



## wwPDB EM Validation Summary Report ⓘ

Sep 27, 2022 – 12:30 am BST

PDB ID : 7P61  
EMDB ID : EMD-13214  
Title : Complex I from *E. coli*, DDM-purified, with NADH, Resting state  
Authors : Kravchuk, V.; Kampjut, D.; Sazanov, L.  
Deposited on : 2021-07-15  
Resolution : 3.20 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

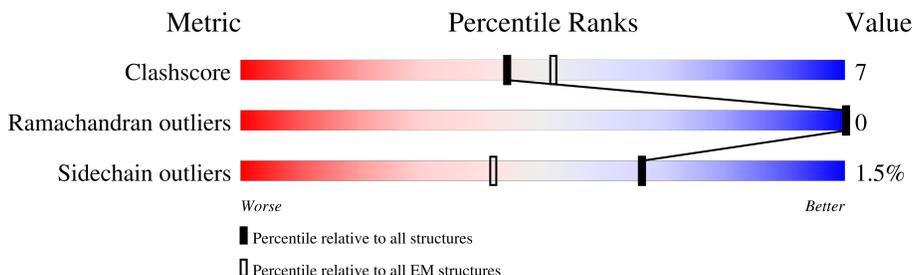
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 Å.

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



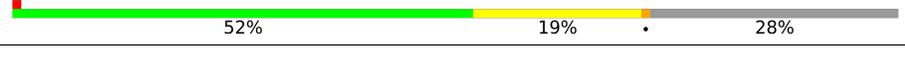
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	F	442	 82% 18%
2	E	156	 85% 15%
3	G	905	 80% 20%
4	C	600	 78% 16% • 5%
5	B	220	 71% 14% • 13%
6	I	147	 76% 24%
7	L	613	 80% 16% ••
8	M	504	 83% 17%

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Mol	Chain	Length	Quality of chain
9	N	485	 80% 19%
10	H	325	 75% 21%
11	A	147	 52% 19% 28%
12	K	100	 81% 19%
13	J	175	 81% 18%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
14	SF4	G	1001	-	-	X	-

## 2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 36690 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	442	3432	2177	601	633	21	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	7022	4388	1269	1328	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	571	4606	2953	801	829	23	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	191	1518	961	261	279	17	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	147	1157	734	194	217	12	0	0

- Molecule 7 is a protein called Proton-translocating NADH-quinone oxidoreductase, chain L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	L	593	4525	3015	717	762	31	0	0

- Molecule 8 is a protein called NADH dehydrogenase I subunit M.

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

- Molecule 9 is a protein called NADH-quinone oxidoreductase subunit N.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	N	479	3630	2424	573	613	20	0	0

- Molecule 10 is a protein called NADH-quinone oxidoreductase subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	H	312	2449	1648	379	404	18	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	A	106	840	573	131	131	5	0	0

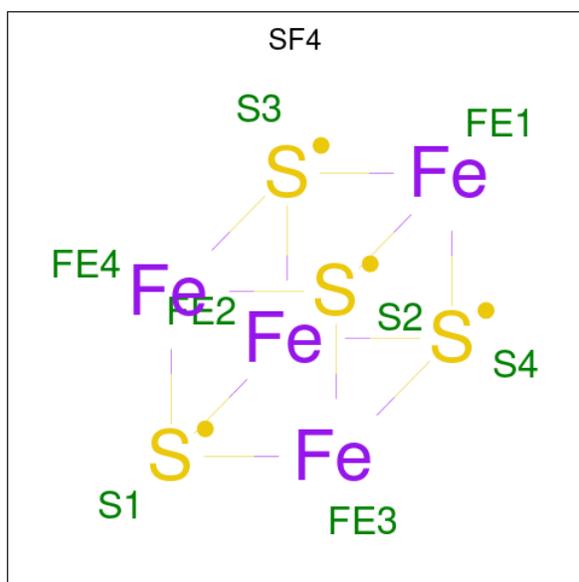
- Molecule 12 is a protein called NADH-quinone oxidoreductase subunit K.

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.

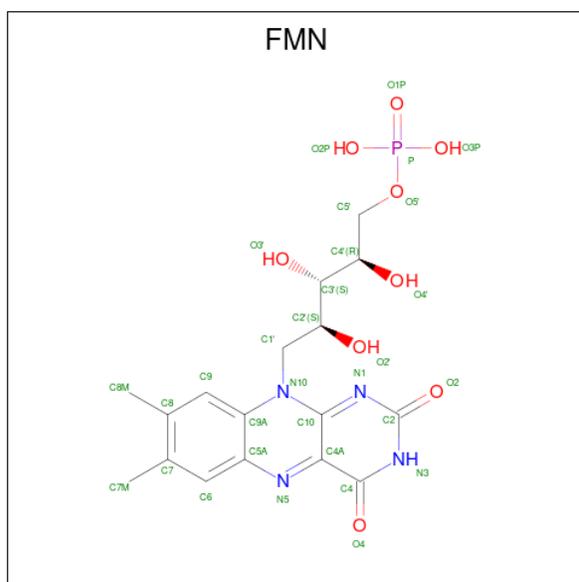
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	J	175	1326	881	209	229	7	0	0

- Molecule 14 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



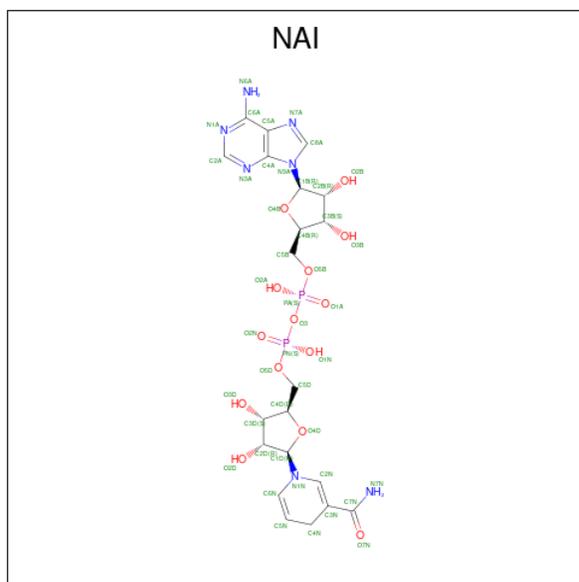
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
14	F	1	8	4	4	0
14	G	1	24	12	12	0
14	G	1	24	12	12	0
14	G	1	24	12	12	0
14	B	1	8	4	4	0
14	I	1	16	8	8	0
14	I	1	16	8	8	0

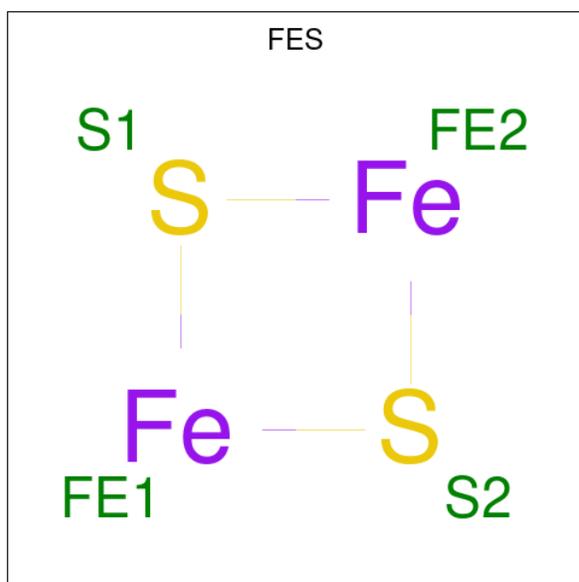
- Molecule 15 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P).



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

- Molecule 16 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula:  $C_{21}H_{29}N_7O_{14}P_2$ ).



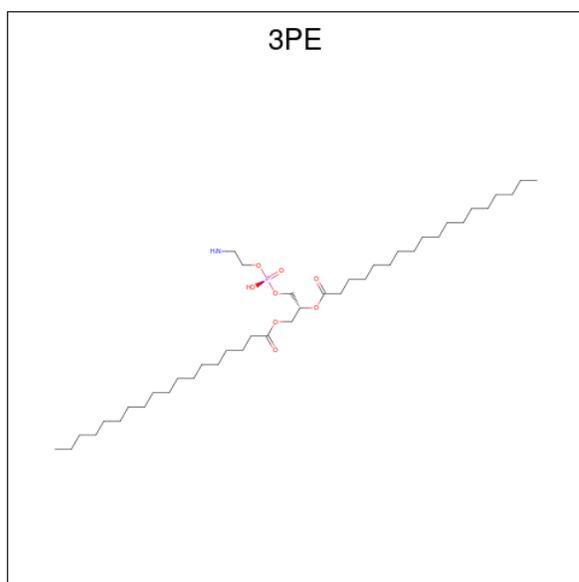


Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
17	E	1	4	2	2	0
17	G	1	4	2	2	0

- Molecule 18 is CALCIUM ION (three-letter code: CA) (formula: Ca).

