LEU
10	3X	18	ILE
10	3Y	16	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	3A	21	ASN
1	3A	126	GLN
1	3A	189	HIS
1	3A	252	HIS
1	3A	271	GLN
1	3A	328	ASN
2	3B	158	GLN
2	3B	162	ASN
2	3B	297	GLN
3	3C	3	ASN
3	3C	16	ASN
3	3C	44	GLN
3	3C	114	ASN
3	3C	196	HIS
3	3C	201	HIS
3	3C	341	GLN
4	3D	194	ASN
4	3D	289	HIS
5	3E	131	ASN
5	3E	194	GLN
5	3E	239	HIS
5	3E	242	HIS
8	3H	51	GLN
9	3J	55	HIS
1	3N	9	GLN
1	3N	85	HIS
1	3N	118	GLN
1	3N	136	GLN

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Mol	Chain	Res	Type
1	3N	264	ASN
1	3N	267	ASN
1	3N	271	GLN
1	3N	289	HIS
1	3N	430	GLN
2	3O	22	GLN
2	3O	343	GLN
2	3O	429	ASN
3	3P	68	HIS
3	3P	263	ASN
4	3Q	105	ASN
4	3Q	121	HIS
5	3R	219	HIS
6	3S	22	ASN
6	3S	79	GLN
8	3U	67	HIS
9	3W	45	HIS
10	3Y	49	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
12	3PE	3A	503	-	31,31,50	0.34	0	34,36,55	0.59	1 (2%)
12	3PE	3C	507	-	33,33,50	0.33	0	36,38,55	0.40	0
11	CDL	3P	506	-	55,55,99	0.35	0	61,67,111	0.49	1 (1%)
13	HEM	3P	501	3	50,50,50	1.64	10 (20%)	67,82,82	1.72	12 (17%)
17	PC1	3R	302	-	44,44,53	0.30	0	50,52,61	0.36	0
14	U10	3P	503	-	23,23,63	0.92	2 (8%)	30,31,79	1.28	5 (16%)
13	HEM	3C	501	3	50,50,50	1.64	9 (18%)	67,82,82	1.71	16 (23%)
12	3PE	3A	502	-	26,26,50	0.36	0	29,31,55	0.56	0
14	U10	3P	504	-	28,28,63	0.83	1 (3%)	36,37,79	1.15	5 (13%)
11	CDL	3A	501	-	57,57,99	0.34	0	63,69,111	0.43	0
16	FES	3E	301	5	0,4,4	-	-	-	-	-
12	3PE	3D	502	-	32,32,50	0.35	0	35,37,55	0.41	0
15	HEC	3D	501	4	48,49,50	2.89	26 (54%)	66,80,82	2.45	24 (36%)
12	3PE	3N	502	-	24,24,50	0.37	0	27,29,55	0.70	1 (3%)
12	3PE	3Q	503	-	46,46,50	0.29	0	49,51,55	0.37	0
12	3PE	3N	501	-	31,31,50	0.35	0	34,36,55	0.38	0
14	U10	3C	504	-	23,23,63	0.93	2 (8%)	30,31,79	1.27	5 (16%)
12	3PE	3P	505	-	32,32,50	0.35	0	35,37,55	0.40	0
17	PC1	3E	302	-	46,46,53	0.30	0	52,54,61	0.30	0
13	HEM	3C	502	-	50,50,50	1.63	9 (18%)	67,82,82	1.65	13 (19%)
11	CDL	3Q	502	-	56,56,99	0.35	0	62,68,111	0.47	0
12	3PE	3G	101	-	28,28,50	0.33	0	31,33,55	0.46	0
14	U10	3C	503	-	24,24,63	1.02	2 (8%)	30,32,79	1.30	6 (20%)
11	CDL	3G	102	-	55,55,99	0.36	0	61,67,111	0.50	0
11	CDL	3C	505	-	51,51,99	0.36	0	57,63,111	0.55	1 (1%)
12	3PE	3Y	101	-	29,29,50	0.36	0	32,34,55	0.42	0
11	CDL	3P	507	-	42,42,99	0.39	0	48,54,111	0.67	1 (2%)
17	PC1	3X	101	-	28,28,53	0.36	0	34,36,61	0.42	0
15	HEC	3Q	501	4	50,50,50	2.85	25 (50%)	68,82,82	2.44	27 (39%)
13	HEM	3P	502	3	50,50,50	1.63	9 (18%)	67,82,82	1.64	13 (19%)
16	FES	3R	301	5	0,4,4	-	-	-	-	-
12	3PE	3C	506	-	34,34,50	0.33	0	37,39,55	0.48	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
12	3PE	3A	503	-	-	7/35/35/54	-
12	3PE	3C	507	-	-	11/37/37/54	-
11	CDL	3P	506	-	-	13/66/66/110	-
13	HEM	3P	501	3	-	6/14/54/54	-
17	PC1	3R	302	-	-	6/48/48/57	-
14	U10	3P	503	-	-	6/15/39/87	0/1/1/1
13	HEM	3C	501	3	-	7/14/54/54	-
12	3PE	3A	502	-	-	4/30/30/54	-
14	U10	3P	504	-	-	4/21/45/87	0/1/1/1
11	CDL	3A	501	-	-	2/68/68/110	-
16	FES	3E	301	5	-	-	0/1/1/1
12	3PE	3D	502	-	-	2/36/36/54	-
15	HEC	3D	501	4	1/1/2/7	6/13/53/54	-
12	3PE	3N	502	-	-	5/28/28/54	-
12	3PE	3Q	503	-	-	5/50/50/54	-
12	3PE	3N	501	-	-	11/35/35/54	-
14	U10	3C	504	-	-	5/15/39/87	0/1/1/1
12	3PE	3P	505	-	-	8/36/36/54	-
17	PC1	3E	302	-	-	1/50/50/57	-
13	HEM	3C	502	-	-	6/14/54/54	-
11	CDL	3Q	502	-	-	17/67/67/110	-
12	3PE	3G	101	-	-	1/32/32/54	-
14	U10	3C	503	-	-	2/17/41/87	0/1/1/1
11	CDL	3G	102	-	-	10/66/66/110	-
11	CDL	3C	505	-	-	14/62/62/110	-
12	3PE	3Y	101	-	-	5/33/33/54	-
11	CDL	3P	507	-	-	10/53/53/110	-
17	PC1	3X	101	-	-	6/32/32/57	-
15	HEC	3Q	501	4	1/1/3/7	9/14/54/54	-
13	HEM	3P	502	3	-	8/14/54/54	-
16	FES	3R	301	5	-	-	0/1/1/1
12	3PE	3C	506	-	-	9/38/38/54	-

All (95) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	3Q	501	HEC	C2A-C3A	5.20	1.48	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	3Q	501	HEC	C3B-C2B	5.13	1.47	1.36
13	3C	501	HEM	FE-NB	5.05	2.10	1.94
15	3D	501	HEC	C3B-C2B	5.03	1.47	1.36
13	3P	501	HEM	FE-NB	4.98	2.10	1.94
13	3P	502	HEM	FE-NB	4.96	2.10	1.94
13	3C	502	HEM	FE-NB	4.95	2.10	1.94
15	3Q	501	HEC	CHB-C4A	4.91	1.48	1.38
15	3D	501	HEC	CHC-C4B	4.84	1.48	1.38
15	3D	501	HEC	C3D-C2D	4.81	1.47	1.36
15	3Q	501	HEC	FE-NB	4.80	2.09	1.94
15	3D	501	HEC	C2A-C3A	4.80	1.47	1.36
15	3D	501	HEC	FE-ND	4.80	2.09	1.94
15	3Q	501	HEC	FE-ND	4.75	2.09	1.94
15	3D	501	HEC	CHA-C1A	4.70	1.47	1.38
15	3D	501	HEC	CHB-C4A	4.69	1.47	1.38
15	3Q	501	HEC	C3D-C2D	4.66	1.46	1.36
15	3Q	501	HEC	CHA-C1A	4.65	1.47	1.38
15	3D	501	HEC	FE-NB	4.64	2.09	1.94
15	3D	501	HEC	CHD-C1D	4.61	1.47	1.38
15	3Q	501	HEC	CHC-C4B	4.57	1.47	1.38
15	3Q	501	HEC	CHD-C1D	4.54	1.47	1.38
15	3Q	501	HEC	FE-NA	4.38	2.09	1.95
15	3D	501	HEC	FE-NC	4.36	2.09	1.95
15	3D	501	HEC	FE-NA	4.34	2.09	1.95
15	3Q	501	HEC	FE-NC	4.33	2.09	1.95
13	3P	502	HEM	FE-NC	4.02	2.08	1.95
13	3C	501	HEM	FE-NC	4.00	2.08	1.95
13	3C	502	HEM	FE-NC	3.93	2.08	1.95
13	3P	501	HEM	FE-NC	3.83	2.07	1.95
15	3Q	501	HEC	CHB-C1B	3.79	1.47	1.39
15	3D	501	HEC	CHC-C1C	3.77	1.47	1.39
13	3C	502	HEM	C1B-NB	-3.70	1.33	1.40
15	3D	501	HEC	CHD-C4C	3.70	1.47	1.39
13	3C	502	HEM	C4D-ND	-3.67	1.33	1.40
15	3D	501	HEC	CHB-C1B	3.65	1.47	1.39
15	3Q	501	HEC	CHA-C4D	3.64	1.47	1.39
13	3P	501	HEM	C1B-NB	-3.63	1.34	1.40
13	3P	502	HEM	C1B-NB	-3.61	1.34	1.40
15	3Q	501	HEC	CHC-C1C	3.61	1.47	1.39
13	3P	501	HEM	C4D-ND	-3.61	1.34	1.40
13	3C	501	HEM	C1B-NB	-3.59	1.34	1.40
15	3D	501	HEC	CHA-C4D	3.59	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	3P	502	HEM	C4D-ND	-3.56	1.34	1.40
15	3Q	501	HEC	CHD-C4C	3.52	1.47	1.39
13	3C	501	HEM	C4D-ND	-3.51	1.34	1.40
15	3D	501	HEC	C3C-C2C	3.37	1.47	1.38
15	3D	501	HEC	C1D-ND	-3.30	1.34	1.40
15	3Q	501	HEC	C1D-ND	-3.30	1.34	1.40
15	3D	501	HEC	C4B-NB	-3.27	1.34	1.40
15	3Q	501	HEC	C4B-NB	-3.25	1.34	1.40
15	3Q	501	HEC	C3C-C2C	3.25	1.47	1.38
14	3P	504	U10	C3-C2	-2.93	1.40	1.48
14	3C	503	U10	C3-C2	-2.82	1.40	1.48
13	3P	501	HEM	FE-ND	-2.77	1.86	1.94
15	3Q	501	HEC	C4C-NC	-2.76	1.34	1.39
13	3C	501	HEM	FE-ND	-2.73	1.86	1.94
13	3P	502	HEM	FE-ND	-2.71	1.86	1.94
13	3C	502	HEM	FE-ND	-2.68	1.86	1.94
13	3P	501	HEM	C3C-C4C	-2.68	1.41	1.46
15	3D	501	HEC	C4A-NA	-2.66	1.34	1.39
15	3Q	501	HEC	C4A-NA	-2.63	1.34	1.39
13	3C	501	HEM	C1C-C2C	-2.62	1.40	1.45
15	3D	501	HEC	C4C-NC	-2.62	1.34	1.39
13	3P	502	HEM	C1C-C2C	-2.61	1.40	1.45
14	3C	504	U10	C4-C5	-2.61	1.41	1.48
13	3C	502	HEM	C1C-C2C	-2.61	1.40	1.45
15	3Q	501	HEC	C1A-NA	-2.61	1.34	1.39
15	3D	501	HEC	C1C-C2C	2.59	1.49	1.43
13	3P	501	HEM	C1C-C2C	-2.59	1.40	1.45
14	3P	503	U10	C4-C5	-2.57	1.41	1.48
15	3D	501	HEC	C1A-NA	-2.50	1.34	1.39
15	3Q	501	HEC	C1C-C2C	2.47	1.48	1.43
14	3C	503	U10	C4-C5	-2.46	1.41	1.48
15	3Q	501	HEC	C1C-NC	-2.42	1.35	1.39
13	3C	501	HEM	C1D-ND	-2.40	1.34	1.38
13	3C	502	HEM	C1D-ND	-2.40	1.34	1.38
15	3D	501	HEC	C1C-NC	-2.40	1.35	1.39
13	3P	502	HEM	C1D-ND	-2.40	1.34	1.38
13	3C	501	HEM	C3C-C4C	-2.38	1.41	1.46
13	3P	501	HEM	C1D-ND	-2.35	1.34	1.38
13	3P	502	HEM	C4B-NB	-2.32	1.34	1.38
13	3P	502	HEM	C3C-C4C	-2.31	1.42	1.46
13	3C	502	HEM	C3C-C4C	-2.28	1.42	1.46
13	3C	502	HEM	C4B-NB	-2.27	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	3C	501	HEM	C4B-NB	-2.20	1.34	1.38
13	3P	501	HEM	C4B-NB	-2.18	1.34	1.38
14	3P	503	U10	C4-C3	2.08	1.43	1.36
14	3C	504	U10	C4-C3	2.07	1.43	1.36
15	3Q	501	HEC	C1B-C2B	2.07	1.48	1.44
15	3D	501	HEC	C4D-ND	-2.06	1.34	1.38
15	3Q	501	HEC	C4D-C3D	2.06	1.48	1.45
13	3P	501	HEM	C1A-C2A	-2.04	1.40	1.44
15	3D	501	HEC	C4B-C3B	2.03	1.48	1.45
15	3D	501	HEC	C4D-C3D	2.01	1.48	1.45

All (131) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	3D	501	HEC	C1B-C2B-C3B	-5.93	100.74	106.98
15	3Q	501	HEC	C2A-C1A-NA	5.57	115.70	110.32
15	3Q	501	HEC	C1B-C2B-C3B	-5.55	101.14	106.98
13	3P	501	HEM	CHC-C4B-NB	5.39	130.22	124.42
13	3C	501	HEM	CHC-C4B-NB	5.32	130.14	124.42
15	3D	501	HEC	C2B-C1B-NB	5.31	116.04	109.90
15	3Q	501	HEC	C1C-C2C-C3C	-5.27	100.79	106.82
13	3C	502	HEM	CHC-C4B-NB	5.11	129.92	124.42
13	3P	502	HEM	CHC-C4B-NB	5.06	129.87	124.42
15	3D	501	HEC	C1C-C2C-C3C	-5.04	101.05	106.82
15	3Q	501	HEC	C3D-C4D-ND	4.99	115.18	110.35
13	3P	501	HEM	CHD-C1D-ND	4.98	129.78	124.42
15	3D	501	HEC	C2A-C1A-NA	4.97	115.12	110.32
15	3D	501	HEC	C3D-C4D-ND	4.92	115.11	110.35
15	3Q	501	HEC	C2B-C1B-NB	4.90	115.57	109.90
15	3D	501	HEC	CBC-CAC-C3C	4.85	125.57	112.42
13	3C	501	HEM	CHD-C1D-ND	4.66	129.44	124.42
15	3D	501	HEC	C2D-C1D-ND	4.66	115.19	109.84
15	3Q	501	HEC	C2D-C1D-ND	4.63	115.16	109.84
15	3Q	501	HEC	CBC-CAC-C3C	4.39	124.33	112.42
15	3D	501	HEC	CBB-CAB-C3B	4.35	124.21	112.42
15	3Q	501	HEC	CBB-CAB-C3B	4.30	124.08	112.42
13	3C	502	HEM	CHD-C1D-ND	4.15	128.89	124.42
13	3P	502	HEM	CHD-C1D-ND	4.14	128.88	124.42
15	3D	501	HEC	C1D-C2D-C3D	-4.01	102.77	106.98
15	3Q	501	HEC	C1D-C2D-C3D	-3.81	102.97	106.98
15	3Q	501	HEC	C1A-C2A-C3A	-3.73	102.19	107.11
15	3Q	501	HEC	C2C-C1C-NC	3.65	115.99	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	3C	501	HEM	CHB-C1B-NB	3.65	128.88	124.37
13	3P	502	HEM	CHA-C4D-ND	3.60	128.82	124.37
15	3Q	501	HEC	C3C-C4C-NC	3.56	114.11	110.15
15	3D	501	HEC	C3C-C4C-NC	3.50	114.03	110.15
13	3C	502	HEM	CHA-C4D-ND	3.48	128.67	124.37
13	3C	501	HEM	CHA-C4D-ND	3.45	128.63	124.37
15	3D	501	HEC	C1A-C2A-C3A	-3.42	102.60	107.11
13	3C	502	HEM	C1B-NB-C4B	3.41	109.24	105.21
15	3D	501	HEC	C2C-C1C-NC	3.40	115.60	110.14
13	3P	501	HEM	CHA-C4D-ND	3.40	128.58	124.37
15	3Q	501	HEC	C3B-C4B-NB	3.35	113.85	110.17
13	3P	502	HEM	C1B-NB-C4B	3.32	109.14	105.21
13	3P	501	HEM	CHD-C4C-NC	3.30	128.05	124.45
13	3P	501	HEM	CHB-C1B-NB	3.29	128.43	124.37
13	3P	502	HEM	CHB-C1B-NB	3.26	128.39	124.37
15	3D	501	HEC	CAC-C3C-C2C	3.24	132.01	126.89
13	3P	501	HEM	C1B-NB-C4B	3.21	109.01	105.21
13	3C	502	HEM	CHB-C1B-NB	3.13	128.23	124.37
13	3C	501	HEM	C1B-NB-C4B	3.08	108.85	105.21
13	3P	501	HEM	CHD-C1D-C2D	-3.05	120.21	125.03
13	3C	502	HEM	C3B-C4B-NB	-2.98	107.33	109.47
15	3Q	501	HEC	C4D-C3D-C2D	-2.96	102.58	106.89
14	3C	503	U10	O3-C3-C4	2.95	134.79	123.64
14	3P	503	U10	O4-C4-C5	-2.92	106.78	116.64
15	3Q	501	HEC	CMC-C2C-C3C	2.91	131.80	125.62
15	3Q	501	HEC	C3A-C4A-NA	2.91	115.01	109.64
15	3D	501	HEC	C3A-C4A-NA	2.90	115.00	109.64
15	3D	501	HEC	C4D-C3D-C2D	-2.89	102.68	106.89
15	3D	501	HEC	C3B-C4B-NB	2.88	113.33	110.17
13	3C	501	HEM	CHD-C4C-NC	2.83	127.54	124.45
14	3C	504	U10	O4-C4-C5	-2.83	107.10	116.64
14	3P	504	U10	C7-C6-C1	-2.79	120.11	124.89
13	3C	501	HEM	CHD-C1D-C2D	-2.77	120.65	125.03
15	3Q	501	HEC	C4A-C3A-C2A	-2.76	102.88	106.97
13	3C	502	HEM	C4A-CHB-C1B	-2.75	119.78	126.25
13	3P	502	HEM	C3B-C4B-NB	-2.75	107.49	109.47
14	3P	503	U10	O3-C3-C2	2.74	125.90	116.64
15	3Q	501	HEC	CAD-C3D-C4D	2.74	129.48	124.70
15	3D	501	HEC	C4A-C3A-C2A	-2.71	102.95	106.97
11	3P	507	CDL	OA6-CA5-C11	2.67	117.26	111.48
14	3C	504	U10	O3-C3-C2	2.66	125.60	116.64
15	3Q	501	HEC	CAC-C3C-C2C	2.60	131.00	126.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	3D	501	HEC	CMC-C2C-C3C	2.59	131.12	125.62
14	3C	503	U10	O4-C4-C3	2.59	133.44	123.64
14	3C	503	U10	O3-C3-C2	-2.57	107.97	116.64
12	3N	502	3PE	O21-C21-C22	2.55	117.00	111.48
13	3C	501	HEM	C3B-C4B-NB	-2.51	107.66	109.47
13	3P	501	HEM	C3B-C4B-NB	-2.50	107.67	109.47
13	3P	502	HEM	C4C-CHD-C1D	-2.50	120.71	126.02
15	3D	501	HEC	CAD-C3D-C4D	2.47	129.00	124.70
13	3P	502	HEM	CHD-C4C-NC	2.47	127.14	124.45
13	3C	502	HEM	CHD-C4C-NC	2.46	127.14	124.45
15	3D	501	HEC	CAA-CBA-CGA	-2.46	107.15	113.67
15	3Q	501	HEC	CAD-CBD-CGD	-2.44	107.18	113.67
13	3P	502	HEM	CHD-C1D-C2D	-2.44	121.17	125.03
14	3P	503	U10	O4-C4-C3	2.42	132.80	123.64
14	3P	504	U10	O3-C3-C2	-2.42	108.49	116.64
13	3C	502	HEM	C1A-CHA-C4D	-2.40	120.60	126.25
14	3C	504	U10	C7-C6-C1	-2.40	120.78	124.89
14	3P	504	U10	C3-C4-C5	-2.40	116.30	120.69
13	3P	502	HEM	C4A-CHB-C1B	-2.39	120.63	126.25
14	3C	503	U10	O4-C4-C5	-2.38	108.59	116.64
14	3C	504	U10	C4-C3-C2	-2.37	116.34	120.69
13	3C	502	HEM	CHD-C1D-C2D	-2.34	121.33	125.03
13	3P	501	HEM	CAD-CBD-CGD	-2.33	107.50	113.67
14	3C	503	U10	C4-C3-C2	-2.30	116.47	120.69
13	3C	502	HEM	C4C-CHD-C1D	-2.30	121.14	126.02
14	3P	503	U10	C4-C3-C2	-2.27	116.52	120.69
14	3P	504	U10	O4-C4-C5	2.27	124.30	116.64
13	3P	501	HEM	C4C-CHD-C1D	-2.26	121.22	126.02
15	3D	501	HEC	CMB-C2B-C3B	2.25	132.25	126.15
14	3P	504	U10	O3-C3-C4	2.24	132.13	123.64
15	3D	501	HEC	CHB-C1B-C2B	-2.24	121.50	125.03
15	3D	501	HEC	CMA-C3A-C4A	2.22	128.64	124.73
14	3C	504	U10	O4-C4-C3	2.21	132.01	123.64
13	3P	501	HEM	C1A-CHA-C4D	-2.20	121.07	126.25
15	3Q	501	HEC	CMB-C2B-C3B	2.19	132.08	126.15
13	3P	502	HEM	C1A-CHA-C4D	-2.18	121.11	126.25
15	3Q	501	HEC	CMD-C2D-C1D	2.17	128.43	125.03
15	3Q	501	HEC	CAB-C3B-C2B	2.17	131.55	127.56
14	3C	503	U10	C7-C6-C1	-2.16	121.19	124.89
13	3C	501	HEM	CHB-C1B-C2B	-2.14	120.85	126.95
15	3Q	501	HEC	CHB-C1B-NB	-2.14	122.12	124.42
15	3D	501	HEC	CMD-C2D-C1D	2.13	128.37	125.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	3Q	501	HEC	CHA-C1A-C2A	-2.13	121.51	124.86
13	3P	502	HEM	CHA-C4D-C3D	-2.12	121.32	125.23
14	3P	503	U10	C7-C6-C1	-2.11	121.27	124.89
13	3C	502	HEM	C4D-ND-C1D	2.11	107.70	105.21
13	3C	501	HEM	C1A-CHA-C4D	-2.11	121.30	126.25
13	3C	501	HEM	CHA-C1A-NA	2.10	127.67	123.86
11	3C	505	CDL	OA6-CA5-C11	2.10	116.02	111.48
13	3C	501	HEM	C4C-CHD-C1D	-2.09	121.58	126.02
13	3C	501	HEM	CHA-C4D-C3D	-2.08	121.39	125.23
13	3C	502	HEM	CHA-C4D-C3D	-2.08	121.40	125.23
15	3Q	501	HEC	CAA-CBA-CGA	-2.05	108.22	113.67
11	3P	506	CDL	OA6-CA5-C11	2.04	115.90	111.48
13	3P	501	HEM	C4A-CHB-C1B	-2.03	121.46	126.25
13	3C	501	HEM	O2D-CGD-CBD	2.03	120.42	114.00
12	3A	503	3PE	O21-C21-C22	2.03	115.87	111.48
13	3C	501	HEM	C4A-CHB-C1B	-2.01	121.51	126.25
15	3Q	501	HEC	CHB-C4A-NA	-2.01	122.26	124.45
13	3C	501	HEM	CAD-CBD-CGD	-2.01	108.33	113.67
13	3P	502	HEM	C4D-ND-C1D	2.01	107.59	105.21

