



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 09:40 PM UTC

PDB ID : 8ZP0 / pdb_00008zp0
EMDB ID : EMD-60323
Title : Cryo-EM structure of YF23694-bound porcine bc1 complex
Authors : Wang, Y.X.; Sun, J.Y.; Cui, G.R.; Yang, G.F.
Deposited on : 2024-05-29
Resolution : 2.44 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:

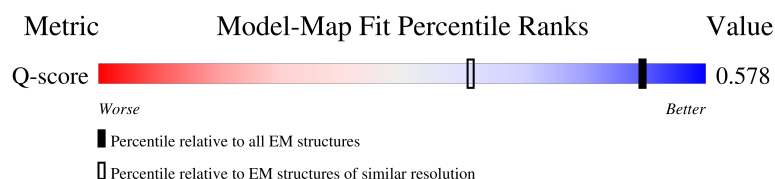
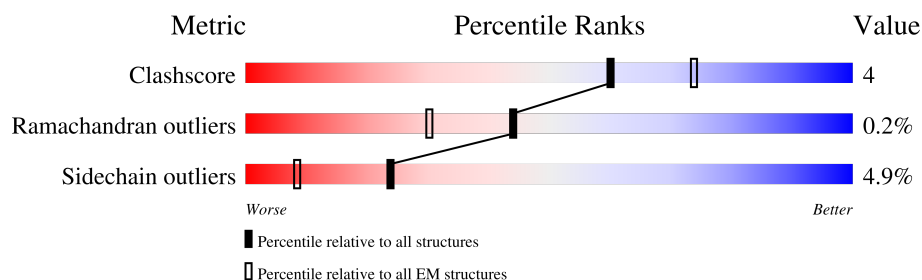
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

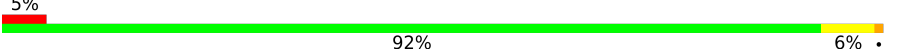
The reported resolution of this entry is 2.44 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5856 (1.94 - 2.94)

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

Mol	Chain	Length	Quality of chain
1	A	378	
1	a	378	
2	B	241	
2	b	241	

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Mol	Chain	Length	Quality of chain
3	C	196	
3	c	196	
4	D	446	
4	d	446	
5	E	418	
5	e	418	
6	F	64	
6	f	64	
7	G	106	
7	g	106	
8	H	79	
8	h	79	
9	I	62	
9	i	62	
10	J	52	
10	j	52	
11	K	57	
11	k	57	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 33585 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	378	Total	C	N	O	S	0	0
			3017	2026	470	501	20		
1	a	378	Total	C	N	O	S	0	0
			3017	2026	470	501	20		

- Molecule 2 is a protein called Cytochrome c1, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	241	Total	C	N	O	S	0	0
			1920	1225	330	349	16		
2	b	239	Total	C	N	O	S	0	0
			1904	1214	327	347	16		

- Molecule 3 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	194	Total	C	N	O	S	0	0
			1502	946	261	288	7		
3	c	196	Total	C	N	O	S	0	0
			1517	954	265	291	7		

- Molecule 4 is a protein called Cytochrome b-c1 complex subunit 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	445	Total	C	N	O	S	0	0
			3452	2157	604	672	19		
4	d	446	Total	C	N	O	S	0	0
			3459	2161	605	674	19		

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	418	Total	C	N	O	S	0	0
			3134	1962	556	607	9		
5	e	418	Total	C	N	O	S	0	0
			3134	1962	556	607	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	64	Total	C	N	O	S	0	0
			528	320	97	106	5		
6	f	64	Total	C	N	O	S	0	0
			528	320	97	106	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	106	Total	C	N	O	S	0	0
			921	589	162	168	2		
7	g	106	Total	C	N	O	S	0	0
			921	589	162	168	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	71	Total	C	N	O	S	0	0
			608	399	112	95	2		
8	h	79	Total	C	N	O	S	0	0
			666	434	122	108	2		

- Molecule 9 is a protein called Complex III subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	62	Total	C	N	O	0	0
			507	331	90	86		
9	i	62	Total	C	N	O	0	0
			507	331	90	86		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	49	Total	C	N	O	S	0	0
			405	269	71	63	2		

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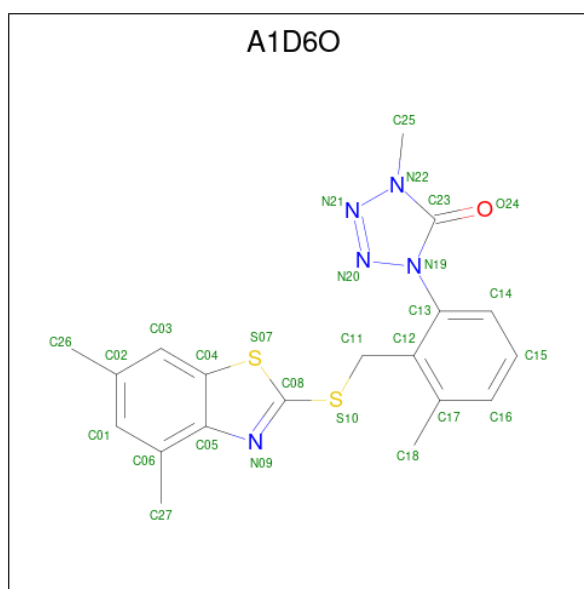
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Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	51	Total	C	N	O	S	0	0
			421	281	74	65	1		

- Molecule 11 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

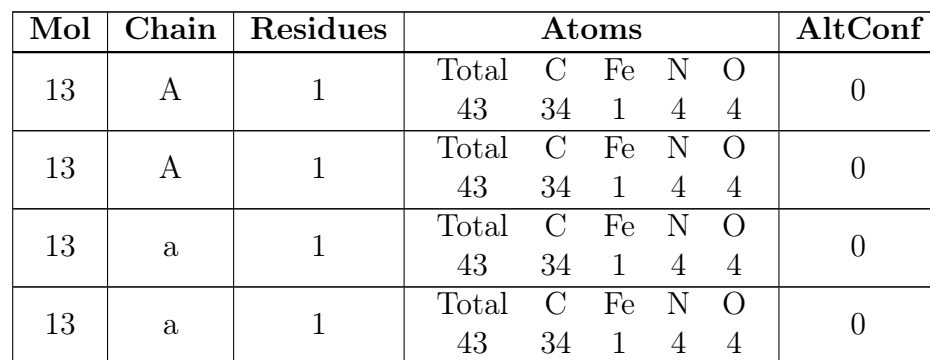
Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	57	Total	C	N	O	S	0	0
			404	252	74	76	2		
11	k	57	Total	C	N	O	S	0	0
			404	252	74	76	2		

- Molecule 12 is 1-[2-[(4,6-dimethyl-1,3-benzothiazol-2-yl)sulfanylmethyl]-3-methyl-phenyl]-4-methyl-1,2,3,4-tetrazol-5-one (CCD ID: A1D6O) (formula: $C_{19}H_{19}N_5OS_2$) (labeled as "Ligand of Interest" by depositor).

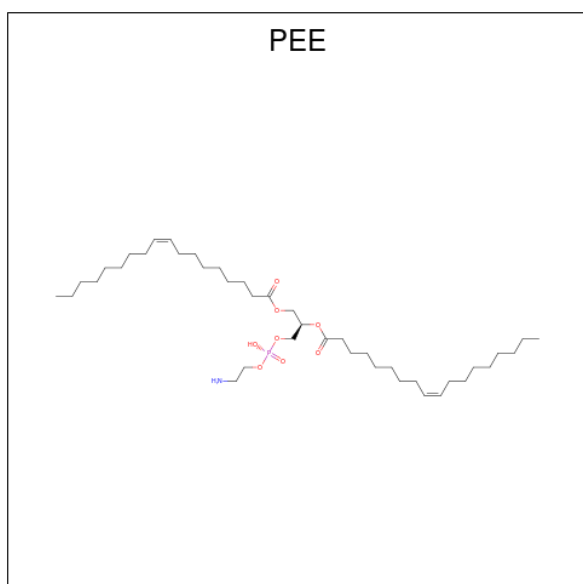


Mol	Chain	Residues	Atoms					AltConf
12	A	1	Total	C	N	O	S	0
			27	19	5	1	2	
12	A	1	Total	C	N	O	S	0
			27	19	5	1	2	
12	a	1	Total	C	N	O	S	0
			27	19	5	1	2	
12	a	1	Total	C	N	O	S	0
			27	19	5	1	2	

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

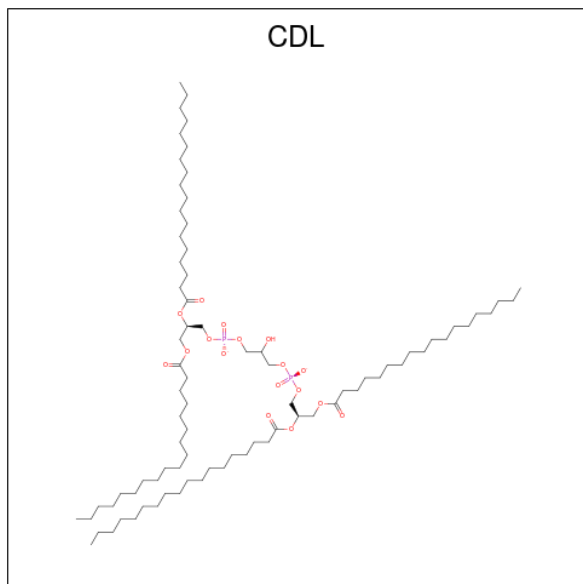


- Molecule 14 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$).



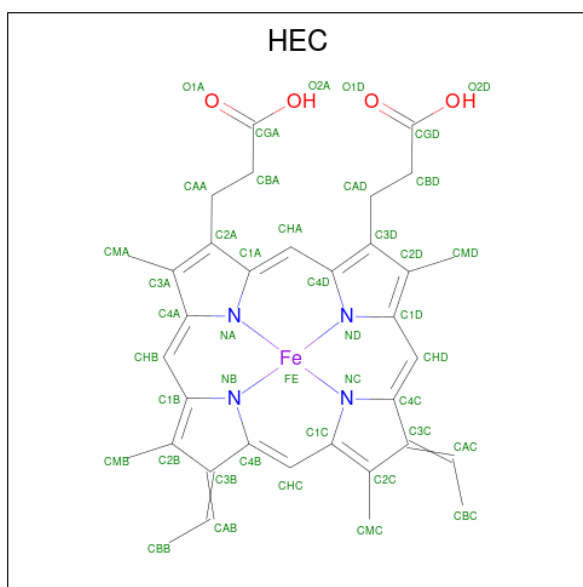
Mol	Chain	Residues	Atoms					AltConf
14	A	1	Total	C	N	O	P	0
			45	35	1	8	1	
14	D	1	Total	C	N	O	P	0
			49	39	1	8	1	
14	a	1	Total	C	N	O	P	0
			49	39	1	8	1	

- Molecule 15 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



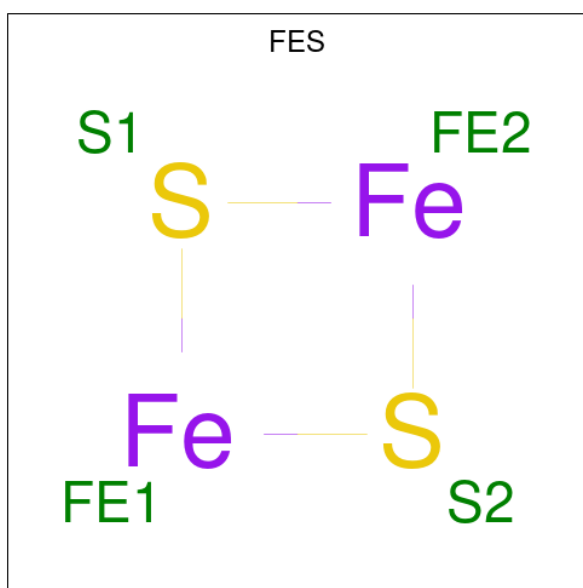
Mol	Chain	Residues	Atoms				AltConf
15	A	1	Total	C	O	P	0
			64	45	17	2	
15	a	1	Total	C	O	P	0
			64	45	17	2	
15	a	1	Total	C	O	P	0
			64	45	17	2	

- Molecule 16 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



Mol	Chain	Residues	Atoms					AltConf
16	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
16	b	1	Total 43	C 34	Fe 1	N 4	O 4	0

- Molecule 17 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).

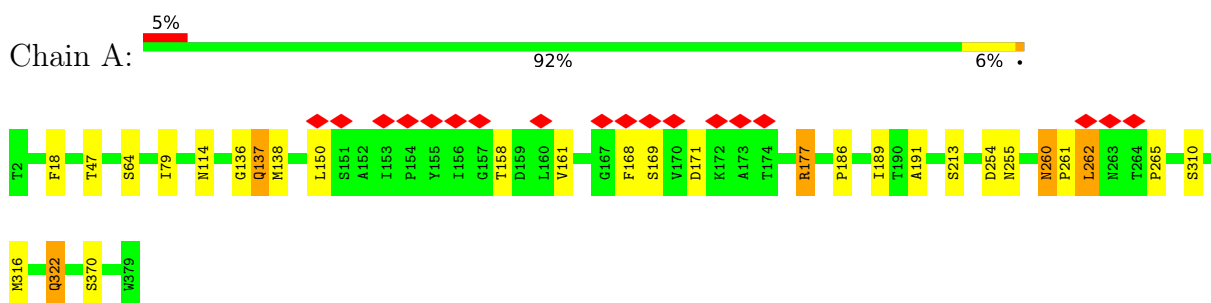


Mol	Chain	Residues	Atoms			AltConf
17	C	1	Total	Fe	S	0
			4	2	2	
17	c	1	Total	Fe	S	0
			4	2	2	

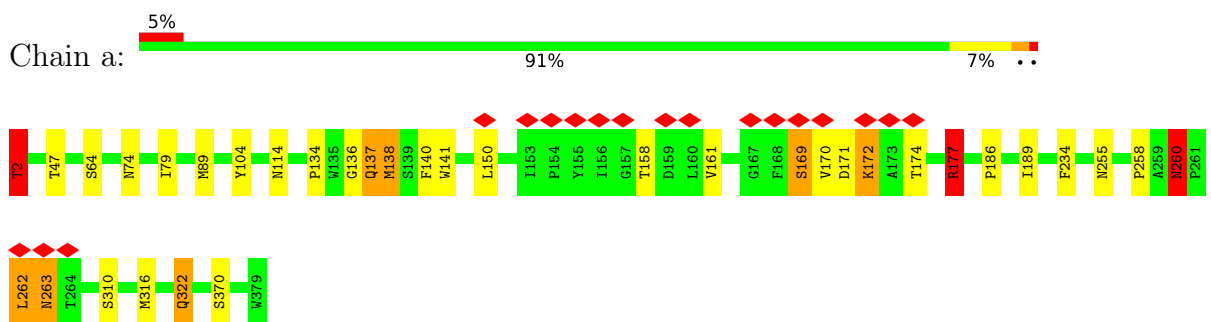
3 Residue-property plots [i](#)

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

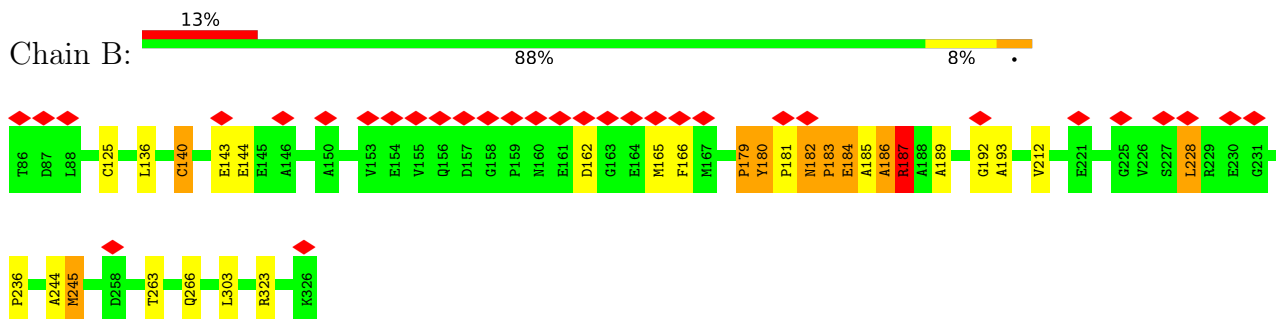
- Molecule 1: Cytochrome b



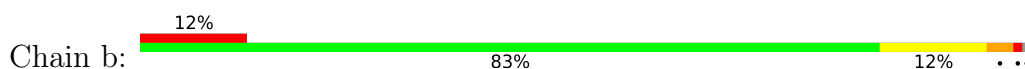
- Molecule 1: Cytochrome b

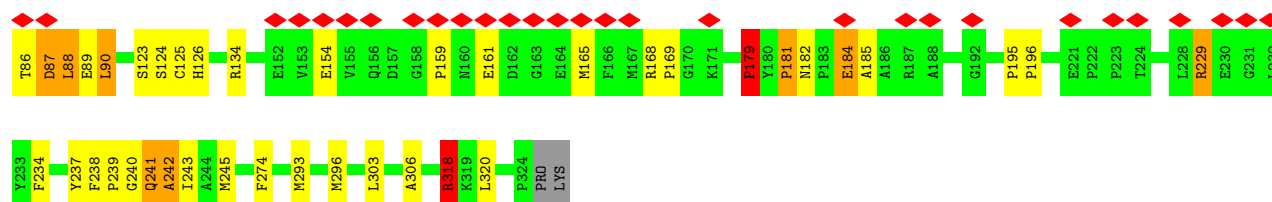


- Molecule 2: Cytochrome c1, heme protein, mitochondrial

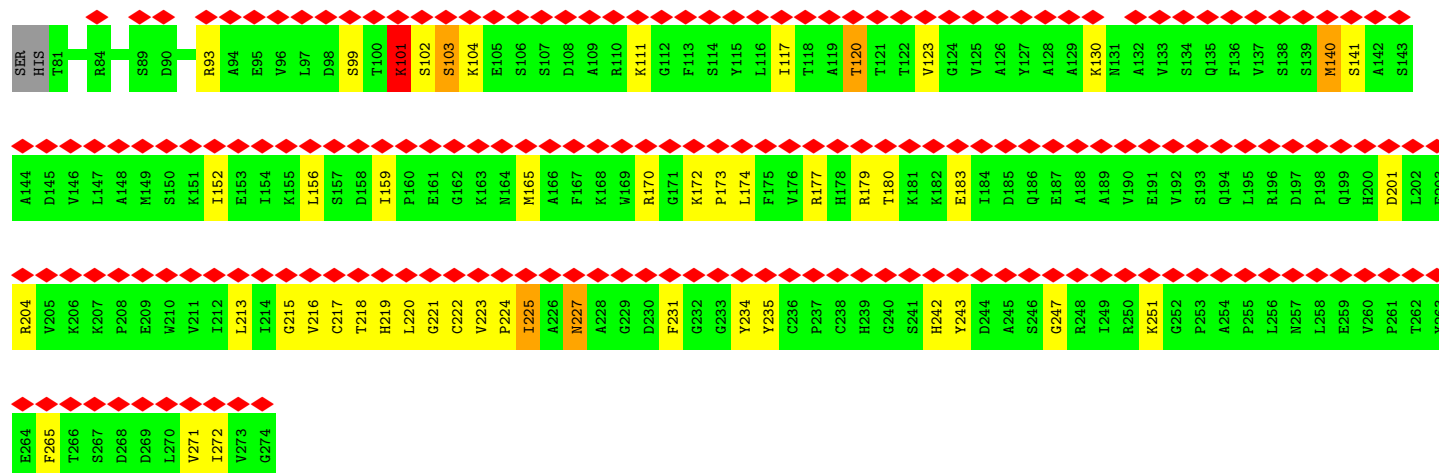
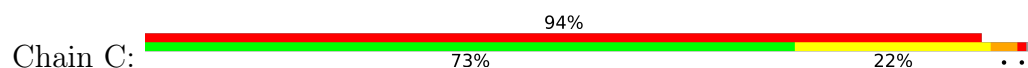


- Molecule 2: Cytochrome c1, heme protein, mitochondrial

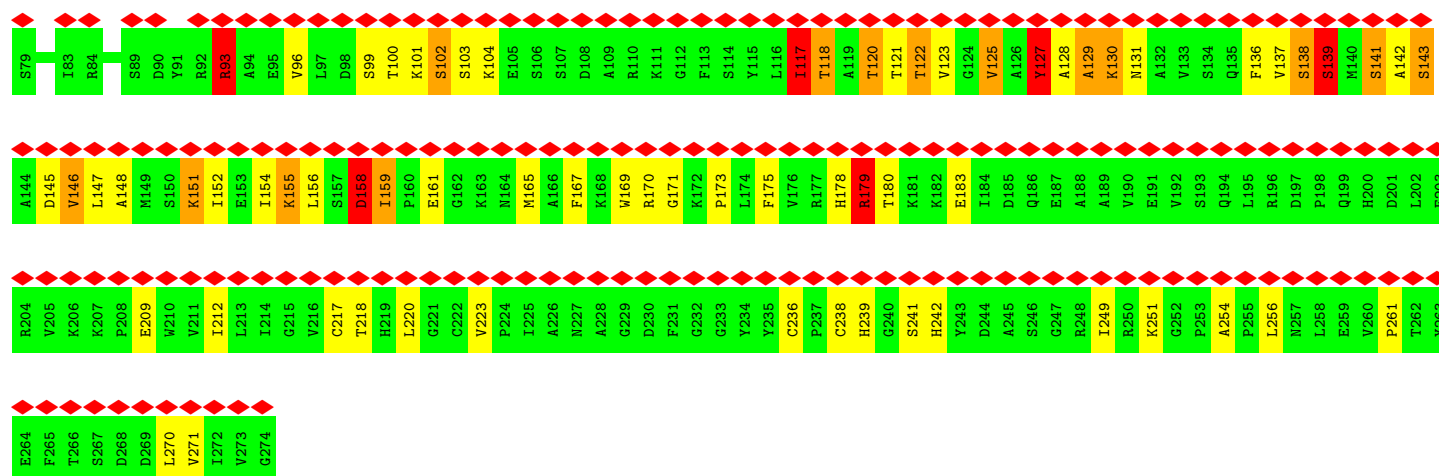




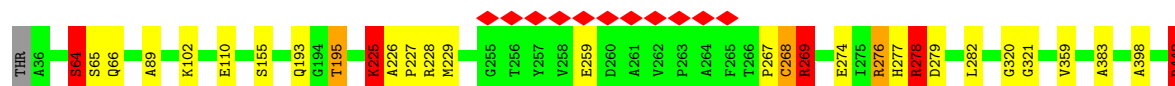
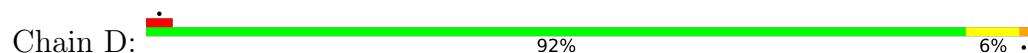
- Molecule 3: Cytochrome b-c1 complex subunit Rieske, mitochondrial

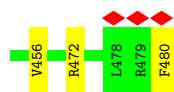


- Molecule 3: Cytochrome b-c1 complex subunit Rieske, mitochondrial



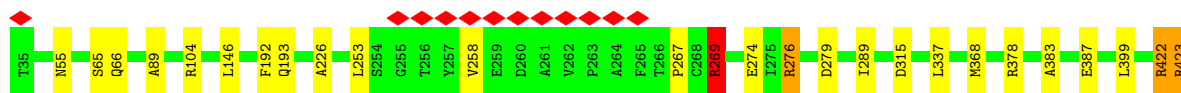
- Molecule 4: Cytochrome b-c1 complex subunit 1, mitochondrial





- Molecule 4: Cytochrome b-c1 complex subunit 1, mitochondrial

Chain d: 92% 7%



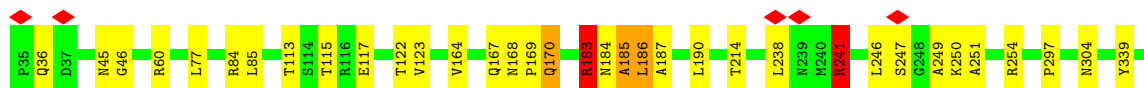
- Molecule 5: Cytochrome b-c1 complex subunit 2, mitochondrial

Chain E: 91% 8%



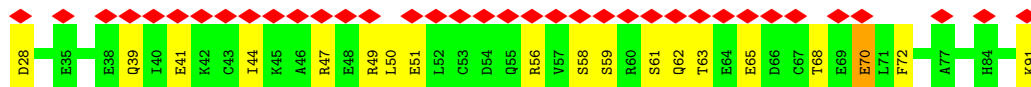
- Molecule 5: Cytochrome b-c1 complex subunit 2, mitochondrial

Chain e: 90% 8%



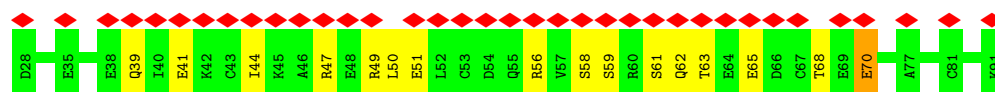
- Molecule 6: Cytochrome b-c1 complex subunit 6

Chain F: 56% 70% 28%

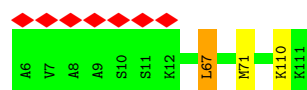


- Molecule 6: Cytochrome b-c1 complex subunit 6

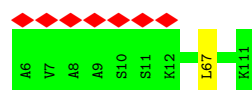
Chain f: 56% 75% 23%



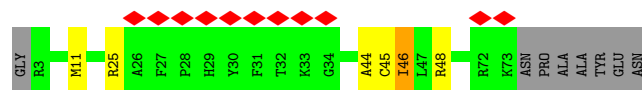
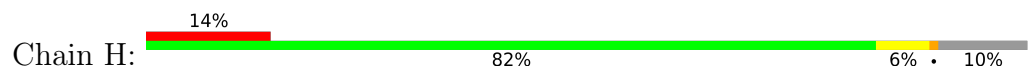
• Molecule 7: Cytochrome b-c1 complex subunit 7



• Molecule 7: Cytochrome b-c1 complex subunit 7



• Molecule 8: Cytochrome b-c1 complex subunit 8



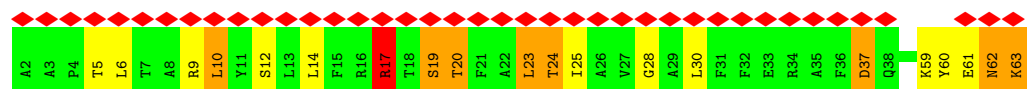
• Molecule 8: Cytochrome b-c1 complex subunit 8



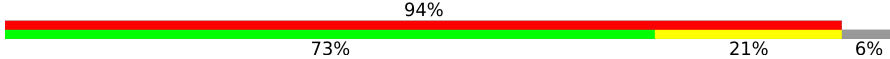
• Molecule 9: Complex III subunit 9



• Molecule 9: Complex III subunit 9

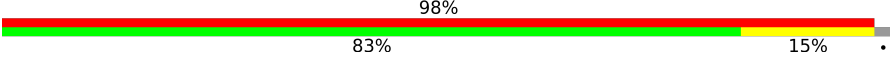


• Molecule 10: Cytochrome b-c1 complex subunit 10

Chain J: 