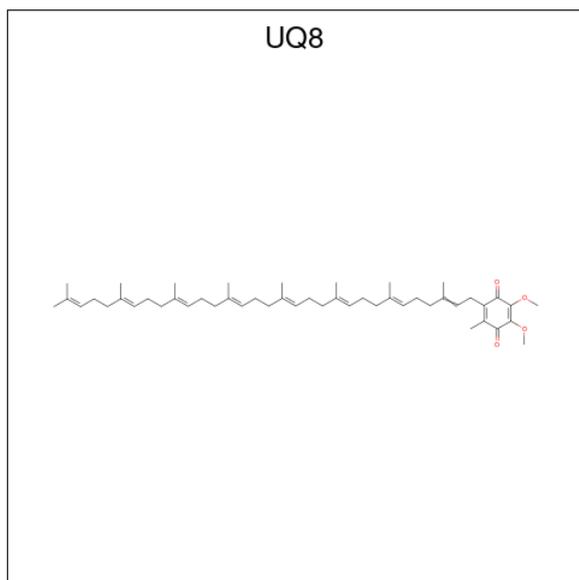
Mol	Chain	Residues	Atoms		AltConf
			Total	Ca	
18	G	1	1	1	0

- Molecule 19 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (three-letter code: 3PE) (formula: C<sub>41</sub>H<sub>82</sub>NO<sub>8</sub>P).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
19	L	1	88	68	2	16	2	0
19	L	1	88	68	2	16	2	0

- Molecule 20 is Ubiquinone-8 (three-letter code: UQ8) (formula:  $C_{49}H_{74}O_4$ ) (labeled as "Ligand of Interest" by depositor).

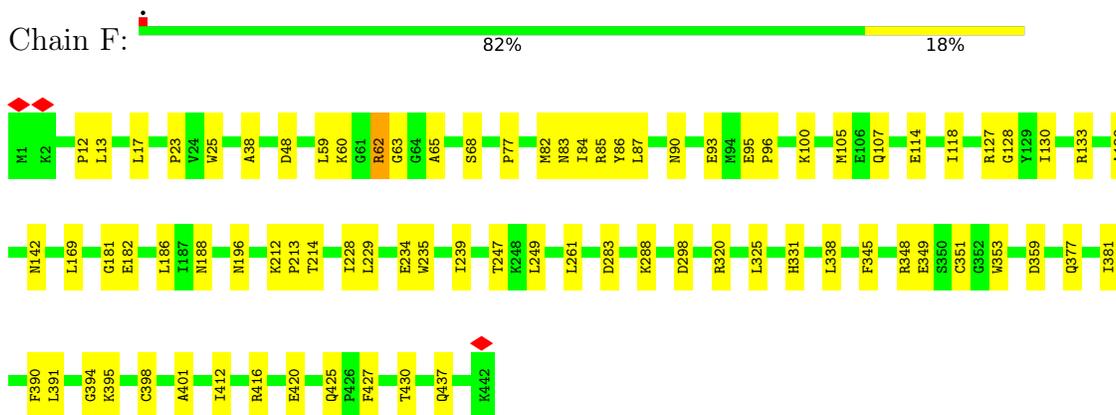


Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
20	H	1	24	20	4	0

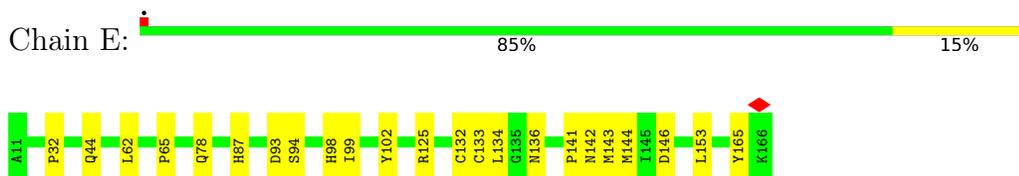
### 3 Residue-property plots [i](#)

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.

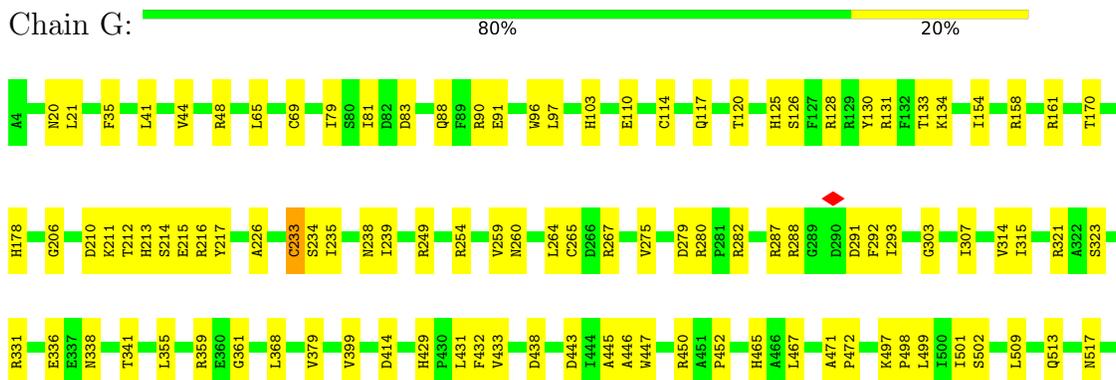
- Molecule 1: NADH-quinone oxidoreductase subunit F

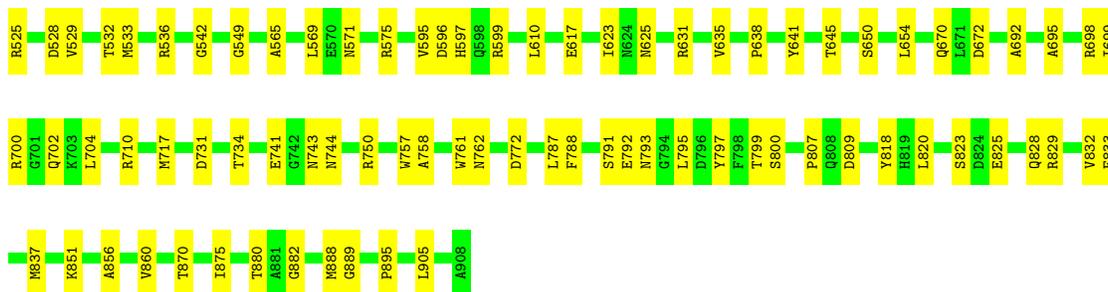


- Molecule 2: NADH dehydrogenase I subunit E



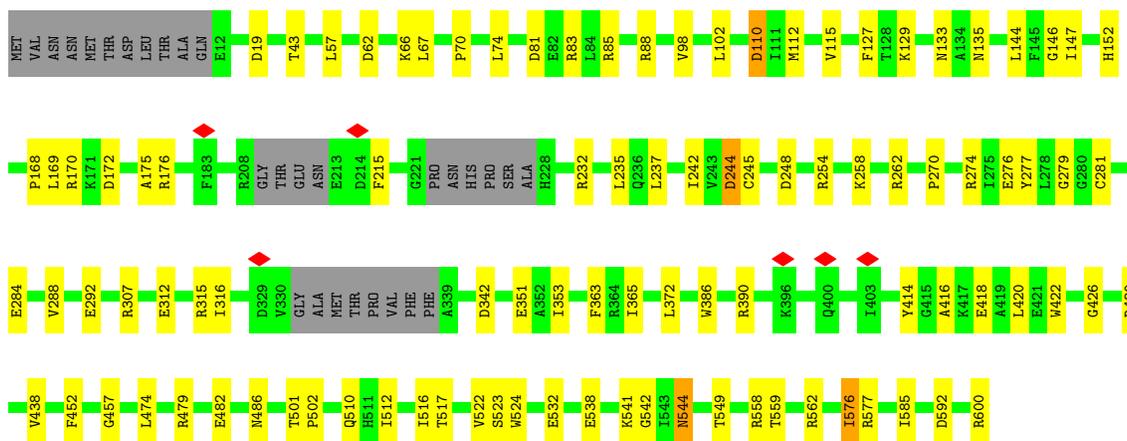
- Molecule 3: NADH-quinone oxidoreductase





