



Full wwPDB EM Validation Report ⓘ

Jun 12, 2024 – 04:57 PM EDT

PDB ID : 8UGK
EMDB ID : EMD-42228
Title : High resolution in-situ structure of complex III in respiratory supercomplex
(composite)
Authors : Zheng, W.; Zhu, J.; Zhang, K.
Deposited on : 2023-10-05
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

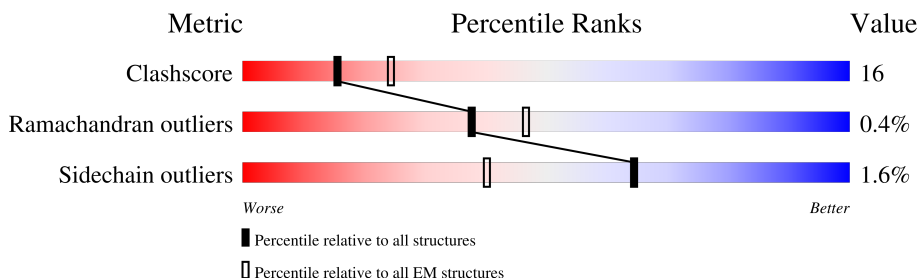
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	 66% 25% 8%
1	3N	480	 66% 26% 7%
2	3B	453	 5% 71% 21% 8%
2	3O	453	 6% 72% 20% 8%
3	3C	379	 73% 26%
3	3P	379	 76% 23%
4	3D	325	 49% 22% 27%
4	3Q	325	 54% 20% 26%

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Mol	Chain	Length	Quality of chain
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	FES	3E	301	-	-	X	-
15	FES	3R	301	-	-	X	-

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 35374 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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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		

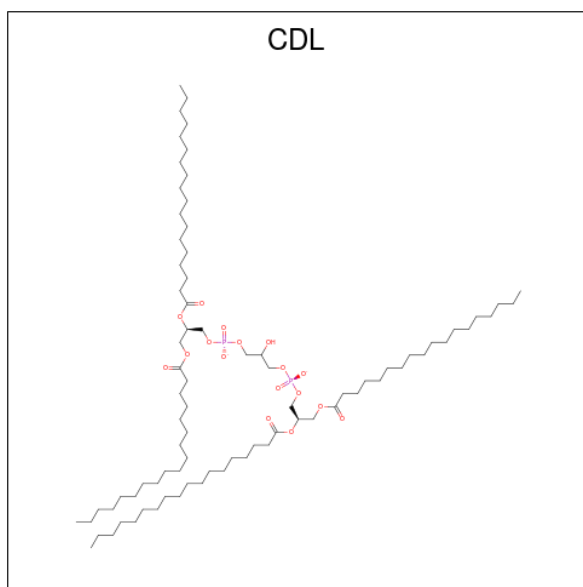
- Molecule 9 is a protein called Ubiquinol-cytochrome c reductase complex 7.2 kDa protein.

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 (three-letter code: 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	3G	1	Total	C	O	P	0
			52	33	17	2	
11	3G	1	Total	C	O	P	0
			56	37	17	2	
11	3N	1	Total	C	O	P	0
			43	24	17	2	
11	3P	1	Total	C	O	P	0
			56	37	17	2	
11	3T	1	Total	C	O	P	0
			57	38	17	2	

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

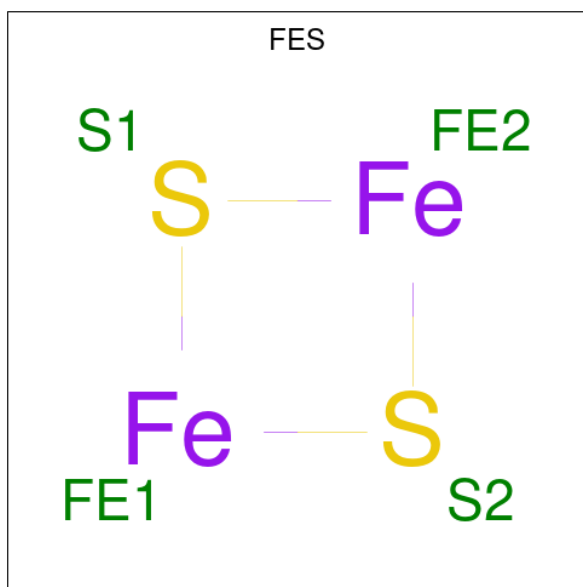


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
12	3A	1	Total 27	C 17	N 1	O 8	P 1	0
12	3A	1	Total 32	C 22	N 1	O 8	P 1	0
12	3C	1	Total 35	C 25	N 1	O 8	P 1	0
12	3C	1	Total 34	C 24	N 1	O 8	P 1	0
12	3D	1	Total 33	C 23	N 1	O 8	P 1	0
12	3G	1	Total 29	C 19	N 1	O 8	P 1	0
12	3N	1	Total 33	C 23	N 1	O 8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

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

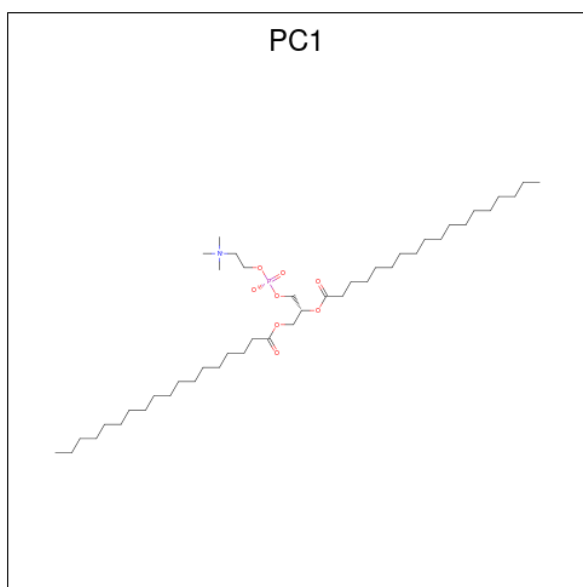
Mol	Chain	Residues	Atoms				AltConf	
14	3D	1	Total	C	Fe	N	O	0
			42	34	1	4	3	
14	3Q	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 15 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms		AltConf
15	3E	1	Total	Fe S	0
			4	2 2	
15	3R	1	Total	Fe S	0
			4	2 2	

- Molecule 16 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: C₄₄H₈₈NO₈P).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
16	3E	1	47	37	1	8	1	0
16	3R	1	45	35	1	8	1	0
16	3X	1	29	19	1	8	1	0

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
17	3A	184	184	184	0
17	3B	110	110	110	0
17	3C	222	222	222	0
17	3D	131	131	131	0
17	3E	45	45	45	0
17	3F	115	115	115	0
17	3G	78	78	78	0
17	3H	26	26	26	0
17	3I	5	5	5	0

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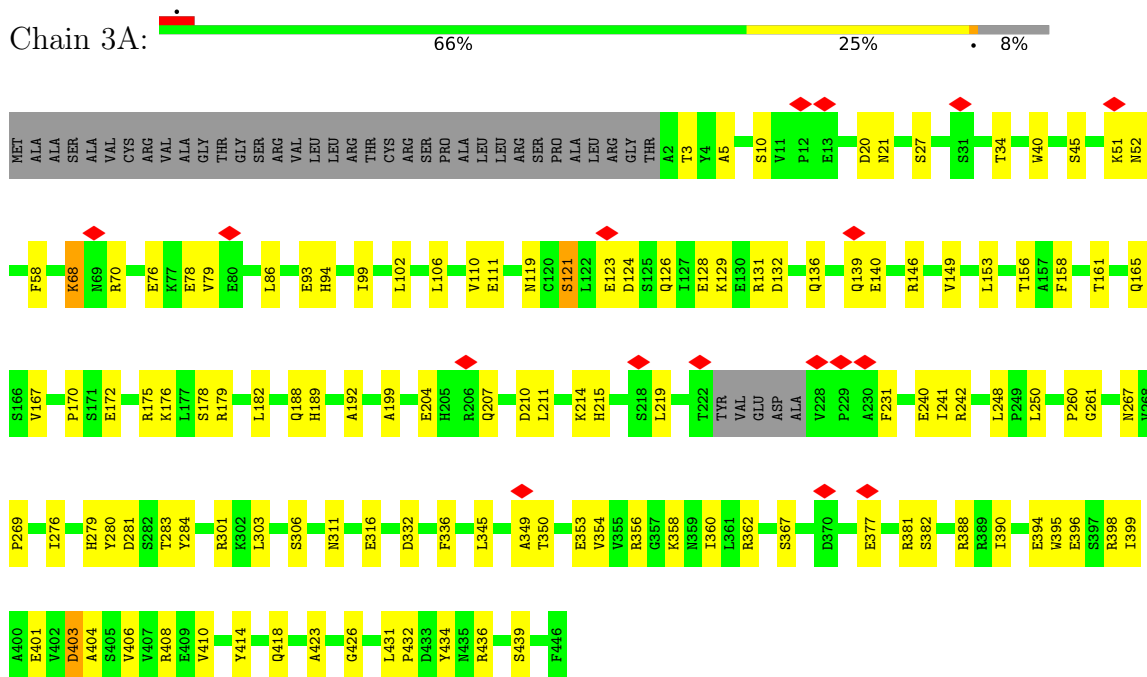
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Mol	Chain	Residues	Atoms		AltConf
17	3J	27	Total 27	O 27	0
17	3N	231	Total 231	O 231	0
17	3O	184	Total 184	O 184	0
17	3P	152	Total 152	O 152	0
17	3Q	98	Total 98	O 98	0
17	3R	47	Total 47	O 47	0
17	3S	71	Total 71	O 71	0
17	3T	25	Total 25	O 25	0
17	3U	110	Total 110	O 110	0
17	3V	7	Total 7	O 7	0
17	3W	29	Total 29	O 29	0
17	3X	25	Total 25	O 25	0
17	3Y	16	Total 16	O 16	0

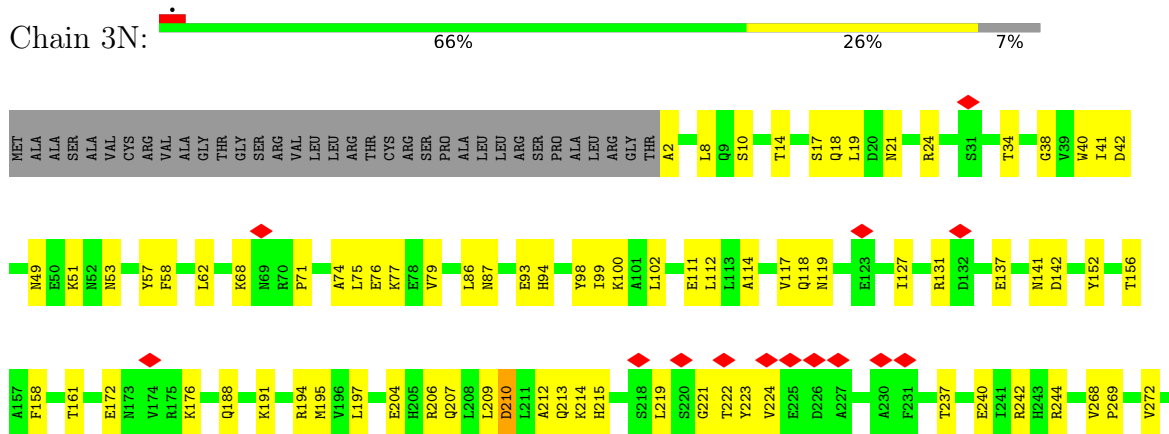
3 Residue-property plots

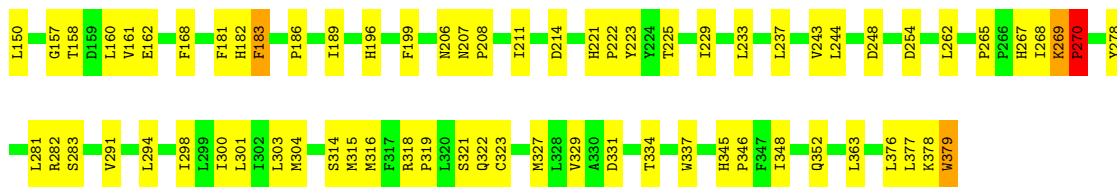
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

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

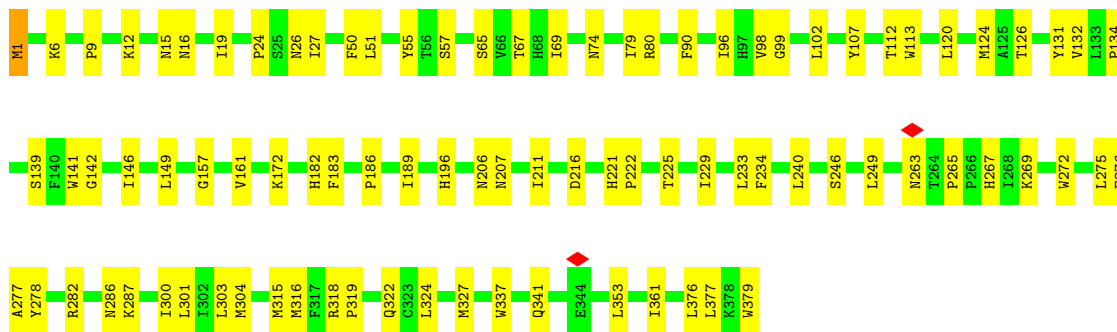
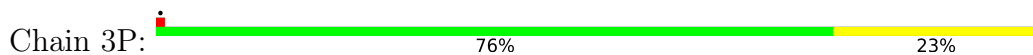


- Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial

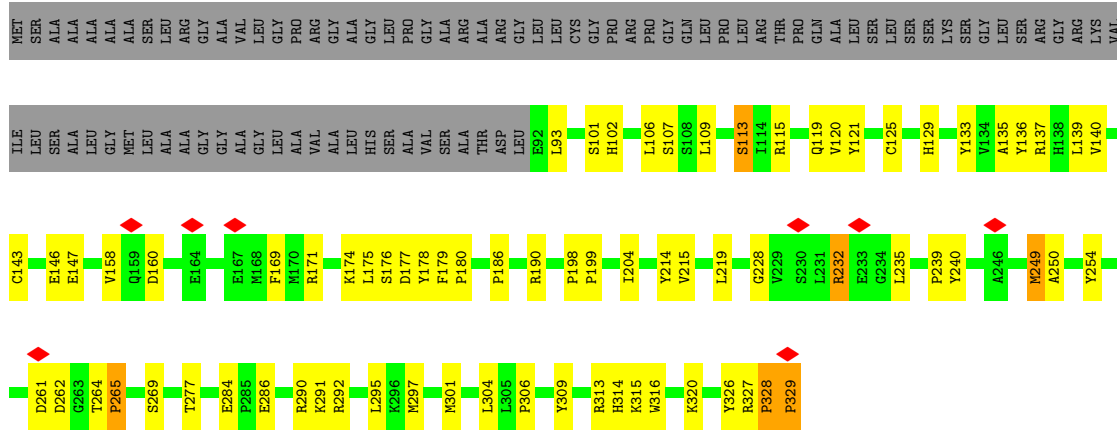




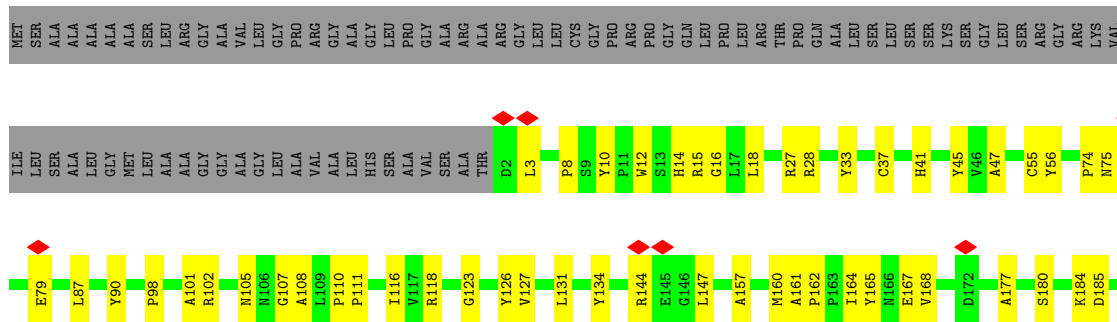
• Molecule 3: Cytochrome b

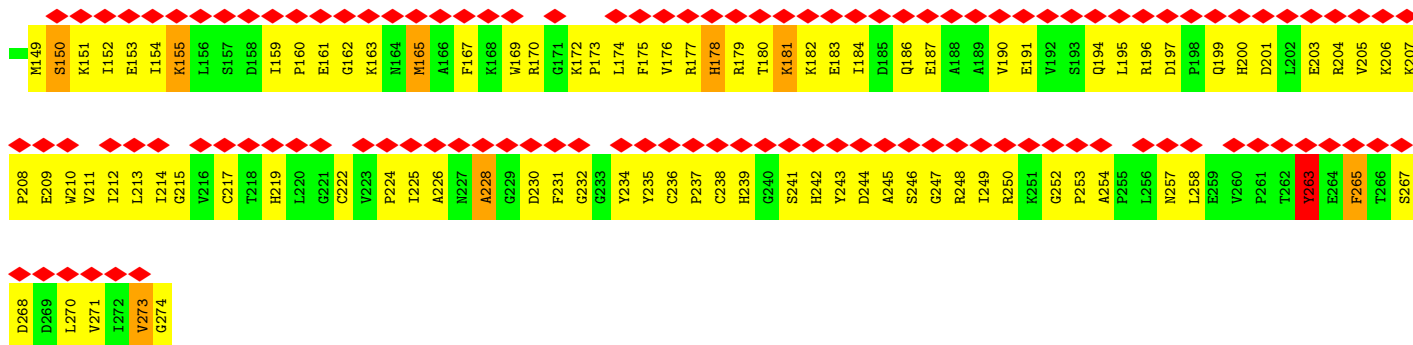


• Molecule 4: Cytochrome c1, heme protein, mitochondrial

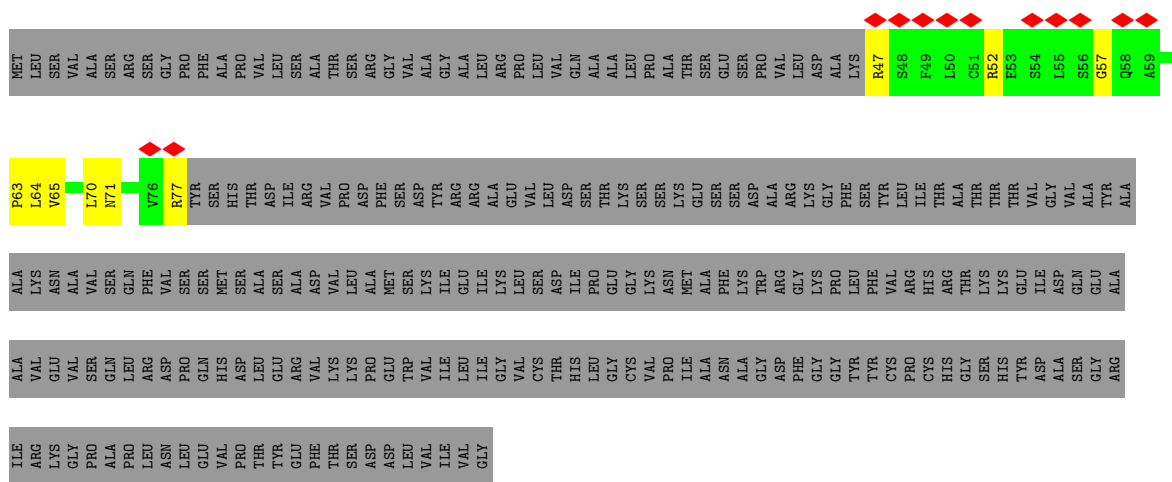


• Molecule 4: Cytochrome c1, heme protein, mitochondrial

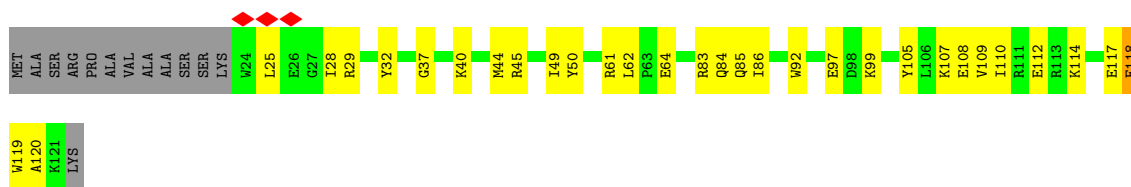




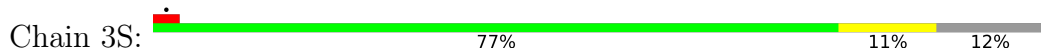
• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



• Molecule 6: Cytochrome b-c1 complex subunit 7

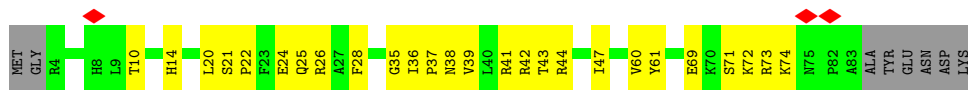


• Molecule 6: Cytochrome b-c1 complex subunit 7

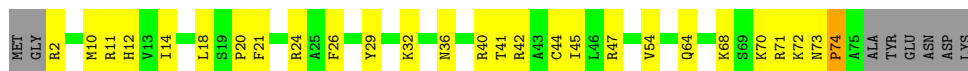


• Molecule 7: Cytochrome b-c1 complex subunit 8

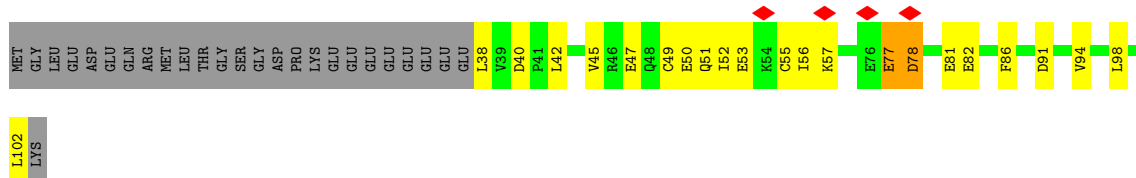




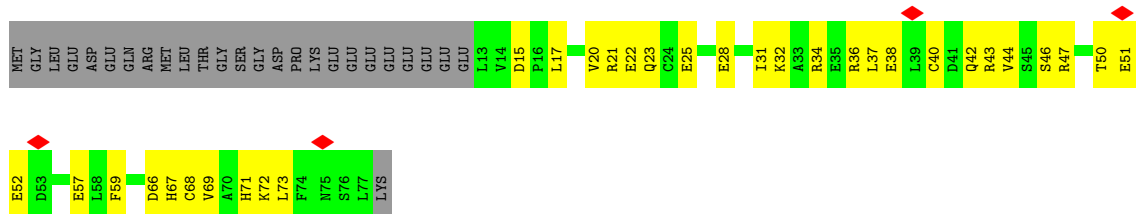
• Molecule 7: Cytochrome b-c1 complex subunit 8



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



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



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



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



• 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	300000	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)	1000	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.626	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	213.824, 213.824, 213.824	wwPDB
Map dimensions	514, 514, 514	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.416, 0.416, 0.416	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: 3PE, FES, HEC, CDL, PC1, HEM

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	0.29	0/3481	0.54	0/4722
1	3N	0.31	0/3496	0.56	0/4723
2	3B	0.29	0/3190	0.52	0/4317
2	3O	0.30	0/3175	0.54	1/4292 (0.0%)
3	3C	0.60	4/3123 (0.1%)	0.74	8/4269 (0.2%)
3	3P	0.29	0/3122	0.48	0/4269
4	3D	0.83	6/1946 (0.3%)	1.00	11/2641 (0.4%)
4	3Q	0.60	3/1962 (0.2%)	0.80	4/2663 (0.2%)
5	3E	0.30	0/1551	0.56	0/2098
5	3I	0.79	2/342 (0.6%)	1.38	7/465 (1.5%)
5	3R	0.42	2/1551 (0.1%)	0.59	0/2098
5	3V	0.29	0/225	0.60	0/303
6	3F	0.32	0/888	0.55	0/1193
6	3S	0.30	0/888	0.53	0/1193
7	3G	0.32	0/649	0.57	0/878
7	3T	1.17	4/649 (0.6%)	1.38	7/878 (0.8%)
8	3H	0.32	0/539	0.67	1/724 (0.1%)
8	3U	0.43	1/539 (0.2%)	0.60	0/724
9	3J	0.51	0/476	0.65	0/641
9	3W	0.31	0/476	0.53	0/641
10	3X	0.29	0/445	0.53	0/608
10	3Y	0.29	0/437	0.54	0/598
All	All	0.45	22/33150 (0.1%)	0.66	39/44938 (0.1%)

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	2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	3D	265	PRO	CG-CD	-22.83	0.75	1.50
7	3T	74	PRO	CG-CD	-21.56	0.79	1.50
3	3C	270	PRO	CB-CG	19.82	2.49	1.50
4	3Q	74	PRO	CG-CD	-19.55	0.86	1.50
3	3C	270	PRO	CG-CD	-17.72	0.92	1.50
7	3T	73	ASN	C-N	13.01	1.58	1.34
4	3D	265	PRO	N-CD	12.29	1.65	1.47
4	3D	329	PRO	CG-CD	-11.51	1.12	1.50
4	3D	265	PRO	CB-CG	11.16	2.05	1.50
5	3I	48	SER	C-N	-11.13	1.08	1.34
7	3T	74	PRO	CB-CG	10.88	2.04	1.50
4	3D	329	PRO	CB-CG	-10.28	0.98	1.50
3	3C	270	PRO	N-CD	7.59	1.58	1.47
3	3C	269	LYS	C-N	7.51	1.48	1.34
4	3Q	74	PRO	CB-CG	6.38	1.81	1.50
4	3D	265	PRO	CA-CB	-6.08	1.41	1.53
8	3U	68	CYS	CB-SG	-5.60	1.72	1.81
7	3T	74	PRO	N-CD	5.53	1.55	1.47
5	3R	263	TYR	CZ-OH	-5.42	1.28	1.37
5	3I	49	PHE	C-N	-5.37	1.21	1.34
4	3Q	74	PRO	N-CD	5.09	1.54	1.47
5	3R	263	TYR	CD1-CE1	-5.09	1.31	1.39

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3C	270	PRO	CB-CG-CD	-25.58	6.72	106.50
4	3Q	74	PRO	N-CD-CG	-23.26	68.30	103.20
7	3T	74	PRO	N-CD-CG	-22.41	69.59	103.20
4	3D	265	PRO	N-CD-CG	-20.80	72.00	103.20
4	3D	329	PRO	CB-CG-CD	18.83	179.94	106.50
4	3D	329	PRO	N-CD-CG	-15.91	79.33	103.20
7	3T	74	PRO	CA-CB-CG	-15.22	75.07	104.00
4	3Q	74	PRO	CA-CB-CG	-14.36	76.72	104.00
5	3I	49	PHE	O-C-N	-14.23	99.93	122.70
4	3D	329	PRO	CA-CB-CG	-13.81	77.77	104.00
7	3T	74	PRO	CB-CG-CD	-13.23	54.92	106.50
3	3C	270	PRO	CA-N-CD	-12.99	93.31	111.50
4	3D	265	PRO	CA-N-CD	-12.72	93.69	111.50
7	3T	74	PRO	N-CA-CB	-12.67	88.09	103.30
3	3C	270	PRO	N-CA-CB	-11.36	89.67	103.30
5	3I	48	SER	O-C-N	-10.65	105.65	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	3T	74	PRO	CA-N-CD	-10.41	96.92	111.50
3	3C	269	LYS	C-N-CD	10.03	149.46	128.40
4	3D	265	PRO	CA-CB-CG	-9.85	85.28	104.00
5	3I	49	PHE	CA-C-N	9.60	138.32	117.20
8	3H	77	GLU	C-N-CA	9.40	145.21	121.70
4	3D	265	PRO	CB-CG-CD	-9.27	70.35	106.50
3	3C	270	PRO	N-CD-CG	-9.08	89.58	103.20
3	3C	270	PRO	CA-CB-CG	-8.57	87.71	104.00
5	3I	48	SER	C-N-CA	8.46	142.84	121.70
7	3T	73	ASN	C-N-CD	7.94	145.07	128.40
5	3I	49	PHE	C-N-CA	7.89	141.44	121.70
4	3D	264	THR	N-CA-CB	-7.75	95.57	110.30
4	3D	328	PRO	C-N-CD	7.44	144.03	128.40
7	3T	73	ASN	CA-C-N	7.44	137.92	117.10
4	3Q	74	PRO	N-CA-CB	-7.27	94.58	103.30
5	3I	48	SER	CA-C-N	7.00	132.59	117.20
4	3D	329	PRO	CA-N-CD	-6.81	101.96	111.50
4	3D	264	THR	C-N-CD	6.53	142.11	128.40
2	3O	33	LEU	CA-CB-CG	5.89	128.85	115.30
3	3C	269	LYS	O-C-N	-5.65	110.37	121.10
4	3Q	74	PRO	CA-N-CD	-5.61	103.65	111.50
5	3I	63	PRO	CA-N-CD	-5.58	103.69	111.50
3	3C	269	LYS	CA-C-N	5.08	131.32	117.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	3R	263	TYR	Sidechain
5	3R	265	PHE	Sidechain

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	3308	85	0
1	3N	3424	0	3350	112	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	3B	3138	0	3116	75	0
2	3O	3124	0	3108	74	0
3	3C	3025	0	3090	117	0
3	3P	3024	0	3090	79	0
4	3D	1888	0	1834	71	0
4	3Q	1904	0	1849	58	0
5	3E	1518	0	1498	89	0
5	3I	337	0	345	32	0
5	3R	1518	0	1498	157	0
5	3V	223	0	233	11	0
6	3F	868	0	857	30	0
6	3S	868	0	857	10	0
7	3G	628	0	634	28	0
7	3T	628	0	634	29	0
8	3H	533	0	513	18	0
8	3U	533	0	513	27	0
9	3J	464	0	467	15	0
9	3W	464	0	467	11	0
10	3X	429	0	430	25	0
10	3Y	421	0	418	14	0
11	3A	58	0	60	12	0
11	3G	108	0	104	9	0
11	3N	43	0	30	7	0
11	3P	56	0	56	7	0
11	3T	57	0	58	6	0
12	3A	59	0	66	14	0
12	3C	69	0	86	14	0
12	3D	33	0	40	6	0
12	3G	29	0	32	2	0
12	3N	58	0	62	10	0
12	3P	33	0	40	5	0
12	3R	47	0	71	6	0
12	3Y	30	0	34	0	0
13	3C	86	0	60	7	0
13	3P	86	0	60	4	0
14	3D	42	0	32	5	0
14	3Q	43	0	32	4	0
15	3E	4	0	0	2	0
15	3R	4	0	0	5	0
16	3E	47	0	68	8	0
16	3R	45	0	64	9	0
16	3X	29	0	32	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	3A	184	0	0	13	0
17	3B	110	0	0	5	0
17	3C	222	0	0	27	0
17	3D	131	0	0	7	0
17	3E	45	0	0	0	0
17	3F	115	0	0	7	0
17	3G	78	0	0	5	0
17	3H	26	0	0	1	0
17	3I	5	0	0	0	0
17	3J	27	0	0	3	0
17	3N	231	0	0	25	0
17	3O	184	0	0	17	0
17	3P	152	0	0	19	0
17	3Q	98	0	0	5	0
17	3R	47	0	0	6	0
17	3S	71	0	0	3	0
17	3T	25	0	0	2	0
17	3U	110	0	0	11	0
17	3V	7	0	0	2	0
17	3W	29	0	0	2	0
17	3X	25	0	0	3	0
17	3Y	16	0	0	0	0
All	All	35374	0	33196	1083	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 16.

