wwPDB EM Validation Summary Report (i)

Aug 26, 2026 – 10:19 am BST

PDB ID	:	7P7C / pdb_00007p7c
EMDB ID	:	EMD-13235
Title	:	Complex I from E. coli, DDM/LMNG-purified, Apo, Open state
Authors	:	Kravchuk, V.; Kampjut, D.; Sazanov, L.
Deposited on	:	2021-07-19
Resolution	:	2.40 Å(reported)
Based on initial models	:	4HEA, 3RKO

This is a wwPDB EM Validation Summary 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 (i) 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 (i)) were used in the production of this report:

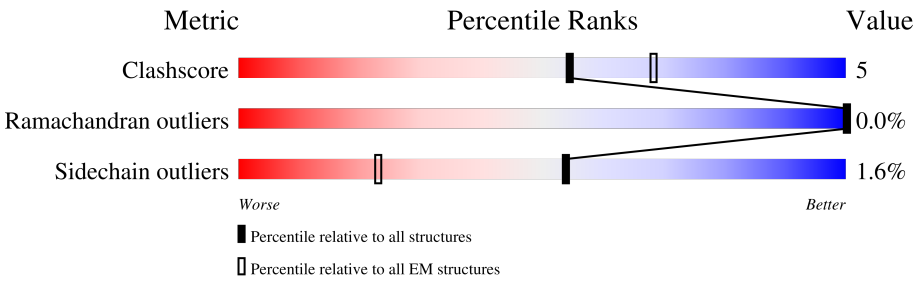
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

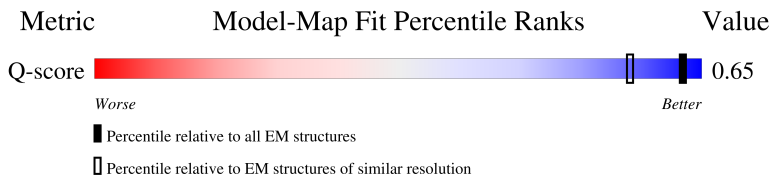
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.40 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	5628 (1.90 - 2.90)

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 <=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	F	439	93% 7%
2	E	156	88% 12%
3	G	905	89% 11%
4	C	600	86% 11%

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Mol	Chain	Length	Quality of chain
5	B	220	76% 14% 10%
6	I	180	93% 7%
7	H	325	75% 20%
8	A	147	53% 15% 31%
9	L	613	5% 85% 12%
10	M	504	82% 18%
11	N	485	80% 17%
12	K	100	88% 12%
13	J	162	81% 19%

2 Entry composition (i)

There are 21 unique types of molecules in this entry. The entry contains 38320 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called NADH-quinone oxidoreductase subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	F	439	3407	2162	596	629	20	0	0

- Molecule 2 is a protein called NADH dehydrogenase I subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	156	1220	768	215	229	8	0	0

- Molecule 3 is a protein called NADH-quinone oxidoreductase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	905	7013	4384	1266	1326	37	0	0

- Molecule 4 is a protein called NADH-quinone oxidoreductase subunit C/D.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	588	4735	3034	822	855	24	0	0

- Molecule 5 is a protein called NADH-quinone oxidoreductase subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	198	1568	994	272	286	16	0	0

- Molecule 6 is a protein called NADH-quinone oxidoreductase subunit I.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	I	180	1436	915	242	264	15	0	0

- Molecule 7 is a protein called NADH-quinone oxidoreductase subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	H	311	2438	1640	383	397	18	0	0

- Molecule 8 is a protein called NADH-quinone oxidoreductase subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	A	101	800	549	123	124	4	0	0

- Molecule 9 is a protein called Proton-translocating NADH-quinone oxidoreductase, chain L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	L	597	4559	3036	725	766	32	0	0

- Molecule 10 is a protein called NADH dehydrogenase I subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	M	504	3953	2661	617	646	29	0	0

- Molecule 11 is a protein called NADH-quinone oxidoreductase subunit N.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	N	476	3602	2408	569	606	19	0	0

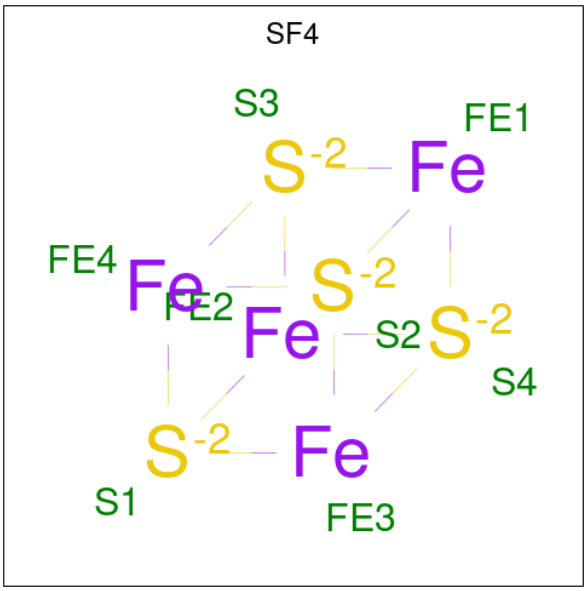
- Molecule 12 is a protein called NADH-quinone oxidoreductase subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	100	760	494	132	129	5	0	0

- Molecule 13 is a protein called NADH-quinone oxidoreductase subunit J.

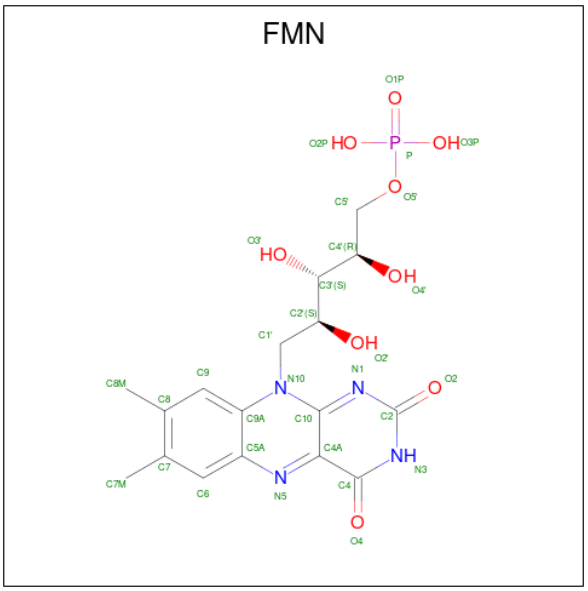
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	J	162	1218	820	187	204	7	0	0

- Molecule 14 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



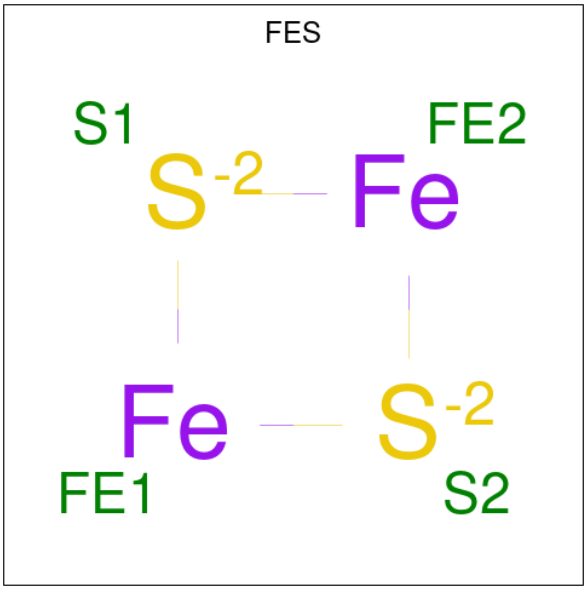
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
14	F	1	8	4	4	0
14	G	1	8	4	4	0
14	G	1	8	4	4	0
14	G	1	8	4	4	0
14	B	1	8	4	4	0
14	I	1	8	4	4	0
14	I	1	8	4	4	0

- Molecule 15 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



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

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

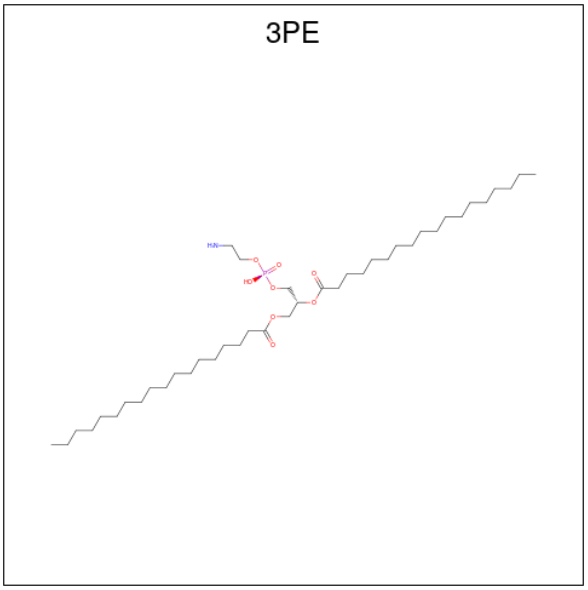


Mol	Chain	Residues	Atoms			AltConf
16	E	1	Total	Fe	S	0
			4	2	2	
16	G	1	Total	Fe	S	0
			4	2	2	

- Molecule 17 is CALCIUM ION (CCD ID: CA) (formula: Ca).

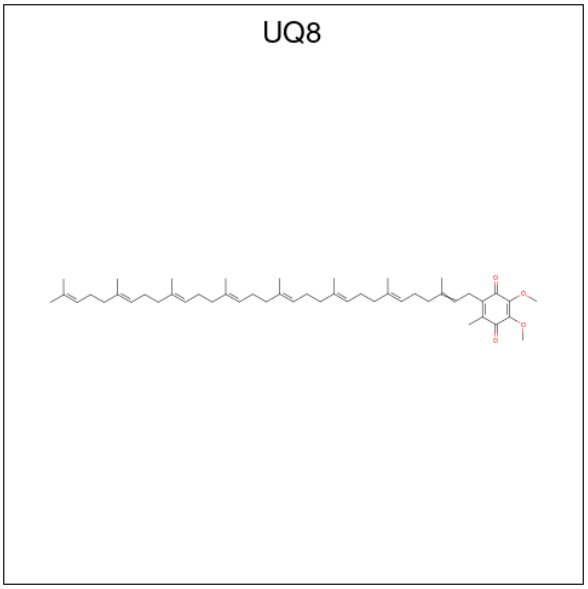
Mol	Chain	Residues	Atoms		AltConf
			Total	Ca	
17	G	1	1	1	0

- Molecule 18 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



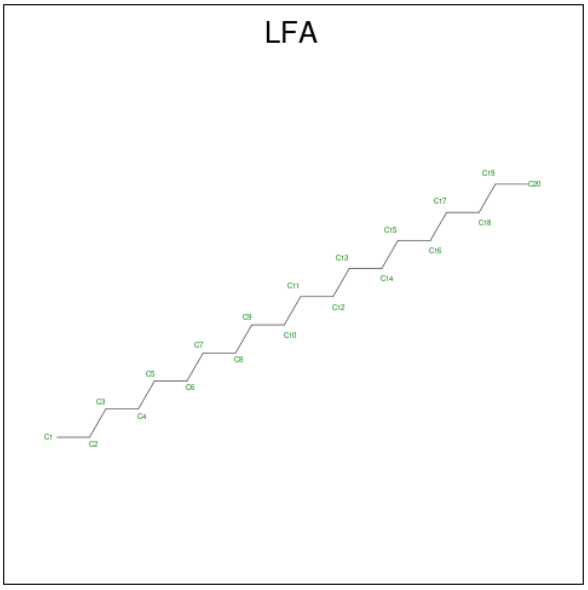
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
18	H	1	51	41	1	8	1	0
			Total	C	N	O	P	
18	H	1	51	41	1	8	1	0
			Total	C	N	O	P	
18	L	1	51	41	1	8	1	0
			Total	C	N	O	P	
18	L	1	44	34	1	8	1	0
			Total	C	N	O	P	
18	L	1	32	22	1	8	1	0
			Total	C	N	O	P	
18	L	1	51	41	1	8	1	0
			Total	C	N	O	P	
18	M	1	51	41	1	8	1	0
			Total	C	N	O	P	
18	M	1	51	41	1	8	1	0
			Total	C	N	O	P	
18	M	1	51	41	1	8	1	0
			Total	C	N	O	P	
18	J	1	51	41	1	8	1	0

- Molecule 19 is Ubiquinone-8 (CCD ID: UQ8) (formula: $C_{49}H_{74}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
19	H	1	29	25	4	0

- Molecule 20 is EICOSANE (CCD ID: LFA) (formula: $C_{20}H_{42}$).