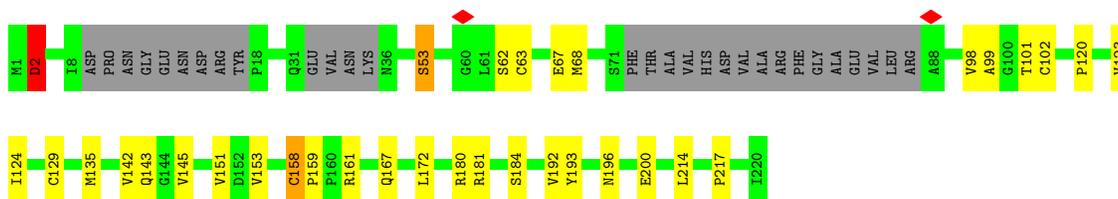
- Molecule 4: NADH-quinone oxidoreductase subunit C/D

Chain C: 78% 16% 5%



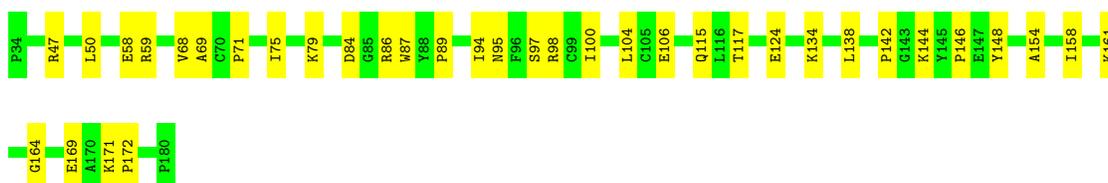
- Molecule 5: NADH-quinone oxidoreductase subunit B

Chain B: 71% 14% 13%



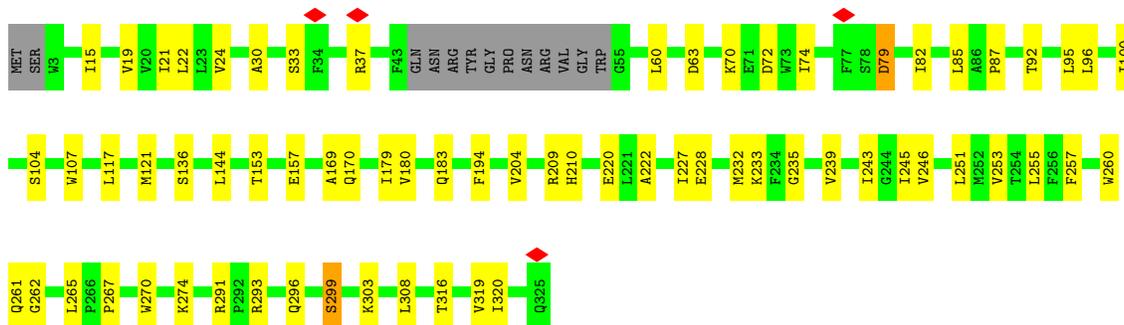
- Molecule 6: NADH-quinone oxidoreductase subunit I

Chain I: 76% 24%

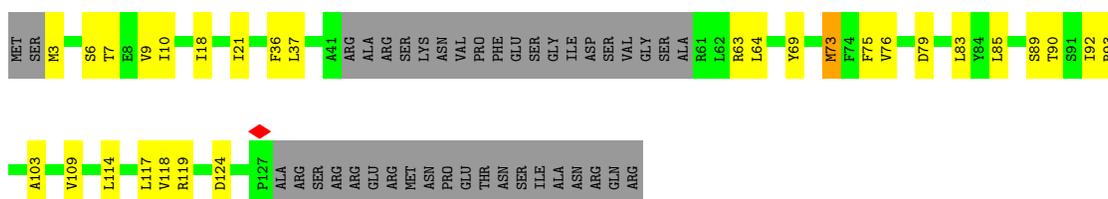


- Molecule 7: Proton-translocating NADH-quinone oxidoreductase, chain L

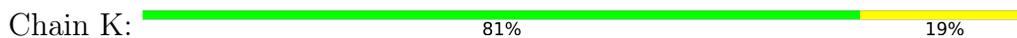




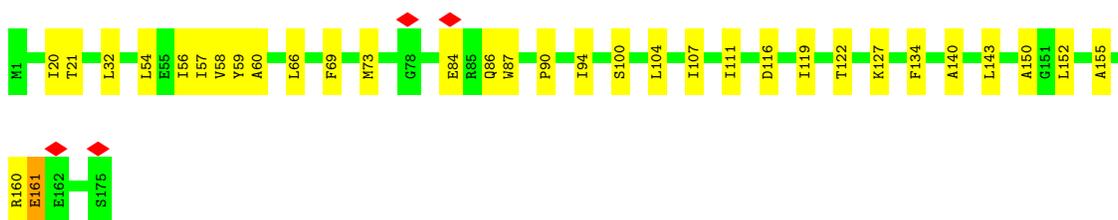
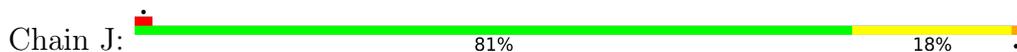
• Molecule 11: NADH-quinone oxidoreductase subunit A



• Molecule 12: NADH-quinone oxidoreductase subunit K



• Molecule 13: NADH-quinone oxidoreductase subunit J



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	145253	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 ( $e^-/\text{\AA}^2$ )	89	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.929	Depositor
Minimum map value	-0.129	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.075	Depositor
Map size (Å)	149.601, 220.688, 237.664	wwPDB
Map dimensions	224, 208, 141	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	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, 3PE, NAI, UQ8, CA, FMN, FES

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	0.27	0/3511	0.56	0/4745
2	E	0.26	0/1248	0.51	0/1691
3	G	0.27	0/7173	0.55	2/9726 (0.0%)
4	C	0.28	0/4728	0.57	1/6413 (0.0%)
5	B	0.28	0/1548	0.59	1/2092 (0.0%)
6	I	0.27	0/1185	0.55	0/1603
7	L	0.29	0/4639	0.55	2/6322 (0.0%)
8	M	0.29	0/4074	0.54	2/5546 (0.0%)
9	N	0.28	0/3718	0.52	2/5071 (0.0%)
10	H	0.30	0/2520	0.61	3/3427 (0.1%)
11	A	0.28	0/865	0.60	1/1176 (0.1%)
12	K	0.26	0/769	0.55	0/1040
13	J	0.29	0/1352	0.56	0/1841
All	All	0.28	0/37330	0.56	14/50693 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	B	0	1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	H	63	ASP	CB-CG-OD1	7.26	124.84	118.30
5	B	2	ASP	CB-CG-OD1	6.83	124.45	118.30
11	A	124	ASP	CB-CG-OD1	6.41	124.07	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	H	72	ASP	CB-CG-OD1	6.33	123.99	118.30
7	L	6	LEU	CA-CB-CG	6.12	129.39	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	B	158	CYS	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	3432	0	3405	55	0
2	E	1220	0	1188	15	0
3	G	7022	0	6825	109	0
4	C	4606	0	4516	65	0
5	B	1518	0	1513	22	0
6	I	1157	0	1121	25	0
7	L	4525	0	4668	65	0
8	M	3953	0	4053	49	0
9	N	3630	0	3799	63	0
10	H	2449	0	2503	42	0
11	A	840	0	855	25	0
12	K	760	0	817	17	0
13	J	1326	0	1394	31	0
14	B	8	0	0	0	0
14	F	8	0	0	0	0
14	G	24	0	0	2	0
14	I	16	0	0	0	0
15	F	31	0	19	2	0
16	F	44	0	27	4	0
17	E	4	0	0	0	0
17	G	4	0	0	0	0
18	G	1	0	0	0	0
19	L	88	0	130	6	0
20	H	24	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	36690	0	36858	510	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 7.