All (1083) 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)
3:3C:270:PRO:CG	3:3C:270:PRO:N	1.82	1.40
3:3C:270:PRO:CD	3:3C:270:PRO:HG3	1.68	1.15
3:3C:150:LEU:HD21	3:3C:160:LEU:HD23	1.34	1.10
3:3C:270:PRO:CD	3:3C:270:PRO:HG2	1.69	1.10
3:3C:270:PRO:CG	3:3C:270:PRO:HD3	1.59	1.09
3:3C:270:PRO:CG	3:3C:270:PRO:HD2	1.59	1.07
5:3R:206:LYS:HG2	5:3R:263:TYR:OH	1.57	1.05
5:3E:237:PRO:HB2	4:3Q:144:ARG:HD3	1.37	1.04
5:3R:219:HIS:CD2	5:3R:239:HIS:CE1	2.55	0.95
5:3R:172:LYS:HD3	5:3R:214:ILE:HG21	1.51	0.93
5:3R:226:ALA:HA	5:3R:234:TYR:HD2	1.34	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:3C:504:3PE:H112	5:3R:138:SER:HB3	1.50	0.92
3:3C:270:PRO:CG	3:3C:270:PRO:CD	0.92	0.92
3:3C:270:PRO:CG	3:3C:270:PRO:CB	2.49	0.91
5:3E:195:LEU:HD22	5:3E:250:ARG:HA	1.53	0.90
5:3R:232:GLY:HA3	5:3R:244:ASP:HA	1.55	0.89
5:3R:219:HIS:CD2	5:3R:239:HIS:NE2	2.41	0.89
1:3N:332:ASP:OD2	3:3P:6:LYS:NZ	2.06	0.88
2:3O:112:LEU:O	17:3O:501:HOH:O	1.91	0.87
5:3I:64:LEU:HA	5:3I:77:ARG:O	1.75	0.86
3:3C:157:GLY:O	17:3C:601:HOH:O	1.94	0.85
2:3O:31:ASN:ND2	17:3O:504:HOH:O	2.09	0.85
1:3N:346:CYS:SG	17:3N:636:HOH:O	2.36	0.83
4:3D:136:TYR:O	17:3D:601:HOH:O	1.96	0.83
10:3X:37:ASP:OD1	10:3X:51:LYS:NZ	2.12	0.82
5:3E:261:PRO:HB2	5:3E:273:VAL:HG11	1.62	0.82
6:3F:97:GLU:OE1	17:3F:201:HOH:O	1.97	0.81
2:3O:78:LYS:HG2	2:3O:129:ALA:HB1	1.62	0.81
2:3B:166:ALA:HB2	2:3B:244:ILE:HG13	1.63	0.81
1:3N:444:LEU:HB2	11:3N:502:CDL:HB31	1.63	0.81
2:3B:47:ILE:HD11	2:3B:211:VAL:HG11	1.63	0.80
5:3R:206:LYS:CG	5:3R:263:TYR:OH	2.29	0.80
6:3S:67:ASP:OD2	17:3S:201:HOH:O	2.00	0.80
12:3N:501:3PE:H31	11:3N:502:CDL:H512	1.64	0.80
8:3U:22:GLU:HA	8:3U:25:GLU:HG2	1.64	0.79
4:3Q:10:TYR:O	4:3Q:15:ARG:NH1	2.16	0.79
5:3R:179:ARG:HH21	5:3R:184:ILE:HA	1.47	0.78
9:3J:54:LYS:HA	9:3J:57:LYS:HE2	1.65	0.78
5:3R:177:ARG:HD2	5:3R:234:TYR:OH	1.84	0.77
6:3S:71:ARG:NH1	17:3S:203:HOH:O	2.16	0.77
2:3B:95:LYS:HE2	5:3I:72:VAL:HB	1.65	0.77
3:3C:6:LYS:NZ	17:3C:605:HOH:O	2.15	0.77
1:3N:14:THR:HG21	1:3N:389:ARG:HB3	1.66	0.76
4:3Q:118:ARG:HG3	4:3Q:194:SER:HB3	1.67	0.76
8:3U:42:GLN:NE2	17:3U:105:HOH:O	2.18	0.76
5:3R:195:LEU:HB3	5:3R:248:ARG:HH21	1.48	0.76
4:3D:240:TYR:OH	8:3H:91:ASP:OD2	2.04	0.76
9:3J:53:TRP:O	9:3J:54:LYS:HB3	1.85	0.75
1:3N:68:LYS:HG2	1:3N:119:ASN:HB3	1.67	0.75
9:3J:41:ASP:O	9:3J:45:GLU:HG3	1.85	0.75
4:3Q:144:ARG:HE	4:3Q:147:LEU:HG	1.50	0.75
1:3N:86:LEU:HB3	2:3O:285:VAL:HG22	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3I:36:ALA:HB3	5:3I:73:PRO:HG2	1.68	0.75
5:3R:219:HIS:HD2	5:3R:239:HIS:NE2	1.84	0.75
2:3B:95:LYS:HD2	5:3I:32:ALA:HB2	1.67	0.75
2:3B:200:THR:HB	2:3B:227:ARG:HG2	1.69	0.75
5:3R:149:MET:O	5:3R:151:LYS:N	2.20	0.75
2:3B:35:ILE:HD12	2:3B:217:LYS:HG2	1.68	0.74
5:3R:236:CYS:SG	5:3R:239:HIS:HB2	2.28	0.74
5:3R:155:LYS:HE2	5:3R:271:VAL:HG23	1.68	0.74
1:3N:351:GLU:OE1	17:3N:601:HOH:O	2.07	0.73
4:3D:301:MET:CE	12:3D:502:3PE:H362	2.19	0.73
4:3D:147:GLU:OE2	17:3D:602:HOH:O	2.05	0.73
5:3R:95:GLU:OE1	17:3R:401:HOH:O	2.06	0.73
5:3R:224:PRO:HA	5:3R:237:PRO:HD3	1.69	0.72
11:3A:501:CDL:H151	11:3A:501:CDL:H321	1.70	0.72
7:3G:60:VAL:O	17:3G:201:HOH:O	2.07	0.72
1:3N:214:LYS:NZ	1:3N:215:HIS:CE1	2.57	0.72
1:3A:250:LEU:HD12	5:3I:44:ASP:HB2	1.72	0.72
3:3C:321:SER:HB2	17:3C:668:HOH:O	1.88	0.72
2:3O:187:THR:O	17:3O:502:HOH:O	2.06	0.72
4:3D:232:ARG:NH1	5:3R:237:PRO:HB2	2.05	0.72
7:3T:36:ASN:ND2	11:3T:101:CDL:OA4	2.21	0.72
2:3B:121:GLU:OE2	2:3B:222:ARG:NH1	2.23	0.72
12:3C:504:3PE:H251	5:3R:137:VAL:HG21	1.70	0.71
2:3O:28:ARG:NH2	2:3O:32:GLY:O	2.23	0.71
5:3R:212:ILE:HB	5:3R:265:PHE:CZ	2.24	0.71
11:3N:502:CDL:H322	3:3P:221:HIS:CD2	2.25	0.71
7:3T:64:GLN:O	7:3T:68:LYS:HG3	1.89	0.71
5:3R:263:TYR:CE1	5:3R:265:PHE:HB2	2.25	0.71
1:3N:76:GLU:O	17:3N:602:HOH:O	2.08	0.71
3:3C:281:LEU:HB2	3:3C:294:LEU:HB2	1.72	0.71
3:3C:221:HIS:O	3:3C:225:THR:OG1	2.04	0.71
2:3O:214:PRO:O	2:3O:218:GLN:HG2	1.90	0.71
1:3N:210:ASP:O	1:3N:214:LYS:HG2	1.90	0.71
5:3R:217:CYS:HB2	5:3R:224:PRO:HD3	1.71	0.71
5:3R:204:ARG:NH1	5:3R:246:SER:O	2.24	0.71
5:3R:176:VAL:HG22	5:3R:212:ILE:HG13	1.73	0.70
5:3E:241:SER:HA	5:3E:252:GLY:HA3	1.72	0.70
1:3N:240:GLU:OE2	1:3N:242:ARG:NH2	2.25	0.70
10:3X:12:GLU:OE1	17:3X:201:HOH:O	2.08	0.70
2:3O:25:GLU:OE2	17:3O:503:HOH:O	2.08	0.70
10:3X:38:TRP:HA	16:3X:101:PC1:H32	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:360:ILE:HG23	5:3I:33:ALA:HA	1.74	0.69
2:3B:201:SER:HB2	2:3B:228:GLY:HA2	1.74	0.69
4:3D:101:SER:O	4:3D:107:SER:OG	2.08	0.69
4:3D:235:LEU:HD11	5:3R:238:CYS:HA	1.73	0.69
5:3E:150:SER:HB3	5:3E:170:ARG:HG3	1.75	0.69
3:3C:318:ARG:HB2	17:3C:668:HOH:O	1.91	0.69
5:3I:49:PHE:HD1	5:3I:54:SER:HG	1.41	0.69
5:3E:264:GLU:H	5:3E:272:ILE:HG12	1.57	0.68
17:3D:630:HOH:O	5:3R:222:CYS:SG	2.51	0.68
2:3O:95:LYS:HE3	5:3V:71:ASN:OD1	1.93	0.68
3:3C:229:ILE:HG23	16:3E:302:PC1:H3A1	1.73	0.68
4:3D:232:ARG:HH11	5:3R:237:PRO:HB2	1.58	0.68
1:3N:214:LYS:HZ2	1:3N:215:HIS:CE1	2.11	0.68
5:3E:238:CYS:SG	17:3Q:619:HOH:O	2.51	0.68
3:3C:150:LEU:CD2	3:3C:160:LEU:HD23	2.20	0.68
1:3A:381:ARG:NH2	1:3A:382:SER:OG	2.26	0.68
5:3E:125:VAL:HG21	16:3E:302:PC1:H362	1.75	0.68
5:3E:219:HIS:HB3	15:3E:301:FES:S1	2.34	0.68
12:3N:503:3PE:O12	17:3N:603:HOH:O	2.11	0.67
8:3U:37:LEU:O	17:3U:102:HOH:O	2.11	0.67
5:3R:199:GLN:HB2	5:3R:248:ARG:HD3	1.75	0.67
4:3D:301:MET:HE1	12:3D:502:3PE:H362	1.76	0.67
1:3N:24:ARG:NH2	1:3N:383:LEU:O	2.25	0.67
8:3U:57:GLU:N	8:3U:57:GLU:OE1	2.28	0.67
1:3N:141:ASN:HA	5:3V:47:ARG:HH21	1.60	0.67
1:3N:42:ASP:HB2	1:3N:194:ARG:HB3	1.75	0.67
5:3E:195:LEU:HD12	5:3E:195:LEU:O	1.95	0.67
3:3C:161:VAL:HB	17:3C:601:HOH:O	1.95	0.66
5:3E:231:PHE:HE1	5:3E:242:HIS:HB3	1.58	0.66
5:3I:69:GLY:HA3	5:3I:72:VAL:HG12	1.76	0.66
5:3R:219:HIS:HB2	15:3R:301:FES:S1	2.36	0.66
6:3F:64:GLU:OE2	17:3F:202:HOH:O	2.13	0.66
1:3A:381:ARG:NH2	17:3A:605:HOH:O	2.29	0.66
5:3E:213:LEU:HD13	5:3E:258:LEU:HB2	1.78	0.66
1:3N:242:ARG:NH2	1:3N:432:PRO:O	2.26	0.66
3:3P:216:ASP:OD1	17:3P:601:HOH:O	2.13	0.66
10:3X:8:PRO:HA	10:3X:11:ARG:HD2	1.77	0.66
8:3U:67:HIS:CE1	8:3U:71:HIS:NE2	2.63	0.66
5:3E:155:LYS:HE3	5:3E:176:VAL:HG21	1.78	0.66
11:3G:102:CDL:O1	11:3G:102:CDL:OA7	2.14	0.65
5:3R:248:ARG:HD2	5:3R:257:ASN:HD22	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3D:306:PRO:HB3	12:3G:101:3PE:H362	1.78	0.65
6:3F:44:MET:HE2	6:3F:99:LYS:H	1.59	0.65
5:3R:162:GLY:H	5:3R:178:HIS:HB3	1.61	0.65
13:3P:501:HEM:O1D	17:3P:602:HOH:O	2.13	0.65
7:3T:2:ARG:O	17:3T:201:HOH:O	2.14	0.65
5:3E:161:GLU:HA	5:3E:178:HIS:HB3	1.78	0.65
1:3N:240:GLU:HG3	1:3N:422:VAL:HB	1.78	0.65
5:3R:196:ARG:NH2	5:3R:254:ALA:O	2.30	0.65
2:3B:120:MET:O	2:3B:124:LEU:HD23	1.97	0.64
2:3O:196:GLN:HA	2:3O:227:ARG:HD3	1.79	0.64
5:3R:212:ILE:HB	5:3R:265:PHE:HZ	1.61	0.64
6:3S:52:GLU:OE2	7:3T:11:ARG:NH1	2.28	0.64
1:3A:70:ARG:HD3	1:3A:78:GLU:OE2	1.98	0.64
13:3C:501:HEM:O2D	17:3C:604:HOH:O	2.14	0.64
5:3R:160:PRO:HD2	5:3R:163:LYS:HB3	1.79	0.64
2:3O:120:MET:CE	2:3O:219:VAL:HG11	2.27	0.64
10:3X:15:ARG:NH1	17:3X:204:HOH:O	2.29	0.64
1:3N:344:ARG:HG2	1:3N:344:ARG:HH11	1.62	0.64
1:3A:106:LEU:HD23	1:3A:207:GLN:NE2	2.13	0.64
3:3C:315:MET:HG2	17:3C:668:HOH:O	1.97	0.64
2:3B:227:ARG:HG3	2:3B:229:GLY:H	1.63	0.63
4:3D:115:ARG:HB2	4:3D:143:CYS:HB2	1.79	0.63
3:3C:237:LEU:HD13	4:3D:301:MET:HG3	1.79	0.63
4:3D:313:ARG:NH2	17:3D:604:HOH:O	2.25	0.63
3:3P:126:THR:HA	17:3P:646:HOH:O	1.98	0.63
6:3F:37:GLY:O	17:3F:203:HOH:O	2.15	0.63
4:3Q:105:ASN:ND2	4:3Q:108:ALA:O	2.31	0.63
1:3N:332:ASP:OD1	1:3N:432:PRO:HG3	1.99	0.63
3:3P:221:HIS:O	3:3P:225:THR:OG1	2.09	0.63
9:3W:10:TYR:HA	9:3W:14:PHE:HB2	1.79	0.63
4:3D:106:LEU:HD22	4:3D:295:LEU:HB2	1.81	0.62
1:3A:86:LEU:HD13	1:3A:99:ILE:HG12	1.81	0.62
2:3B:78:LYS:HB2	2:3B:129:ALA:HB1	1.80	0.62
4:3D:232:ARG:HD3	5:3R:237:PRO:HB3	1.79	0.62
5:3R:207:LYS:HG2	5:3R:265:PHE:HB3	1.82	0.62
2:3O:203:ARG:NH1	2:3O:232:LEU:O	2.32	0.62
8:3U:46:SER:OG	17:3U:101:HOH:O	2.03	0.62
3:3C:377:LEU:HG	6:3F:32:TYR:HE2	1.63	0.62
1:3N:19:LEU:HD21	17:3N:607:HOH:O	1.99	0.62
5:3R:263:TYR:CD1	5:3R:263:TYR:C	2.73	0.62
6:3F:118:GLU:OE1	17:3F:204:HOH:O	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3R:179:ARG:HE	5:3R:184:ILE:HG12	1.65	0.62
7:3G:69:GLU:HA	7:3G:72:LYS:HE2	1.81	0.62
1:3N:269:PRO:O	17:3N:606:HOH:O	2.16	0.62
4:3Q:12:TRP:HD1	4:3Q:15:ARG:HH12	1.47	0.62
1:3A:242:ARG:NH2	1:3A:431:LEU:O	2.32	0.62
5:3E:174:LEU:HD13	5:3E:214:ILE:HD13	1.82	0.61
10:3Y:11:ARG:HG3	10:3Y:15:ARG:NH1	2.16	0.61
1:3A:132:ASP:O	1:3A:136:GLN:HG2	2.00	0.61
2:3O:51:ILE:HG12	2:3O:204:MET:HG2	1.82	0.61
3:3C:379:TRP:OXT	17:3C:606:HOH:O	2.16	0.61
1:3N:356:ARG:O	1:3N:360:ILE:HG13	2.01	0.61
3:3P:376:LEU:O	17:3P:603:HOH:O	2.16	0.61
1:3A:121:SER:HB3	1:3A:123:GLU:HG3	1.82	0.61
3:3C:150:LEU:O	3:3C:150:LEU:HD23	2.00	0.61
4:3Q:177:ALA:O	17:3Q:602:HOH:O	2.16	0.61
4:3D:292:ARG:HG3	17:3J:112:HOH:O	2.00	0.61
5:3E:169:TRP:CE2	5:3E:273:VAL:HG12	2.36	0.61
4:3Q:144:ARG:HG2	4:3Q:147:LEU:HD12	1.82	0.61
3:3C:281:LEU:HD13	3:3C:294:LEU:HD13	1.84	0.60
5:3E:179:ARG:HH12	5:3E:184:ILE:HG12	1.66	0.60
3:3C:81:TYR:HB2	17:3C:635:HOH:O	2.01	0.60
2:3B:99:THR:HG1	5:3I:67:SER:HG	1.45	0.60
1:3N:429:GLU:O	17:3N:605:HOH:O	2.16	0.60
4:3D:314:HIS:CE1	7:3G:22:PRO:HB2	2.37	0.60
1:3N:114:ALA:O	1:3N:118:GLN:HB2	2.01	0.60
5:3R:226:ALA:HA	5:3R:234:TYR:CD2	2.25	0.60
11:3A:501:CDL:H332	11:3A:501:CDL:H171	1.84	0.60
4:3D:129:HIS:HE1	4:3D:199:PRO:HD2	1.67	0.60
5:3R:199:GLN:HG3	5:3R:257:ASN:ND2	2.17	0.60
2:3B:37:SER:HB3	2:3B:216:LEU:HD12	1.83	0.60
4:3D:160:ASP:HB2	4:3D:171:ARG:HG2	1.84	0.60
5:3R:179:ARG:HH11	5:3R:211:VAL:HB	1.67	0.60
1:3A:269:PRO:HB2	1:3A:410:VAL:HG11	1.84	0.59
2:3B:314:ALA:CB	5:3I:63:PRO:HG3	2.32	0.59
5:3R:211:VAL:HG11	5:3R:245:ALA:O	2.01	0.59
4:3D:139:LEU:HD13	17:3D:725:HOH:O	2.02	0.59
1:3N:34:THR:HG22	1:3N:102:LEU:HD23	1.82	0.59
3:3P:300:ILE:HG13	3:3P:303:LEU:HD12	1.82	0.59
3:3P:316:MET:HA	12:3P:503:3PE:H111	1.84	0.59
5:3R:207:LYS:H	5:3R:265:PHE:HD2	1.50	0.59
3:3C:196:HIS:HE1	13:3C:502:HEM:ND	1.99	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3E:235:TYR:HA	5:3E:243:TYR:H	1.68	0.59
5:3R:174:LEU:HD11	5:3R:212:ILE:HG23	1.85	0.59
3:3C:182:HIS:HA	17:3C:740:HOH:O	2.01	0.59
1:3A:390:ILE:HG21	17:3A:708:HOH:O	2.02	0.59
2:3B:124:LEU:HD12	2:3B:223:PHE:HB2	1.85	0.59
1:3N:446:PHE:HB2	17:3N:797:HOH:O	2.03	0.59
2:3B:153:GLN:HE22	5:3I:42:VAL:HA	1.67	0.59
3:3C:168:PHE:CZ	5:3R:151:LYS:HB2	2.37	0.59
5:3E:263:TYR:HB2	5:3E:272:ILE:H	1.68	0.59
5:3R:165:MET:HG3	5:3R:167:PHE:CZ	2.38	0.59
1:3A:240:GLU:OE1	1:3A:242:ARG:NH1	2.36	0.59
5:3E:169:TRP:HD1	5:3E:214:ILE:HD11	1.68	0.59
5:3E:238:CYS:HA	4:3Q:147:LEU:HD11	1.84	0.59
1:3N:344:ARG:NH2	17:3N:617:HOH:O	2.35	0.58
2:3O:25:GLU:HG2	2:3O:213:HIS:CD2	2.38	0.58
5:3R:267:SER:O	5:3R:271:VAL:HG13	2.02	0.58
7:3T:54:VAL:HG22	17:3T:223:HOH:O	2.03	0.58
3:3P:278:TYR:CE2	3:3P:282:ARG:HD3	2.39	0.58
4:3Q:3:LEU:HD22	7:3T:71:ARG:HH11	1.68	0.58
5:3R:197:ASP:HB3	5:3R:248:ARG:NH1	2.17	0.58
1:3N:209:LEU:O	17:3N:607:HOH:O	2.16	0.58
2:3O:109:VAL:HB	2:3O:119:LEU:HD23	1.85	0.58
4:3Q:216:LEU:HB3	11:3T:101:CDL:H562	1.86	0.58
2:3O:342:ASP:HA	2:3O:345:LYS:HD3	1.86	0.58
12:3R:302:3PE:H391	12:3R:302:3PE:H261	1.85	0.58
11:3A:501:CDL:H132	12:3A:503:3PE:H372	1.86	0.58
7:3G:42:ARG:NH2	17:3G:206:HOH:O	2.37	0.58
4:3Q:12:TRP:HD1	4:3Q:15:ARG:NH1	2.01	0.58
10:3X:45:VAL:HG23	17:3X:202:HOH:O	2.03	0.57
4:3D:313:ARG:HD3	7:3G:28:PHE:CE2	2.39	0.57
2:3B:71:LEU:HD23	5:3I:68:VAL:HG11	1.86	0.57
2:3O:166:ALA:HB2	2:3O:244:ILE:HG13	1.86	0.57
3:3C:223:TYR:HA	17:3C:721:HOH:O	2.04	0.57
3:3C:278:TYR:CZ	3:3C:282:ARG:HD3	2.39	0.57
4:3Q:18:LEU:HD22	4:3Q:206:LEU:HB2	1.86	0.57
1:3A:204:GLU:HG2	1:3A:207:GLN:H	1.70	0.57
5:3E:80:HIS:HA	5:3E:83:ILE:HD12	1.85	0.57
5:3E:156:LEU:HG	5:3E:157:SER:H	1.70	0.57
8:3H:82:GLU:N	8:3H:82:GLU:OE1	2.37	0.57
5:3R:235:TYR:HA	5:3R:242:HIS:HA	1.86	0.57
1:3A:126:GLN:HA	1:3A:129:LYS:HD3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3P:157:GLY:O	3:3P:161:VAL:HG23	2.04	0.57
9:3W:9:LEU:HD23	9:3W:13:LEU:HD12	1.87	0.57
2:3B:109:VAL:HG13	2:3B:123:LEU:HD13	1.87	0.57
9:3J:44:TYR:OH	17:3J:101:HOH:O	2.14	0.57
1:3N:272:VAL:HG12	17:3N:806:HOH:O	2.05	0.57
2:3B:136:GLU:OE2	17:3B:501:HOH:O	2.17	0.56
1:3N:354:VAL:HG21	1:3N:404:ALA:HA	1.87	0.56
5:3R:161:GLU:HA	5:3R:178:HIS:HB3	1.87	0.56
1:3A:204:GLU:HG3	17:3A:744:HOH:O	2.05	0.56
3:3C:331:ASP:HA	3:3C:334:THR:HG22	1.87	0.56
1:3N:443:TRP:HE3	17:3N:797:HOH:O	1.88	0.56
5:3R:153:GLU:O	5:3R:155:LYS:NZ	2.37	0.56
3:3C:104:TYR:HA	3:3C:314:SER:HB2	1.86	0.56
2:3O:163:LEU:HD11	2:3O:258:VAL:HG22	1.87	0.56
9:3W:29:LEU:HA	10:3X:34:TRP:CD1	2.41	0.56
2:3B:197:ASN:HB3	2:3B:232:LEU:HB2	1.87	0.56
2:3O:87:ARG:NH2	17:3O:516:HOH:O	2.38	0.56
4:3Q:180:SER:OG	8:3U:15:ASP:OD1	2.22	0.56
1:3N:152:TYR:CE1	5:3R:83:ILE:HD11	2.41	0.56
2:3O:211:VAL:HG11	2:3O:216:LEU:HD13	1.88	0.56
12:3D:502:3PE:H351	5:3E:128:ALA:HB1	1.87	0.56
1:3N:439:SER:HB3	12:3N:503:3PE:H111	1.88	0.56
3:3P:361:ILE:HD12	17:3P:702:HOH:O	2.04	0.56
1:3A:21:ASN:OD1	17:3A:601:HOH:O	2.18	0.55
5:3E:173:PRO:O	5:3E:215:GLY:N	2.37	0.55
1:3N:62:LEU:HD11	1:3N:127:ILE:HG12	1.87	0.55
5:3R:125:VAL:HG21	16:3R:303:PC1:H361	1.88	0.55
5:3R:201:ASP:O	5:3R:205:VAL:HG12	2.06	0.55
10:3Y:12:GLU:HG2	10:3Y:15:ARG:NH2	2.22	0.55
11:3G:102:CDL:H512	17:3G:206:HOH:O	2.06	0.55
2:3O:102:ARG:NH2	17:3O:517:HOH:O	2.39	0.55
3:3P:99:GLY:HA3	12:3P:503:3PE:H281	1.88	0.55
5:3R:179:ARG:NE	5:3R:184:ILE:HG12	2.22	0.55
10:3X:8:PRO:O	10:3X:12:GLU:HG3	2.06	0.55
2:3B:22:GLN:OE1	2:3B:39:GLU:HB3	2.06	0.55
3:3C:67:THR:HG23	3:3C:71:ARG:HD2	1.87	0.55
4:3D:204:ILE:HG12	14:3D:501:HEC:HMA3	1.88	0.55
2:3O:25:GLU:HG2	2:3O:213:HIS:CG	2.41	0.55
2:3B:117:GLU:O	2:3B:121:GLU:HG2	2.06	0.55
3:3C:150:LEU:HD21	3:3C:160:LEU:CD2	2.22	0.55
2:3O:56:ARG:HD2	2:3O:103:GLU:HG2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:3S:44:LYS:NZ	17:3S:202:HOH:O	2.15	0.55
9:3J:11:TYR:HA	9:3J:15:PHE:HB2	1.89	0.55
1:3N:161:THR:HG22	5:3R:99:SER:HB2	1.88	0.55
5:3R:128:ALA:HB1	12:3R:302:3PE:H361	1.89	0.55
2:3B:49:LEU:HD23	2:3B:127:THR:HG21	1.89	0.55
4:3D:140:VAL:HG23	17:3D:601:HOH:O	2.06	0.55
12:3A:502:3PE:H32	16:3E:302:PC1:H31	1.89	0.55
1:3A:93:GLU:HG3	1:3A:94:HIS:CD2	2.42	0.55
3:3C:8:HIS:ND1	3:3C:11:MET:HG2	2.22	0.55
3:3C:222:PRO:HB2	17:3C:762:HOH:O	2.07	0.55
5:3E:187:GLU:O	5:3E:190:VAL:HB	2.07	0.55
3:3C:207:ASN:ND2	3:3C:211:ILE:O	2.38	0.55
2:3O:186:VAL:HG12	17:3O:502:HOH:O	2.06	0.55
1:3A:214:LYS:HE3	1:3A:215:HIS:CE1	2.41	0.55
1:3A:358:LYS:O	1:3A:362:ARG:HG3	2.07	0.55
3:3C:345:HIS:ND1	17:3C:607:HOH:O	2.17	0.55
3:3P:377:LEU:HG	6:3S:20:TYR:HE2	1.72	0.55
5:3E:183:GLU:O	5:3E:187:GLU:HG2	2.07	0.54
8:3H:45:VAL:HG12	8:3H:94:VAL:HG22	1.89	0.54
11:3N:502:CDL:OA9	3:3P:221:HIS:CE1	2.60	0.54
4:3Q:147:LEU:HD13	4:3Q:157:ALA:HB1	1.89	0.54
12:3C:503:3PE:H281	12:3C:503:3PE:H242	1.89	0.54
2:3O:350:GLY:HA2	2:3O:411:ILE:HD13	1.89	0.54
2:3O:365:LYS:HG2	2:3O:399:LEU:HD22	1.89	0.54
2:3O:76:THR:HG23	2:3O:81:SER:HA	1.89	0.54
2:3O:328:SER:OG	17:3O:505:HOH:O	2.12	0.54
3:3P:149:LEU:HD23	3:3P:287:LYS:HZ2	1.73	0.54
1:3A:140:GLU:OE2	5:3I:50:LEU:N	2.40	0.54
3:3C:214:ASP:HB3	7:3G:10:THR:HG23	1.90	0.54
7:3G:41:ARG:HA	7:3G:44:ARG:HH21	1.72	0.54
1:3N:358:LYS:O	1:3N:362:ARG:HG3	2.08	0.54
7:3G:20:LEU:HD23	7:3G:25:GLN:HB3	1.90	0.54
3:3P:318:ARG:NH2	17:3P:618:HOH:O	2.40	0.54
1:3A:280:TYR:HA	1:3A:284:TYR:CE2	2.43	0.54
2:3B:39:GLU:OE1	2:3B:113:ARG:NH2	2.39	0.54
3:3C:112:THR:O	3:3C:196:HIS:NE2	2.40	0.54
9:3J:38:GLN:OE1	10:3Y:47:TYR:OH	2.20	0.54
5:3R:263:TYR:C	5:3R:263:TYR:HD1	2.10	0.54
3:3C:319:PRO:O	17:3C:608:HOH:O	2.19	0.54
11:3G:103:CDL:H562	11:3G:103:CDL:H522	1.89	0.54
3:3P:57:SER:O	17:3P:604:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3R:225:ILE:HG12	5:3R:237:PRO:HG3	1.89	0.54
2:3B:95:LYS:HB2	5:3I:32:ALA:HB2	1.90	0.54
7:3G:42:ARG:HD2	11:3G:102:CDL:OB3	2.08	0.54
2:3O:253:VAL:HB	17:3O:505:HOH:O	2.07	0.54
2:3B:35:ILE:CD1	2:3B:217:LYS:HG2	2.35	0.53
1:3N:100:LYS:HD3	1:3N:373:THR:OG1	2.08	0.53
1:3N:204:GLU:HB3	1:3N:207[B]:GLN:HG2	1.89	0.53
1:3N:212:ALA:HB3	17:3N:607:HOH:O	2.07	0.53
2:3O:78:LYS:HD2	17:3O:546:HOH:O	2.08	0.53
3:3P:207:ASN:ND2	3:3P:211:ILE:O	2.41	0.53
1:3A:248:LEU:HD12	1:3A:426:GLY:HA2	1.88	0.53
5:3E:98:ASP:HB3	5:3E:101:LYS:HG2	1.89	0.53
7:3G:26:ARG:O	17:3G:202:HOH:O	2.18	0.53
5:3R:172:LYS:HB3	5:3R:214:ILE:HG23	1.89	0.53
5:3R:199:GLN:HG3	5:3R:257:ASN:HD21	1.71	0.53
1:3A:170:PRO:HB2	1:3A:172:GLU:CD	2.28	0.53
8:3U:28:GLU:HA	8:3U:31:ILE:HB	1.91	0.53
1:3N:269:PRO:HB2	1:3N:410:VAL:HG21	1.90	0.53
3:3P:98:VAL:O	3:3P:102:LEU:HG	2.09	0.53
5:3R:92:ARG:O	7:3T:24:ARG:NH1	2.42	0.53
5:3E:242:HIS:O	5:3E:250:ARG:N	2.41	0.53
12:3N:503:3PE:H322	16:3R:303:PC1:H31	1.90	0.53
2:3O:359:ALA:O	2:3O:363:LYS:HG3	2.08	0.53
1:3A:110:VAL:HG11	1:3A:211:LEU:HB3	1.89	0.53
2:3B:334:GLY:O	2:3B:338:LYS:HD3	2.09	0.53
3:3C:126:THR:HA	17:3C:740:HOH:O	2.07	0.53
1:3A:192:ALA:HB2	1:3A:219:LEU:HB3	1.91	0.53
1:3A:423:ALA:HB2	17:3A:655:HOH:O	2.09	0.53
3:3C:141:TRP:HB3	3:3C:268:ILE:HD13	1.91	0.53
7:3G:73:ARG:NE	8:3H:81:GLU:OE2	2.40	0.53
3:3P:316:MET:HG3	12:3P:503:3PE:H112	1.89	0.53
12:3C:504:3PE:H2A1	5:3R:130:LYS:HA	1.91	0.53
1:3N:79:VAL:HB	17:3N:602:HOH:O	2.07	0.53
1:3N:86:LEU:HD13	1:3N:99:ILE:HG12	1.91	0.53
1:3N:444:LEU:HD22	16:3R:303:PC1:H221	1.91	0.53
2:3O:283:PRO:HG3	5:3V:57:GLY:HA3	1.90	0.53
4:3Q:218:LEU:HB2	17:3R:426:HOH:O	2.08	0.53
10:3Y:15:ARG:HA	10:3Y:18:ILE:HD12	1.91	0.53
2:3O:161:GLU:OE2	17:3O:506:HOH:O	2.19	0.52
4:3Q:195:GLU:OE1	4:3Q:201:ARG:NE	2.41	0.52
3:3P:50:PHE:HZ	12:3R:302:3PE:H2I3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3R:236:CYS:H	5:3R:242:HIS:HA	1.74	0.52
10:3X:9:ARG:NH1	10:3X:13:LEU:HD11	2.24	0.52
3:3C:51:LEU:HD13	13:3C:501:HEM:HBD1	1.90	0.52
4:3Q:3:LEU:HD12	8:3U:59:PHE:HD2	1.75	0.52
4:3Q:27:ARG:HB2	4:3Q:55:CYS:HB2	1.91	0.52
9:3W:56:LYS:NZ	17:3W:105:HOH:O	2.41	0.52
1:3A:27:SER:HA	1:3A:199:ALA:O	2.10	0.52
2:3B:163:LEU:HD12	17:3B:553:HOH:O	2.10	0.52
8:3U:47:ARG:HD3	8:3U:50:THR:HB	1.90	0.52
1:3N:18:GLN:HG3	1:3N:24:ARG:HG3	1.92	0.52
1:3N:322:ALA:HB1	17:3N:808:HOH:O	2.08	0.52
5:3R:153:GLU:HG3	5:3R:169:TRP:CD2	2.44	0.52
5:3R:182:LYS:HD3	5:3R:182:LYS:H	1.74	0.52
6:3F:84:GLN:HB2	11:3G:103:CDL:HA22	1.90	0.52
7:3G:74:LYS:NZ	8:3H:82:GLU:OE2	2.42	0.52
2:3O:157:ALA:O	2:3O:161:GLU:HG2	2.10	0.52
1:3A:76:GLU:HG3	2:3B:285:VAL:HG21	1.92	0.52
2:3B:74:SER:O	2:3B:82:SER:OG	2.21	0.52
3:3C:281:LEU:HD12	3:3C:291:VAL:HA	1.91	0.52
9:3W:56:LYS:NZ	17:3W:102:HOH:O	2.29	0.52
3:3C:104:TYR:CE2	12:3C:503:3PE:H251	2.45	0.52
5:3E:180:THR:O	5:3E:184:ILE:HG13	2.10	0.52
5:3E:266:THR:HB	5:3E:270:LEU:HG	1.91	0.52
1:3A:395:TRP:O	1:3A:399:ILE:HG13	2.10	0.51
2:3B:56:ARG:HD2	2:3B:103:GLU:HG2	1.92	0.51
1:3N:191:LYS:HD3	1:3N:221:GLY:HA2	1.91	0.51
1:3N:240:GLU:CD	1:3N:242:ARG:HE	2.13	0.51
3:3P:132:VAL:HA	3:3P:139:SER:HB3	1.91	0.51
5:3R:213:LEU:HD22	5:3R:258:LEU:HB2	1.91	0.51
1:3A:414:TYR:O	1:3A:418:GLN:HG3	2.11	0.51
2:3B:227:ARG:HG3	2:3B:229:GLY:N	2.25	0.51
3:3C:379:TRP:CZ3	6:3F:49:ILE:HD12	2.45	0.51
1:3A:79:VAL:HG21	1:3A:86:LEU:HD22	1.91	0.51
2:3B:207:ILE:HD13	2:3B:383:GLY:HA2	1.92	0.51
4:3D:309:TYR:OH	11:3G:103:CDL:OB3	2.22	0.51
2:3O:169:ARG:HG3	2:3O:240:ARG:HB3	1.92	0.51
3:3P:267:HIS:HD2	3:3P:269:LYS:HG2	1.76	0.51
9:3W:55:ILE:O	9:3W:58:LYS:HG2	2.10	0.51
5:3E:178:HIS:HA	5:3E:210:TRP:CD1	2.45	0.51
4:3Q:105:ASN:ND2	4:3Q:110:PRO:HD3	2.26	0.51
5:3R:179:ARG:NH1	5:3R:246:SER:OG	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:3Y:14:ALA:O	10:3Y:18:ILE:HG13	2.10	0.51
1:3A:349:ALA:O	1:3A:353:GLU:OE1	2.28	0.51
1:3A:354:VAL:HG21	1:3A:404:ALA:HA	1.92	0.51
2:3B:435:PHE:H	2:3B:438:GLU:HG3	1.75	0.51
2:3O:197:ASN:HB3	2:3O:232:LEU:HB2	1.93	0.51
5:3R:219:HIS:NE2	5:3R:239:HIS:CE1	2.77	0.51
3:3C:283:SER:HA	17:3C:748:HOH:O	2.09	0.51
1:3N:244:ARG:HG2	7:3T:10:MET:HB3	1.92	0.51
1:3N:436:ARG:HD3	3:3P:222:PRO:HD3	1.92	0.51
11:3P:504:CDL:HA61	11:3P:504:CDL:H532	1.93	0.51
11:3A:501:CDL:H352	3:3C:225:THR:HG21	1.93	0.51
2:3B:166:ALA:HB3	17:3B:553:HOH:O	2.11	0.51
3:3C:103:TYR:HA	3:3C:315:MET:SD	2.51	0.51
4:3D:219:LEU:HD11	14:3D:501:HEC:HMB2	1.91	0.51
3:3P:319:PRO:HB3	7:3T:47:ARG:CZ	2.40	0.51
5:3R:85:VAL:O	17:3R:402:HOH:O	2.18	0.51
8:3U:20:VAL:HG13	17:3U:128:HOH:O	2.10	0.51
4:3Q:238:ARG:CZ	5:3R:83:ILE:HG22	2.40	0.51
5:3E:220:LEU:HD12	3:3P:263:ASN:HD21	1.74	0.51
2:3O:78:LYS:CG	2:3O:129:ALA:HB1	2.37	0.51
11:3P:504:CDL:OB4	7:3T:40:ARG:NE	2.41	0.51
5:3R:219:HIS:HE1	5:3R:253:PRO:HG2	1.76	0.51
12:3R:302:3PE:H242	17:3R:443:HOH:O	2.09	0.51
7:3T:29:TYR:CZ	11:3T:101:CDL:HA61	2.46	0.51
1:3A:111:GLU:HG3	1:3A:215:HIS:CE1	2.46	0.51
1:3A:336:PHE:HZ	12:3A:503:3PE:H112	1.76	0.51
2:3B:424:MET:HB2	2:3B:436:VAL:HG23	1.93	0.51
6:3F:120:ALA:HB3	10:3X:4:ARG:HH12	1.76	0.51
5:3R:241:SER:HB3	5:3R:249:ILE:HG23	1.93	0.51
5:3E:195:LEU:HD13	5:3E:249:ILE:O	2.12	0.50
7:3G:71:SER:HB3	17:3G:208:HOH:O	2.11	0.50
4:3Q:101:ALA:O	4:3Q:105:ASN:ND2	2.44	0.50
5:3R:150:SER:HB3	5:3R:170:ARG:H	1.76	0.50
5:3R:222:CYS:HB2	15:3R:301:FES:S2	2.50	0.50
4:3D:186:PRO:O	4:3D:190:ARG:HG3	2.12	0.50
4:3Q:224:ARG:HD3	7:3T:26:PHE:CE2	2.45	0.50
5:3R:234:TYR:HB2	5:3R:243:TYR:HB2	1.93	0.50
3:3C:376:LEU:O	6:3F:29:ARG:HD3	2.10	0.50
5:3E:199:GLN:O	5:3E:248:ARG:HD3	2.11	0.50
1:3N:57:TYR:OH	1:3N:137:GLU:OE1	2.27	0.50
11:3P:504:CDL:HB32	7:3T:44:CYS:SG	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3Q:131:LEU:HB3	4:3Q:164:ILE:HD11	1.94	0.50
4:3Q:224:ARG:NH2	17:3Q:608:HOH:O	2.43	0.50
10:3X:4:ARG:NH1	10:3X:10:TYR:OH	2.44	0.50
1:3A:124:ASP:OD1	1:3A:179:ARG:HD2	2.11	0.50
5:3E:231:PHE:CE1	5:3E:242:HIS:HB3	2.45	0.50
5:3R:119:ALA:HB3	17:3R:439:HOH:O	2.12	0.50
1:3A:279:HIS:ND1	1:3A:284:TYR:OH	2.43	0.50
12:3A:503:3PE:N	3:3C:3:ASN:OD1	2.28	0.50
3:3C:4:ILE:HG13	3:3C:8:HIS:HB2	1.93	0.50
3:3C:8:HIS:CE1	3:3C:10:LEU:HB2	2.47	0.50
3:3C:19:ILE:HA	3:3C:221:HIS:HB2	1.93	0.50
3:3P:149:LEU:HD23	3:3P:287:LYS:NZ	2.26	0.50
5:3I:42:VAL:HG22	5:3I:43:LEU:HD12	1.92	0.50
5:3E:186:GLN:O	5:3E:190:VAL:HG23	2.11	0.50
1:3N:41:ILE:HG23	1:3N:195:MET:HG3	1.92	0.50
4:3Q:105:ASN:HD21	4:3Q:110:PRO:HD3	1.77	0.50
17:3C:762:HOH:O	4:3D:315:LYS:HB3	2.12	0.50
4:3D:316:TRP:O	4:3D:320:LYS:HG2	2.11	0.50
8:3H:42:LEU:HD13	8:3H:98:LEU:HD22	1.94	0.50
1:3N:195:MET:SD	1:3N:219:LEU:HD21	2.52	0.50
3:3P:79:ILE:HG12	17:3P:738:HOH:O	2.12	0.50
11:3P:504:CDL:OB9	7:3T:41:THR:HG23	2.11	0.50
4:3Q:167:GLU:N	17:3Q:602:HOH:O	2.45	0.50
5:3V:65:VAL:HB	5:3V:77:ARG:HG3	1.92	0.50
2:3O:40:ASN:OD1	2:3O:40:ASN:N	2.38	0.49
8:3U:72:LYS:HE2	17:3U:128:HOH:O	2.12	0.49
3:3C:67:THR:CG2	3:3C:71:ARG:HD2	2.42	0.49
3:3C:103:TYR:CG	12:3C:503:3PE:H241	2.47	0.49
5:3E:236:CYS:HB2	5:3E:241:SER:O	2.12	0.49
1:3N:280:TYR:HA	1:3N:284:TYR:CE2	2.47	0.49
4:3Q:98:PRO:O	4:3Q:102:ARG:HG3	2.12	0.49
5:3R:212:ILE:HB	5:3R:265:PHE:CE1	2.47	0.49
5:3R:230:ASP:OD1	5:3R:231:PHE:N	2.46	0.49
5:3V:63:PRO:HG2	17:3V:305:HOH:O	2.12	0.49
1:3A:241:ILE:HG12	17:3A:661:HOH:O	2.11	0.49
3:3C:97:HIS:HE1	13:3C:502:HEM:O1A	1.95	0.49
4:3D:120:VAL:HG22	4:3D:258:LEU:HD21	1.94	0.49
3:3P:319:PRO:HB3	7:3T:47:ARG:NH2	2.28	0.49
1:3A:149:VAL:HG13	17:3A:698:HOH:O	2.12	0.49
4:3D:249:MET:HG2	4:3D:250:ALA:O	2.12	0.49
5:3R:116:LEU:HD12	17:3R:439:HOH:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3R:154:ILE:HD11	5:3R:270:LEU:HA	1.95	0.49
2:3B:385:GLN:OE1	2:3B:393:VAL:HG22	2.13	0.49
3:3C:248:ASP:OD2	17:3C:609:HOH:O	2.20	0.49
1:3N:214:LYS:HZ1	1:3N:215:HIS:CE1	2.28	0.49
1:3N:351:GLU:HB3	17:3N:788:HOH:O	2.13	0.49
5:3R:98:ASP:HB3	5:3R:101:LYS:HG2	1.95	0.49
5:3R:173:PRO:O	5:3R:215:GLY:N	2.35	0.49
1:3A:207:GLN:HE21	1:3A:211:LEU:HD11	1.76	0.49
2:3B:357:VAL:HG21	2:3B:407:ASP:OD1	2.12	0.49
5:3I:64:LEU:CA	5:3I:77:ARG:O	2.57	0.49
4:3Q:234:LYS:HD3	5:3R:86:PRO:HG2	1.93	0.49
4:3D:135:ALA:HA	4:3D:178:TYR:HA	1.93	0.49
5:3E:186:GLN:O	5:3E:190:VAL:N	2.44	0.49
8:3H:50:GLU:HG2	8:3H:86:PHE:HZ	1.77	0.49
4:3Q:27:ARG:NE	4:3Q:55:CYS:O	2.45	0.49
5:3R:243:TYR:HB3	5:3R:247:GLY:HA2	1.95	0.49
1:3A:45:SER:O	1:3A:165:GLN:NE2	2.45	0.49
5:3E:181:LYS:HA	5:3E:184:ILE:HB	1.95	0.49
5:3E:185:ASP:OD1	5:3E:186:GLN:N	2.44	0.49
1:3N:14:THR:HG21	1:3N:389:ARG:CB	2.38	0.49
3:3P:26:ASN:O	17:3P:605:HOH:O	2.20	0.49
3:3P:324:LEU:HD23	3:3P:327:MET:SD	2.52	0.49
2:3B:58:GLU:HG2	17:3B:541:HOH:O	2.12	0.49
5:3E:109:ALA:HA	9:3J:7:THR:HG23	1.95	0.49
2:3O:56:ARG:NH1	2:3O:103:GLU:OE2	2.44	0.49
4:3D:269:SER:OG	8:3H:40:ASP:OD1	2.29	0.48
11:3A:501:CDL:H1	12:3A:503:3PE:H32	1.94	0.48
3:3C:29:SER:O	3:3C:32:ASN:HB2	2.14	0.48
5:3E:155:LYS:HD2	5:3E:167:PHE:CZ	2.48	0.48
8:3H:53:GLU:O	8:3H:57:LYS:HG2	2.13	0.48
5:3R:123:VAL:HG13	9:3W:28:ALA:HA	1.95	0.48
3:3C:379:TRP:CE3	6:3F:45:ARG:HD3	2.48	0.48
5:3E:207:LYS:O	5:3E:209:GLU:N	2.45	0.48
5:3I:36:ALA:CB	5:3I:73:PRO:HG2	2.39	0.48
8:3U:21:ARG:O	8:3U:25:GLU:HG2	2.13	0.48
1:3A:301:ARG:HB2	1:3A:303:LEU:HG	1.96	0.48
3:3C:322:GLN:NE2	12:3C:503:3PE:H111	2.27	0.48
4:3D:214:TYR:OH	14:3D:501:HEC:O2A	2.26	0.48
5:3E:151:LYS:HG2	5:3E:152:ILE:HG23	1.95	0.48
5:3R:191:GLU:HG3	5:3R:194:GLN:H	1.78	0.48
3:3C:100:ARG:HA	12:3C:503:3PE:H252	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3C:244:LEU:HD12	4:3D:297:MET:HE2	1.95	0.48
2:3O:357:VAL:HG21	2:3O:407:ASP:OD1	2.14	0.48
8:3U:44:VAL:HG13	17:3U:109:HOH:O	2.13	0.48
4:3D:137:ARG:HD3	4:3D:176:SER:HA	1.94	0.48
5:3R:178:HIS:CE1	5:3R:209:GLU:HB3	2.49	0.48
1:3A:68:LYS:CG	1:3A:119:ASN:HB3	2.44	0.48
1:3A:276:ILE:HG21	1:3A:345:LEU:HD21	1.96	0.48
11:3A:501:CDL:H172	12:3A:503:3PE:H3A2	1.96	0.48
3:3C:316:MET:HA	12:3C:503:3PE:C11	2.44	0.48