Mol	Chain	Residues	Atoms		AltConf
			Total	C	
20	H	1	20	20	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	C	
20	N	1	20	20	0
			Total	C	
20	N	1	14	14	0

- Molecule 21 is water.

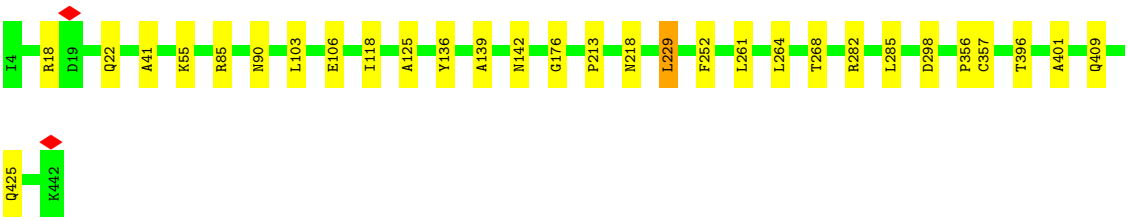
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
21	F	86	86	86	0
			Total	O	
21	E	24	24	24	0
			Total	O	
21	G	328	328	328	0
			Total	O	
21	C	150	150	150	0
			Total	O	
21	B	28	28	28	0
			Total	O	
21	I	72	72	72	0
			Total	O	
21	H	32	32	32	0
			Total	O	
21	A	9	9	9	0
			Total	O	
21	L	49	49	49	0
			Total	O	
21	M	74	74	74	0
			Total	O	
21	N	59	59	59	0
			Total	O	
21	K	19	19	19	0
			Total	O	
21	J	18	18	18	0

3 Residue-property plots (i)

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

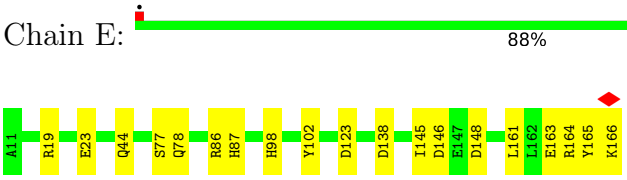
• Molecule 1: NADH-quinone oxidoreductase subunit F

Chain F: 93% 7%



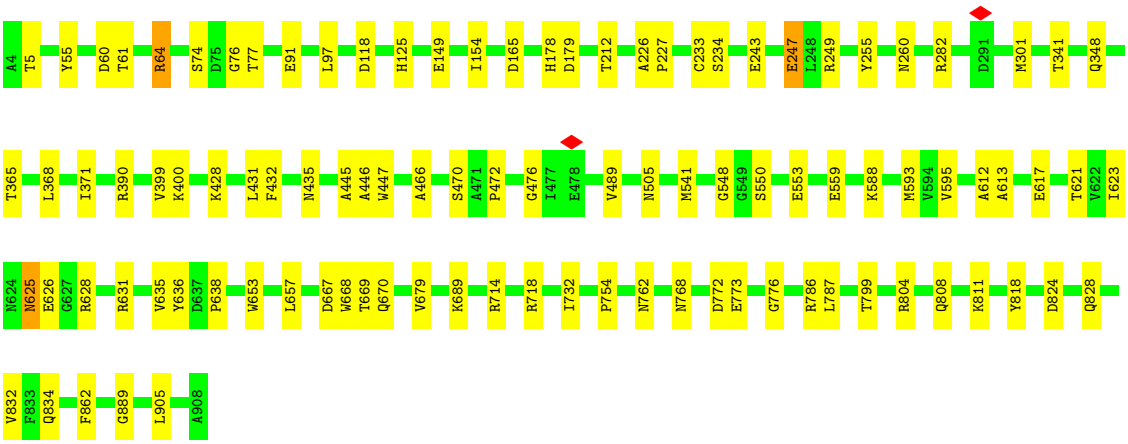
• Molecule 2: NADH dehydrogenase I subunit E

Chain E: 88% 12%



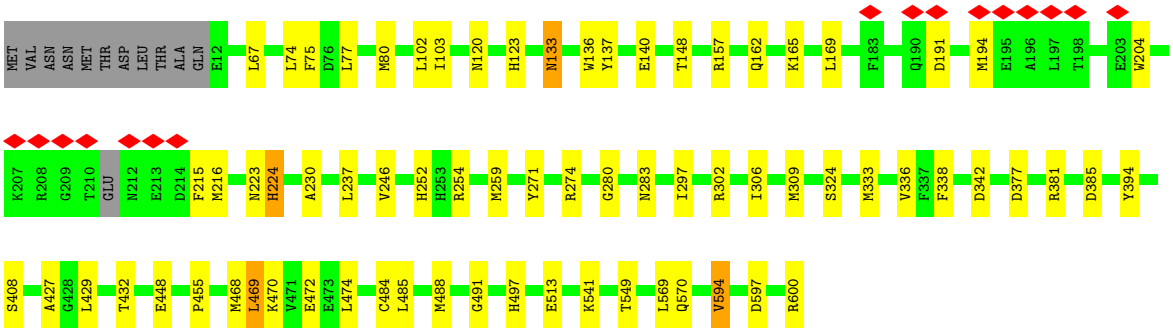
• Molecule 3: NADH-quinone oxidoreductase

Chain G: 89% 11%



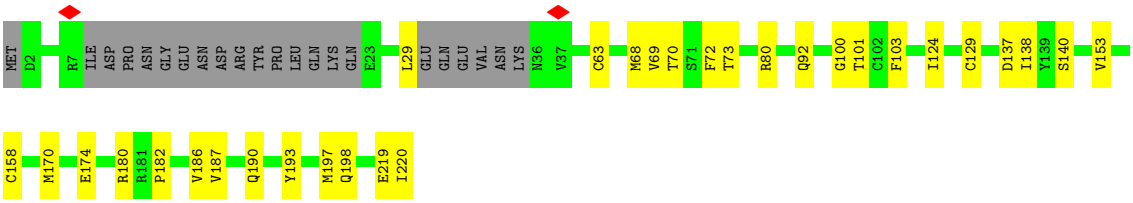
• Molecule 4: NADH-quinone oxidoreductase subunit C/D

Chain C:



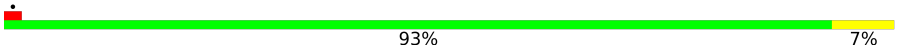
- Molecule 5: NADH-quinone oxidoreductase subunit B

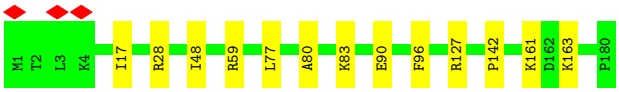
Chain B:



- Molecule 6: NADH-quinone oxidoreductase subunit I

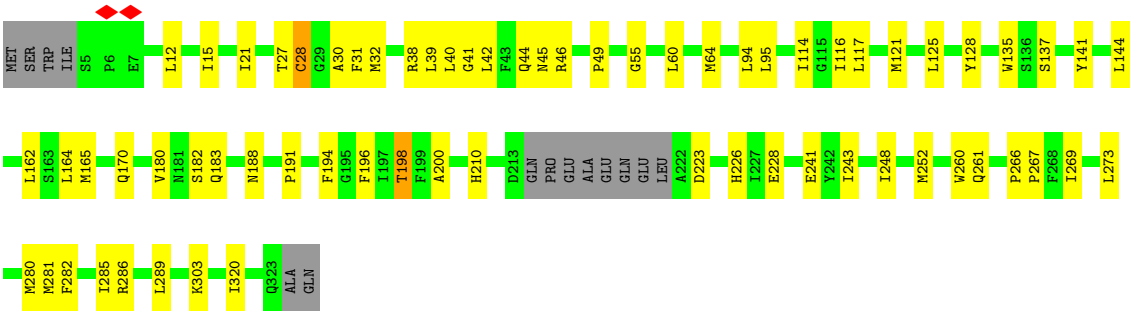
Chain I:





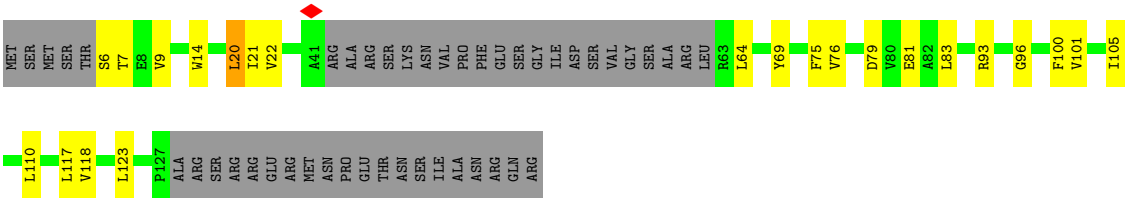
- Molecule 7: NADH-quinone oxidoreductase subunit H

Chain H:



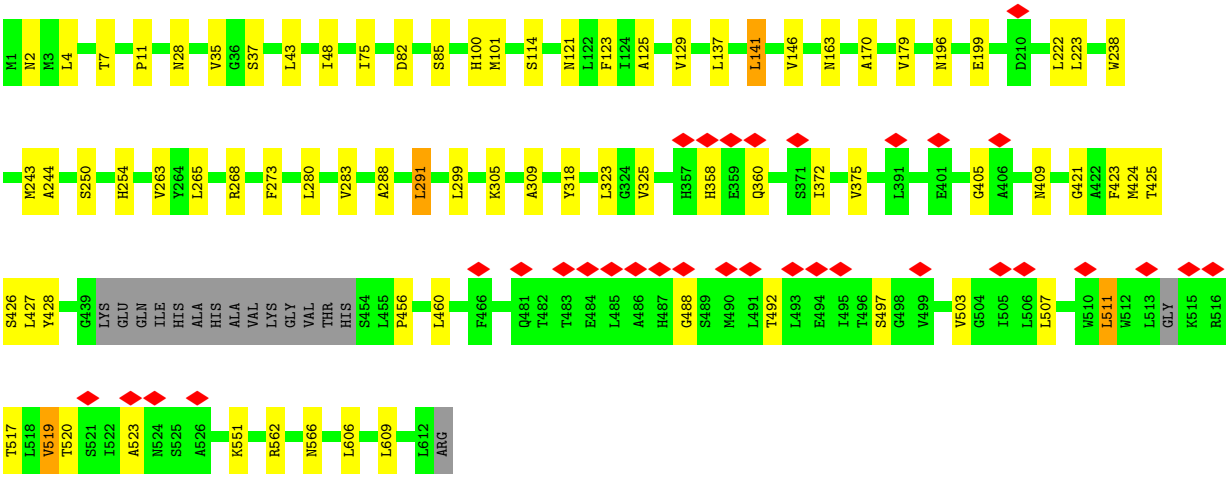
- Molecule 8: NADH-quinone oxidoreductase subunit A

Chain A:



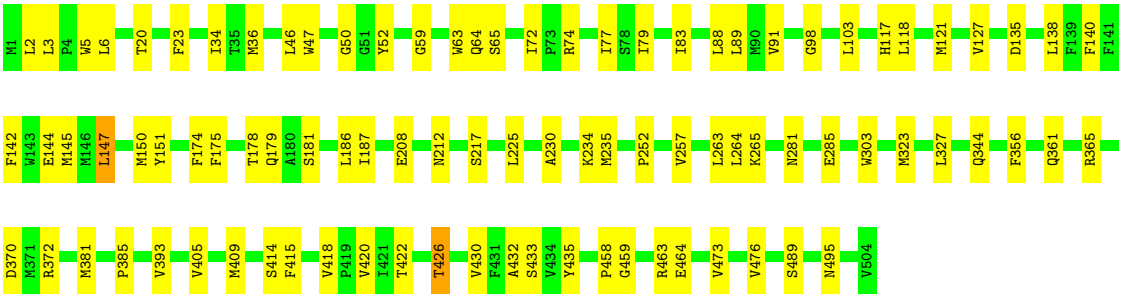
- Molecule 9: Proton-translocating NADH-quinone oxidoreductase, chain L