The worst 5 of 510 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)
13:J:69:PHE:O	13:J:73:MET:HB2	1.78	0.82
4:C:215:PHE:HA	4:C:237:LEU:O	1.88	0.74
4:C:416:ALA:O	4:C:420:LEU:HB2	1.89	0.72
10:H:104:SER:HB3	10:H:107:TRP:HB2	1.70	0.72
10:H:227:ILE:HG13	10:H:228:GLU:HG2	1.74	0.69

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	440/442 (100%)	427 (97%)	13 (3%)	0	100	100
2	E	154/156 (99%)	149 (97%)	5 (3%)	0	100	100
3	G	903/905 (100%)	866 (96%)	37 (4%)	0	100	100
4	C	563/600 (94%)	543 (96%)	20 (4%)	0	100	100
5	B	183/220 (83%)	172 (94%)	11 (6%)	0	100	100
6	I	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
7	L	585/613 (95%)	563 (96%)	22 (4%)	0	100	100
8	M	502/504 (100%)	484 (96%)	18 (4%)	0	100	100
9	N	473/485 (98%)	460 (97%)	13 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	H	308/325 (95%)	292 (95%)	16 (5%)	0	100	100
11	A	102/147 (69%)	95 (93%)	7 (7%)	0	100	100
12	K	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
13	J	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
All	All	4629/4819 (96%)	4447 (96%)	182 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	356/356 (100%)	350 (98%)	6 (2%)	60	83
2	E	129/129 (100%)	127 (98%)	2 (2%)	62	84
3	G	732/732 (100%)	724 (99%)	8 (1%)	73	88
4	C	489/519 (94%)	483 (99%)	6 (1%)	71	88
5	B	168/192 (88%)	164 (98%)	4 (2%)	49	77
6	I	124/126 (98%)	124 (100%)	0	100	100
7	L	470/486 (97%)	461 (98%)	9 (2%)	57	81
8	M	413/413 (100%)	404 (98%)	9 (2%)	52	79
9	N	381/385 (99%)	378 (99%)	3 (1%)	81	93
10	H	258/269 (96%)	253 (98%)	5 (2%)	57	81
11	A	84/119 (71%)	83 (99%)	1 (1%)	71	88
12	K	79/79 (100%)	78 (99%)	1 (1%)	69	87
13	J	139/139 (100%)	136 (98%)	3 (2%)	52	79
All	All	3822/3944 (97%)	3765 (98%)	57 (2%)	66	85

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	L	162	LYS
13	J	116	ASP
8	M	74	ARG
13	J	59	TYR
10	H	170	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
7	L	135	ASN
7	L	78	ASN
3	G	702	GLN
3	G	670	GLN
4	C	510	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 1 is monoatomic - leaving 14 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
14	SF4	B	301	5	0,12,12	-	-	-		
16	NAI	F	503	-	42,48,48	0.50	0	47,73,73	0.58	1 (2%)
14	SF4	G	1003	3	0,12,12	-	-	-		
14	SF4	G	1001	3	0,12,12	-	-	-		
17	FES	G	1004	3	0,4,4	-	-	-		
14	SF4	I	201	6	0,12,12	-	-	-		
20	UQ8	H	401	-	24,24,53	0.30	0	29,32,67	0.91	2 (6%)
14	SF4	F	501	1	0,12,12	-	-	-		
19	3PE	L	801	-	50,50,50	0.30	0	53,55,55	0.28	0
19	3PE	L	802	-	36,36,50	0.36	0	39,41,55	0.33	0
14	SF4	I	202	6	0,12,12	-	-	-		
15	FMN	F	502	-	33,33,33	1.06	2 (6%)	48,50,50	1.22	7 (14%)
17	FES	E	201	2	0,4,4	-	-	-		
14	SF4	G	1002	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
14	SF4	B	301	5	-	-	0/6/5/5
16	NAI	F	503	-	-	4/25/72/72	0/5/5/5
14	SF4	G	1003	3	-	-	0/6/5/5
14	SF4	G	1001	3	-	-	0/6/5/5
17	FES	G	1004	3	-	-	0/1/1/1
14	SF4	I	201	6	-	-	0/6/5/5
20	UQ8	H	401	-	-	5/17/41/75	0/1/1/1
19	3PE	L	801	-	-	6/54/54/54	-
14	SF4	F	501	1	-	-	0/6/5/5
19	3PE	L	802	-	-	8/40/40/54	-
14	SF4	I	202	6	-	-	0/6/5/5
15	FMN	F	502	-	-	5/18/18/18	0/3/3/3
17	FES	E	201	2	-	-	0/1/1/1
14	SF4	G	1002	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	3.65	1.37	1.30
15	F	502	FMN	C10-N1	2.45	1.38	1.33

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	H	401	UQ8	C8-C7-C6	3.78	122.23	112.05
15	F	502	FMN	C4-N3-C2	-3.21	119.71	125.64
15	F	502	FMN	O4-C4-C4A	-2.69	119.46	126.60
15	F	502	FMN	C4A-C4-N3	2.67	119.97	113.19
15	F	502	FMN	C4A-C10-N10	2.54	120.19	116.48

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

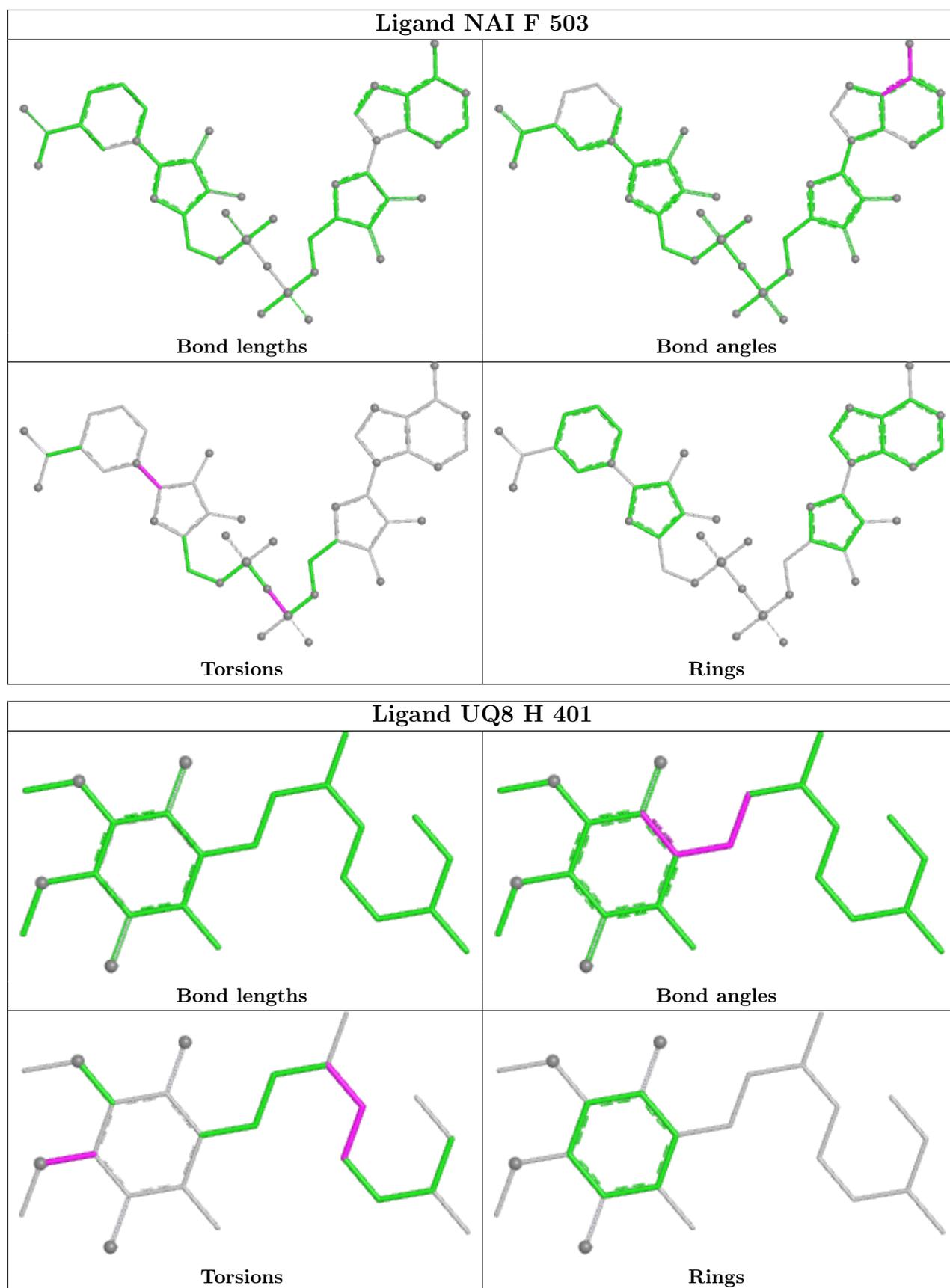
Mol	Chain	Res	Type	Atoms
15	F	502	FMN	N10-C1'-C2'-O2'
15	F	502	FMN	N10-C1'-C2'-C3'
15	F	502	FMN	C5'-O5'-P-O2P
15	F	502	FMN	C5'-O5'-P-O3P
19	L	802	3PE	C1-O11-P-O12