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
15	3D	501	HEC	NA
15	3Q	501	HEC	NA

All (206) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	3C	505	CDL	OA7-CA5-OA6-CA4
11	3C	505	CDL	C11-CA5-OA6-CA4
11	3C	505	CDL	CB3-OB5-PB2-OB2
11	3C	505	CDL	CB3-OB5-PB2-OB4
11	3C	505	CDL	CB4-CB3-OB5-PB2
11	3G	102	CDL	CA3-OA5-PA1-OA3
11	3G	102	CDL	CA4-CA3-OA5-PA1
11	3G	102	CDL	OA7-CA5-OA6-CA4
11	3G	102	CDL	C11-CA5-OA6-CA4
11	3G	102	CDL	OA9-CA7-OA8-CA6
11	3G	102	CDL	C31-CA7-OA8-CA6
11	3P	506	CDL	C1-CA2-OA2-PA1
11	3P	506	CDL	CA2-OA2-PA1-OA3

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Mol	Chain	Res	Type	Atoms
11	3P	507	CDL	OA7-CA5-OA6-CA4
11	3P	507	CDL	C11-CA5-OA6-CA4
11	3P	507	CDL	CB3-OB5-PB2-OB2
11	3Q	502	CDL	CA2-OA2-PA1-OA4
11	3Q	502	CDL	CA2-OA2-PA1-OA5
11	3Q	502	CDL	CA3-OA5-PA1-OA3
11	3Q	502	CDL	OA6-CA4-CA6-OA8
11	3Q	502	CDL	CB3-OB5-PB2-OB3
11	3Q	502	CDL	OB9-CB7-OB8-CB6
11	3Q	502	CDL	C71-CB7-OB8-CB6
12	3A	502	3PE	O32-C31-O31-C3
12	3A	502	3PE	C32-C31-O31-C3
12	3A	502	3PE	O22-C21-O21-C2
12	3A	502	3PE	C22-C21-O21-C2
12	3A	503	3PE	C1-O11-P-O14
12	3A	503	3PE	O32-C31-O31-C3
12	3A	503	3PE	C32-C31-O31-C3
12	3A	503	3PE	O22-C21-O21-C2
12	3A	503	3PE	C22-C21-O21-C2
12	3C	506	3PE	C11-O13-P-O11
12	3C	506	3PE	C11-O13-P-O12
12	3C	507	3PE	C11-O13-P-O11
12	3C	507	3PE	C11-O13-P-O12
12	3C	507	3PE	C2-C1-O11-P
12	3C	507	3PE	C12-C11-O13-P
12	3N	502	3PE	C11-O13-P-O14
12	3N	502	3PE	O22-C21-O21-C2
12	3N	502	3PE	C22-C21-O21-C2
12	3P	505	3PE	C11-O13-P-O14
13	3C	501	HEM	C2B-C3B-CAB-CBB
13	3C	501	HEM	C4B-C3B-CAB-CBB
13	3C	502	HEM	C2B-C3B-CAB-CBB
13	3C	502	HEM	C2C-C3C-CAC-CBC
13	3P	501	HEM	C2B-C3B-CAB-CBB
13	3P	501	HEM	C4B-C3B-CAB-CBB
13	3P	502	HEM	C2B-C3B-CAB-CBB
13	3P	502	HEM	C2C-C3C-CAC-CBC
17	3R	302	PC1	C1-O11-P-O13
17	3X	101	PC1	C1-O11-P-O14
17	3X	101	PC1	C1-O11-P-O13
15	3D	501	HEC	C4C-C3C-CAC-CBC
15	3Q	501	HEC	C4C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
15	3D	501	HEC	C4B-C3B-CAB-CBB
15	3Q	501	HEC	C4B-C3B-CAB-CBB
15	3D	501	HEC	C2B-C3B-CAB-CBB
15	3Q	501	HEC	C2B-C3B-CAB-CBB
15	3D	501	HEC	C2C-C3C-CAC-CBC
15	3Q	501	HEC	C2C-C3C-CAC-CBC
14	3C	504	U10	C12-C11-C9-C10
14	3C	504	U10	C12-C11-C9-C8
15	3Q	501	HEC	C1A-C2A-CAA-CBA
14	3C	504	U10	C4-C3-O3-C3M
14	3P	503	U10	C4-C3-O3-C3M
14	3P	504	U10	C3-C4-O4-C4M
15	3Q	501	HEC	C3A-C2A-CAA-CBA
11	3C	505	CDL	O1-C1-CB2-OB2
12	3N	501	3PE	C2-C1-O11-P
14	3P	503	U10	C2-C3-O3-C3M
11	3G	102	CDL	C51-C52-C53-C54
12	3P	505	3PE	C33-C34-C35-C36
12	3N	501	3PE	C32-C33-C34-C35
11	3Q	502	CDL	CA7-C31-C32-C33
14	3C	504	U10	C2-C3-O3-C3M
11	3P	506	CDL	OB5-CB3-CB4-OB6
13	3C	502	HEM	C4B-C3B-CAB-CBB
13	3C	502	HEM	C4C-C3C-CAC-CBC
13	3P	502	HEM	C4B-C3B-CAB-CBB
13	3P	502	HEM	C4C-C3C-CAC-CBC
12	3P	505	3PE	C31-C32-C33-C34
12	3C	507	3PE	O21-C2-C3-O31
11	3Q	502	CDL	CA4-CA3-OA5-PA1
11	3Q	502	CDL	CB4-CB3-OB5-PB2
12	3Q	503	3PE	C38-C39-C3A-C3B
13	3C	501	HEM	C3D-CAD-CBD-CGD
12	3Y	101	3PE	C34-C35-C36-C37
11	3C	505	CDL	CA3-CA4-CA6-OA8
12	3C	507	3PE	C1-C2-C3-O31
12	3Y	101	3PE	C2-C1-O11-P
12	3P	505	3PE	O11-C1-C2-O21
12	3C	506	3PE	C25-C26-C27-C28
11	3A	501	CDL	C32-C33-C34-C35
11	3P	507	CDL	C1-CA2-OA2-PA1
11	3Q	502	CDL	C1-CB2-OB2-PB2
17	3R	302	PC1	C2-C1-O11-P

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Mol	Chain	Res	Type	Atoms
11	3P	506	CDL	OA5-CA3-CA4-CA6
11	3P	506	CDL	OB5-CB3-CB4-CB6
12	3P	505	3PE	O11-C1-C2-C3
17	3X	101	PC1	O21-C21-C22-C23
12	3C	507	3PE	O21-C21-C22-C23
11	3C	505	CDL	C52-C51-CB5-OB6
12	3C	507	3PE	C22-C23-C24-C25
11	3Q	502	CDL	CA3-CA4-CA6-OA8
12	3N	501	3PE	C1-C2-C3-O31
11	3P	506	CDL	OA5-CA3-CA4-OA6
12	3C	506	3PE	O11-C1-C2-O21
11	3C	505	CDL	C1-CB2-OB2-PB2
11	3P	506	CDL	C12-C11-CA5-OA6
13	3C	501	HEM	C2C-C3C-CAC-CBC
13	3P	501	HEM	C2C-C3C-CAC-CBC
12	3C	507	3PE	O11-C1-C2-O21
12	3C	506	3PE	C12-C11-O13-P
12	3D	502	3PE	C12-C11-O13-P
12	3N	501	3PE	C12-C11-O13-P
12	3N	502	3PE	C12-C11-O13-P
12	3P	505	3PE	C12-C11-O13-P
12	3Y	101	3PE	C12-C11-O13-P
11	3C	505	CDL	C52-C53-C54-C55
11	3A	501	CDL	C1-CB2-OB2-PB2
17	3R	302	PC1	C38-C39-C3A-C3B
11	3C	505	CDL	OA6-CA4-CA6-OA8
12	3N	501	3PE	O21-C2-C3-O31
12	3Y	101	3PE	O21-C2-C3-O31
11	3P	506	CDL	CB3-OB5-PB2-OB3
11	3P	507	CDL	CB3-OB5-PB2-OB3
11	3Q	502	CDL	CA3-OA5-PA1-OA2
11	3Q	502	CDL	CA3-OA5-PA1-OA4
12	3C	506	3PE	C1-O11-P-O14
12	3N	501	3PE	C11-O13-P-O14
17	3R	302	PC1	C1-O11-P-O14
11	3P	506	CDL	CA4-CA3-OA5-PA1
11	3P	507	CDL	CA4-CA3-OA5-PA1
12	3G	101	3PE	C31-C32-C33-C34
12	3C	507	3PE	O11-C1-C2-C3
12	3Q	503	3PE	C23-C24-C25-C26
17	3R	302	PC1	C32-C33-C34-C35
17	3X	101	PC1	O31-C31-C32-C33

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Mol	Chain	Res	Type	Atoms
12	3N	502	3PE	C31-C32-C33-C34
11	3P	506	CDL	C72-C71-CB7-OB8
12	3D	502	3PE	C31-C32-C33-C34
14	3P	503	U10	C12-C11-C9-C10
12	3P	505	3PE	O21-C2-C3-O31
14	3P	503	U10	C5-C4-O4-C4M
13	3C	501	HEM	CAA-CBA-CGA-O2A
12	3C	506	3PE	C1-C2-O21-C21
13	3C	501	HEM	CAA-CBA-CGA-O1A
14	3P	503	U10	C12-C11-C9-C8
11	3P	507	CDL	C72-C71-CB7-OB9
11	3P	507	CDL	C72-C71-CB7-OB8
11	3G	102	CDL	CB4-CB3-OB5-PB2
13	3C	502	HEM	CAA-CBA-CGA-O1A
12	3N	501	3PE	O11-C1-C2-C3
13	3P	502	HEM	CAD-CBD-CGD-O1D
14	3C	504	U10	C5-C4-O4-C4M
14	3P	504	U10	C5-C4-O4-C4M
17	3R	302	PC1	C36-C37-C38-C39
13	3P	501	HEM	CAD-CBD-CGD-O1D
17	3E	302	PC1	C38-C39-C3A-C3B
13	3P	502	HEM	CAD-CBD-CGD-O2D
12	3C	506	3PE	C21-C22-C23-C24
13	3C	502	HEM	CAA-CBA-CGA-O2A
13	3P	502	HEM	CAA-CBA-CGA-O1A
12	3N	501	3PE	O11-C1-C2-O21
12	3Q	503	3PE	C37-C38-C39-C3A
12	3C	507	3PE	O22-C21-C22-C23
11	3Q	502	CDL	CA5-C11-C12-C13
12	3Q	503	3PE	C21-C22-C23-C24
15	3D	501	HEC	CAA-CBA-CGA-O2A
11	3P	506	CDL	C52-C51-CB5-OB6
15	3Q	501	HEC	CAA-CBA-CGA-O2A
13	3P	501	HEM	CAD-CBD-CGD-O2D
11	3P	507	CDL	CB6-CB4-OB6-CB5
12	3A	503	3PE	C33-C34-C35-C36
11	3C	505	CDL	C52-C51-CB5-OB7
15	3D	501	HEC	CAA-CBA-CGA-O1A
12	3P	505	3PE	C1-C2-C3-O31
13	3C	501	HEM	C4C-C3C-CAC-CBC
13	3P	501	HEM	C4C-C3C-CAC-CBC
13	3P	502	HEM	CAA-CBA-CGA-O2A

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Mol	Chain	Res	Type	Atoms
12	3N	501	3PE	O31-C31-C32-C33
11	3G	102	CDL	OB6-CB4-CB6-OB8
15	3Q	501	HEC	CAA-CBA-CGA-O1A
11	3P	506	CDL	C12-C11-CA5-OA7
14	3P	504	U10	C2-C3-O3-C3M
12	3C	506	3PE	C29-C2A-C2B-C2C
11	3P	507	CDL	CB3-CB4-OB6-CB5
14	3P	503	U10	C3-C4-O4-C4M
12	3A	503	3PE	C34-C35-C36-C37
17	3X	101	PC1	C2-C1-O11-P
17	3X	101	PC1	O22-C21-C22-C23
14	3C	503	U10	C5-C4-O4-C4M
12	3N	501	3PE	C22-C23-C24-C25
14	3P	504	U10	C1-C6-C7-C8
12	3Y	101	3PE	C32-C33-C34-C35
12	3N	501	3PE	O32-C31-C32-C33
11	3Q	502	CDL	C72-C73-C74-C75
11	3P	506	CDL	C32-C31-CA7-OA8
11	3C	505	CDL	C12-C11-CA5-OA6
12	3Q	503	3PE	C36-C37-C38-C39
11	3C	505	CDL	C12-C11-CA5-OA7
11	3Q	502	CDL	C32-C31-CA7-OA8
14	3C	503	U10	C2-C3-O3-C3M
15	3Q	501	HEC	CAD-CBD-CGD-O1D
11	3G	102	CDL	C76-C77-C78-C79

There are no ring outliers.

31 monomers are involved in 131 short contacts:

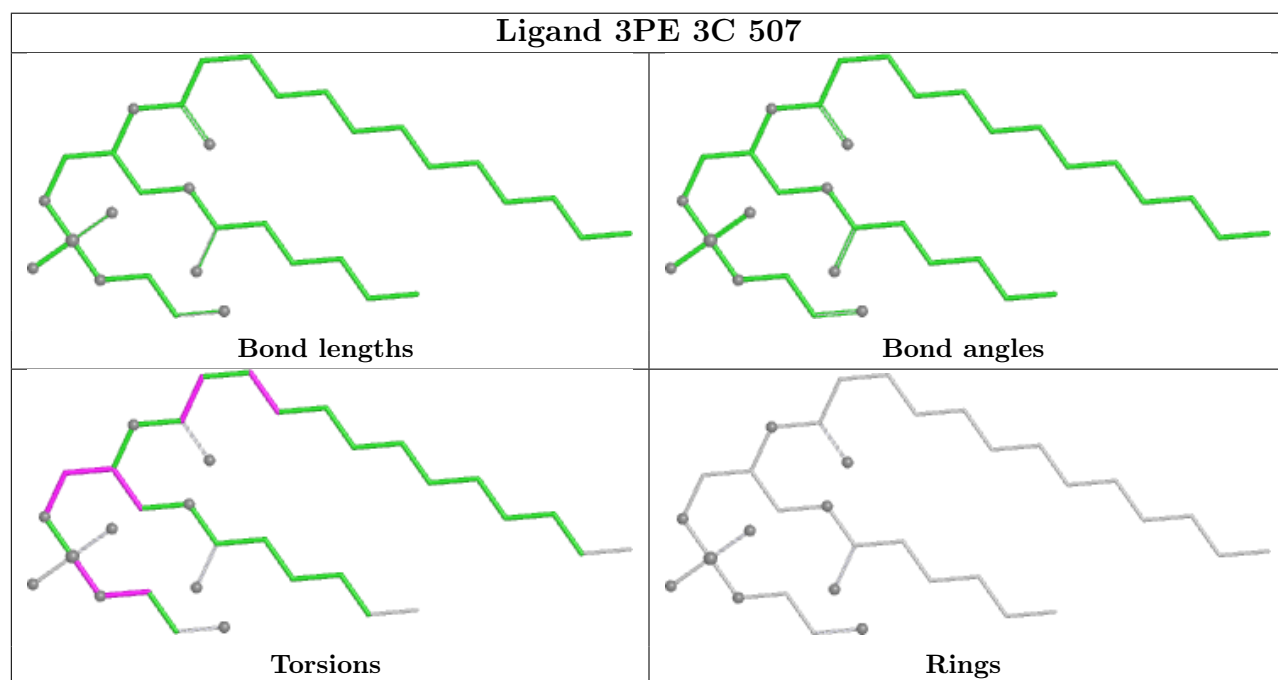
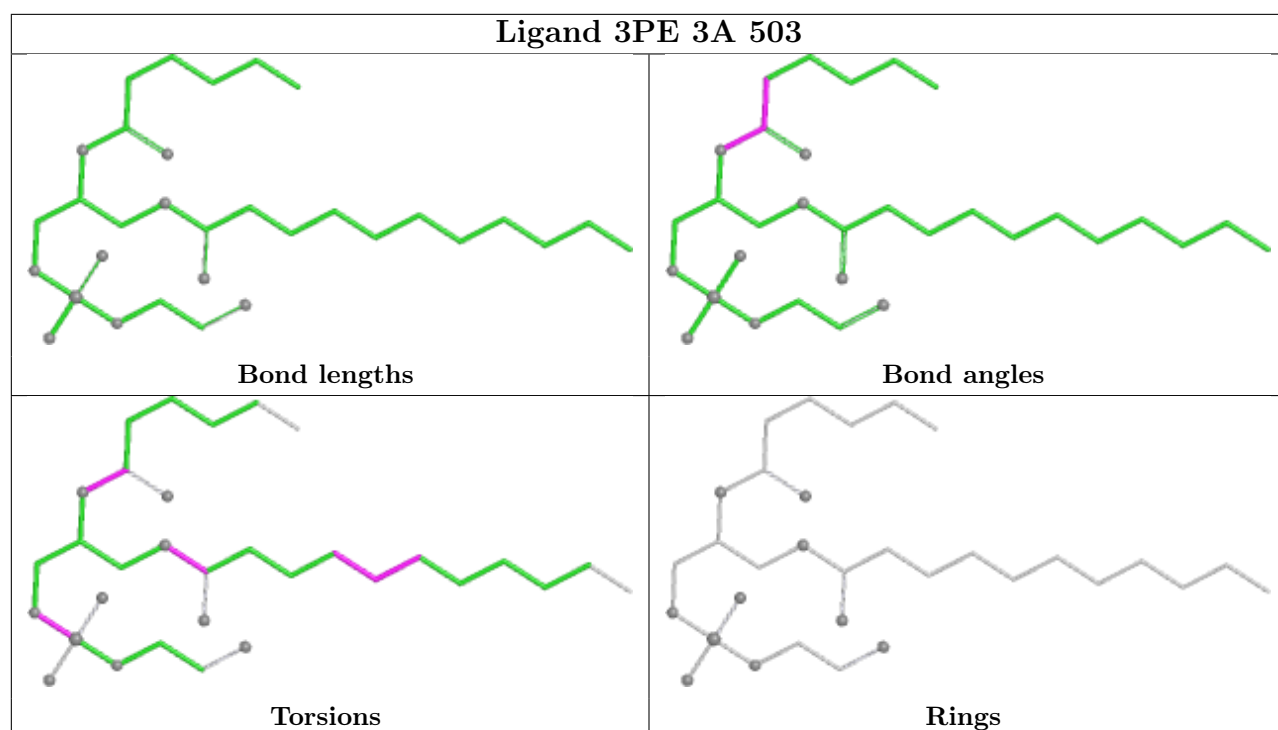
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	3A	503	3PE	5	0
12	3C	507	3PE	3	0
11	3P	506	CDL	10	0
13	3P	501	HEM	2	0
17	3R	302	PC1	5	0
14	3P	503	U10	3	0
13	3C	501	HEM	3	0
12	3A	502	3PE	7	0
14	3P	504	U10	2	0
11	3A	501	CDL	7	0
16	3E	301	FES	1	0
12	3D	502	3PE	4	0