Chain L:



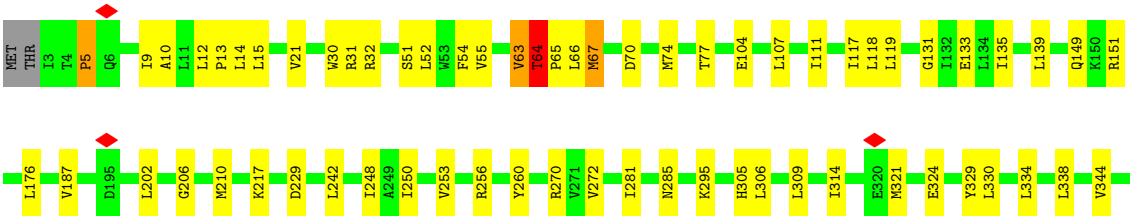
- Molecule 10: NADH dehydrogenase I subunit M

Chain M:



- Molecule 11: NADH-quinone oxidoreductase subunit N

Chain N:

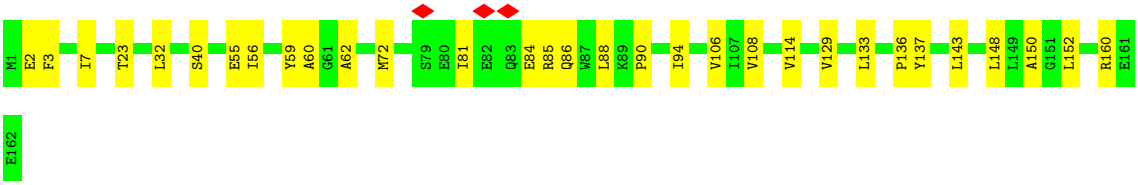


- Molecule 12: NADH-quinone oxidoreductase subunit K

Chain K:

- Molecule 13: NADH-quinone oxidoreductase subunit J

Chain J:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	167032	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 ($e^-/Å^2$)	78	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.680	Depositor
Minimum map value	-0.077	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.055	Depositor
Map size (Å)	154.5, 208.5, 243.0	wwPDB
Map dimensions	486, 417, 309	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.5, 0.5, 0.5	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: SF4, UQ8, FES, FMN, CA, LFA, 3PE

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	F	0.18	0/3486	0.36	0/4713
2	E	0.18	0/1248	0.42	0/1691
3	G	0.20	0/7164	0.41	0/9715
4	C	0.20	0/4865	0.39	0/6605
5	B	0.20	0/1601	0.42	0/2168
6	I	0.20	0/1470	0.42	0/1985
7	H	0.27	0/2510	0.48	0/3415
8	A	0.24	0/825	0.49	0/1123
9	L	0.20	0/4675	0.44	1/6371 (0.0%)
10	M	0.23	0/4074	0.46	0/5546
11	N	0.28	1/3691 (0.0%)	0.54	4/5037 (0.1%)
12	K	0.19	0/769	0.34	0/1040
13	J	0.22	0/1244	0.50	0/1698
All	All	0.22	1/37622 (0.0%)	0.44	5/51107 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	G	0	2
11	N	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	N	5	PRO	CG-CD	-8.27	1.22	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	N	5	PRO	N-CD-CG	-10.30	87.75	103.20
11	N	5	PRO	CA-N-CD	-6.16	103.38	112.00
11	N	5	PRO	CA-CB-CG	-5.29	94.45	104.50
11	N	64	THR	N-CA-C	-5.15	98.42	109.81
9	L	511	LEU	CA-CB-CG	5.01	133.84	116.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	G	260	ASN	Peptide
3	G	668	TRP	Peptide
11	N	63	VAL	Peptide
11	N	64	THR	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3407	0	3374	18	0
2	E	1220	0	1187	12	0
3	G	7013	0	6811	60	0
4	C	4735	0	4635	43	0
5	B	1568	0	1553	19	0
6	I	1436	0	1415	9	0
7	H	2438	0	2488	45	0
8	A	800	0	810	18	0
9	L	4559	0	4701	46	0
10	M	3953	0	4053	56	0
11	N	3602	0	3769	58	0
12	K	760	0	817	9	0
13	J	1218	0	1287	26	0
14	B	8	0	0	1	0
14	F	8	0	0	0	0
14	G	24	0	0	0	0
14	I	16	0	0	0	0
15	F	31	0	19	2	0
16	E	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	G	4	0	0	0	0
17	G	1	0	0	0	0
18	H	102	0	164	6	0
18	J	51	0	82	2	0
18	L	178	0	267	5	0
18	M	153	0	246	3	0
19	H	29	0	33	0	0
20	H	20	0	42	2	0
20	N	34	0	69	0	0
21	A	9	0	0	2	0
21	B	28	0	0	0	0
21	C	150	0	0	1	0
21	E	24	0	0	0	0
21	F	86	0	0	0	0
21	G	328	0	0	4	0
21	H	32	0	0	0	0
21	I	72	0	0	2	0
21	J	18	0	0	0	0
21	K	19	0	0	0	0
21	L	49	0	0	1	0
21	M	74	0	0	3	0
21	N	59	0	0	2	0
All	All	38320	0	37822	385	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 385 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)
11:N:63:VAL:O	11:N:67:MET:HB3	1.82	0.79
7:H:116:ILE:HD11	7:H:164:LEU:HB3	1.71	0.71
7:H:141:TYR:HB3	7:H:223:ASP:H	1.57	0.69
10:M:181:SER:HB2	10:M:230:ALA:HA	1.74	0.68
5:B:197:MET:HE3	5:B:198:GLN:H	1.62	0.65

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	F	437/439 (100%)	432 (99%)	5 (1%)	0	100	100
2	E	154/156 (99%)	150 (97%)	4 (3%)	0	100	100
3	G	903/905 (100%)	881 (98%)	21 (2%)	1 (0%)	48	64
4	C	584/600 (97%)	569 (97%)	15 (3%)	0	100	100
5	B	192/220 (87%)	184 (96%)	8 (4%)	0	100	100
6	I	178/180 (99%)	174 (98%)	4 (2%)	0	100	100
7	H	307/325 (94%)	298 (97%)	9 (3%)	0	100	100
8	A	97/147 (66%)	95 (98%)	2 (2%)	0	100	100
9	L	591/613 (96%)	579 (98%)	12 (2%)	0	100	100
10	M	502/504 (100%)	488 (97%)	14 (3%)	0	100	100
11	N	472/485 (97%)	459 (97%)	12 (2%)	1 (0%)	43	58
12	K	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
13	J	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
All	All	4675/4836 (97%)	4561 (98%)	112 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	N	64	THR
3	G	669	THR

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	F	353/353 (100%)	350 (99%)	3 (1%)	73	86
2	E	129/129 (100%)	128 (99%)	1 (1%)	73	86
3	G	730/732 (100%)	723 (99%)	7 (1%)	68	84
4	C	504/519 (97%)	495 (98%)	9 (2%)	51	73
5	B	171/192 (89%)	168 (98%)	3 (2%)	51	73
6	I	154/154 (100%)	153 (99%)	1 (1%)	78	89
7	H	256/269 (95%)	249 (97%)	7 (3%)	39	62
8	A	79/119 (66%)	77 (98%)	2 (2%)	42	64
9	L	473/486 (97%)	462 (98%)	11 (2%)	44	66
10	M	413/413 (100%)	403 (98%)	10 (2%)	43	65
11	N	377/385 (98%)	372 (99%)	5 (1%)	61	80
12	K	79/79 (100%)	79 (100%)	0	100	100
13	J	126/128 (98%)	123 (98%)	3 (2%)	43	65
All	All	3844/3958 (97%)	3782 (98%)	62 (2%)	54	76

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	H	198	THR
11	N	359	LEU
9	L	114	SER
11	N	67	MET
13	J	2	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
10	M	64	GLN
11	N	404	GLN
10	M	117	HIS
10	M	308	GLN
3	G	625	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 25 ligands modelled in this entry, 1 is monoatomic - leaving 24 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
18	3PE	M	1203	-	50,50,50	0.29	0	53,55,55	0.28	0
14	SF4	I	201	6	0,12,12	-	-	-		
14	SF4	F	501	1	0,12,12	-	-	-		
18	3PE	H	401	-	50,50,50	0.31	0	53,55,55	0.29	0
18	3PE	L	802	-	43,43,50	0.33	0	46,48,55	0.31	0
14	SF4	G	1002	3	0,12,12	-	-	-		
16	FES	G	1004	3	0,4,4	-	-	-		
16	FES	E	201	2	0,4,4	-	-	-		
18	3PE	L	803	-	31,31,50	0.37	0	34,36,55	0.36	0
14	SF4	B	301	5	0,12,12	-	-	-		
15	FMN	F	502	-	33,33,33	1.06	2 (6%)	48,50,50	1.27	6 (12%)
18	3PE	J	201	-	50,50,50	0.30	0	53,55,55	0.29	0
19	UQ8	H	402	-	29,29,53	0.26	0	35,38,67	0.52	1 (2%)
18	3PE	M	1202	-	50,50,50	0.31	0	53,55,55	0.30	0
18	3PE	L	801	-	50,50,50	0.30	0	53,55,55	0.28	0
14	SF4	I	202	6	0,12,12	-	-	-		
18	3PE	H	404	-	50,50,50	0.31	0	53,55,55	0.31	0
18	3PE	L	804	-	50,50,50	0.30	0	53,55,55	0.27	0
18	3PE	M	1201	-	50,50,50	0.29	0	53,55,55	0.32	0
20	LFA	N	501	-	19,19,19	0.14	0	18,18,18	0.16	0
14	SF4	G	1003	3	0,12,12	-	-	-		
20	LFA	N	502	-	13,13,19	0.13	0	12,12,18	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
20	LFA	H	403	-	19,19,19	0.14	0	18,18,18	0.11	0
14	SF4	G	1001	3	0,12,12	-	-	-		

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
18	3PE	M	1203	-	-	13/54/54/54	-
14	SF4	I	201	6	-	-	0/6/5/5
18	3PE	H	401	-	-	8/54/54/54	-
14	SF4	F	501	1	-	-	0/6/5/5
18	3PE	L	802	-	-	14/47/47/54	-
14	SF4	G	1002	3	-	-	0/6/5/5
16	FES	G	1004	3	-	-	0/1/1/1
16	FES	E	201	2	-	-	0/1/1/1
18	3PE	L	803	-	-	8/35/35/54	-
14	SF4	B	301	5	-	-	0/6/5/5
15	FMN	F	502	-	-	6/18/18/18	0/3/3/3
18	3PE	J	201	-	-	12/54/54/54	-
19	UQ8	H	402	-	-	3/23/47/75	0/1/1/1
18	3PE	M	1202	-	-	9/54/54/54	-
18	3PE	L	801	-	-	8/54/54/54	-
18	3PE	H	404	-	-	13/54/54/54	-
14	SF4	I	202	6	-	-	0/6/5/5
18	3PE	L	804	-	-	12/54/54/54	-
18	3PE	M	1201	-	-	13/54/54/54	-
20	LFA	N	501	-	-	0/17/17/17	-
14	SF4	G	1003	3	-	-	0/6/5/5
20	LFA	N	502	-	-	0/11/11/17	-
20	LFA	H	403	-	-	1/17/17/17	-
14	SF4	G	1001	3	-	-	0/6/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	F	502	FMN	C4A-N5	3.55	1.37	1.30
15	F	502	FMN	C10-N1	2.22	1.37	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	F	502	FMN	C4-N3-C2	-3.25	119.64	125.64
15	F	502	FMN	C4A-C10-N10	2.91	120.73	116.48
15	F	502	FMN	C4A-C4-N3	2.72	120.09	113.19
15	F	502	FMN	O4-C4-C4A	-2.53	119.89	126.60
15	F	502	FMN	C4A-C10-N1	-2.41	119.15	124.73

There are no chirality outliers.