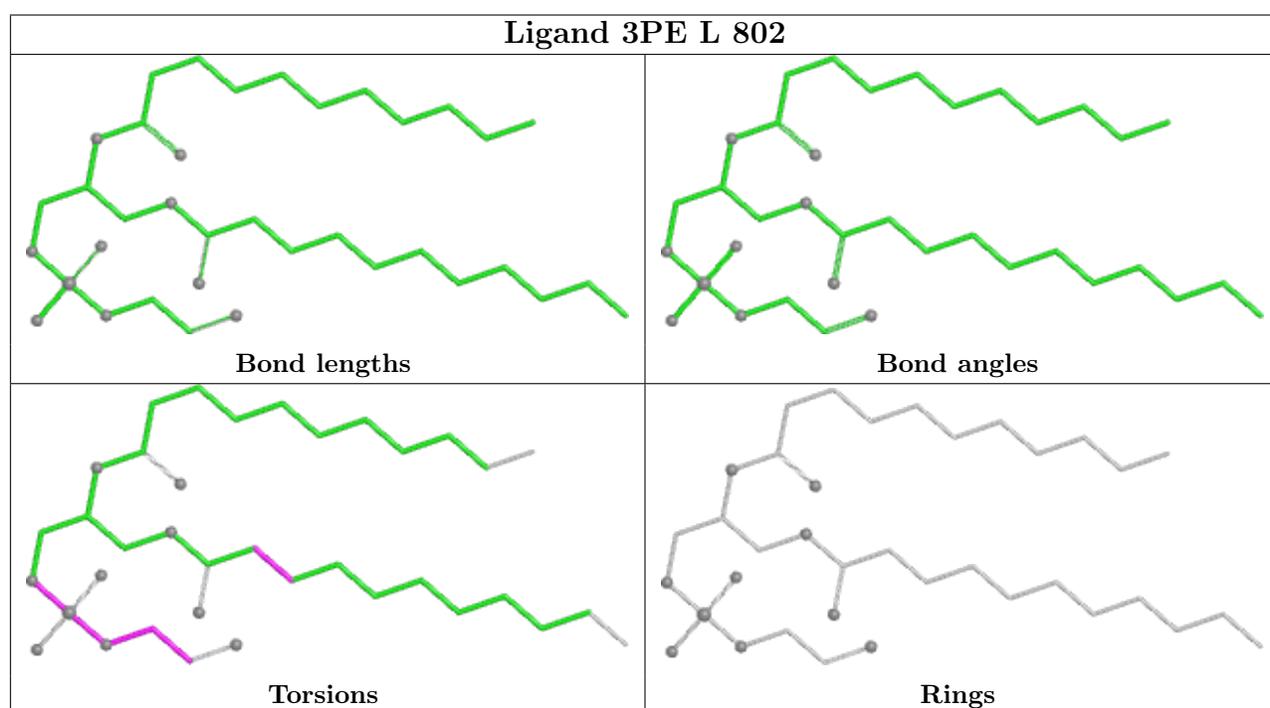
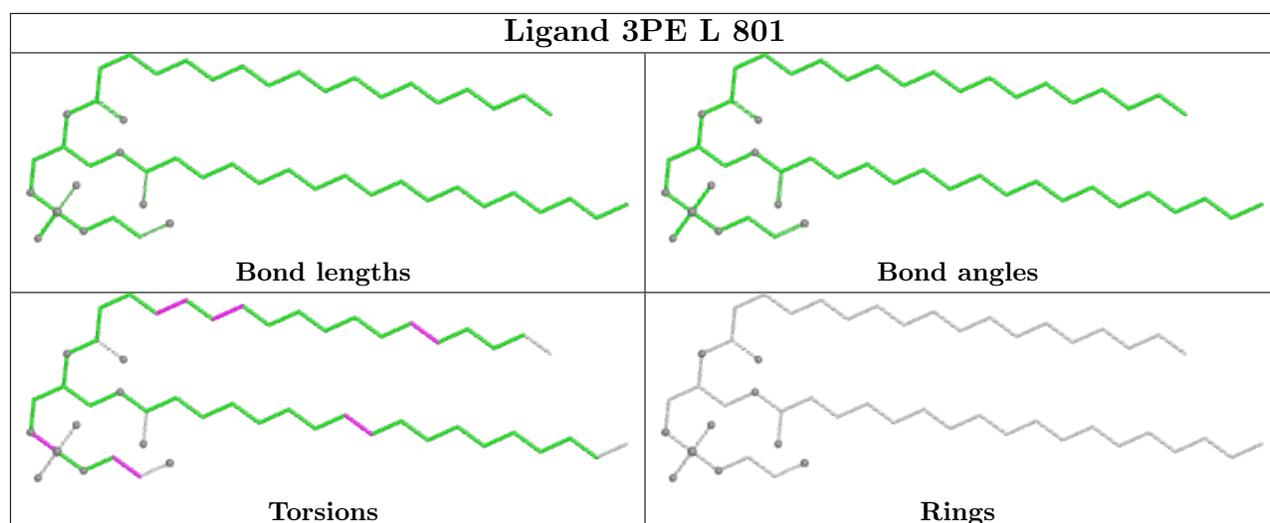
There are no ring outliers.

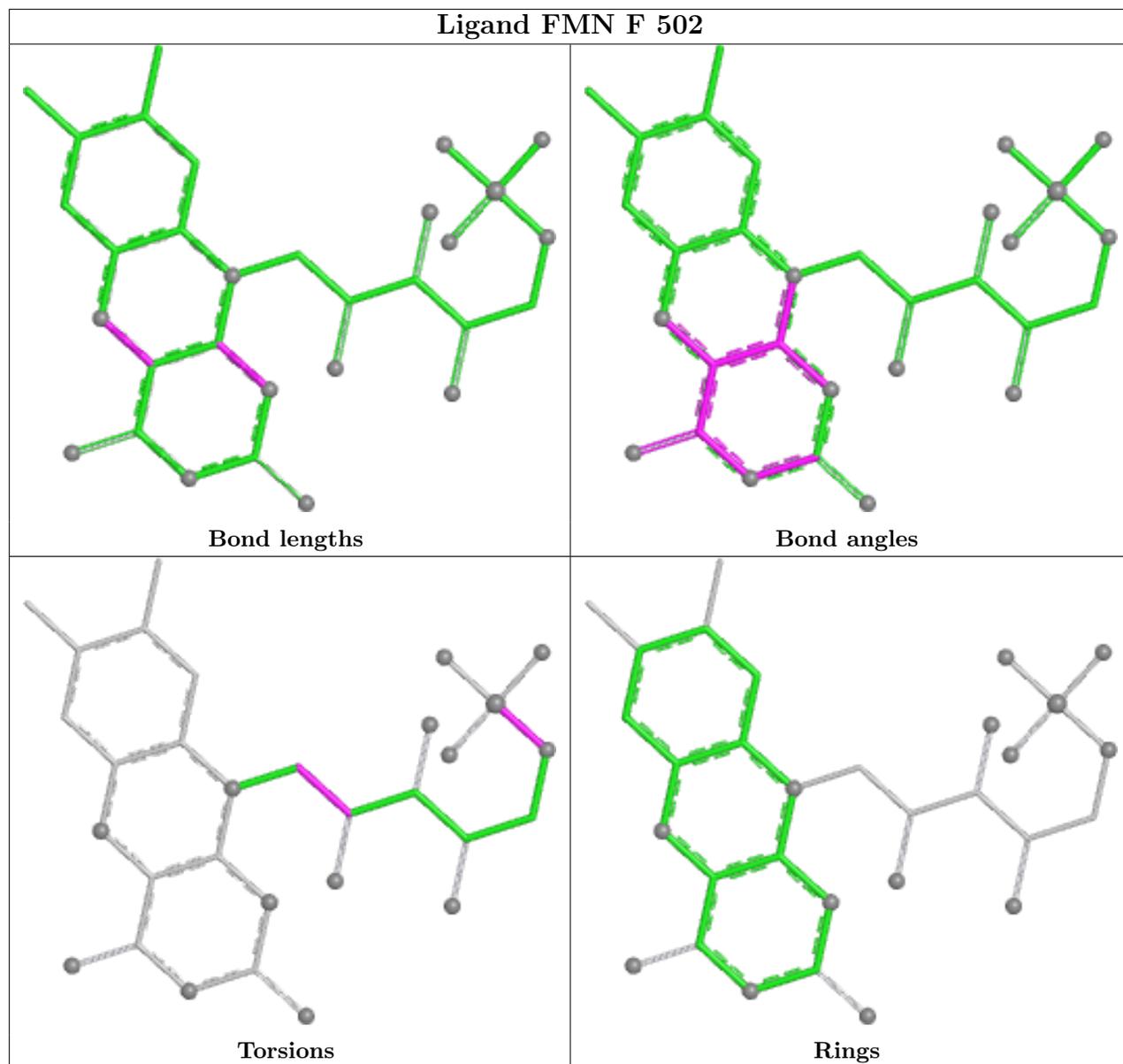
6 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	F	503	NAI	4	0
14	G	1001	SF4	2	0
20	H	401	UQ8	1	0
19	L	801	3PE	1	0
19	L	802	3PE	5	0
15	F	502	FMN	2	0

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







## 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.

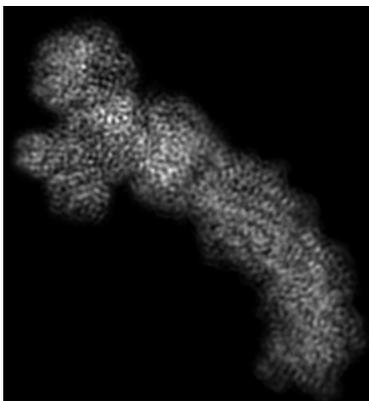
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13214. These allow visual inspection of the internal detail of the map and identification of artifacts.