4:3D:180:PRO:HD2	17:3D:711:HOH:O	2.13	0.48
2:3O:120:MET:HE3	2:3O:219:VAL:HG11	1.94	0.48
3:3P:206:ASN:HB3	13:3P:502:HEM:O1D	2.13	0.48
10:3X:23:MET:O	10:3X:27:VAL:HG23	2.13	0.48
4:3D:102:HIS:O	4:3D:291:LYS:NZ	2.47	0.48
7:3G:21:SER:O	7:3G:25:GLN:HG2	2.13	0.48
1:3N:444:LEU:HD12	11:3N:502:CDL:HB31	1.95	0.48
2:3O:94:GLY:O	17:3O:507:HOH:O	2.20	0.48
4:3Q:33:TYR:HA	4:3Q:37:CYS:SG	2.54	0.48
2:3B:424:MET:HB2	2:3B:436:VAL:CG2	2.43	0.48
12:3C:504:3PE:H111	3:3P:74:ASN:ND2	2.29	0.48
1:3N:19:LEU:HD22	1:3N:213:GLN:OE1	2.14	0.48
1:3N:191:LYS:HE3	1:3N:222:THR:C	2.34	0.48
7:3T:42:ARG:HD2	7:3T:42:ARG:HA	1.64	0.48
1:3N:40:TRP:HB3	1:3N:384:LEU:HD11	1.95	0.48
3:3P:315:MET:HG3	3:3P:318:ARG:NH2	2.29	0.48
5:3R:241:SER:OG	5:3R:252:GLY:HA3	2.13	0.48
4:3D:284:GLU:OE2	4:3D:290:ARG:NE	2.47	0.47
2:3O:56:ARG:HA	2:3O:171:ALA:O	2.14	0.47
3:3P:234:PHE:CZ	11:3T:101:CDL:H532	2.49	0.47
11:3T:101:CDL:HB61	11:3T:101:CDL:H711	1.50	0.47
8:3U:20:VAL:HG12	8:3U:69:VAL:HG22	1.96	0.47
1:3A:153:LEU:HA	17:3A:655:HOH:O	2.13	0.47
1:3A:176:LYS:HA	1:3A:176:LYS:HD3	1.55	0.47
1:3A:280:TYR:O	1:3A:306:SER:HA	2.13	0.47
1:3A:349:ALA:CB	1:3A:408:ARG:HG3	2.45	0.47
2:3B:181:TYR:CZ	2:3B:182:ARG:HG2	2.49	0.47
2:3B:369:LEU:HD11	2:3B:399:LEU:HD11	1.95	0.47
3:3C:150:LEU:HD22	17:3C:601:HOH:O	2.13	0.47
5:3E:234:TYR:HD2	5:3E:247:GLY:HA2	1.78	0.47
1:3N:49:ASN:OD1	1:3N:51:LYS:HB2	2.13	0.47
1:3N:342:TRP:O	17:3N:608:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:332:ASP:OD1	1:3A:432:PRO:HG3	2.13	0.47
4:3D:329:PRO:HD3	7:3G:14:HIS:CE1	2.49	0.47
5:3R:263:TYR:CD1	5:3R:265:PHE:CD1	3.01	0.47
5:3E:190:VAL:HG22	5:3E:250:ARG:CZ	2.44	0.47
2:3O:128:ALA:HA	2:3O:227:ARG:HH22	1.78	0.47
2:3O:129:ALA:N	2:3O:130:PRO:HD3	2.29	0.47
3:3P:229:ILE:CG2	16:3R:303:PC1:H371	2.44	0.47
8:3U:50:THR:OG1	8:3U:51:GLU:N	2.47	0.47
10:3Y:23:MET:O	10:3Y:27:VAL:HG23	2.14	0.47
5:3E:213:LEU:CD1	5:3E:247:GLY:HA3	2.44	0.47
5:3E:220:LEU:HA	3:3P:263:ASN:OD1	2.15	0.47
7:3G:38:ASN:ND2	11:3G:103:CDL:OA3	2.30	0.47
8:3H:49:CYS:O	8:3H:52:ILE:HB	2.15	0.47
1:3N:74:ALA:HA	1:3N:77:LYS:HG2	1.96	0.47
5:3R:244:ASP:OD1	5:3R:248:ARG:N	2.38	0.47
10:3X:38:TRP:HD1	16:3X:101:PC1:O12	1.96	0.47
2:3O:78:LYS:NZ	2:3O:131:GLU:HG2	2.30	0.47
5:3R:248:ARG:NH2	5:3R:249:ILE:O	2.48	0.47
1:3A:188:GLN:HG3	1:3A:189:HIS:CD2	2.50	0.47
4:3D:158:VAL:HG11	4:3D:177:ASP:OD2	2.14	0.47
6:3F:50:TYR:O	17:3F:206:HOH:O	2.20	0.47
8:3H:53:GLU:HA	8:3H:56:ILE:HB	1.97	0.47
1:3N:93:GLU:HG3	1:3N:94:HIS:CE1	2.50	0.47
4:3Q:165:TYR:CZ	4:3Q:168:VAL:HG23	2.50	0.47
5:3R:167:PHE:O	5:3R:173:PRO:HA	2.14	0.47
5:3R:183:GLU:O	5:3R:187:GLU:HG2	2.15	0.47
8:3U:38:GLU:HG2	17:3U:198:HOH:O	2.15	0.47
10:3X:39:ARG:HE	10:3X:39:ARG:HB3	1.57	0.47
1:3A:21:ASN:HD22	1:3A:192:ALA:HB1	1.80	0.47
1:3A:398:ARG:O	1:3A:401:GLU:HG2	2.14	0.47
4:3D:136:TYR:HA	4:3D:139:LEU:HD12	1.96	0.47
3:3P:141:TRP:CD1	3:3P:265:PRO:HD3	2.49	0.47
3:3P:337:TRP:O	3:3P:341:GLN:HG2	2.15	0.47
3:3C:300:ILE:HA	3:3C:303:LEU:HD12	1.97	0.47
13:3C:502:HEM:O2A	17:3C:610:HOH:O	2.20	0.47
4:3D:301:MET:HE2	12:3D:502:3PE:H362	1.95	0.47
5:3E:169:TRP:HB2	5:3E:174:LEU:HD22	1.97	0.47
2:3O:86:THR:HG23	5:3V:70:LEU:HD11	1.96	0.47
1:3A:367:SER:OG	5:3I:34:LEU:HD12	2.15	0.47
2:3B:213:HIS:O	2:3B:217:LYS:HG3	2.15	0.47
2:3B:260:GLU:O	2:3B:416:LYS:NZ	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3E:244:ASP:HB2	5:3E:250:ARG:HG2	1.96	0.47
8:3H:47:GLU:O	8:3H:51:GLN:HG2	2.15	0.47
3:3P:272:TRP:HA	3:3P:275:LEU:HG	1.97	0.47
5:3R:167:PHE:HB3	5:3R:169:TRP:CE2	2.50	0.47
5:3R:263:TYR:HA	5:3R:273:VAL:HA	1.97	0.47
3:3C:300:ILE:HG13	3:3C:303:LEU:HD12	1.97	0.46
4:3D:301:MET:HE1	12:3D:502:3PE:C36	2.44	0.46
1:3N:79:VAL:HG21	1:3N:86:LEU:HD22	1.97	0.46
1:3N:298:ALA:HA	1:3N:303:LEU:HB2	1.95	0.46
1:3N:411:CYS:HB3	17:3N:608:HOH:O	2.15	0.46
5:3R:236:CYS:HB2	5:3R:241:SER:O	2.15	0.46
3:3C:323:CYS:O	3:3C:327:MET:HG3	2.15	0.46
1:3N:156:THR:HA	5:3R:85:VAL:HG21	1.97	0.46
2:3O:78:LYS:HD3	2:3O:131:GLU:HG2	1.97	0.46
5:3R:184:ILE:HD11	5:3R:209:GLU:HA	1.97	0.46
5:3R:263:TYR:CD1	5:3R:263:TYR:O	2.69	0.46
3:3C:337:TRP:CH2	7:3G:61:TYR:HA	2.50	0.46
2:3B:73:SER:O	2:3B:74:SER:HB3	2.16	0.46
8:3H:52:ILE:HG22	8:3H:55:CYS:H	1.80	0.46
9:3J:54:LYS:HG2	9:3J:55:HIS:N	2.28	0.46
3:3C:379:TRP:CZ3	6:3F:45:ARG:HD3	2.50	0.46
4:3D:232:ARG:HD3	5:3R:237:PRO:CB	2.44	0.46
8:3H:77:GLU:HA	8:3H:78:ASP:HB2	1.97	0.46
3:3C:8:HIS:HE1	3:3C:10:LEU:HB2	1.80	0.46
2:3O:243:GLU:HG3	2:3O:424:MET:HB3	1.98	0.46
3:3P:319:PRO:HG3	7:3T:47:ARG:HH22	1.81	0.46
10:3X:39:ARG:HG2	10:3X:52:PHE:CE2	2.51	0.46
1:3A:281:ASP:OD1	1:3A:283:THR:OG1	2.28	0.46
3:3C:4:ILE:CD1	3:3C:8:HIS:HB2	2.46	0.46
3:3C:78:VAL:O	3:3C:82:LEU:HB2	2.15	0.46
3:3C:124:MET:CE	3:3C:298:ILE:HD13	2.45	0.46
3:3C:262:LEU:HD11	5:3R:172:LYS:HA	1.98	0.46
3:3C:377:LEU:HG	6:3F:32:TYR:CE2	2.48	0.46
8:3U:34:ARG:O	8:3U:38:GLU:HG3	2.16	0.46
2:3B:365:LYS:HG2	2:3B:399:LEU:HD22	1.97	0.46
3:3C:137:GLN:OE1	17:3C:611:HOH:O	2.20	0.46
3:3C:168:PHE:HZ	5:3R:151:LYS:HB2	1.79	0.46
4:3D:115:ARG:O	4:3D:119:GLN:HG3	2.15	0.46
7:3G:38:ASN:O	7:3G:42:ARG:HG3	2.16	0.46
9:3J:34:ARG:HD3	10:3Y:48:ILE:HA	1.98	0.46
1:3N:49:ASN:O	1:3N:53:ASN:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:3N:501:3PE:H262	11:3N:502:CDL:HB62	1.97	0.46
3:3P:172:LYS:HD2	17:3P:604:HOH:O	2.14	0.46
3:3P:286:ASN:HB3	17:3P:685:HOH:O	2.15	0.46
5:3R:187:GLU:CD	5:3R:244:ASP:HB2	2.36	0.46
3:3C:229:ILE:HG21	16:3E:302:PC1:H351	1.98	0.46
4:3D:171:ARG:NH1	4:3D:174:LYS:HD2	2.31	0.46
4:3D:304:LEU:HD21	5:3E:124:GLY:HA3	1.98	0.46
5:3I:42:VAL:HG22	5:3I:43:LEU:CD1	2.46	0.46
2:3O:65:THR:HA	2:3O:186:VAL:HG11	1.97	0.46
2:3O:219:VAL:HG12	2:3O:222:ARG:NH2	2.31	0.46
3:3P:376:LEU:O	6:3S:17:ARG:HD3	2.16	0.46
4:3Q:160:MET:HG2	4:3Q:161:ALA:O	2.15	0.46
1:3A:40:TRP:CZ2	1:3A:377:GLU:HA	2.51	0.46
11:3A:501:CDL:H142	12:3A:502:3PE:O22	2.16	0.46
2:3B:109:VAL:HG22	2:3B:123:LEU:HD22	1.98	0.46
3:3C:81:TYR:HD1	17:3C:723:HOH:O	1.98	0.46
12:3C:504:3PE:H262	5:3R:133:VAL:HG12	1.98	0.46
12:3C:504:3PE:H11	5:3R:137:VAL:HG12	1.98	0.46
4:3D:171:ARG:NH1	4:3D:177:ASP:OD2	2.45	0.46
3:3P:12:LYS:HE3	3:3P:16:ASN:OD1	2.16	0.46
4:3Q:12:TRP:HB3	4:3Q:14:HIS:CE1	2.51	0.46
5:3R:109:ALA:HA	9:3W:6:THR:HG23	1.97	0.46
3:3C:141:TRP:CD1	3:3C:265:PRO:HD3	2.51	0.45
4:3D:113:SER:HB3	4:3D:277:THR:HG21	1.99	0.45
1:3N:111:GLU:HG3	1:3N:215:HIS:CD2	2.50	0.45
11:3P:504:CDL:HB62	11:3P:504:CDL:H712	1.55	0.45
5:3R:167:PHE:HB3	5:3R:169:TRP:CZ2	2.51	0.45
9:3W:30:PHE:HA	10:3X:48:ILE:HD11	1.97	0.45
1:3A:260:PRO:HG2	1:3A:267:ASN:OD1	2.15	0.45
5:3E:263:TYR:HB3	5:3E:273:VAL:HG22	1.99	0.45
5:3R:162:GLY:N	5:3R:178:HIS:HB3	2.28	0.45
5:3R:263:TYR:CE1	5:3R:265:PHE:CB	2.98	0.45
5:3E:223:VAL:HG22	4:3Q:107:GLY:O	2.15	0.45
9:3J:54:LYS:HA	9:3J:57:LYS:CE	2.43	0.45
2:3O:306:PRO:HA	5:3V:52:ARG:HD3	1.97	0.45
4:3Q:37:CYS:SG	14:3Q:501:HEC:HBB3	2.55	0.45
4:3Q:116:ILE:HG12	14:3Q:501:HEC:HMA3	1.98	0.45
9:3W:53:LYS:HB3	9:3W:53:LYS:HE3	1.78	0.45
11:3A:501:CDL:H132	12:3A:503:3PE:H342	1.99	0.45
3:3C:126:THR:HG21	3:3C:186:PRO:HG3	1.98	0.45
3:3C:346:PRO:HA	17:3C:607:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3E:234:TYR:HB2	5:3E:243:TYR:HB3	1.98	0.45
5:3I:32:ALA:N	5:3I:71:ASN:HB3	2.31	0.45
5:3I:35:PRO:O	5:3I:36:ALA:HB3	2.17	0.45
2:3O:111:CYS:SG	2:3O:119:LEU:HD22	2.56	0.45
5:3R:159:ILE:HG21	5:3R:176:VAL:HG12	1.97	0.45
1:3A:281:ASP:OD2	5:3I:73:PRO:HG3	2.17	0.45
2:3B:154:ASN:ND2	5:3I:78:TYR:CE1	2.84	0.45
3:3C:158:THR:O	3:3C:162:GLU:HG3	2.15	0.45
3:3C:300:ILE:HD11	3:3C:363:LEU:HG	1.99	0.45
7:3G:43:THR:O	7:3G:47:ILE:HB	2.17	0.45
3:3P:246:SER:HB2	3:3P:249:LEU:HB2	1.98	0.45
2:3B:276:GLN:HG2	2:3B:281:ALA:HB2	1.99	0.45
3:3C:67:THR:HG23	3:3C:71:ARG:CD	2.46	0.45
7:3G:21:SER:HB3	7:3G:24:GLU:HG2	1.98	0.45
1:3N:17:SER:HB2	1:3N:209:LEU:CD1	2.46	0.45
3:3P:51:LEU:HB3	17:3P:701:HOH:O	2.16	0.45
5:3E:242:HIS:HB2	5:3E:251:LYS:HB3	1.98	0.45
3:3P:353:LEU:HB2	17:3P:651:HOH:O	2.16	0.45
5:3R:150:SER:HB2	5:3R:170:ARG:HD3	1.98	0.45
5:3R:243:TYR:HA	5:3R:248:ARG:O	2.17	0.45
1:3A:388:ARG:HH22	1:3A:394:GLU:CD	2.19	0.45
2:3B:107:TYR:HB3	2:3B:123:LEU:HD11	1.98	0.45
5:3E:177:ARG:HD2	5:3E:179:ARG:HG2	1.98	0.45
5:3E:217:CYS:HB3	5:3E:221:GLY:HA2	1.99	0.45
1:3N:214:LYS:HE2	1:3N:214:LYS:HB2	1.73	0.45
1:3N:414:TYR:O	1:3N:418:GLN:HG3	2.17	0.45
11:3P:504:CDL:H542	11:3P:504:CDL:OA7	2.16	0.45
5:3R:121:THR:O	5:3R:125:VAL:HG23	2.17	0.45
4:3D:198:PRO:HA	4:3D:199:PRO:HD3	1.89	0.45
1:3N:336:PHE:HZ	12:3N:501:3PE:H112	1.81	0.45
1:3N:347:THR:HG21	17:3N:797:HOH:O	2.17	0.45
13:3P:501:HEM:HBD1	17:3P:701:HOH:O	2.17	0.45
2:3B:207:ILE:CD1	2:3B:383:GLY:HA2	2.47	0.45
2:3B:286:LYS:HG2	2:3B:287:ARG:HG3	1.99	0.45
5:3E:155:LYS:CE	5:3E:176:VAL:HG21	2.46	0.45
2:3O:181:TYR:CZ	2:3O:182:ARG:HG2	2.52	0.45
3:3P:96:ILE:HA	12:3P:503:3PE:H291	1.98	0.45
3:3P:98:VAL:HG22	13:3P:502:HEM:HAC	1.99	0.45
4:3Q:16:GLY:O	4:3Q:202:LYS:NZ	2.43	0.45
4:3Q:238:ARG:HD2	7:3T:14:ILE:HD12	1.99	0.45
5:3R:93:ARG:NH2	7:3T:21:PHE:HA	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:156:THR:HA	5:3E:85:VAL:HG21	1.98	0.44
2:3B:36:ALA:O	2:3B:207:ILE:HA	2.18	0.44
2:3B:359:ALA:O	2:3B:363:LYS:HG3	2.16	0.44
4:3D:121:TYR:CD1	4:3D:125:CYS:HB2	2.52	0.44
1:3N:344:ARG:HG2	1:3N:344:ARG:NH1	2.29	0.44
2:3O:75:LEU:HB2	17:3O:634:HOH:O	2.17	0.44
5:3E:154:ILE:HA	5:3E:274:GLY:O	2.18	0.44
6:3F:86:ILE:HD12	6:3F:92:TRP:HZ2	1.82	0.44
3:3P:96:ILE:HG22	17:3P:654:HOH:O	2.18	0.44
8:3U:23:GLN:NE2	17:3U:103:HOH:O	2.15	0.44
3:3C:104:TYR:HE2	12:3C:503:3PE:H251	1.82	0.44
4:3D:228:GLY:HA3	8:3H:78:ASP:H	1.82	0.44
6:3F:119:TRP:CH2	2:3O:87:ARG:HB3	2.53	0.44
3:3P:182:HIS:HA	17:3P:646:HOH:O	2.17	0.44
3:3P:316:MET:HA	12:3P:503:3PE:C11	2.47	0.44
4:3Q:225:HIS:CE1	7:3T:20:PRO:HB2	2.52	0.44
7:3T:18:LEU:HD12	7:3T:18:LEU:HA	1.81	0.44
2:3B:95:LYS:HE2	5:3I:72:VAL:CB	2.39	0.44
13:3C:501:HEM:HMC1	13:3C:501:HEM:HBC2	2.00	0.44
5:3E:164:ASN:HA	5:3E:177:ARG:HB2	2.00	0.44
6:3F:61:ARG:NH2	6:3F:112:GLU:OE1	2.46	0.44
1:3N:41:ILE:HG12	1:3N:195:MET:HG2	1.98	0.44
1:3N:127:ILE:O	1:3N:131:ARG:HG3	2.18	0.44
5:3R:159:ILE:HD13	5:3R:176:VAL:HG11	1.99	0.44
5:3R:175:PHE:CE2	5:3R:234:TYR:CE2	3.05	0.44
6:3F:44:MET:HE1	6:3F:99:LYS:HB2	1.99	0.44
3:3P:276:PHE:CG	3:3P:277:ALA:N	2.86	0.44
5:3R:195:LEU:HD13	5:3R:248:ARG:HE	1.82	0.44
2:3B:153:GLN:OE1	5:3I:46:LYS:HE3	2.18	0.44
4:3D:121:TYR:HA	4:3D:125:CYS:SG	2.58	0.44
9:3J:46:HIS:HB2	17:3J:105:HOH:O	2.17	0.44
1:3N:8:LEU:HD22	1:3N:392:LEU:HB3	2.00	0.44
2:3O:39:GLU:OE2	2:3O:113:ARG:NH2	2.51	0.44
3:3P:301:LEU:HD23	3:3P:304:MET:HE3	1.98	0.44
5:3R:225:ILE:HG22	5:3R:228:ALA:HB3	2.00	0.44
10:3X:39:ARG:HG2	10:3X:52:PHE:CZ	2.52	0.44
2:3B:327:ILE:HG21	5:3I:55:LEU:HD11	1.98	0.44
3:3C:237:LEU:HB2	4:3D:301:MET:SD	2.57	0.44
2:3O:78:LYS:HZ3	2:3O:131:GLU:HA	1.82	0.44
3:3P:186:PRO:HA	3:3P:189:ILE:HD12	1.99	0.44
10:3Y:39:ARG:HA	10:3Y:42:LEU:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3D:249:MET:HB2	14:3D:501:HEC:C1D	2.48	0.44
3:3P:161:VAL:HB	17:3P:692:HOH:O	2.17	0.44
10:3X:32:LEU:HD21	16:3X:101:PC1:H341	2.00	0.44
10:3X:39:ARG:N	16:3X:101:PC1:O12	2.49	0.44
2:3B:47:ILE:HD12	2:3B:216:LEU:HD21	2.00	0.44
3:3C:24:PRO:HB2	3:3C:27:ILE:HG23	1.99	0.44
5:3E:159:ILE:HD12	5:3E:159:ILE:H	1.83	0.44
9:3J:54:LYS:HD3	9:3J:55:HIS:CG	2.53	0.44
2:3O:307:PHE:CD2	5:3V:52:ARG:HD2	2.53	0.44
3:3P:16:ASN:ND2	17:3P:617:HOH:O	2.50	0.44
4:3Q:184:LYS:NZ	17:3Q:607:HOH:O	2.40	0.44
5:3R:186:GLN:O	5:3R:190:VAL:N	2.49	0.44
4:3D:215:VAL:O	4:3D:219:LEU:HG	2.18	0.43
10:3Y:11:ARG:O	10:3Y:15:ARG:HG3	2.18	0.43
3:3C:186:PRO:HA	3:3C:189:ILE:HD12	2.00	0.43
4:3D:129:HIS:CE1	4:3D:199:PRO:HD2	2.52	0.43
3:3P:65:SER:O	3:3P:69:ILE:HG13	2.17	0.43
2:3O:232:LEU:HD23	2:3O:232:LEU:HA	1.83	0.43
5:3R:239:HIS:CD2	15:3R:301:FES:S2	3.11	0.43
5:3R:248:ARG:HH22	5:3R:249:ILE:HB	1.83	0.43
3:3C:67:THR:HG21	4:3D:133:TYR:CG	2.54	0.43
4:3D:265:PRO:HB3	4:3D:265:PRO:HD3	1.50	0.43
5:3E:169:TRP:CE3	5:3E:273:VAL:HA	2.54	0.43
8:3H:50:GLU:HG2	8:3H:86:PHE:CZ	2.53	0.43
1:3N:111:GLU:HG3	1:3N:215:HIS:NE2	2.33	0.43
3:3P:233:LEU:HD13	16:3R:303:PC1:H3B2	2.01	0.43
8:3U:32:LYS:O	8:3U:36:ARG:HD3	2.19	0.43
1:3A:131:ARG:HD3	1:3A:175:ARG:HA	2.00	0.43
1:3A:139:GLN:HB2	5:3I:50:LEU:HD12	2.00	0.43
1:3A:158:PHE:HB3	1:3A:161:THR:OG1	2.17	0.43
3:3C:348:ILE:HB	17:3C:676:HOH:O	2.17	0.43
3:3C:378:LYS:HE2	3:3C:378:LYS:HB2	1.69	0.43
7:3G:36:ILE:HB	7:3G:37:PRO:HD3	2.00	0.43
1:3N:19:LEU:HD22	1:3N:213:GLN:CD	2.39	0.43
4:3Q:33:TYR:CD1	4:3Q:37:CYS:HB2	2.53	0.43
4:3Q:41:HIS:HE1	4:3Q:111:PRO:HD2	1.83	0.43
5:3R:175:PHE:HB2	5:3R:213:LEU:O	2.19	0.43
2:3B:78:LYS:HA	2:3B:131:GLU:OE2	2.19	0.43
4:3D:327:ARG:O	7:3G:14:HIS:HB3	2.18	0.43
6:3F:97:GLU:HG3	17:3F:239:HOH:O	2.19	0.43
2:3O:238:LYS:HE3	2:3O:239:TYR:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3Q:126:TYR:OH	14:3Q:501:HEC:O2A	2.21	0.43
5:3R:180:THR:N	5:3R:183:GLU:OE1	2.52	0.43
7:3T:32:LYS:HE2	7:3T:32:LYS:HB2	1.72	0.43
1:3A:167:VAL:HG13	17:3A:613:HOH:O	2.19	0.43
12:3A:502:3PE:H32	12:3A:502:3PE:H322	1.58	0.43
12:3A:503:3PE:O14	12:3A:503:3PE:H2	2.19	0.43
6:3F:99:LYS:HD3	6:3F:99:LYS:HA	1.70	0.43
3:3P:126:THR:HG21	3:3P:186:PRO:HG3	2.01	0.43
4:3Q:75:ASN:OD1	4:3Q:79:GLU:HG2	2.19	0.43
5:3R:187:GLU:HA	5:3R:190:VAL:HB	2.01	0.43
5:3R:224:PRO:HB3	5:3R:243:TYR:CE2	2.53	0.43
1:3A:349:ALA:O	1:3A:350:THR:HB	2.18	0.43
5:3I:36:ALA:HB2	5:3I:73:PRO:HD2	2.00	0.43
1:3N:68:LYS:HE3	1:3N:68:LYS:HB2	1.82	0.43
1:3N:188:GLN:O	1:3N:223:TYR:HE1	2.02	0.43
5:3R:197:ASP:H	5:3R:248:ARG:NH2	2.16	0.43
5:3R:248:ARG:NH2	5:3R:249:ILE:HB	2.34	0.43
4:3D:125:CYS:SG	14:3D:501:HEC:HBB3	2.59	0.43
4:3D:160:ASP:HB3	4:3D:169:PHE:CZ	2.54	0.43
5:3E:197:ASP:OD1	5:3E:197:ASP:N	2.49	0.43
7:3G:38:ASN:HD22	11:3G:103:CDL:PA1	2.41	0.43
1:3N:40:TRP:CZ2	1:3N:377:GLU:HA	2.53	0.43
2:3O:125:ASN:HB2	17:3O:622:HOH:O	2.18	0.43
3:3P:234:PHE:HZ	11:3T:101:CDL:H532	1.84	0.43
4:3Q:8:PRO:HG3	8:3U:66:ASP:HB3	2.00	0.43
5:3R:152:ILE:O	5:3R:153:GLU:HG2	2.18	0.43
1:3A:436:ARG:HD3	3:3C:222:PRO:HD3	2.01	0.43
4:3D:93:LEU:HD23	4:3D:239:PRO:HB2	1.99	0.43
5:3E:155:LYS:HE2	5:3E:159:ILE:HD11	2.01	0.43
9:3J:30:LEU:HA	10:3Y:34:TRP:CD1	2.54	0.43
1:3N:343:MET:HE2	17:3N:636:HOH:O	2.18	0.43
1:3A:3:THR:C	1:3A:5:ALA:H	2.23	0.42
3:3C:111:GLU:OE2	17:3C:612:HOH:O	2.21	0.42
3:3P:112:THR:O	3:3P:196:HIS:CE1	2.72	0.42
5:3R:200:HIS:O	5:3R:204:ARG:HG3	2.18	0.42
8:3U:17:LEU:HD13	8:3U:73:LEU:HD22	2.00	0.42
4:3D:254:TYR:CZ	4:3D:257:VAL:HG23	2.54	0.42
6:3F:86:ILE:HD12	6:3F:92:TRP:CZ2	2.54	0.42
3:3P:107:TYR:HB3	3:3P:113:TRP:CD2	2.54	0.42
5:3R:195:LEU:HB3	5:3R:248:ARG:NH2	2.24	0.42
5:3R:219:HIS:HB3	15:3R:301:FES:S2	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3R:222:CYS:HB3	5:3R:238:CYS:HB3	1.48	0.42
2:3O:199:PHE:O	2:3O:227:ARG:NE	2.41	0.42
3:3P:240:LEU:HD11	12:3R:302:3PE:H381	2.01	0.42
7:3T:71:ARG:HA	7:3T:71:ARG:HD2	1.85	0.42
1:3A:124:ASP:O	1:3A:128:GLU:HG2	2.20	0.42
2:3B:163:LEU:HD11	2:3B:258:VAL:HG22	2.00	0.42
2:3B:340:ALA:O	2:3B:344:VAL:HG23	2.19	0.42
12:3D:502:3PE:H351	5:3E:128:ALA:CB	2.49	0.42
5:3E:235:TYR:HD1	5:3E:242:HIS:HA	1.85	0.42
6:3F:110:ILE:O	6:3F:114:LYS:HG2	2.19	0.42
1:3N:237:THR:HG21	7:3T:18:LEU:HD11	2.02	0.42
1:3N:277:ILE:HB	1:3N:309:THR:HG21	2.02	0.42
7:3T:70:LYS:HE2	7:3T:70:LYS:HB3	1.85	0.42
9:3W:33:ARG:HG2	10:3X:47:TYR:CE2	2.54	0.42
10:3Y:6:LEU:O	10:3Y:10:TYR:HD2	2.02	0.42
2:3B:76:THR:HG23	2:3B:81:SER:HA	2.01	0.42
2:3B:244:ILE:O	2:3B:425:ALA:HA	2.19	0.42
3:3C:181:PHE:HZ	5:3R:140:MET:HE1	1.85	0.42
5:3E:212:ILE:O	5:3E:261:PRO:HD2	2.20	0.42
1:3N:2:ALA:HB1	17:3N:768:HOH:O	2.20	0.42
5:3R:210:TRP:CD1	5:3R:268:ASP:HB3	2.54	0.42
1:3A:51:LYS:HG3	1:3A:52:ASN:N	2.33	0.42
12:3A:503:3PE:H121	3:3C:4:ILE:H	1.85	0.42
2:3B:95:LYS:CD	5:3I:32:ALA:HB2	2.45	0.42
3:3C:112:THR:O	3:3C:196:HIS:CD2	2.73	0.42
3:3C:199:PHE:HE1	3:3P:9:PRO:HG2	1.85	0.42
6:3F:114:LYS:HD2	17:3F:224:HOH:O	2.19	0.42
1:3N:351:GLU:HG2	10:3X:12:GLU:OE2	2.20	0.42
5:3V:70:LEU:HA	17:3V:304:HOH:O	2.18	0.42
1:3A:403:ASP:OD1	1:3A:406:VAL:HG23	2.20	0.42
3:3C:137:GLN:HB2	3:3C:254:ASP:O	2.20	0.42
5:3E:177:ARG:CD	5:3E:179:ARG:HG2	2.50	0.42
5:3E:270:LEU:O	5:3E:271:VAL:HG22	2.20	0.42
1:3N:444:LEU:CD2	16:3R:303:PC1:H221	2.48	0.42
3:3P:120:LEU:O	3:3P:124:MET:HG3	2.20	0.42
5:3R:207:LYS:O	5:3R:208:PRO:C	2.58	0.42
1:3A:146:ARG:HA	1:3A:149:VAL:HG12	2.02	0.42
11:3A:501:CDL:H311	3:3C:221:HIS:CE1	2.54	0.42
2:3B:156:GLN:NE2	5:3I:78:TYR:CE2	2.87	0.42
17:3N:705:HOH:O	4:3Q:226:LYS:HE3	2.18	0.42
2:3O:228:GLY:HA3	17:3O:660:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3P:142:GLY:O	3:3P:146:ILE:HG13	2.19	0.42
5:3R:150:SER:HB3	5:3R:170:ARG:N	2.33	0.42
3:3C:158:THR:O	3:3C:161:VAL:HG12	2.19	0.42
3:3C:183:PHE:HB3	3:3P:183:PHE:CZ	2.55	0.42
3:3C:233:LEU:HB2	16:3E:302:PC1:H3A2	2.02	0.42
3:3C:267:HIS:CE1	3:3C:269:LYS:HB3	2.54	0.42
5:3E:206:LYS:O	5:3E:207:LYS:HD3	2.20	0.42
1:3N:297:VAL:HA	3:3P:1:MET:HE1	2.02	0.42
1:3N:324:PHE:HE1	1:3N:326:CYS:HG	1.68	0.42
1:3N:444:LEU:HD11	12:3N:503:3PE:H12	2.02	0.42
5:3R:242:HIS:C	5:3R:250:ARG:HG2	2.40	0.42
6:3S:28:LYS:HA	6:3S:80:TRP:CD1	2.55	0.42
1:3A:390:ILE:HD13	17:3A:670:HOH:O	2.20	0.42
2:3B:232:LEU:HD12	2:3B:232:LEU:HA	1.70	0.42
6:3F:40:LYS:HA	6:3F:92:TRP:CD1	2.55	0.42
9:3J:34:ARG:HG2	10:3Y:47:TYR:CE2	2.54	0.42
1:3N:75:LEU:O	1:3N:79:VAL:HG23	2.19	0.42
1:3N:87:ASN:HB3	1:3N:98:TYR:CZ	2.55	0.42
1:3N:268:VAL:HB	1:3N:269:PRO:HD3	2.01	0.42
1:3N:358:LYS:HE3	1:3N:399:ILE:O	2.20	0.42
1:3N:442:PHE:CD1	16:3R:303:PC1:H122	2.55	0.42
2:3O:295:LEU:HD23	2:3O:343:GLN:HB3	2.02	0.42
7:3T:45:ILE:HD12	7:3T:45:ILE:HA	1.88	0.42
4:3D:139:LEU:HD11	4:3D:179:PHE:HZ	1.85	0.41
1:3N:19:LEU:HB2	1:3N:21:ASN:OD1	2.20	0.41
1:3N:443:TRP:HB3	1:3N:445:ARG:HG2	2.02	0.41
4:3Q:87:LEU:HD23	4:3Q:87:LEU:HA	1.89	0.41
4:3Q:238:ARG:O	7:3T:12:HIS:HB3	2.20	0.41
5:3R:180:THR:O	5:3R:182:LYS:N	2.53	0.41
17:3A:716:HOH:O	5:3E:104:LYS:HE3	2.19	0.41
2:3B:406:ALA:HB1	17:3B:558:HOH:O	2.19	0.41
5:3E:241:SER:HB2	15:3E:301:FES:S1	2.60	0.41
5:3E:248:ARG:HE	5:3E:248:ARG:HB3	1.64	0.41
7:3G:35:GLY:O	7:3G:39:VAL:HG23	2.20	0.41
1:3N:242:ARG:NH1	17:3N:609:HOH:O	2.25	0.41
2:3O:169:ARG:HD2	2:3O:238:LYS:HG3	2.02	0.41
4:3Q:27:ARG:HH21	4:3Q:56:TYR:HA	1.83	0.41
4:3Q:131:LEU:HD11	14:3Q:501:HEC:HMB2	2.01	0.41
5:3R:163:LYS:O	5:3R:177:ARG:HA	2.19	0.41
5:3R:244:ASP:OD1	5:3R:248:ARG:HB2	2.20	0.41
3:3C:329:VAL:HG13	17:3C:757:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3E:226:ALA:HA	5:3E:234:TYR:HD1	1.85	0.41
7:3G:73:ARG:HA	7:3G:73:ARG:HD2	1.78	0.41
11:3G:102:CDL:OA9	11:3G:103:CDL:H741	2.20	0.41
3:3P:55:TYR:HB2	17:3P:701:HOH:O	2.20	0.41
3:3P:131:TYR:O	3:3P:134:PRO:HD2	2.20	0.41
3:3P:315:MET:HB3	3:3P:315:MET:HE2	1.91	0.41
5:3R:207:LYS:HE3	5:3R:210:TRP:HZ3	1.85	0.41
2:3B:109:VAL:HB	2:3B:119:LEU:HD12	2.02	0.41
3:3C:77:TRP:CD2	4:3D:286:GLU:HG3	2.56	0.41
5:3E:117:ILE:HD11	12:3G:101:3PE:O32	2.21	0.41
5:3E:179:ARG:NH2	5:3E:201:ASP:OD1	2.53	0.41
5:3E:235:TYR:N	5:3E:243:TYR:HB2	2.35	0.41
1:3N:158:PHE:HB3	1:3N:161:THR:OG1	2.20	0.41
2:3O:160:LEU:HD12	5:3V:64:LEU:HD13	2.03	0.41
3:3P:15:ASN:HA	3:3P:19:ILE:HD12	2.01	0.41
3:3P:318:ARG:O	3:3P:322:GLN:HG3	2.20	0.41
5:3R:180:THR:O	5:3R:180:THR:HG23	2.21	0.41
2:3B:74:SER:O	2:3B:74:SER:OG	2.36	0.41
3:3C:206:ASN:HB3	13:3C:502:HEM:O2D	2.21	0.41
5:3E:206:LYS:HD2	5:3E:265:PHE:HD1	1.85	0.41
6:3F:107:LYS:HD3	6:3F:108:GLU:N	2.35	0.41
2:3O:240:ARG:O	2:3O:421:ARG:NH1	2.53	0.41
4:3Q:47:ALA:HA	4:3Q:90:TYR:HA	2.01	0.41
5:3R:224:PRO:HB3	5:3R:243:TYR:HE2	1.85	0.41
16:3R:303:PC1:H32	16:3R:303:PC1:H321	1.31	0.41
8:3U:47:ARG:HG3	17:3U:101:HOH:O	2.20	0.41
3:3C:98:VAL:O	3:3C:102:LEU:HG	2.21	0.41
3:3C:104:TYR:CD1	3:3C:208:PRO:HA	2.55	0.41
3:3C:301:LEU:HD23	3:3C:304:MET:HE3	2.02	0.41
4:3D:106:LEU:HD13	4:3D:295:LEU:HD13	2.02	0.41
5:3E:199:GLN:OE1	5:3E:204:ARG:HB3	2.21	0.41
6:3F:117:GLU:HB3	10:3X:4:ARG:HG2	2.02	0.41
1:3N:281:ASP:HB3	1:3N:284:TYR:CE1	2.56	0.41
1:3A:178:SER:O	1:3A:182:LEU:HG	2.21	0.41
1:3A:311:ASN:HB2	17:3A:658:HOH:O	2.21	0.41
1:3A:362:ARG:HE	1:3A:396:GLU:CD	2.24	0.41
4:3D:269:SER:HB2	8:3H:102:LEU:HD11	2.03	0.41
1:3N:38:GLY:O	1:3N:197:LEU:HD12	2.20	0.41
12:3N:501:3PE:H332	11:3N:502:CDL:H111	2.01	0.41
2:3O:195:VAL:O	2:3O:199:PHE:HB2	2.20	0.41
2:3O:221:GLU:O	2:3O:225:ASN:ND2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3P:67:THR:HG21	4:3Q:45:TYR:CD1	2.56	0.41
5:3R:183:GLU:HB3	5:3R:245:ALA:HB2	2.02	0.41
3:3C:348:ILE:HG22	3:3C:352:GLN:OE1	2.21	0.41
5:3E:108:ASP:O	5:3E:112:GLY:N	2.50	0.41
5:3E:191:GLU:HG3	5:3E:194:GLN:H	1.86	0.41
5:3E:224:PRO:HA	5:3E:235:TYR:O	2.21	0.41
7:3G:47:ILE:HD12	7:3G:47:ILE:HA	1.91	0.41
4:3Q:134:TYR:CD2	4:3Q:162:PRO:HG3	2.56	0.41
5:3R:134:SER:O	5:3R:138:SER:OG	2.28	0.41
6:3S:16:ILE:H	6:3S:16:ILE:HG12	1.64	0.41
8:3U:72:LYS:HB2	17:3U:128:HOH:O	2.21	0.41
1:3A:172:GLU:OE1	1:3A:172:GLU:N	2.47	0.41
1:3A:439:SER:OG	12:3A:502:3PE:O14	2.28	0.41
11:3A:501:CDL:H152	12:3A:503:3PE:H381	2.03	0.41
11:3A:501:CDL:HB22	17:3A:705:HOH:O	2.20	0.41
2:3B:341:TYR:O	2:3B:345:LYS:HG3	2.20	0.41
3:3C:82:LEU:HD12	3:3C:243:VAL:HG21	2.02	0.41
4:3D:146:GLU:HG2	4:3D:175:LEU:HD11	2.03	0.41
6:3F:25:LEU:HD13	6:3F:28:ILE:HB	2.02	0.41
7:3G:72:LYS:HE3	7:3G:72:LYS:HB2	1.82	0.41
2:3O:314:ALA:HA	5:3V:63:PRO:HD3	2.01	0.41
4:3Q:123:GLY:O	4:3Q:127:VAL:HG23	2.20	0.41
5:3R:133:VAL:O	5:3R:137:VAL:HG23	2.21	0.41
5:3R:200:HIS:HB3	5:3R:203:GLU:HB3	2.01	0.41
5:3R:249:ILE:HG12	5:3R:257:ASN:HA	2.02	0.41
7:3T:72:LYS:HD2	8:3U:52:GLU:HG3	2.03	0.41
10:3X:8:PRO:O	10:3X:11:ARG:HG2	2.21	0.41
11:3A:501:CDL:H722	16:3E:302:PC1:H232	2.03	0.41
2:3B:83:PHE:CE2	6:3S:104:ARG:HG3	2.55	0.41
5:3E:168:LYS:HD2	5:3E:168:LYS:HA	1.86	0.41
6:3F:62:LEU:HD23	6:3F:62:LEU:HA	1.96	0.41
1:3N:172:GLU:O	1:3N:176:LYS:HG2	2.21	0.41
1:3N:209:LEU:HA	1:3N:209:LEU:HD12	1.83	0.41
4:3Q:28:ARG:HE	4:3Q:185:ASP:CG	2.24	0.41
8:3U:40:CYS:HA	8:3U:43:ARG:NH1	2.36	0.41
1:3A:316:GLU:OE1	1:3A:316:GLU:N	2.54	0.40
3:3C:115:ILE:HB	3:3C:196:HIS:HD2	1.86	0.40
3:3C:158:THR:HA	3:3C:161:VAL:HG12	2.03	0.40
4:3D:261:ASP:OD1	4:3D:262:ASP:N	2.54	0.40
5:3E:263:TYR:HB3	5:3E:273:VAL:HG13	2.03	0.40
1:3N:432:PRO:HB2	1:3N:437:ILE:HG13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3N:445:ARG:NH2	12:3N:501:3PE:O12	2.39	0.40
11:3P:504:CDL:HB31	7:3T:40:ARG:HB3	2.02	0.40
5:3R:213:LEU:CD2	5:3R:258:LEU:HB2	2.50	0.40
6:3S:105:GLU:HG2	10:3Y:4:ARG:HG3	2.04	0.40
8:3U:69:VAL:HA	17:3U:128:HOH:O	2.21	0.40
1:3A:240:GLU:CD	1:3A:434:TYR:HB2	2.42	0.40
5:3E:103:SER:O	5:3E:110:ARG:NH2	2.49	0.40
5:3E:172:LYS:HB3	5:3E:214:ILE:HD12	2.03	0.40
7:3G:20:LEU:HG	7:3G:24:GLU:HB2	2.03	0.40
3:3P:24:PRO:HB2	3:3P:27:ILE:HG23	2.02	0.40
10:3X:42:LEU:HD23	10:3X:42:LEU:HA	1.80	0.40
1:3A:261:GLY:O	1:3A:267:ASN:ND2	2.46	0.40
12:3A:502:3PE:C3	16:3E:302:PC1:H31	2.52	0.40
2:3B:51:ILE:HG12	2:3B:204:MET:HG2	2.03	0.40
3:3C:376:LEU:O	17:3C:614:HOH:O	2.22	0.40
12:3C:504:3PE:H32	16:3X:101:PC1:H222	2.03	0.40
1:3N:215:HIS:CE1	17:3N:639:HOH:O	2.74	0.40
1:3N:406:VAL:O	1:3N:410:VAL:HG13	2.22	0.40
2:3O:169:ARG:CG	2:3O:240:ARG:HB3	2.50	0.40
4:3Q:15:ARG:NH1	4:3Q:15:ARG:HG3	2.35	0.40
5:3R:184:ILE:HG21	5:3R:184:ILE:HD13	1.80	0.40
1:3A:34:THR:HG22	1:3A:102:LEU:HD23	2.03	0.40
1:3A:34:THR:OG1	2:3B:373:GLU:OE2	2.30	0.40
3:3C:149:LEU:HD22	3:3C:281:LEU:HD11	2.02	0.40
4:3D:326:TYR:CZ	4:3D:328:PRO:HB3	2.56	0.40
5:3E:130:LYS:NZ	10:3Y:34:TRP:O	2.48	0.40
16:3E:302:PC1:H271	9:3J:22:ALA:HB1	2.04	0.40
6:3F:83:ARG:O	6:3F:85:GLN:HG2	2.22	0.40
8:3H:38:LEU:HD12	17:3H:207:HOH:O	2.22	0.40
2:3O:190:GLN:HB2	17:3O:502:HOH:O	2.20	0.40
2:3O:411:ILE:HG12	17:3O:514:HOH:O	2.22	0.40
3:3P:240:LEU:HD13	4:3Q:208:MET:HG3	2.03	0.40
3:3P:377:LEU:HD23	3:3P:377:LEU:HA	1.91	0.40
5:3R:170:ARG:HG2	5:3R:274:GLY:O	2.21	0.40
5:3R:182:LYS:HE2	5:3R:182:LYS:HB2	1.93	0.40
12:3R:302:3PE:H3B1	16:3R:303:PC1:H3F2	2.02	0.40
1:3A:20:ASP:N	1:3A:20:ASP:OD1	2.55	0.40
1:3A:284:TYR:CD2	5:3I:71:ASN:HA	2.57	0.40
1:3A:356:ARG:HG3	2:3B:91:ALA:HA	2.03	0.40
2:3B:101:THR:HG22	5:3I:65:VAL:HG12	2.03	0.40
6:3F:105:TYR:O	6:3F:109:VAL:HG23	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3N:142:ASP:OD1	5:3R:80:HIS:ND1	2.39	0.40
1:3N:439:SER:HB3	12:3N:503:3PE:C11	2.50	0.40
17:3N:797:HOH:O	10:3X:17:TRP:HH2	2.03	0.40
5:3R:182:LYS:O	5:3R:186:GLN:N	2.37	0.40
5:3R:241:SER:HB2	15:3R:301:FES:S1	2.61	0.40
5:3R:248:ARG:HH11	5:3R:257:ASN:HB3	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3A	436/480 (91%)	423 (97%)	12 (3%)	1 (0%)	47	49
1	3N	444/480 (92%)	424 (96%)	18 (4%)	2 (0%)	29	26
2	3B	414/453 (91%)	397 (96%)	17 (4%)	0	100	100
2	3O	413/453 (91%)	402 (97%)	10 (2%)	1 (0%)	47	49
3	3C	377/379 (100%)	370 (98%)	6 (2%)	1 (0%)	41	41
3	3P	377/379 (100%)	369 (98%)	8 (2%)	0	100	100
4	3D	235/325 (72%)	232 (99%)	3 (1%)	0	100	100
4	3Q	237/325 (73%)	228 (96%)	9 (4%)	0	100	100
5	3E	194/274 (71%)	169 (87%)	24 (12%)	1 (0%)	29	26
5	3I	45/274 (16%)	40 (89%)	4 (9%)	1 (2%)	6	2
5	3R	194/274 (71%)	167 (86%)	23 (12%)	4 (2%)	7	3
5	3V	29/274 (11%)	28 (97%)	1 (3%)	0	100	100
6	3F	96/111 (86%)	94 (98%)	2 (2%)	0	100	100
6	3S	96/111 (86%)	95 (99%)	1 (1%)	0	100	100
7	3G	72/82 (88%)	70 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	3T	72/82 (88%)	71 (99%)	0	1 (1%)	11	6
8	3H	63/91 (69%)	61 (97%)	1 (2%)	1 (2%)	9	5
8	3U	63/91 (69%)	62 (98%)	1 (2%)	0	100	100
9	3J	54/64 (84%)	51 (94%)	1 (2%)	2 (4%)	3	1
9	3W	54/64 (84%)	53 (98%)	1 (2%)	0	100	100
10	3X	50/56 (89%)	47 (94%)	3 (6%)	0	100	100
10	3Y	49/56 (88%)	45 (92%)	4 (8%)	0	100	100
All	All	4064/5178 (78%)	3898 (96%)	151 (4%)	15 (0%)	38	32