5 of 120 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	F	502	FMN	N10-C1'-C2'-O2'
15	F	502	FMN	N10-C1'-C2'-C3'
15	F	502	FMN	C5'-O5'-P-O2P
15	F	502	FMN	C5'-O5'-P-O3P
18	H	401	3PE	C11-O13-P-O12

There are no ring outliers.

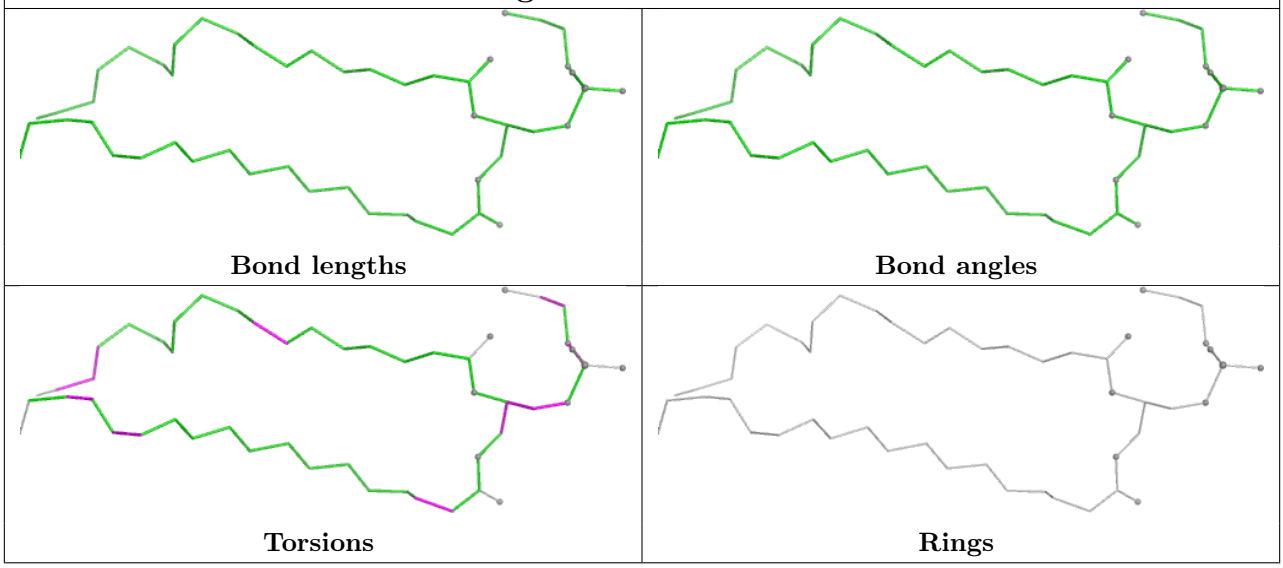
12 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	H	401	3PE	2	0
18	L	802	3PE	1	0
18	L	803	3PE	1	0
14	B	301	SF4	1	0
15	F	502	FMN	2	0
18	J	201	3PE	2	0
18	M	1202	3PE	1	0
18	L	801	3PE	2	0
18	H	404	3PE	4	0
18	L	804	3PE	1	0
18	M	1201	3PE	2	0
20	H	403	LFA	2	0

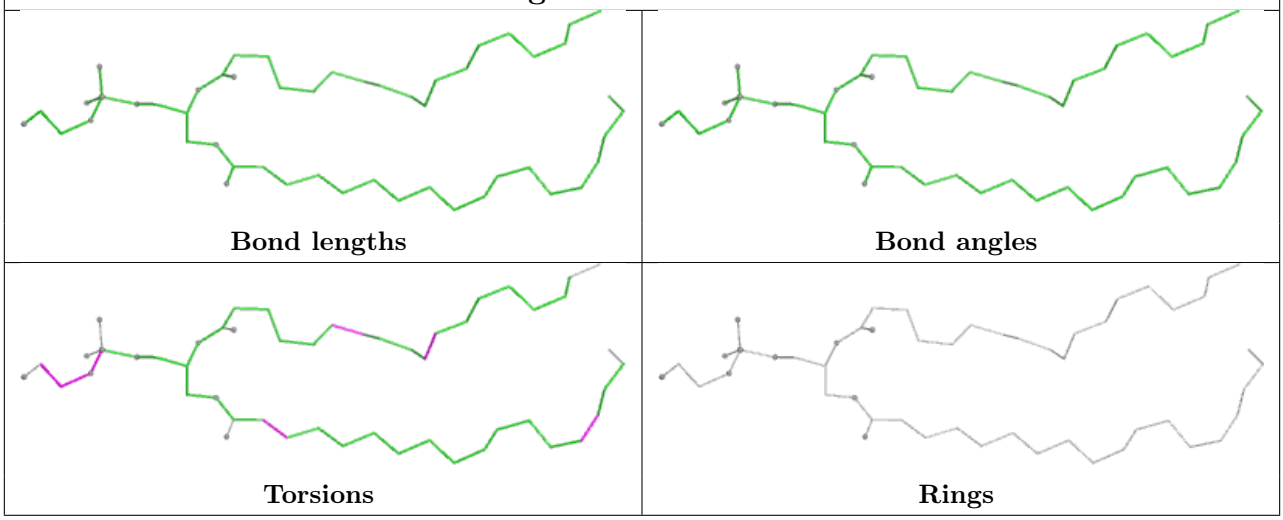
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