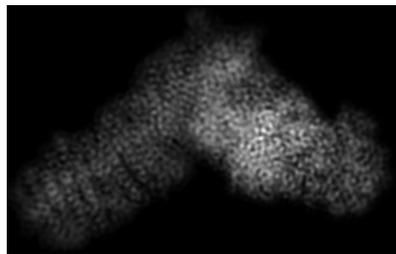
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

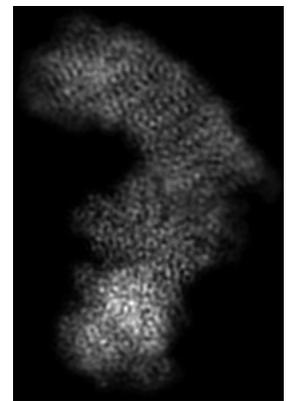
#### 6.1.1 Primary map



X



Y

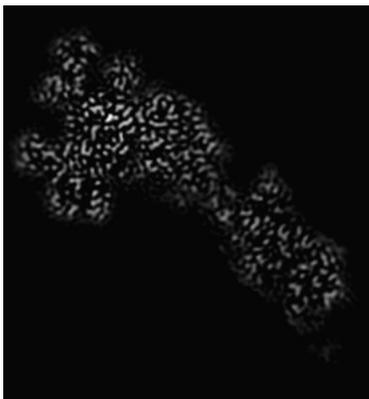


Z

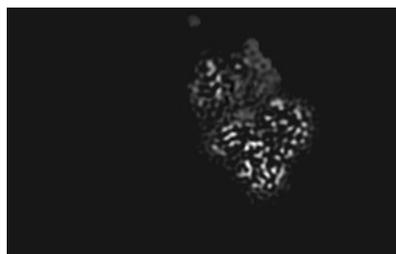
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

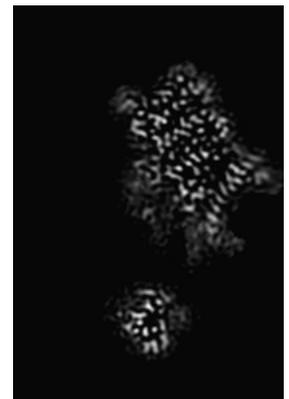
#### 6.2.1 Primary map



X Index: 70



Y Index: 104

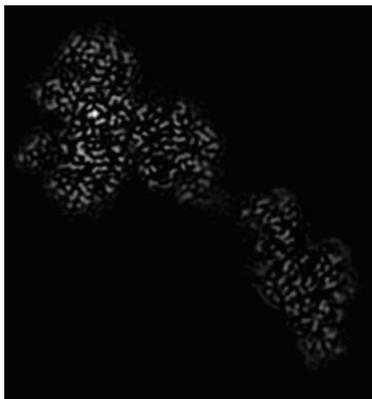


Z Index: 112

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: 62



Y Index: 59



Z Index: 143

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

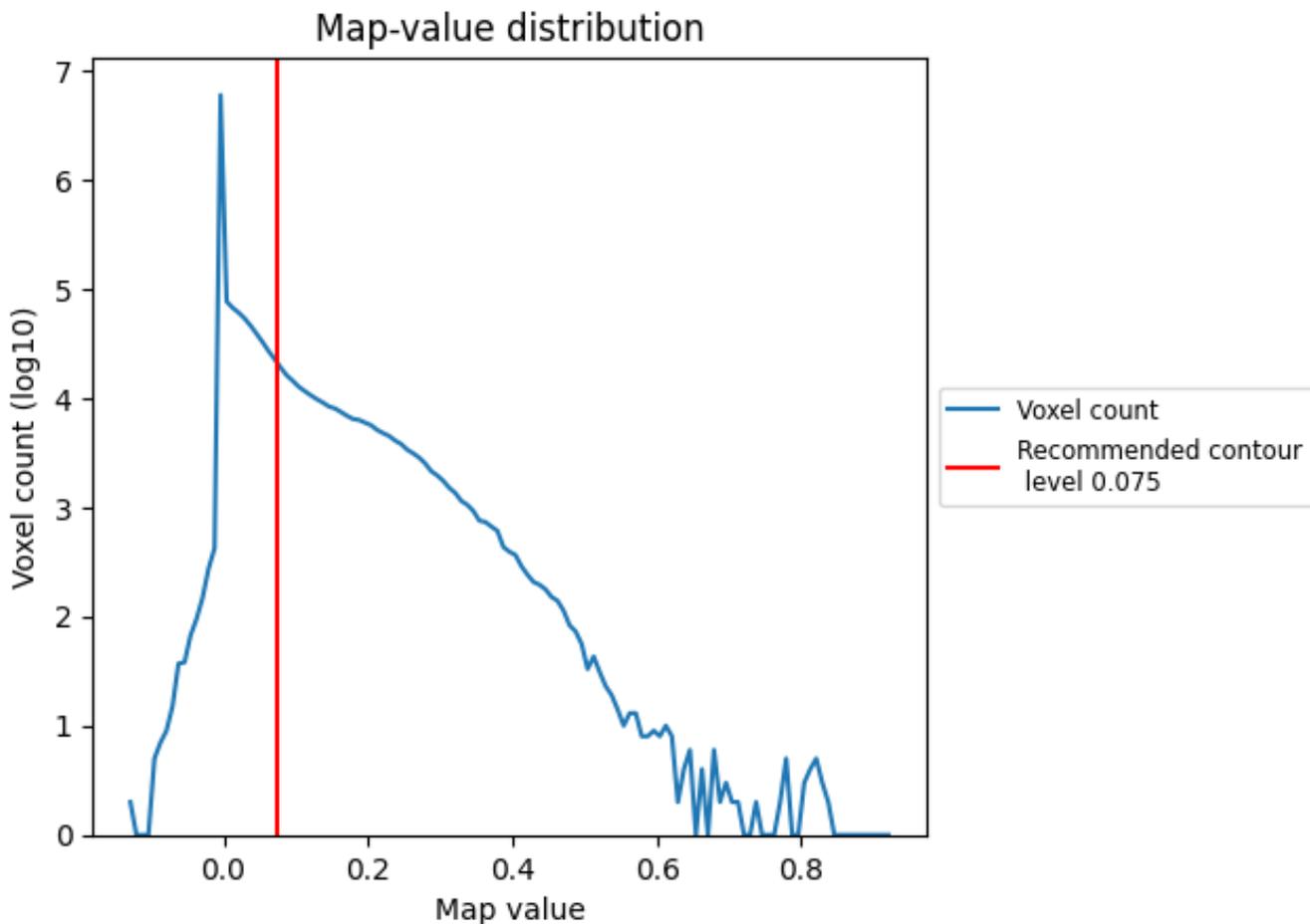
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