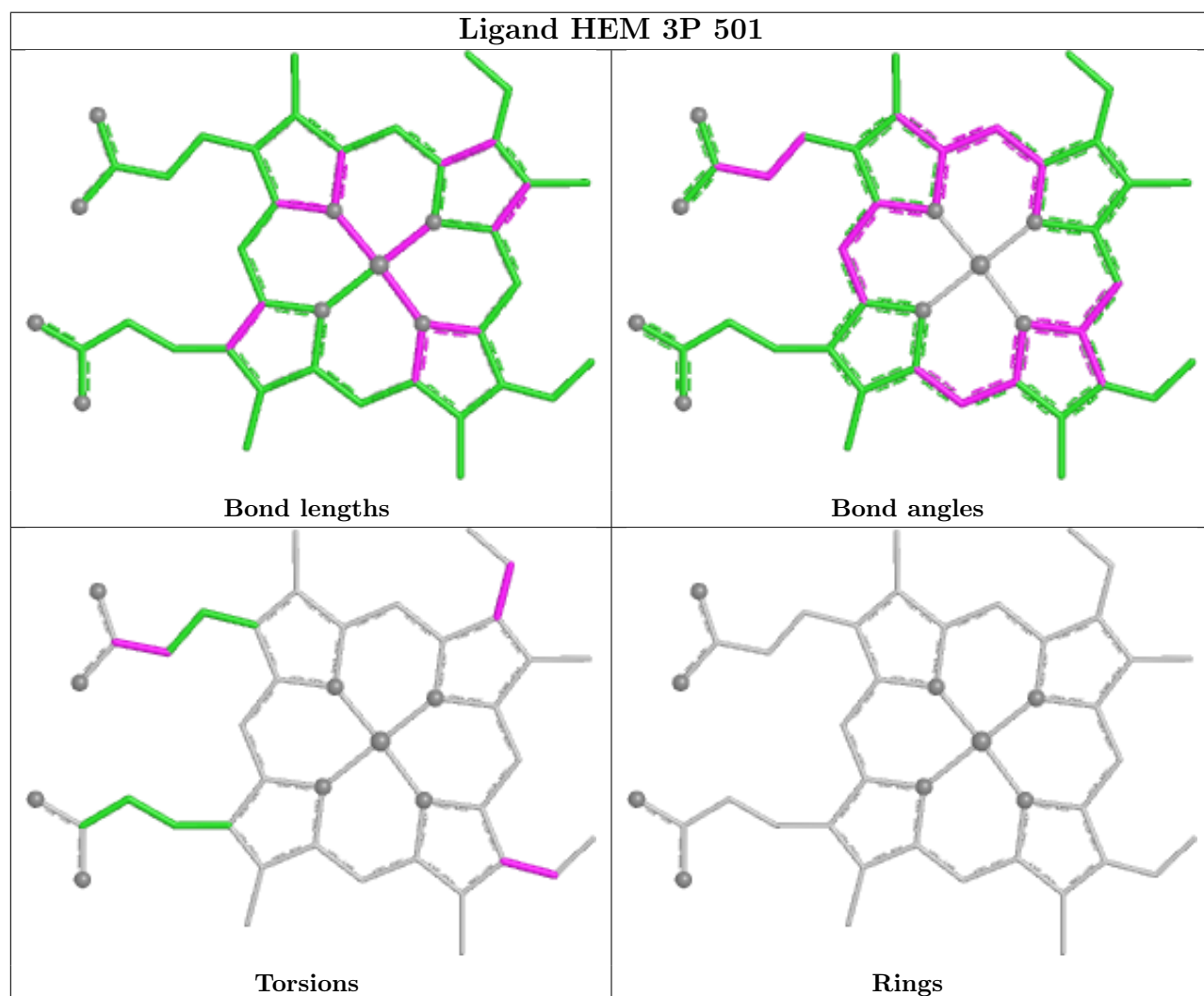
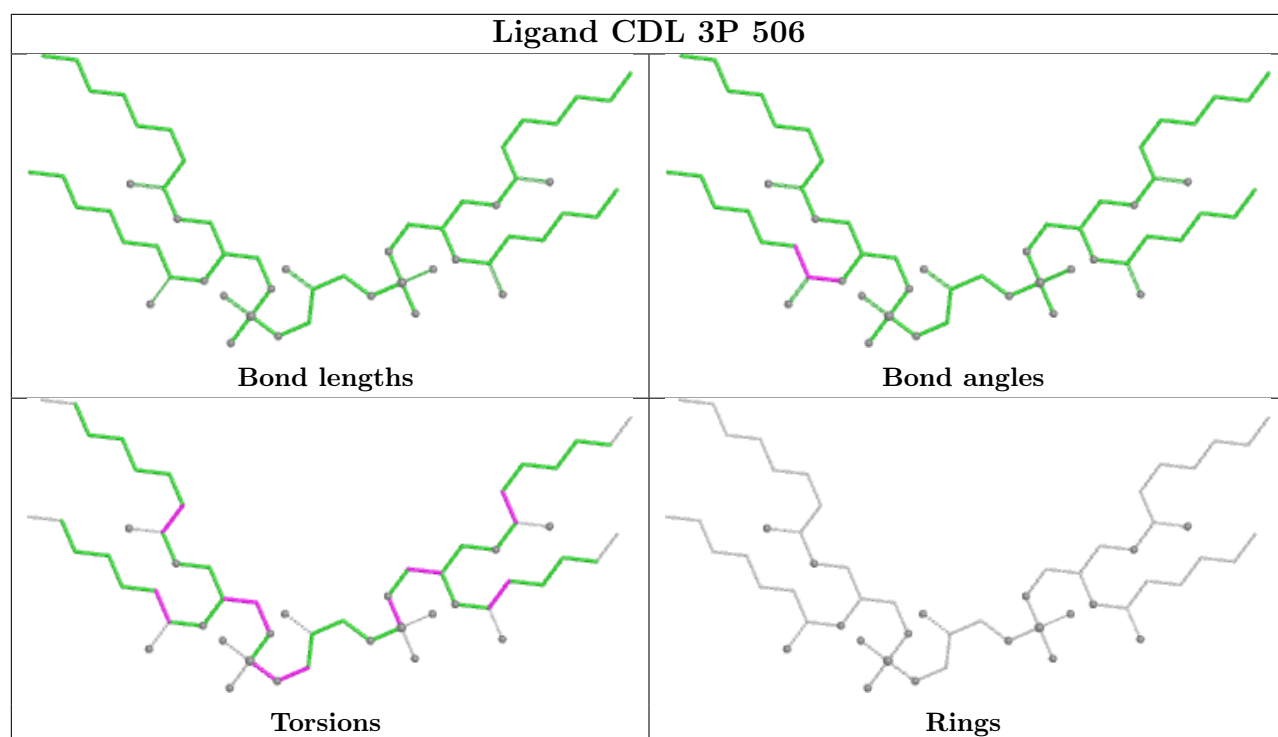
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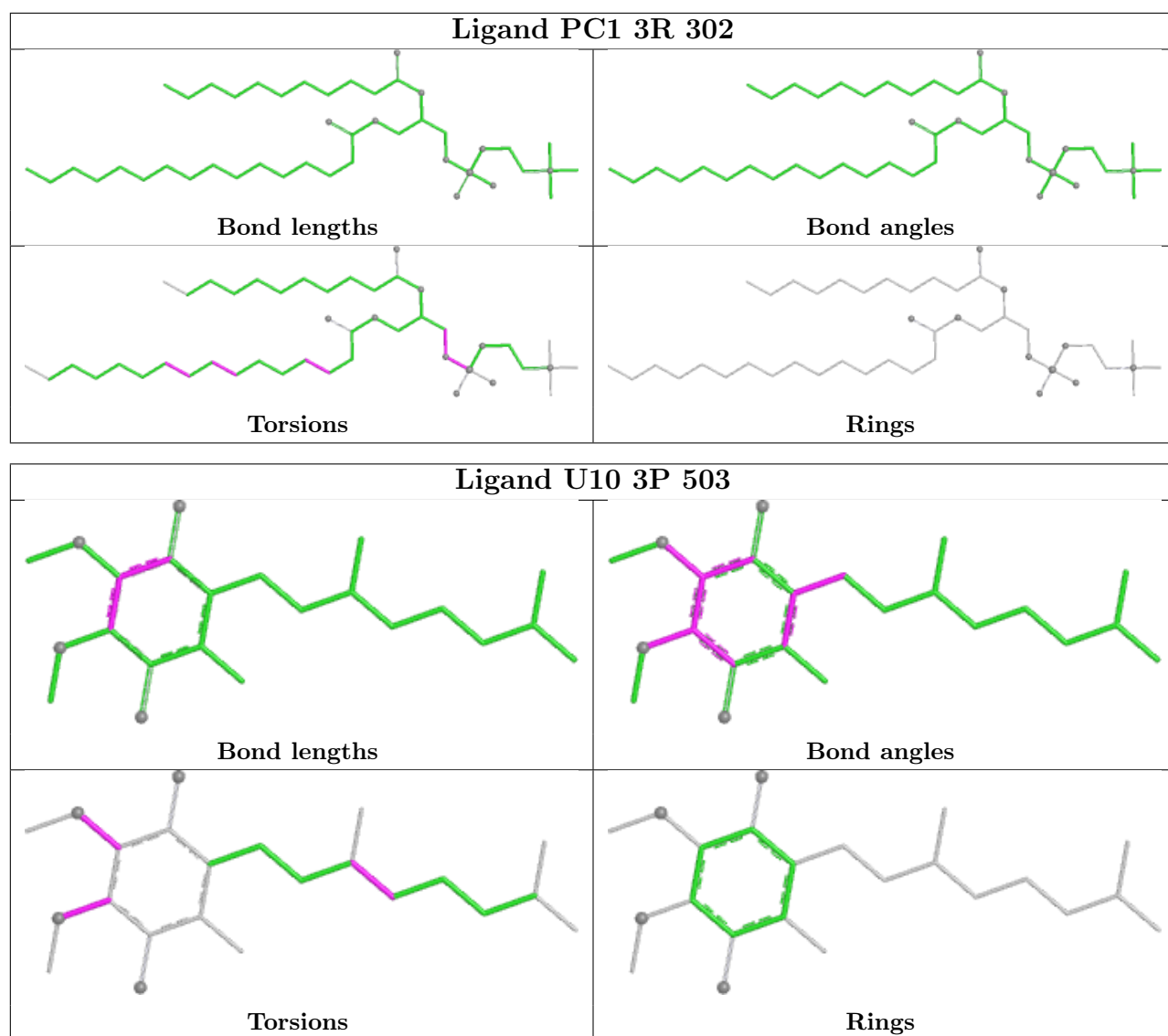
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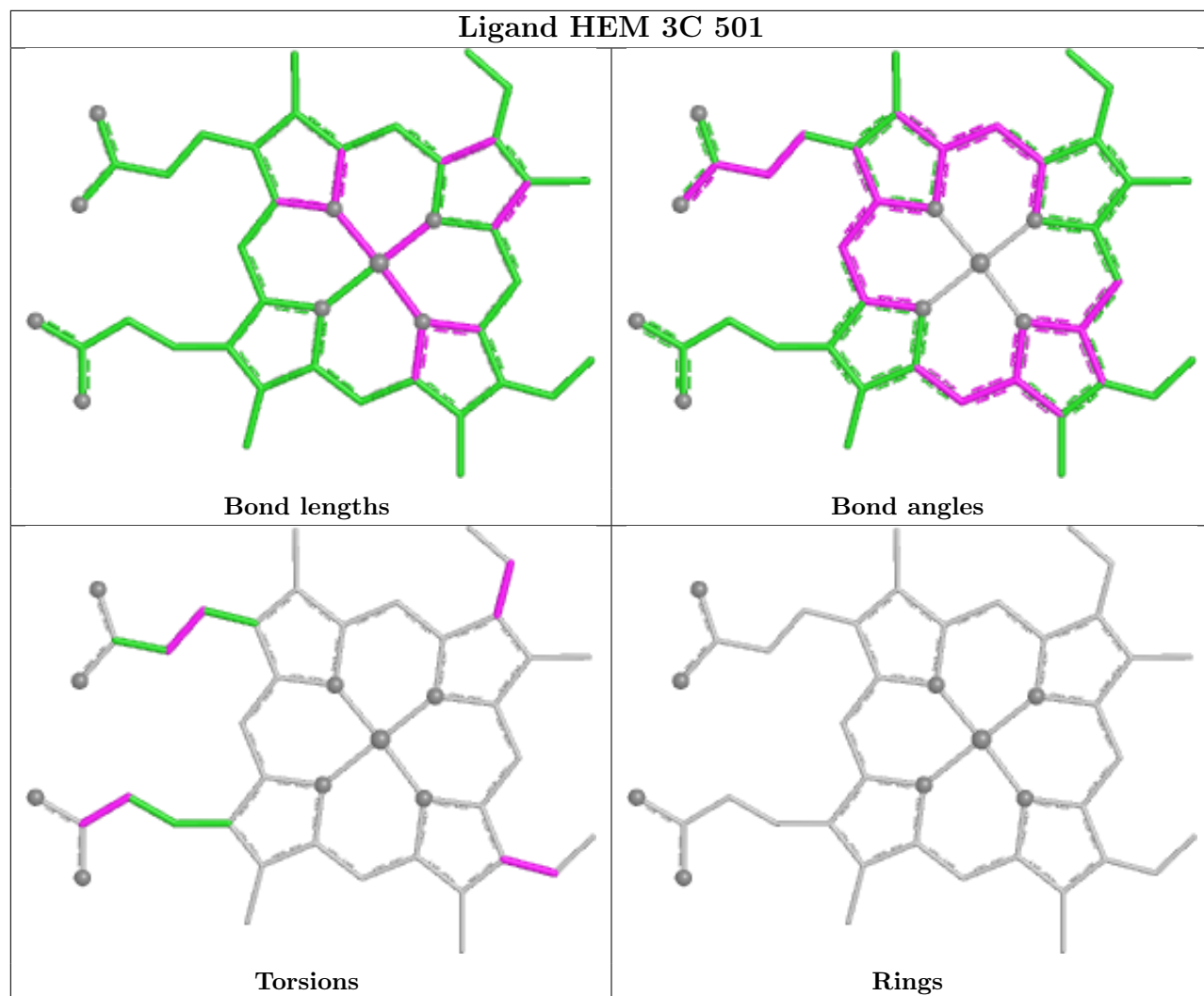
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	3D	501	HEC	15	0
12	3N	502	3PE	4	0
12	3Q	503	3PE	8	0
12	3N	501	3PE	2	0
14	3C	504	U10	4	0
12	3P	505	3PE	3	0
17	3E	302	PC1	7	0
13	3C	502	HEM	5	0
11	3Q	502	CDL	13	0
12	3G	101	3PE	1	0
14	3C	503	U10	7	0
11	3G	102	CDL	3	0
11	3C	505	CDL	5	0
11	3P	507	CDL	2	0
17	3X	101	PC1	5	0
15	3Q	501	HEC	3	0
13	3P	502	HEM	3	0
16	3R	301	FES	1	0
12	3C	506	3PE	2	0

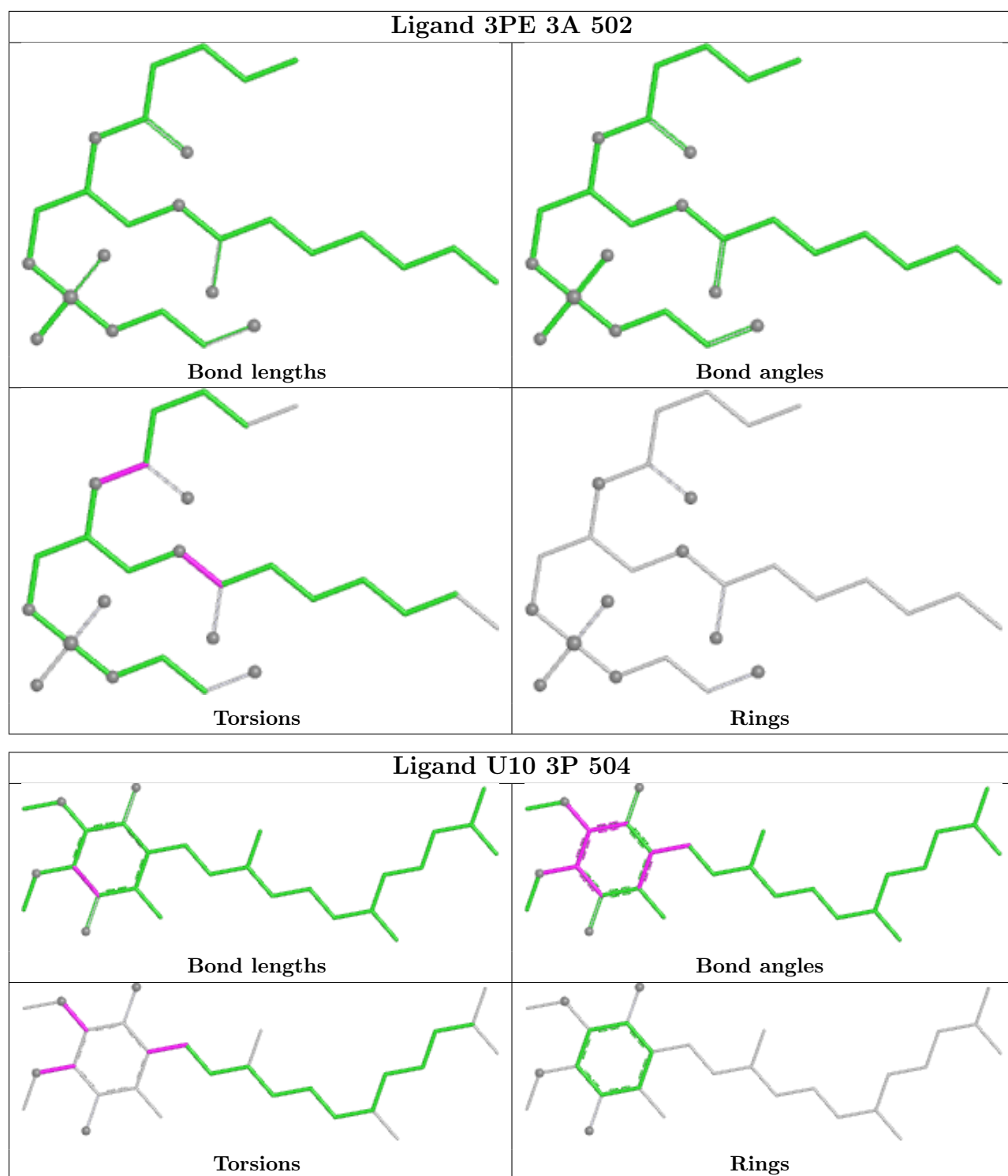
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