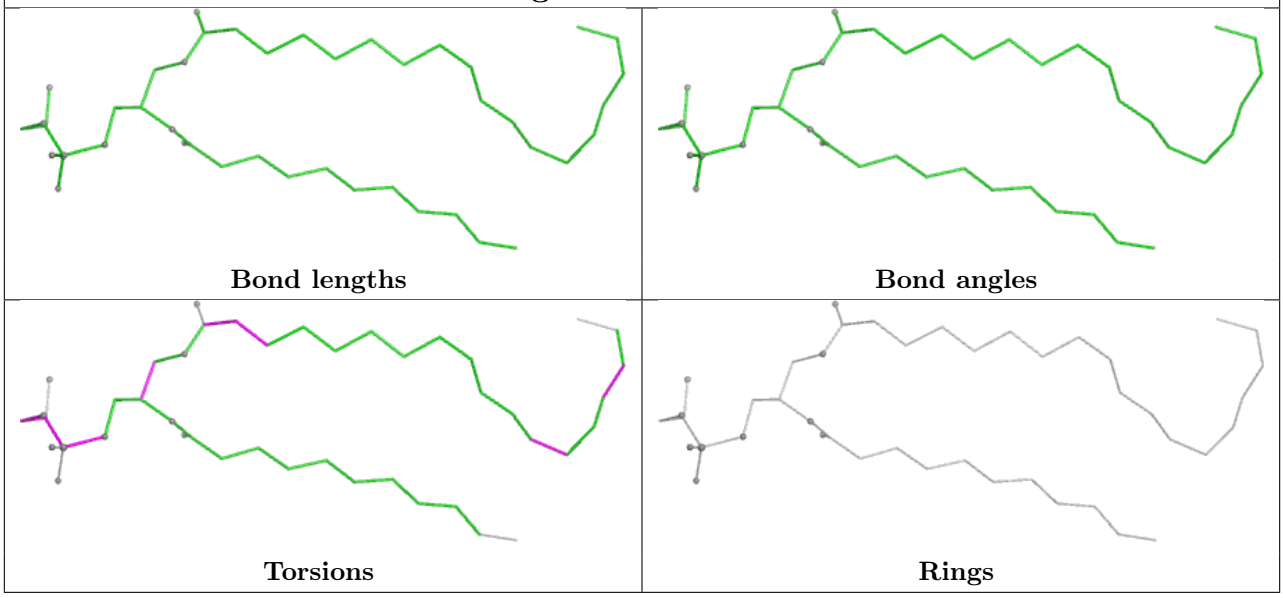
Ligand 3PE M 1203



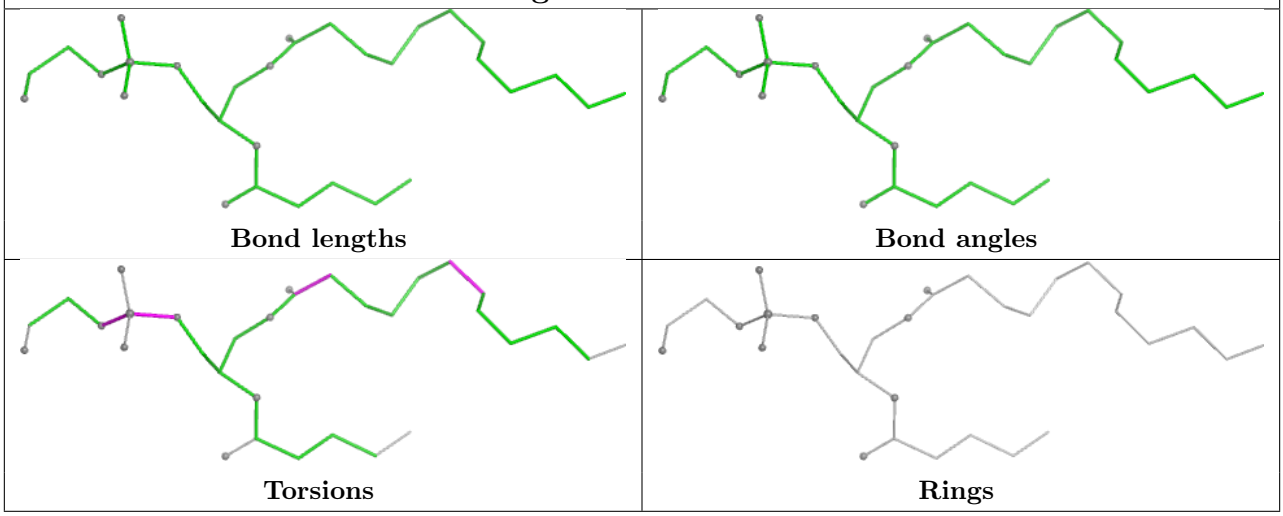
Ligand 3PE H 401



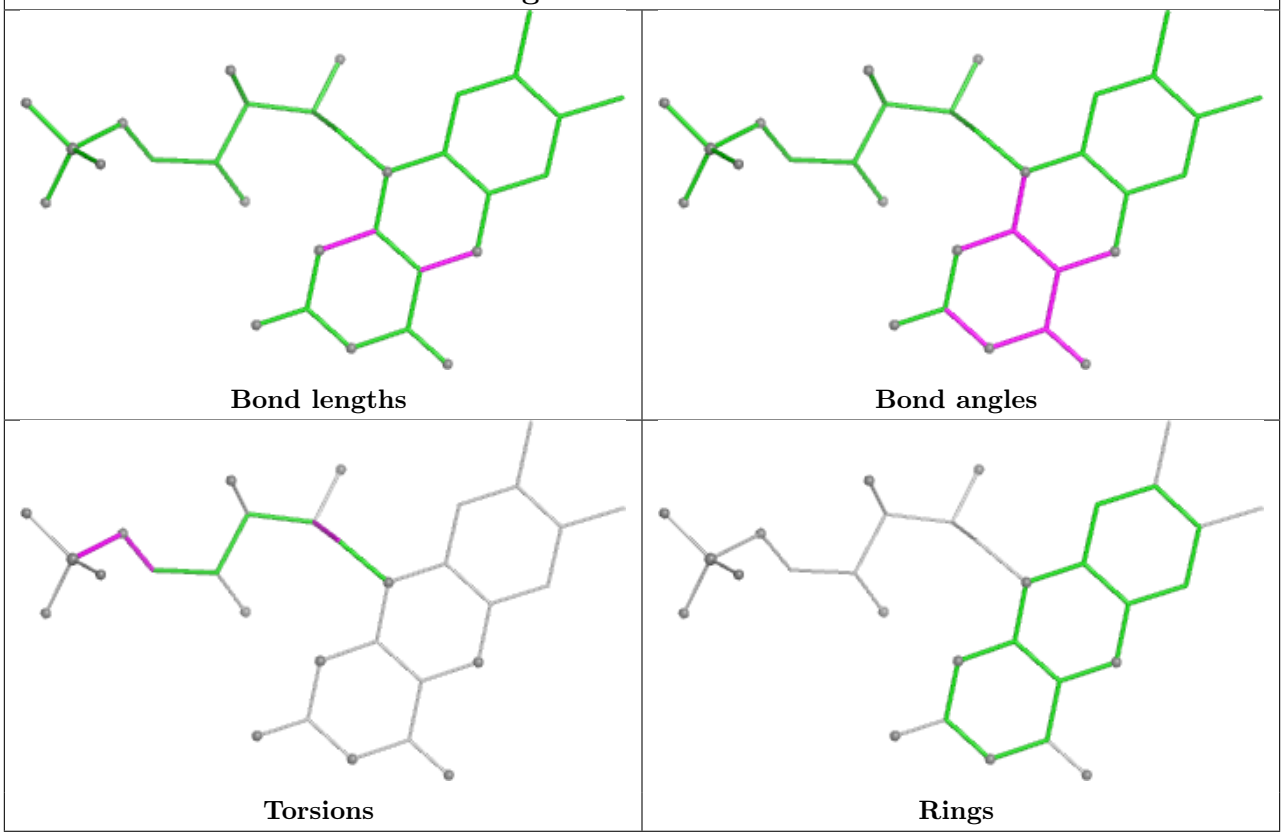
Ligand 3PE L 802



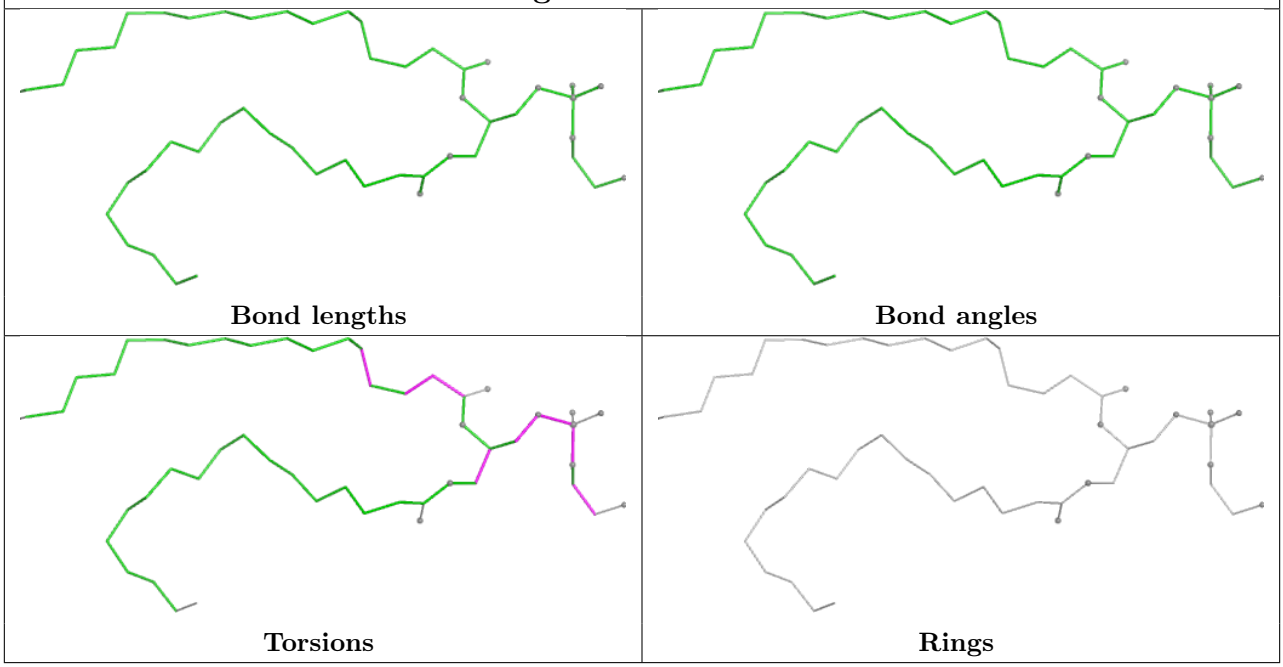
Ligand 3PE L 803



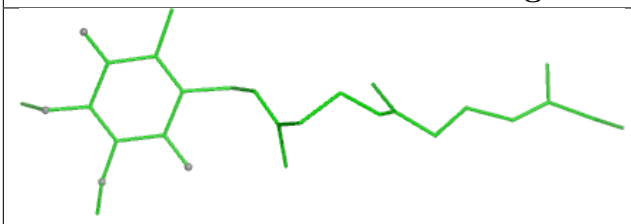
Ligand FMN F 502



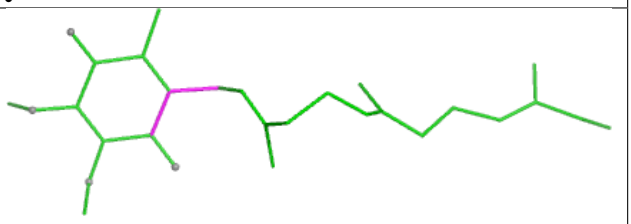
Ligand 3PE J 201



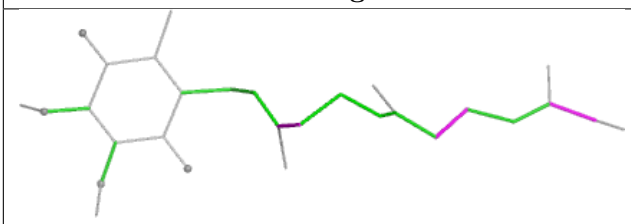
Ligand UQ8 H 402



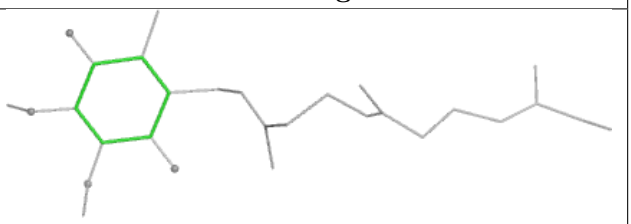
Bond lengths



Bond angles

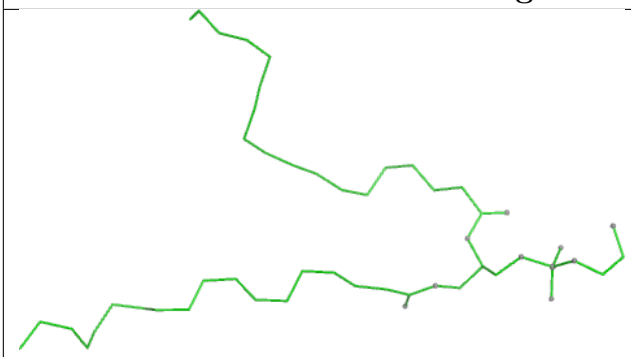


Torsions

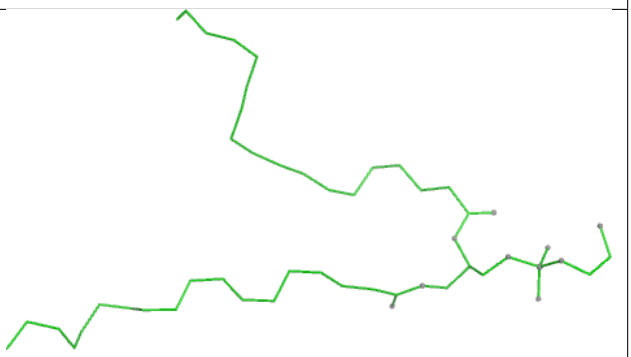


Rings

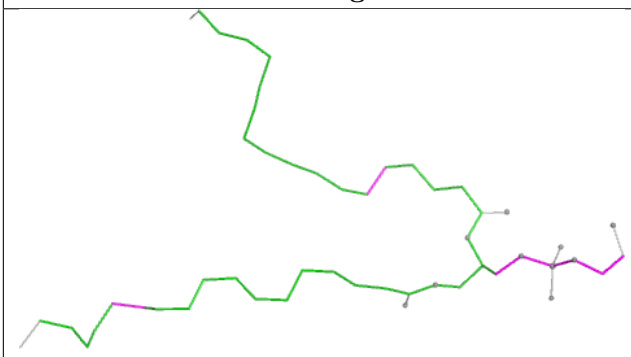
Ligand 3PE M 1202



Bond lengths



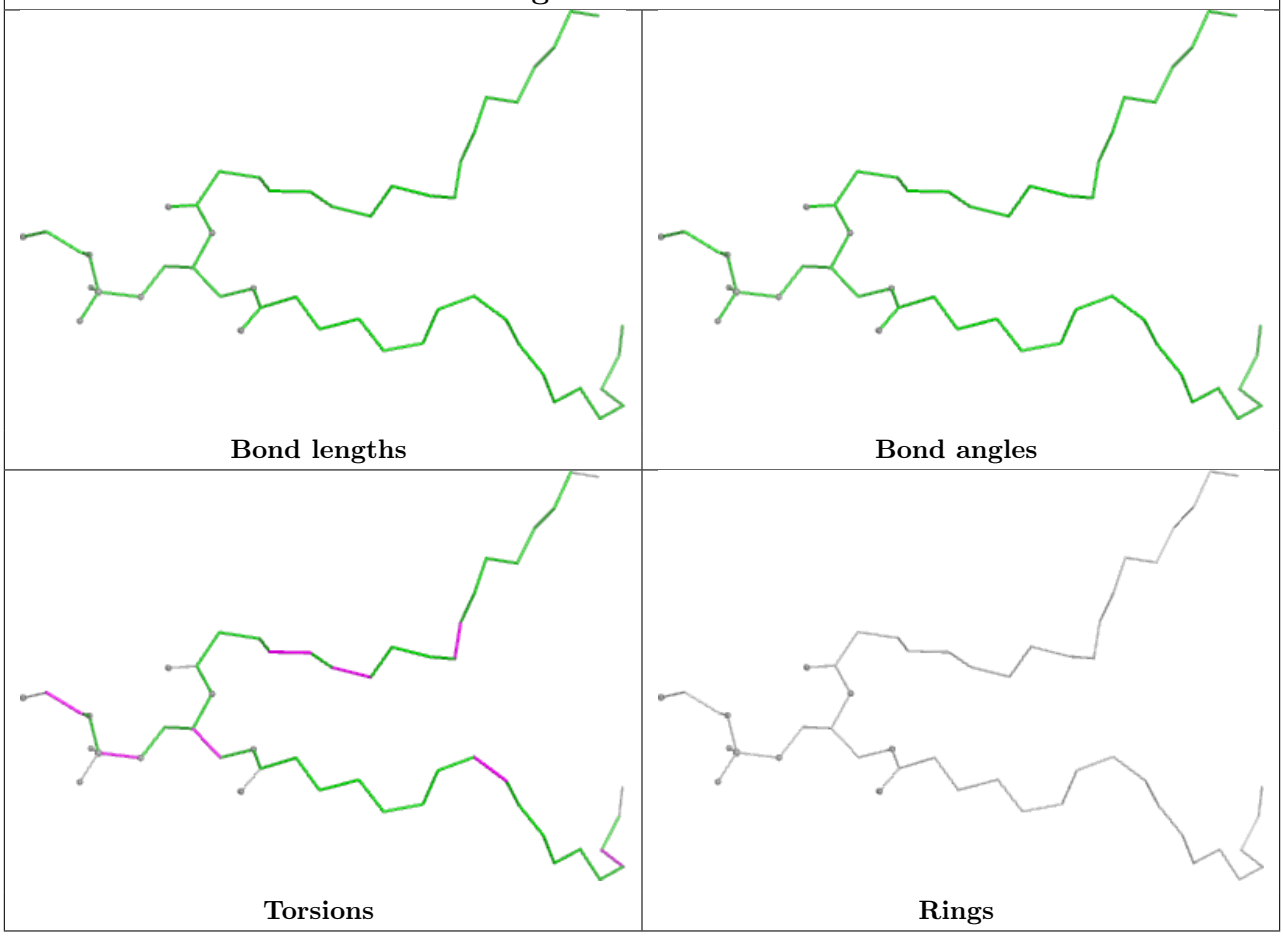
Bond angles



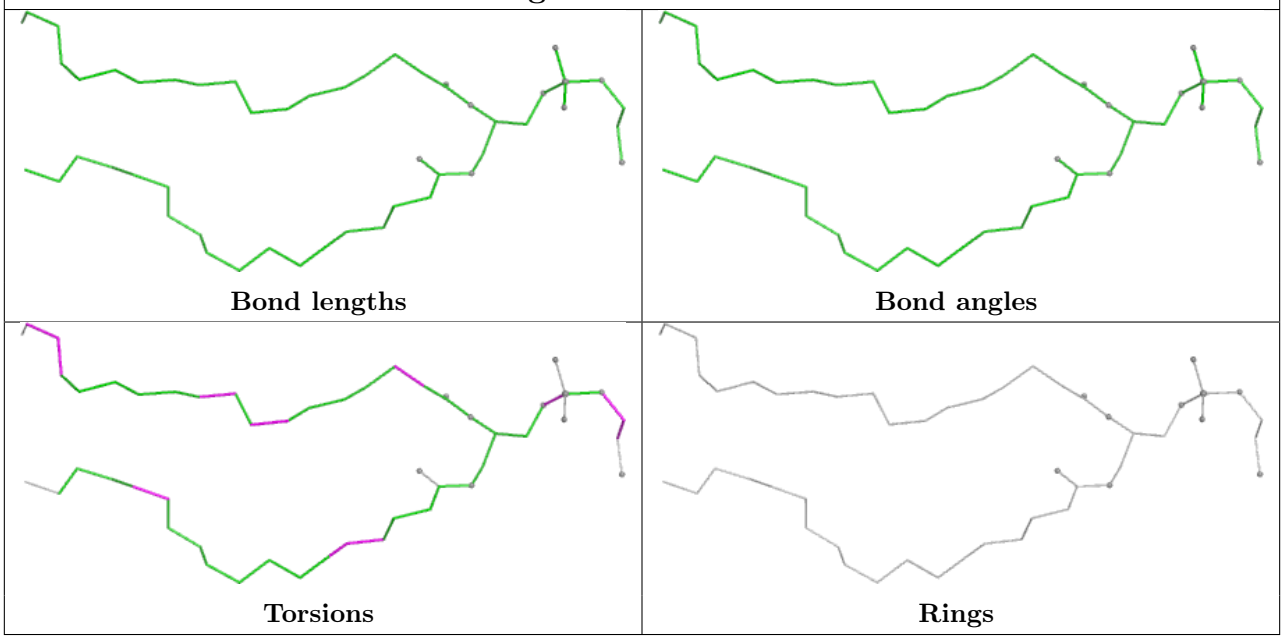
Torsions

Rings