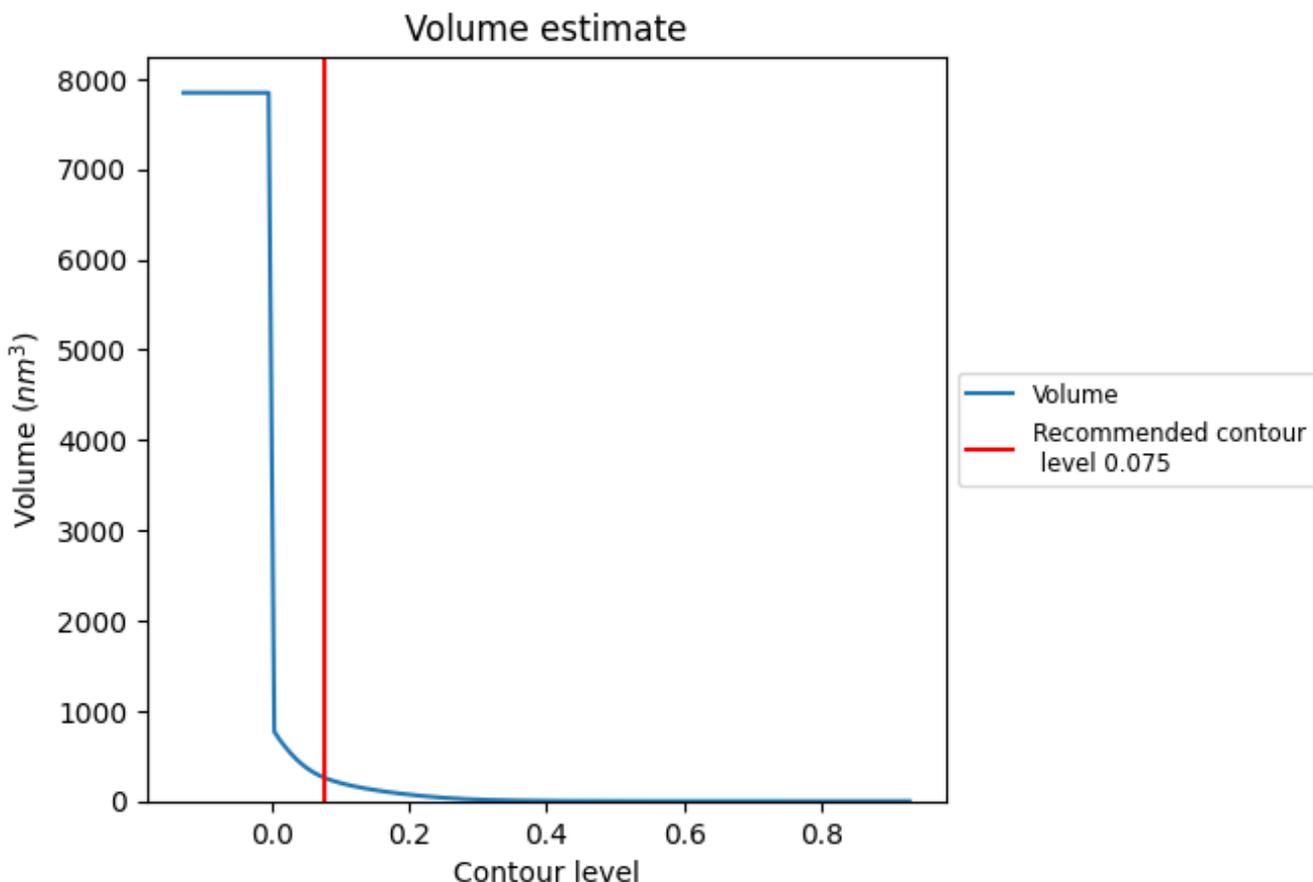
This section contains the results of statistical analysis of the map.

### 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  $264 \text{ nm}^3$ ; this corresponds to an approximate mass of 239 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.

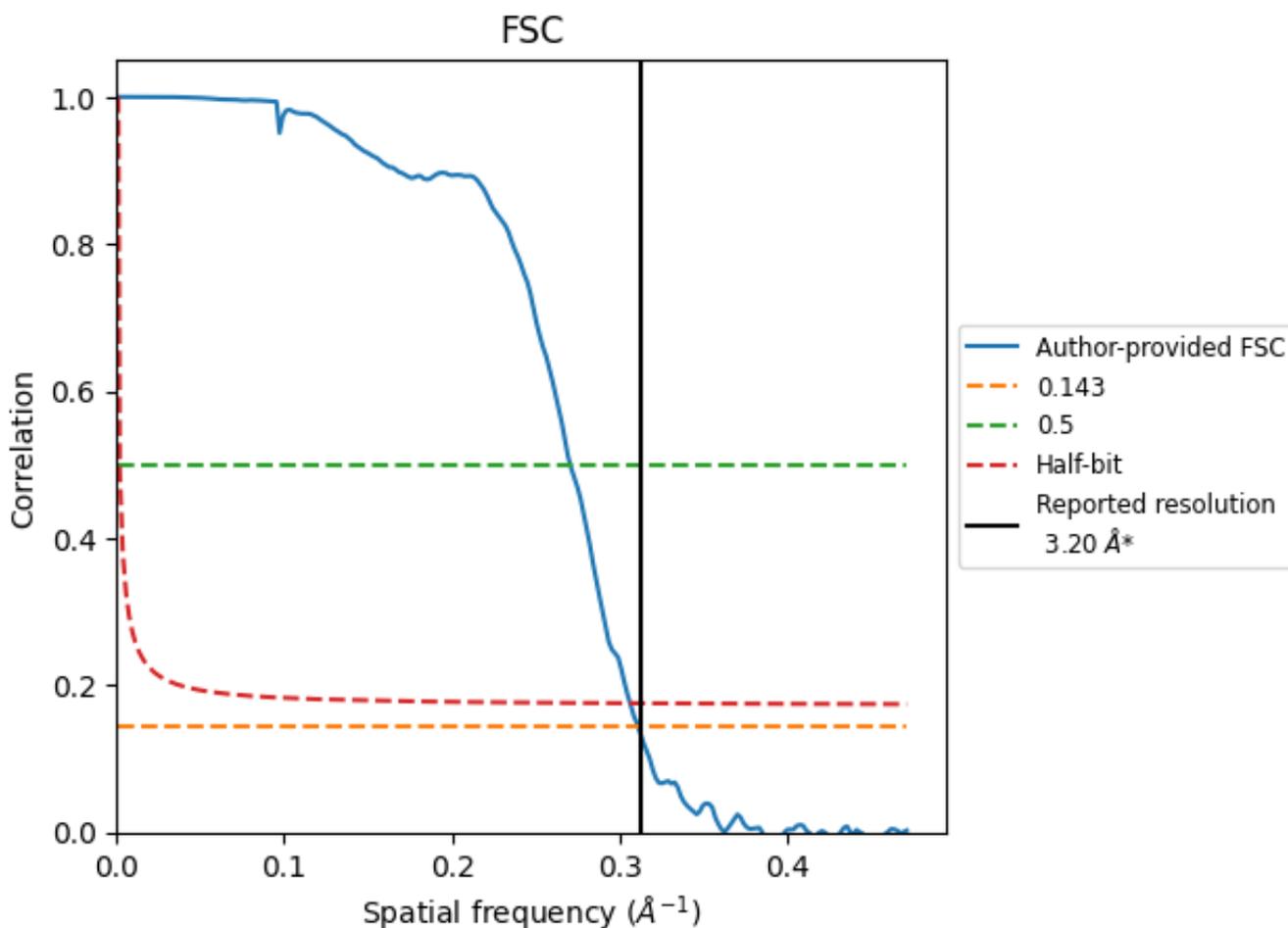
## 7.3 Rotationally averaged power spectrum [i](#)

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 0.312 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

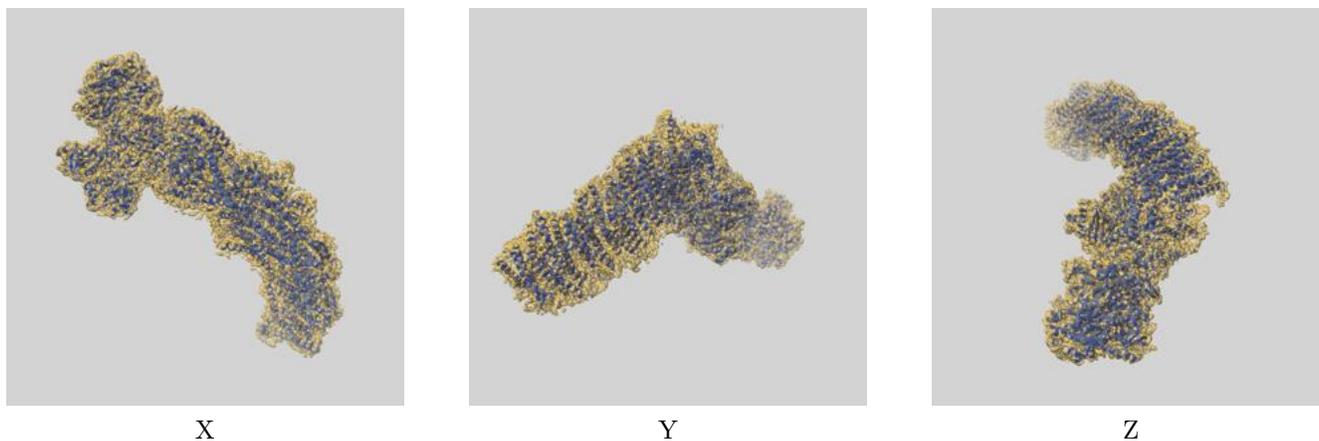
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.21	3.70	3.26
Unmasked-calculated*	-	-	-