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	3C	270	PRO
5	3E	271	VAL
1	3N	224	VAL
5	3R	150	SER
5	3I	36	ALA
9	3J	54	LYS
5	3R	228	ALA
5	3R	273	VAL
2	3O	171	ALA
5	3R	181	LYS
8	3H	78	ASP
9	3J	58	HIS
7	3T	74	PRO
1	3A	231	PHE
1	3N	71	PRO

5.3.2 Protein sidechains [i](#)

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%)	361 (98%)	6 (2%)	62	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3N	372/397 (94%)	363 (98%)	9 (2%)	49	53
2	3B	328/355 (92%)	323 (98%)	5 (2%)	65	71
2	3O	327/355 (92%)	323 (99%)	4 (1%)	71	77
3	3C	332/332 (100%)	328 (99%)	4 (1%)	71	77
3	3P	332/332 (100%)	328 (99%)	4 (1%)	71	77
4	3D	202/258 (78%)	197 (98%)	5 (2%)	47	52
4	3Q	204/258 (79%)	204 (100%)	0	100	100
5	3E	166/225 (74%)	161 (97%)	5 (3%)	41	44
5	3I	36/225 (16%)	35 (97%)	1 (3%)	43	47
5	3R	166/225 (74%)	160 (96%)	6 (4%)	35	36
5	3V	24/225 (11%)	24 (100%)	0	100	100
6	3F	90/99 (91%)	89 (99%)	1 (1%)	73	79
6	3S	90/99 (91%)	89 (99%)	1 (1%)	73	79
7	3G	67/73 (92%)	67 (100%)	0	100	100
7	3T	67/73 (92%)	67 (100%)	0	100	100
8	3H	62/85 (73%)	62 (100%)	0	100	100
8	3U	62/85 (73%)	62 (100%)	0	100	100
9	3J	46/52 (88%)	42 (91%)	4 (9%)	10	7
9	3W	46/52 (88%)	46 (100%)	0	100	100
10	3X	42/46 (91%)	41 (98%)	1 (2%)	49	53
10	3Y	41/46 (89%)	40 (98%)	1 (2%)	49	53
All	All	3469/4294 (81%)	3412 (98%)	57 (2%)	64	69

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	3A	10	SER
1	3A	58	PHE
1	3A	68	LYS
1	3A	121	SER
1	3A	210	ASP
1	3A	403	ASP
2	3B	110	GLU
2	3B	189	ASP
2	3B	315	SER

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Mol	Chain	Res	Type
2	3B	342	ASP
2	3B	421	ARG
3	3C	80	ARG
3	3C	90	PHE
3	3C	183	PHE
3	3C	379	TRP
4	3D	109	LEU
4	3D	113	SER
4	3D	232	ARG
4	3D	249	MET
4	3D	258	LEU
5	3E	155	LYS
5	3E	161	GLU
5	3E	177	ARG
5	3E	230	ASP
5	3E	242	HIS
6	3F	118	GLU
5	3I	67	SER
9	3J	54	LYS
9	3J	56	ILE
9	3J	57	LYS
9	3J	58	HIS
1	3N	10	SER
1	3N	58	PHE
1	3N	112	LEU
1	3N	117	VAL
1	3N	206	ARG
1	3N	210	ASP
1	3N	284	TYR
1	3N	307	PHE
1	3N	403	ASP
2	3O	110	GLU
2	3O	223	PHE
2	3O	339	SER
2	3O	437	ASP
3	3P	1	MET
3	3P	80	ARG
3	3P	90	PHE
3	3P	379	TRP
5	3R	82	ASP
5	3R	155	LYS
5	3R	165	MET

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Mol	Chain	Res	Type
5	3R	178	HIS
5	3R	181	LYS
5	3R	263	TYR
6	3S	39	GLU
10	3X	4	ARG
10	3Y	11	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	3A	21	ASN
1	3A	207	GLN
1	3A	215	HIS
3	3C	54	HIS
9	3J	49	GLN
1	3N	9	GLN
1	3N	215	HIS
3	3P	16	ASN
3	3P	221	HIS
4	3Q	105	ASN
5	3R	219	HIS
5	3R	257	ASN
8	3U	67	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

28 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
12	3PE	3D	502	-	32,32,50	0.35	0	35,37,55	0.52	0
12	3PE	3C	503	-	34,34,50	0.35	0	37,39,55	0.54	0
12	3PE	3N	501	-	31,31,50	0.35	0	34,36,55	0.73	1 (2%)
12	3PE	3A	502	-	26,26,50	0.37	0	29,31,55	0.67	1 (3%)
16	PC1	3E	302	-	46,46,53	0.28	0	52,54,61	0.38	0
12	3PE	3C	504	-	33,33,50	0.35	0	36,38,55	0.53	0
11	CDL	3T	101	-	56,56,99	0.36	0	62,68,111	0.70	2 (3%)
11	CDL	3N	502	-	42,42,99	0.39	0	48,54,111	0.61	0
15	FES	3E	301	5	0,4,4	-	-	-	-	-
12	3PE	3P	503	-	32,32,50	0.33	0	35,37,55	0.55	0
11	CDL	3A	501	-	57,57,99	0.34	0	63,69,111	0.54	0
16	PC1	3X	101	-	28,28,53	0.37	0	34,36,61	0.63	1 (2%)
11	CDL	3G	102	-	51,51,99	0.36	0	57,63,111	0.65	1 (1%)
12	3PE	3N	503	-	24,24,50	0.37	0	27,29,55	0.53	0
13	HEM	3C	502	3	41,50,50	1.31	4 (9%)	45,82,82	1.72	10 (22%)
13	HEM	3P	501	3	41,50,50	1.30	4 (9%)	45,82,82	1.85	8 (17%)
14	HEC	3D	501	4	31,49,50	2.38	12 (38%)	22,80,82	2.62	5 (22%)
12	3PE	3R	302	-	46,46,50	0.28	0	49,51,55	0.34	0
16	PC1	3R	303	-	44,44,53	0.30	0	50,52,61	0.42	0
12	3PE	3A	503	-	31,31,50	0.34	0	34,36,55	0.41	0
12	3PE	3Y	101	-	29,29,50	0.36	0	32,34,55	0.46	0
13	HEM	3P	502	3	41,50,50	1.33	6 (14%)	45,82,82	1.81	11 (24%)
14	HEC	3Q	501	4	32,50,50	2.39	12 (37%)	24,82,82	2.64	6 (25%)
13	HEM	3C	501	3	41,50,50	1.31	6 (14%)	45,82,82	1.83	9 (20%)
15	FES	3R	301	5	0,4,4	-	-	-	-	-
12	3PE	3G	101	-	28,28,50	0.34	0	31,33,55	0.43	0
11	CDL	3P	504	-	55,55,99	0.37	0	61,67,111	0.61	1 (1%)
11	CDL	3G	103	-	55,55,99	0.35	0	61,67,111	0.47	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	3D	502	-	-	3/36/36/54	-
12	3PE	3C	503	-	-	12/38/38/54	-
12	3PE	3N	501	-	-	11/35/35/54	-
12	3PE	3A	502	-	-	7/30/30/54	-
16	PC1	3E	302	-	-	3/50/50/57	-
12	3PE	3C	504	-	-	9/37/37/54	-
11	CDL	3T	101	-	-	14/67/67/110	-
11	CDL	3N	502	-	-	9/53/53/110	-
15	FES	3E	301	5	-	-	0/1/1/1
12	3PE	3P	503	-	-	11/36/36/54	-
11	CDL	3A	501	-	-	8/68/68/110	-
16	PC1	3X	101	-	-	6/32/32/57	-
11	CDL	3G	102	-	-	10/62/62/110	-
12	3PE	3N	503	-	-	9/28/28/54	-
13	HEM	3C	502	3	-	4/12/54/54	-
13	HEM	3P	501	3	-	6/12/54/54	-
14	HEC	3D	501	4	-	3/8/53/54	-
12	3PE	3R	302	-	-	9/50/50/54	-
16	PC1	3R	303	-	-	6/48/48/57	-
12	3PE	3A	503	-	-	8/35/35/54	-
12	3PE	3Y	101	-	-	3/33/33/54	-
13	HEM	3P	502	3	-	6/12/54/54	-
14	HEC	3Q	501	4	-	4/10/54/54	-
13	HEM	3C	501	3	-	5/12/54/54	-
15	FES	3R	301	5	-	-	0/1/1/1
12	3PE	3G	101	-	-	10/32/32/54	-
11	CDL	3P	504	-	-	14/66/66/110	-
11	CDL	3G	103	-	-	13/66/66/110	-