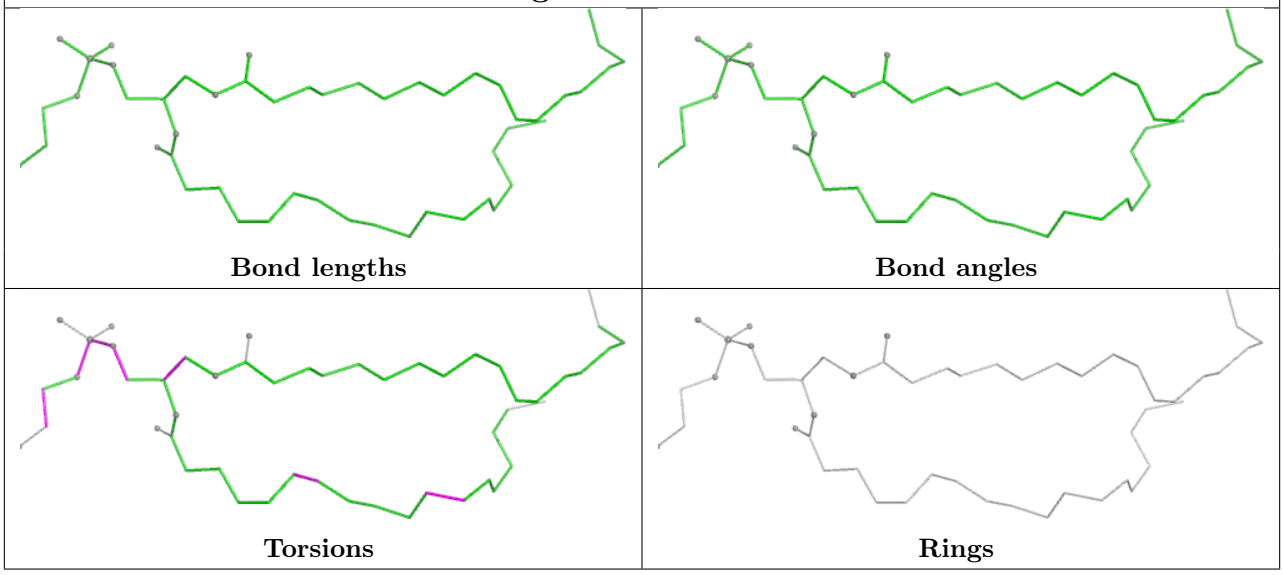
Ligand 3PE L 801



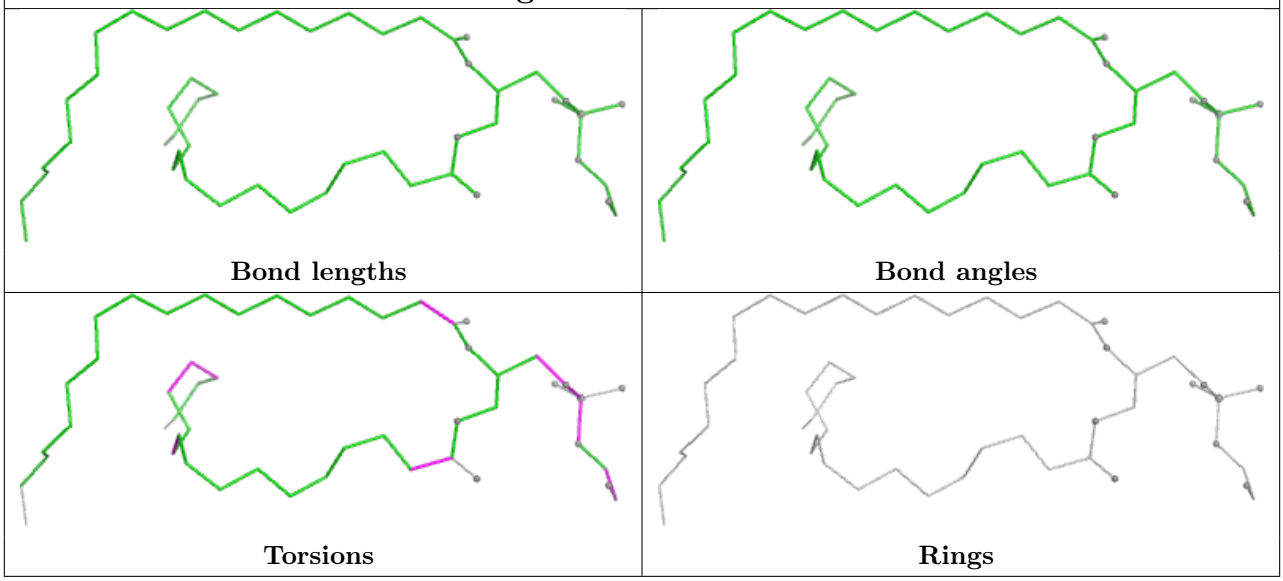
Ligand 3PE H 404



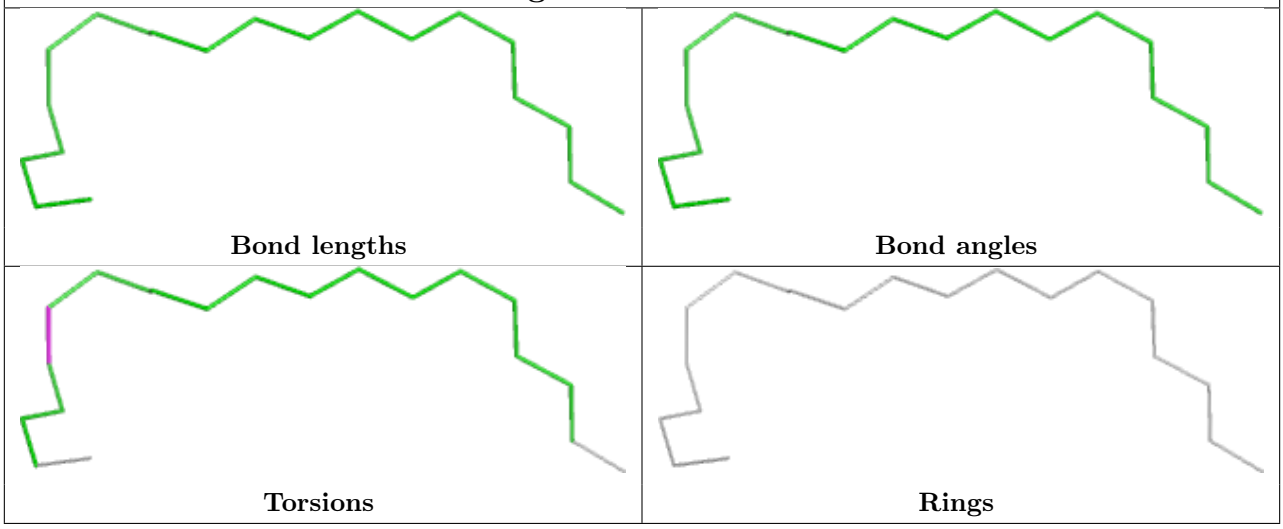
Ligand 3PE L 804



Ligand 3PE M 1201



Ligand LFA H 403



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.

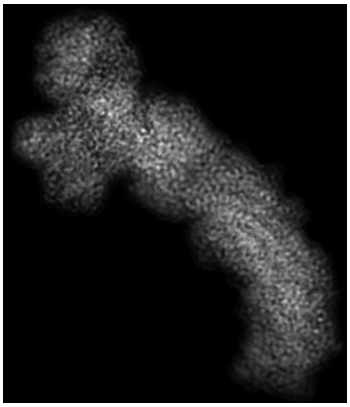
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-13235. These allow visual inspection of the internal detail of the map and identification of artifacts.

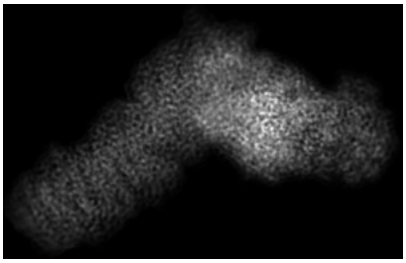
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

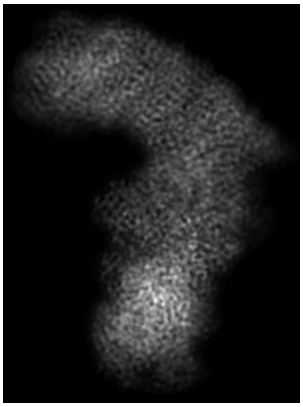
6.1.1 Primary map



X



Y

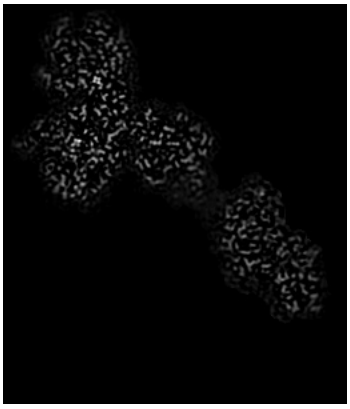


Z

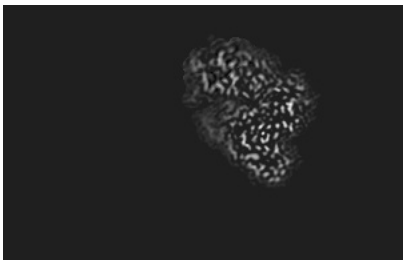
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 154