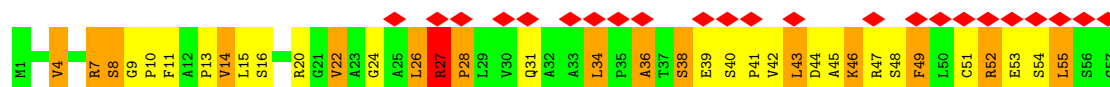
- Molecule 10: Cytochrome b-c1 complex subunit 10

Chain j: 



- Molecule 11: Cytochrome b-c1 complex subunit Rieske, mitochondrial

Chain K: 



- Molecule 11: Cytochrome b-c1 complex subunit Rieske, mitochondrial

Chain k: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	493233	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 ($e^-/\text{\AA}^2$)	49.72	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	10.253	Depositor
Minimum map value	-6.629	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.286	Depositor
Recommended contour level	1.06	Depositor
Map size (Å)	307.19998, 307.19998, 307.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9599999, 0.9599999, 0.9599999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HEC, PEE, A1D6O, HEM, FES, CDL

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.51	3/3115 (0.1%)	0.81	8/4259 (0.2%)
1	a	0.59	7/3115 (0.2%)	0.89	17/4259 (0.4%)
2	B	0.64	4/1978 (0.2%)	1.02	10/2684 (0.4%)
2	b	0.66	4/1961 (0.2%)	1.06	15/2661 (0.6%)
3	C	0.53	2/1534 (0.1%)	1.05	3/2075 (0.1%)
3	c	0.87	7/1549 (0.5%)	1.23	18/2095 (0.9%)
4	D	0.69	12/3524 (0.3%)	0.90	17/4783 (0.4%)
4	d	0.77	12/3531 (0.3%)	0.96	26/4793 (0.5%)
5	E	0.55	3/3187 (0.1%)	0.78	6/4314 (0.1%)
5	e	0.59	5/3187 (0.2%)	0.84	13/4314 (0.3%)
6	F	0.35	0/534	0.84	0/714
6	f	0.41	0/534	0.96	2/714 (0.3%)
7	G	0.42	0/941	0.64	0/1262
7	g	0.42	0/941	0.64	0/1262
8	H	0.52	1/628 (0.2%)	1.01	1/848 (0.1%)
8	h	0.40	0/688	0.90	1/931 (0.1%)
9	I	0.59	1/520 (0.2%)	1.22	8/701 (1.1%)
9	i	0.64	1/520 (0.2%)	1.37	8/701 (1.1%)
10	J	0.32	0/420	0.76	0/576
10	j	0.37	0/437	0.85	1/598 (0.2%)
11	K	1.49	7/410 (1.7%)	2.06	17/556 (3.1%)
11	k	1.51	7/410 (1.7%)	2.04	21/556 (3.8%)
All	All	0.65	76/33664 (0.2%)	0.97	192/45656 (0.4%)

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
1	A	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	a	0	2
2	B	0	2
2	b	0	2
3	C	0	2
3	c	0	6
4	D	0	4
4	d	0	7
5	E	0	3
5	e	0	4
8	h	0	1
9	I	0	3
9	i	0	1
11	K	0	4
11	k	0	5
All	All	0	47

All (76) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	K	46	LYS	C-N	14.87	1.56	1.33
3	c	102	SER	C-N	11.54	1.49	1.33
4	d	466	PRO	C-O	-11.40	1.10	1.23
3	c	128	ALA	C-N	10.13	1.47	1.33
4	D	64	SER	C-N	10.04	1.47	1.33
3	c	142	ALA	C-N	10.02	1.48	1.33
4	d	378	ARG	C-O	-9.68	1.11	1.24
4	d	279	ASP	C-O	-9.67	1.12	1.23
4	D	279	ASP	C-O	-9.67	1.12	1.23
4	D	229	MET	C-O	-9.40	1.12	1.23
4	d	424	ILE	C-O	-9.35	1.12	1.24
11	K	9	GLY	C-O	-9.33	1.11	1.24
11	k	9	GLY	C-O	-9.27	1.11	1.24
4	D	227	PRO	C-O	-8.94	1.12	1.24
4	d	452	GLN	C-O	-8.89	1.12	1.23
4	D	442	ARG	C-O	-8.89	1.12	1.24
4	d	276	ARG	C-O	-8.63	1.14	1.24
11	k	16	SER	C-O	-8.62	1.11	1.24
5	e	187	ALA	C-O	-8.54	1.13	1.24
4	d	442	ARG	C-O	-8.45	1.13	1.24
5	E	252	LYS	C-O	-8.21	1.14	1.24
2	b	318	ARG	C-O	-8.16	1.14	1.23
5	e	183	ARG	C-O	-7.87	1.13	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	K	45	ALA	C-N	7.78	1.44	1.33
4	d	425	PRO	C-O	-7.78	1.13	1.23
11	k	14	VAL	C-O	-7.78	1.15	1.24
5	e	185	ALA	C-O	-7.63	1.14	1.24
4	D	228	ARG	C-O	-7.59	1.14	1.24
11	k	8	SER	C-O	7.53	1.33	1.24
4	D	277	HIS	C-O	-7.49	1.14	1.23
11	K	8	SER	C-O	7.41	1.33	1.24
11	k	16	SER	CA-CB	-7.40	1.41	1.53
9	i	59	LYS	C-N	7.39	1.46	1.33
1	a	169	SER	C-N	7.37	1.43	1.33
1	A	136	GLY	C-O	-7.37	1.17	1.24
1	a	136	GLY	C-O	-7.28	1.17	1.24
5	e	249	ALA	CA-CB	-7.19	1.41	1.53
3	c	129	ALA	C-N	7.17	1.43	1.33
5	E	249	ALA	CA-CB	-7.11	1.41	1.53
11	k	18	THR	C-O	-7.08	1.15	1.24
2	b	320	LEU	C-O	-7.01	1.16	1.24
3	C	101	LYS	C-N	6.85	1.43	1.33
1	a	138	MET	C-O	-6.57	1.15	1.24
4	d	450	TYR	C-N	-6.45	1.25	1.33
1	a	322	GLN	C-O	-6.37	1.15	1.24
1	A	322	GLN	C-O	-6.30	1.15	1.24
2	b	242	ALA	C-N	6.09	1.42	1.33
4	d	269	ARG	C-O	-6.08	1.16	1.23
9	I	60	TYR	CA-C	-5.96	1.44	1.52
11	K	54	SER	C-N	5.85	1.41	1.33
4	D	268	CYS	C-O	-5.83	1.17	1.24
3	c	220	LEU	C-N	5.77	1.42	1.33
4	d	65	SER	C-N	5.75	1.42	1.33
4	D	225	LYS	C-O	-5.68	1.17	1.23
4	D	269	ARG	C-O	-5.62	1.16	1.23
4	D	282	LEU	C-O	-5.59	1.16	1.24
1	a	104	TYR	C-O	-5.57	1.16	1.24
2	B	244	ALA	CA-CB	-5.55	1.45	1.53
1	a	258	PRO	C-O	-5.53	1.17	1.23
3	c	239	HIS	C-N	5.52	1.41	1.33
4	D	64	SER	CA-CB	-5.49	1.45	1.54
2	b	126	HIS	N-CA	5.32	1.52	1.45
3	c	179	ARG	C-N	5.29	1.41	1.33
1	A	168	PHE	C-N	-5.27	1.25	1.33
2	B	180	TYR	CA-C	-5.26	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	140	CYS	C-O	-5.25	1.17	1.24
2	B	184	GLU	C-N	-5.25	1.26	1.33
5	e	251	ALA	C-O	-5.22	1.17	1.24
8	H	46	ILE	C-O	-5.21	1.18	1.24
11	k	8	SER	CA-CB	-5.20	1.46	1.53
4	d	422	ARG	C-O	-5.19	1.18	1.23
5	E	251	ALA	C-O	-5.09	1.17	1.23
11	K	8	SER	CA-CB	-5.07	1.46	1.53
1	a	2	THR	C-N	-5.06	1.26	1.33
11	K	28	PRO	N-CA	-5.05	1.39	1.48
3	C	227	ASN	C-N	5.00	1.40	1.33

All (192) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	28	PRO	N-CA-CB	-16.94	91.13	102.65
9	i	60	TYR	N-CA-CB	-14.42	89.66	110.57
3	c	118	THR	CB-CA-C	-13.00	83.16	109.55
4	D	442	ARG	CB-CG-CD	-12.84	81.77	111.30
9	i	37	ASP	N-CA-C	-12.59	97.38	113.12
1	a	2	THR	CB-CA-C	-11.36	84.11	109.10
5	e	184	ASN	CA-C-O	-10.01	110.75	121.36
11	k	16	SER	N-CA-C	9.84	125.51	109.96
11	k	44	ASP	N-CA-C	-9.77	100.55	114.12
4	d	425	PRO	N-CA-CB	-9.54	90.83	103.42
2	B	183	PRO	CB-CA-C	-9.49	95.91	111.56
2	b	126	HIS	CA-C-N	9.41	133.63	122.44
2	b	126	HIS	C-N-CA	9.41	133.63	122.44
11	k	43	LEU	N-CA-CB	-9.34	96.22	110.42
4	d	450	TYR	O-C-N	-9.32	111.39	122.11
1	a	260	ASN	CB-CA-C	-9.27	91.91	110.17
1	A	322	GLN	CB-CA-C	9.27	125.45	109.24
11	K	28	PRO	CB-CA-C	9.22	126.66	112.27
1	a	322	GLN	CB-CA-C	9.20	125.34	109.24
5	E	241	ARG	CB-CA-C	9.02	123.37	111.82
2	B	183	PRO	N-CA-C	8.92	130.85	112.47
9	I	60	TYR	N-CA-C	-8.92	99.80	113.89
6	f	62	GLN	CA-CB-CG	8.80	131.71	114.10
11	k	7	ARG	CB-CA-C	8.79	124.03	109.53
10	j	22	SER	N-CA-C	-8.76	101.85	112.54
11	K	42	VAL	N-CA-C	-8.72	95.25	107.99
1	A	260	ASN	CB-CA-C	-8.56	93.31	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	b	179	PRO	N-CA-CB	-8.45	94.38	103.25
3	c	93	ARG	CB-CA-C	8.41	122.28	110.16
4	d	451	ASP	CA-CB-CG	8.41	121.01	112.60
11	K	8	SER	CA-C-N	-8.39	108.69	121.87
11	K	8	SER	C-N-CA	-8.39	108.69	121.87
11	k	8	SER	CA-C-N	-8.39	108.70	121.87
11	k	8	SER	C-N-CA	-8.39	108.70	121.87
4	D	321	GLY	N-CA-C	8.32	122.70	112.64
11	K	46	LYS	O-C-N	8.09	133.35	122.59
11	K	7	ARG	CB-CA-C	8.01	122.93	109.48
8	H	44	ALA	CA-C-O	-7.84	112.11	120.42
9	i	61	GLU	N-CA-C	-7.83	100.11	111.30
1	a	262	LEU	CA-C-N	-7.70	109.57	121.74
1	a	262	LEU	C-N-CA	-7.70	109.57	121.74
3	c	118	THR	N-CA-CB	7.69	122.43	110.44
11	k	43	LEU	CA-C-O	-7.69	112.90	121.89
2	B	189	ALA	N-CA-C	-7.66	103.93	113.20
9	I	38	GLN	CB-CA-C	7.66	124.66	110.11
4	d	450	TYR	N-CA-C	7.62	123.95	111.37
11	K	51	CYS	CA-C-O	-7.56	112.31	122.44
2	B	186	ALA	N-CA-C	-7.55	103.96	113.02
11	k	9	GLY	CA-C-N	-7.37	113.09	120.31
11	k	9	GLY	C-N-CA	-7.37	113.09	120.31
11	k	43	LEU	N-CA-C	7.26	121.12	110.59
3	C	141	SER	CA-C-N	7.24	131.47	120.82
3	C	141	SER	C-N-CA	7.24	131.47	120.82
2	B	180	TYR	CB-CA-C	-7.23	95.93	110.17
3	c	93	ARG	CA-C-N	7.22	131.66	120.82
3	c	93	ARG	C-N-CA	7.22	131.66	120.82
9	i	60	TYR	CA-CB-CG	7.17	126.81	113.90
3	c	117	ILE	O-C-N	-7.17	113.89	122.06
11	K	9	GLY	CA-C-N	-7.13	113.32	120.31
11	K	9	GLY	C-N-CA	-7.13	113.32	120.31
5	e	247	SER	CA-C-N	-7.13	111.79	121.06
5	e	247	SER	C-N-CA	-7.13	111.79	121.06
5	e	169	PRO	CA-C-N	7.08	132.55	120.72
5	e	169	PRO	C-N-CA	7.08	132.55	120.72
11	k	44	ASP	N-CA-CB	7.07	120.64	110.88
4	d	269	ARG	N-CA-CB	-7.06	100.01	110.17
4	d	425	PRO	CB-CA-C	7.03	121.84	111.22
11	K	51	CYS	N-CA-C	7.01	121.57	110.70
2	b	126	HIS	CB-CA-C	7.01	123.14	109.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	204	ARG	N-CA-C	-6.98	105.70	114.56
2	b	126	HIS	CA-CB-CG	6.97	120.77	113.80
4	D	269	ARG	N-CA-CB	-6.96	99.71	110.29
11	K	36	ALA	O-C-N	6.86	131.72	122.59
4	d	387	GLU	CB-CG-CD	-6.80	101.04	112.60
1	a	262	LEU	CA-C-O	-6.74	113.96	120.90
5	E	247	SER	CA-C-N	-6.67	112.39	121.06
5	E	247	SER	C-N-CA	-6.67	112.39	121.06
1	a	322	GLN	CB-CG-CD	-6.66	101.27	112.60
1	a	137	GLN	N-CA-CB	-6.58	100.38	110.44
3	c	141	SER	N-CA-C	6.58	120.98	109.80
1	a	138	MET	N-CA-C	-6.50	105.47	113.41
1	a	2	THR	N-CA-C	6.45	129.06	111.00
6	f	62	GLN	CB-CG-CD	6.44	123.55	112.60
4	d	387	GLU	CA-C-O	-6.44	112.57	119.97
4	d	422	ARG	CA-C-O	-6.43	114.40	121.28
4	D	278	ARG	CB-CG-CD	-6.42	96.53	111.30
1	A	322	GLN	N-CA-C	-6.38	105.63	113.41
11	K	49	PHE	CA-CB-CG	6.35	120.15	113.80
1	a	169	SER	O-C-N	6.34	129.59	122.11
5	e	187	ALA	CA-C-O	-6.31	112.72	119.97
1	A	322	GLN	CB-CG-CD	-6.30	101.88	112.60
4	d	442	ARG	CB-CG-CD	-6.29	96.83	111.30
4	D	64	SER	CA-C-N	-6.27	109.57	121.54
4	D	64	SER	C-N-CA	-6.27	109.57	121.54
3	c	139	SER	N-CA-C	-6.25	104.46	111.28
1	a	263	ASN	O-C-N	6.24	129.53	121.79
5	e	184	ASN	CA-C-N	6.21	133.41	121.54
5	e	184	ASN	C-N-CA	6.21	133.41	121.54
11	K	38	SER	N-CA-C	-6.21	97.00	108.24
5	E	244	LEU	N-CA-C	-6.20	102.53	110.53
1	a	322	GLN	N-CA-C	-6.20	105.85	113.41
4	D	279	ASP	CB-CA-C	-6.18	103.32	111.42
11	k	48	SER	CB-CA-C	6.16	119.70	109.53
4	D	229	MET	CA-C-O	-6.15	113.91	121.11
2	b	179	PRO	N-CA-C	6.14	125.11	112.47
3	c	142	ALA	O-C-N	6.12	130.73	122.59
4	d	279	ASP	CB-CA-C	-6.07	103.47	111.42
4	d	66	GLN	N-CA-CB	-6.07	101.31	110.05
1	a	134	PRO	CA-C-N	6.04	130.73	122.34
1	a	134	PRO	C-N-CA	6.04	130.73	122.34
9	I	37	ASP	N-CA-C	-6.01	98.00	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	c	128	ALA	O-C-N	6.00	130.41	122.43
1	A	136	GLY	CA-C-O	-6.00	115.78	121.90
3	c	139	SER	N-CA-CB	5.96	118.88	110.12
11	k	16	SER	CA-C-N	5.93	133.34	122.79
11	k	16	SER	C-N-CA	5.93	133.34	122.79
3	c	102	SER	N-CA-C	5.91	119.34	107.41
4	d	425	PRO	CA-N-CD	5.86	120.21	112.00
2	B	166	PHE	CA-CB-CG	5.85	119.65	113.80
11	K	7	ARG	N-CA-C	-5.85	100.17	109.76
2	B	193	ALA	N-CA-C	-5.84	97.44	107.61
5	e	46	GLY	CA-C-O	-5.80	113.06	119.27
4	d	450	TYR	CA-C-N	-5.80	114.15	122.67
4	d	450	TYR	C-N-CA	-5.80	114.15	122.67
2	b	237	TYR	CA-C-O	-5.79	114.00	121.17
11	k	7	ARG	N-CA-C	-5.78	100.24	109.96
1	A	168	PHE	CA-C-N	5.76	131.37	121.86
1	A	168	PHE	C-N-CA	5.76	131.37	121.86
2	b	123	SER	O-C-N	5.74	127.52	121.89
11	k	41	PRO	CA-C-O	-5.74	115.01	122.12
9	i	59	LYS	CA-C-N	-5.69	111.01	122.55
9	i	59	LYS	C-N-CA	-5.69	111.01	122.55
4	d	269	ARG	CA-C-O	-5.68	115.37	121.56
2	B	180	TYR	CA-CB-CG	-5.67	103.69	113.90
5	E	46	GLY	CA-C-O	-5.66	113.22	119.27
4	d	441	VAL	CA-C-N	5.62	128.38	120.28
4	d	441	VAL	C-N-CA	5.62	128.38	120.28
9	I	60	TYR	CA-C-O	5.62	125.38	119.03
2	B	183	PRO	N-CD-CG	-5.58	94.83	103.20
3	c	127	TYR	N-CA-CB	5.57	118.41	110.06
11	k	44	ASP	CB-CA-C	5.56	118.71	109.38
4	D	259	GLU	CA-C-N	5.54	132.12	121.54
4	D	259	GLU	C-N-CA	5.54	132.12	121.54
3	c	122	THR	N-CA-C	-5.54	104.55	112.13
11	k	17	ALA	CA-C-N	5.53	130.61	121.99
11	k	17	ALA	C-N-CA	5.53	130.61	121.99
1	A	136	GLY	N-CA-C	-5.50	104.73	112.60
9	I	38	GLN	N-CA-C	-5.50	106.54	113.20
11	K	39	GLU	CB-CA-C	5.50	119.46	109.62
5	e	186	LEU	N-CA-CB	-5.50	100.77	110.39
1	a	136	GLY	N-CA-C	-5.48	104.77	112.60
4	D	320	GLY	CA-C-N	5.48	126.18	119.99
4	D	320	GLY	C-N-CA	5.48	126.18	119.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	k	16	SER	N-CA-CB	-5.47	100.73	110.14
4	d	89	ALA	N-CA-C	5.43	117.20	111.28
3	c	158	ASP	CB-CA-C	5.42	120.19	110.81
2	b	274	PHE	N-CA-C	-5.42	102.26	110.28
3	c	151	LYS	CA-C-N	5.40	128.97	122.16
3	c	151	LYS	C-N-CA	5.40	128.97	122.16
4	d	258	VAL	CA-C-N	5.40	133.32	124.31
4	d	258	VAL	C-N-CA	5.40	133.32	124.31
2	b	90	LEU	N-CA-C	-5.38	99.76	108.52
2	b	238	PHE	CA-CB-CG	5.36	119.16	113.80
5	e	249	ALA	N-CA-CB	-5.35	101.91	110.46
4	D	89	ALA	N-CA-C	5.34	117.11	111.28
5	e	187	ALA	CA-C-N	5.34	128.43	120.95
5	e	187	ALA	C-N-CA	5.34	128.43	120.95
2	b	181	PRO	O-C-N	5.33	128.37	122.24
4	d	192	PHE	CA-C-N	5.32	128.79	120.82
4	d	192	PHE	C-N-CA	5.32	128.79	120.82
4	D	226	ALA	N-CA-C	5.30	120.81	113.45
5	E	249	ALA	N-CA-CB	-5.27	102.03	110.46
2	b	318	ARG	CB-CA-C	5.23	117.87	109.61
4	D	442	ARG	CA-C-O	-5.22	114.21	120.10
2	b	242	ALA	O-C-N	5.21	129.19	122.93
2	b	293	MET	N-CA-C	-5.17	107.04	113.55
11	K	44	ASP	N-CA-C	-5.16	108.01	114.56
4	D	269	ARG	N-CA-C	5.14	118.09	110.48
11	k	44	ASP	CA-C-O	5.14	124.55	118.90
4	d	269	ARG	CB-CA-C	5.12	118.96	109.54
4	D	193	GLN	N-CA-C	5.12	119.82	111.37
3	c	93	ARG	CA-C-O	-5.11	114.83	120.70
9	I	36	PHE	N-CA-C	-5.08	104.58	111.55
2	B	166	PHE	N-CA-CB	-5.07	102.59	110.04
4	d	65	SER	N-CA-C	5.05	121.57	110.80
4	d	193	GLN	N-CA-C	5.05	119.71	111.37
8	h	65	GLN	N-CA-C	-5.04	108.40	114.75
9	i	30	LEU	CA-C-N	5.04	130.47	122.61
9	i	30	LEU	C-N-CA	5.04	130.47	122.61
1	a	138	MET	CB-CA-C	5.02	118.02	109.24
9	I	30	LEU	CA-C-N	5.01	130.43	122.61
9	I	30	LEU	C-N-CA	5.01	130.43	122.61

There are no chirality outliers.

All (47) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	177	ARG	Sidechain
2	B	187	ARG	Sidechain
2	B	323	ARG	Sidechain
3	C	231	PHE	Peptide
3	C	247	GLY	Peptide
4	D	269	ARG	Sidechain
4	D	276	ARG	Sidechain
4	D	278	ARG	Sidechain
4	D	442	ARG	Mainchain
5	E	236	ARG	Sidechain
5	E	246	LEU	Peptide
5	E	36	GLN	Peptide
9	I	17	ARG	Sidechain
9	I	35	ALA	Mainchain
9	I	58	HIS	Mainchain
11	K	26	LEU	Mainchain
11	K	27	ARG	Sidechain
11	K	52	ARG	Sidechain
11	K	7	ARG	Sidechain
1	a	177	ARG	Sidechain
1	a	2	THR	Mainchain
2	b	229	ARG	Sidechain
2	b	318	ARG	Sidechain
3	c	117	ILE	Mainchain
3	c	136	PHE	Mainchain
3	c	169	TRP	Peptide
3	c	179	ARG	Sidechain
3	c	93	ARG	Sidechain
3	c	99	SER	Mainchain
4	d	226	ALA	Peptide
4	d	269	ARG	Sidechain
4	d	276	ARG	Sidechain
4	d	422	ARG	Sidechain
4	d	423	ARG	Sidechain
4	d	442	ARG	Sidechain,Mainchain
5	e	183	ARG	Sidechain
5	e	241	ARG	Sidechain
5	e	246	LEU	Peptide
5	e	36	GLN	Peptide
8	h	45	CYS	Peptide
9	i	17	ARG	Sidechain
11	k	27	ARG	Sidechain
11	k	34	LEU	Peptide

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Mol	Chain	Res	Type	Group
11	k	35	PRO	Peptide
11	k	47	ARG	Sidechain
11	k	7	ARG	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	A	3017	0	3078	20	0
1	a	3017	0	3078	26	0
2	B	1920	0	1869	25	0
2	b	1904	0	1849	29	0
3	C	1502	0	1490	38	0
3	c	1517	0	1497	43	0
4	D	3452	0	3343	24	0
4	d	3459	0	3350	10	0
5	E	3134	0	3112	23	0
5	e	3134	0	3112	19	0
6	F	528	0	510	5	0
6	f	528	0	510	2	0
7	G	921	0	917	3	0
7	g	921	0	917	0	0
8	H	608	0	616	4	0
8	h	666	0	663	5	0
9	I	507	0	509	13	0
9	i	507	0	509	10	0
10	J	405	0	405	12	0
10	j	421	0	418	5	0
11	K	404	0	425	30	0
11	k	404	0	425	28	0
12	A	54	0	0	0	0
12	a	54	0	0	0	0
13	A	86	0	60	0	0
13	a	86	0	60	0	0
14	A	45	0	65	2	0
14	D	49	0	71	5	0
14	a	49	0	73	5	0
15	A	64	0	72	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	a	128	0	144	9	0
16	B	43	0	32	5	0
16	b	43	0	32	5	0
17	C	4	0	0	0	0
17	c	4	0	0	0	0
All	All	33585	0	33211	300	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 4.