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	3Q	501	HEC	C3C-C2C	7.04	1.48	1.40
14	3D	501	HEC	C3C-C2C	6.92	1.48	1.40
14	3Q	501	HEC	C2B-C3B	6.87	1.47	1.40
14	3D	501	HEC	C2B-C3B	6.67	1.47	1.40
13	3P	502	HEM	C1B-NB	-3.44	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	3P	502	HEM	C4D-ND	-3.37	1.34	1.40
13	3C	502	HEM	C1B-NB	-3.35	1.34	1.40
14	3D	501	HEC	C3D-C2D	3.27	1.47	1.37
14	3Q	501	HEC	C3D-C2D	3.27	1.47	1.37
13	3C	501	HEM	C1B-NB	-3.26	1.34	1.40
14	3D	501	HEC	C2A-C3A	3.22	1.47	1.37
13	3C	502	HEM	C4D-ND	-3.20	1.34	1.40
13	3P	501	HEM	C4D-ND	-3.19	1.34	1.40
13	3P	501	HEM	C1B-NB	-3.18	1.34	1.40
14	3Q	501	HEC	C2A-C3A	3.16	1.47	1.37
13	3C	501	HEM	C4D-ND	-3.15	1.34	1.40
14	3Q	501	HEC	C3C-C4C	3.12	1.48	1.43
14	3D	501	HEC	C4B-C3B	3.06	1.48	1.43
14	3D	501	HEC	C3C-C4C	3.06	1.48	1.43
14	3Q	501	HEC	C4B-C3B	3.05	1.48	1.43
13	3P	501	HEM	FE-NB	3.03	2.11	1.96
13	3C	501	HEM	FE-NB	2.97	2.11	1.96
13	3C	502	HEM	FE-NB	2.92	2.11	1.96
13	3P	502	HEM	FE-NB	2.79	2.10	1.96
14	3Q	501	HEC	C3A-C4A	2.63	1.48	1.42
14	3D	501	HEC	C3A-C4A	2.61	1.48	1.42
14	3D	501	HEC	C2A-C1A	2.59	1.48	1.42
14	3Q	501	HEC	C2A-C1A	2.58	1.48	1.42
14	3Q	501	HEC	C1D-CHD	2.56	1.48	1.41
14	3D	501	HEC	C4D-CHA	2.50	1.47	1.41
14	3D	501	HEC	C1D-CHD	2.47	1.47	1.41
14	3Q	501	HEC	C4D-CHA	2.39	1.47	1.41
14	3Q	501	HEC	C1C-CHC	2.38	1.47	1.41
14	3D	501	HEC	C1C-CHC	2.31	1.47	1.41
14	3D	501	HEC	C1B-CHB	2.20	1.47	1.41
14	3Q	501	HEC	C1B-CHB	2.19	1.47	1.41
13	3C	501	HEM	CHB-C1B	2.19	1.40	1.35
13	3P	501	HEM	CHB-C1B	2.17	1.40	1.35
13	3P	502	HEM	C4B-NB	-2.10	1.34	1.38
13	3C	501	HEM	C1D-ND	-2.05	1.34	1.38
13	3P	502	HEM	C1D-ND	-2.05	1.34	1.38
13	3C	502	HEM	C1D-ND	-2.03	1.34	1.38
13	3C	501	HEM	C4B-NB	-2.02	1.34	1.38
13	3P	502	HEM	FE-ND	-2.00	1.87	1.96

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	3Q	501	HEC	C1D-C2D-C3D	-6.40	102.55	107.00
14	3D	501	HEC	C1D-C2D-C3D	-6.24	102.65	107.00
14	3Q	501	HEC	CMC-C2C-C3C	5.82	132.66	125.82
14	3D	501	HEC	CMC-C2C-C3C	5.74	132.57	125.82
14	3D	501	HEC	CMB-C2B-C3B	5.66	132.48	125.82
14	3Q	501	HEC	CMB-C2B-C3B	5.56	132.35	125.82
13	3C	501	HEM	CHC-C4B-NB	5.45	130.35	124.43
13	3P	501	HEM	CHC-C4B-NB	5.21	130.09	124.43
13	3P	502	HEM	CHC-C4B-NB	4.64	129.47	124.43
13	3C	502	HEM	CHC-C4B-NB	4.56	129.38	124.43
13	3C	501	HEM	CHD-C1D-ND	4.50	129.32	124.43
13	3P	501	HEM	CHD-C1D-ND	4.49	129.31	124.43
13	3C	502	HEM	CHD-C1D-ND	4.20	129.00	124.43
13	3P	502	HEM	CHD-C1D-ND	4.18	128.98	124.43
13	3P	501	HEM	CBA-CAA-C2A	-4.12	105.59	112.62
13	3P	502	HEM	C1B-NB-C4B	4.10	109.31	105.07
13	3P	502	HEM	CHA-C4D-ND	4.08	129.42	124.38
14	3Q	501	HEC	CAA-CBA-CGA	-4.05	102.39	113.76
14	3D	501	HEC	CAA-CBA-CGA	-3.99	102.57	113.76
13	3C	502	HEM	C1B-NB-C4B	3.95	109.16	105.07
13	3C	501	HEM	C1B-NB-C4B	3.73	108.92	105.07
13	3P	501	HEM	C1B-NB-C4B	3.65	108.85	105.07
14	3Q	501	HEC	CBD-CAD-C3D	-3.58	106.52	112.62
13	3P	502	HEM	CHB-C1B-NB	3.52	128.74	124.38
13	3C	502	HEM	CHA-C4D-ND	3.39	128.57	124.38
13	3C	502	HEM	CHB-C1B-NB	3.32	128.48	124.38
13	3C	501	HEM	CHA-C4D-ND	3.25	128.40	124.38
13	3P	501	HEM	CHA-C4D-ND	3.05	128.15	124.38
13	3P	501	HEM	CHD-C1D-C2D	-2.97	120.34	124.98
13	3C	501	HEM	CHD-C1D-C2D	-2.96	120.36	124.98
13	3P	501	HEM	CHB-C1B-NB	2.93	128.00	124.38
13	3C	501	HEM	CHB-C1B-NB	2.85	127.91	124.38
13	3P	502	HEM	C4D-ND-C1D	2.75	107.92	105.07
13	3C	502	HEM	CHD-C1D-C2D	-2.66	120.83	124.98
13	3C	501	HEM	CBA-CAA-C2A	-2.52	108.32	112.62
13	3P	502	HEM	CHA-C4D-C3D	-2.40	120.83	125.33
11	3G	102	CDL	OA6-CA4-CA3	2.31	116.78	108.40
13	3C	502	HEM	C4D-ND-C1D	2.31	107.46	105.07
16	3X	101	PC1	O21-C21-C22	2.29	116.44	111.50
14	3D	501	HEC	CMA-C3A-C2A	2.25	129.18	124.94
13	3P	502	HEM	CHD-C1D-C2D	-2.23	121.49	124.98
13	3P	502	HEM	O2D-CGD-CBD	2.22	121.15	114.03
12	3N	501	3PE	O21-C2-C1	2.22	116.43	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	3C	501	HEM	CMC-C2C-C3C	2.16	128.72	124.68
12	3A	502	3PE	O21-C21-C22	2.14	116.11	111.50
13	3C	502	HEM	O2A-CGA-CBA	2.14	120.90	114.03
14	3Q	501	HEC	CMA-C3A-C2A	2.11	128.92	124.94
11	3P	504	CDL	OB6-CB4-CB6	-2.08	100.86	108.40
13	3C	501	HEM	C4D-ND-C1D	2.07	107.21	105.07
11	3T	101	CDL	OA6-CA4-CA3	2.06	115.85	108.40
13	3P	502	HEM	CHB-C1B-C2B	-2.06	121.03	126.72
11	3T	101	CDL	OA8-CA6-CA4	2.05	114.41	108.43
13	3C	502	HEM	CBD-CAD-C3D	-2.02	107.01	112.63
13	3P	501	HEM	CAD-C3D-C4D	2.02	128.19	124.66
13	3P	502	HEM	O2A-CGA-CBA	2.01	120.48	114.03
13	3C	502	HEM	CHB-C1B-C2B	-2.00	121.19	126.72

There are no chirality outliers.

All (203) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	3A	501	CDL	CB2-OB2-PB2-OB4
11	3G	102	CDL	CA3-OA5-PA1-OA3
11	3G	102	CDL	CB2-OB2-PB2-OB4
11	3G	103	CDL	CB2-OB2-PB2-OB5
11	3G	103	CDL	CB3-OB5-PB2-OB3
11	3P	504	CDL	OB5-CB3-CB4-OB6
11	3P	504	CDL	OB9-CB7-OB8-CB6
11	3P	504	CDL	C71-CB7-OB8-CB6
11	3T	101	CDL	OB9-CB7-OB8-CB6
11	3T	101	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	C2-C1-O11-P
12	3C	503	3PE	C1-O11-P-O14
12	3C	503	3PE	C11-O13-P-O14
12	3C	504	3PE	C1-O11-P-O12
12	3C	504	3PE	C2-C1-O11-P
12	3C	504	3PE	O13-C11-C12-N
12	3G	101	3PE	C1-O11-P-O12
12	3G	101	3PE	C1-O11-P-O13
12	3G	101	3PE	C1-O11-P-O14

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Mol	Chain	Res	Type	Atoms
12	3G	101	3PE	O32-C31-O31-C3
12	3G	101	3PE	C32-C31-O31-C3
12	3N	501	3PE	C1-O11-P-O14
12	3N	503	3PE	O22-C21-O21-C2
12	3N	503	3PE	C22-C21-O21-C2
12	3P	503	3PE	C11-O13-P-O11
12	3P	503	3PE	C11-O13-P-O12
12	3P	503	3PE	C11-O13-P-O14
13	3C	501	HEM	C2B-C3B-CAB-CBB
13	3C	502	HEM	C2B-C3B-CAB-CBB
13	3P	502	HEM	C2B-C3B-CAB-CBB
16	3R	303	PC1	C1-O11-P-O14
16	3R	303	PC1	O32-C31-O31-C3
16	3R	303	PC1	C32-C31-O31-C3
16	3X	101	PC1	C1-O11-P-O14
16	3X	101	PC1	O13-C11-C12-N
11	3G	102	CDL	O1-C1-CB2-OB2
12	3Y	101	3PE	C2-C1-O11-P
11	3N	502	CDL	OA6-CA4-CA6-OA8
11	3P	504	CDL	CB5-C51-C52-C53
12	3C	503	3PE	C21-C22-C23-C24
11	3A	501	CDL	CB2-OB2-PB2-OB5
11	3G	102	CDL	CA3-OA5-PA1-OA2
11	3G	102	CDL	CB2-OB2-PB2-OB5
11	3T	101	CDL	CA3-OA5-PA1-OA2
12	3C	503	3PE	C11-O13-P-O11
12	3N	501	3PE	C1-O11-P-O13
12	3G	101	3PE	C31-C32-C33-C34
12	3C	504	3PE	C31-C32-C33-C34
12	3R	302	3PE	C35-C36-C37-C38
11	3T	101	CDL	CA4-CA3-OA5-PA1
12	3N	501	3PE	C2-C1-O11-P
12	3A	503	3PE	C32-C33-C34-C35
12	3R	302	3PE	C21-C22-C23-C24
12	3A	503	3PE	C36-C37-C38-C39
16	3R	303	PC1	C26-C27-C28-C29
11	3G	103	CDL	CA5-C11-C12-C13
12	3P	503	3PE	C21-C22-C23-C24
12	3Y	101	3PE	C31-C32-C33-C34
12	3A	502	3PE	O11-C1-C2-O21
13	3C	501	HEM	C4B-C3B-CAB-CBB
13	3C	502	HEM	C4B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
13	3P	502	HEM	C4B-C3B-CAB-CBB
12	3N	501	3PE	C33-C34-C35-C36
12	3R	302	3PE	C27-C28-C29-C2A
11	3G	103	CDL	CB3-OB5-PB2-OB2
12	3C	504	3PE	C1-O11-P-O13
12	3A	503	3PE	O11-C1-C2-C3
11	3P	504	CDL	CA5-C11-C12-C13
11	3G	102	CDL	CA2-C1-CB2-OB2
12	3P	503	3PE	C1-C2-C3-O31
12	3P	503	3PE	C27-C28-C29-C2A
12	3R	302	3PE	C23-C24-C25-C26
11	3T	101	CDL	C31-CA7-OA8-CA6
13	3C	501	HEM	C3D-CAD-CBD-CGD
11	3G	102	CDL	C72-C71-CB7-OB8
11	3T	101	CDL	C52-C53-C54-C55
11	3P	504	CDL	OB5-CB3-CB4-CB6
12	3P	503	3PE	C22-C23-C24-C25
11	3N	502	CDL	CA3-CA4-CA6-OA8
12	3C	504	3PE	C29-C2A-C2B-C2C
11	3G	103	CDL	OA6-CA4-CA6-OA8
12	3G	101	3PE	O21-C2-C3-O31
11	3N	502	CDL	CA2-C1-CB2-OB2
11	3P	504	CDL	C51-CB5-OB6-CB4
12	3C	504	3PE	O31-C31-C32-C33
11	3G	103	CDL	C52-C53-C54-C55
13	3P	501	HEM	C2B-C3B-CAB-CBB
12	3N	503	3PE	C1-C2-C3-O31
12	3A	503	3PE	O11-C1-C2-O21
12	3A	502	3PE	O21-C2-C3-O31
12	3N	501	3PE	O21-C2-C3-O31
12	3P	503	3PE	C25-C26-C27-C28
11	3A	501	CDL	O1-C1-CA2-OA2
11	3N	502	CDL	CB4-CB3-OB5-PB2
11	3G	102	CDL	CA3-OA5-PA1-OA4
11	3G	103	CDL	CB2-OB2-PB2-OB4
11	3T	101	CDL	CA3-OA5-PA1-OA3
11	3T	101	CDL	CA3-OA5-PA1-OA4
12	3C	503	3PE	C11-O13-P-O12
12	3C	504	3PE	C1-O11-P-O14
12	3N	501	3PE	C1-O11-P-O12
11	3A	501	CDL	C52-C53-C54-C55
12	3A	502	3PE	O11-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
12	3A	503	3PE	O13-C11-C12-N
12	3C	503	3PE	C12-C11-O13-P
12	3C	504	3PE	C12-C11-O13-P
12	3G	101	3PE	C36-C37-C38-C39
12	3R	302	3PE	C26-C27-C28-C29
12	3N	503	3PE	O21-C2-C3-O31
12	3P	503	3PE	O21-C2-C3-O31
12	3R	302	3PE	C32-C33-C34-C35
12	3C	503	3PE	C29-C2A-C2B-C2C
11	3G	103	CDL	C11-C12-C13-C14
12	3N	501	3PE	C1-C2-O21-C21
12	3N	501	3PE	C3-C2-O21-C21
12	3C	503	3PE	C2C-C2D-C2E-C2F
16	3X	101	PC1	O21-C21-C22-C23
11	3A	501	CDL	CA7-C31-C32-C33
11	3A	501	CDL	CB3-OB5-PB2-OB2
11	3G	103	CDL	CA2-OA2-PA1-OA5
11	3N	502	CDL	CB3-OB5-PB2-OB2
11	3P	504	CDL	CA3-OA5-PA1-OA2
11	3P	504	CDL	CB3-OB5-PB2-OB2
11	3T	101	CDL	CA2-OA2-PA1-OA5
12	3A	503	3PE	C1-O11-P-O13
12	3N	501	3PE	C11-O13-P-O11
12	3N	503	3PE	C11-O13-P-O11
12	3Y	101	3PE	C1-O11-P-O13
16	3R	303	PC1	C1-O11-P-O13
16	3X	101	PC1	C11-O13-P-O11
16	3X	101	PC1	C1-O11-P-O13
12	3N	501	3PE	C1-C2-C3-O31
11	3G	102	CDL	C72-C71-CB7-OB9
11	3N	502	CDL	C1-CB2-OB2-PB2
13	3C	501	HEM	CAA-CBA-CGA-O2A
12	3C	503	3PE	C23-C24-C25-C26
13	3P	501	HEM	CAA-CBA-CGA-O1A
13	3P	502	HEM	CAA-CBA-CGA-O1A
13	3P	501	HEM	CAD-CBD-CGD-O1D
14	3D	501	HEC	C3D-CAD-CBD-CGD
13	3P	502	HEM	CAA-CBA-CGA-O2A
12	3C	503	3PE	C1-C2-O21-C21
13	3C	502	HEM	CAA-CBA-CGA-O1A
13	3C	502	HEM	CAA-CBA-CGA-O2A
13	3P	501	HEM	CAA-CBA-CGA-O2A

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Mol	Chain	Res	Type	Atoms
13	3P	501	HEM	CAD-CBD-CGD-O2D
12	3C	503	3PE	O11-C1-C2-O21
11	3T	101	CDL	C53-C54-C55-C56
12	3D	502	3PE	C35-C36-C37-C38
13	3C	501	HEM	CAA-CBA-CGA-O1A
12	3R	302	3PE	C22-C23-C24-C25
16	3X	101	PC1	C21-C22-C23-C24
11	3T	101	CDL	OA5-CA3-CA4-CA6
11	3G	102	CDL	C12-C13-C14-C15
12	3C	503	3PE	C1-O11-P-O13
11	3N	502	CDL	CB6-CB4-OB6-CB5
14	3D	501	HEC	CAA-CBA-CGA-O2A
11	3P	504	CDL	C32-C31-CA7-OA8
14	3Q	501	HEC	CAA-CBA-CGA-O2A
13	3P	502	HEM	CAD-CBD-CGD-O1D
14	3D	501	HEC	CAA-CBA-CGA-O1A
14	3Q	501	HEC	CAA-CBA-CGA-O1A
13	3P	501	HEM	C4B-C3B-CAB-CBB
13	3P	502	HEM	CAD-CBD-CGD-O2D
11	3A	501	CDL	CB2-C1-CA2-OA2
11	3G	103	CDL	OB6-CB4-CB6-OB8
11	3T	101	CDL	OB6-CB4-CB6-OB8
11	3G	103	CDL	C72-C73-C74-C75
11	3T	101	CDL	C52-C51-CB5-OB6
11	3N	502	CDL	C52-C51-CB5-OB6
16	3R	303	PC1	C39-C3A-C3B-C3C
12	3R	302	3PE	C37-C38-C39-C3A
11	3P	504	CDL	C32-C31-CA7-OA9
12	3G	101	3PE	C1-C2-C3-O31
12	3D	502	3PE	C31-C32-C33-C34
12	3N	503	3PE	C31-C32-C33-C34
11	3P	504	CDL	C72-C71-CB7-OB9
11	3A	501	CDL	CB3-OB5-PB2-OB3
11	3G	103	CDL	CA2-OA2-PA1-OA3
11	3G	103	CDL	CB3-OB5-PB2-OB4
11	3N	502	CDL	CB3-OB5-PB2-OB3
11	3P	504	CDL	CA3-OA5-PA1-OA3
12	3G	101	3PE	C11-O13-P-O14
12	3N	501	3PE	C11-O13-P-O14
12	3N	503	3PE	C11-O13-P-O14
12	3D	502	3PE	C24-C25-C26-C27
14	3Q	501	HEC	CAD-CBD-CGD-O2D

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Mol	Chain	Res	Type	Atoms
12	3P	503	3PE	C12-C11-O13-P
16	3E	302	PC1	C12-C11-O13-P
16	3E	302	PC1	C3B-C3C-C3D-C3E
16	3E	302	PC1	C36-C37-C38-C39
14	3Q	501	HEC	CAD-CBD-CGD-O1D
12	3P	503	3PE	C24-C25-C26-C27
12	3R	302	3PE	C34-C35-C36-C37
11	3P	504	CDL	C72-C71-CB7-OB8
12	3N	503	3PE	O31-C31-C32-C33
12	3N	503	3PE	O32-C31-C32-C33
11	3T	101	CDL	C52-C51-CB5-OB7

There are no ring outliers.

27 monomers are involved in 132 short contacts:

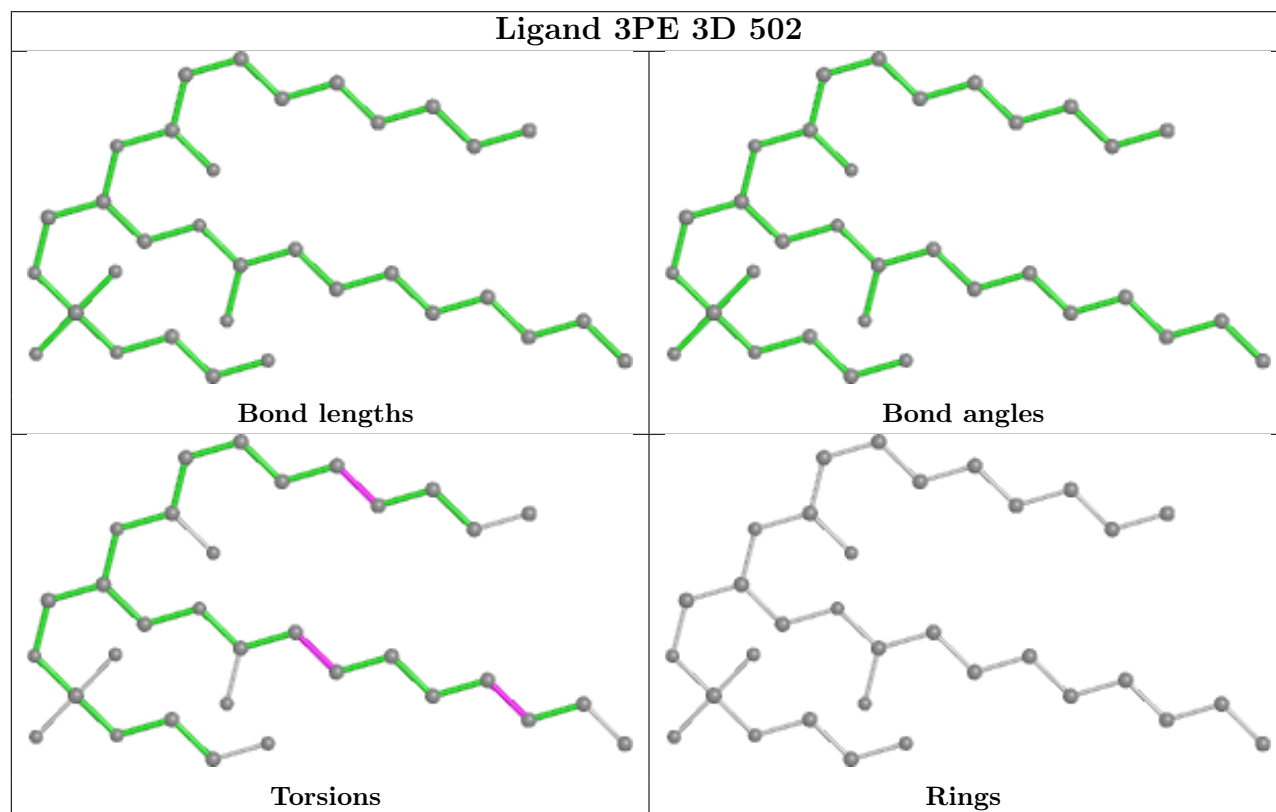
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	3D	502	3PE	6	0
12	3C	503	3PE	7	0
12	3N	501	3PE	5	0
12	3A	502	3PE	5	0
16	3E	302	PC1	8	0
12	3C	504	3PE	7	0
11	3T	101	CDL	6	0
11	3N	502	CDL	7	0
15	3E	301	FES	2	0
12	3P	503	3PE	5	0
11	3A	501	CDL	12	0
16	3X	101	PC1	5	0
11	3G	102	CDL	4	0
12	3N	503	3PE	5	0
13	3C	502	HEM	4	0
13	3P	501	HEM	2	0
14	3D	501	HEC	5	0
12	3R	302	3PE	6	0
16	3R	303	PC1	9	0
12	3A	503	3PE	9	0
13	3P	502	HEM	2	0
14	3Q	501	HEC	4	0
13	3C	501	HEM	3	0
15	3R	301	FES	5	0
12	3G	101	3PE	2	0
11	3P	504	CDL	7	0

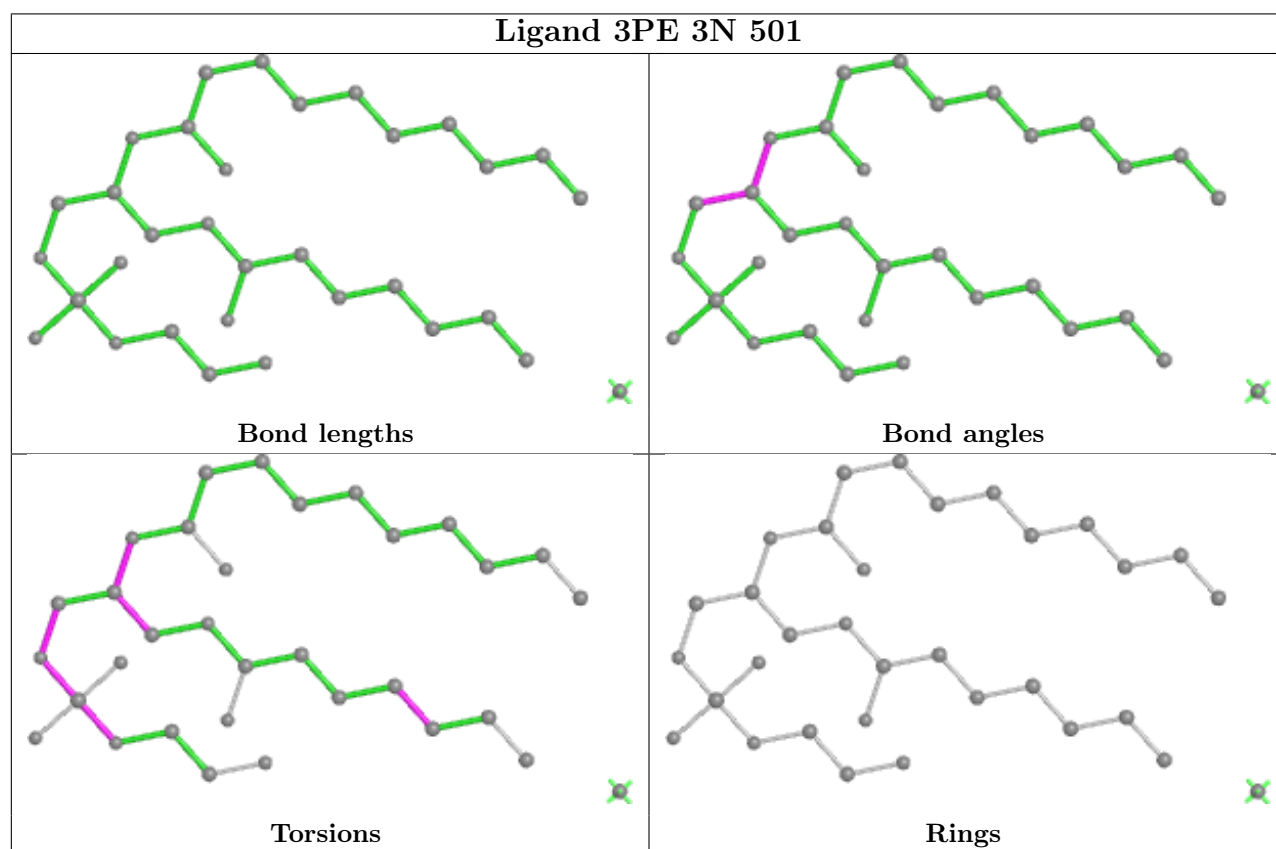
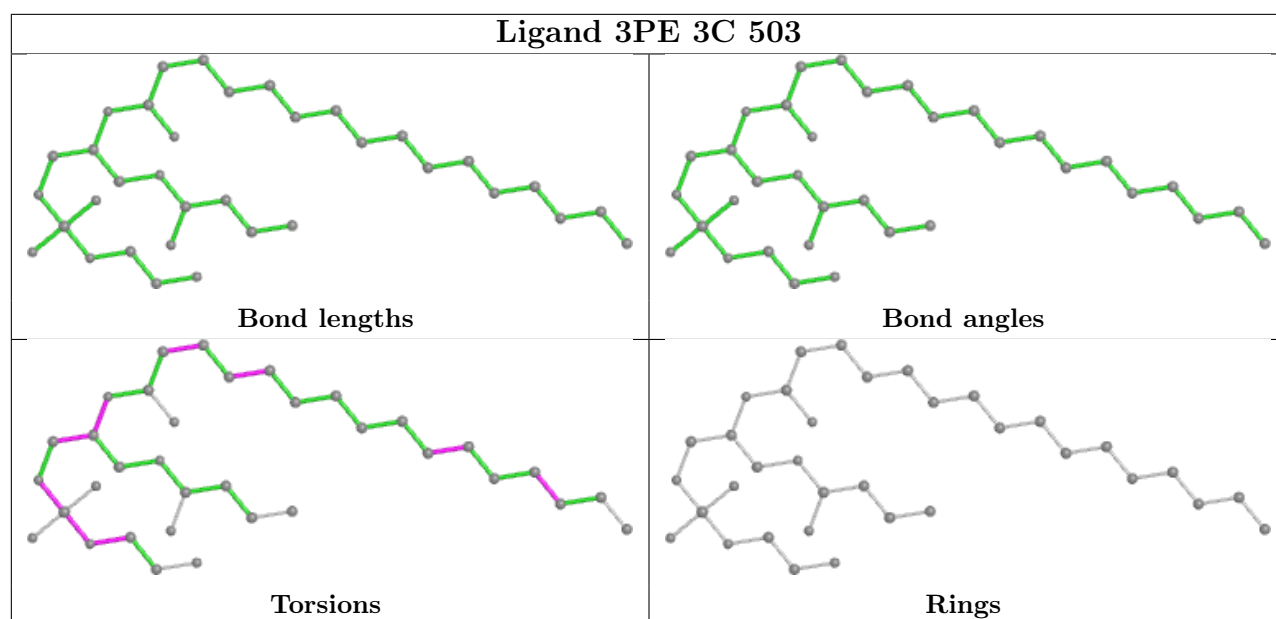
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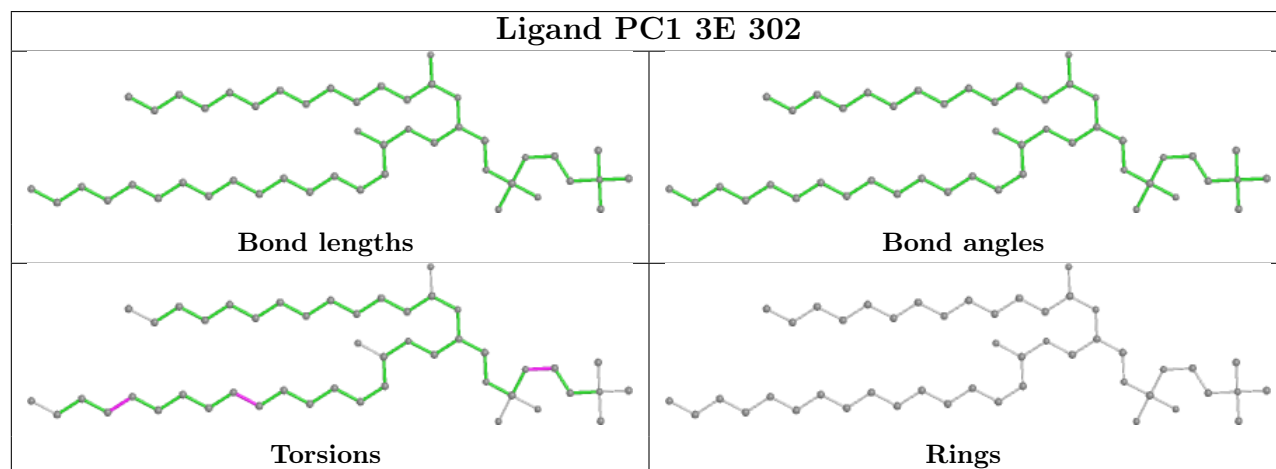
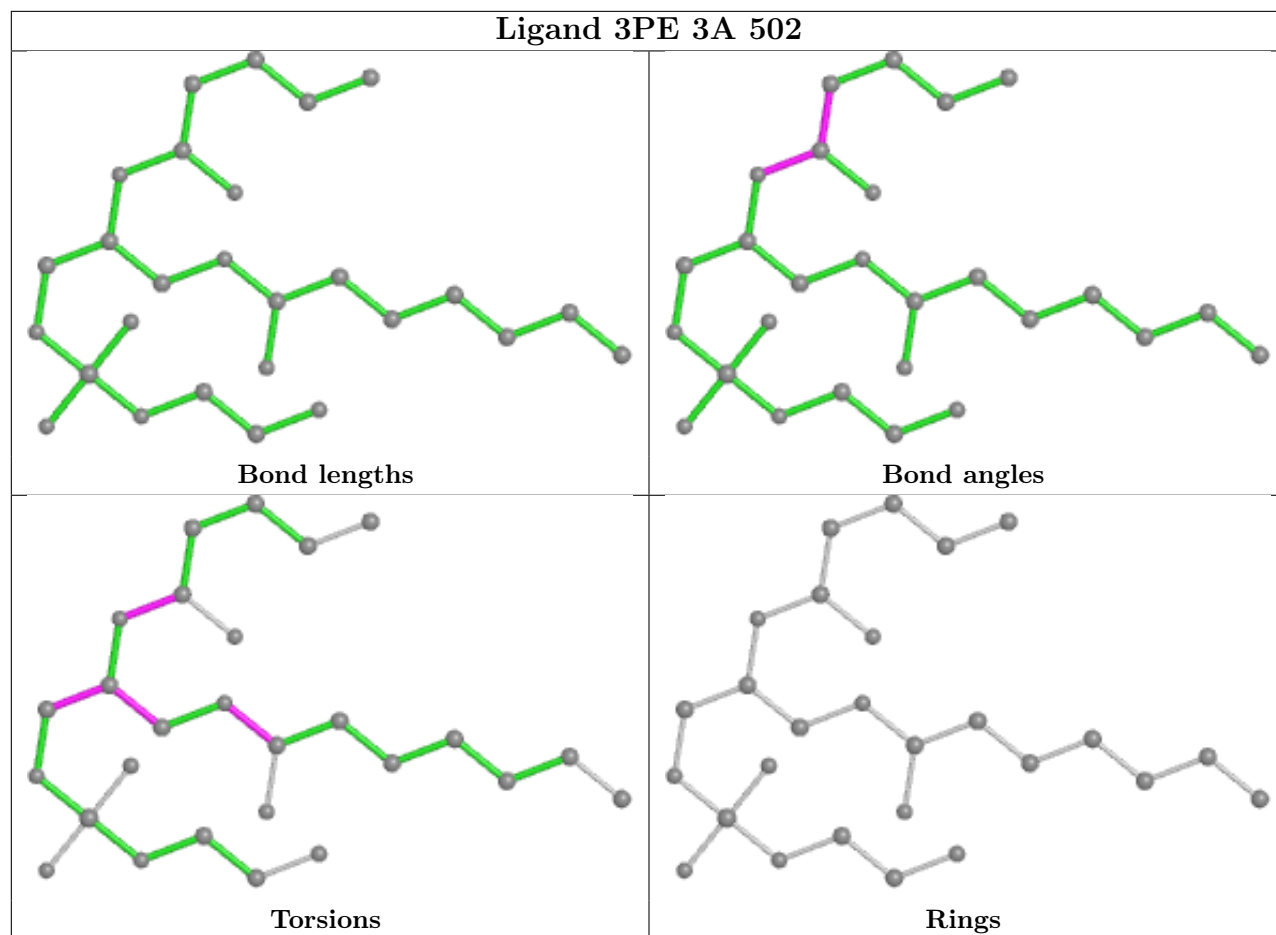
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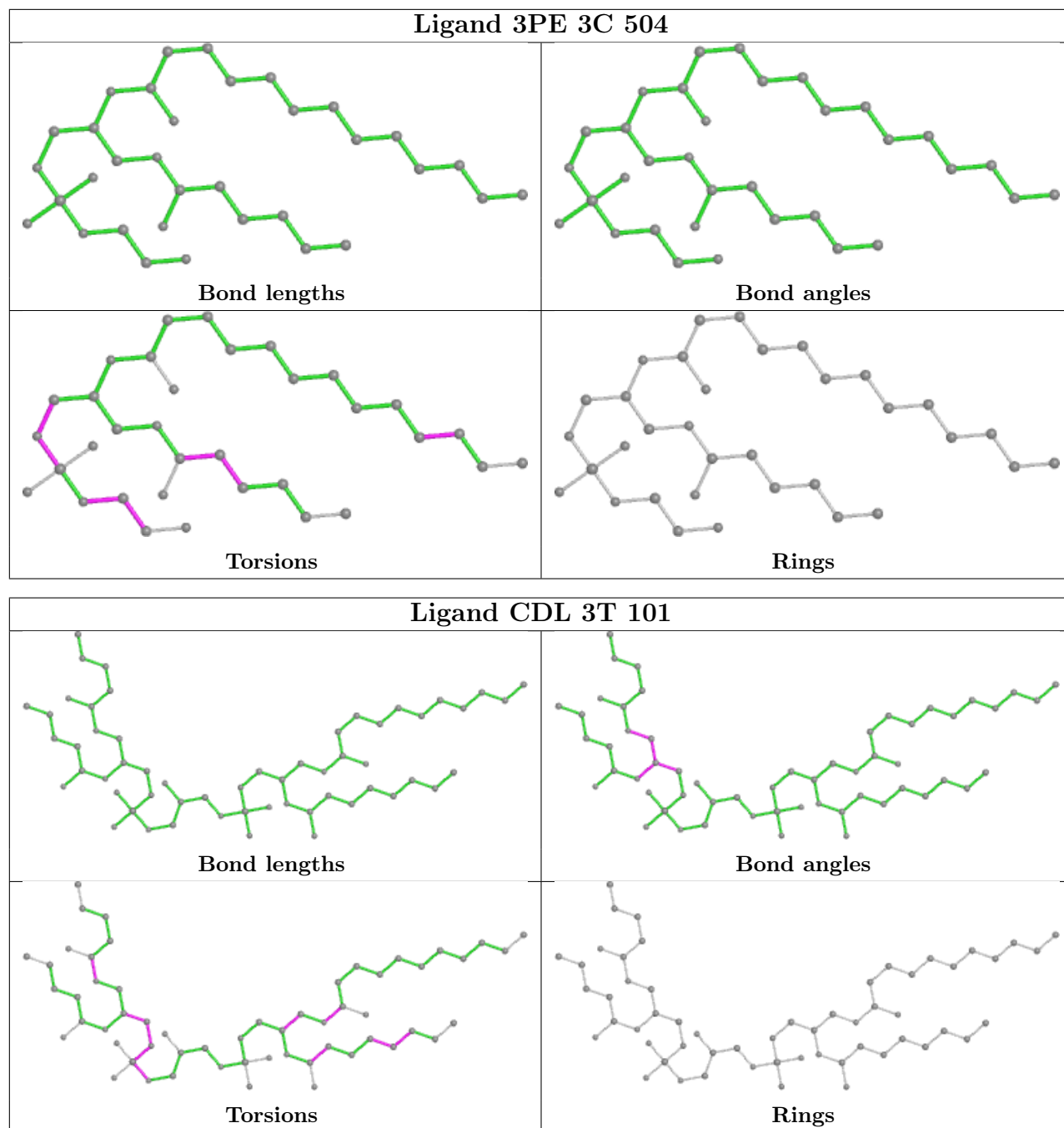
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	3G	103	CDL	6	0