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

## 9 Map-model fit [i](#)

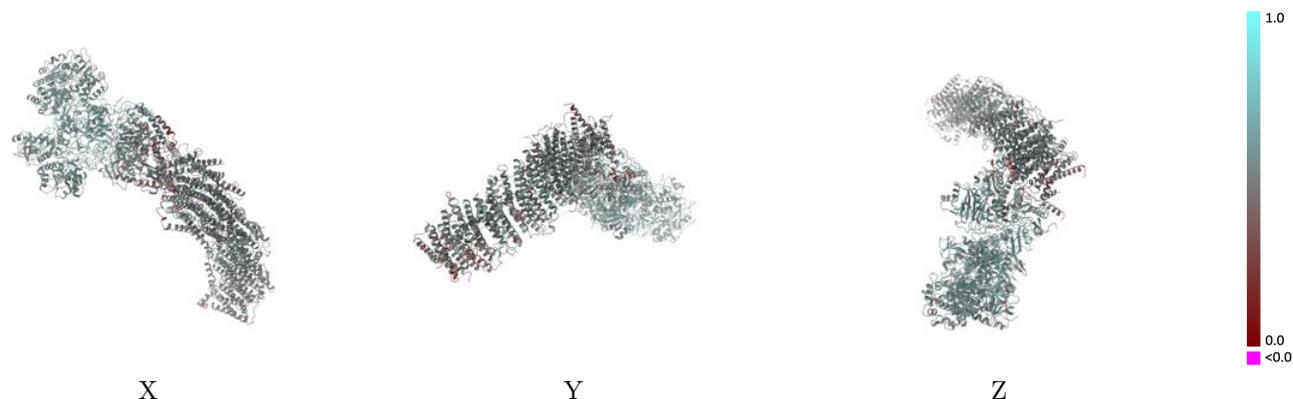
This section contains information regarding the fit between EMDB map EMD-13214 and PDB model 7P61. Per-residue inclusion information can be found in section 3 on page 10.

### 9.1 Map-model overlay [i](#)



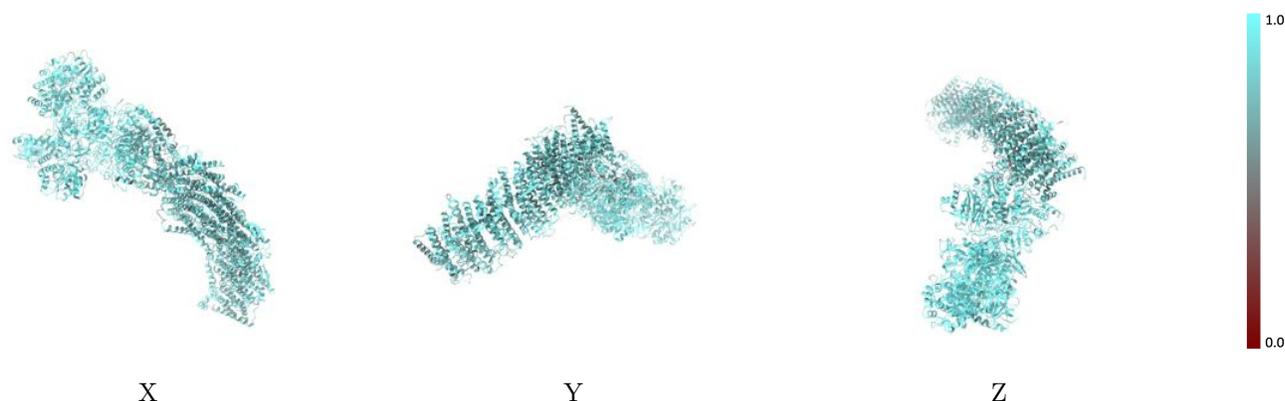
The images above show the 3D surface view of the map at the recommended contour level 0.075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



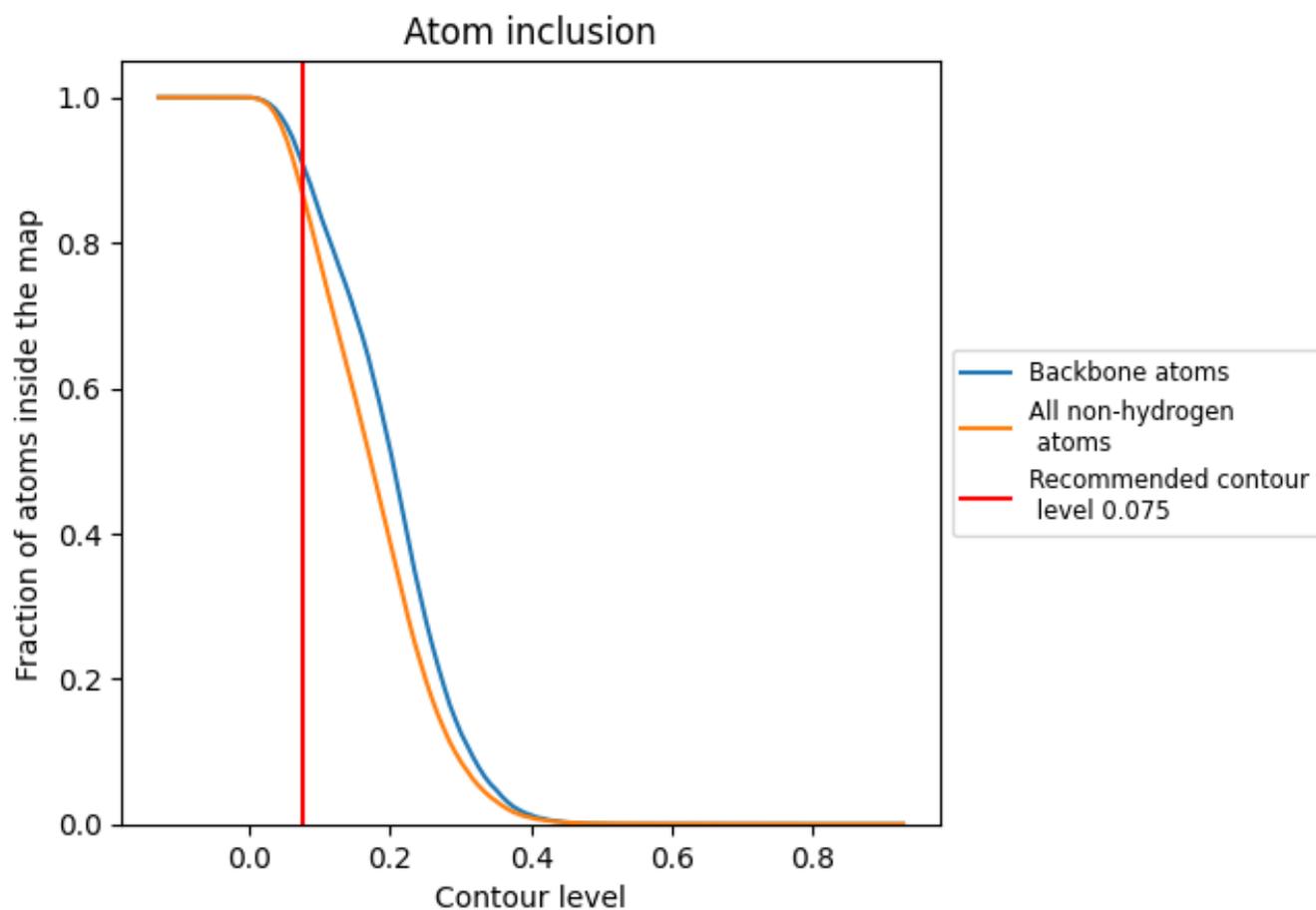
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.075).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8685	 0.5240
A	 0.8187	 0.4820
B	 0.8803	 0.5230
C	 0.8851	 0.5410
E	 0.9110	 0.5520
F	 0.9128	 0.5530
G	 0.9282	 0.5690
H	 0.8152	 0.4680
I	 0.9301	 0.5770
J	 0.8081	 0.4810
K	 0.8564	 0.5230
L	 0.8073	 0.4680
M	 0.8461	 0.5090
N	 0.8257	 0.5100