All (300) 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)
2:B:125:CYS:SG	16:B:401:HEC:HBC3	1.77	1.21
2:B:125:CYS:SG	16:B:401:HEC:CAC	2.31	1.19
2:B:125:CYS:SG	16:B:401:HEC:CBC	2.35	1.14
2:b:125:CYS:SG	16:b:401:HEC:HBC3	1.90	1.09
2:b:125:CYS:SG	16:b:401:HEC:CBC	2.41	1.08
11:K:8:SER:HB3	11:K:26:LEU:HD13	1.32	1.08
2:b:125:CYS:SG	16:b:401:HEC:CAC	2.43	1.07
11:k:8:SER:HB3	11:k:26:LEU:HD13	1.31	1.07
2:B:184:GLU:C	2:B:186:ALA:H	1.63	0.97
2:B:187:ARG:HB2	2:B:192:GLY:HA2	1.43	0.96
5:E:320:PRO:HG2	11:K:36:ALA:HB2	1.52	0.92
5:e:164:VAL:HG22	11:k:46:LYS:HA	1.53	0.91
5:e:164:VAL:HG13	11:k:46:LYS:HG2	1.60	0.83
2:B:184:GLU:C	2:B:186:ALA:N	2.33	0.83
2:b:182:ASN:HD21	2:b:184:GLU:HB2	1.41	0.81
2:B:182:ASN:HB3	2:b:161:GLU:HB3	1.62	0.80
1:A:262:LEU:HD13	3:c:223:VAL:HG13	1.64	0.80
3:C:220:LEU:HB3	1:a:141:TRP:CD1	2.19	0.78
3:c:102:SER:O	3:c:104:LYS:HG2	1.83	0.77
1:A:316:MET:HG3	14:A:405:PEE:H10	1.69	0.75
4:D:278:ARG:HD3	8:H:11:MET:HB3	1.69	0.75
5:e:183:ARG:HG3	5:e:254:ARG:HB2	1.68	0.75
2:B:125:CYS:SG	16:B:401:HEC:C3C	2.74	0.74
11:k:43:LEU:HD13	11:k:46:LYS:CB	2.16	0.73
9:I:9:ARG:HH21	9:I:10:LEU:HD13	1.54	0.72
3:C:218:THR:HG23	3:C:219:HIS:HD2	1.54	0.71
5:e:164:VAL:CG2	11:k:46:LYS:HA	2.20	0.71
9:i:9:ARG:HH21	9:i:10:LEU:HD13	1.54	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:214:THR:HG22	5:E:241:ARG:HG2	1.71	0.71
2:B:187:ARG:CB	2:B:192:GLY:HA2	2.20	0.71
2:b:240:GLY:O	2:b:242:ALA:N	2.23	0.70
4:d:315:ASP:OD2	11:k:47:ARG:HA	1.91	0.70
3:c:155:LYS:HB2	3:c:271:VAL:HB	1.72	0.69
3:C:101:LYS:HG3	4:D:267:PRO:HG2	1.75	0.68
11:K:8:SER:CB	11:K:26:LEU:HD13	2.19	0.68
5:e:85:LEU:HA	11:k:15:LEU:HD13	1.76	0.68
3:c:137:VAL:C	3:c:141:SER:HB2	2.20	0.67
5:E:301:ARG:HG2	11:K:34:LEU:HD21	1.77	0.67
2:b:296:MET:HG2	3:c:127:TYR:CE1	2.31	0.66
2:b:88:LEU:HD21	8:h:72:ARG:HE	1.61	0.66
1:A:262:LEU:HA	3:c:223:VAL:HG13	1.79	0.64
3:C:120:THR:HA	3:C:123:VAL:HG12	1.79	0.64
11:k:8:SER:HB3	11:k:26:LEU:CD1	2.17	0.64
5:E:190:LEU:HD13	11:K:13:PRO:HD3	1.80	0.64
4:d:55:ASN:HD21	4:d:253:LEU:HB2	1.63	0.64
5:e:113:THR:HG23	11:k:14:VAL:HG22	1.81	0.63
5:E:168:ASN:ND2	11:K:27:ARG:HD2	2.14	0.63
11:K:8:SER:HB3	11:K:26:LEU:CD1	2.18	0.63
3:C:173:PRO:HG2	3:C:223:VAL:HG21	1.80	0.62
5:E:85:LEU:HA	11:K:15:LEU:HD22	1.81	0.62
2:B:184:GLU:O	2:B:186:ALA:N	2.31	0.62
5:E:320:PRO:CG	11:K:36:ALA:HB2	2.28	0.62
9:I:20:THR:HA	9:I:23:LEU:HB2	1.81	0.62
11:K:14:VAL:HB	11:K:22:VAL:HG12	1.80	0.62
2:B:266:GLN:HE22	6:F:91:LYS:H	1.48	0.62
11:k:43:LEU:HD13	11:k:46:LYS:HB3	1.81	0.62
4:D:64:SER:O	4:D:65:SER:HB3	2.00	0.62
3:c:159:ILE:HD11	3:c:165:MET:HB3	1.81	0.62
2:B:303:LEU:HD11	3:C:117:ILE:HG12	1.82	0.61
3:C:156:LEU:HD21	3:C:271:VAL:HG22	1.81	0.61
11:K:4:VAL:HG13	11:K:10:PRO:HG2	1.83	0.61
9:i:20:THR:HA	9:i:23:LEU:HB2	1.83	0.61
11:k:31:GLN:H	11:k:34:LEU:HD13	1.65	0.61
7:G:110:LYS:HB2	10:j:8:PRO:HD2	1.83	0.61
4:d:337:LEU:HB3	4:d:368:MET:HE1	1.82	0.60
3:c:138:SER:HB3	3:c:143:SER:HB3	1.81	0.60
4:D:383:ALA:HB3	4:D:442:ARG:HG3	1.83	0.60
5:E:115:THR:HG23	5:E:117:GLU:H	1.67	0.60
5:e:115:THR:HG23	5:e:117:GLU:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:159:ILE:HG21	3:C:165:MET:HG3	1.82	0.59
11:k:4:VAL:HG13	11:k:10:PRO:HG2	1.83	0.59
14:a:405:PEE:H11	15:a:406:CDL:H141	1.85	0.58
4:d:383:ALA:HB3	4:d:442:ARG:HG3	1.86	0.58
1:A:137:GLN:NE2	1:A:265:PRO:HB3	2.19	0.57
2:b:243:ILE:HG12	2:b:245:MET:HB3	1.86	0.57
1:A:262:LEU:HD13	3:c:223:VAL:CG1	2.34	0.57
3:C:99:SER:HA	4:D:269:ARG:HH21	1.70	0.57
3:c:158:ASP:HB2	3:c:167:PHE:HZ	1.70	0.57
9:I:24:THR:HA	9:I:28:GLY:H	1.70	0.56
5:e:167:GLN:OE1	11:k:46:LYS:HG3	2.04	0.56
4:D:102:LYS:HE3	4:D:155:SER:HB3	1.86	0.56
4:d:274:GLU:HG3	4:d:456:VAL:HB	1.88	0.56
3:C:102:SER:HB3	4:D:269:ARG:NH1	2.21	0.56
2:b:154:GLU:HA	2:b:169:PRO:HA	1.88	0.56
2:B:303:LEU:HD21	3:C:120:THR:HG23	1.88	0.55
3:C:220:LEU:HB3	1:a:141:TRP:HD1	1.70	0.55
5:E:399:GLN:HE22	5:E:407:MET:H	1.53	0.55
5:E:183:ARG:HG3	5:E:254:ARG:HB2	1.87	0.55
5:e:190:LEU:HD13	11:k:13:PRO:HD3	1.89	0.55
4:D:480:PHE:HA	9:I:17:ARG:O	2.07	0.55
5:e:399:GLN:HE22	5:e:407:MET:H	1.54	0.55
4:D:398:ALA:HB1	11:K:55:LEU:O	2.07	0.55
10:J:45:VAL:HG12	10:J:47:TYR:H	1.72	0.54
1:A:137:GLN:HE22	1:A:265:PRO:HB3	1.72	0.54
4:D:274:GLU:HG3	4:D:456:VAL:HB	1.89	0.54
5:e:168:ASN:HD21	11:k:27:ARG:HB3	1.73	0.54
10:j:21:ALA:O	10:j:24:TRP:HB3	2.06	0.54
11:k:20:ARG:HH11	11:k:48:SER:HB3	1.73	0.54
15:a:406:CDL:H512	15:a:406:CDL:H761	1.88	0.54
4:D:195:THR:HG23	4:D:268:CYS:SG	2.47	0.54
11:k:43:LEU:HD13	11:k:46:LYS:HB2	1.89	0.54
11:k:46:LYS:CG	11:k:47:ARG:H	2.20	0.54
3:C:140:MET:HB3	1:a:177:ARG:HE	1.72	0.54
9:I:23:LEU:HD22	10:J:27:VAL:HG11	1.90	0.54
5:e:214:THR:HG22	5:e:241:ARG:HD2	1.89	0.53
3:C:93:ARG:HA	8:H:25:ARG:HG3	1.91	0.53
1:a:316:MET:HA	14:a:405:PEE:H9	1.90	0.53
3:C:102:SER:HB3	4:D:269:ARG:HH12	1.72	0.53
2:B:181:PRO:O	2:B:182:ASN:HB2	2.09	0.53
3:C:111:LYS:HZ3	4:D:472:ARG:HH21	1.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:120:THR:HA	3:c:123:VAL:HG12	1.90	0.53
3:c:158:ASP:HB2	3:c:167:PHE:CZ	2.43	0.53
11:K:20:ARG:HB3	11:K:47:ARG:HD3	1.91	0.52
1:A:47:THR:HG23	1:A:79:ILE:HG23	1.91	0.52
11:k:51:CYS:C	11:k:53:GLU:H	2.18	0.52
5:E:297:PRO:HG3	11:K:31:GLN:HG2	1.92	0.52
11:k:8:SER:CB	11:k:26:LEU:HD13	2.20	0.52
1:A:262:LEU:HD11	3:c:175:PHE:HZ	1.75	0.52
3:c:167:PHE:H	3:c:173:PRO:HB3	1.74	0.52
11:k:20:ARG:NH1	11:k:48:SER:HB3	2.24	0.52
3:C:223:VAL:HB	1:a:262:LEU:HD13	1.92	0.52
3:C:265:PHE:HA	3:C:271:VAL:HB	1.92	0.52
2:b:125:CYS:HG	16:b:401:HEC:CAC	2.23	0.52
1:A:169:SER:HB2	3:c:171:GLY:HA3	1.92	0.51
15:a:406:CDL:H162	15:a:406:CDL:H111	1.93	0.51
1:a:47:THR:HG23	1:a:79:ILE:HG23	1.91	0.51
3:C:170:ARG:HD2	3:C:174:LEU:HD22	1.92	0.51
15:a:406:CDL:H512	15:a:406:CDL:H742	1.92	0.51
1:a:74:ASN:HB3	3:c:139:SER:HA	1.93	0.51
2:b:303:LEU:HG	3:c:117:ILE:HG23	1.93	0.51
9:i:17:ARG:C	9:i:19:SER:H	2.19	0.51
3:C:179:ARG:HD3	3:C:183:GLU:HG2	1.92	0.51
5:e:297:PRO:HB3	5:e:304:ASN:HD21	1.76	0.51
4:D:359:VAL:HG21	11:K:46:LYS:HD2	1.92	0.50
11:k:31:GLN:HA	11:k:34:LEU:HB2	1.92	0.50
3:C:224:PRO:HD2	3:C:234:TYR:CD1	2.47	0.50
1:a:114:ASN:HD22	15:a:407:CDL:H711	1.75	0.50
4:D:480:PHE:HB3	10:J:17:TRP:HZ3	1.76	0.50
5:E:297:PRO:HB3	5:E:304:ASN:HD21	1.76	0.50
3:c:148:ALA:HA	3:c:152:ILE:HG13	1.92	0.50
4:d:399:LEU:HB3	11:k:57:GLY:HA3	1.94	0.50
1:A:191:ALA:HB1	15:A:406:CDL:H762	1.94	0.49
11:K:47:ARG:HD2	11:K:48:SER:H	1.77	0.49
5:E:168:ASN:HD22	11:K:27:ARG:HD2	1.75	0.49
1:A:261:PRO:O	3:c:223:VAL:HG12	2.12	0.49
10:j:18:ILE:HA	10:j:21:ALA:HB3	1.93	0.49
5:E:60:ARG:HH21	5:E:122:THR:HG21	1.78	0.49
5:E:301:ARG:HB3	11:K:34:LEU:HD11	1.95	0.49
1:a:114:ASN:HD21	15:a:407:CDL:H761	1.78	0.49
4:D:225:LYS:HB3	4:D:225:LYS:HE2	1.25	0.49
2:b:88:LEU:CD2	8:h:72:ARG:HB3	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:k:20:ARG:HG2	11:k:48:SER:H	1.78	0.48
4:d:479:ARG:HE	10:j:20:THR:HG21	1.78	0.48
5:e:84:ARG:O	11:k:15:LEU:HD22	2.14	0.48
15:a:407:CDL:H532	15:a:407:CDL:HB31	1.95	0.48
2:b:88:LEU:HD21	8:h:72:ARG:NE	2.28	0.48
3:c:179:ARG:HB3	3:c:209:GLU:HA	1.95	0.48
1:A:114:ASN:HD22	15:A:406:CDL:H561	1.79	0.48
1:a:322:GLN:HE21	8:h:48:ARG:NH1	2.10	0.48
1:a:186:PRO:HA	1:a:189:ILE:HD12	1.96	0.48
3:c:102:SER:HB3	4:d:267:PRO:HB2	1.95	0.48
9:I:23:LEU:HD13	10:J:27:VAL:HG21	1.96	0.48
3:C:123:VAL:HG23	9:I:28:GLY:O	2.14	0.47
3:c:161:GLU:HA	3:c:178:HIS:HB2	1.96	0.47
3:C:130:LYS:HD2	10:J:34:TRP:HE1	1.80	0.47
3:C:177:ARG:HH22	3:C:213:LEU:HB2	1.79	0.47
2:b:182:ASN:ND2	2:b:184:GLU:HB2	2.19	0.47
3:c:218:THR:HG21	3:c:256:LEU:HB2	1.95	0.47
10:J:27:VAL:HA	10:J:30:VAL:HG12	1.97	0.47
3:c:159:ILE:CD1	3:c:165:MET:HB3	2.44	0.47
5:e:60:ARG:HH21	5:e:122:THR:HG21	1.78	0.47
1:a:89:MET:HE1	15:a:406:CDL:H772	1.97	0.46
5:e:170:GLN:HG3	5:e:339:TYR:OH	2.15	0.46
14:D:501:PEE:H23	14:D:501:PEE:H35	1.98	0.46
10:J:18:ILE:HD12	10:J:21:ALA:HB3	1.97	0.46
2:B:179:PRO:HG2	2:B:180:TYR:H	1.80	0.46
3:C:234:TYR:HB2	3:C:243:TYR:HB2	1.98	0.46
14:a:405:PEE:H69	14:a:405:PEE:H34	1.98	0.46
2:b:234:PHE:CE1	2:b:241:GLN:HB3	2.50	0.46
5:e:164:VAL:HG13	11:k:46:LYS:CG	2.38	0.46
1:A:186:PRO:HA	1:A:189:ILE:HD12	1.96	0.46
1:a:172:LYS:H	1:a:172:LYS:HG2	1.39	0.46
2:b:241:GLN:OE1	2:b:241:GLN:N	2.49	0.46
3:c:242:HIS:N	3:c:251:LYS:HG3	2.30	0.46
3:C:242:HIS:HB2	3:C:251:LYS:HB2	1.98	0.46
4:D:442:ARG:NH1	10:J:16:ASN:HD22	2.14	0.46
3:c:154:ILE:HG23	3:c:270:LEU:HB3	1.97	0.46
1:a:137:GLN:CD	1:a:141:TRP:HZ3	2.24	0.45
2:B:180:TYR:CD2	2:B:186:ALA:HB1	2.51	0.45
3:C:103:SER:HA	4:D:269:ARG:HA	1.99	0.45
3:C:172:LYS:HZ1	1:a:140:PHE:HE1	1.64	0.45
5:E:168:ASN:HD21	11:K:27:ARG:HB2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:245:MET:HB2	16:B:401:HEC:C1D	2.47	0.45
9:I:59:LYS:H	9:I:59:LYS:HG3	1.53	0.45
11:K:55:LEU:HD23	11:K:55:LEU:HA	1.73	0.45
10:j:33:VAL:HG23	10:j:38:TRP:HB3	1.98	0.45
3:C:217:CYS:H	3:C:221:GLY:HA2	1.82	0.45
3:C:224:PRO:HG2	3:C:234:TYR:HB3	1.99	0.45
11:K:43:LEU:H	11:K:43:LEU:HG	1.59	0.45
1:a:234:PHE:HD1	15:a:406:CDL:H722	1.81	0.45
4:D:480:PHE:CD2	9:I:17:ARG:HB3	2.51	0.45
3:c:249:ILE:HG12	3:c:254:ALA:HB3	1.99	0.45
2:B:228:LEU:HD23	2:B:228:LEU:HA	1.74	0.44
3:c:236:CYS:HB2	3:c:241:SER:HB3	1.99	0.44
1:A:18:PHE:CB	14:D:501:PEE:H38	2.48	0.44
3:C:220:LEU:HB3	1:a:141:TRP:NE1	2.33	0.44
4:D:480:PHE:HD2	9:I:17:ARG:HB3	1.82	0.44
3:c:121:THR:O	3:c:125:VAL:HB	2.17	0.44
3:C:140:MET:CB	1:a:177:ARG:HE	2.31	0.44
11:K:15:LEU:HG	11:K:16:SER:N	2.32	0.44
14:D:501:PEE:H40	14:D:501:PEE:H34	1.45	0.44
1:a:260:ASN:HB3	1:a:263:ASN:OD1	2.18	0.44
3:c:154:ILE:HG23	3:c:270:LEU:CB	2.48	0.44
3:c:158:ASP:O	3:c:159:ILE:HG13	2.17	0.44
10:J:24:TRP:HA	10:J:27:VAL:HG23	1.99	0.44
2:b:87:ASP:HB2	2:b:88:LEU:HD23	1.99	0.44
1:A:310:SER:HB2	1:A:370:SER:HB3	2.00	0.44
2:b:229:ARG:HE	2:b:229:ARG:HB2	1.61	0.44
14:A:405:PEE:H27	14:A:405:PEE:H21	1.42	0.43
2:B:303:LEU:HD12	2:B:303:LEU:HA	1.81	0.43
1:A:213:SER:HB3	7:G:67:LEU:HD21	2.01	0.43
3:c:130:LYS:HG3	3:c:131:ASN:OD1	2.18	0.43
3:c:151:LYS:HD3	3:c:170:ARG:HD2	2.01	0.43
14:a:405:PEE:H32	14:a:405:PEE:H25	1.87	0.43
3:C:99:SER:HA	4:D:269:ARG:HD2	2.00	0.43
2:B:182:ASN:HA	2:B:183:PRO:HD3	1.83	0.43
6:f:50:LEU:HD13	6:f:70:GLU:HB3	2.01	0.43
6:F:50:LEU:HD13	6:F:70:GLU:HB3	2.00	0.43
9:I:17:ARG:H	9:I:17:ARG:HG2	1.43	0.43
2:b:195:PRO:HA	2:b:196:PRO:HD3	1.83	0.42
1:A:322:GLN:HE21	8:H:48:ARG:NH1	2.16	0.42
2:B:182:ASN:OD1	2:b:161:GLU:HA	2.18	0.42
4:D:278:ARG:NH2	4:D:278:ARG:HB2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:233:VAL:O	5:E:236:ARG:HB2	2.19	0.42
9:I:30:LEU:HD11	10:J:30:VAL:HG22	1.99	0.42
1:a:310:SER:HB2	1:a:370:SER:HB3	2.00	0.42
3:c:125:VAL:HG12	9:i:25:ILE:HG22	2.00	0.42
2:b:159:PRO:HD3	2:b:165:MET:HE2	2.02	0.42
2:B:187:ARG:H	2:B:187:ARG:HG2	1.54	0.42
1:a:158:THR:HA	1:a:161:VAL:HG12	2.02	0.42
2:b:125:CYS:SG	16:b:401:HEC:C3C	3.07	0.42
7:G:71:MET:HE2	7:G:71:MET:HB3	1.98	0.42
8:H:45:CYS:SG	8:H:46:ILE:N	2.93	0.42
14:D:501:PEE:H72	14:D:501:PEE:H66	1.68	0.42
1:a:138:MET:HB2	1:a:255:ASN:ND2	2.35	0.42
5:e:379:LYS:HG2	5:e:413:LEU:HG	2.02	0.42
1:A:158:THR:HA	1:A:161:VAL:HG12	2.02	0.42
2:B:236:PRO:HB3	6:F:72:PHE:HE1	1.84	0.42
3:C:177:ARG:HB2	3:C:179:ARG:CZ	2.50	0.42
3:c:127:TYR:C	3:c:129:ALA:N	2.78	0.42
4:d:269:ARG:NH1	4:d:269:ARG:HG3	2.33	0.42
4:D:110:GLU:HG3	5:E:299:VAL:HG21	2.02	0.42
5:E:379:LYS:HG2	5:E:413:LEU:HG	2.02	0.42
2:b:90:LEU:HD12	2:b:90:LEU:HA	1.89	0.42
3:c:123:VAL:HA	9:i:28:GLY:O	2.19	0.41
5:e:45:ASN:HD21	5:e:238:LEU:HG	1.84	0.41
6:f:47:ARG:HD2	6:f:47:ARG:HA	1.86	0.41
10:J:23:MET:HE3	10:J:23:MET:HB3	1.69	0.41
11:K:20:ARG:HE	11:K:48:SER:HB3	1.85	0.41
11:K:24:GLY:HA3	11:K:27:ARG:HG2	2.02	0.41
3:c:122:THR:CG2	9:i:24:THR:HB	2.50	0.41
3:C:225:ILE:HD11	3:C:235:TYR:HD1	1.85	0.41
5:E:45:ASN:HD21	5:E:238:LEU:HG	1.84	0.41
1:A:138:MET:HB2	1:A:255:ASN:ND2	2.36	0.41
1:a:316:MET:HG3	14:a:405:PEE:H9	2.02	0.41
9:i:63:LYS:HD3	9:i:63:LYS:N	2.35	0.41
11:k:50:LEU:C	11:k:52:ARG:H	2.28	0.41
14:D:501:PEE:O1P	14:D:501:PEE:H11	2.21	0.41
3:c:127:TYR:C	3:c:129:ALA:H	2.29	0.41
8:h:80:ASN:HD22	8:h:80:ASN:HA	1.66	0.41
9:i:17:ARG:H	9:i:17:ARG:HG3	1.57	0.41
2:B:136:LEU:HD23	2:B:140:CYS:SG	2.61	0.41
5:E:85:LEU:HD22	11:K:15:LEU:HD13	2.01	0.41
6:F:47:ARG:HA	6:F:47:ARG:HD2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:31:GLN:OE1	11:K:34:LEU:HG	2.21	0.41
3:c:125:VAL:CG1	9:i:25:ILE:HG22	2.50	0.41
1:A:137:GLN:HG3	1:A:254:ASP:O	2.21	0.41
2:B:263:THR:HG1	6:F:28:ASP:N	2.19	0.41
5:E:301:ARG:CB	11:K:34:LEU:HD11	2.50	0.41
10:J:18:ILE:HA	10:J:21:ALA:HB3	2.02	0.41
11:K:46:LYS:HE3	11:K:49:PHE:CD2	2.56	0.41
9:i:62:ASN:C	9:i:63:LYS:HD3	2.45	0.41
3:C:140:MET:HB3	1:a:177:ARG:NE	2.35	0.41
1:a:260:ASN:CG	1:a:263:ASN:H	2.29	0.41
4:d:104:ARG:HH12	4:d:146:LEU:HD12	1.86	0.41
5:E:171:ALA:HA	11:K:11:PHE:CE2	2.55	0.40
2:b:134:ARG:HH12	3:c:146:VAL:HG12	1.86	0.40
2:b:168:ARG:HH11	2:b:169:PRO:HD2	1.86	0.40
3:C:152:ILE:HG21	3:C:272:ILE:HB	2.03	0.40
2:b:181:PRO:HG2	2:b:185:ALA:HB3	2.03	0.40
2:b:306:ALA:HB3	3:c:117:ILE:HG21	2.03	0.40
3:c:212:ILE:HD12	3:c:261:PRO:HG2	2.02	0.40
11:k:47:ARG:HH21	11:k:49:PHE:HA	1.87	0.40
11:K:34:LEU:HD22	11:K:34:LEU:HA	1.89	0.40
9:I:23:LEU:HD23	9:I:23:LEU:HA	1.91	0.40
2:b:168:ARG:HD2	2:b:169:PRO:HD2	2.03	0.40
3:c:138:SER:O	3:c:139:SER:C	2.60	0.40
3:C:215:GLY:O	3:C:223:VAL:HG13	2.22	0.40
4:D:64:SER:HB2	4:D:66:GLN:HE21	1.86	0.40
1:a:172:LYS:C	1:a:174:THR:H	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	376/378 (100%)	370 (98%)	6 (2%)	0	100	100
1	a	376/378 (100%)	368 (98%)	8 (2%)	0	100	100
2	B	239/241 (99%)	209 (87%)	27 (11%)	3 (1%)	9	9
2	b	237/241 (98%)	210 (89%)	24 (10%)	3 (1%)	9	9
3	C	192/196 (98%)	164 (85%)	28 (15%)	0	100	100
3	c	194/196 (99%)	148 (76%)	46 (24%)	0	100	100
4	D	443/446 (99%)	430 (97%)	13 (3%)	0	100	100
4	d	444/446 (100%)	420 (95%)	24 (5%)	0	100	100
5	E	416/418 (100%)	405 (97%)	11 (3%)	0	100	100
5	e	416/418 (100%)	405 (97%)	10 (2%)	1 (0%)	43	53
6	F	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
6	f	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
7	G	104/106 (98%)	103 (99%)	1 (1%)	0	100	100
7	g	104/106 (98%)	103 (99%)	1 (1%)	0	100	100
8	H	69/79 (87%)	66 (96%)	3 (4%)	0	100	100
8	h	77/79 (98%)	70 (91%)	7 (9%)	0	100	100
9	I	60/62 (97%)	47 (78%)	13 (22%)	0	100	100
9	i	60/62 (97%)	48 (80%)	12 (20%)	0	100	100
10	J	47/52 (90%)	44 (94%)	3 (6%)	0	100	100
10	j	49/52 (94%)	45 (92%)	4 (8%)	0	100	100
11	K	55/57 (96%)	42 (76%)	13 (24%)	0	100	100
11	k	55/57 (96%)	40 (73%)	15 (27%)	0	100	100
All	All	4137/4198 (98%)	3856 (93%)	274 (7%)	7 (0%)	44	53

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	b	241	GLN
2	B	179	PRO
2	B	185	ALA
5	e	185	ALA
2	b	239	PRO
2	B	182	ASN
2	b	179	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	331/331 (100%)	324 (98%)	7 (2%)	47	60
1	a	331/331 (100%)	322 (97%)	9 (3%)	39	52
2	B	206/206 (100%)	198 (96%)	8 (4%)	28	40
2	b	204/206 (99%)	196 (96%)	8 (4%)	28	40
3	C	164/166 (99%)	153 (93%)	11 (7%)	15	19
3	c	165/166 (99%)	140 (85%)	25 (15%)	3	2
4	D	371/372 (100%)	365 (98%)	6 (2%)	55	68
4	d	372/372 (100%)	366 (98%)	6 (2%)	55	68
5	E	327/328 (100%)	322 (98%)	5 (2%)	57	69
5	e	327/328 (100%)	320 (98%)	7 (2%)	47	60
6	F	61/61 (100%)	47 (77%)	14 (23%)	1	0
6	f	61/61 (100%)	48 (79%)	13 (21%)	1	0
7	G	95/95 (100%)	94 (99%)	1 (1%)	65	75
7	g	95/95 (100%)	94 (99%)	1 (1%)	65	75
8	H	65/70 (93%)	65 (100%)	0	100	100
8	h	70/70 (100%)	69 (99%)	1 (1%)	59	70
9	I	50/50 (100%)	37 (74%)	13 (26%)	0	0
9	i	50/50 (100%)	37 (74%)	13 (26%)	0	0
10	J	40/42 (95%)	40 (100%)	0	100	100
10	j	41/42 (98%)	41 (100%)	0	100	100
11	K	44/44 (100%)	31 (70%)	13 (30%)	0	0
11	k	44/44 (100%)	33 (75%)	11 (25%)	0	0
All	All	3514/3530 (100%)	3342 (95%)	172 (5%)	24	31

All (172) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	SER
1	A	137	GLN
1	A	150	LEU
1	A	171	ASP
1	A	177	ARG
1	A	260	ASN
1	A	262	LEU
2	B	143	GLU
2	B	144	GLU
2	B	162	ASP
2	B	165	MET
2	B	187	ARG
2	B	212	VAL
2	B	228	LEU
2	B	245	MET
3	C	101	LYS
3	C	103	SER
3	C	104	LYS
3	C	120	THR
3	C	140	MET
3	C	180	THR
3	C	201	ASP
3	C	216	VAL
3	C	222	CYS
3	C	225	ILE
3	C	227	ASN
4	D	64	SER
4	D	195	THR
4	D	225	LYS
4	D	269	ARG
4	D	276	ARG
4	D	278	ARG
5	E	77	LEU
5	E	123	VAL
5	E	236	ARG
5	E	250	LYS
5	E	390	GLU
6	F	39	GLN
6	F	41	GLU
6	F	44	ILE
6	F	49	ARG
6	F	51	GLU
6	F	56	ARG