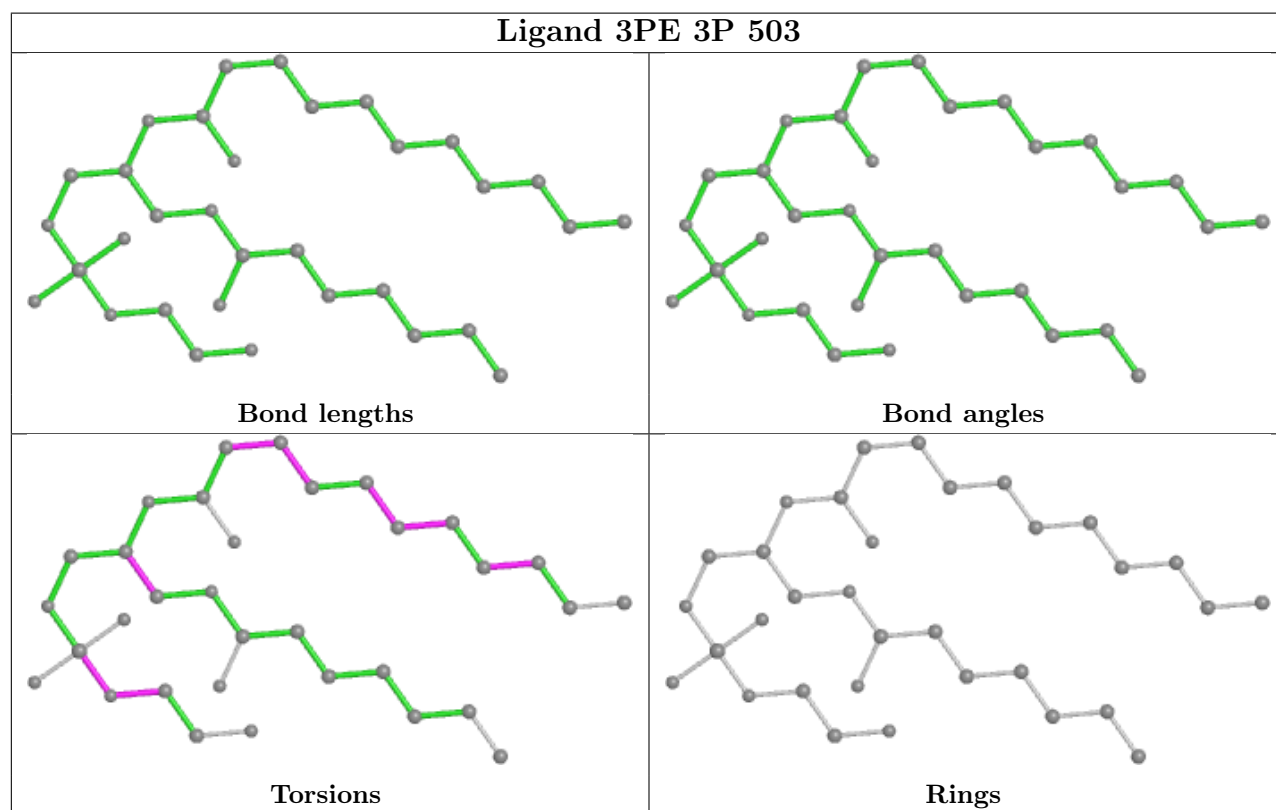
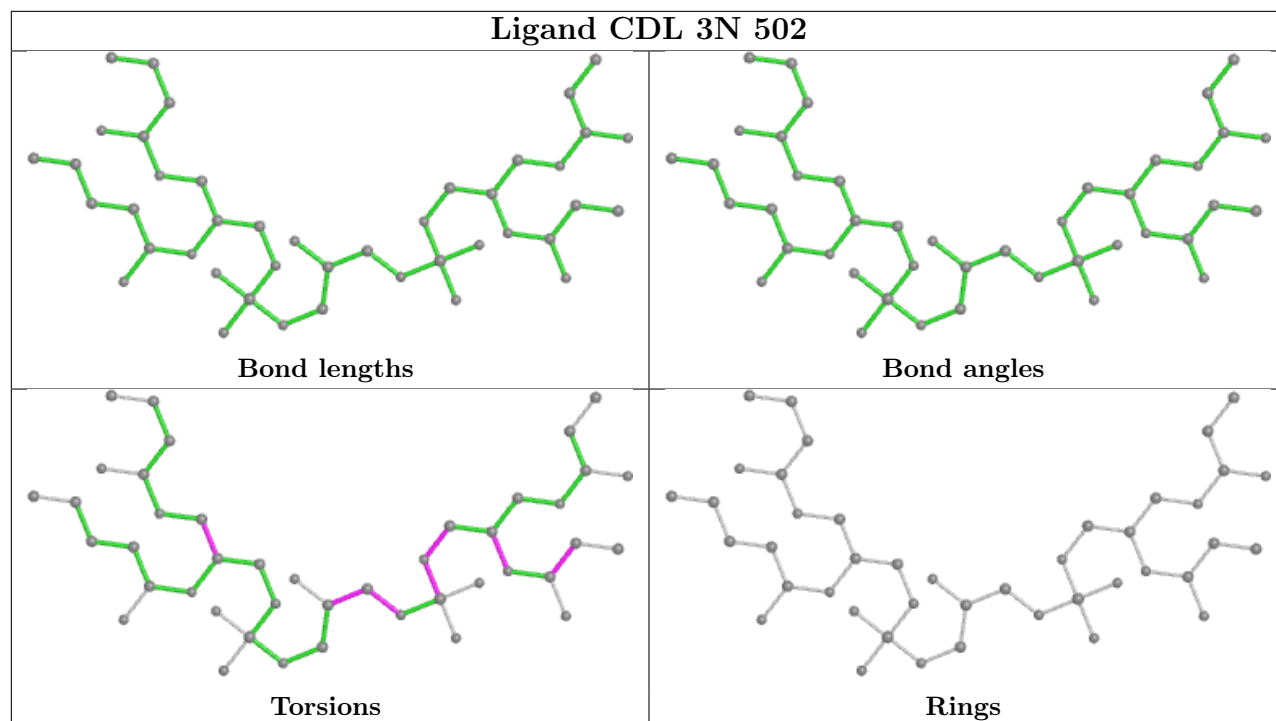
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

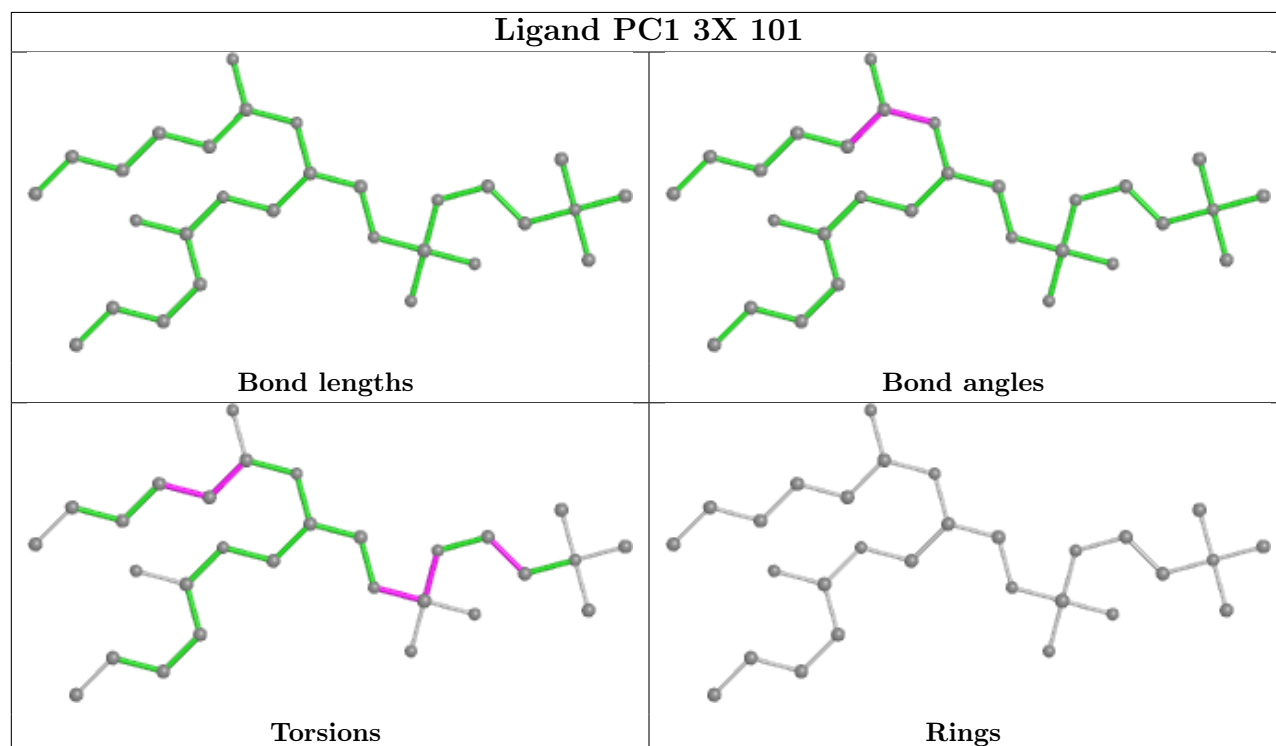
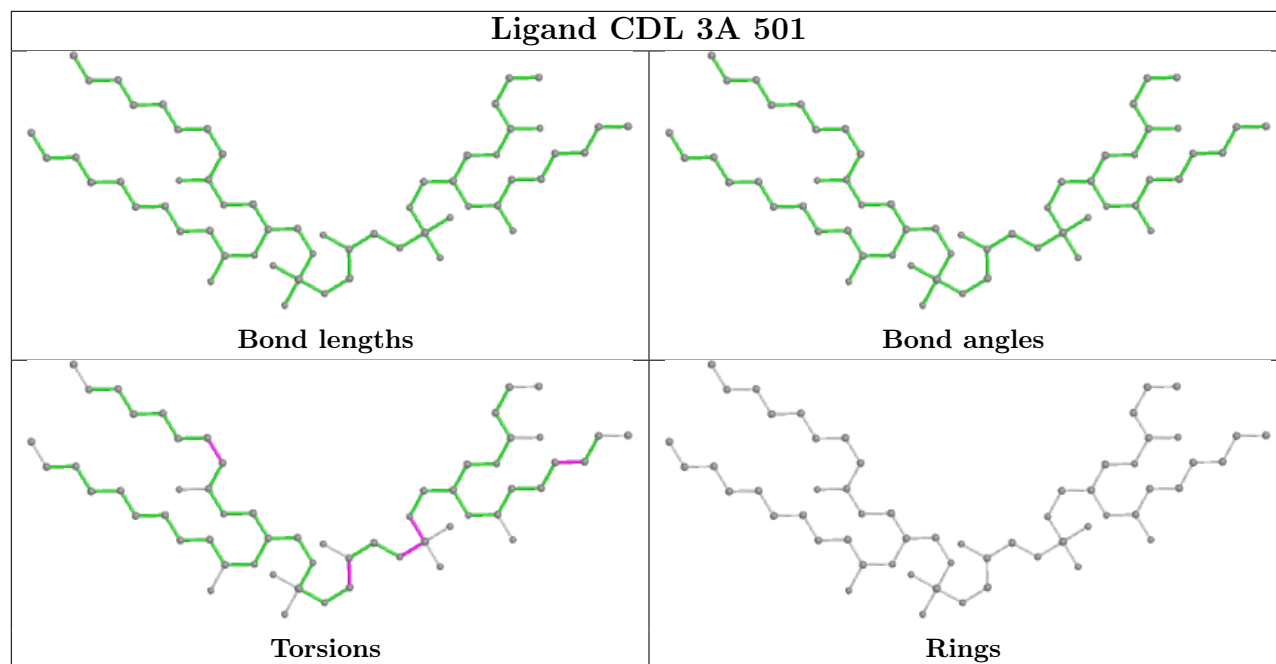


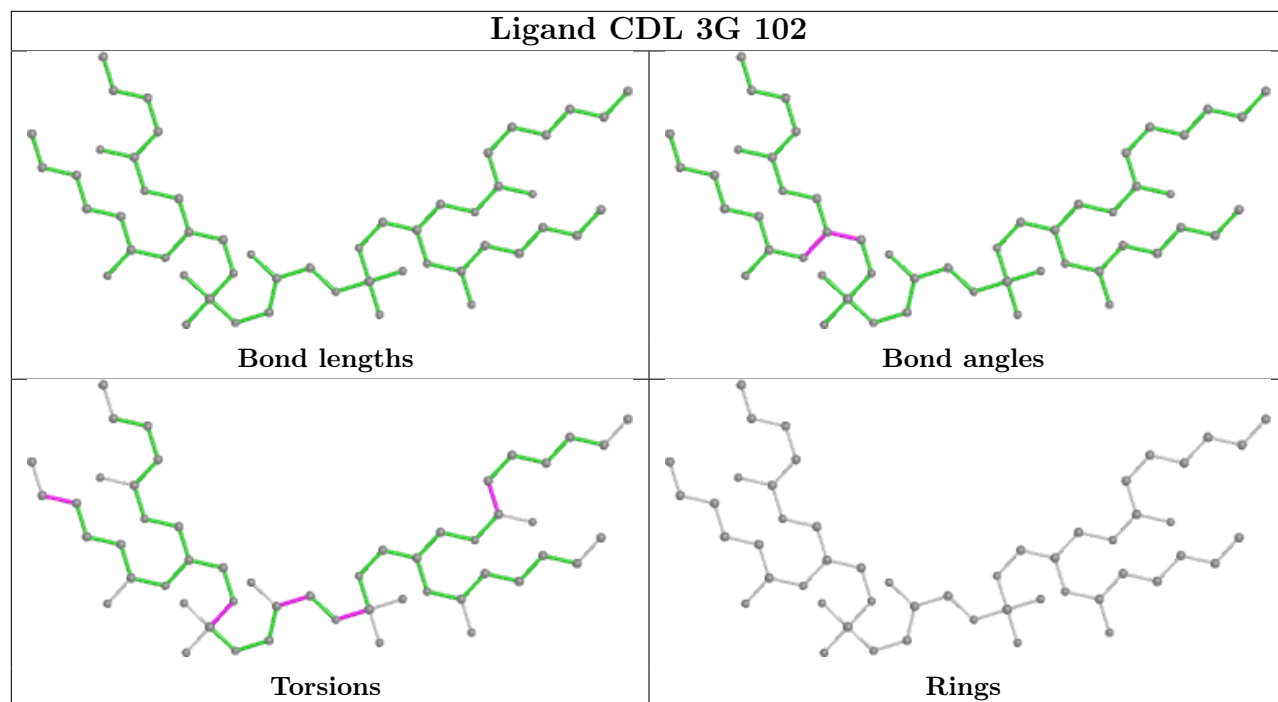


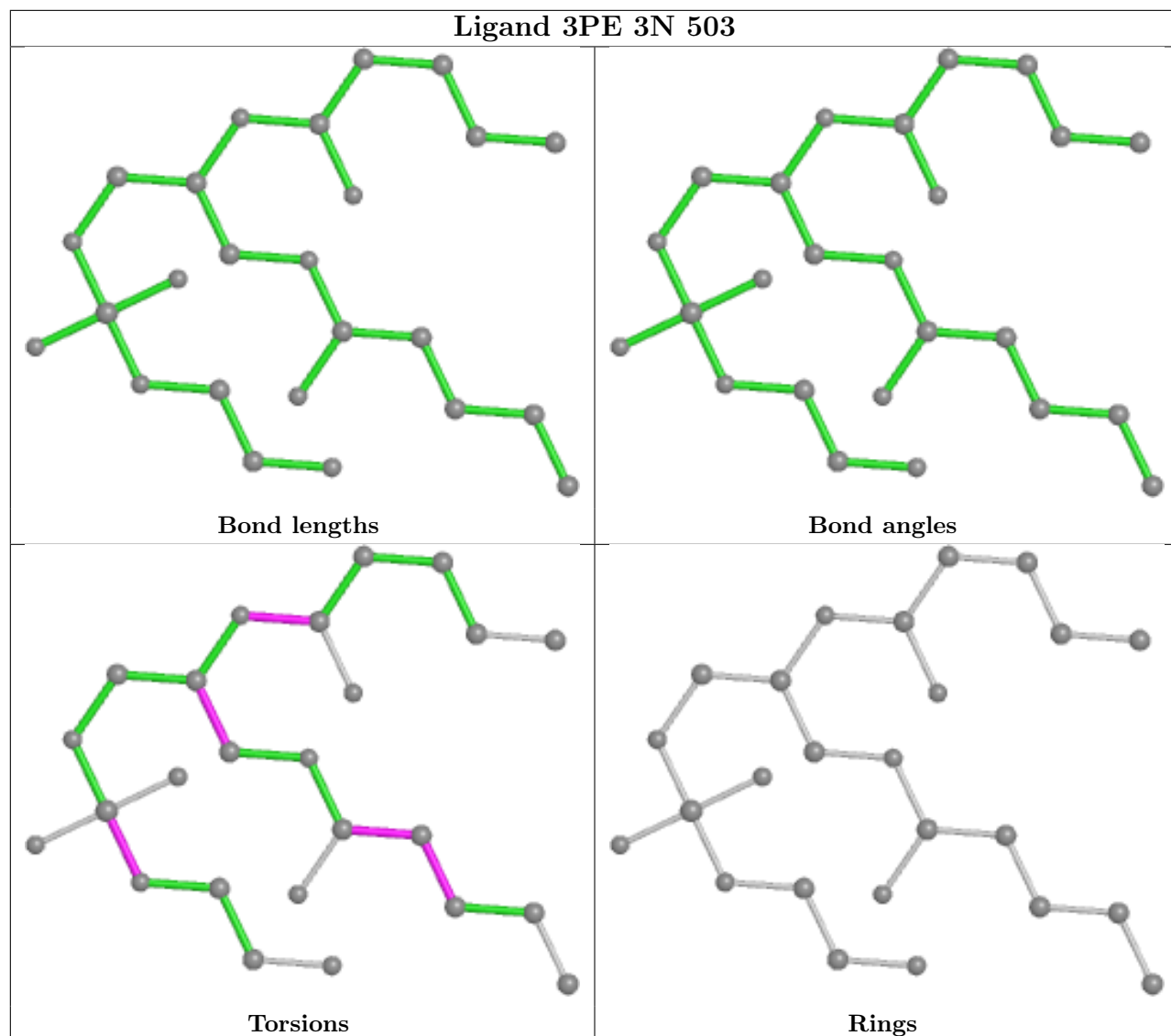


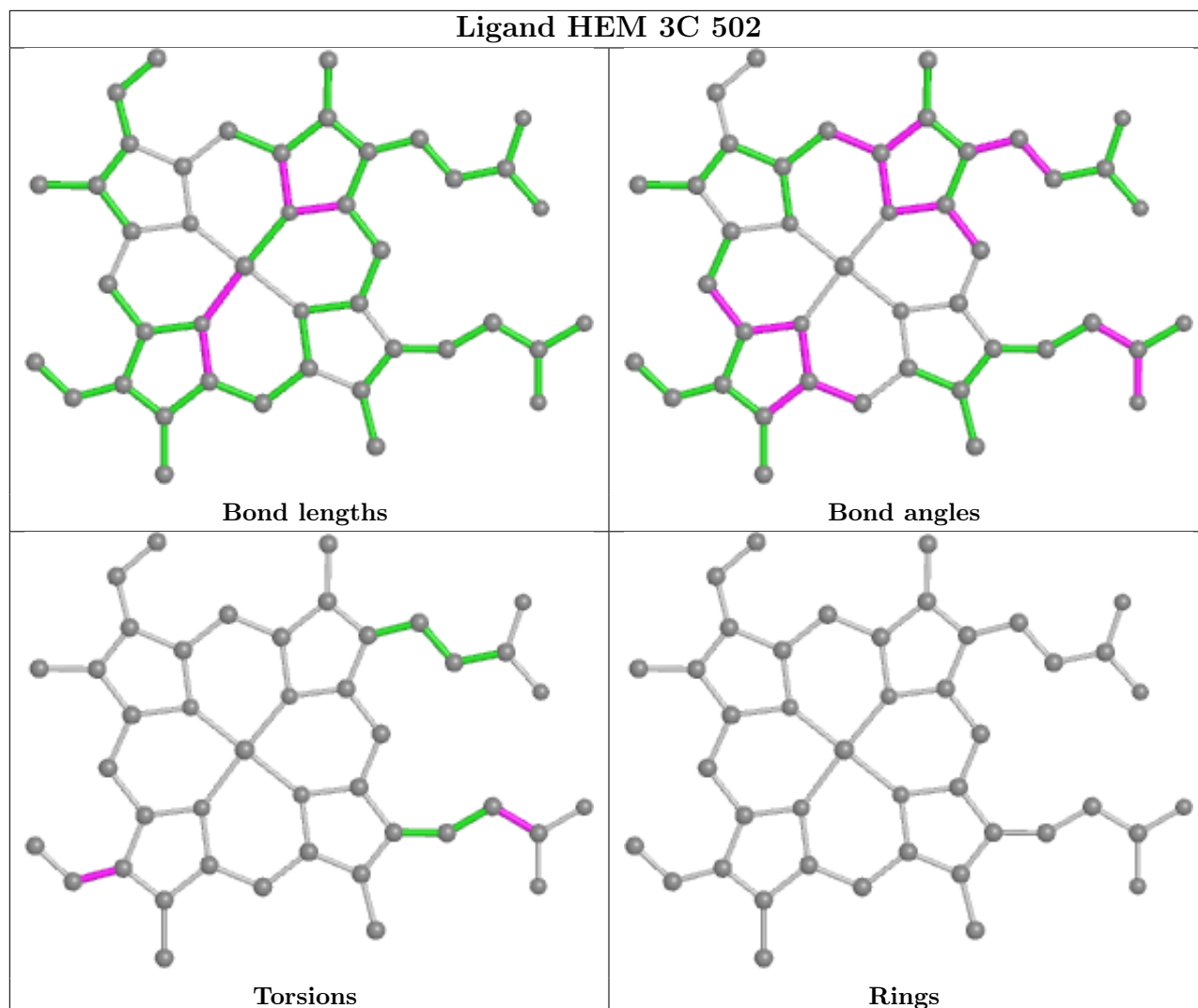


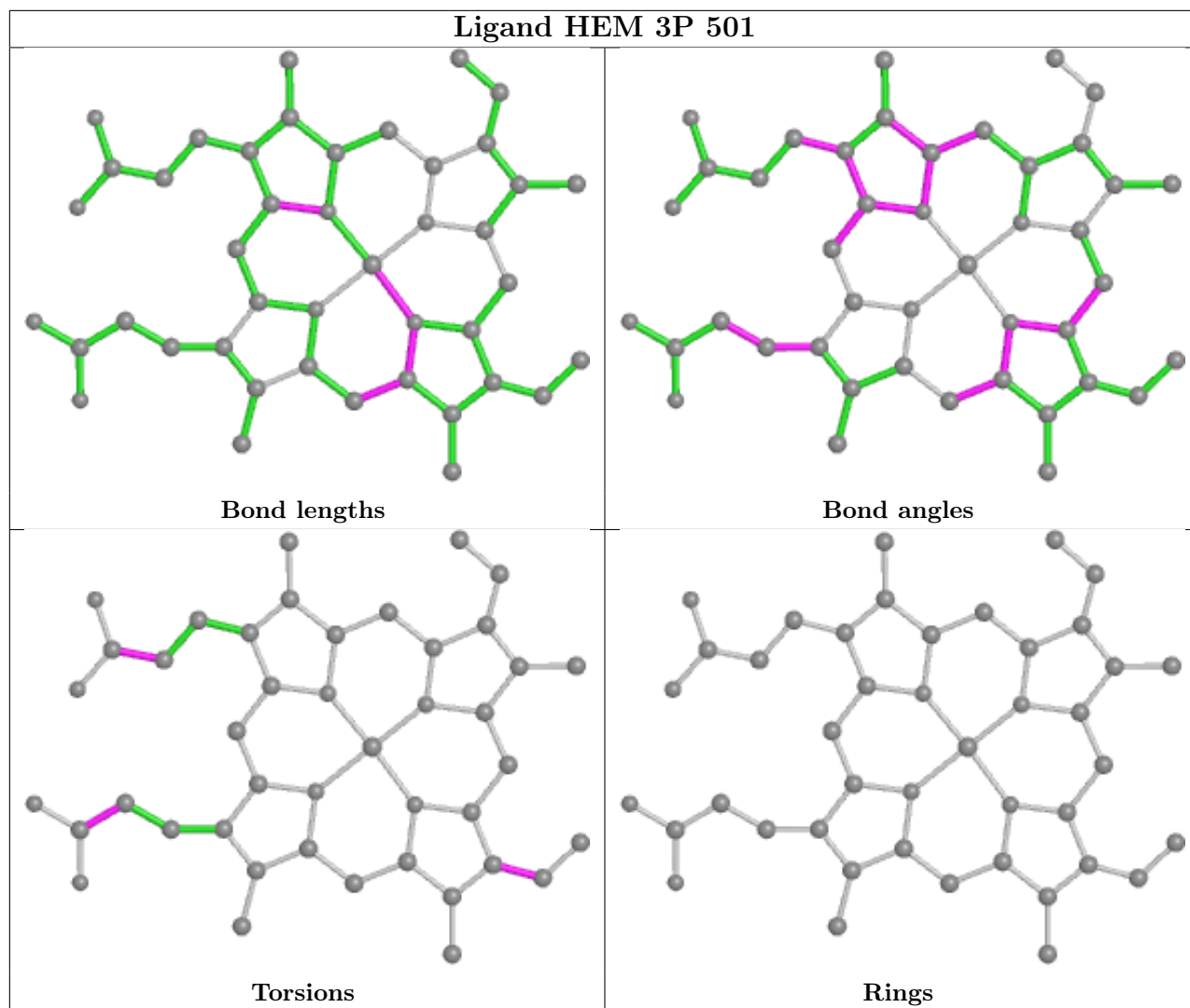


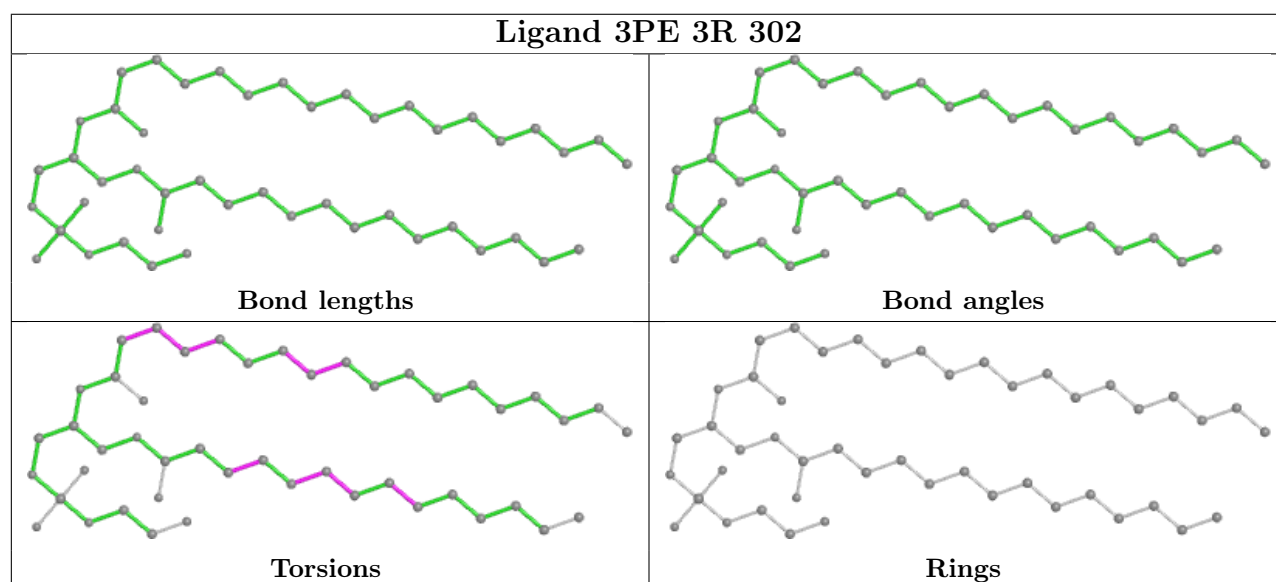
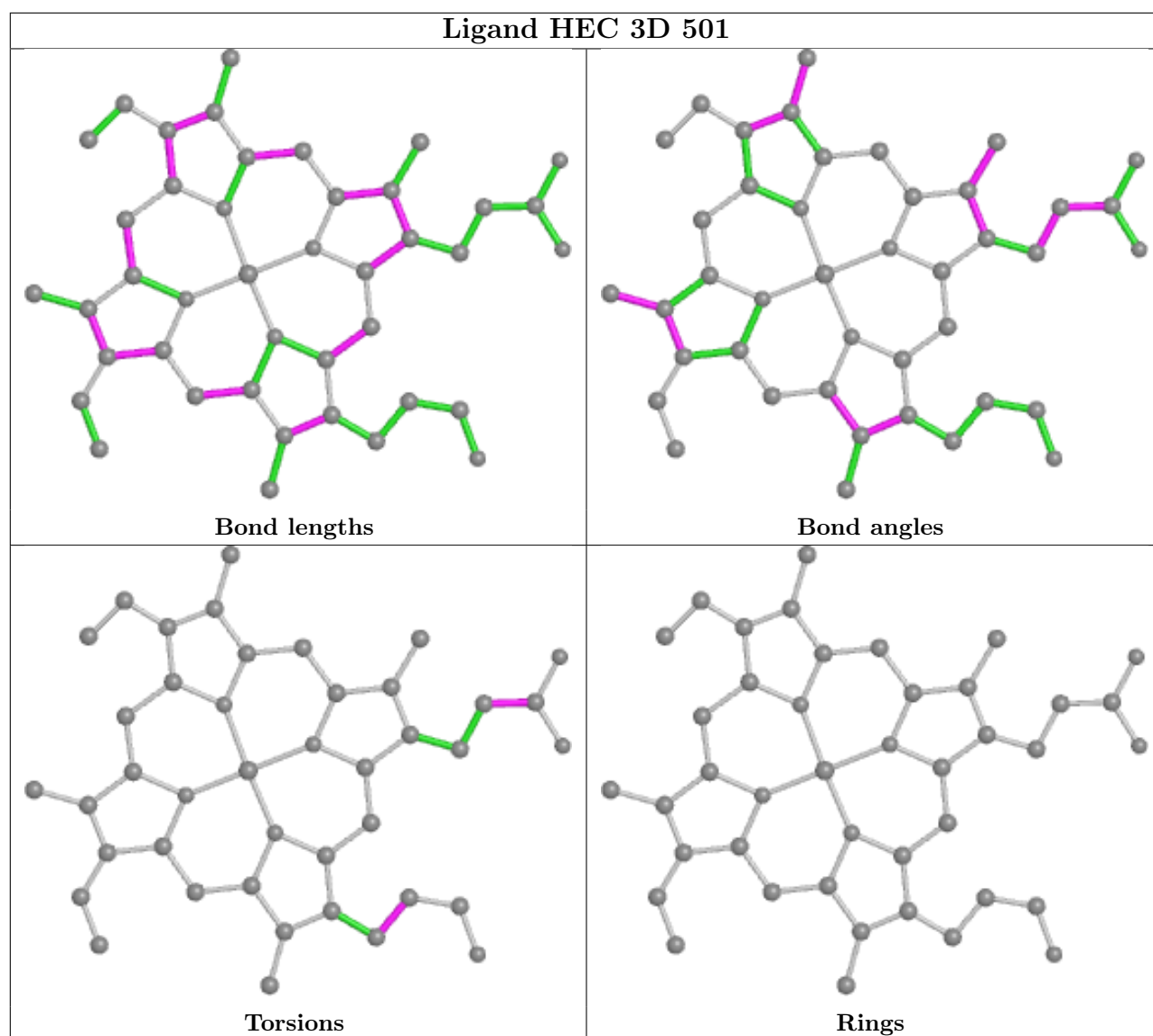