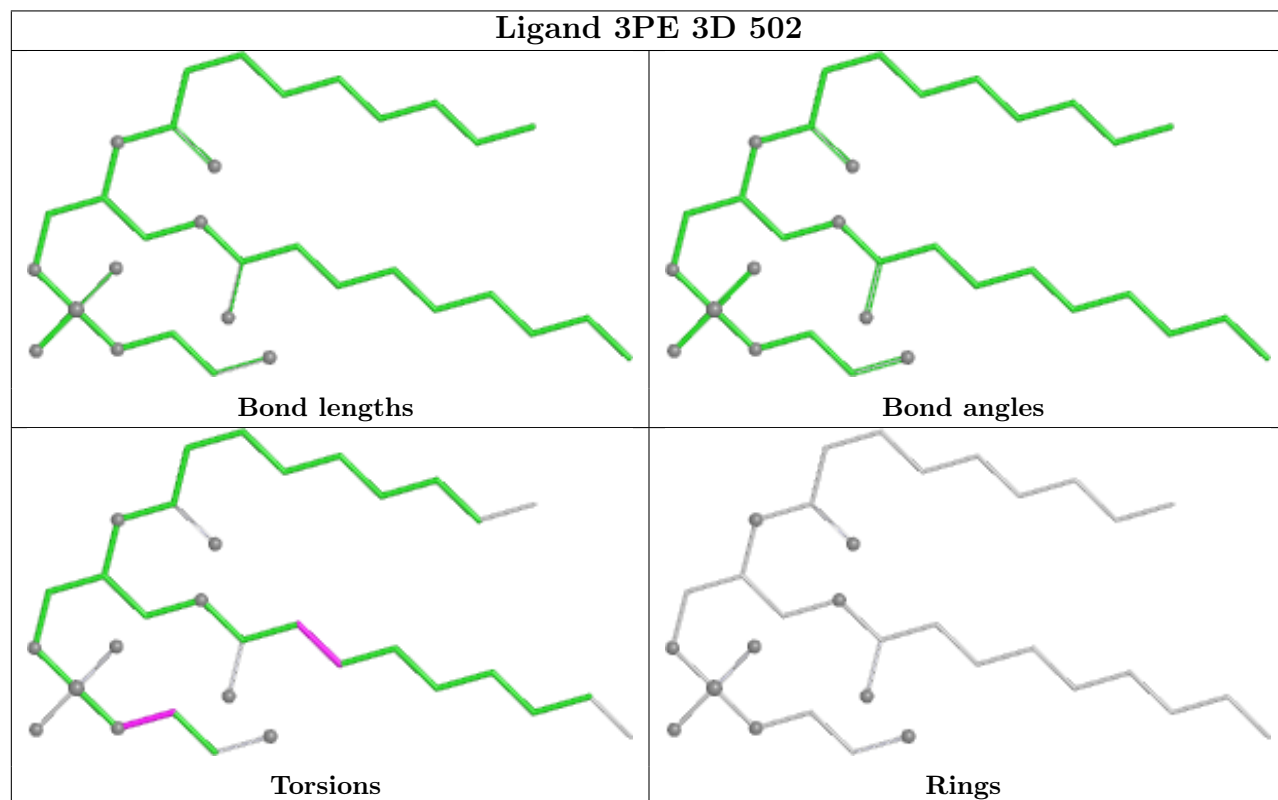
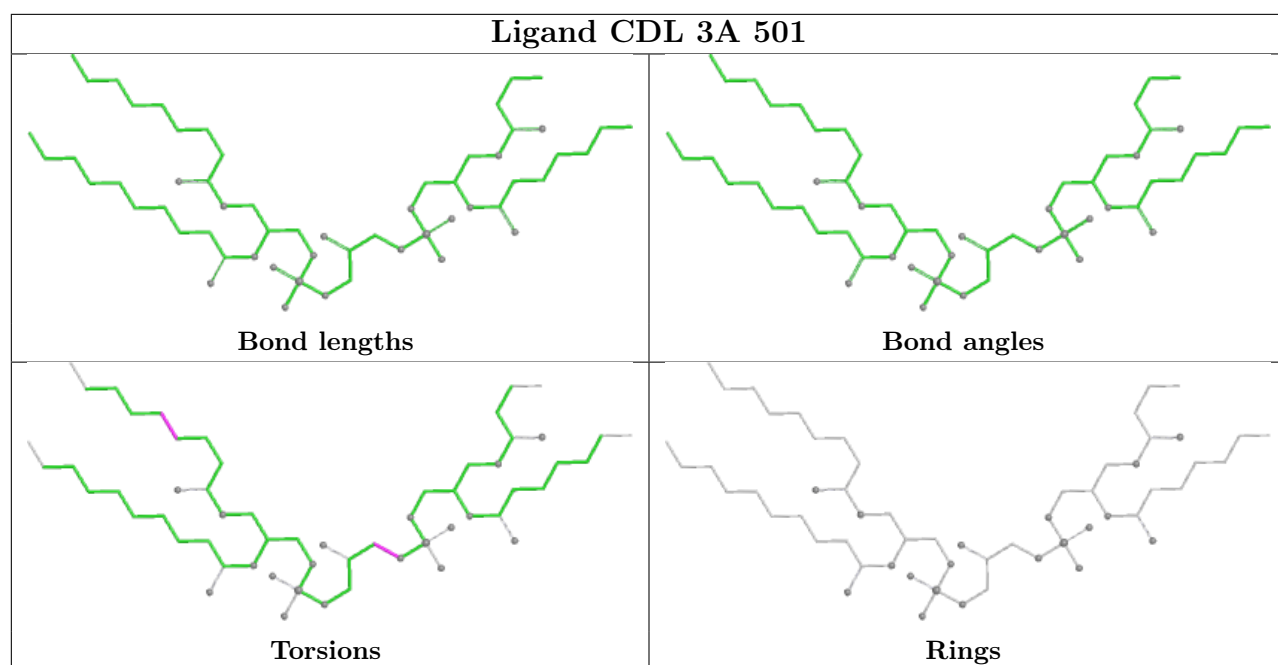


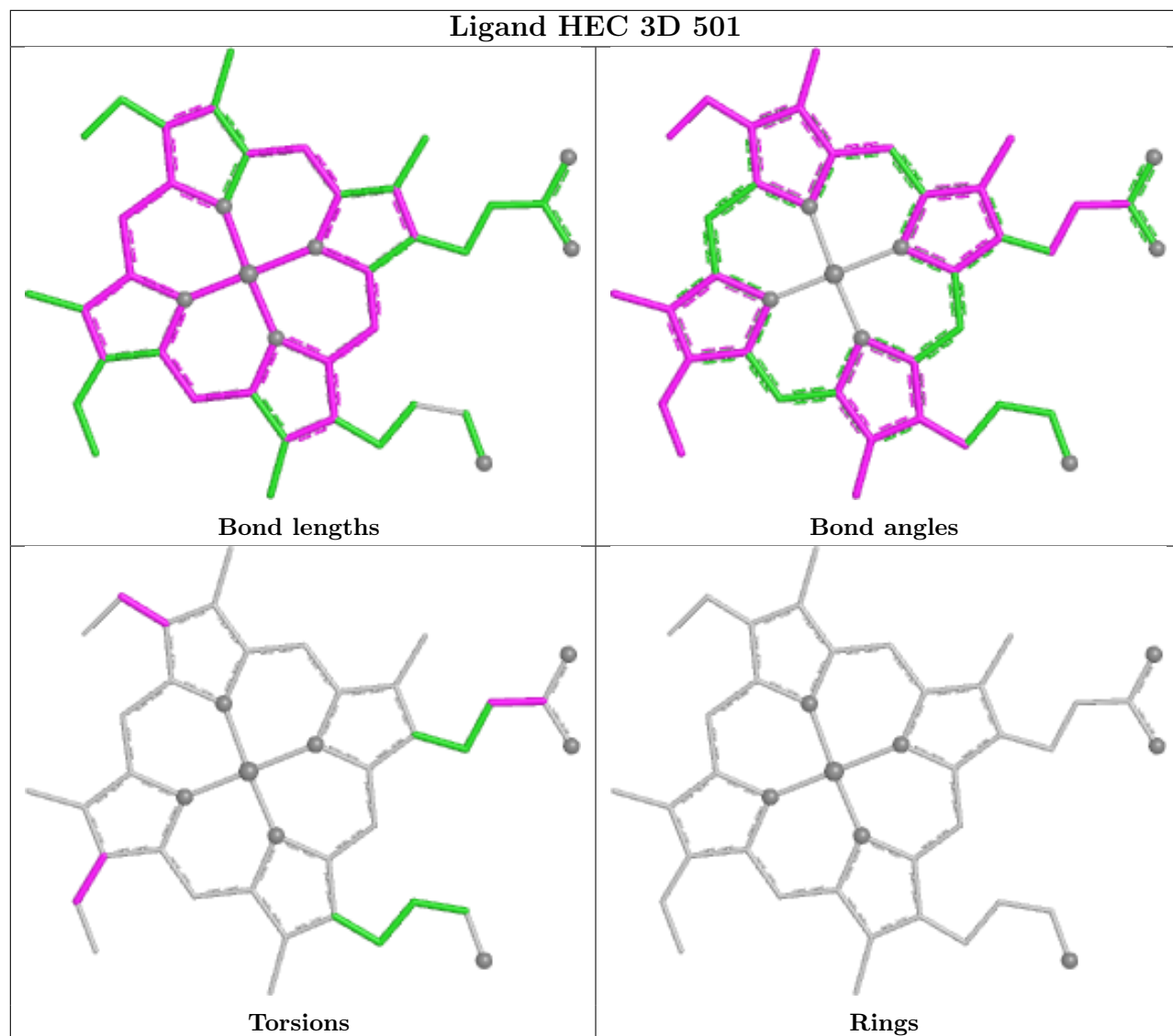


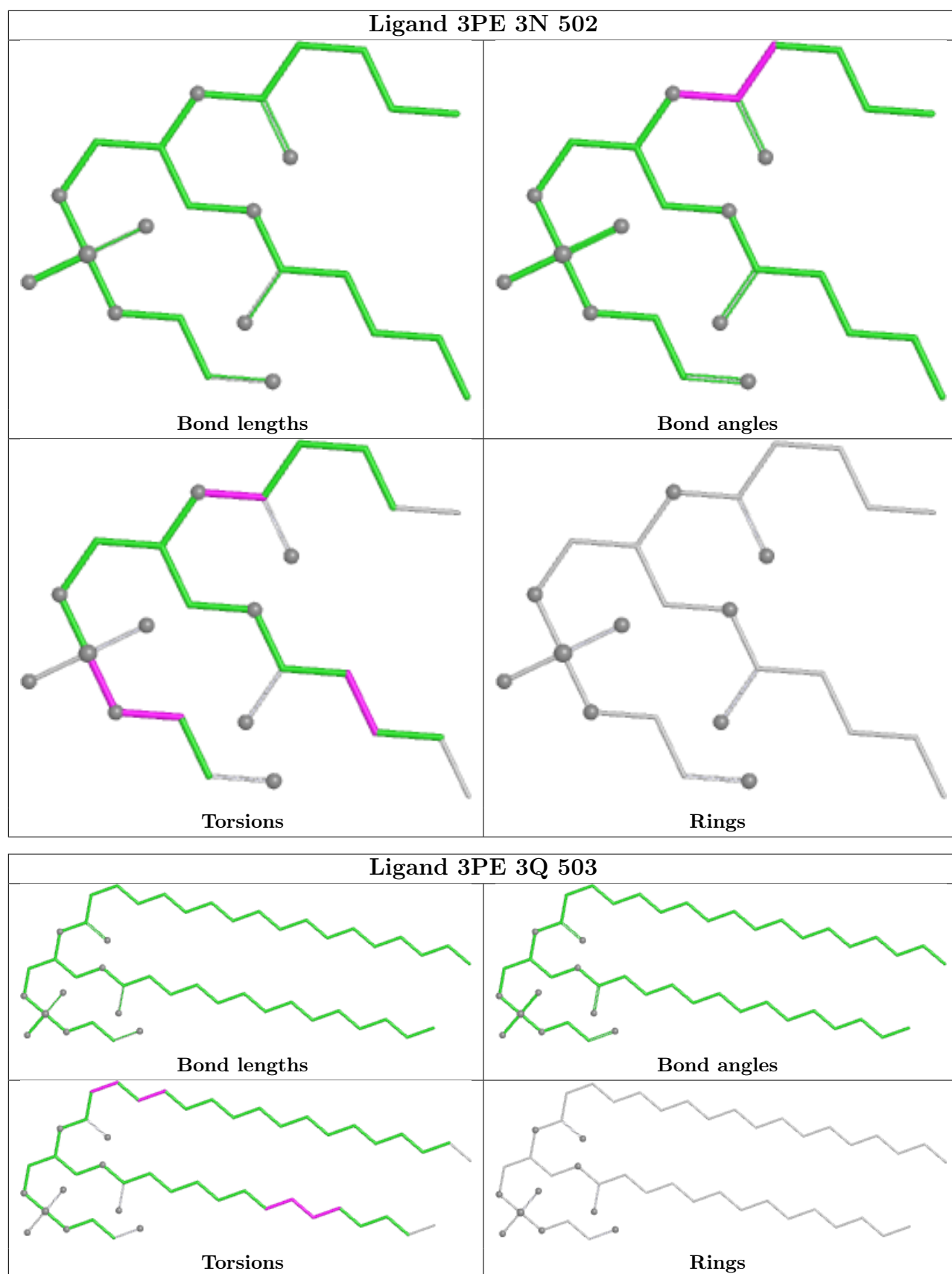


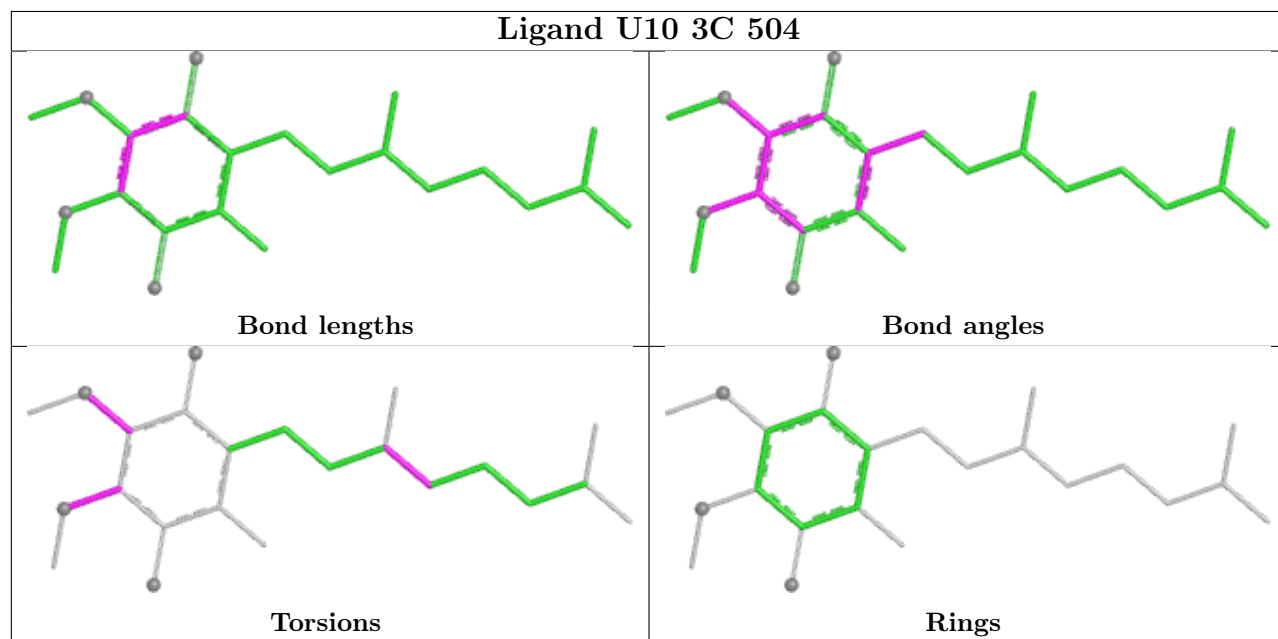
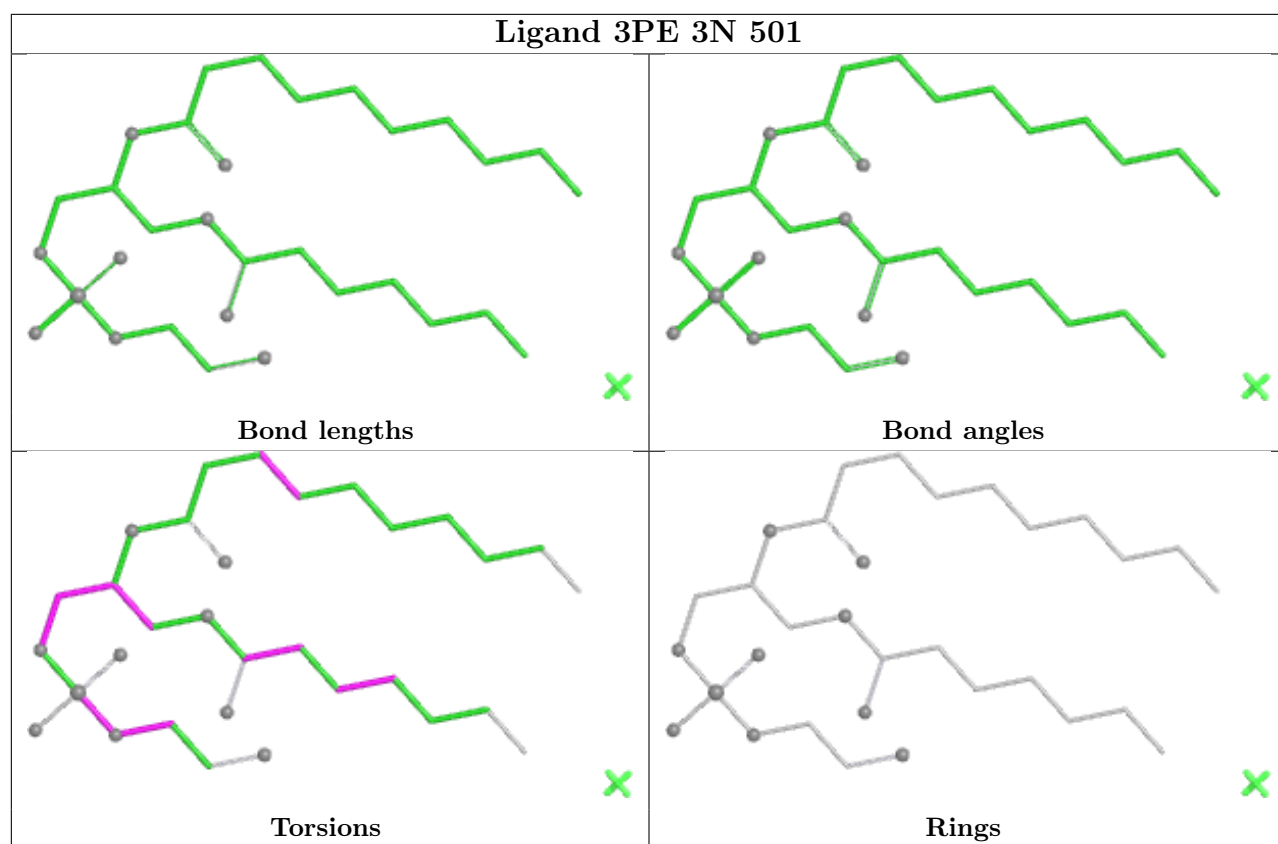