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Mol	Chain	Res	Type
6	F	58	SER
6	F	59	SER
6	F	61	SER
6	F	62	GLN
6	F	63	THR
6	F	65	GLU
6	F	68	THR
6	F	70	GLU
7	G	67	LEU
9	I	5	THR
9	I	6	LEU
9	I	10	LEU
9	I	12	SER
9	I	14	LEU
9	I	17	ARG
9	I	19	SER
9	I	20	THR
9	I	37	ASP
9	I	38	GLN
9	I	59	LYS
9	I	62	ASN
9	I	63	LYS
11	K	4	VAL
11	K	14	VAL
11	K	22	VAL
11	K	27	ARG
11	K	28	PRO
11	K	34	LEU
11	K	38	SER
11	K	40	SER
11	K	41	PRO
11	K	43	LEU
11	K	52	ARG
11	K	53	GLU
11	K	55	LEU
1	a	2	THR
1	a	64	SER
1	a	150	LEU
1	a	169	SER
1	a	170	VAL
1	a	171	ASP
1	a	172	LYS

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Mol	Chain	Res	Type
1	a	177	ARG
1	a	260	ASN
2	b	86	THR
2	b	87	ASP
2	b	88	LEU
2	b	89	GLU
2	b	124	SER
2	b	179	PRO
2	b	184	GLU
2	b	318	ARG
3	c	93	ARG
3	c	96	VAL
3	c	100	THR
3	c	101	LYS
3	c	103	SER
3	c	118	THR
3	c	120	THR
3	c	125	VAL
3	c	127	TYR
3	c	130	LYS
3	c	138	SER
3	c	139	SER
3	c	143	SER
3	c	145	ASP
3	c	146	VAL
3	c	147	LEU
3	c	155	LYS
3	c	156	LEU
3	c	158	ASP
3	c	159	ILE
3	c	179	ARG
3	c	180	THR
3	c	183	GLU
3	c	217	CYS
3	c	238	CYS
4	d	269	ARG
4	d	289	ILE
4	d	423	ARG
4	d	442	ARG
4	d	451	ASP
4	d	452	GLN
5	e	77	LEU

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Mol	Chain	Res	Type
5	e	123	VAL
5	e	170	GLN
5	e	186	LEU
5	e	241	ARG
5	e	250	LYS
5	e	390	GLU
6	f	39	GLN
6	f	41	GLU
6	f	44	ILE
6	f	49	ARG
6	f	51	GLU
6	f	56	ARG
6	f	58	SER
6	f	59	SER
6	f	61	SER
6	f	63	THR
6	f	65	GLU
6	f	68	THR
6	f	70	GLU
7	g	67	LEU
8	h	9	THR
9	i	5	THR
9	i	6	LEU
9	i	10	LEU
9	i	12	SER
9	i	14	LEU
9	i	17	ARG
9	i	19	SER
9	i	20	THR
9	i	23	LEU
9	i	24	THR
9	i	37	ASP
9	i	62	ASN
9	i	63	LYS
11	k	4	VAL
11	k	7	ARG
11	k	15	LEU
11	k	22	VAL
11	k	44	ASP
11	k	47	ARG
11	k	48	SER
11	k	51	CYS

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Mol	Chain	Res	Type
11	k	52	ARG
11	k	53	GLU
11	k	54	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	137	GLN
1	A	255	ASN
1	A	267	HIS
2	B	156	GLN
2	B	206	HIS
2	B	241	GLN
2	B	266	GLN
3	C	219	HIS
4	D	66	GLN
4	D	87	ASN
4	D	95	HIS
4	D	222	GLN
4	D	305	GLN
4	D	323	HIS
4	D	339	GLN
4	D	375	GLN
5	E	75	ASN
5	E	155	GLN
5	E	268	HIS
5	E	290	GLN
5	E	399	GLN
6	F	39	GLN
8	H	29	HIS
9	I	48	ASN
10	J	16	ASN
1	a	54	HIS
1	a	74	ASN
1	a	114	ASN
1	a	255	ASN
1	a	260	ASN
1	a	267	HIS
2	b	206	HIS
2	b	283	HIS
2	b	285	HIS

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Mol	Chain	Res	Type
2	b	310	HIS
3	c	199	GLN
3	c	257	ASN
4	d	49	GLN
4	d	55	ASN
4	d	87	ASN
4	d	95	HIS
4	d	222	GLN
4	d	223	HIS
4	d	286	HIS
4	d	323	HIS
4	d	375	GLN
4	d	452	GLN
4	d	469	ASN
5	e	75	ASN
5	e	155	GLN
5	e	168	ASN
5	e	170	GLN
5	e	268	HIS
5	e	290	GLN
5	e	399	GLN
6	f	39	GLN
8	h	80	ASN
9	i	58	HIS
10	j	16	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

18 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	A1D6O	a	402	-	30,30,30	1.49	4 (13%)	40,44,44	3.97	17 (42%)
17	FES	C	301	-	0,4,4	-	-	-	-	-
14	PEE	D	501	-	48,48,50	0.42	0	51,53,55	0.61	2 (3%)
15	CDL	a	406	-	63,63,99	1.12	7 (11%)	69,75,111	1.08	4 (5%)
15	CDL	a	407	-	63,63,99	1.08	7 (11%)	69,75,111	1.13	6 (8%)
15	CDL	A	406	-	63,63,99	1.10	8 (12%)	69,75,111	1.10	4 (5%)
14	PEE	A	405	-	44,44,50	0.80	2 (4%)	47,49,55	0.84	2 (4%)
13	HEM	A	403	1	50,50,50	1.60	10 (20%)	67,82,82	1.29	8 (11%)
16	HEC	b	401	2	46,50,50	2.53	23 (50%)	58,82,82	2.15	23 (39%)
12	A1D6O	A	402	-	30,30,30	1.48	4 (13%)	40,44,44	4.01	16 (40%)
17	FES	c	301	-	0,4,4	-	-	-	-	-
12	A1D6O	A	401	-	30,30,30	1.64	4 (13%)	40,44,44	4.04	15 (37%)
14	PEE	a	405	-	48,48,50	0.82	2 (4%)	51,53,55	0.85	2 (3%)
16	HEC	B	401	2	46,50,50	2.53	23 (50%)	58,82,82	2.16	24 (41%)
13	HEM	a	404	1	50,50,50	1.61	10 (20%)	67,82,82	1.29	9 (13%)
12	A1D6O	a	401	-	30,30,30	1.64	4 (13%)	40,44,44	4.04	15 (37%)
13	HEM	A	404	1	50,50,50	1.64	6 (12%)	67,82,82	1.71	15 (22%)
13	HEM	a	403	1	50,50,50	1.60	6 (12%)	67,82,82	1.30	9 (13%)

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	A1D6O	a	402	-	-	3/9/9/9	0/4/4/4
17	FES	C	301	-	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	PEE	D	501	-	-	32/52/52/54	-
15	CDL	a	406	-	-	43/74/74/110	-
15	CDL	a	407	-	-	41/74/74/110	-
15	CDL	A	406	-	-	33/74/74/110	-
14	PEE	A	405	-	-	23/48/48/54	-
13	HEM	A	403	1	-	2/14/54/54	-
16	HEC	b	401	2	-	0/14/54/54	-
12	A1D6O	A	402	-	-	3/9/9/9	0/4/4/4
17	FES	c	301	-	-	-	0/1/1/1
12	A1D6O	A	401	-	-	1/9/9/9	0/4/4/4
14	PEE	a	405	-	-	27/52/52/54	-
16	HEC	B	401	2	-	0/14/54/54	-
13	HEM	a	404	1	-	2/14/54/54	-
12	A1D6O	a	401	-	-	1/9/9/9	0/4/4/4
13	HEM	A	404	1	-	5/14/54/54	-
13	HEM	a	403	1	-	5/14/54/54	-

All (120) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	b	401	HEC	CHA-C1A	5.51	1.49	1.38
16	B	401	HEC	CHA-C1A	5.49	1.49	1.38
13	A	404	HEM	FE-ND	5.23	2.11	1.94
13	a	403	HEM	FE-ND	4.85	2.09	1.94
16	b	401	HEC	C2A-C3A	4.78	1.47	1.36
16	B	401	HEC	C2A-C3A	4.71	1.46	1.36
12	A	401	A1D6O	C08-S10	4.70	1.83	1.74
12	a	401	A1D6O	C08-S10	4.68	1.83	1.74
12	A	401	A1D6O	C08-S07	-4.60	1.69	1.75
12	a	401	A1D6O	C08-S07	-4.58	1.69	1.75
16	b	401	HEC	CHB-C4A	4.57	1.47	1.38
16	B	401	HEC	CHB-C4A	4.52	1.47	1.38
13	A	403	HEM	FE-NC	4.49	2.10	1.95
12	A	402	A1D6O	C08-S07	-4.45	1.70	1.75
12	a	402	A1D6O	C08-S07	-4.43	1.70	1.75
13	A	404	HEM	FE-NB	4.42	2.08	1.94
13	a	404	HEM	FE-NC	4.39	2.09	1.95
16	b	401	HEC	CHA-C4D	4.31	1.49	1.39
13	a	404	HEM	FE-ND	4.24	2.07	1.94
16	B	401	HEC	CAC-C3C	4.24	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	b	401	HEC	CAC-C3C	4.22	1.48	1.35
16	B	401	HEC	CHA-C4D	4.21	1.48	1.39
13	a	403	HEM	FE-NC	4.17	2.08	1.95
13	A	403	HEM	FE-ND	4.16	2.07	1.94
13	a	403	HEM	FE-NB	4.15	2.07	1.94
13	a	404	HEM	FE-NA	4.14	2.08	1.95
16	B	401	HEC	CAB-C3B	4.10	1.48	1.35
16	b	401	HEC	CAB-C3B	4.06	1.48	1.35
12	A	402	A1D6O	C08-S10	4.00	1.81	1.74
13	A	403	HEM	FE-NA	3.99	2.08	1.95
12	a	402	A1D6O	C08-S10	3.97	1.81	1.74
16	B	401	HEC	CHB-C1B	3.90	1.48	1.39
16	b	401	HEC	CHB-C1B	3.90	1.48	1.39
13	A	404	HEM	FE-NC	3.88	2.08	1.95
16	B	401	HEC	CHD-C4C	3.83	1.45	1.38
16	b	401	HEC	C4C-NC	-3.60	1.32	1.39
16	b	401	HEC	CHD-C4C	3.60	1.45	1.38
16	B	401	HEC	CHC-C4B	3.53	1.45	1.38
15	a	406	CDL	OA6-CA4	-3.51	1.38	1.46
16	B	401	HEC	C4C-NC	-3.50	1.33	1.39
16	b	401	HEC	CHC-C4B	3.50	1.45	1.38
16	B	401	HEC	CHC-C1C	3.45	1.47	1.39
16	b	401	HEC	CHC-C1C	3.39	1.47	1.39
13	A	403	HEM	CAC-C3C	3.22	1.56	1.47
13	a	404	HEM	CAC-C3C	3.21	1.56	1.47
13	a	404	HEM	CAB-C3B	3.16	1.55	1.47
13	A	403	HEM	CAB-C3B	3.15	1.55	1.47
16	b	401	HEC	C3D-C2D	3.14	1.47	1.38
13	a	403	HEM	CAB-C3B	3.13	1.55	1.47
16	B	401	HEC	C4B-NB	-3.12	1.33	1.39
13	A	404	HEM	CAB-C3B	3.11	1.55	1.47
16	b	401	HEC	C4B-NB	-3.10	1.33	1.39
16	B	401	HEC	CHD-C1D	3.03	1.46	1.39
16	B	401	HEC	C3D-C2D	3.03	1.46	1.38
13	a	403	HEM	CAC-C3C	3.02	1.55	1.47
13	A	404	HEM	CAC-C3C	3.01	1.55	1.47
16	b	401	HEC	CHD-C1D	3.01	1.46	1.39
15	a	407	CDL	OA6-CA4	-2.88	1.39	1.46
16	b	401	HEC	C1D-ND	-2.80	1.34	1.39
16	B	401	HEC	O2D-CGD	-2.75	1.21	1.30
16	b	401	HEC	C1A-NA	-2.71	1.34	1.39
15	a	406	CDL	OB6-CB4	-2.70	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	b	401	HEC	O2D-CGD	-2.70	1.21	1.30
16	B	401	HEC	C1D-ND	-2.70	1.34	1.39
16	b	401	HEC	C4A-NA	-2.66	1.34	1.39
16	B	401	HEC	C1A-NA	-2.65	1.34	1.39
15	a	407	CDL	OB6-CB5	2.65	1.41	1.34
16	B	401	HEC	C4A-NA	-2.62	1.34	1.39
15	a	406	CDL	OA8-CA6	-2.61	1.39	1.45
16	B	401	HEC	C1C-NC	-2.58	1.34	1.39
14	A	405	PEE	C12-C11	-2.57	1.42	1.52
14	a	405	PEE	C12-C11	-2.57	1.42	1.52
16	b	401	HEC	C1C-NC	-2.54	1.34	1.39
12	a	401	A1D6O	O24-C23	-2.54	1.17	1.22
12	A	401	A1D6O	O24-C23	-2.53	1.17	1.22
15	A	406	CDL	OB6-CB4	-2.48	1.40	1.46
15	A	406	CDL	OA8-CA7	2.47	1.40	1.33
12	A	401	A1D6O	C11-C12	2.47	1.55	1.51
13	A	403	HEM	FE-NB	2.46	2.02	1.94
13	a	404	HEM	FE-NB	2.45	2.02	1.94
12	a	401	A1D6O	C11-C12	2.45	1.55	1.51
15	A	406	CDL	OA6-CA4	-2.43	1.40	1.46
15	A	406	CDL	OA6-CA5	2.40	1.41	1.34
12	a	402	A1D6O	O24-C23	-2.39	1.18	1.22
16	b	401	HEC	C4D-ND	-2.38	1.35	1.39
15	A	406	CDL	OB8-CB6	-2.37	1.39	1.45
12	A	402	A1D6O	O24-C23	-2.35	1.18	1.22
15	a	406	CDL	OB8-CB7	2.35	1.40	1.33
15	A	406	CDL	OB8-CB7	2.35	1.40	1.33
15	a	407	CDL	OB8-CB7	2.34	1.40	1.33
16	B	401	HEC	C4D-ND	-2.32	1.35	1.39
14	a	405	PEE	O4-C10	-2.32	1.15	1.22
15	a	407	CDL	OA8-CA7	2.23	1.39	1.33
15	A	406	CDL	OA8-CA6	-2.23	1.40	1.45
15	a	406	CDL	OB6-CB5	2.22	1.40	1.34
13	a	404	HEM	CMD-C2D	2.22	1.55	1.50
15	a	407	CDL	OA8-CA6	-2.20	1.40	1.45
12	a	402	A1D6O	C13-N19	2.20	1.46	1.43
13	A	403	HEM	CMD-C2D	2.18	1.55	1.50
16	b	401	HEC	C4D-C3D	2.18	1.48	1.44
15	A	406	CDL	OB6-CB5	2.18	1.40	1.34
16	b	401	HEC	C1B-C2B	2.17	1.48	1.43
12	A	402	A1D6O	C13-N19	2.17	1.46	1.43
15	a	407	CDL	OA6-CA5	2.15	1.40	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	405	PEE	O4-C10	-2.14	1.16	1.22
13	a	404	HEM	CMA-C3A	2.13	1.55	1.50
13	A	403	HEM	CMA-C3A	2.13	1.55	1.50
16	B	401	HEC	O2A-CGA	-2.12	1.23	1.30
13	A	403	HEM	CMB-C2B	2.12	1.55	1.50
16	b	401	HEC	O2A-CGA	-2.11	1.23	1.30
16	B	401	HEC	C1B-C2B	2.11	1.48	1.43
13	A	404	HEM	CMC-C2C	2.11	1.55	1.50
13	a	404	HEM	CMB-C2B	2.10	1.55	1.50
13	a	403	HEM	CMC-C2C	2.10	1.55	1.50
15	a	406	CDL	OA8-CA7	2.09	1.39	1.33
16	B	401	HEC	C4D-C3D	2.06	1.48	1.44
13	a	404	HEM	CMC-C2C	2.05	1.55	1.50
15	a	407	CDL	OB8-CB6	-2.04	1.40	1.45
15	a	406	CDL	OB8-CB6	-2.02	1.40	1.45
13	A	403	HEM	CMC-C2C	2.01	1.54	1.50

All (171) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A	402	A1D6O	N19-C23-N22	15.79	108.67	101.46
12	a	402	A1D6O	N19-C23-N22	15.55	108.56	101.46
12	A	401	A1D6O	N19-C23-N22	15.40	108.49	101.46
12	a	401	A1D6O	N19-C23-N22	15.32	108.46	101.46
12	a	401	A1D6O	C04-S07-C08	11.02	97.93	88.77
12	A	401	A1D6O	C04-S07-C08	10.97	97.89	88.77
12	A	402	A1D6O	C04-S07-C08	9.71	96.85	88.77
12	a	402	A1D6O	C04-S07-C08	9.69	96.82	88.77
12	a	401	A1D6O	S07-C08-N09	-8.31	106.45	116.34
12	A	401	A1D6O	S07-C08-N09	-8.28	106.49	116.34
12	A	402	A1D6O	C23-N19-N20	-8.14	105.13	110.53
12	a	402	A1D6O	C23-N19-N20	-7.99	105.23	110.53
12	A	402	A1D6O	S07-C08-N09	-7.77	107.10	116.34
12	a	402	A1D6O	S07-C08-N09	-7.73	107.14	116.34
12	a	401	A1D6O	C05-C04-S07	-6.77	104.62	109.71
12	A	401	A1D6O	C05-C04-S07	-6.76	104.64	109.71
12	A	401	A1D6O	C23-N19-N20	-6.30	106.35	110.53
12	a	401	A1D6O	C23-N19-N20	-6.29	106.36	110.53
12	A	402	A1D6O	C05-C04-S07	-5.80	105.35	109.71
12	a	402	A1D6O	C05-C04-S07	-5.80	105.36	109.71
12	A	401	A1D6O	C11-S10-C08	5.63	112.14	102.46
12	a	401	A1D6O	C11-S10-C08	5.63	112.14	102.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	404	HEM	CAD-C3D-C4D	5.62	134.49	124.70
12	a	402	A1D6O	C14-C13-N19	-5.06	112.23	118.98
12	A	402	A1D6O	C14-C13-N19	-5.05	112.25	118.98
13	A	404	HEM	CAD-C3D-C2D	-4.94	118.62	127.87
16	b	401	HEC	CBD-CAD-C3D	-4.80	99.26	112.53
16	B	401	HEC	CBD-CAD-C3D	-4.75	99.40	112.53
16	B	401	HEC	CAA-CBA-CGA	-4.45	101.88	113.67
16	B	401	HEC	C3D-C4D-ND	4.34	114.96	110.15
16	b	401	HEC	CAA-CBA-CGA	-4.24	102.43	113.67
16	b	401	HEC	C3D-C4D-ND	4.23	114.85	110.15
16	b	401	HEC	C2C-C1C-NC	4.20	116.88	110.14
16	B	401	HEC	C2C-C1C-NC	4.15	116.80	110.14
16	B	401	HEC	C2A-C1A-NA	4.14	114.32	110.32
15	A	406	CDL	OB6-CB5-C51	4.11	120.37	111.48
16	b	401	HEC	C2A-C1A-NA	3.92	114.10	110.32
16	b	401	HEC	C2D-C1D-ND	3.87	116.34	110.14
15	a	406	CDL	OB6-CB5-C51	3.83	119.77	111.48
16	B	401	HEC	C2D-C1D-ND	3.80	116.23	110.14
15	a	407	CDL	OB6-CB5-C51	3.80	119.69	111.48
12	A	402	A1D6O	C03-C04-S07	3.75	135.43	126.07
12	a	402	A1D6O	C03-C04-S07	3.74	135.40	126.07
16	b	401	HEC	C1D-C2D-C3D	-3.71	102.56	106.82
12	A	401	A1D6O	C03-C04-S07	3.71	135.32	126.07
12	a	401	A1D6O	C03-C04-S07	3.70	135.32	126.07
16	B	401	HEC	C1D-C2D-C3D	-3.69	102.59	106.82
15	A	406	CDL	OA6-CA5-C11	3.55	119.15	111.48
15	a	407	CDL	OA6-CA5-C11	3.54	119.13	111.48
12	a	401	A1D6O	C12-C11-S10	3.53	119.64	109.83
16	B	401	HEC	C2B-C1B-NB	3.51	115.77	110.14
12	A	401	A1D6O	C12-C11-S10	3.51	119.58	109.83
16	b	401	HEC	C2B-C1B-NB	3.43	115.64	110.14
13	A	404	HEM	CHA-C4D-C3D	3.31	131.33	125.23
13	a	403	HEM	C2A-C1A-NA	-3.30	106.49	110.15
13	A	404	HEM	C2A-C1A-NA	-3.25	106.55	110.15
16	b	401	HEC	C3A-C4A-NA	3.23	115.61	109.64
12	A	402	A1D6O	C05-N09-C08	3.22	116.28	110.14
16	B	401	HEC	C3A-C4A-NA	3.21	115.58	109.64
12	a	401	A1D6O	C05-N09-C08	3.20	116.23	110.14
14	a	405	PEE	O2P-P-O4P	-3.20	93.08	107.57
13	a	404	HEM	C1B-NB-C4B	3.19	108.99	105.21
12	A	401	A1D6O	C05-N09-C08	3.19	116.21	110.14
16	b	401	HEC	C4A-C3A-C2A	-3.19	102.25	106.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	a	402	A1D6O	C05-N09-C08	3.17	116.18	110.14
13	A	403	HEM	C1B-NB-C4B	3.17	108.96	105.21
12	a	402	A1D6O	S07-C08-S10	3.13	126.91	118.20
12	A	402	A1D6O	S07-C08-S10	3.13	126.88	118.20
12	a	402	A1D6O	C25-N22-N21	3.12	126.21	121.08
12	A	402	A1D6O	C25-N22-N21	3.12	126.20	121.08
12	a	401	A1D6O	C25-N22-N21	3.11	126.18	121.08
12	A	401	A1D6O	C25-N22-N21	3.09	126.16	121.08
16	B	401	HEC	C4A-C3A-C2A	-3.04	102.46	106.97
14	a	405	PEE	O4P-P-O1P	3.02	120.92	108.94
13	A	404	HEM	C4D-ND-C1D	3.01	108.77	105.21
13	a	404	HEM	C4D-ND-C1D	2.97	108.72	105.21
15	a	407	CDL	CB4-OB6-CB5	2.92	124.79	117.80
13	A	403	HEM	C4D-ND-C1D	2.91	108.65	105.21
15	a	406	CDL	OB8-CB7-C71	2.91	120.71	111.83
16	B	401	HEC	C1A-C2A-C3A	-2.89	103.31	107.11
12	a	402	A1D6O	C11-S10-C08	2.87	107.39	102.46
12	A	402	A1D6O	C11-S10-C08	2.87	107.39	102.46
12	a	402	A1D6O	C06-C01-C02	-2.85	119.42	122.13
12	A	402	A1D6O	C06-C01-C02	-2.83	119.44	122.13
13	A	404	HEM	CBD-CAD-C3D	2.81	120.29	112.53
12	A	402	A1D6O	N19-N20-N21	2.76	110.85	107.56
13	A	404	HEM	C3D-C4D-ND	-2.76	107.15	110.17
16	b	401	HEC	C4D-C3D-C2D	-2.75	102.61	106.87
12	a	402	A1D6O	C16-C17-C12	2.75	121.58	118.39
12	A	402	A1D6O	C16-C17-C12	2.74	121.57	118.39
16	b	401	HEC	C1A-C2A-C3A	-2.74	103.51	107.11
12	a	402	A1D6O	N19-N20-N21	2.69	110.77	107.56
16	B	401	HEC	C4D-C3D-C2D	-2.68	102.72	106.87
12	a	401	A1D6O	S07-C08-S10	2.67	125.62	118.20
16	b	401	HEC	CHC-C4B-C3B	-2.67	120.71	125.21
12	A	401	A1D6O	S07-C08-S10	2.66	125.60	118.20
12	a	401	A1D6O	C13-N19-N20	2.64	124.67	120.14
15	a	407	CDL	OA8-CA7-C31	2.64	119.89	111.83
15	A	406	CDL	OA8-CA7-C31	2.64	119.87	111.83
12	A	401	A1D6O	C13-N19-N20	2.63	124.64	120.14
14	A	405	PEE	O2P-P-O4P	2.58	119.25	107.57
13	a	403	HEM	C4D-ND-C1D	2.57	108.25	105.21
16	B	401	HEC	CHC-C4B-C3B	-2.57	120.88	125.21
16	b	401	HEC	CHC-C1C-C2C	-2.54	120.05	127.43
16	b	401	HEC	CMD-C2D-C3D	2.54	131.01	125.62
15	a	406	CDL	OA8-CA7-C31	2.53	119.55	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	B	401	HEC	CMC-C2C-C3C	2.53	132.50	126.55
16	B	401	HEC	CHC-C1C-C2C	-2.53	120.09	127.43
15	A	406	CDL	OB8-CB7-C71	2.53	119.54	111.83
13	a	404	HEM	C3B-C4B-NB	-2.53	107.65	109.47
13	A	403	HEM	C2A-C1A-NA	-2.52	107.36	110.15
13	a	404	HEM	C2A-C1A-NA	-2.51	107.37	110.15
15	a	406	CDL	OA6-CA5-C11	2.50	116.90	111.48
13	A	403	HEM	C3B-C4B-NB	-2.50	107.67	109.47
16	b	401	HEC	CMC-C2C-C3C	2.49	132.41	126.55
12	a	401	A1D6O	C14-C13-N19	-2.45	115.71	118.98
12	A	401	A1D6O	C14-C13-N19	-2.41	115.77	118.98
16	b	401	HEC	CHD-C1D-C2D	-2.39	120.49	127.43
12	a	401	A1D6O	C11-C12-C17	2.37	121.94	119.60
12	A	401	A1D6O	C11-C12-C17	2.37	121.94	119.60
13	a	403	HEM	C1B-NB-C4B	2.36	108.01	105.21
13	a	403	HEM	CHD-C4C-NC	2.36	127.03	124.45
16	B	401	HEC	CHD-C1D-C2D	-2.35	120.60	127.43
16	B	401	HEC	O2A-CGA-CBA	2.35	121.43	114.00
13	A	403	HEM	CMB-C2B-C1B	-2.34	121.38	125.03
13	A	404	HEM	CHD-C4C-NC	2.34	127.00	124.45
13	A	404	HEM	C1B-NB-C4B	2.33	107.96	105.21
13	a	403	HEM	C3D-C4D-ND	-2.32	107.62	110.17
14	D	501	PEE	O2P-P-O4P	-2.32	97.07	107.57
13	a	404	HEM	CMB-C2B-C1B	-2.32	121.42	125.03
12	a	401	A1D6O	C18-C17-C16	-2.31	115.82	120.28
16	b	401	HEC	O2A-CGA-CBA	2.31	121.30	114.00
13	A	404	HEM	CHA-C4D-ND	-2.30	121.52	124.37
12	A	401	A1D6O	C18-C17-C16	-2.30	115.84	120.28
14	A	405	PEE	O3P-P-O1P	-2.29	99.84	108.94
13	a	403	HEM	C4A-NA-C1A	2.29	109.55	105.82
15	a	407	CDL	OB8-CB7-C71	2.28	118.79	111.83
13	A	404	HEM	C1D-C2D-C3D	2.28	109.38	106.98
16	B	401	HEC	O1A-CGA-CBA	-2.25	115.95	123.09
13	A	404	HEM	CAC-C3C-C4C	-2.24	119.46	124.82
13	a	404	HEM	C3D-C4D-ND	-2.24	107.72	110.17
16	b	401	HEC	O1A-CGA-CBA	-2.22	116.05	123.09
13	a	403	HEM	CAC-C3C-C4C	-2.21	119.54	124.82
16	B	401	HEC	CMD-C2D-C3D	2.18	130.26	125.62
13	A	403	HEM	C3D-C4D-ND	-2.18	107.78	110.17
13	A	404	HEM	C4A-NA-C1A	2.17	109.36	105.82
13	a	404	HEM	C2D-C1D-ND	-2.17	107.39	109.90
16	b	401	HEC	CHA-C1A-NA	-2.16	122.10	124.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	a	403	HEM	C3A-C4A-NA	-2.15	106.69	110.14
15	a	407	CDL	OB6-CB4-CB3	2.15	116.07	108.34
13	A	403	HEM	C2D-C1D-ND	-2.15	107.42	109.90
16	B	401	HEC	CHA-C1A-NA	-2.14	122.12	124.45
16	B	401	HEC	CHB-C4A-C3A	-2.14	121.04	125.49
13	a	403	HEM	C3B-C2B-C1B	2.13	108.01	106.41
16	b	401	HEC	CMB-C2B-C3B	2.12	131.54	126.55
16	B	401	HEC	CMB-C2B-C3B	2.11	131.52	126.55
13	A	404	HEM	C3B-C2B-C1B	2.11	107.99	106.41
16	b	401	HEC	CHB-C4A-C3A	-2.08	121.16	125.49
13	A	404	HEM	C3A-C4A-NA	-2.06	106.84	110.14
16	B	401	HEC	CAD-C3D-C4D	2.05	128.95	124.94
12	A	402	A1D6O	C12-C11-S10	2.05	115.53	109.83
12	a	402	A1D6O	C12-C11-S10	2.04	115.50	109.83
16	b	401	HEC	CHD-C4C-C3C	-2.04	121.78	125.21
12	a	402	A1D6O	C01-C06-C05	2.03	120.57	118.45
12	A	402	A1D6O	C15-C14-C13	2.03	122.39	118.28
12	a	402	A1D6O	C15-C14-C13	2.03	122.38	118.28
16	B	401	HEC	CHB-C1B-C2B	-2.03	121.53	127.43
14	D	501	PEE	O2P-P-O1P	2.03	121.87	112.44
13	a	404	HEM	C2B-C1B-NB	-2.03	107.51	109.84
13	a	404	HEM	C4C-NC-C1C	2.02	109.12	105.82
13	A	403	HEM	C2B-C1B-NB	-2.01	107.53	109.84

There are no chirality outliers.