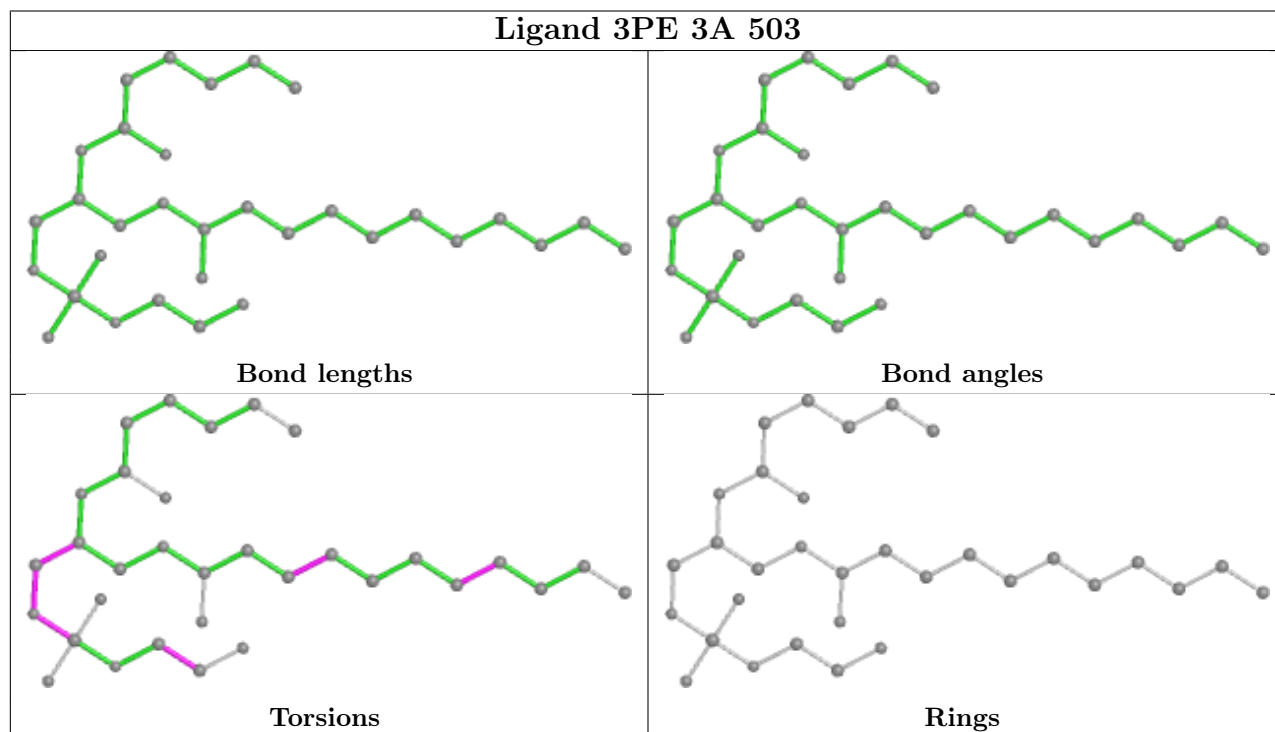
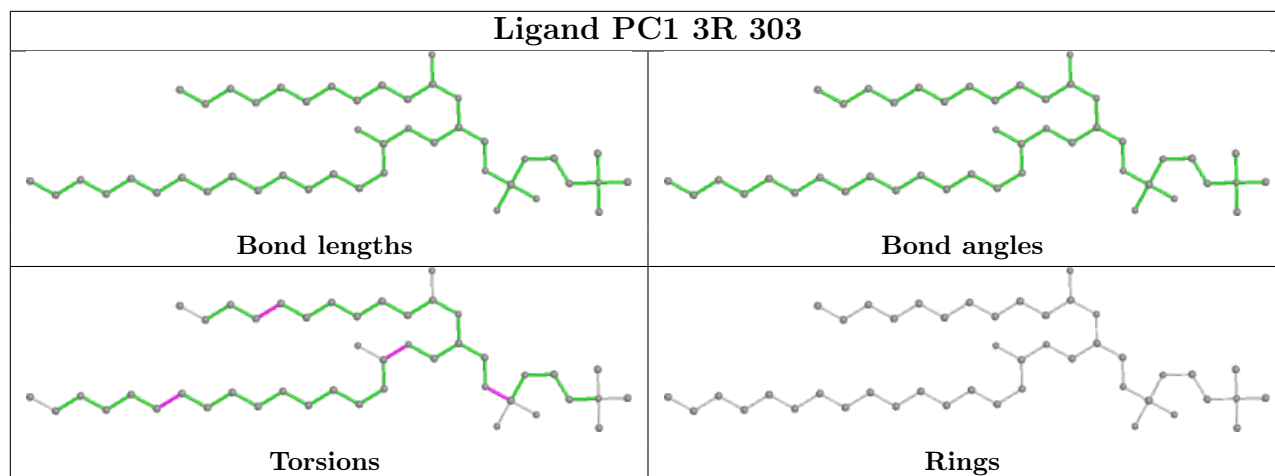


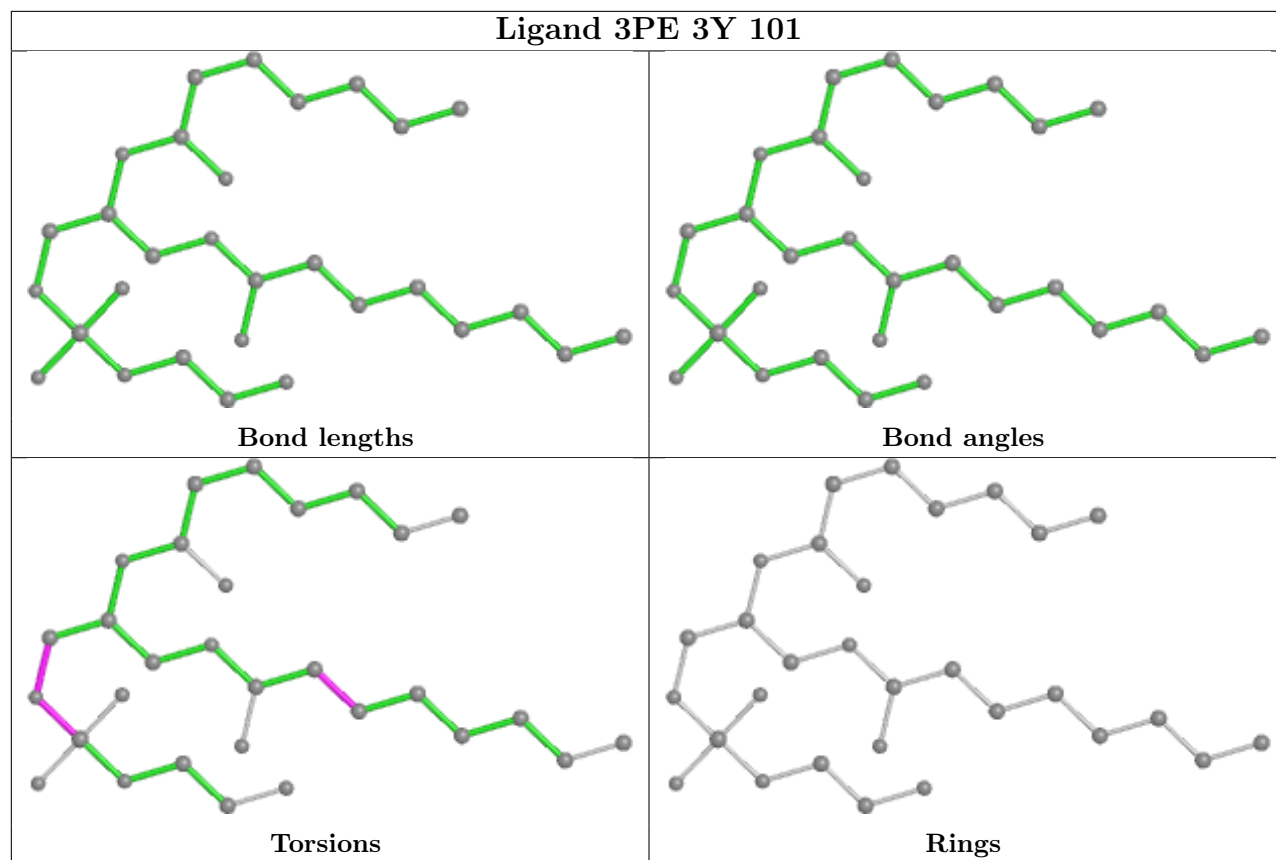


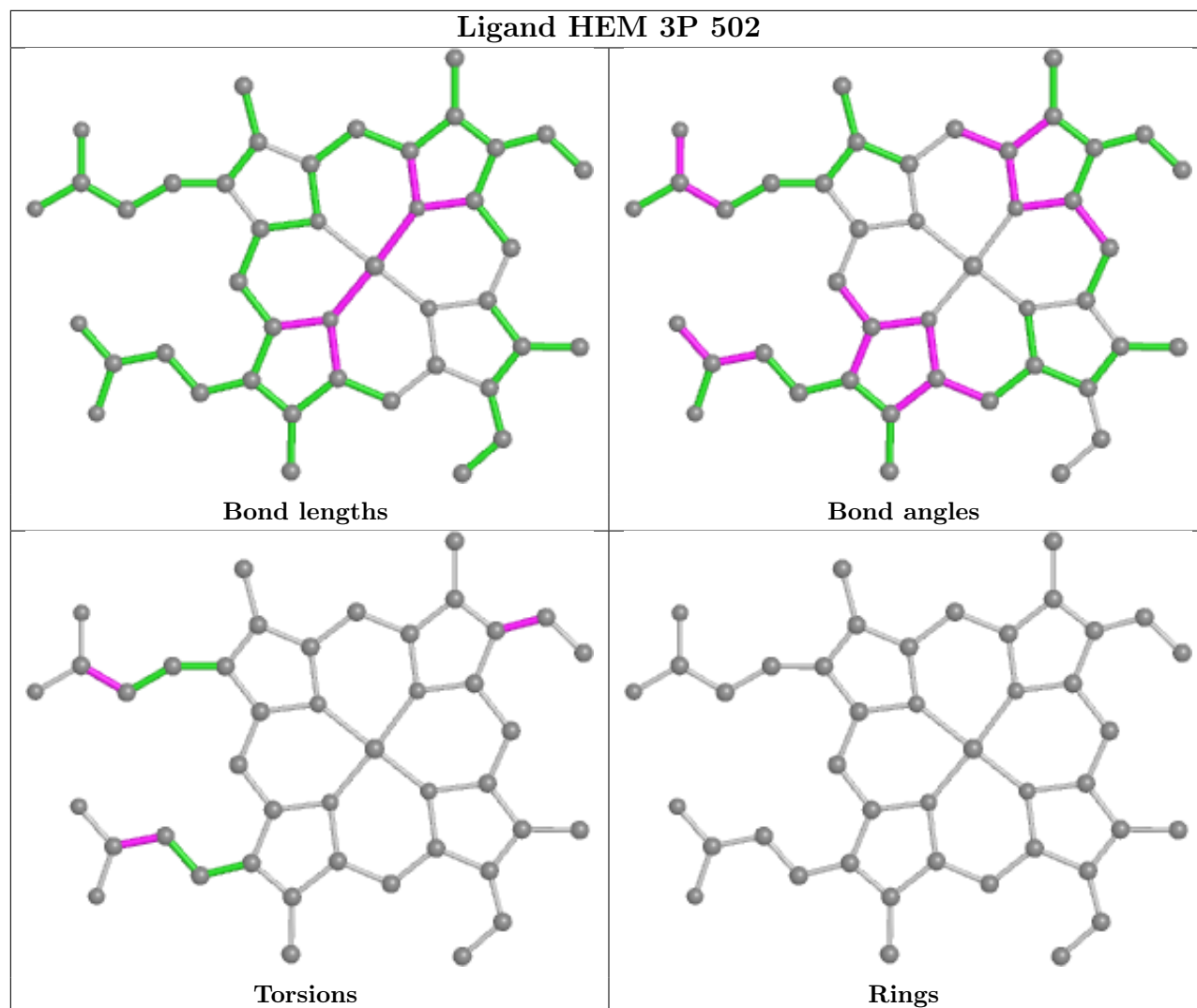


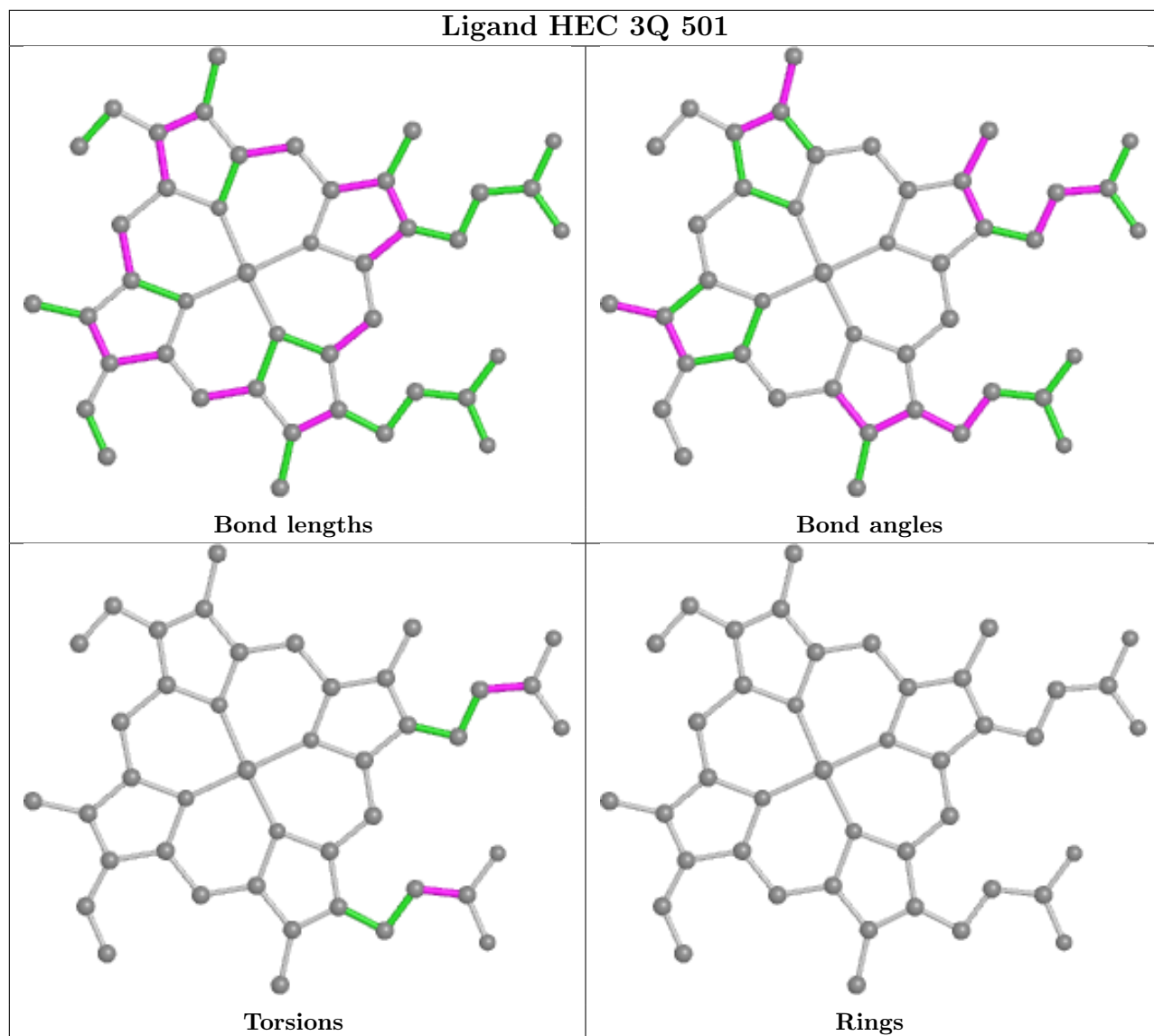


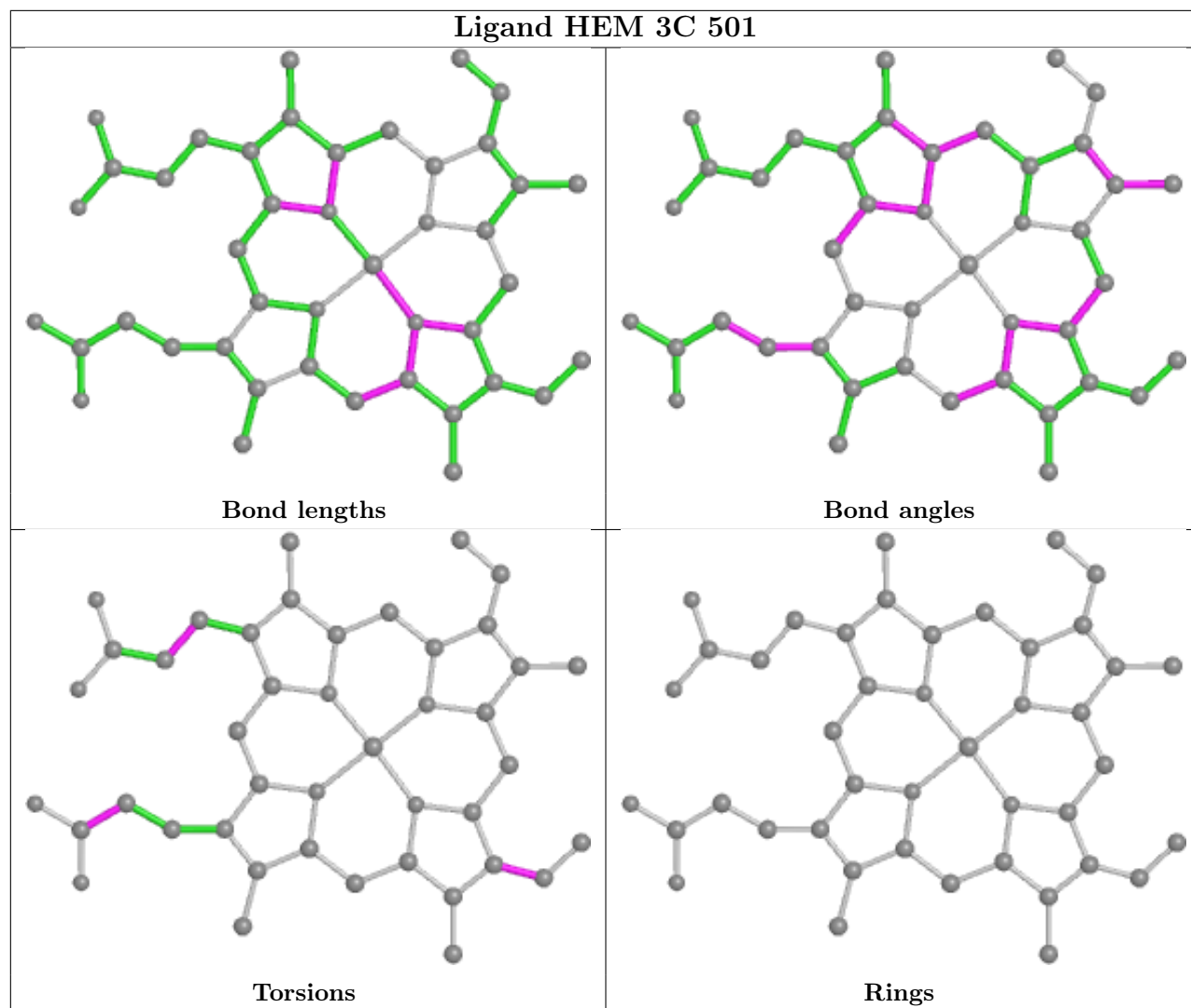


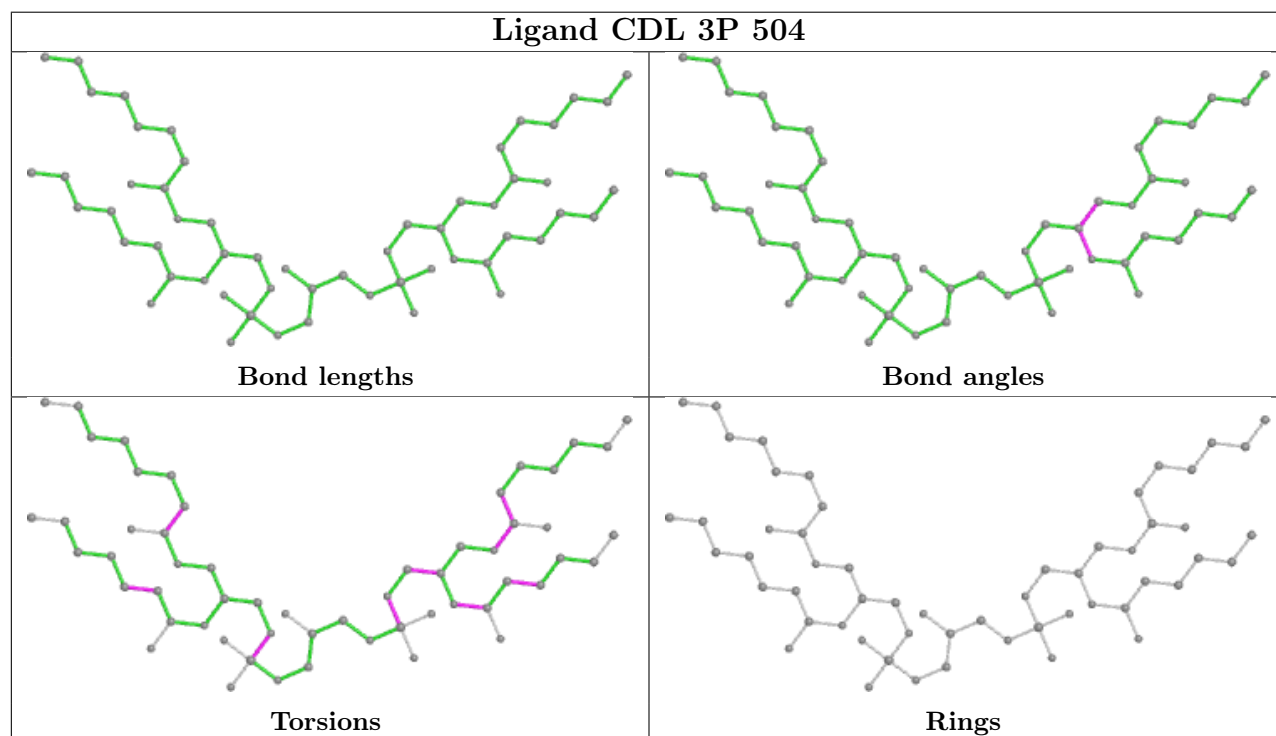
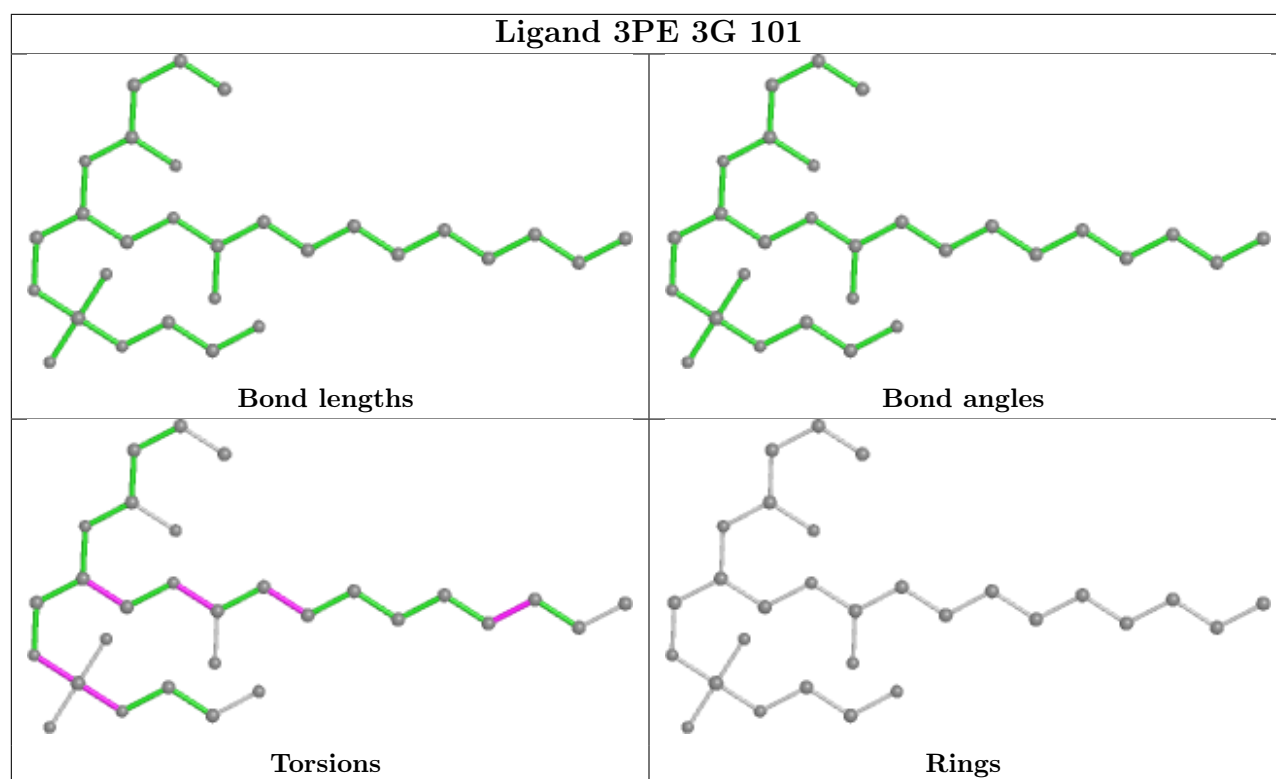


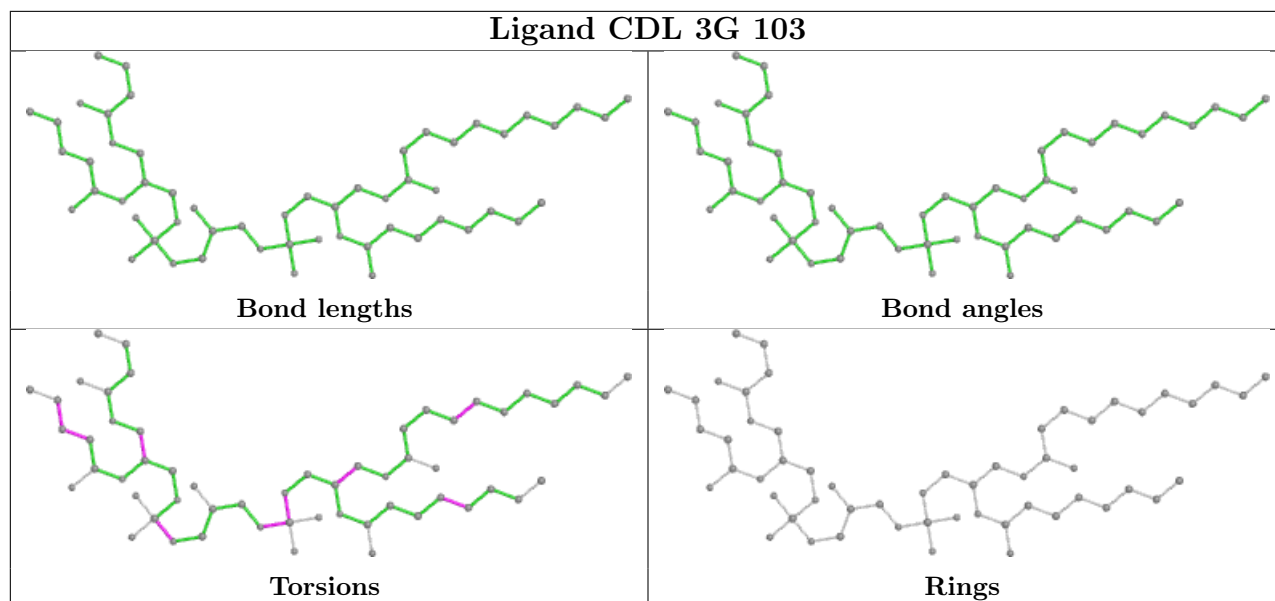












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	3I	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	3I	48:SER	C	49:PHE	N	1.08

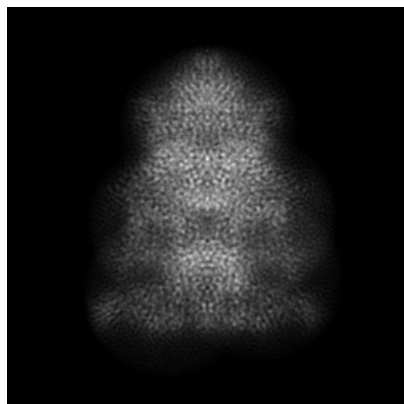
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42228. These allow visual inspection of the internal detail of the map and identification of artifacts.