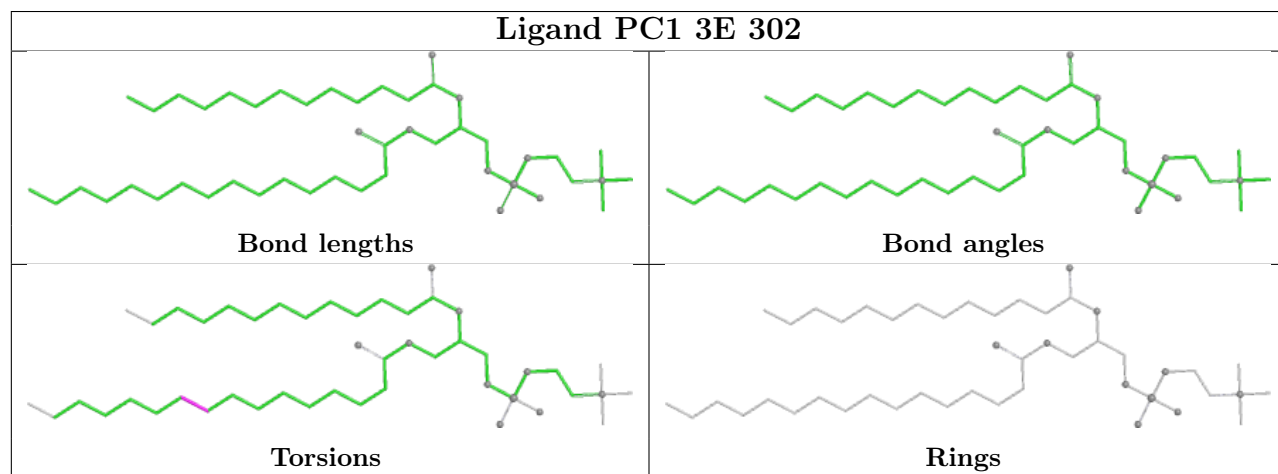
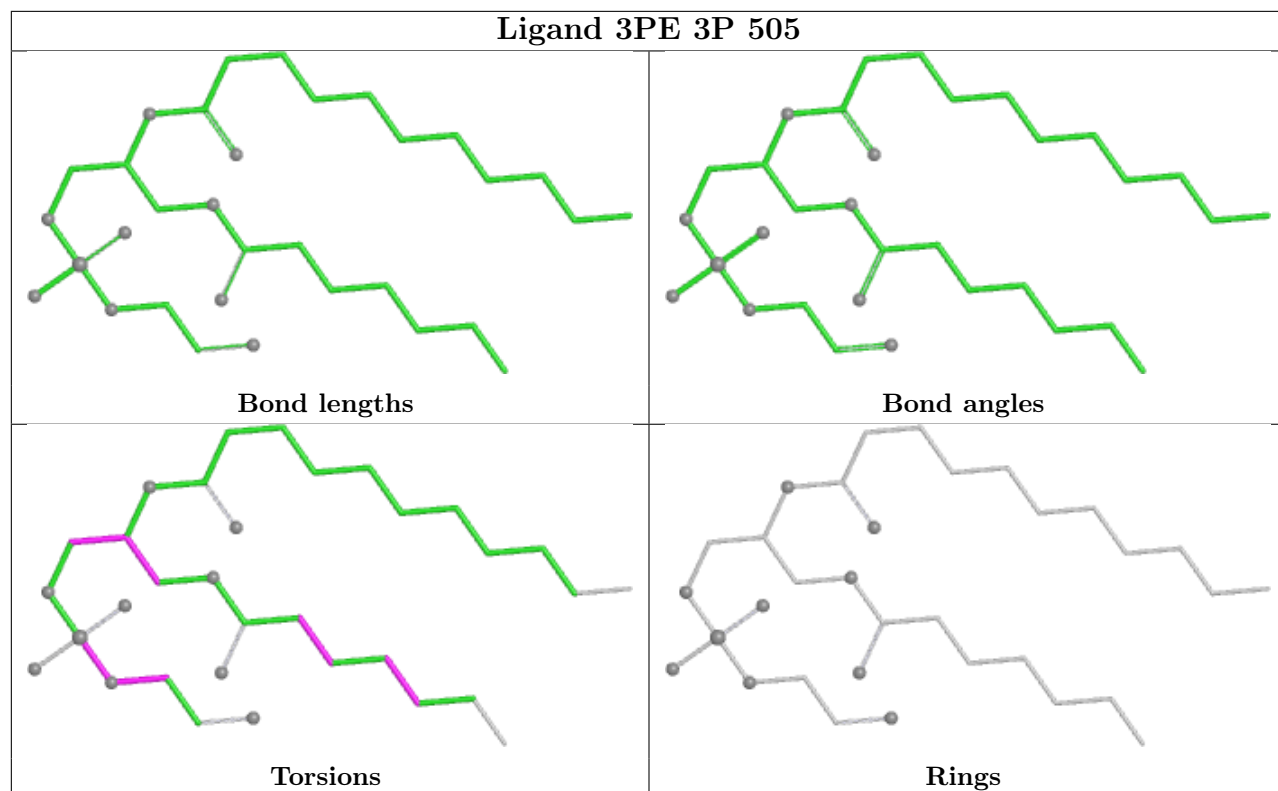




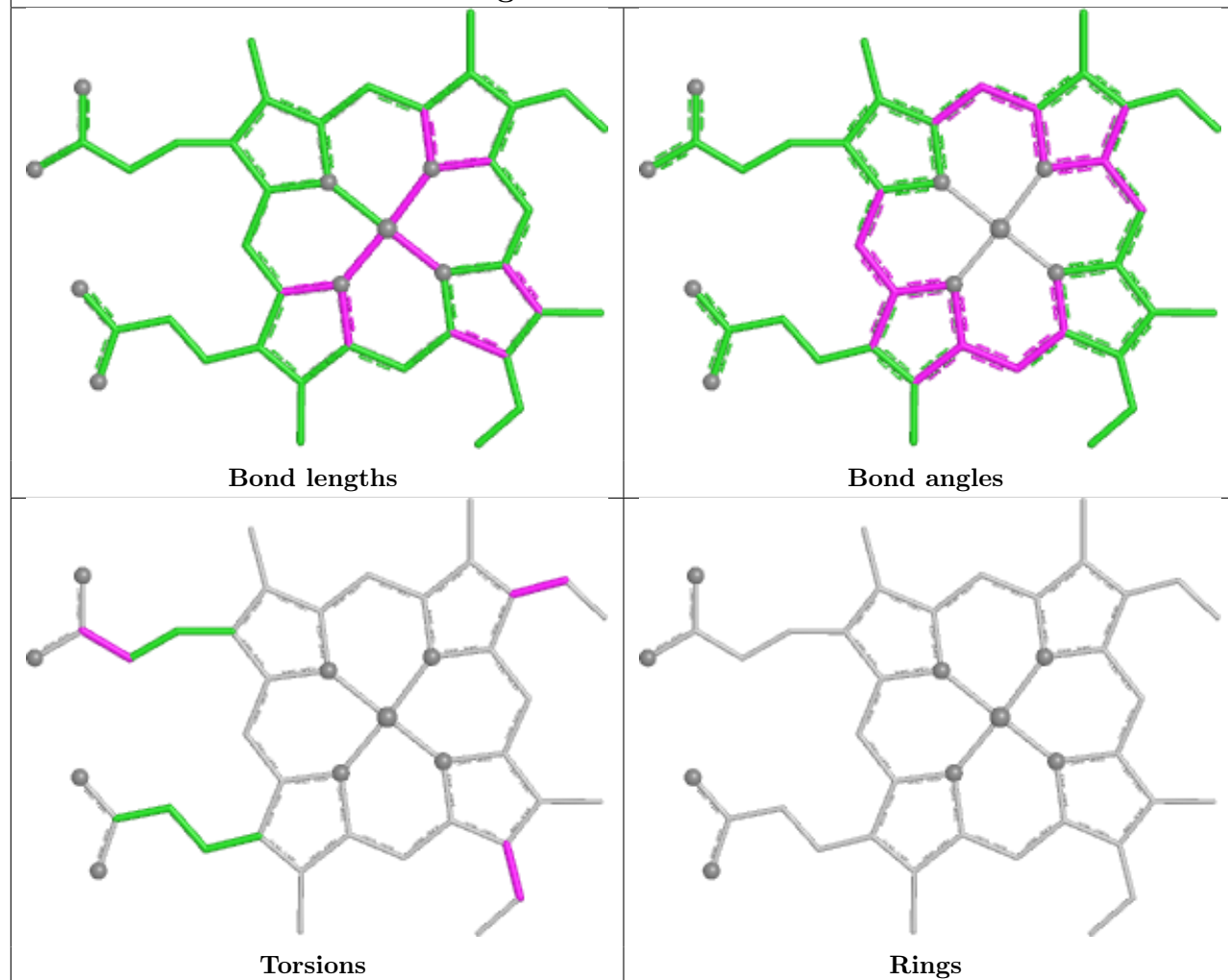




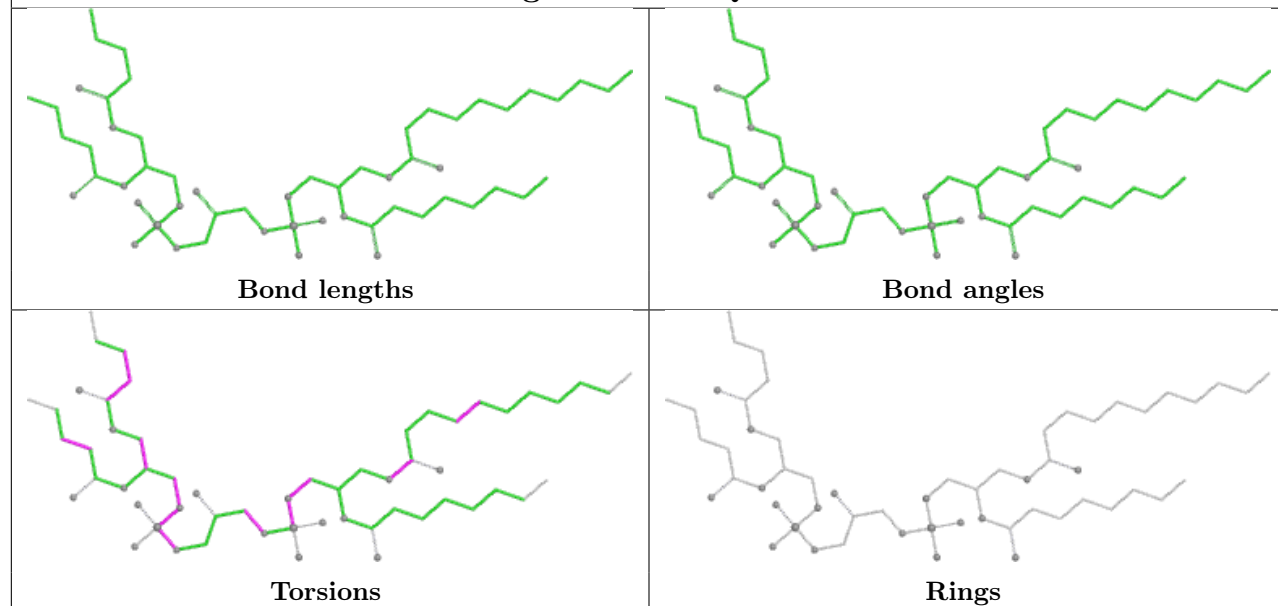


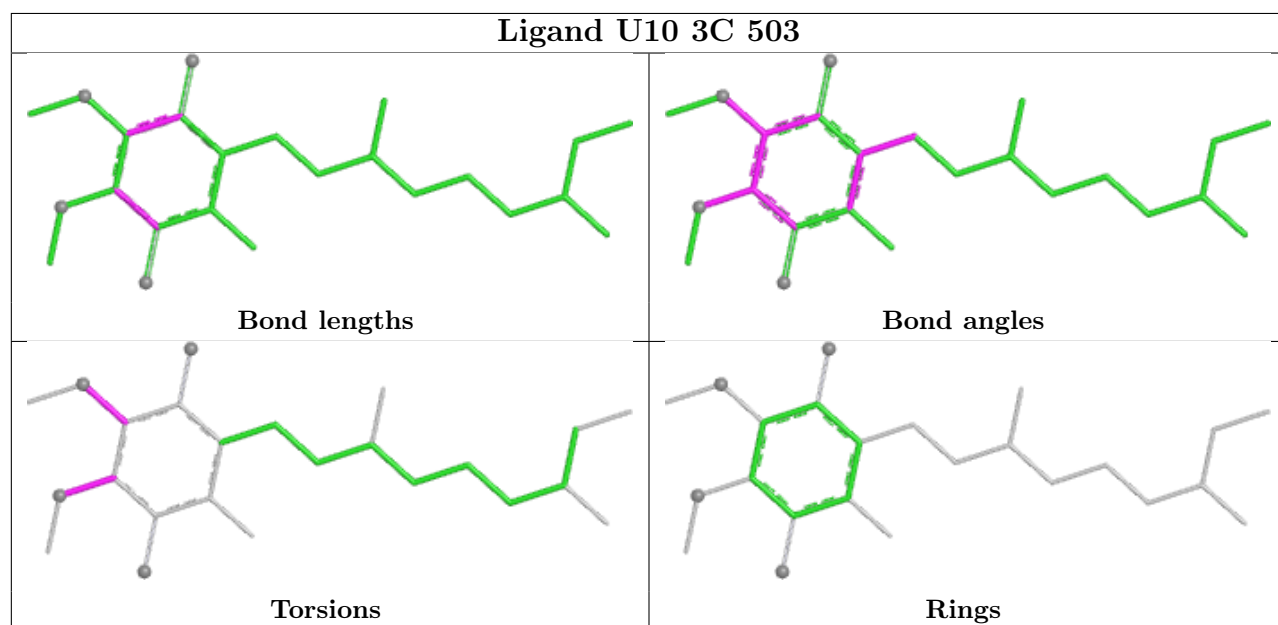
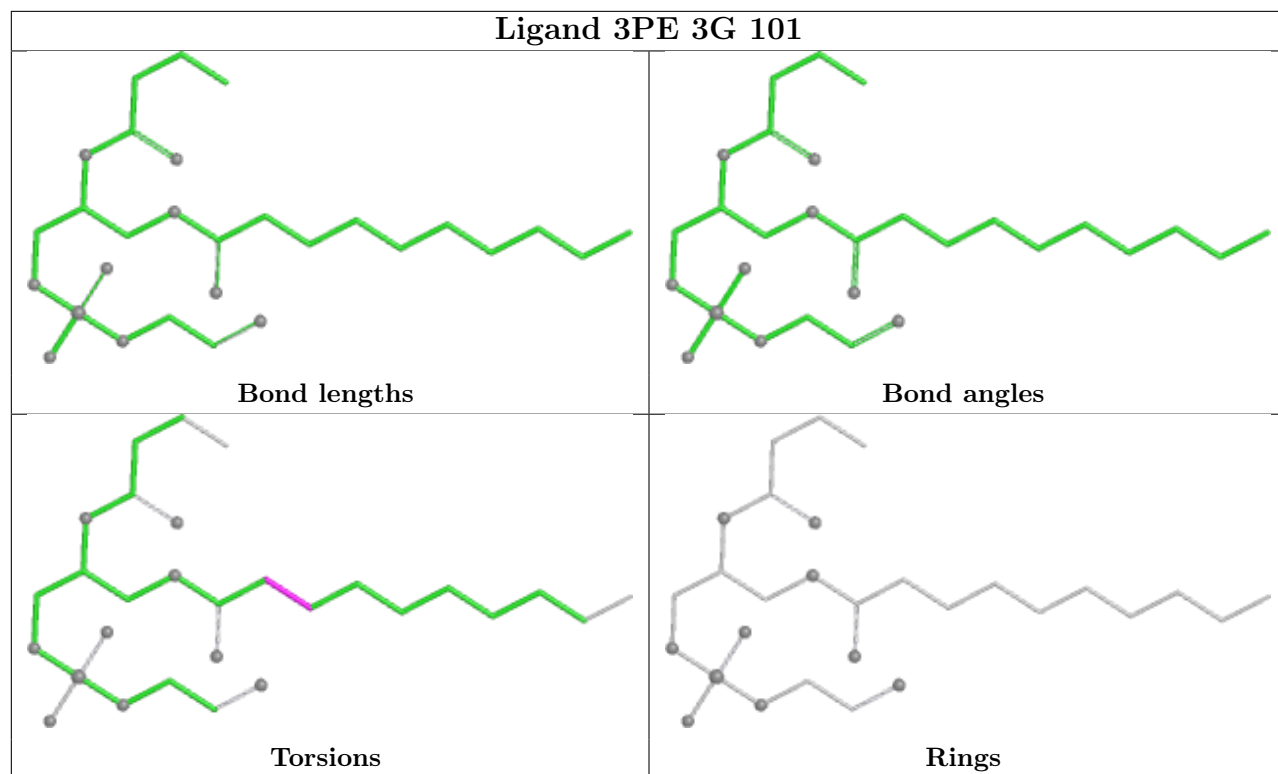


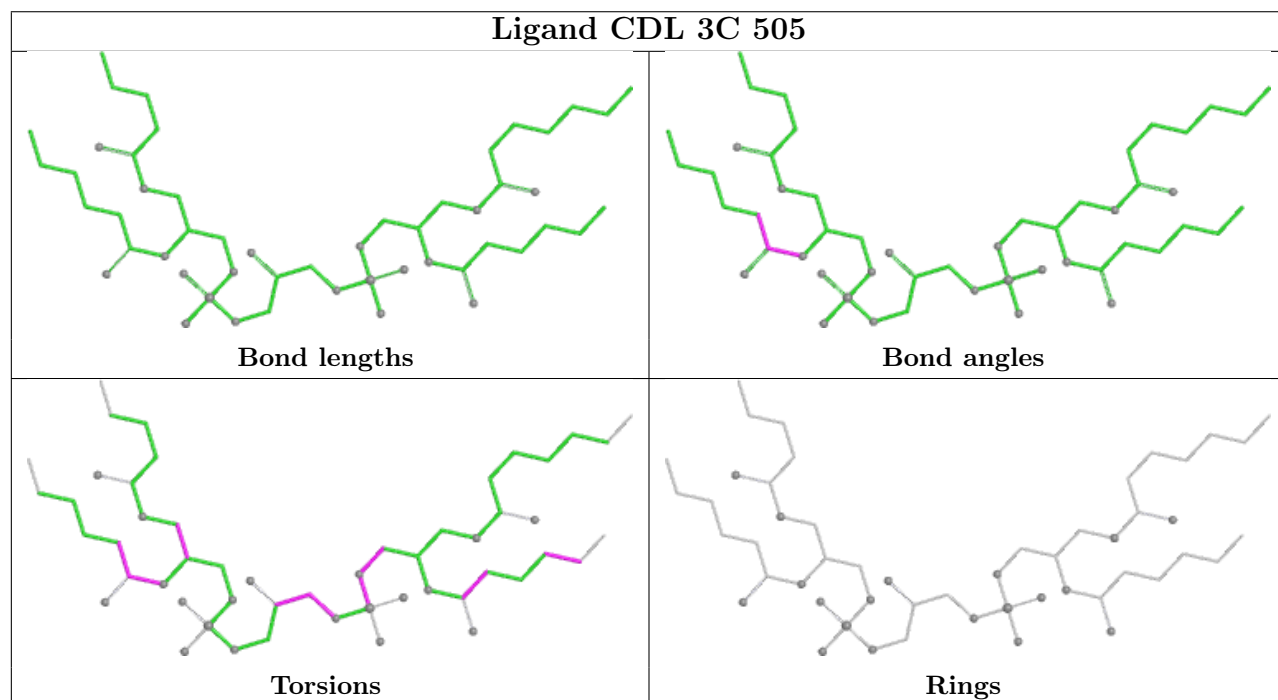
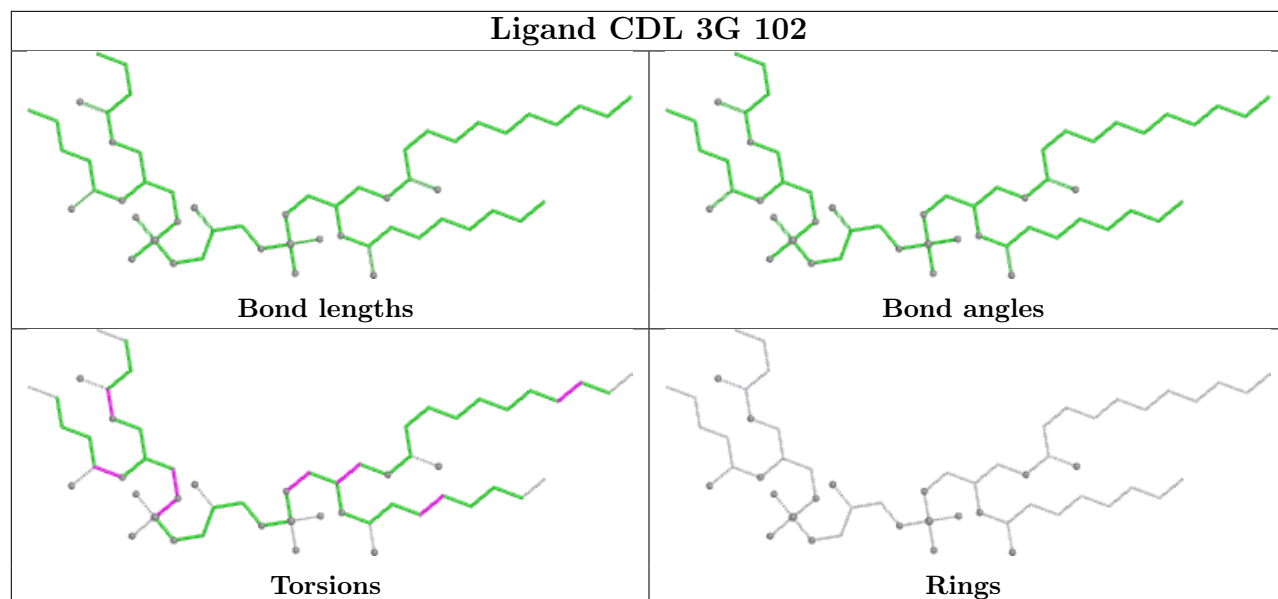
Ligand HEM 3C 502