All (221) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	A	404	HEM	C2D-C3D-CAD-CBD
13	A	404	HEM	C4D-C3D-CAD-CBD
14	A	405	PEE	C1-O3P-P-O1P
14	A	405	PEE	C4-O4P-P-O3P
14	A	405	PEE	C4-O4P-P-O2P
14	A	405	PEE	C4-O4P-P-O1P
14	A	405	PEE	O4P-C4-C5-N
14	D	501	PEE	C11-C10-O2-C2
14	D	501	PEE	O4-C10-O2-C2
14	D	501	PEE	O2-C2-C3-O3
14	D	501	PEE	C2-C1-O3P-P
14	D	501	PEE	C1-O3P-P-O2P
14	a	405	PEE	C4-O4P-P-O3P
14	a	405	PEE	C4-O4P-P-O2P

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Mol	Chain	Res	Type	Atoms
14	a	405	PEE	C4-O4P-P-O1P
14	a	405	PEE	O4P-C4-C5-N
15	A	406	CDL	CB2-C1-CA2-OA2
15	A	406	CDL	CA2-OA2-PA1-OA4
15	A	406	CDL	CA2-OA2-PA1-OA5
15	A	406	CDL	CA3-OA5-PA1-OA2
15	a	406	CDL	CA2-OA2-PA1-OA3
15	a	406	CDL	CA2-OA2-PA1-OA5
15	a	406	CDL	CB3-OB5-PB2-OB3
15	a	406	CDL	OB6-CB4-CB6-OB8
15	a	406	CDL	OB7-CB5-OB6-CB4
15	a	406	CDL	C51-CB5-OB6-CB4
15	a	407	CDL	CB3-OB5-PB2-OB2
15	a	407	CDL	CB3-OB5-PB2-OB3
15	a	407	CDL	CB3-OB5-PB2-OB4
15	a	407	CDL	OB7-CB5-OB6-CB4
14	A	405	PEE	O5-C30-O3-C3
15	a	406	CDL	OB9-CB7-OB8-CB6
14	A	405	PEE	C31-C30-O3-C3
15	a	406	CDL	C71-CB7-OB8-CB6
15	a	407	CDL	C51-CB5-OB6-CB4
15	a	406	CDL	OA9-CA7-OA8-CA6
15	A	406	CDL	O1-C1-CA2-OA2
15	a	406	CDL	C31-CA7-OA8-CA6
15	A	406	CDL	C11-CA5-OA6-CA4
15	a	406	CDL	C11-C12-C13-C14
15	A	406	CDL	OA7-CA5-OA6-CA4
15	A	406	CDL	CA2-C1-CB2-OB2
15	a	407	CDL	CA2-C1-CB2-OB2
14	a	405	PEE	C31-C30-O3-C3
14	D	501	PEE	C21-C22-C23-C24
14	a	405	PEE	C22-C23-C24-C25
14	A	405	PEE	C15-C16-C17-C18
14	D	501	PEE	C40-C41-C42-C43
14	a	405	PEE	C14-C15-C16-C17
14	D	501	PEE	C17-C18-C19-C20
15	a	406	CDL	CB5-C51-C52-C53
14	a	405	PEE	O5-C30-O3-C3
15	A	406	CDL	O1-C1-CB2-OB2
15	a	406	CDL	O1-C1-CB2-OB2
15	a	407	CDL	O1-C1-CB2-OB2
15	a	406	CDL	CA5-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
14	D	501	PEE	C19-C20-C21-C22
14	D	501	PEE	C32-C33-C34-C35
15	A	406	CDL	CA7-C31-C32-C33
15	a	406	CDL	CA2-C1-CB2-OB2
15	a	407	CDL	CB3-CB4-OB6-CB5
14	A	405	PEE	C20-C21-C22-C23
15	a	407	CDL	C71-C72-C73-C74
15	a	407	CDL	C54-C55-C56-C57
15	A	406	CDL	C33-C34-C35-C36
14	D	501	PEE	C39-C40-C41-C42
15	a	407	CDL	C11-C12-C13-C14
14	a	405	PEE	C30-C31-C32-C33
14	D	501	PEE	C31-C32-C33-C34
15	a	406	CDL	C13-C14-C15-C16
15	a	406	CDL	C74-C75-C76-C77
14	a	405	PEE	C34-C35-C36-C37
14	D	501	PEE	C30-C31-C32-C33
15	A	406	CDL	CB7-C71-C72-C73
15	a	406	CDL	CA7-C31-C32-C33
14	A	405	PEE	C13-C14-C15-C16
14	A	405	PEE	C31-C32-C33-C34
14	D	501	PEE	C20-C21-C22-C23
15	A	406	CDL	C13-C14-C15-C16
15	a	406	CDL	C12-C13-C14-C15
15	a	406	CDL	C54-C55-C56-C57
15	a	407	CDL	C72-C73-C74-C75
14	D	501	PEE	C11-C12-C13-C14
14	A	405	PEE	C11-C12-C13-C14
14	A	405	PEE	C14-C15-C16-C17
14	a	405	PEE	C15-C16-C17-C18
14	a	405	PEE	C37-C38-C39-C40
14	D	501	PEE	C24-C25-C26-C27
15	A	406	CDL	C51-C52-C53-C54
15	A	406	CDL	C74-C75-C76-C77
15	a	407	CDL	CB7-C71-C72-C73
15	a	406	CDL	C14-C15-C16-C17
15	A	406	CDL	C73-C74-C75-C76
15	a	407	CDL	C53-C54-C55-C56
14	D	501	PEE	C37-C38-C39-C40
15	A	406	CDL	OA5-CA3-CA4-OA6
15	a	406	CDL	OA5-CA3-CA4-OA6
15	a	407	CDL	CA7-C31-C32-C33

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Mol	Chain	Res	Type	Atoms
15	A	406	CDL	C53-C54-C55-C56
14	A	405	PEE	C19-C20-C21-C22
14	a	405	PEE	C20-C21-C22-C23
15	a	406	CDL	C1-CB2-OB2-PB2
14	D	501	PEE	C41-C42-C43-C44
15	a	407	CDL	C74-C75-C76-C77
12	A	402	A1D6O	S07-C08-S10-C11
12	a	402	A1D6O	S07-C08-S10-C11
14	A	405	PEE	C23-C24-C25-C26
14	a	405	PEE	C32-C33-C34-C35
15	a	406	CDL	C34-C35-C36-C37
15	a	406	CDL	C52-C53-C54-C55
14	D	501	PEE	C13-C14-C15-C16
14	a	405	PEE	C19-C20-C21-C22
14	a	405	PEE	C35-C36-C37-C38
15	a	406	CDL	C33-C34-C35-C36
15	A	406	CDL	OA5-CA3-CA4-CA6
15	a	407	CDL	OA5-CA3-CA4-CA6
14	D	501	PEE	C10-C11-C12-C13
15	a	407	CDL	C73-C74-C75-C76
14	D	501	PEE	C1-C2-C3-O3
15	a	407	CDL	CA5-C11-C12-C13
14	a	405	PEE	C11-C12-C13-C14
14	D	501	PEE	C35-C36-C37-C38
14	a	405	PEE	C17-C18-C19-C20
14	a	405	PEE	C23-C24-C25-C26
14	A	405	PEE	C24-C25-C26-C27
14	A	405	PEE	C34-C35-C36-C37
12	A	402	A1D6O	N09-C08-S10-C11
12	a	402	A1D6O	N09-C08-S10-C11
15	a	407	CDL	OA6-CA4-CA6-OA8
15	a	407	CDL	C15-C16-C17-C18
15	a	407	CDL	C71-CB7-OB8-CB6
15	a	406	CDL	C15-C16-C17-C18
15	A	406	CDL	C12-C11-CA5-OA6
15	a	406	CDL	C31-C32-C33-C34
15	a	407	CDL	CB4-CB3-OB5-PB2
14	a	405	PEE	C1-C2-C3-O3
15	a	406	CDL	CB3-CB4-CB6-OB8
15	A	406	CDL	C54-C55-C56-C57
14	D	501	PEE	C12-C13-C14-C15
15	A	406	CDL	OB5-CB3-CB4-OB6

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Mol	Chain	Res	Type	Atoms
15	A	406	CDL	C1-CA2-OA2-PA1
14	a	405	PEE	C31-C32-C33-C34
14	a	405	PEE	O2-C2-C3-O3
15	a	406	CDL	C75-C76-C77-C78
15	A	406	CDL	C75-C76-C77-C78
15	a	407	CDL	C55-C56-C57-C58
15	a	407	CDL	CB2-C1-CA2-OA2
15	A	406	CDL	OB5-CB3-CB4-CB6
13	a	403	HEM	C3D-CAD-CBD-CGD
15	a	407	CDL	OB9-CB7-OB8-CB6
14	D	501	PEE	C1-C2-O2-C10
15	A	406	CDL	CA6-CA4-OA6-CA5
14	D	501	PEE	C22-C23-C24-C25
15	a	407	CDL	OA5-CA3-CA4-OA6
15	a	406	CDL	CA3-CA4-CA6-OA8
14	a	405	PEE	C40-C41-C42-C43
14	D	501	PEE	C5-C4-O4P-P
15	a	406	CDL	OA6-CA4-CA6-OA8
15	a	407	CDL	OB6-CB4-CB6-OB8
15	a	406	CDL	C73-C74-C75-C76
14	a	405	PEE	C12-C13-C14-C15
14	A	405	PEE	C32-C33-C34-C35
15	A	406	CDL	C71-C72-C73-C74
15	a	407	CDL	O1-C1-CA2-OA2
14	A	405	PEE	C33-C34-C35-C36
15	a	407	CDL	CA3-CA4-CA6-OA8
15	a	407	CDL	CB3-CB4-CB6-OB8
14	A	405	PEE	C1-O3P-P-O4P
14	D	501	PEE	C4-O4P-P-O2P
15	A	406	CDL	CA2-OA2-PA1-OA3
15	a	406	CDL	CA2-OA2-PA1-OA4
15	a	407	CDL	CB2-OB2-PB2-OB3
15	A	406	CDL	C1-CB2-OB2-PB2
15	a	407	CDL	CA4-CA3-OA5-PA1
14	A	405	PEE	C12-C13-C14-C15
15	a	406	CDL	OA5-CA3-CA4-CA6
14	A	405	PEE	C21-C22-C23-C24
15	a	407	CDL	OA9-CA7-OA8-CA6
15	a	406	CDL	CA4-CA3-OA5-PA1
15	a	407	CDL	C31-CA7-OA8-CA6
15	a	407	CDL	C52-C53-C54-C55
15	a	407	CDL	C32-C33-C34-C35

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Mol	Chain	Res	Type	Atoms
15	a	406	CDL	O1-C1-CA2-OA2
15	a	407	CDL	C1-CA2-OA2-PA1
15	A	406	CDL	C12-C11-CA5-OA7
14	D	501	PEE	O3P-C1-C2-O2
14	D	501	PEE	C31-C30-O3-C3
13	a	403	HEM	CAA-CBA-CGA-O1A
14	D	501	PEE	C42-C43-C44-C45
13	A	404	HEM	CAA-CBA-CGA-O1A
13	A	403	HEM	CAA-CBA-CGA-O2A
13	a	404	HEM	CAA-CBA-CGA-O2A
13	A	404	HEM	CAA-CBA-CGA-O2A
13	a	404	HEM	CAA-CBA-CGA-O1A
15	a	407	CDL	C51-C52-C53-C54
13	A	403	HEM	CAA-CBA-CGA-O1A
13	a	403	HEM	CAA-CBA-CGA-O2A
15	a	407	CDL	C52-C51-CB5-OB6
14	D	501	PEE	C16-C17-C18-C19
15	a	406	CDL	C53-C54-C55-C56
15	a	407	CDL	C1-CB2-OB2-PB2
14	A	405	PEE	C16-C17-C18-C19
15	A	406	CDL	OB6-CB4-CB6-OB8
14	D	501	PEE	O3P-C1-C2-C3
12	A	401	A1D6O	S10-C11-C12-C13
12	a	401	A1D6O	S10-C11-C12-C13
15	a	406	CDL	C32-C31-CA7-OA8
14	a	405	PEE	C38-C39-C40-C41
15	a	406	CDL	C12-C11-CA5-OA6
13	a	403	HEM	CAD-CBD-CGD-O1D
14	a	405	PEE	C18-C19-C20-C21
15	a	406	CDL	C52-C51-CB5-OB6
13	a	403	HEM	CAD-CBD-CGD-O2D
15	A	406	CDL	C72-C73-C74-C75
15	A	406	CDL	CB3-CB4-CB6-OB8
15	a	406	CDL	C12-C11-CA5-OA7
15	a	406	CDL	C52-C51-CB5-OB7
12	A	402	A1D6O	C12-C13-N19-N20
12	a	402	A1D6O	C12-C13-N19-N20
13	A	404	HEM	CAD-CBD-CGD-O2D
14	a	405	PEE	C33-C34-C35-C36

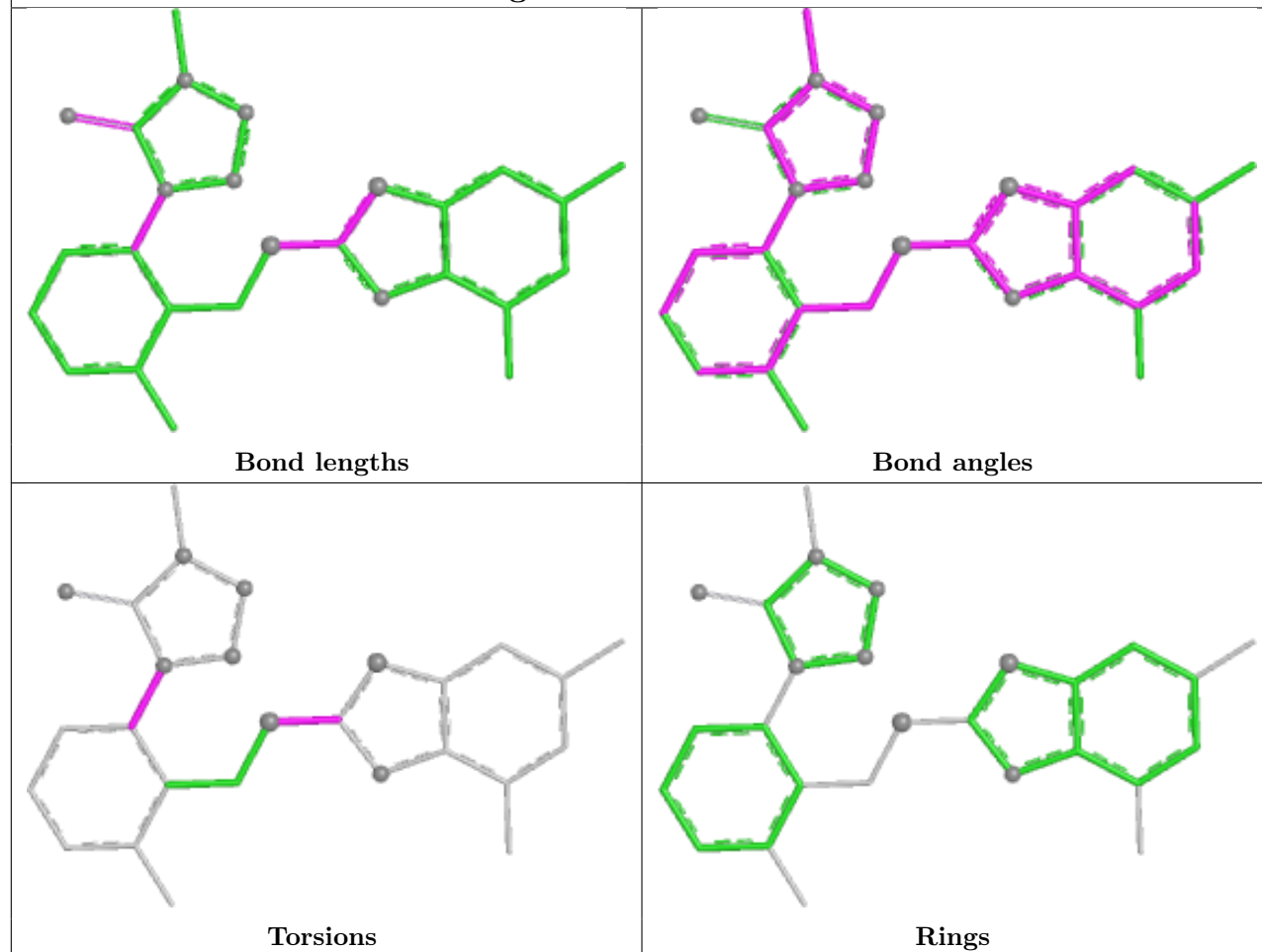
There are no ring outliers.

8 monomers are involved in 32 short contacts:

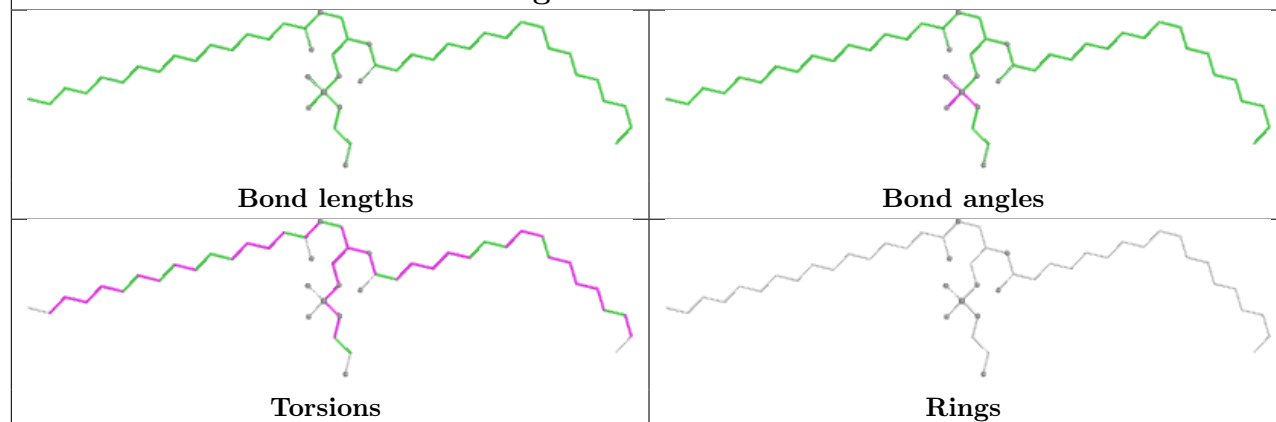
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	D	501	PEE	5	0
15	a	406	CDL	6	0
15	a	407	CDL	3	0
15	A	406	CDL	2	0
14	A	405	PEE	2	0
16	b	401	HEC	5	0
14	a	405	PEE	5	0
16	B	401	HEC	5	0

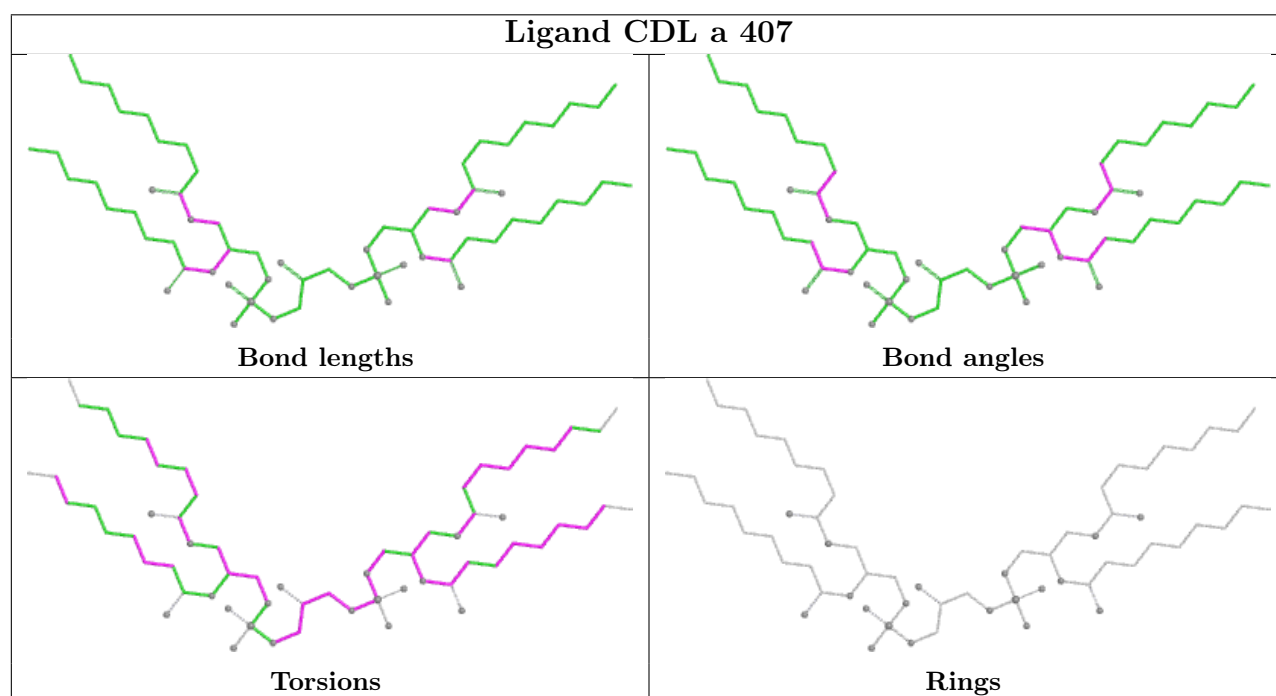
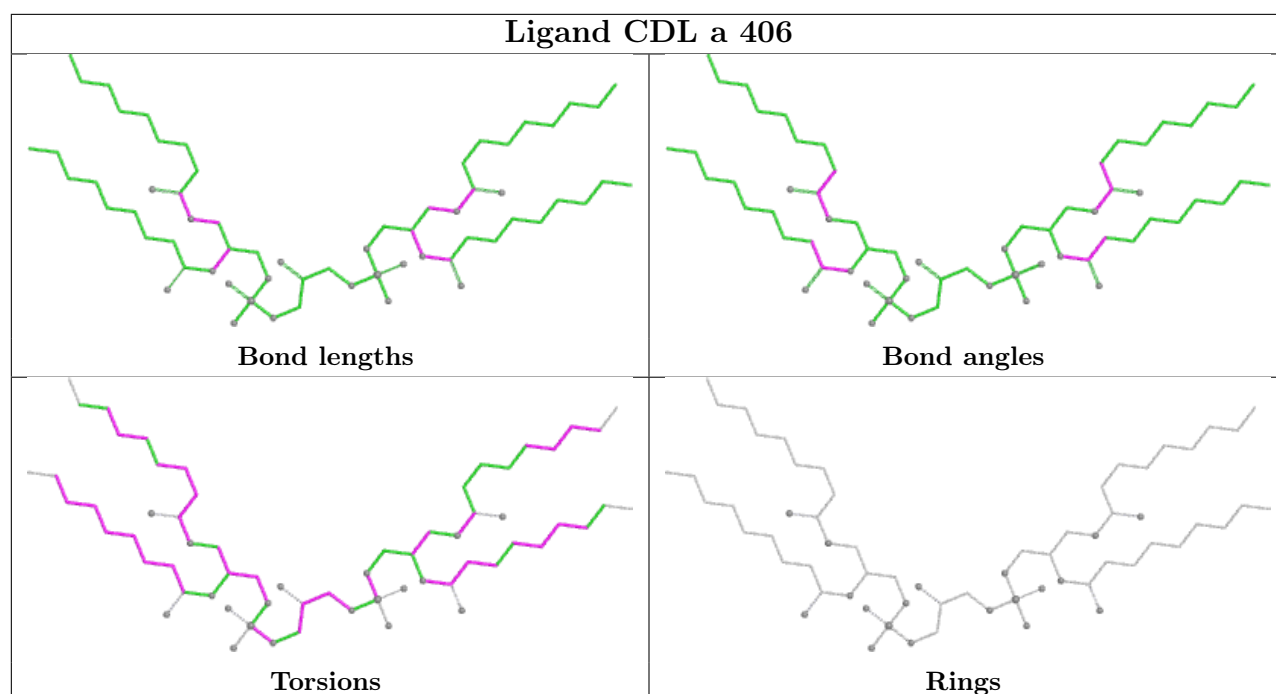
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