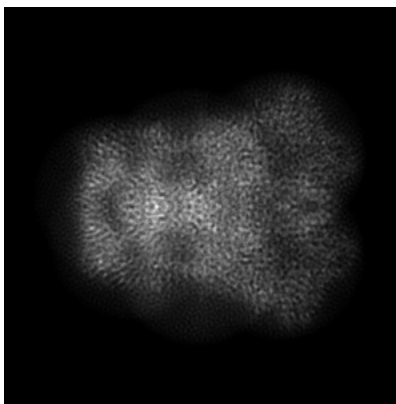
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

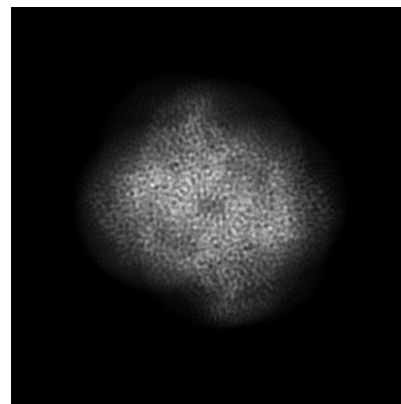
6.1.1 Primary map



X

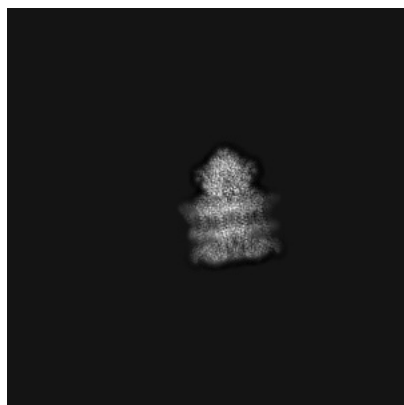


Y

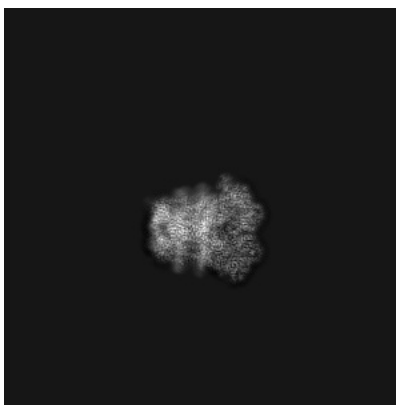


Z

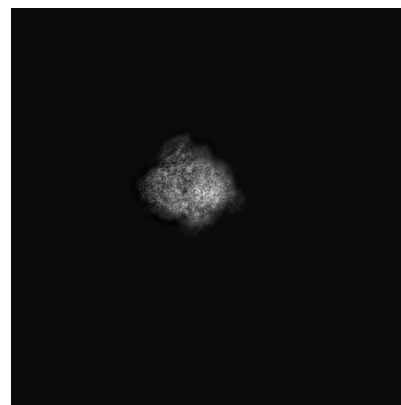
6.1.2 Raw map



X



Y

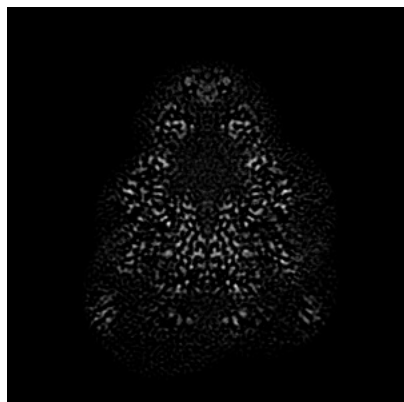


Z

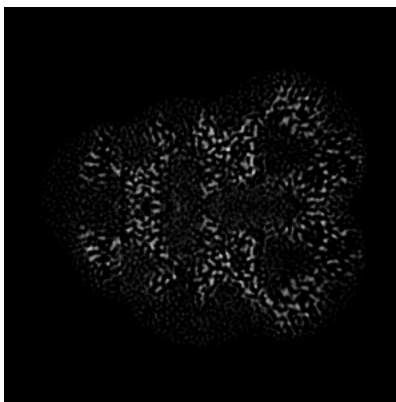
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

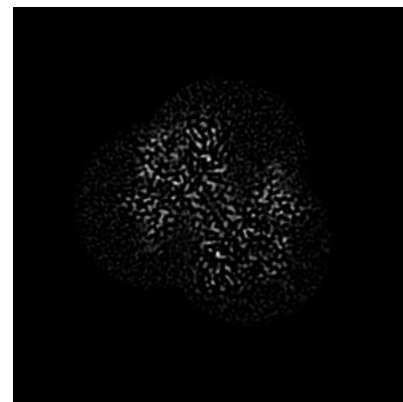
6.2.1 Primary map



X Index: 257



Y Index: 257

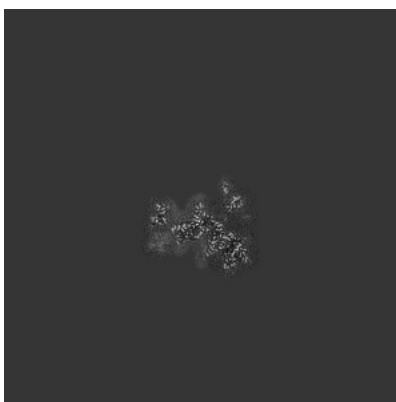


Z Index: 257

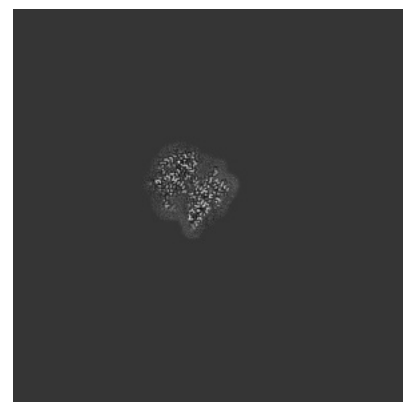
6.2.2 Raw map



X Index: 256



Y Index: 256

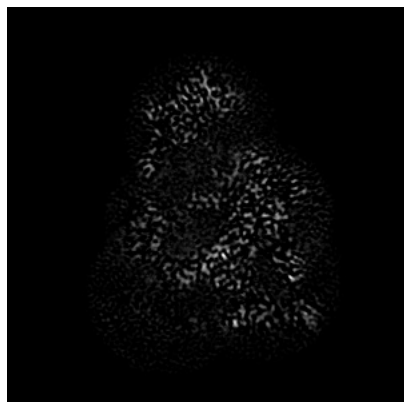


Z Index: 256

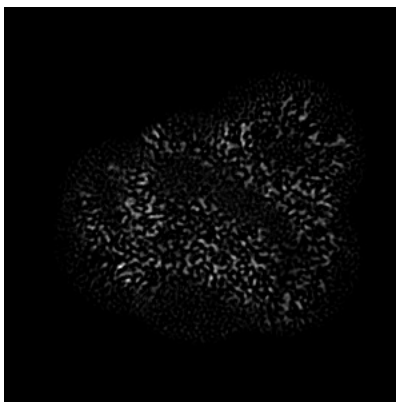
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

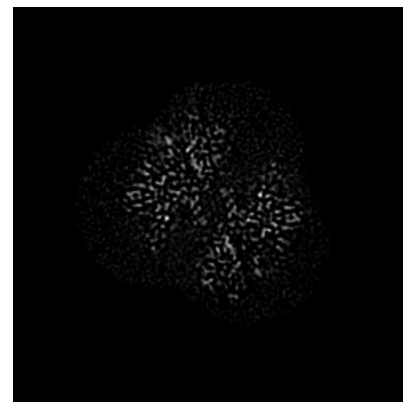
6.3.1 Primary map



X Index: 237

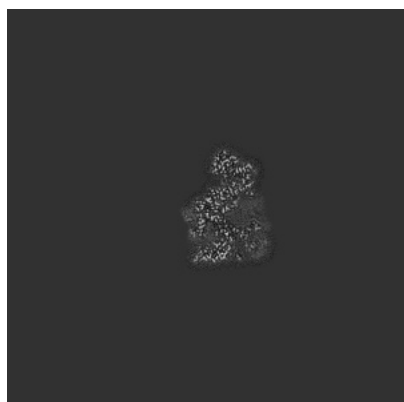


Y Index: 285



Z Index: 264

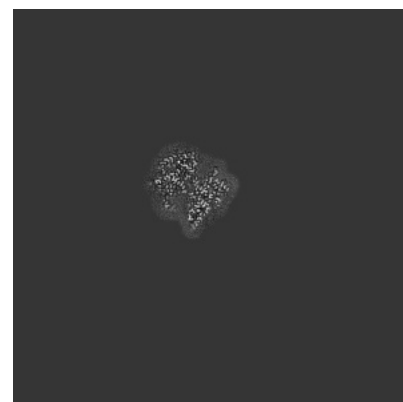
6.3.2 Raw map



X Index: 240



Y Index: 276

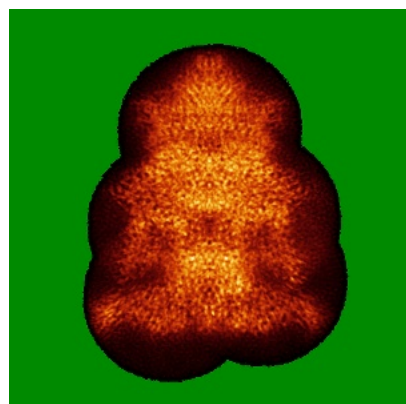


Z Index: 256

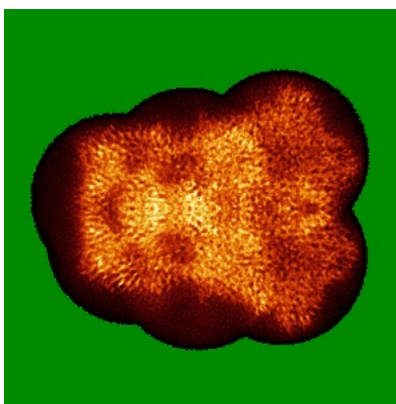
The images above show the largest variance slices of the map in three orthogonal directions.

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

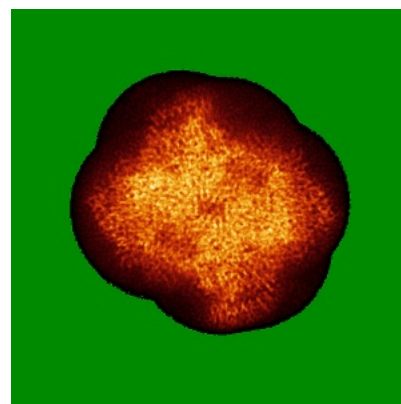
6.4.1 Primary map



X



Y

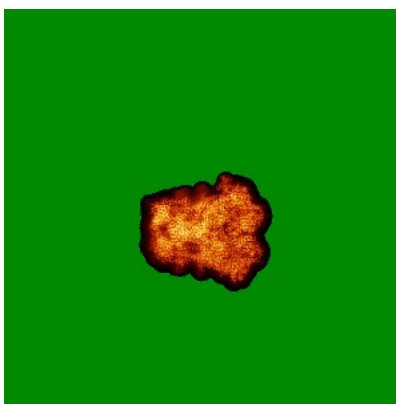


Z

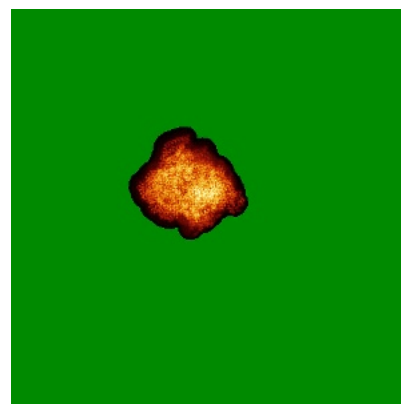
6.4.2 Raw map



X



Y

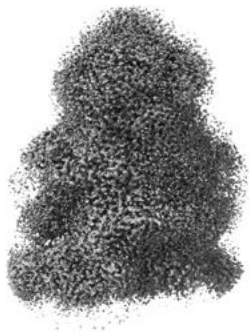


Z

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



X



Y



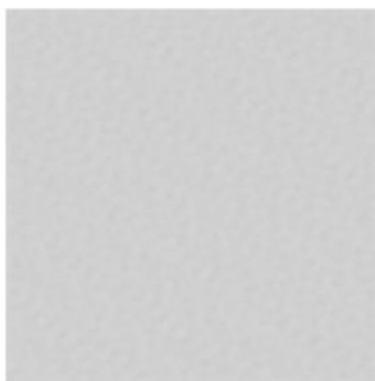
Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. 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



X



Y



Z

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.

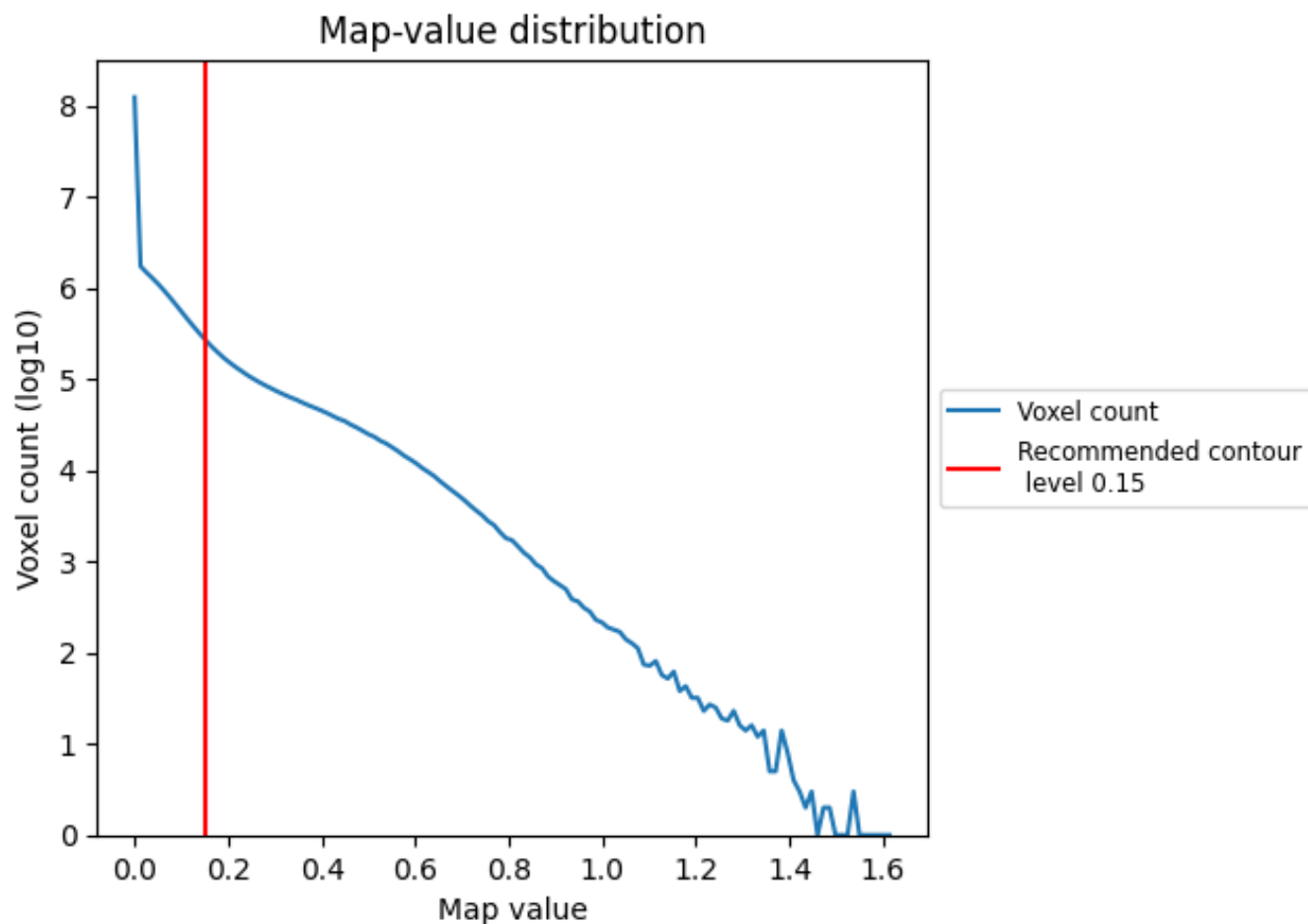
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

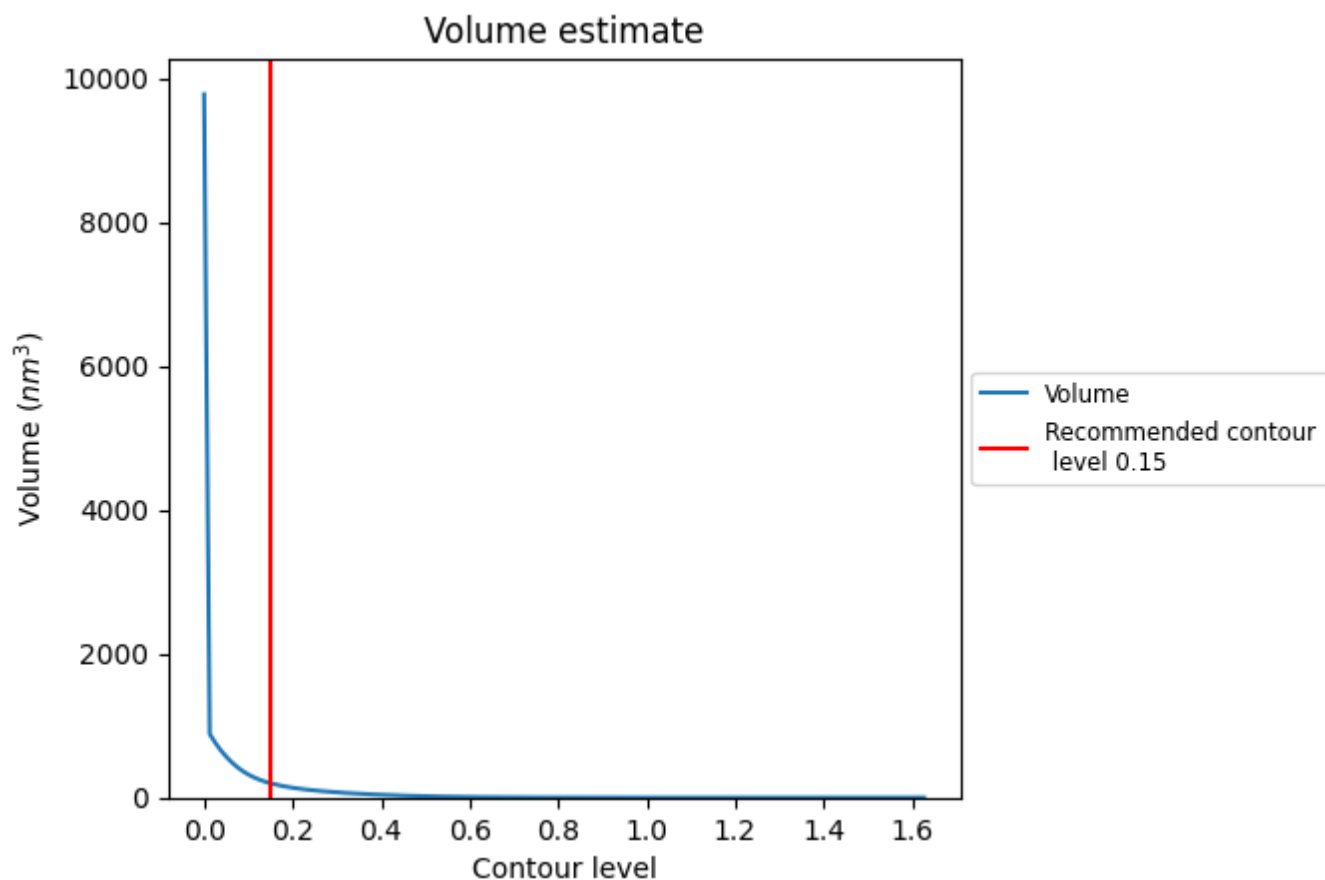
This section contains the results of statistical analysis of the map.

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.

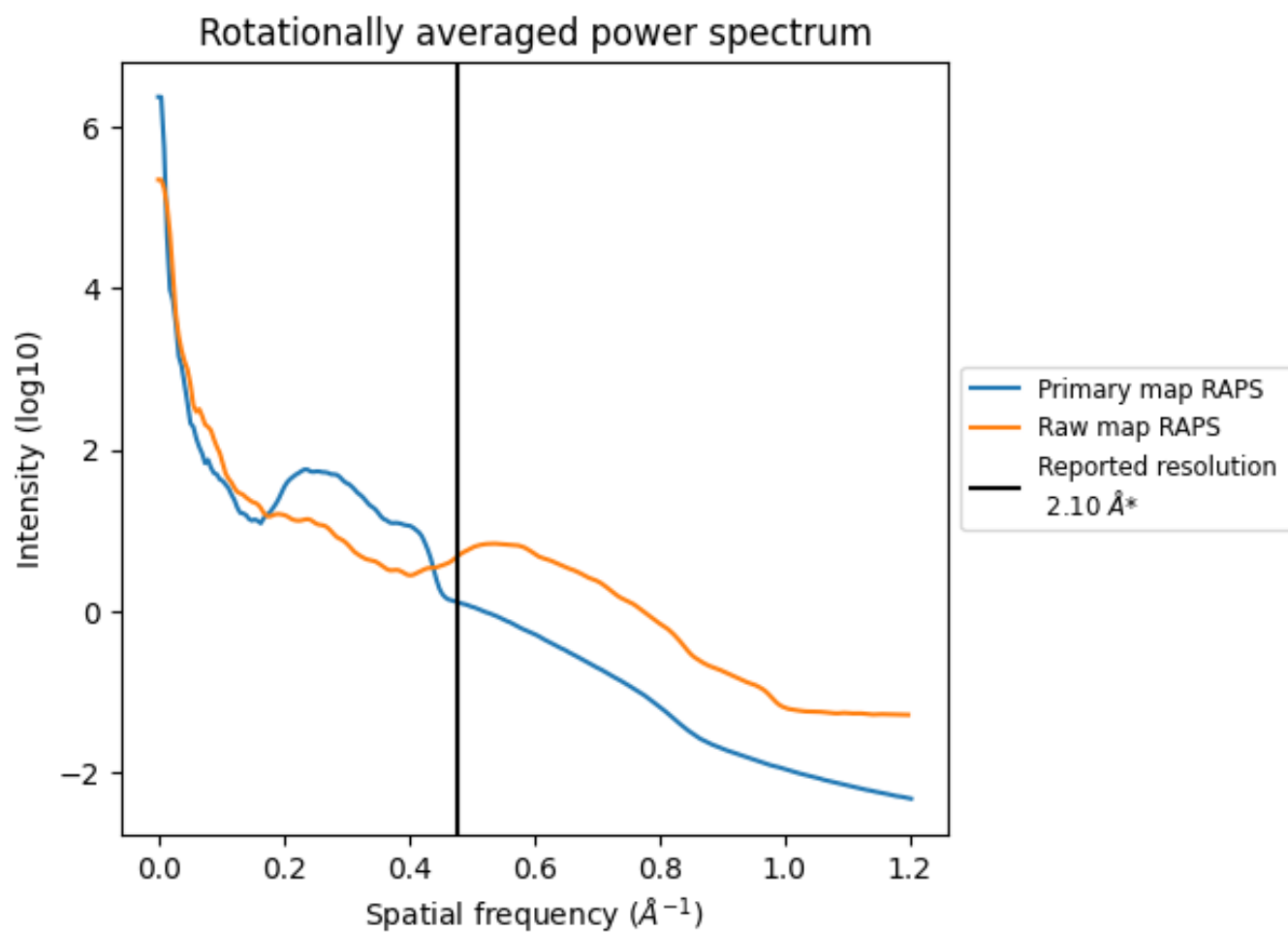
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 199 nm³; this corresponds to an approximate mass of 180 kDa.

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

7.3 Rotationally averaged power spectrum i

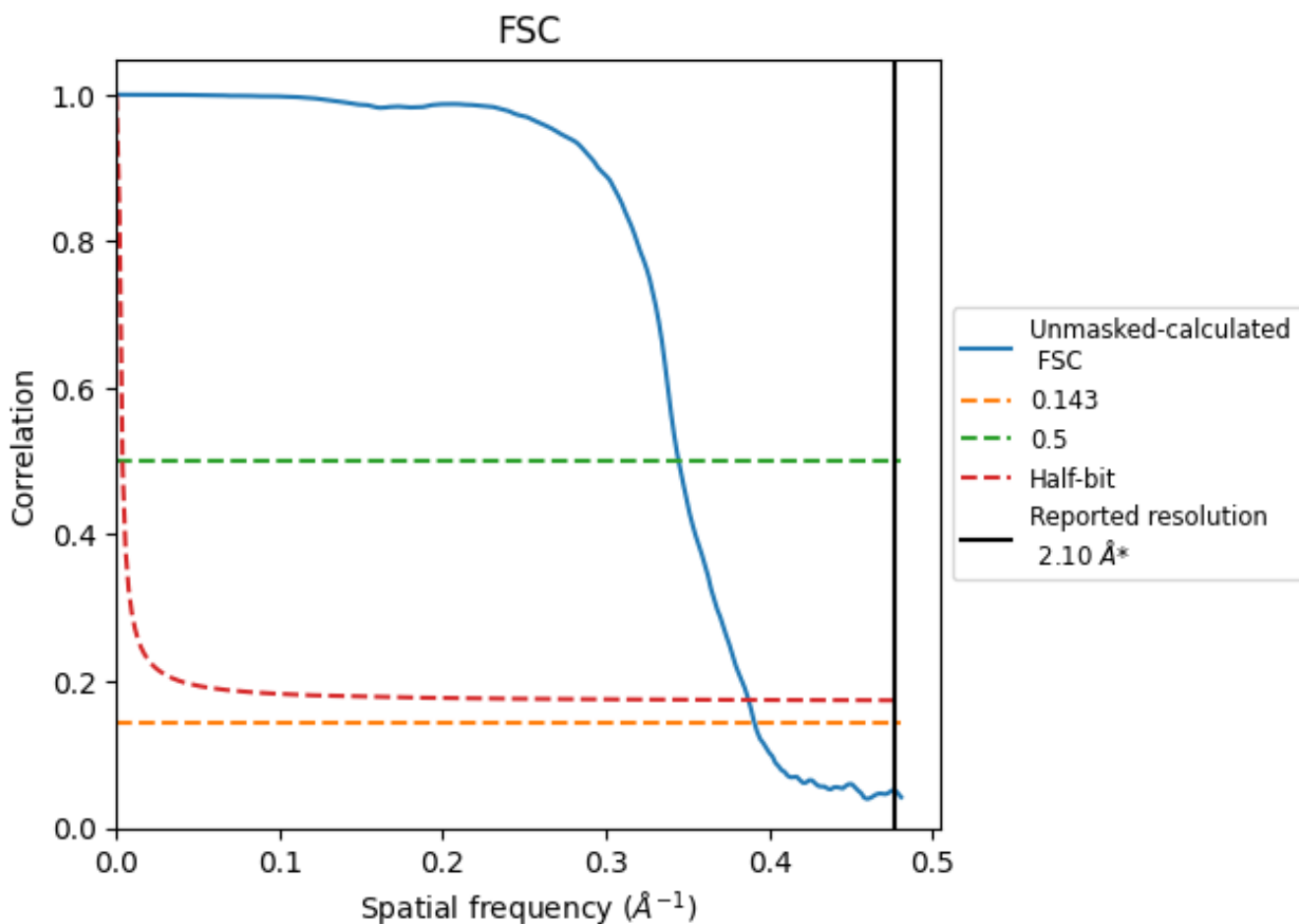


*Reported resolution corresponds to spatial frequency of 0.476 Å⁻¹

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 0.476\AA^{-1}

8.2 Resolution estimates [i](#)

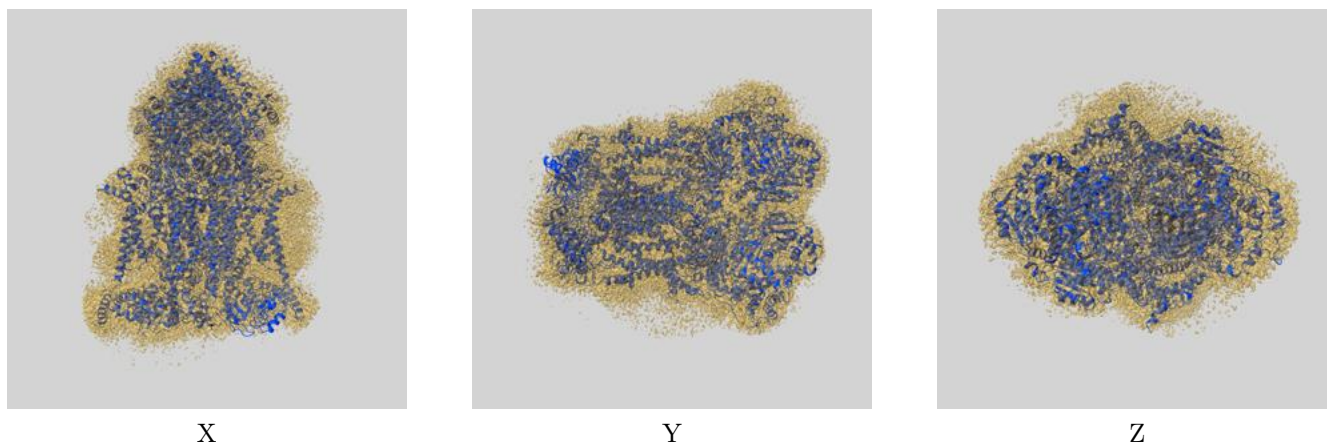
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.56	2.90	2.58

*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 2.56 differs from the reported value 2.1 by more than 10 %

9 Map-model fit [i](#)

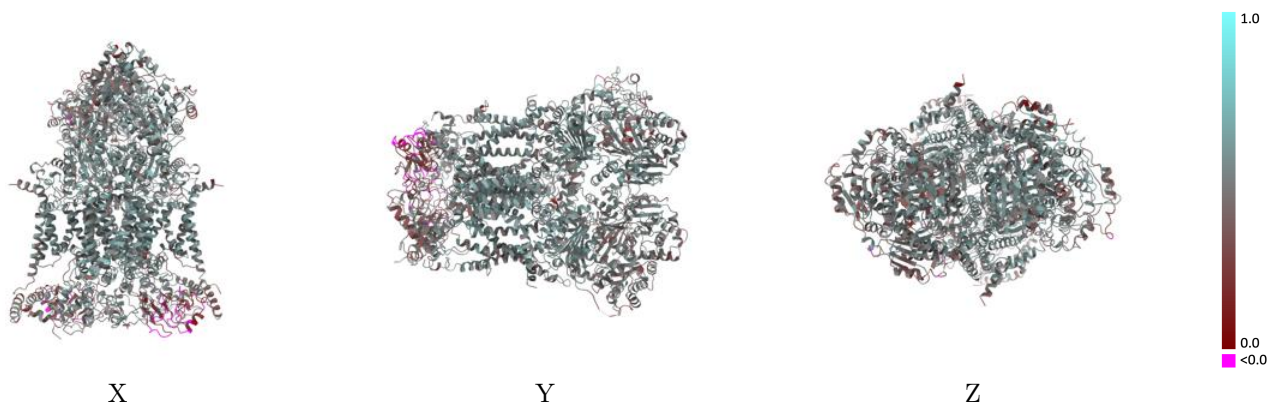
This section contains information regarding the fit between EMDB map EMD-42228 and PDB model 8UGK. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



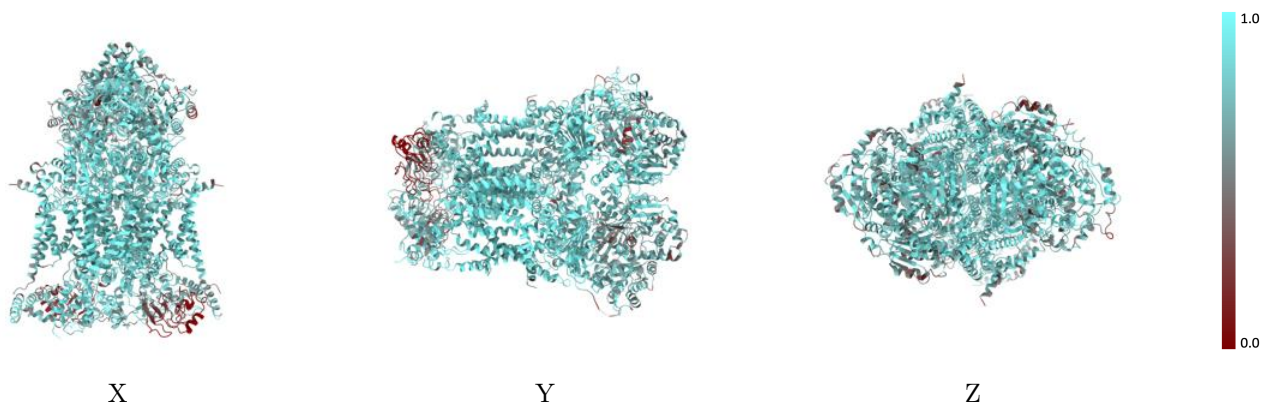
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



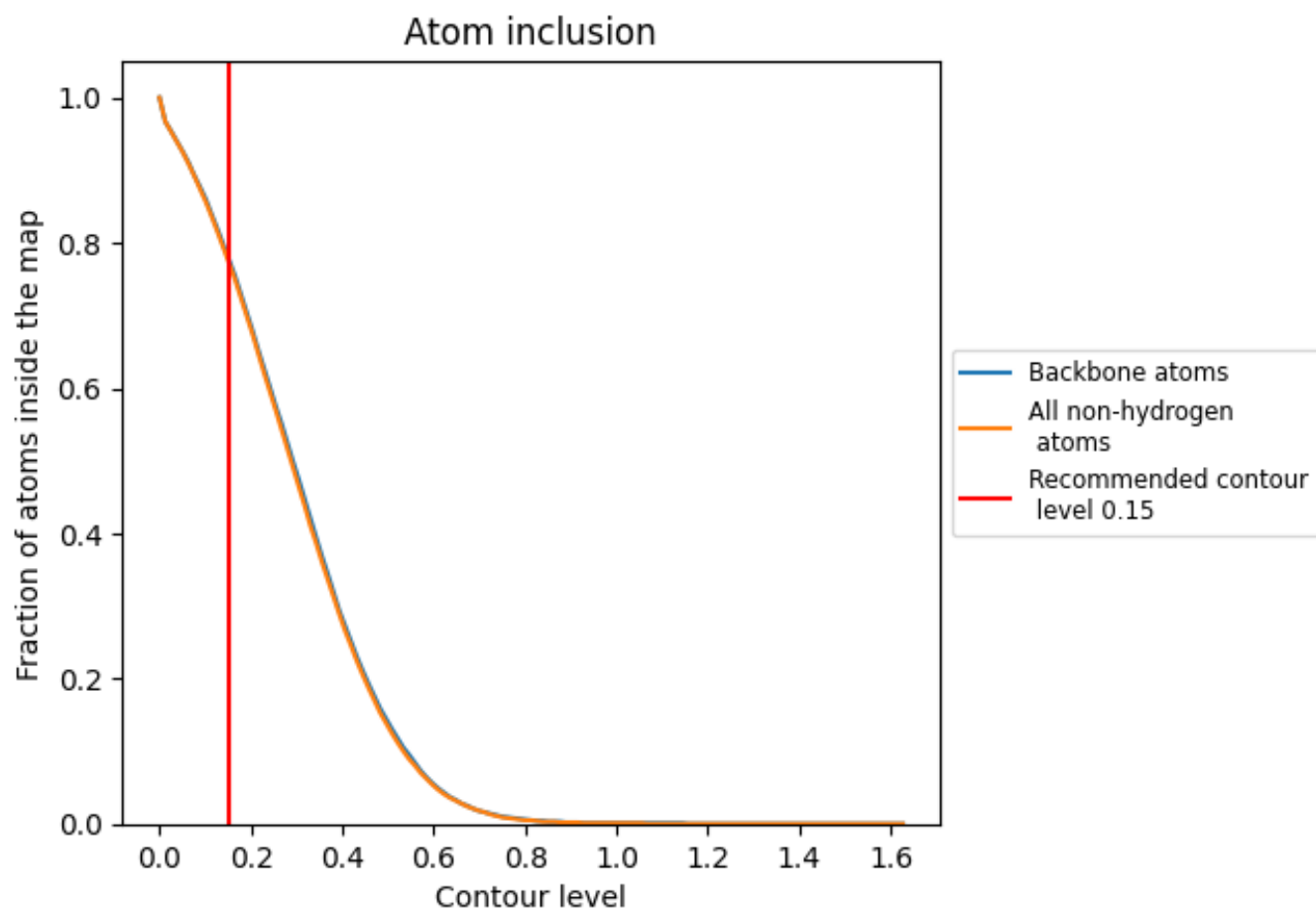
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 78% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7760	 0.4780
3A	 0.8010	 0.4930
3B	 0.7630	 0.4780
3C	 0.9070	 0.5380
3D	 0.8430	 0.5030
3E	 0.4020	 0.3040
3F	 0.8600	 0.5040
3G	 0.8240	 0.4690
3H	 0.6870	 0.3890
3I	 0.4600	 0.3850
3J	 0.8800	 0.5100
3N	 0.8170	 0.5070
3O	 0.7900	 0.5050
3P	 0.8940	 0.5270
3Q	 0.8120	 0.4950
3R	 0.4120	 0.2710
3S	 0.8200	 0.5020
3T	 0.8040	 0.5000
3U	 0.7220	 0.4220
3V	 0.4790	 0.4070
3W	 0.8450	 0.5180
3X	 0.7640	 0.4760
3Y	 0.7420	 0.4620