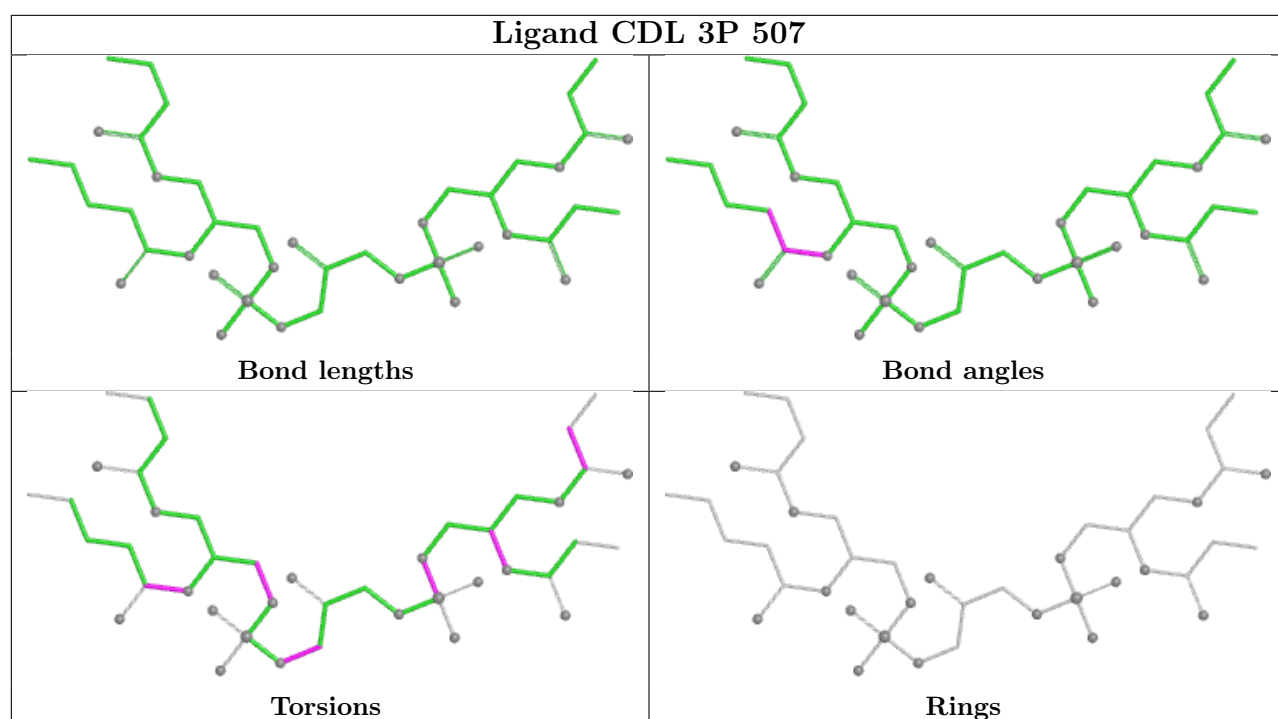
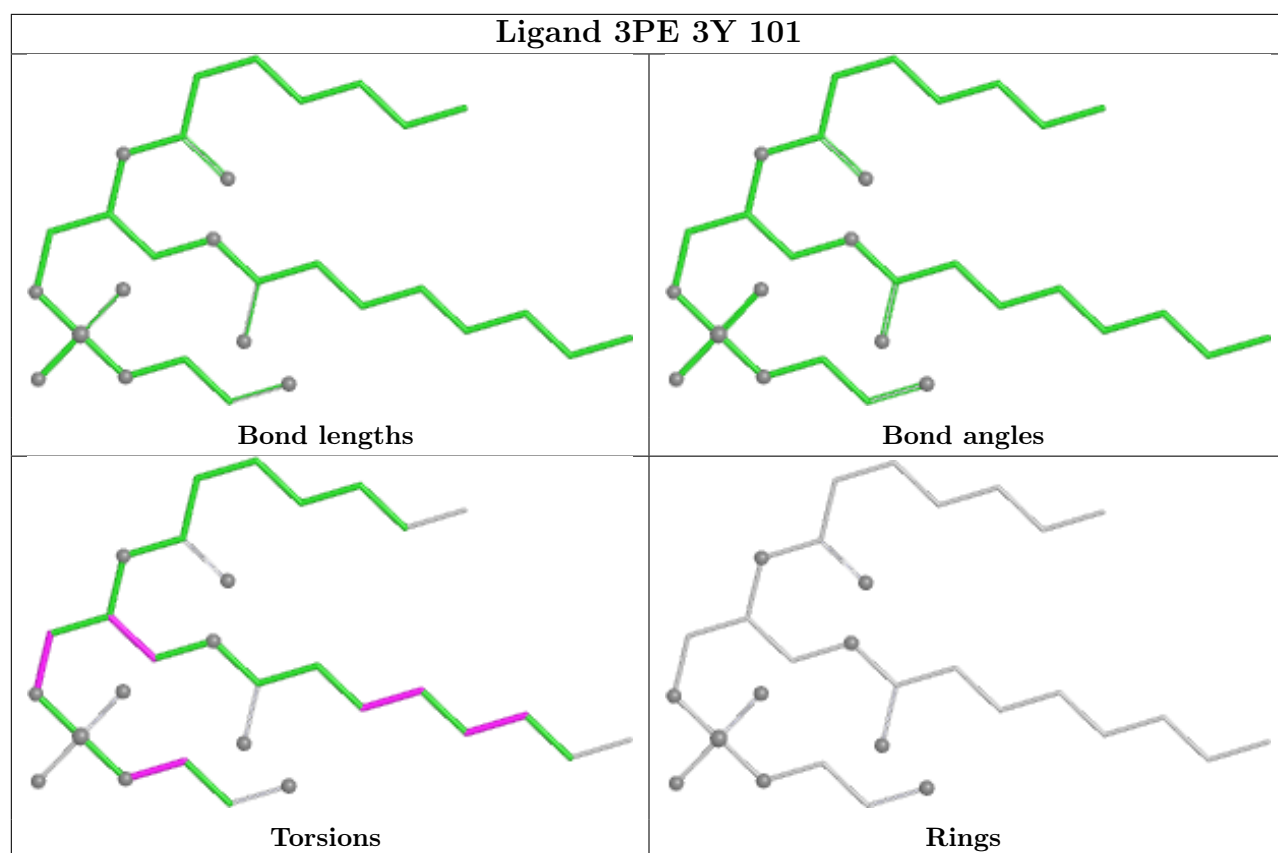


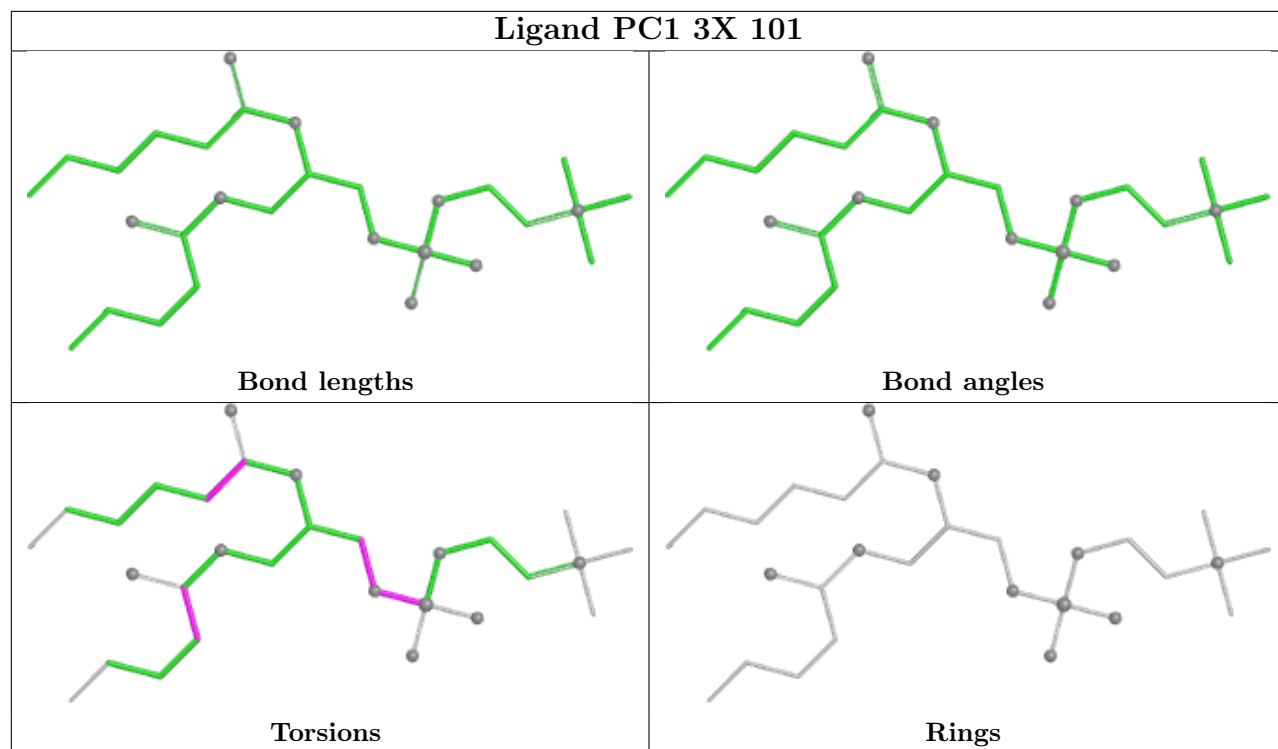
Ligand CDL 3Q 502



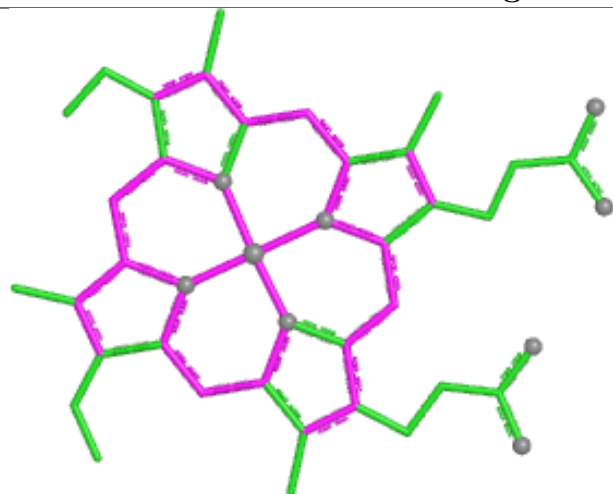




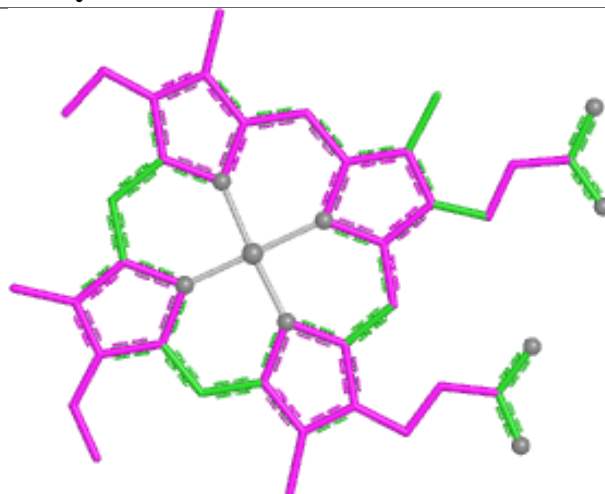




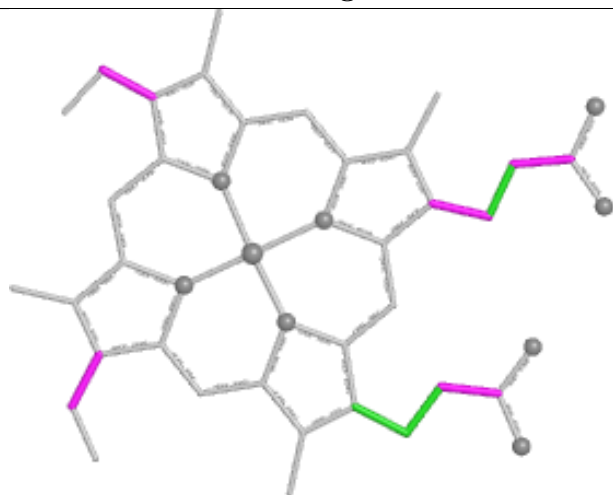
Ligand HEC 3Q 501



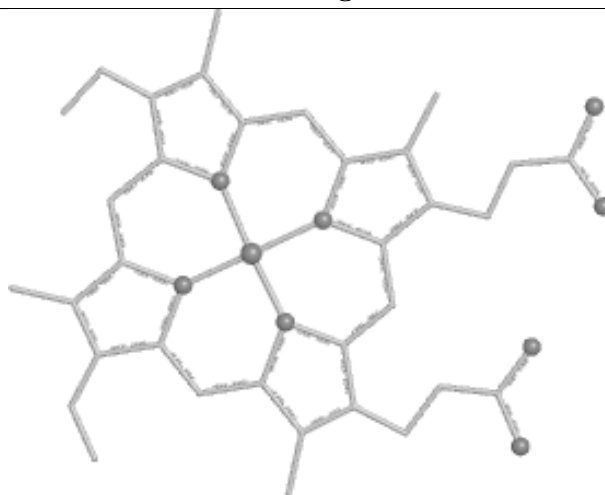
Bond lengths



Bond angles

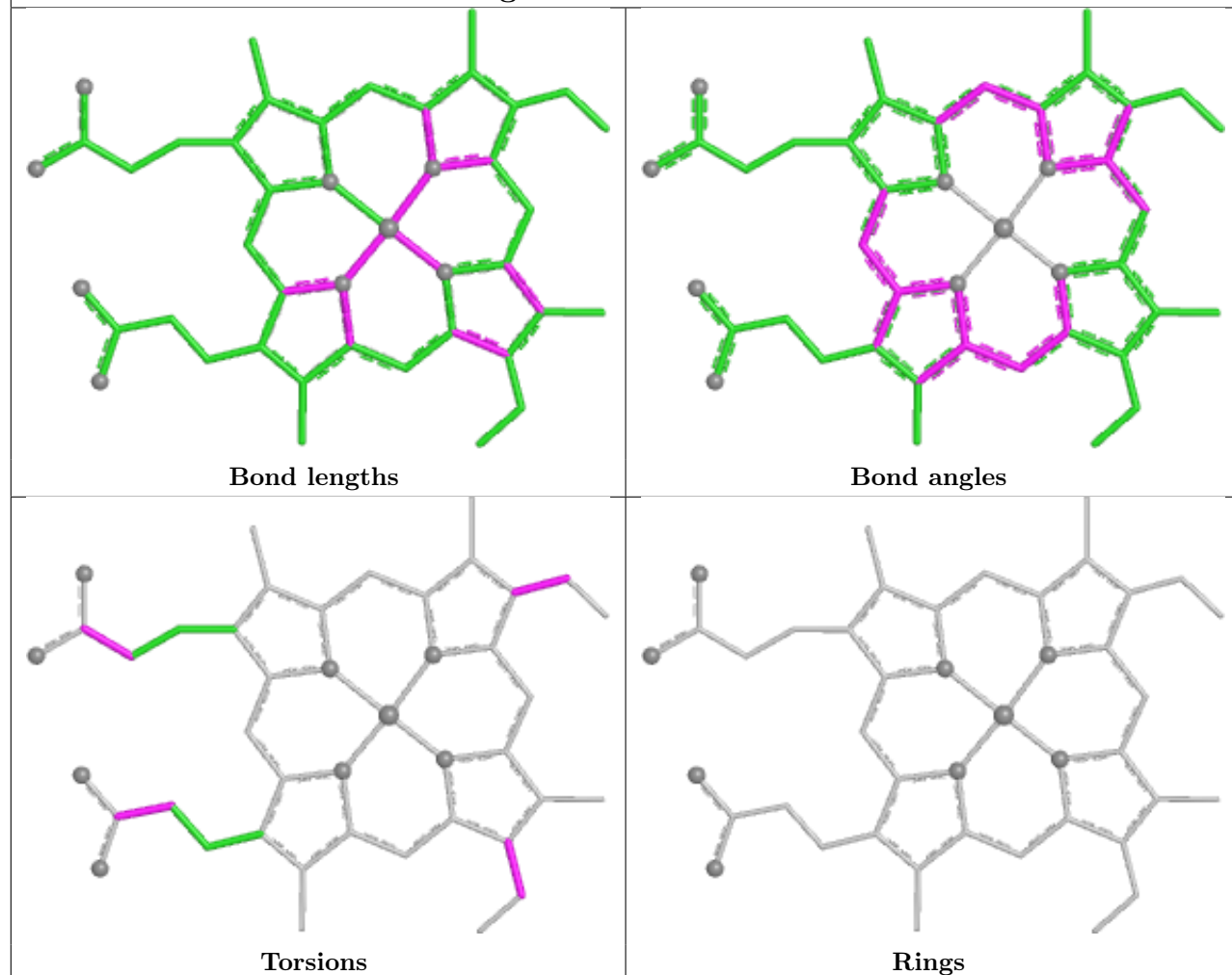


Torsions

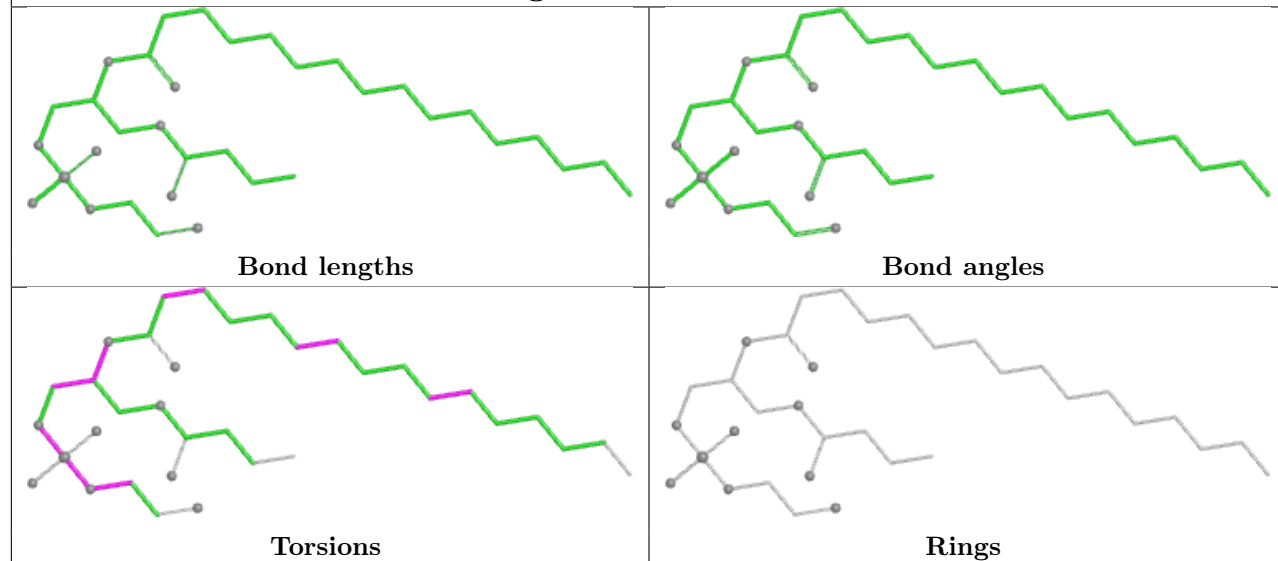


Rings

Ligand HEM 3P 502



Ligand 3PE 3C 506



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	3H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	3H	77:GLU	C	78:ASP	N	3.32

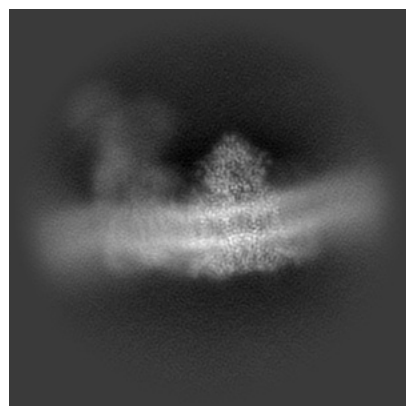
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42222. These allow visual inspection of the internal detail of the map and identification of artifacts.