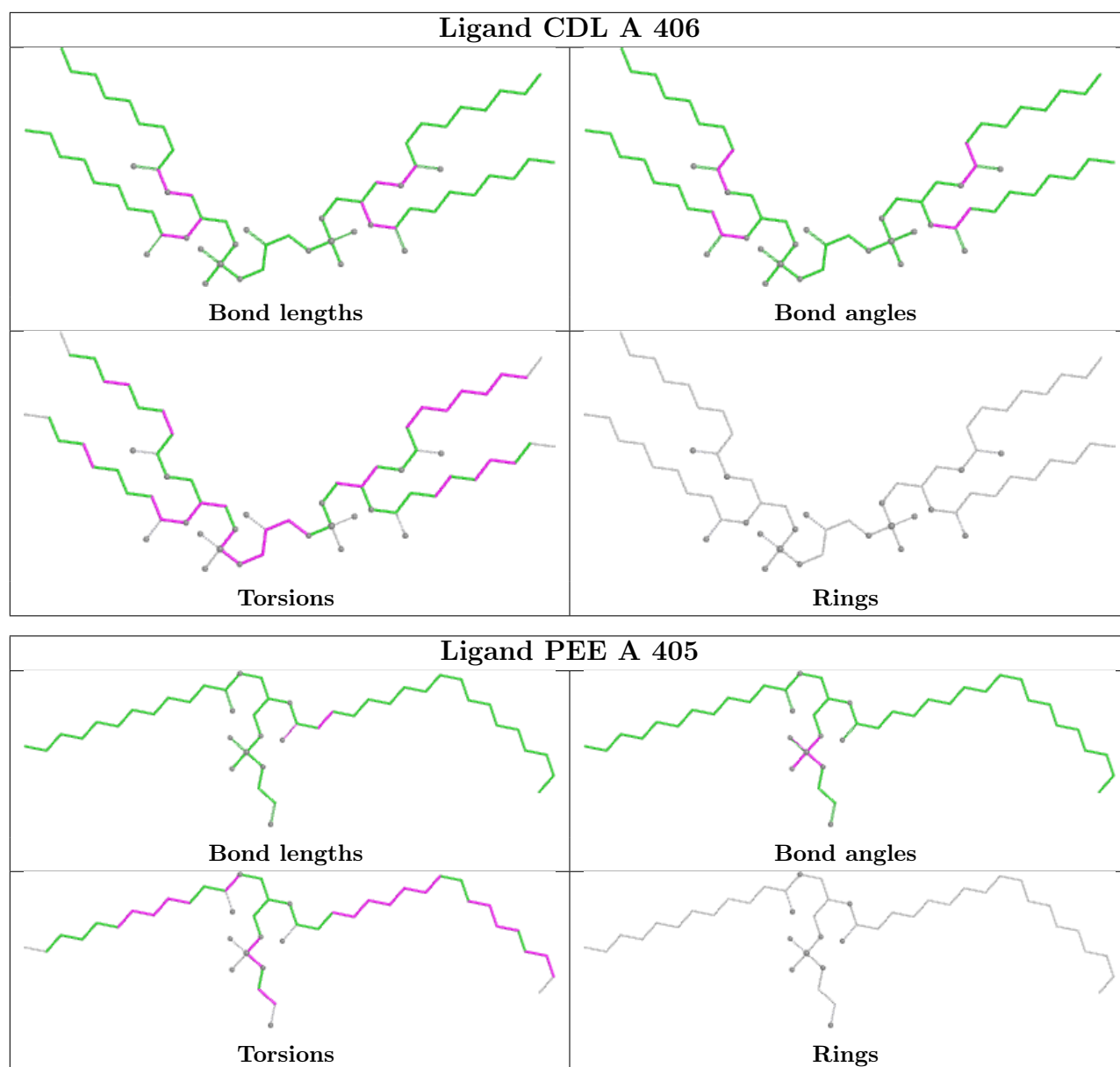
Ligand A1D6O a 402

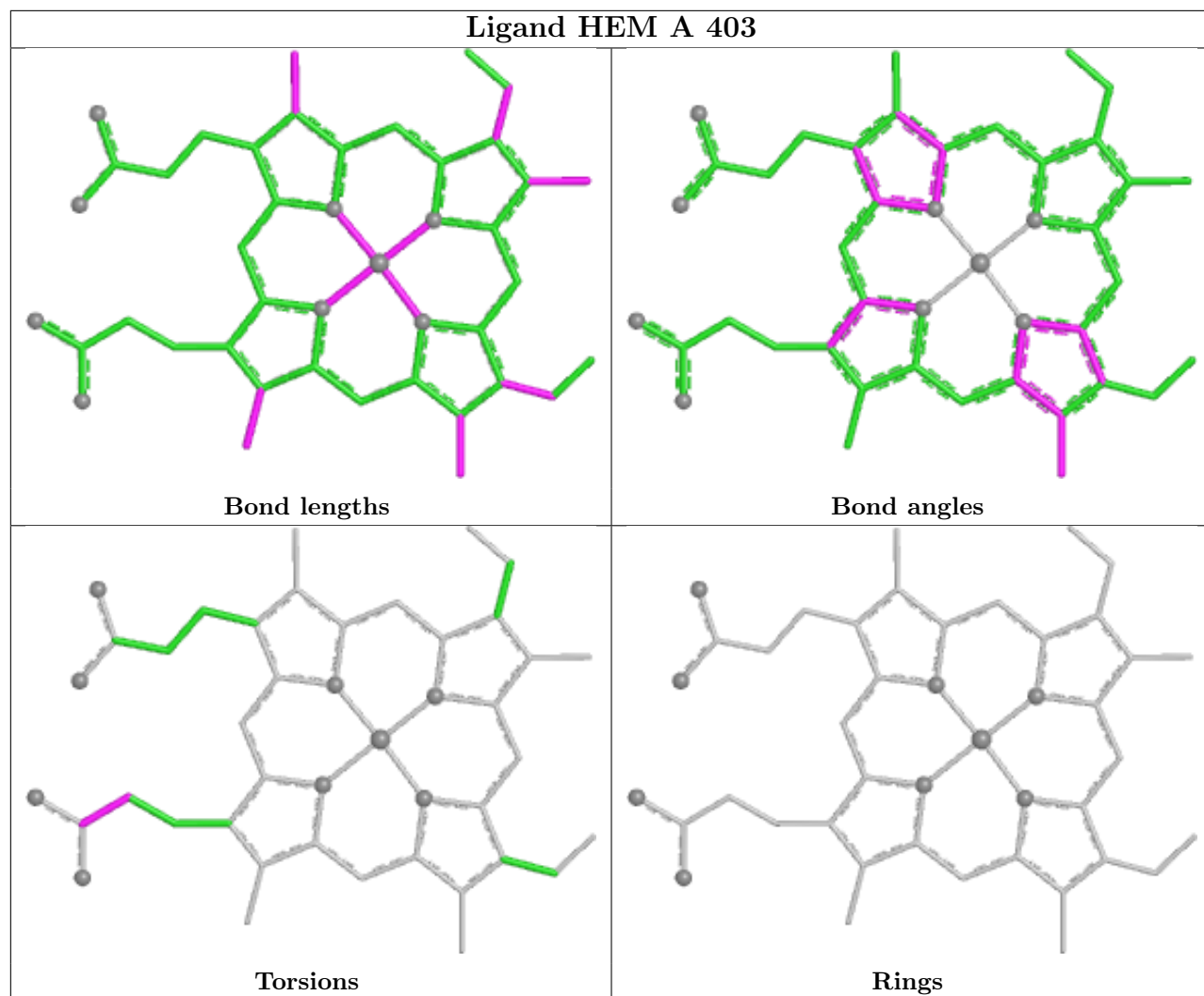


Ligand PEE D 501

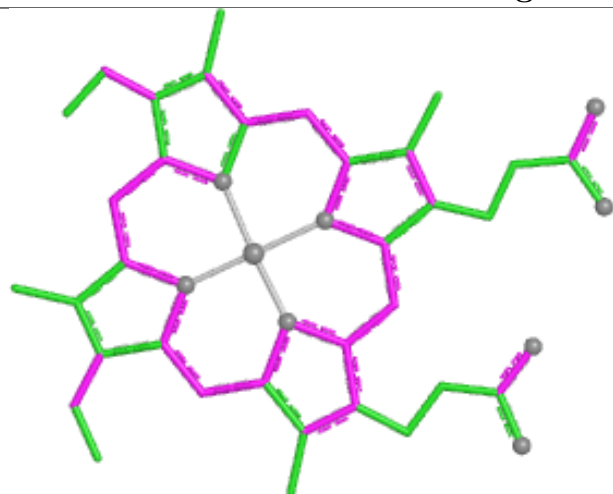




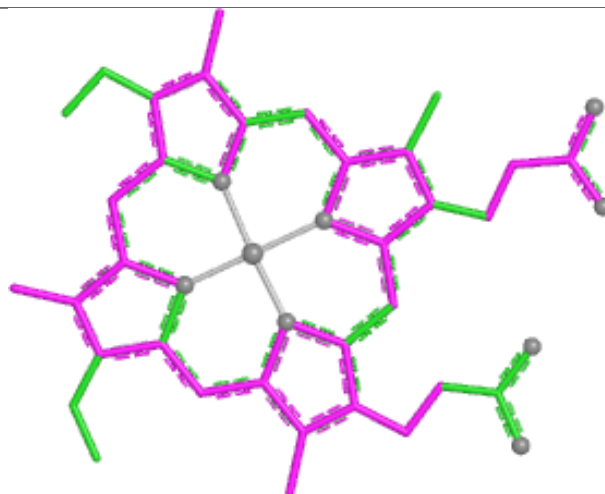




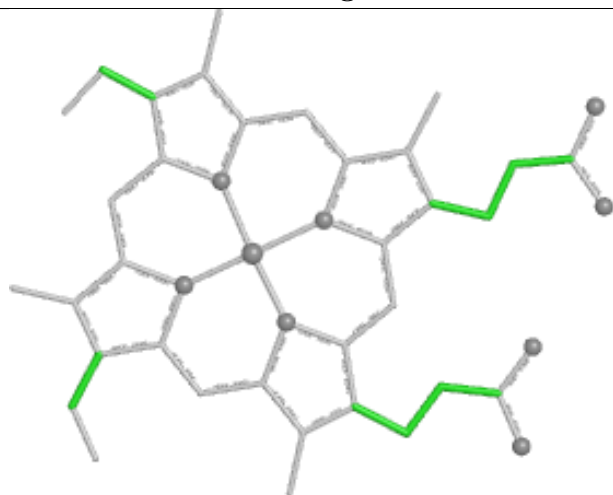
Ligand HEC b 401



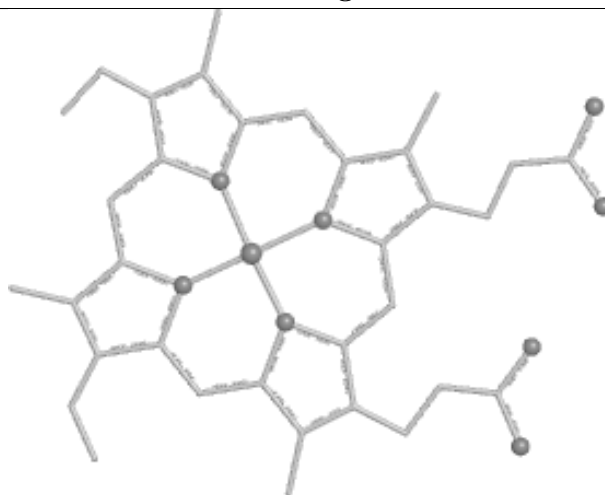
Bond lengths



Bond angles

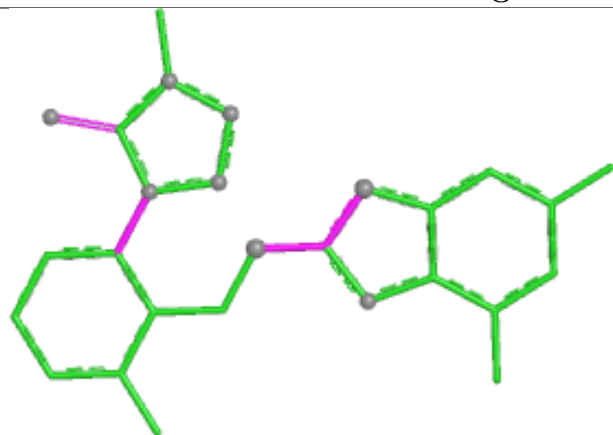


Torsions

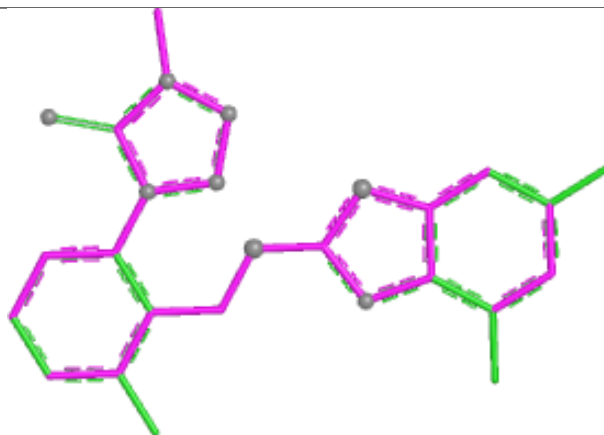


Rings

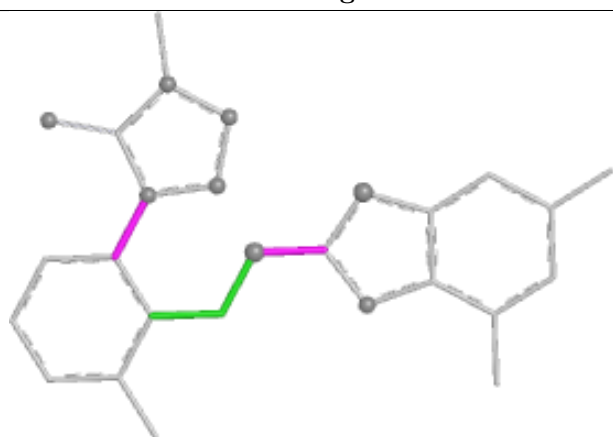
Ligand A1D6O A 402



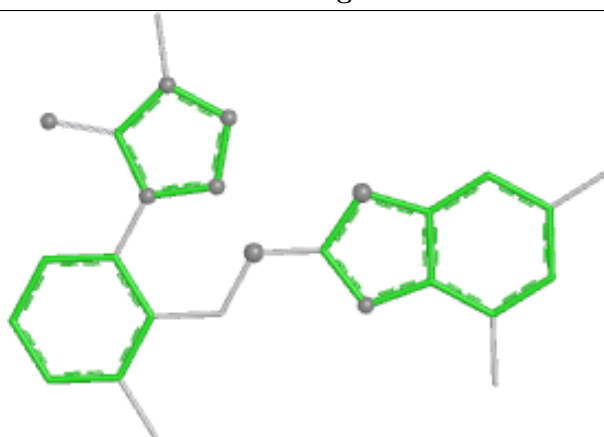
Bond lengths



Bond angles

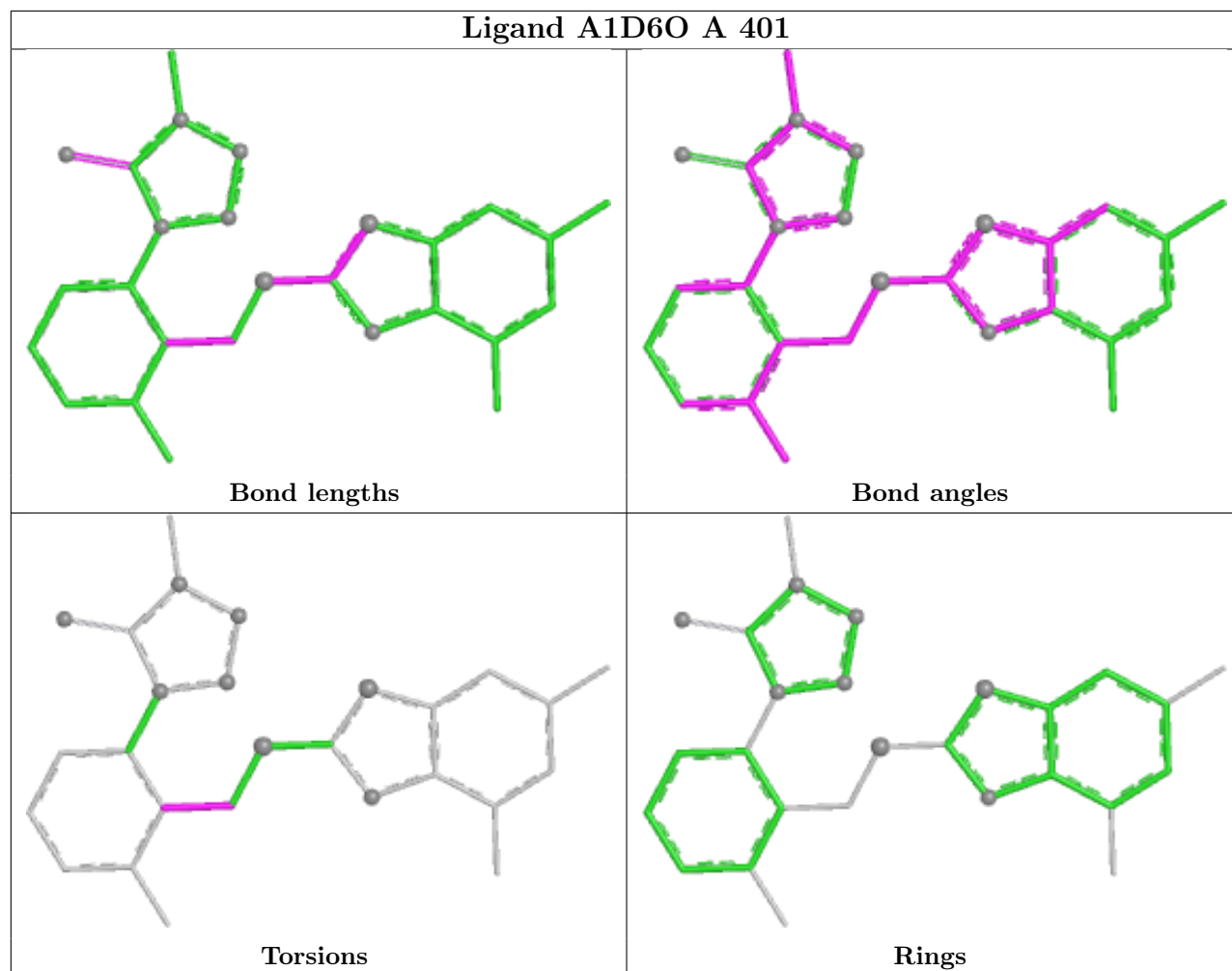


Torsions

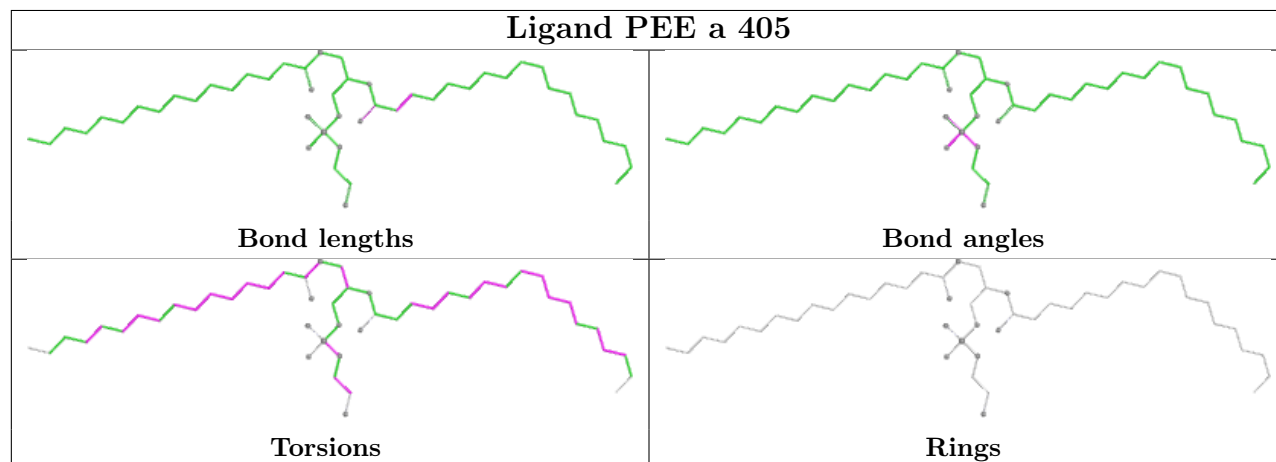


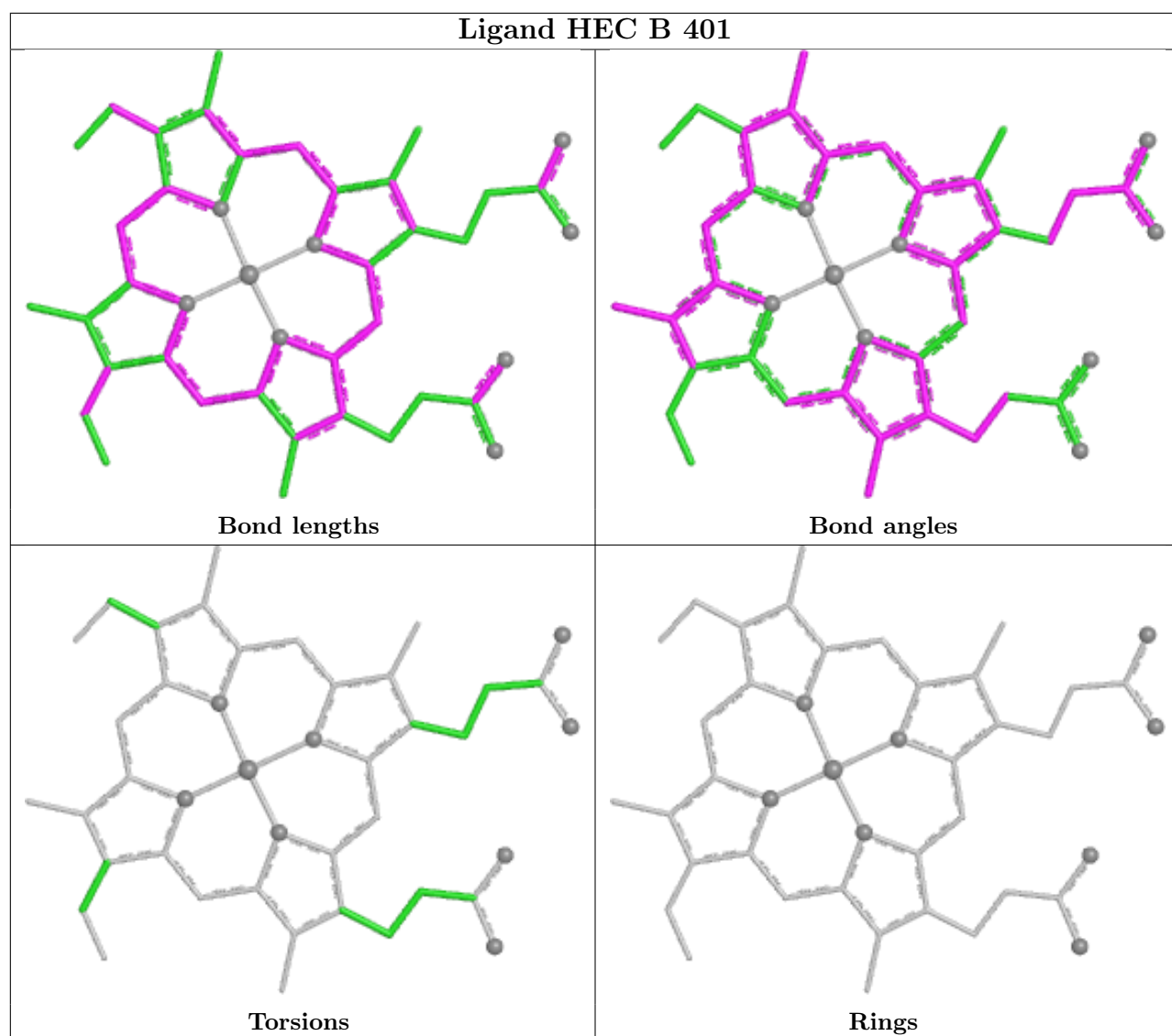
Rings

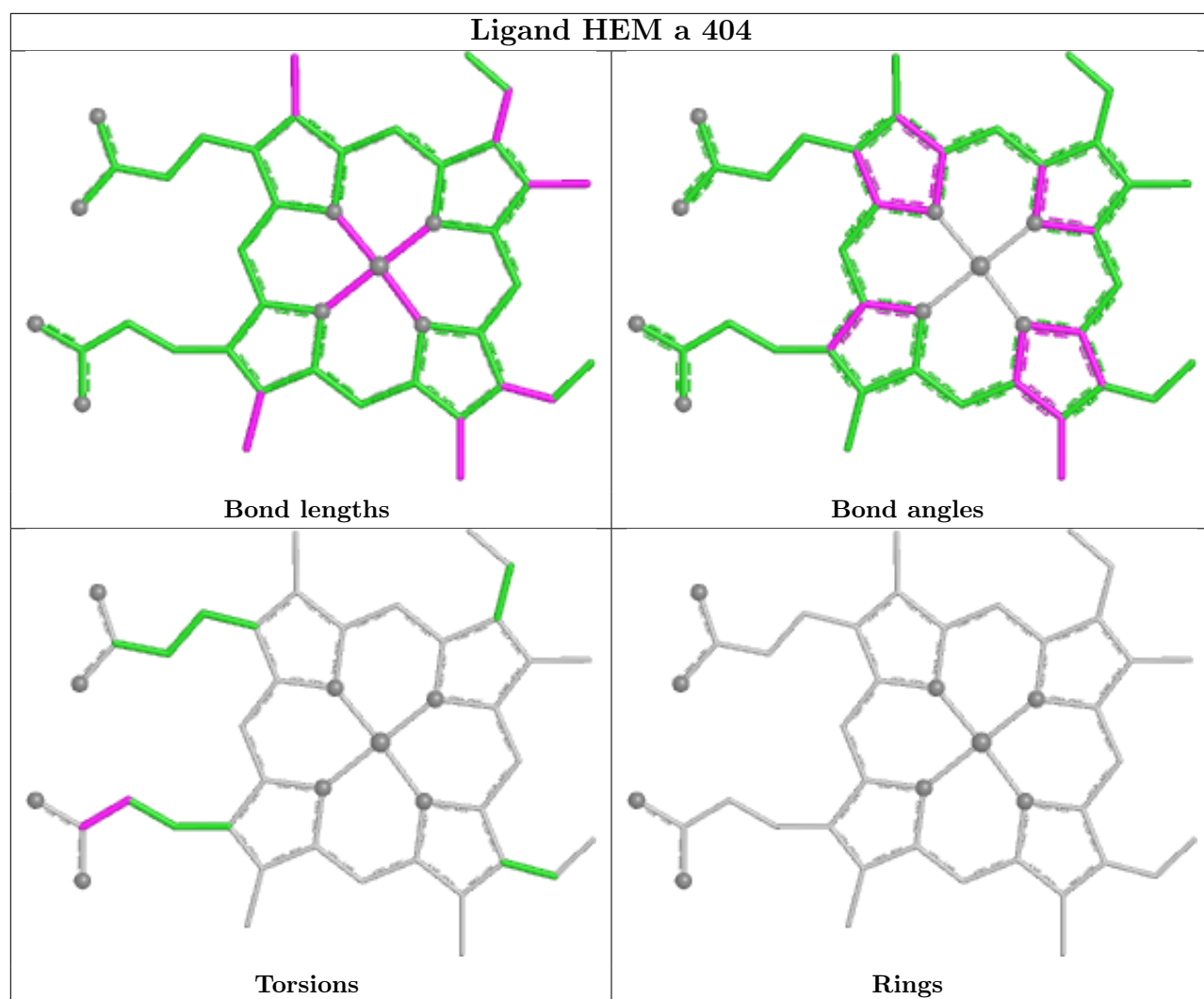
Ligand A1D6O A 401



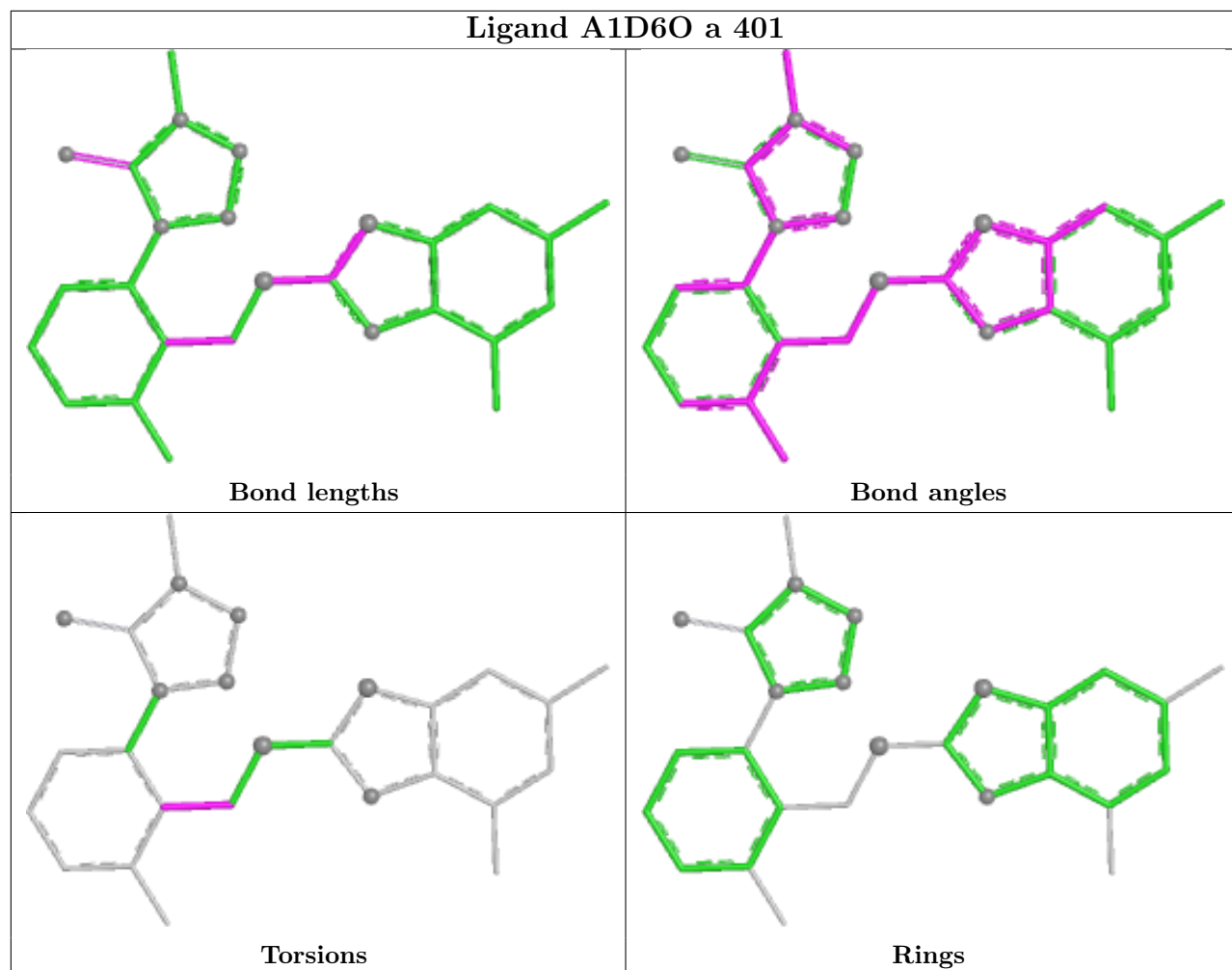
Ligand PEE a 405

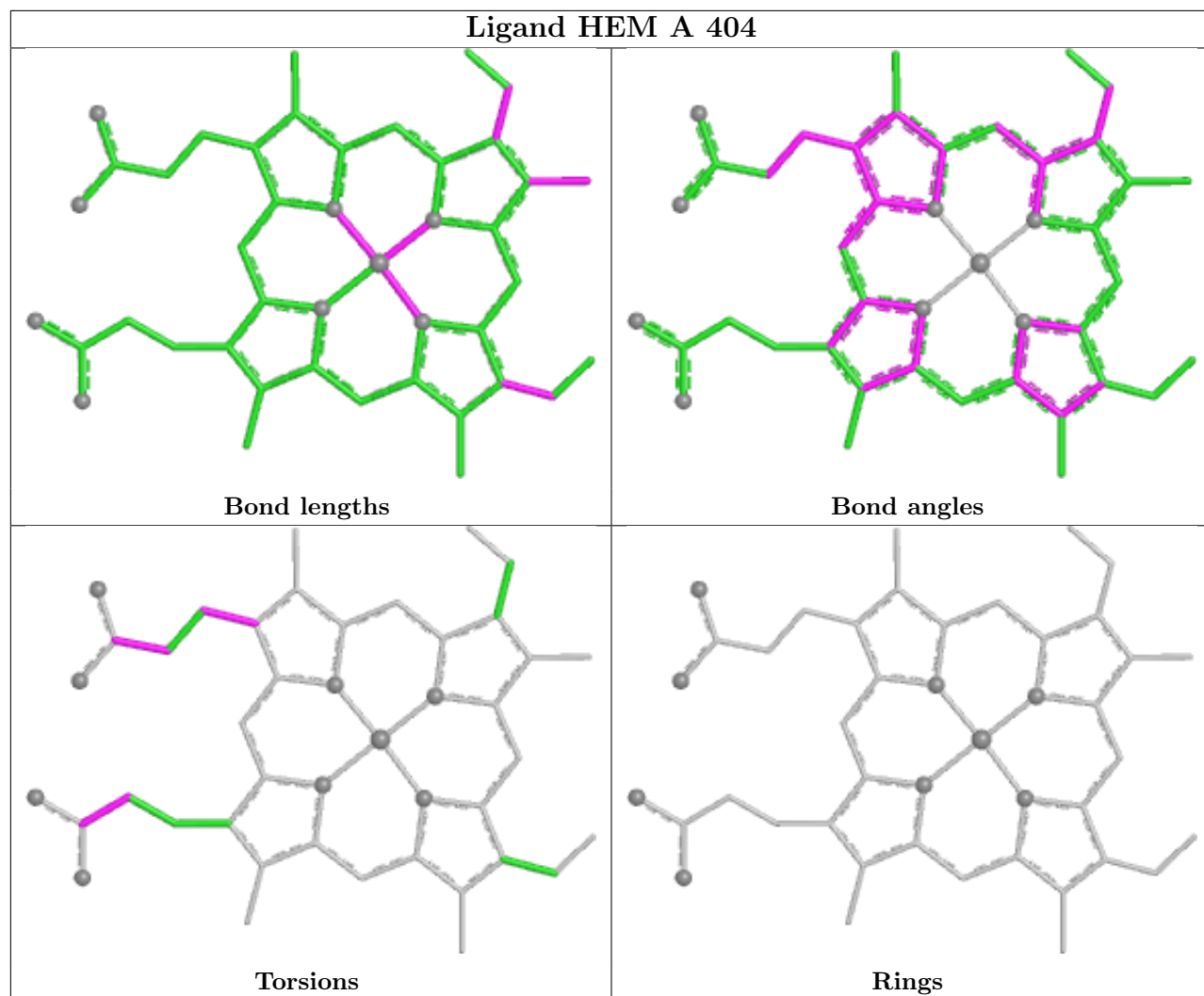


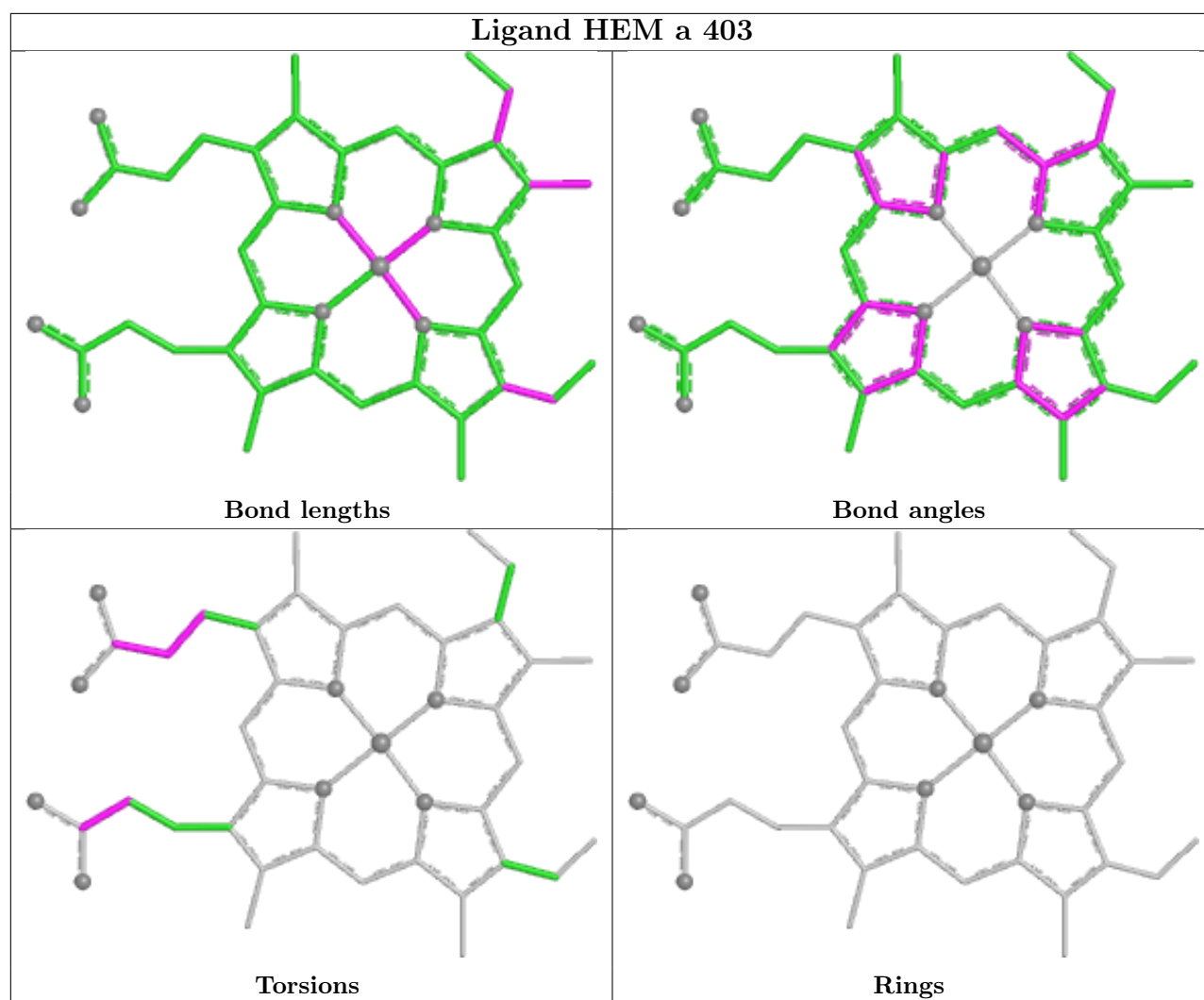




Ligand A1D6O a 401







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

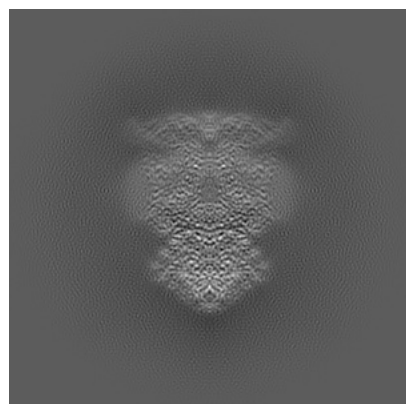
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60323. These allow visual inspection of the internal detail of the map and identification of artifacts.

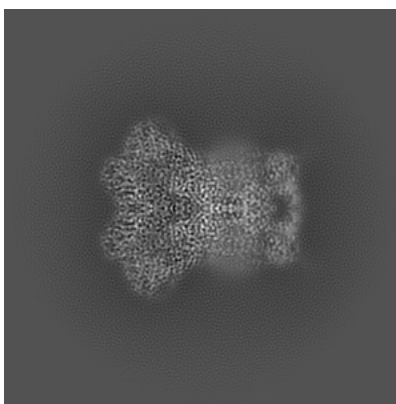
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