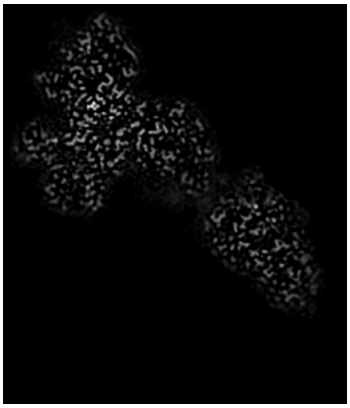
Y Index: 208

Z Index: 243

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: 167

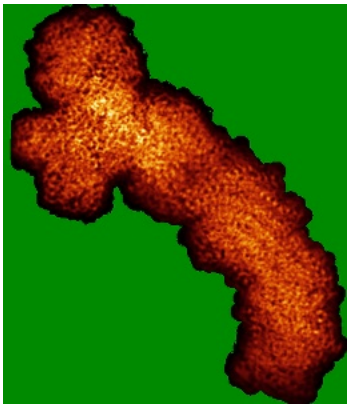
Y Index: 112

Z Index: 320

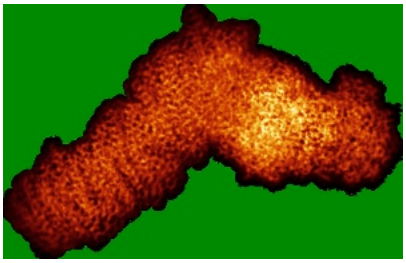
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

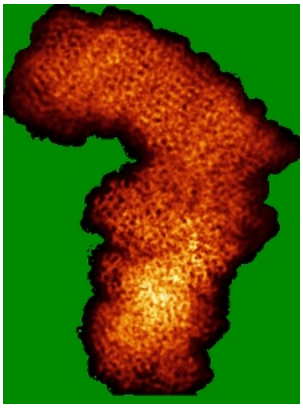
6.4.1 Primary map



X



Y

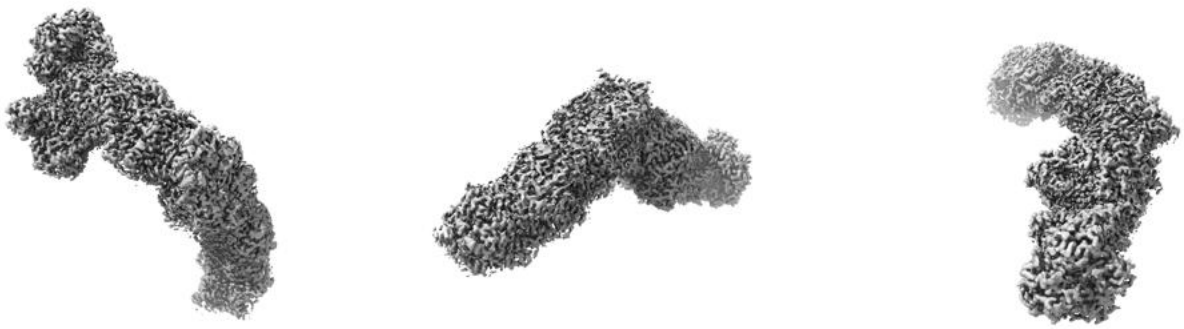


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

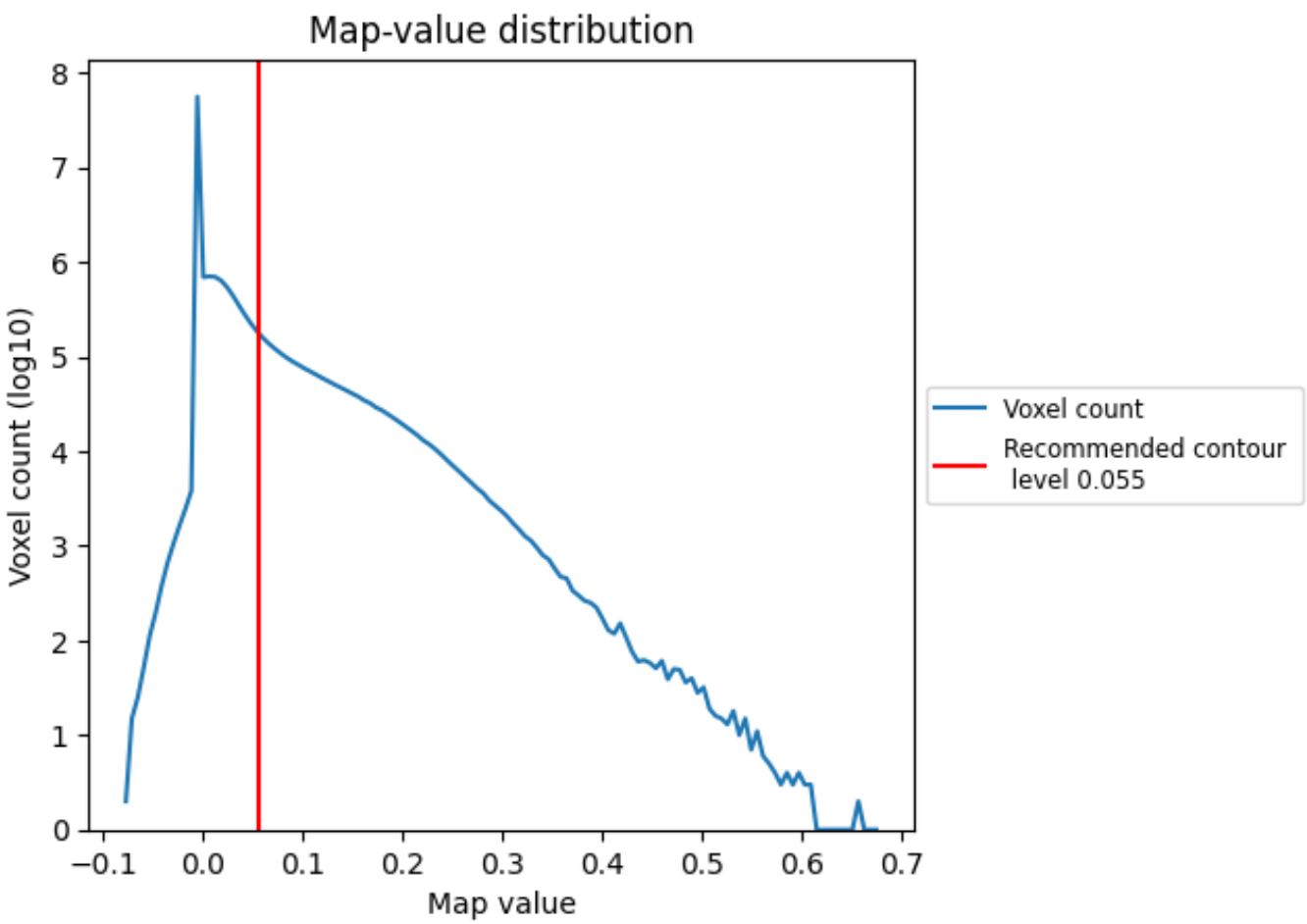
6.6 Mask visualisation (i)

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

7 Map analysis (i)

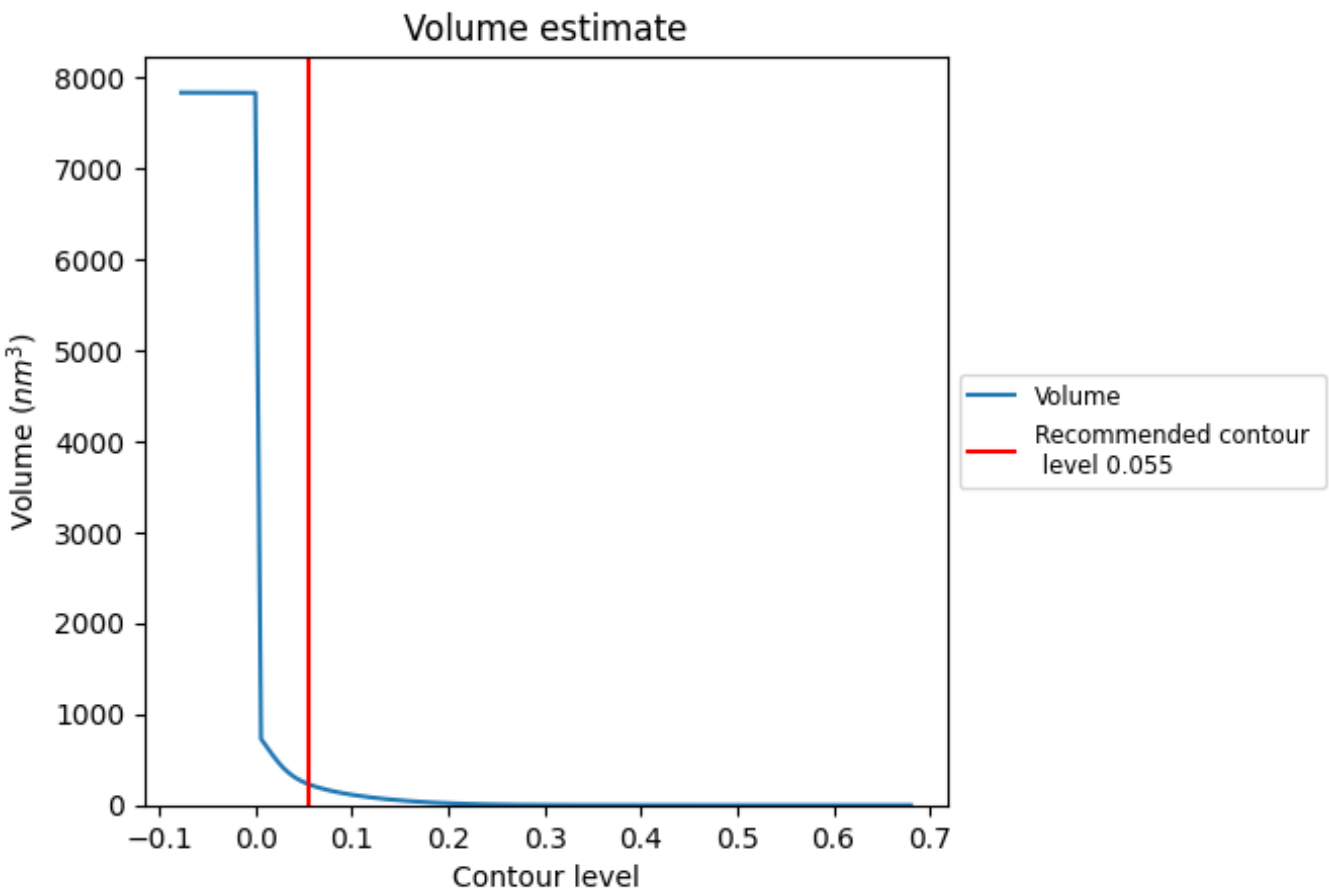
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

7.2 Volume estimate (i)



The volume at the recommended contour level is 231 nm^3; this corresponds to an approximate mass of 208 kDa.