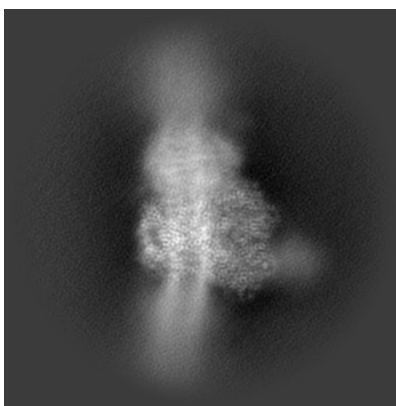
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

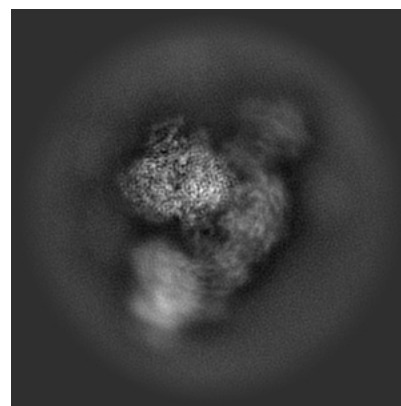
6.1.1 Primary map



X

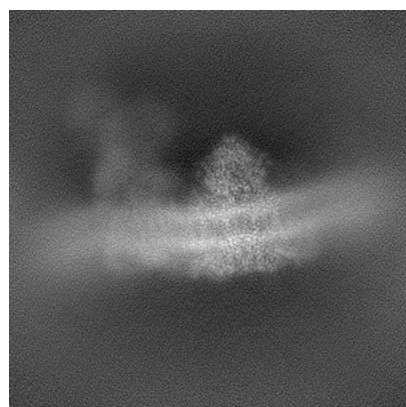


Y

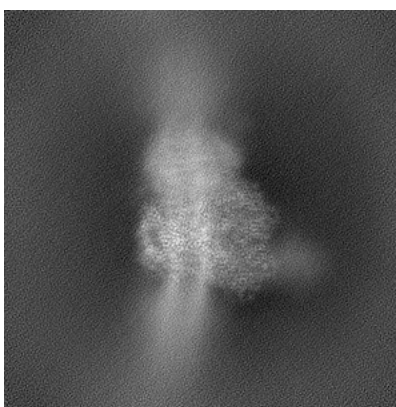


Z

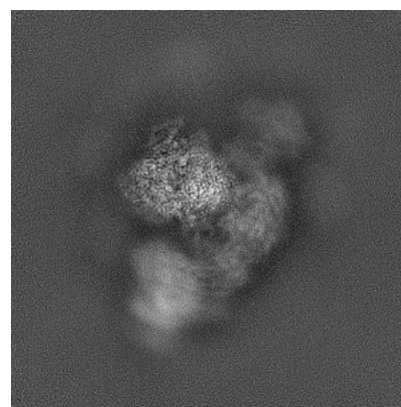
6.1.2 Raw map



X



Y

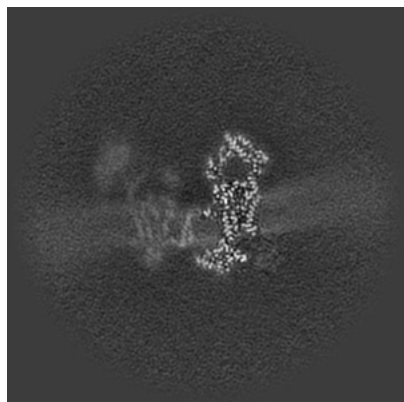


Z

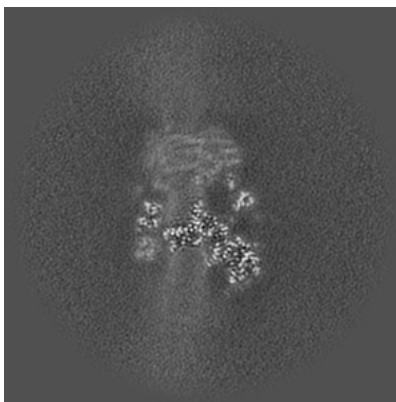
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

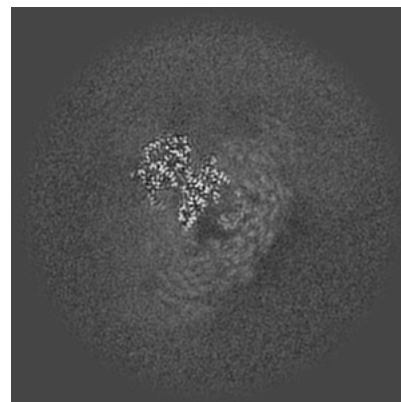
6.2.1 Primary map



X Index: 160

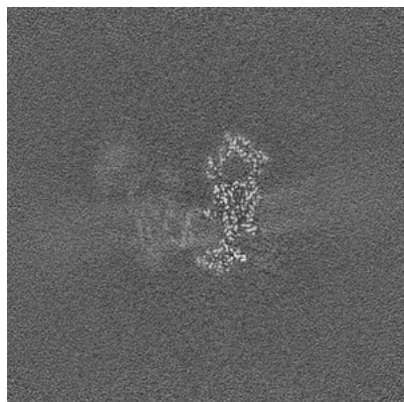


Y Index: 160

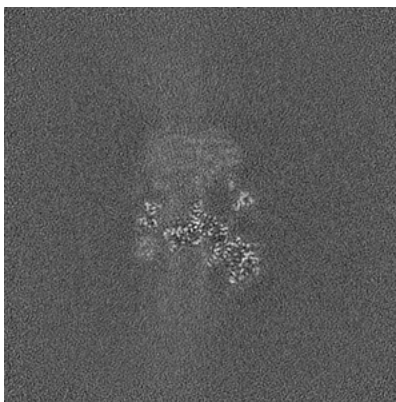


Z Index: 160

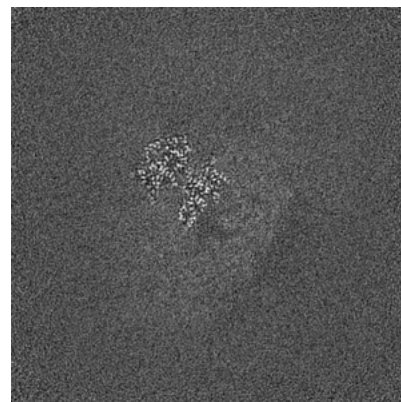
6.2.2 Raw map



X Index: 160



Y Index: 160

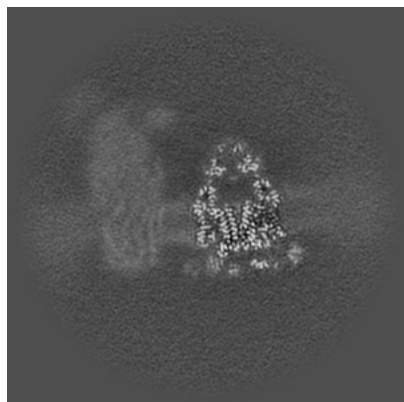


Z Index: 160

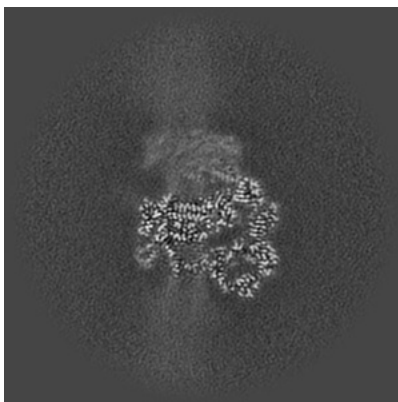
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

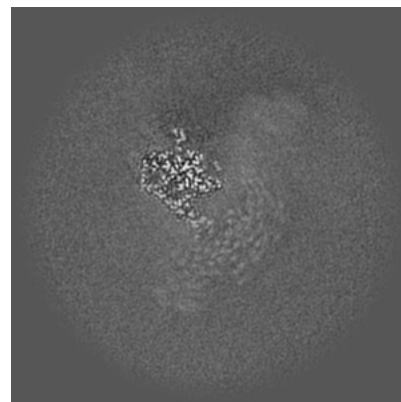
6.3.1 Primary map



X Index: 135

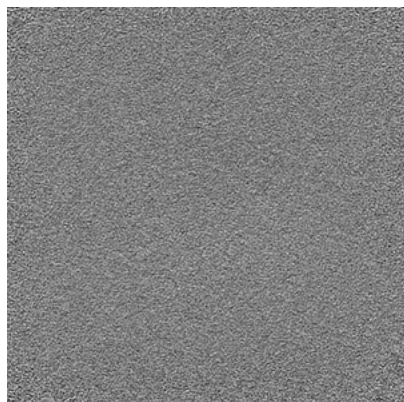


Y Index: 175

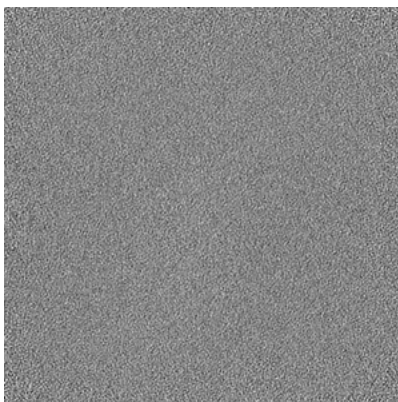


Z Index: 136

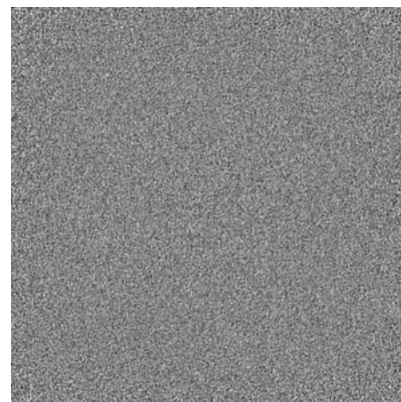
6.3.2 Raw map



X Index: 0



Y Index: 0

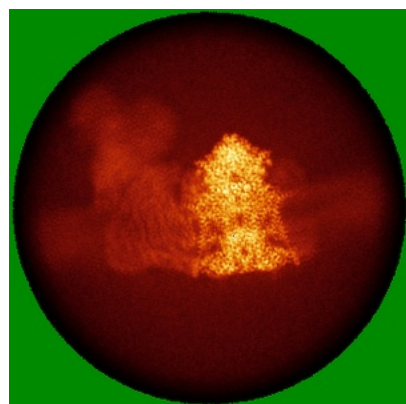


Z Index: 0

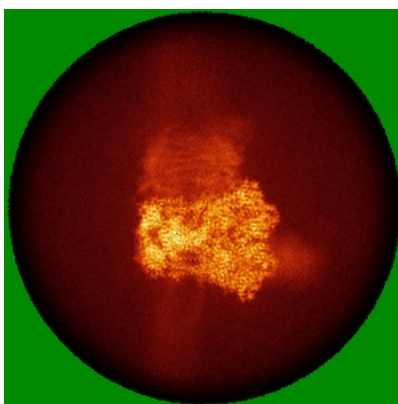
The images above show the largest variance slices of the map in three orthogonal directions.

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

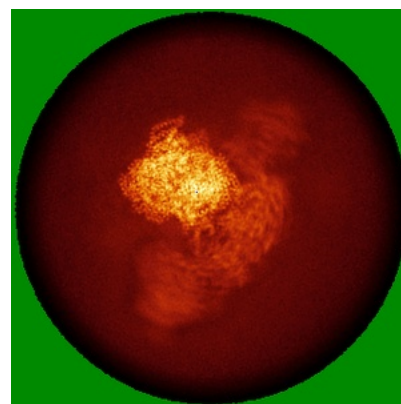
6.4.1 Primary map



X

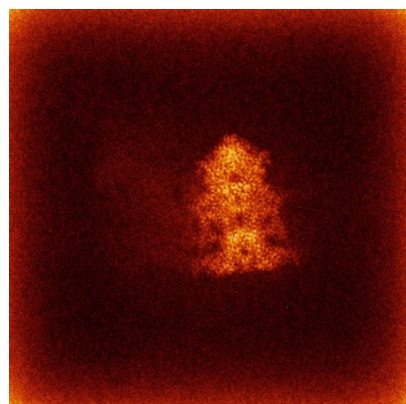


Y

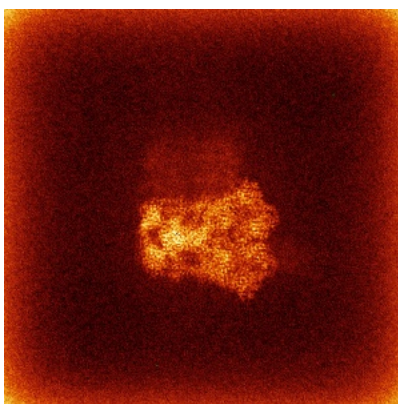


Z

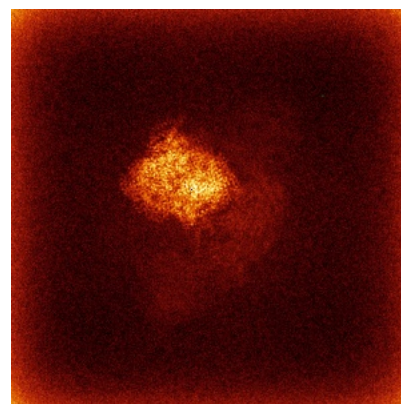
6.4.2 Raw map



X



Y

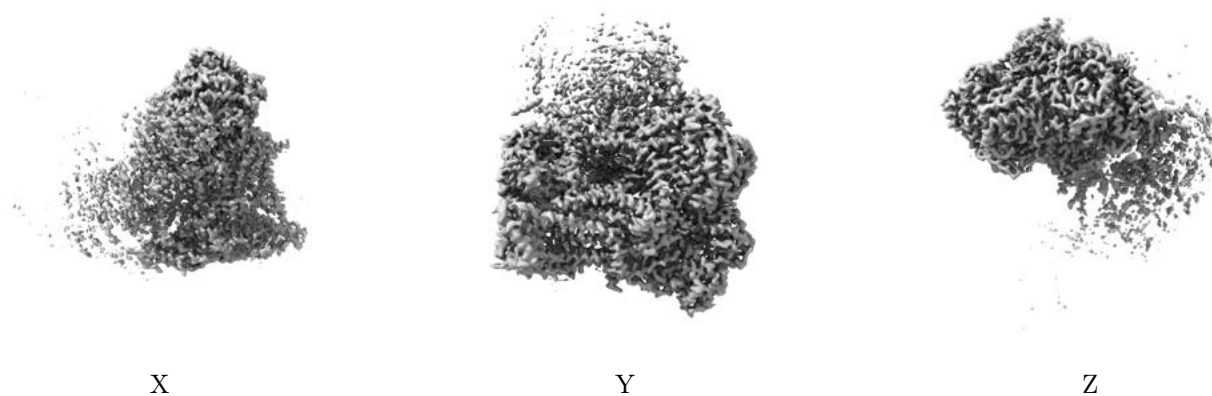


Z

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.

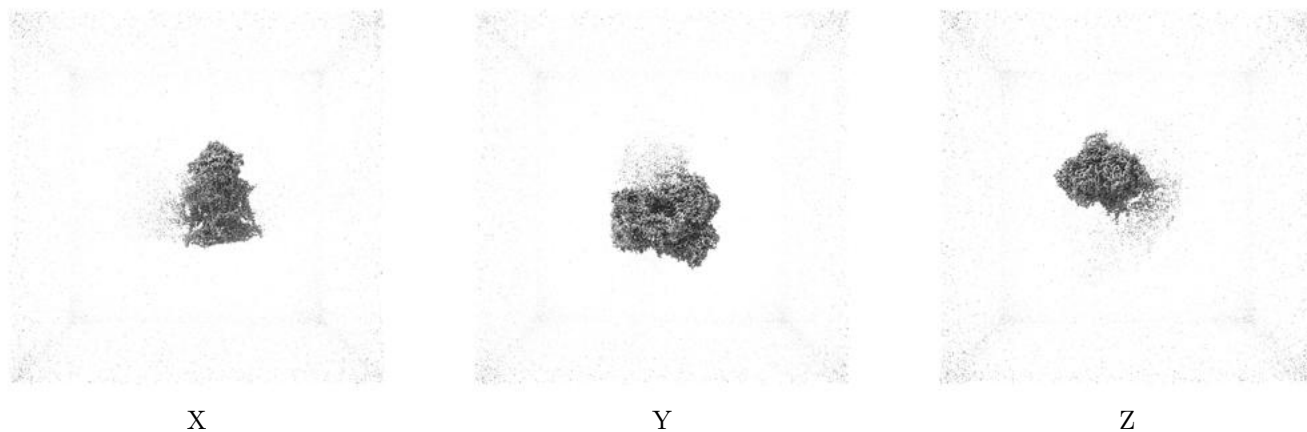
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

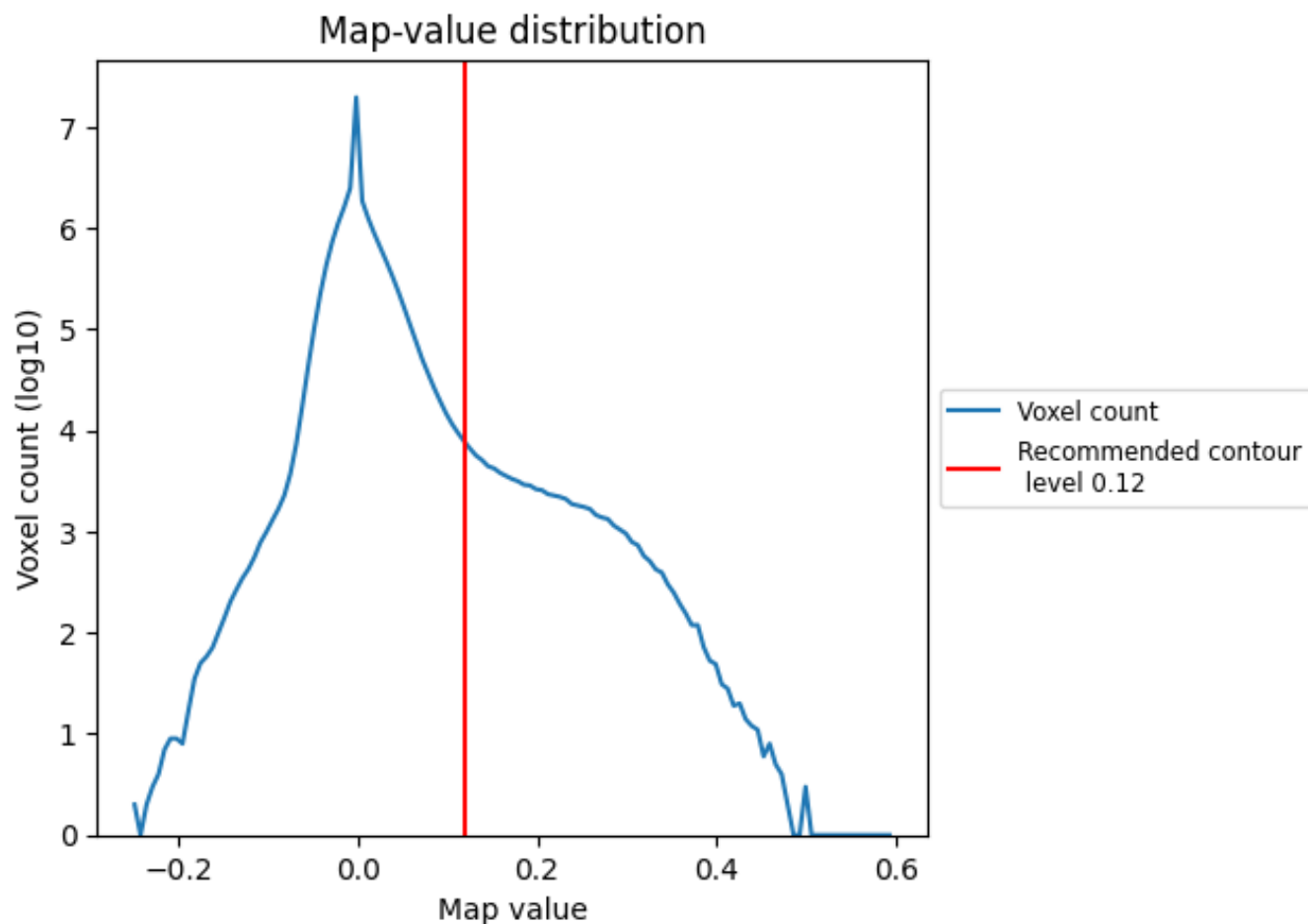
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