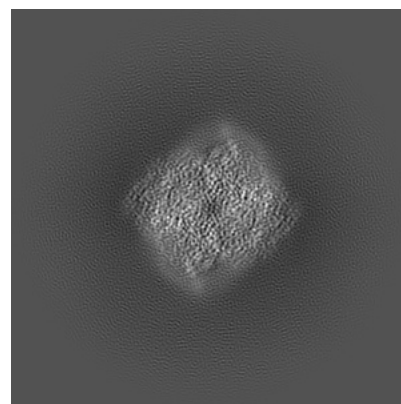
6.1.1 Primary map



X

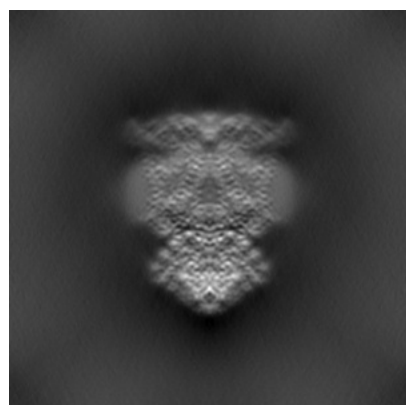


Y

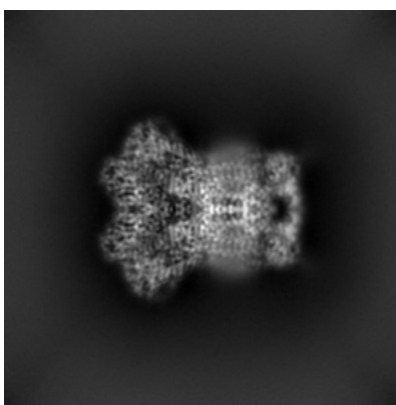


Z

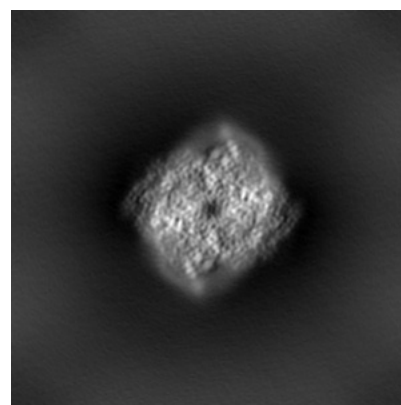
6.1.2 Raw map



X



Y

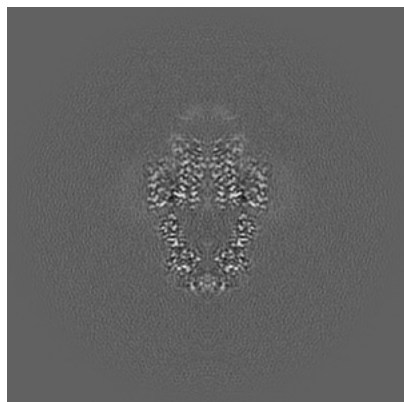


Z

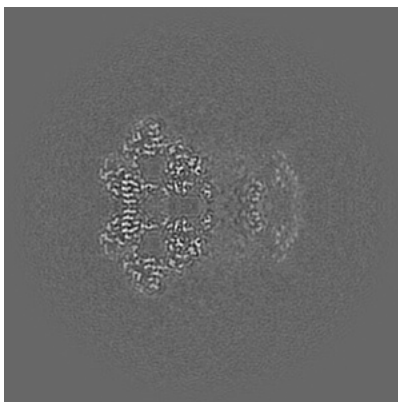
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

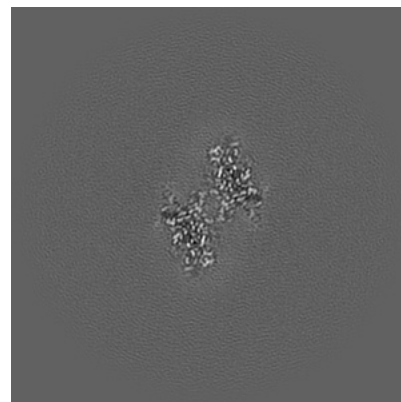
6.2.1 Primary map



X Index: 160

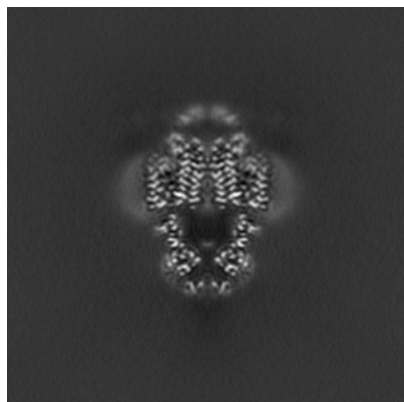


Y Index: 160

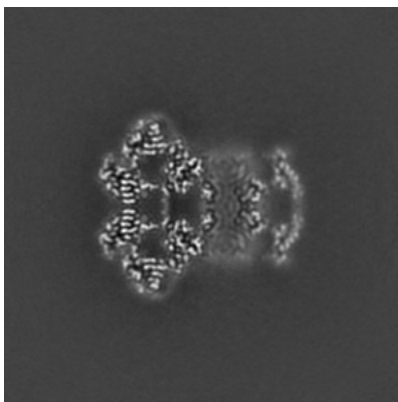


Z Index: 160

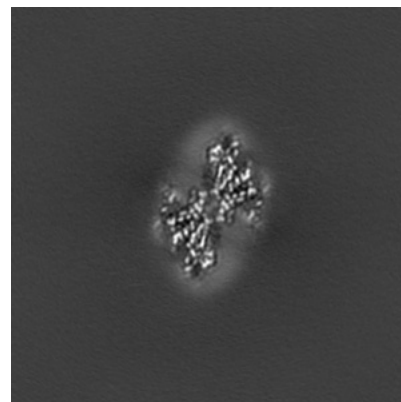
6.2.2 Raw map



X Index: 160



Y Index: 160

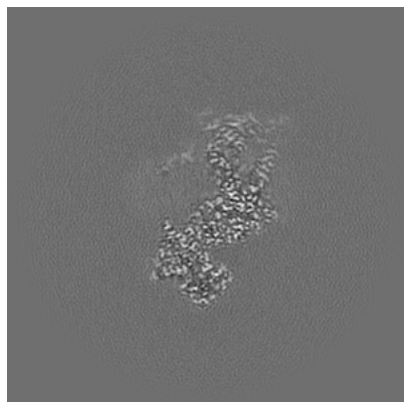


Z Index: 160

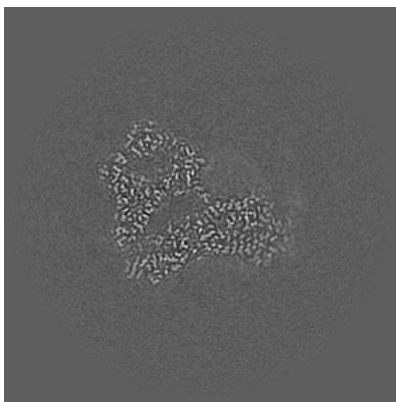
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

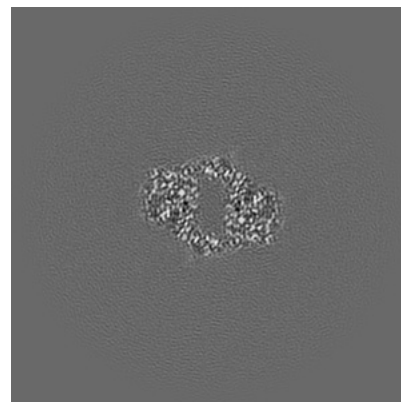
6.3.1 Primary map



X Index: 176

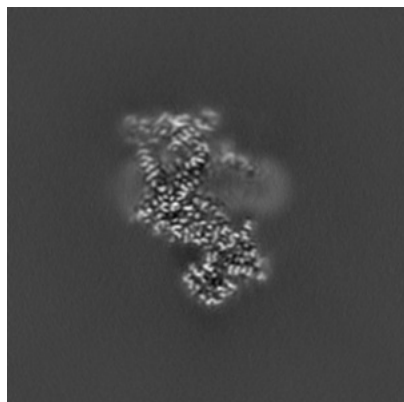


Y Index: 150

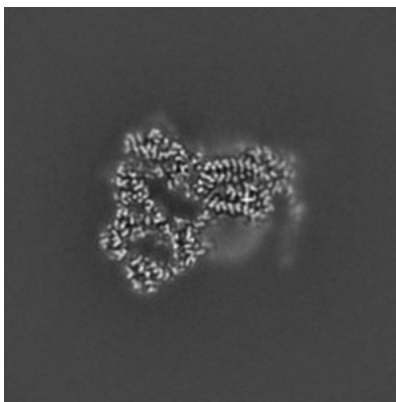


Z Index: 138

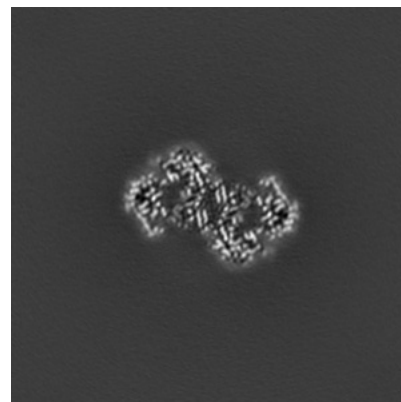
6.3.2 Raw map



X Index: 144



Y Index: 170

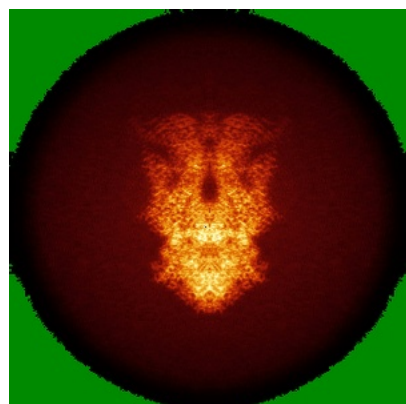


Z Index: 108

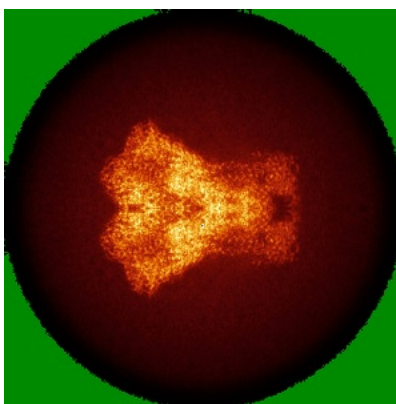
The images above show the largest variance slices of the map in three orthogonal directions.