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

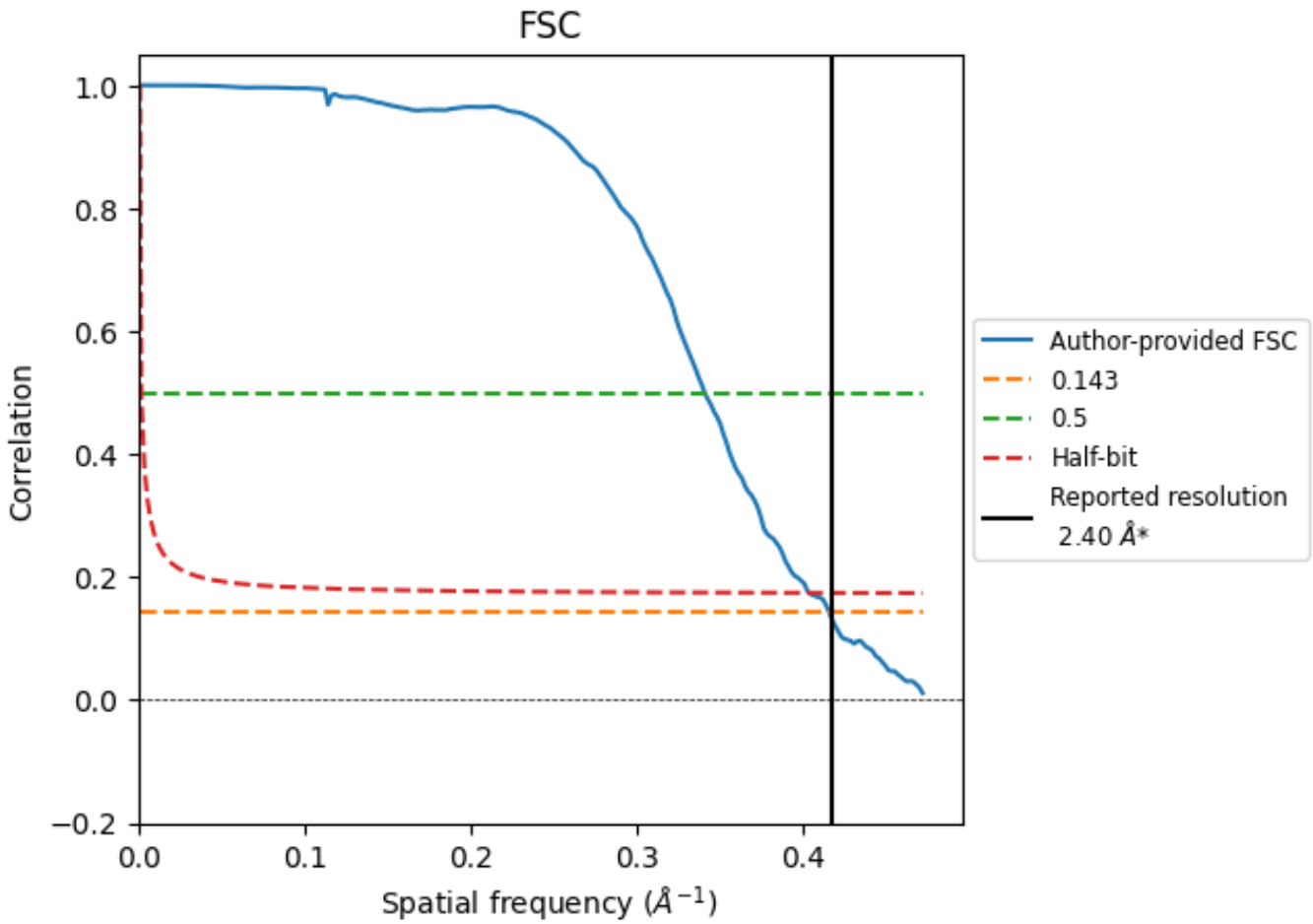
7.3 Rotationally averaged power spectrum (i)

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

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.417 Å^{-1}

8.2 Resolution estimates (i)

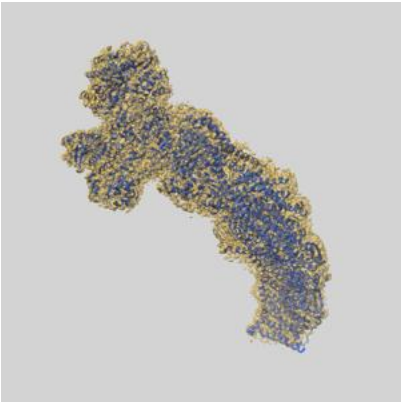
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.41	2.94	2.48
Unmasked-calculated*	-	-	-

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

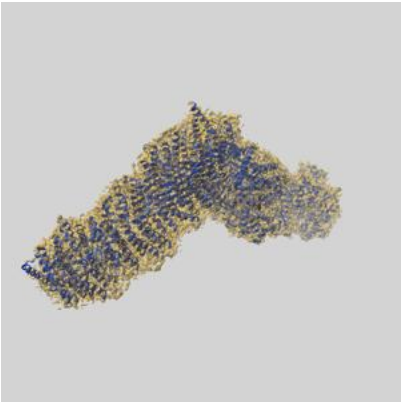
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-13235 and PDB model 7P7C. Per-residue inclusion information can be found in section 3 on page 11.

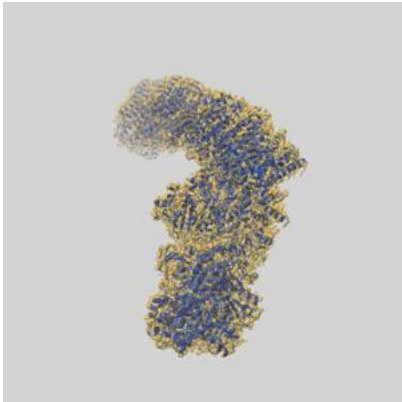
9.1 Map-model overlay (i)



X



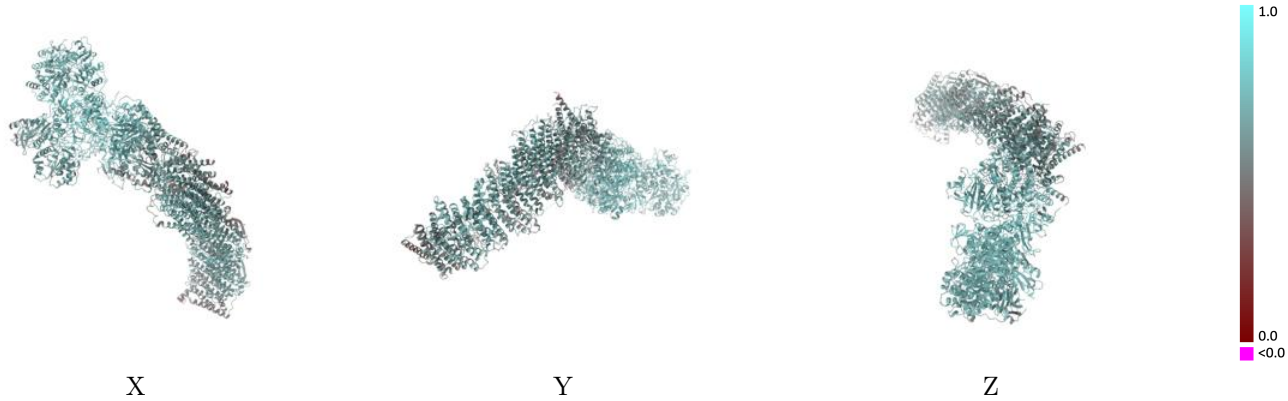
Y



Z

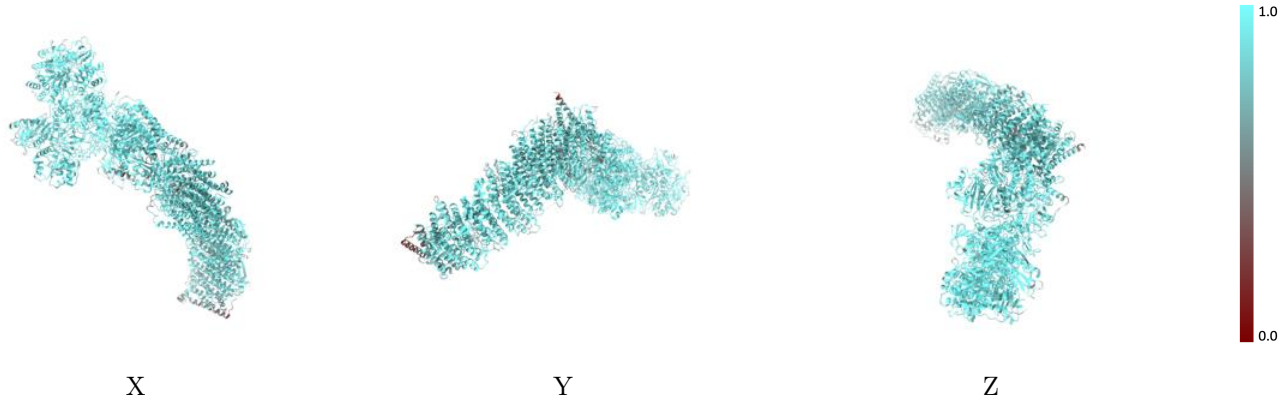
The images above show the 3D surface view of the map at the recommended contour level 0.055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



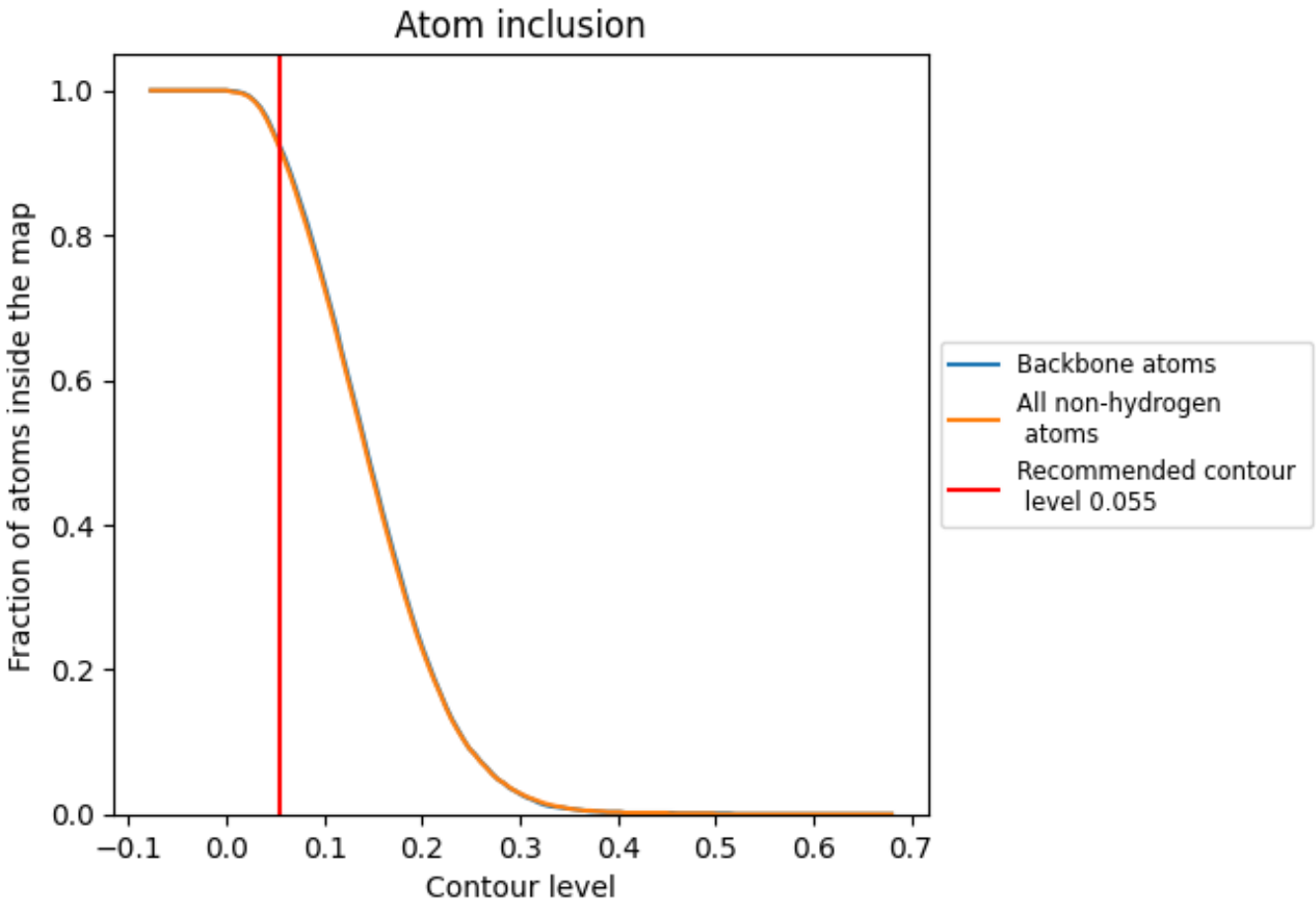
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.055).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9190	0.6500
A	0.8930	0.5810
B	0.9330	0.6690
C	0.9420	0.6920
E	0.9430	0.6860
F	0.9450	0.6850
G	0.9510	0.6900
H	0.8890	0.5860
I	0.9390	0.7040
J	0.9070	0.6260
K	0.9750	0.6940
L	0.8380	0.5800
M	0.9210	0.6270
N	0.9250	0.6230