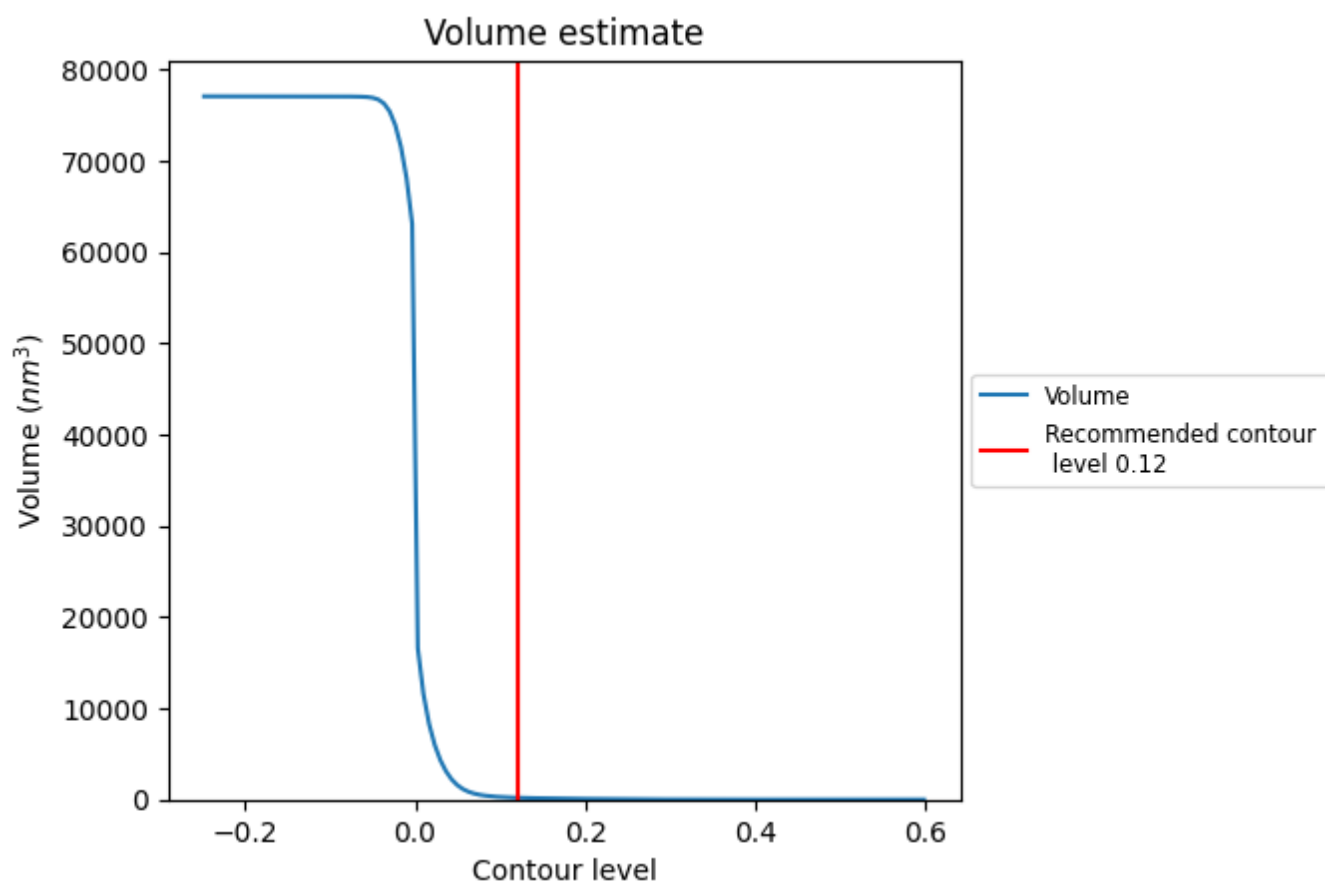
This section contains the results of statistical analysis of the map.

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.

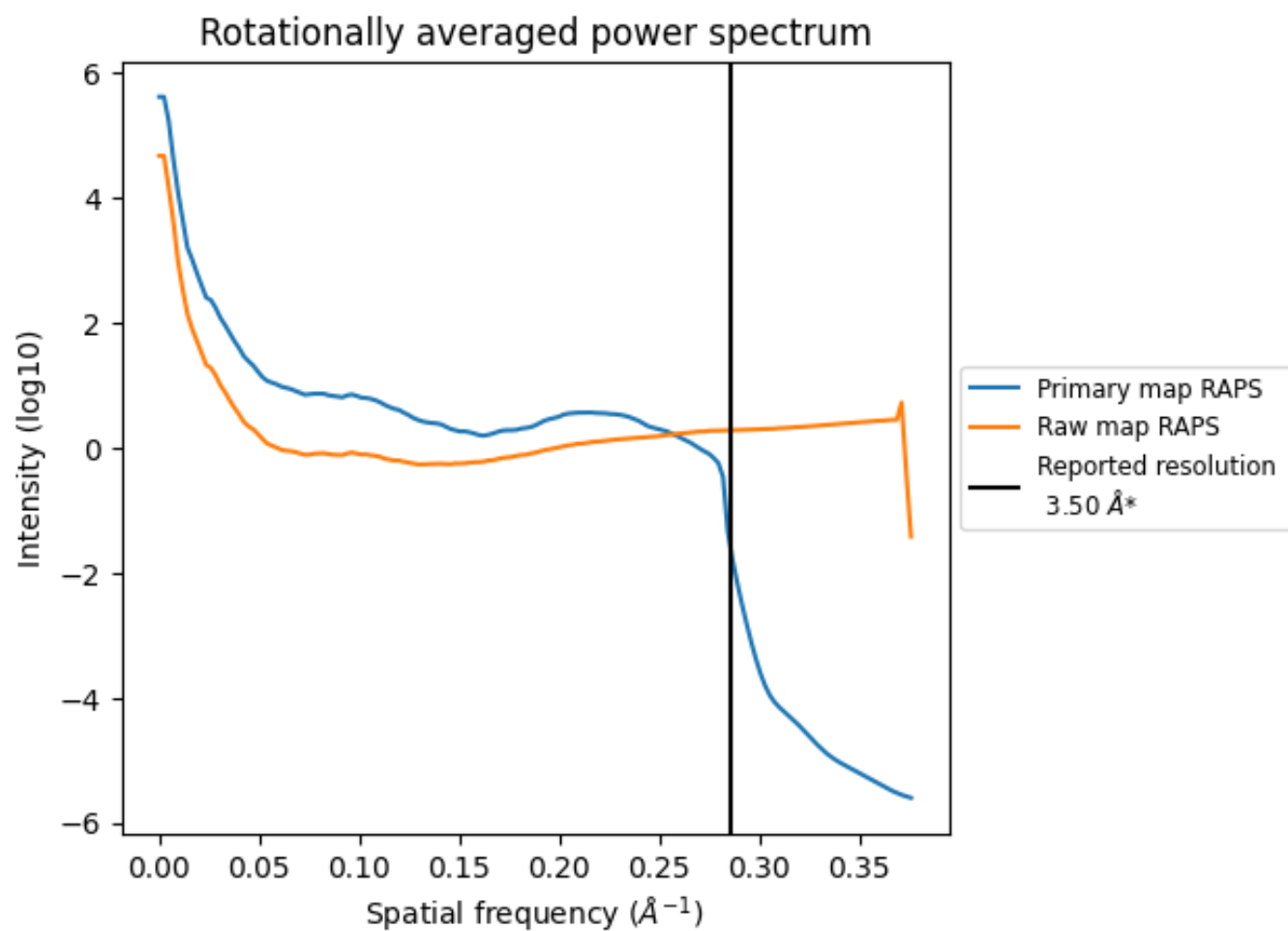
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 201 nm³; this corresponds to an approximate mass of 181 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 ⓘ

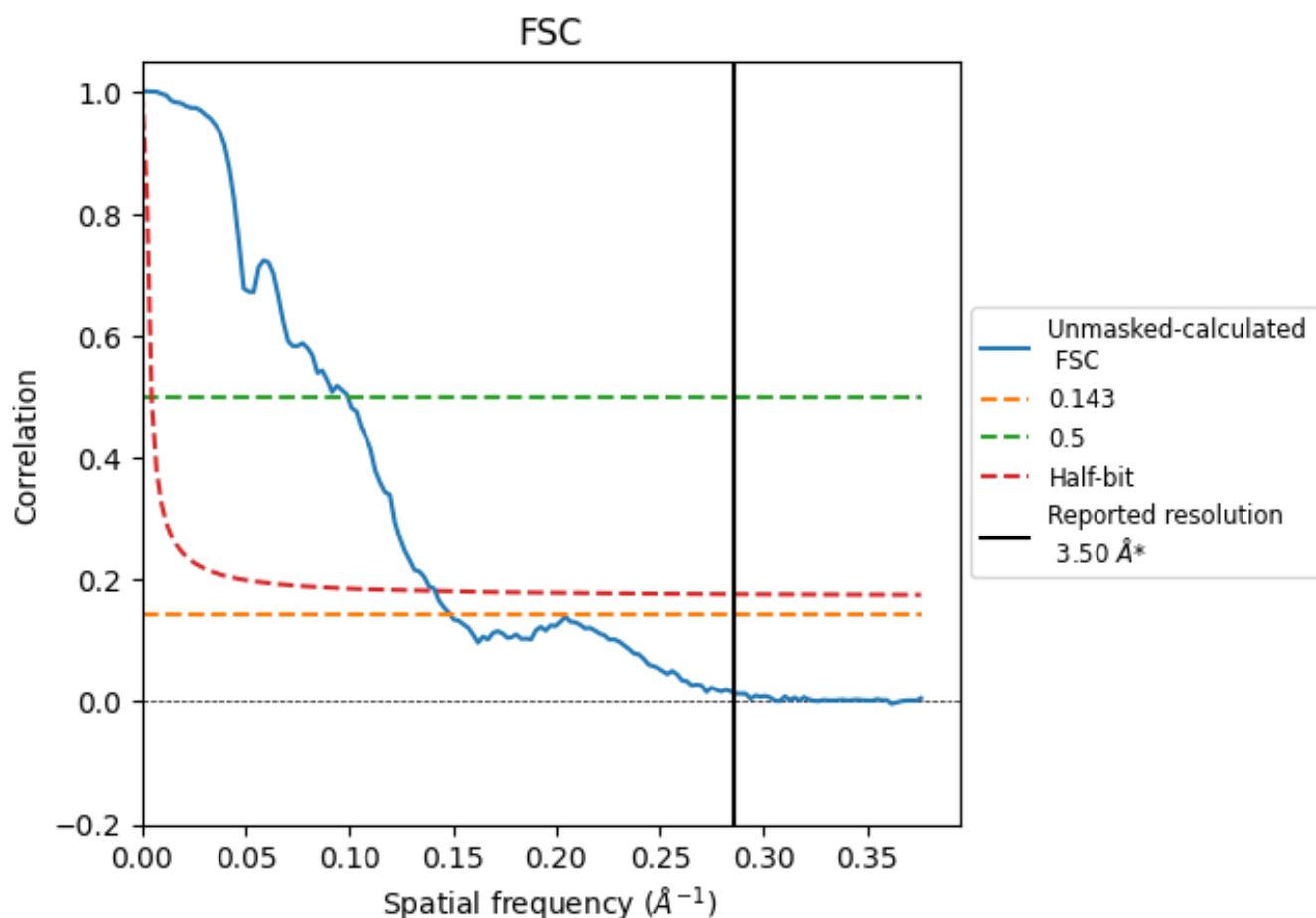


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

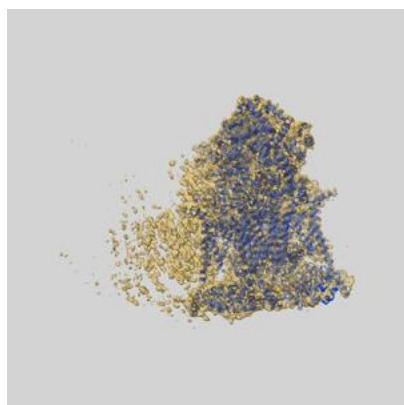
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.72	10.10	7.07

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.72 differs from the reported value 3.5 by more than 10 %

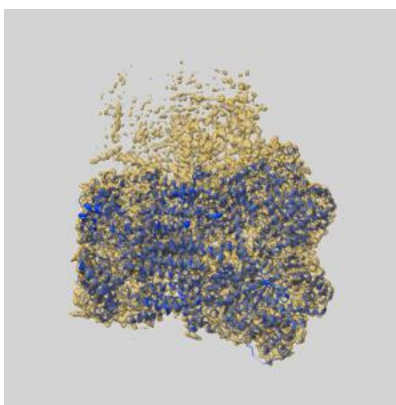
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42222 and PDB model 8UGE. Per-residue inclusion information can be found in section [3](#) on page [12](#).

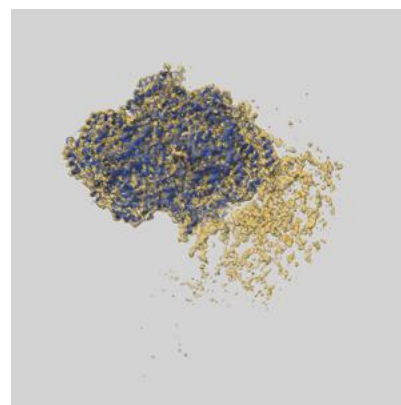
9.1 Map-model overlay [i](#)



X



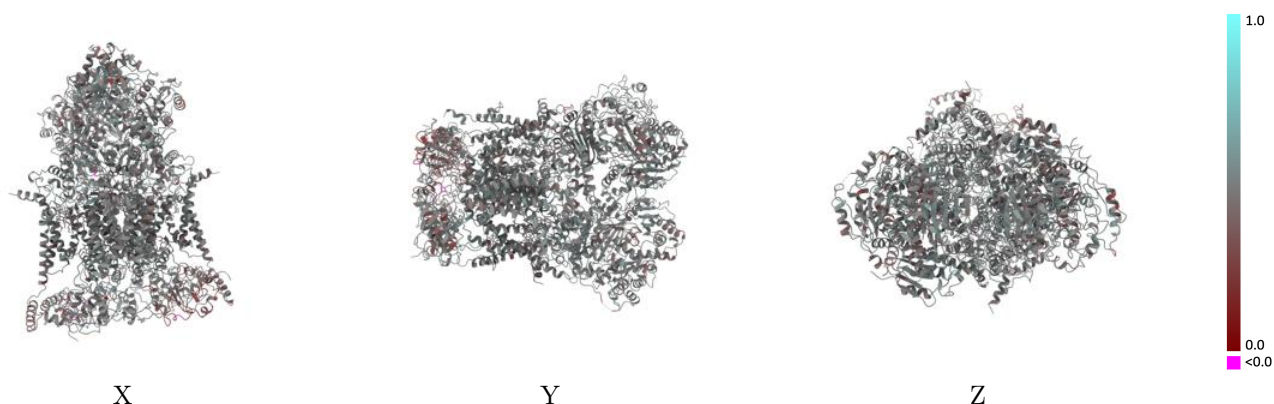
Y



Z

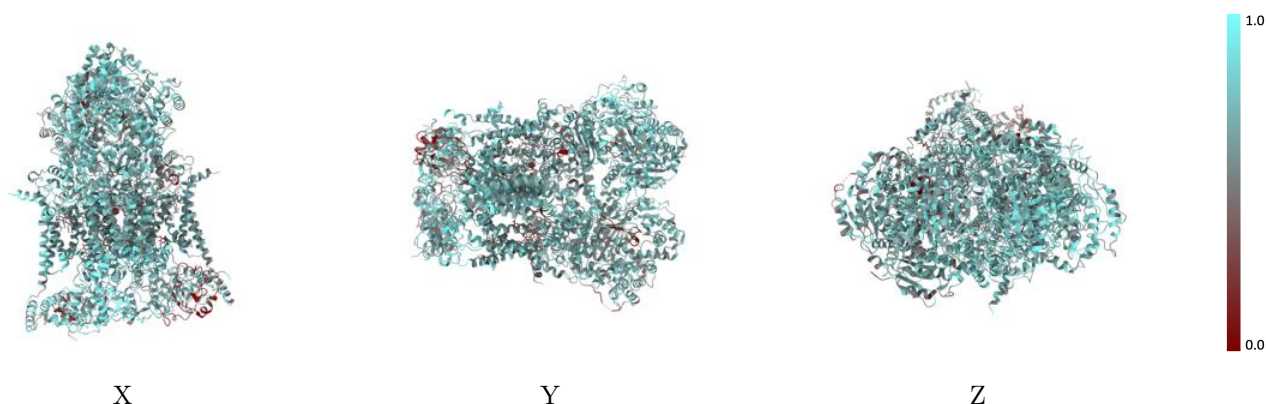
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



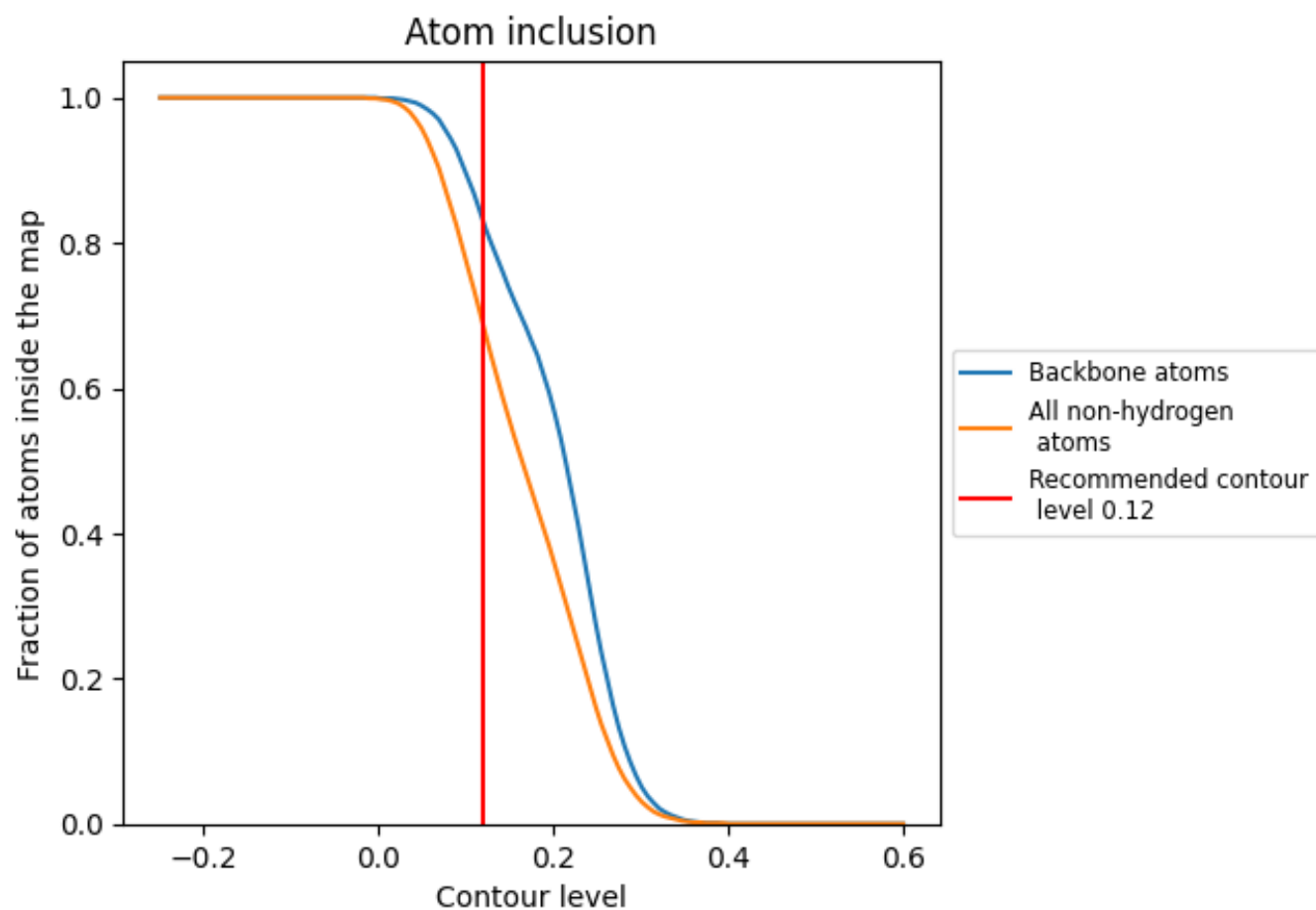
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 69% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6860	 0.4780
3A	 0.6670	 0.4890
3B	 0.6840	 0.4880
3C	 0.7050	 0.4930
3D	 0.7530	 0.4970
3E	 0.4800	 0.4050
3F	 0.6740	 0.4900
3G	 0.6330	 0.4870
3H	 0.6830	 0.4360
3I	 0.2410	 0.3820
3J	 0.6990	 0.4880
3N	 0.7470	 0.4860
3O	 0.7290	 0.4840
3P	 0.7440	 0.4920
3Q	 0.7690	 0.4930
3R	 0.4620	 0.3790
3S	 0.7560	 0.5010
3T	 0.7970	 0.4960
3U	 0.7060	 0.4460
3V	 0.4610	 0.4500
3W	 0.7790	 0.4950
3X	 0.6240	 0.4740
3Y	 0.5580	 0.4900