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

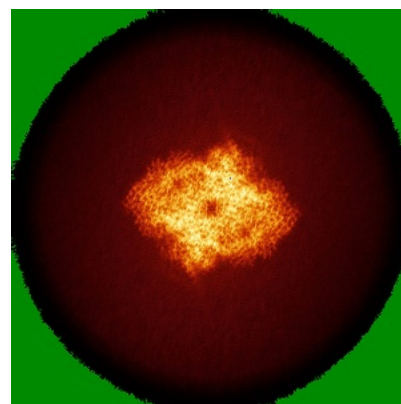
6.4.1 Primary map



X

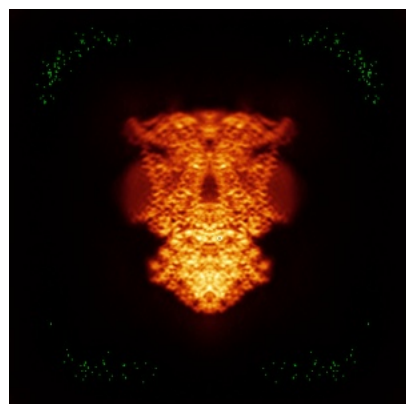


Y

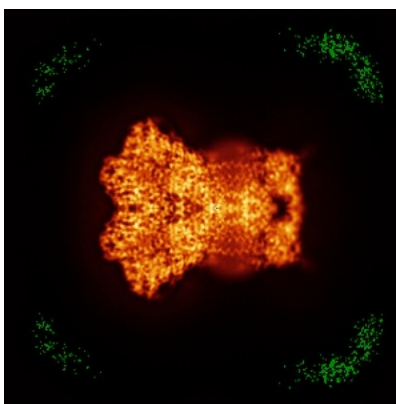


Z

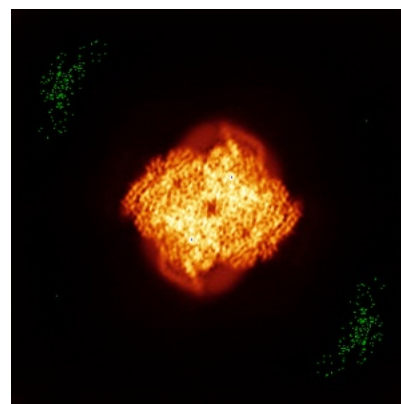
6.4.2 Raw map



X



Y

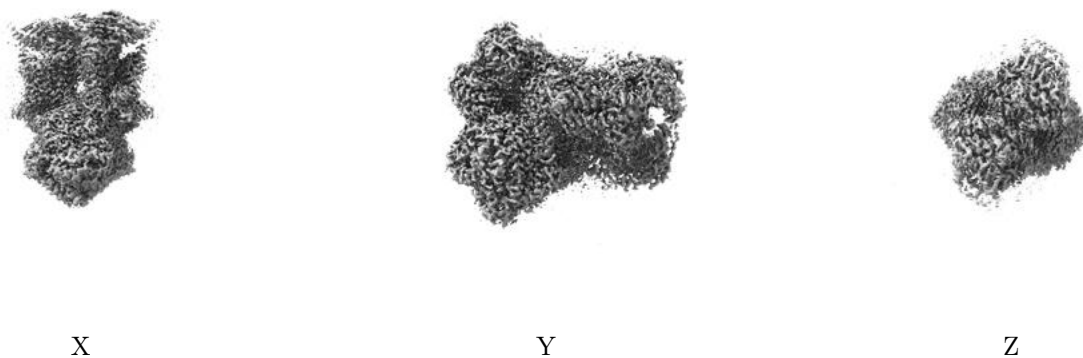


Z

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

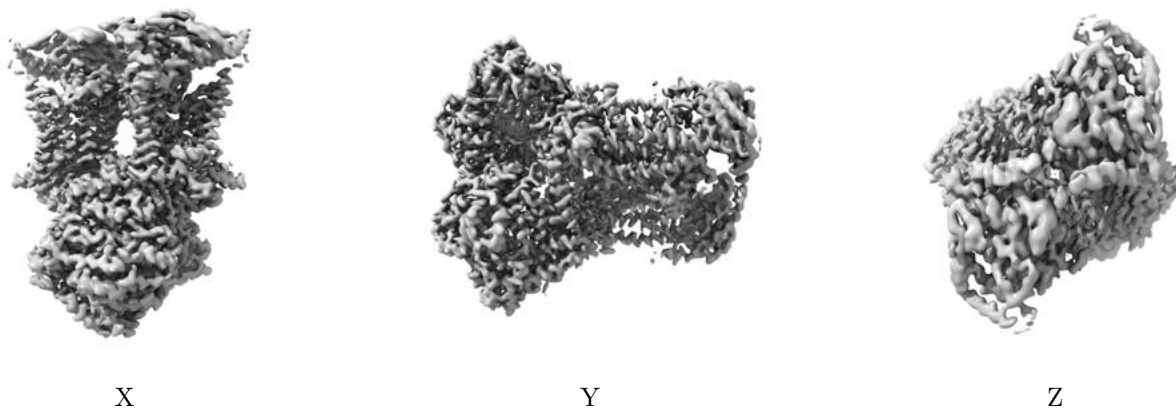
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

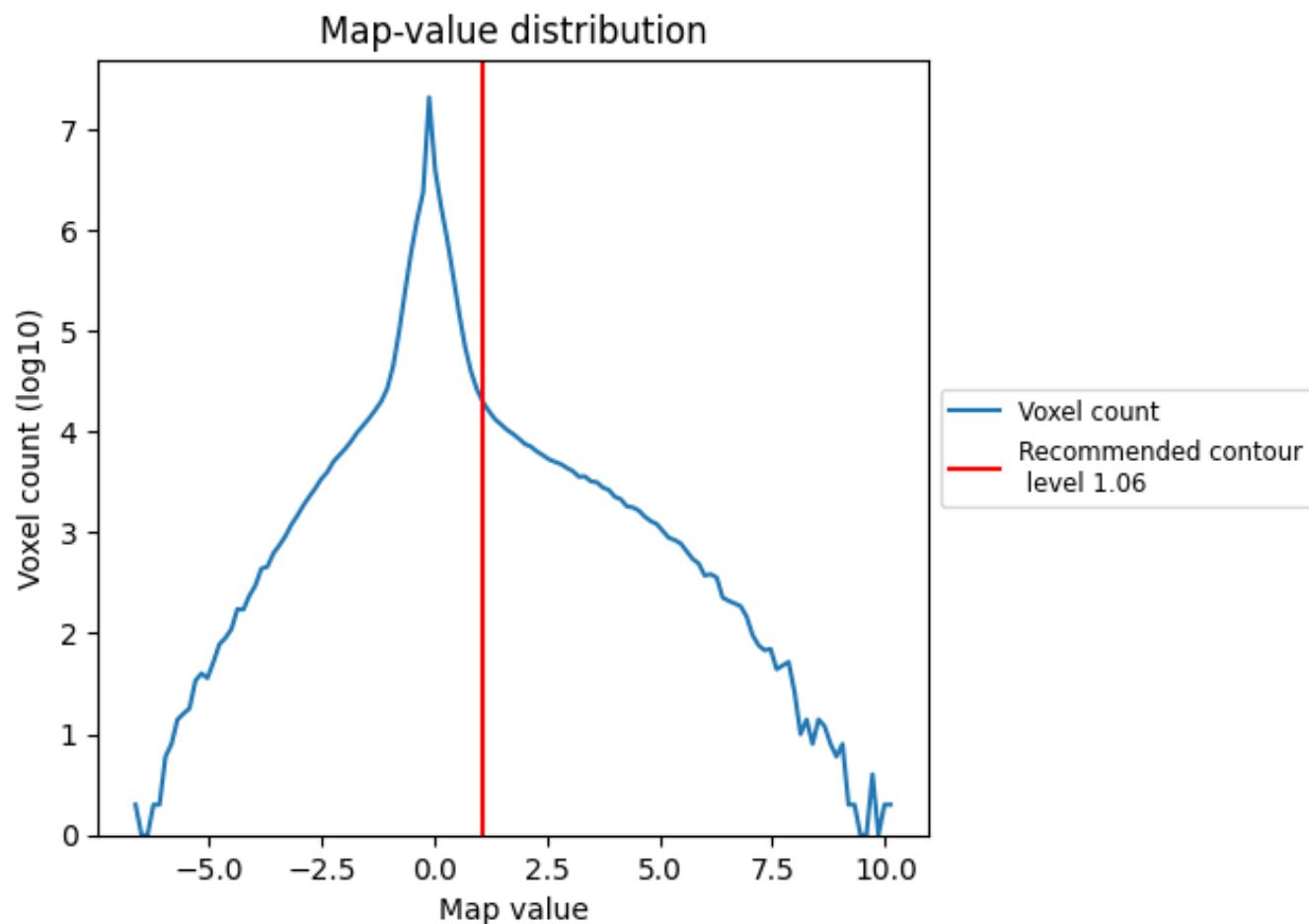
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

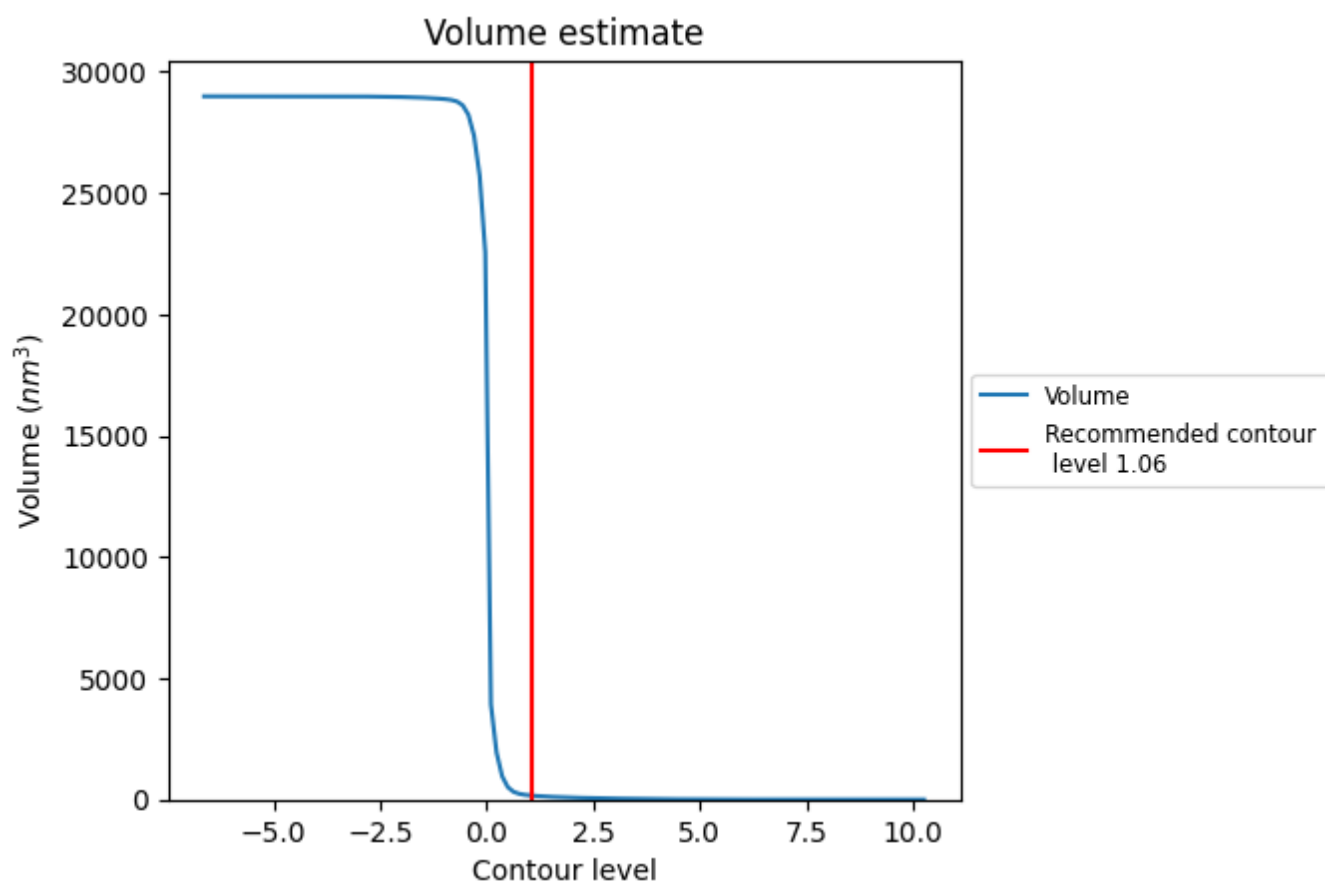
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

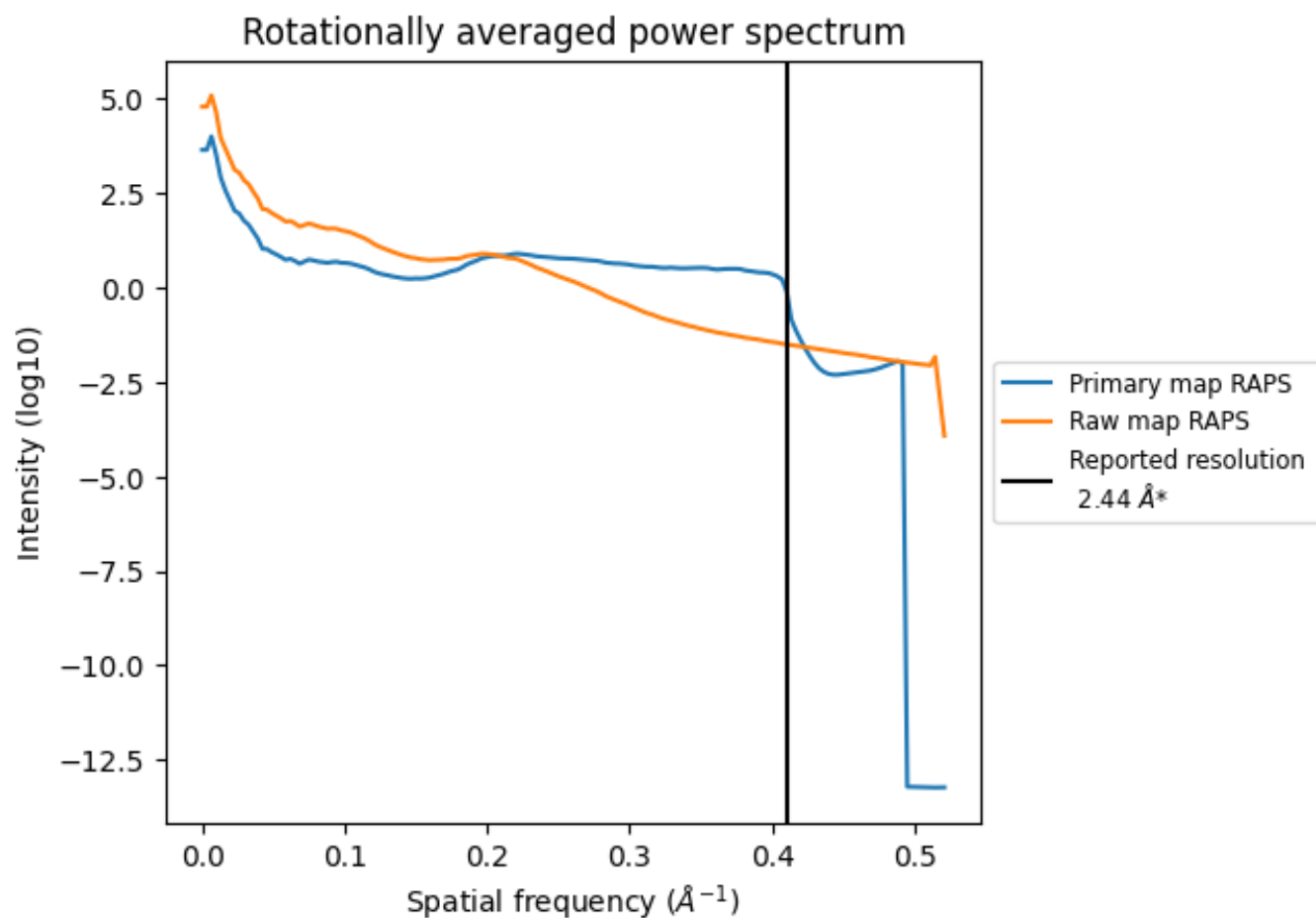
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 163 nm^3 ; this corresponds to an approximate mass of 147 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

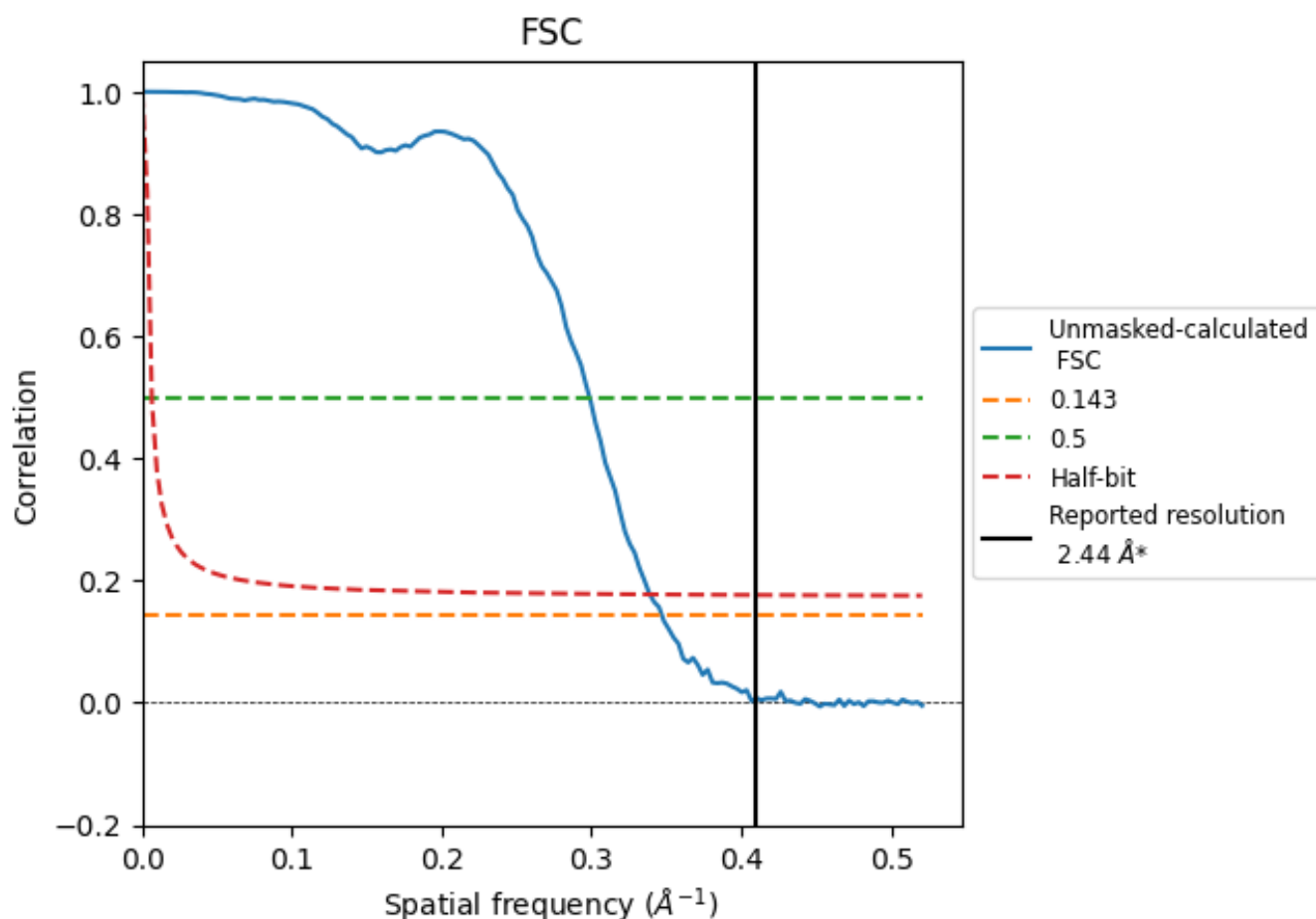


*Reported resolution corresponds to spatial frequency of 0.410 Å⁻¹

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 0.410 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

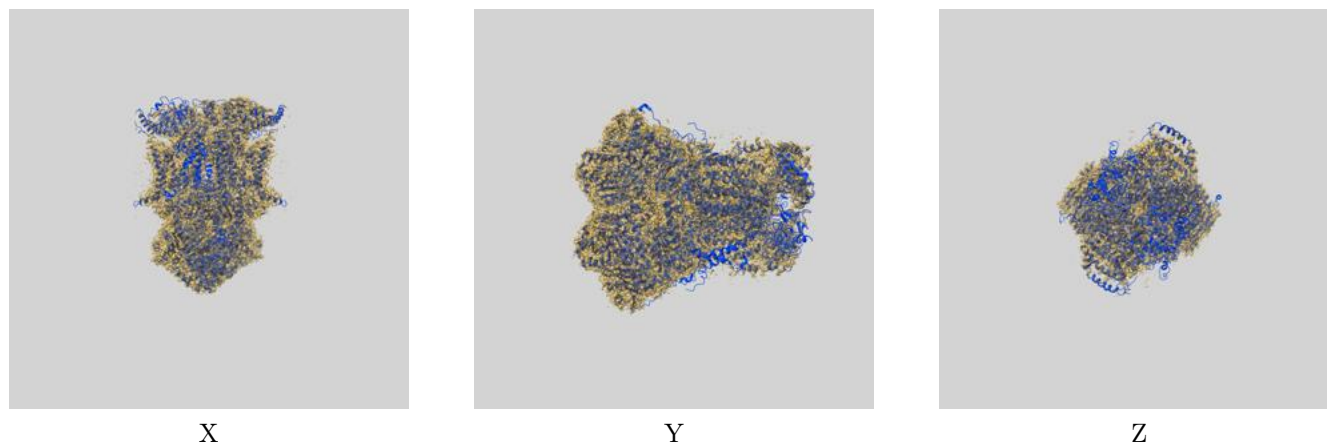
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.44	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.88	3.35	2.95

*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 2.88 differs from the reported value 2.44 by more than 10 %

9 Map-model fit [i](#)

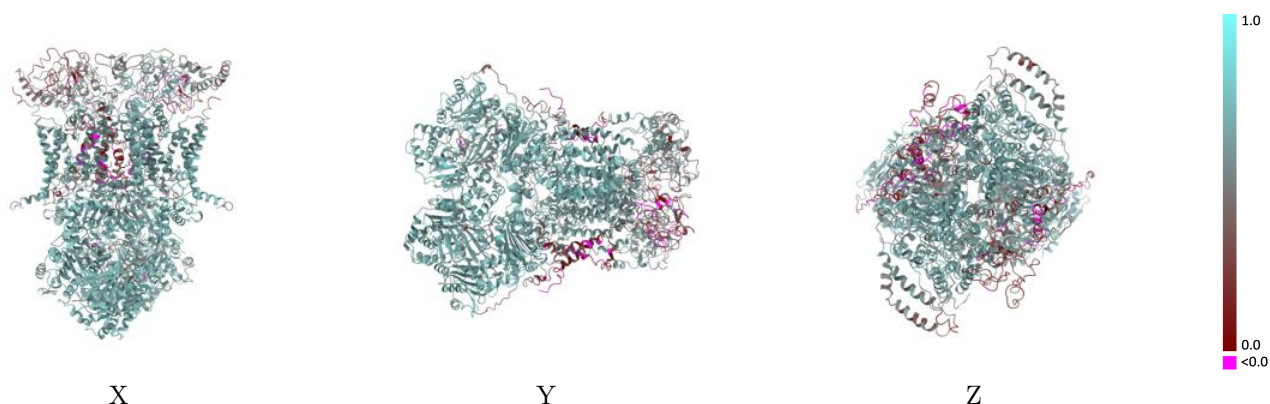
This section contains information regarding the fit between EMDB map EMD-60323 and PDB model 8ZP0. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



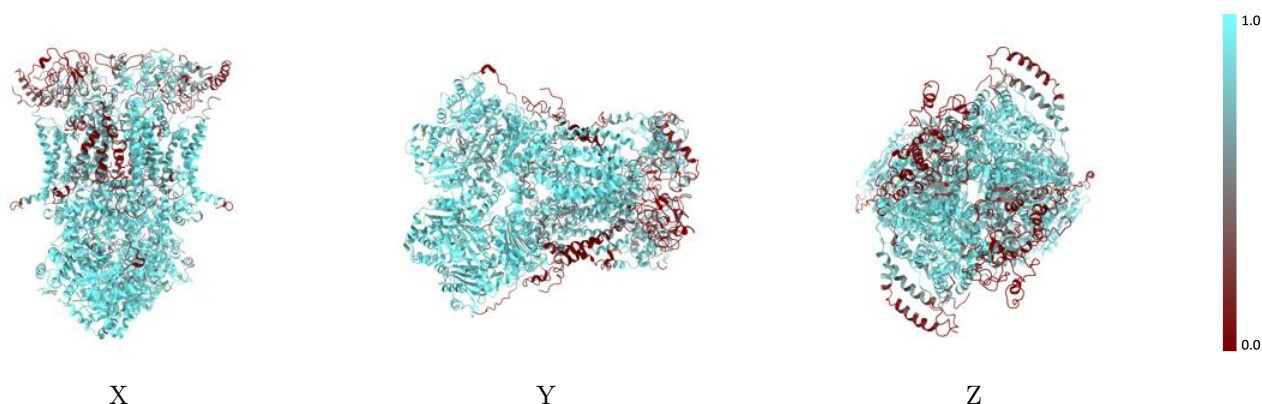
The images above show the 3D surface view of the map at the recommended contour level 1.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



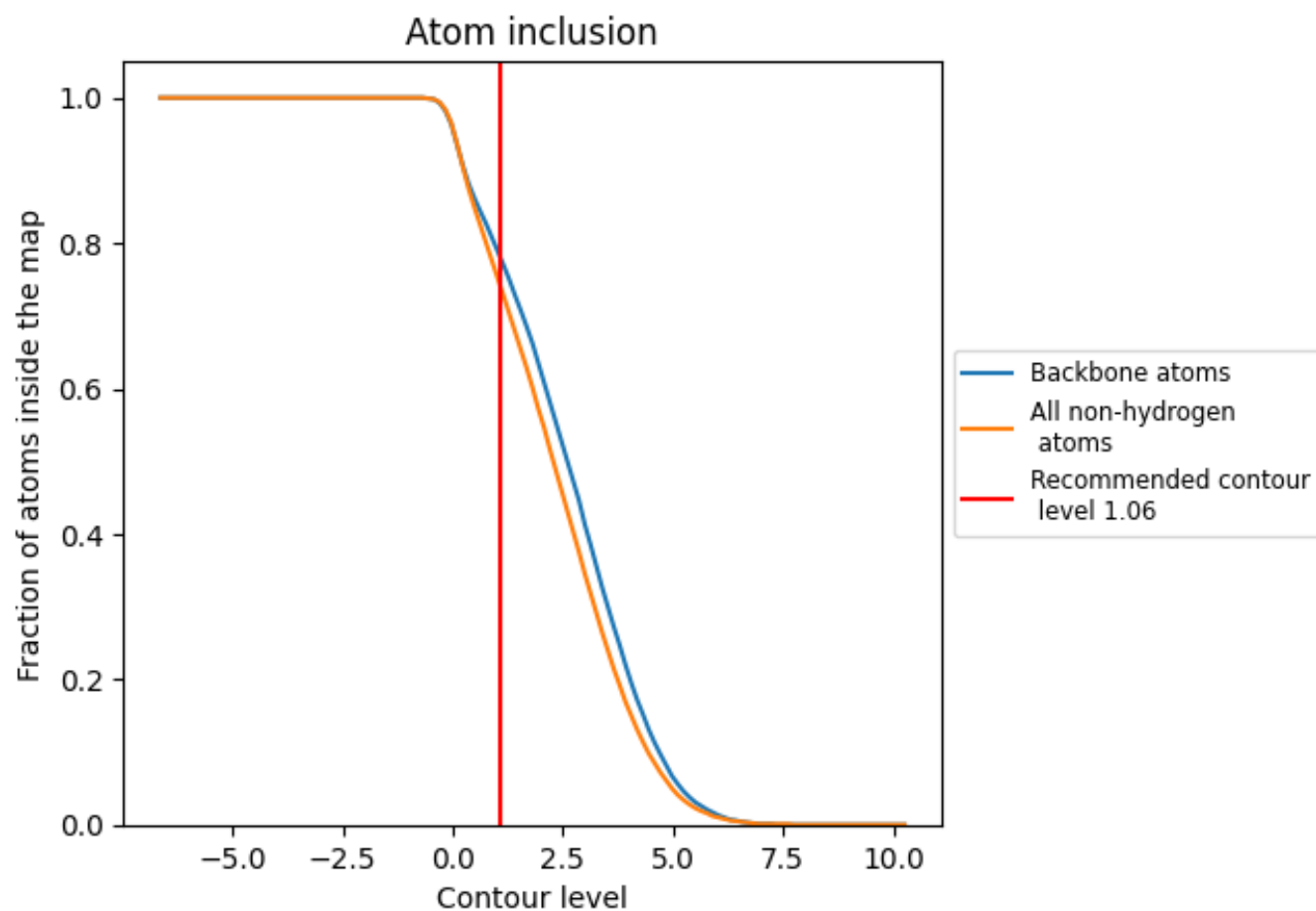
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 74% 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 (1.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7450	 0.5780
A	 0.8930	 0.6450
B	 0.7460	 0.5820
C	 0.0530	 0.2900
D	 0.9110	 0.6610
E	 0.9440	 0.6680
F	 0.3820	 0.4860
G	 0.8940	 0.6630
H	 0.7760	 0.6080
I	 0.3170	 0.3120
J	 0.0050	 0.1980
K	 0.4870	 0.4200
a	 0.8860	 0.6430
b	 0.7610	 0.5910
c	 0.0600	 0.2220
d	 0.9160	 0.6620
e	 0.9450	 0.6690
f	 0.3900	 0.4780
g	 0.8930	 0.6630
h	 0.7240	 0.5740
i	 0.3190	 0.2970
j	 0.0030	 0.1840
k	 0.5000	 0.4250

