Full wwPDB EM Validation Report ⓘ

Sep 10, 2024 – 06:53 PM JST

PDB ID	:	8IBF
EMDB ID	:	EMD-35342
Title	:	Respiratory complex Membrane domain of CI, focus-refined of type II, Wild type mouse under cold temperature
Authors	:	Shin, Y.-C.; Liao, M.
Deposited on	:	2023-02-10
Resolution	:	3.30 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:

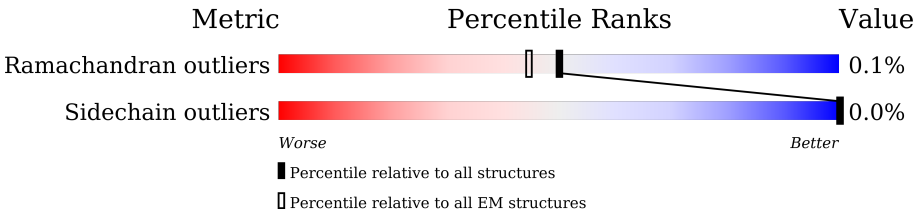
EMDB validation analysis	:	0.0.1.dev112
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.2

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 3.30 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	D	463	5% 9% 91%
2	J	172	30% 94% • 5%
3	K	98	7% 97% • •
4	L	607	• 97% •
5	M	459	97% •
6	N	345	• 98% •
7	O	355	37% 86% • 10%
8	U	156	• 56% • 43%
9	X	172	15% • 84%

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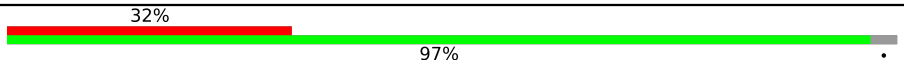
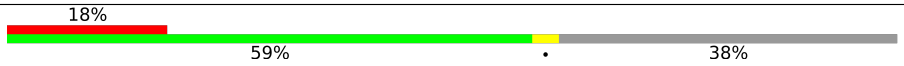
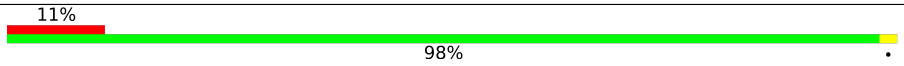
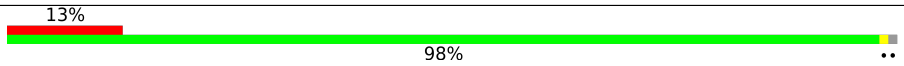
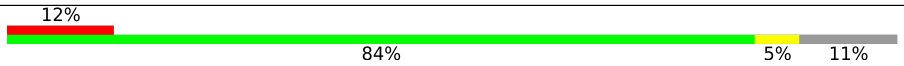
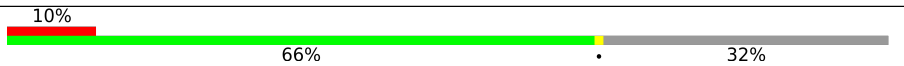
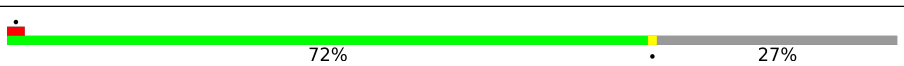
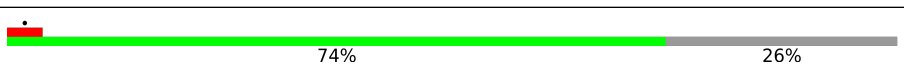
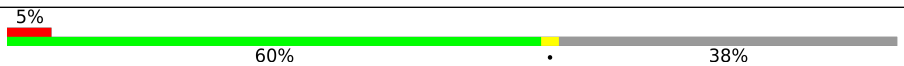
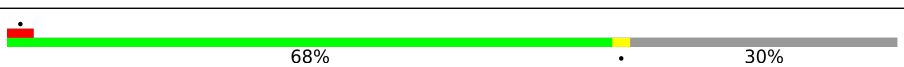
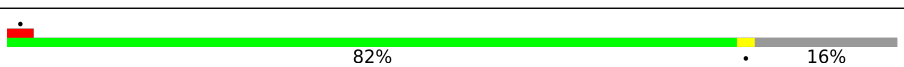
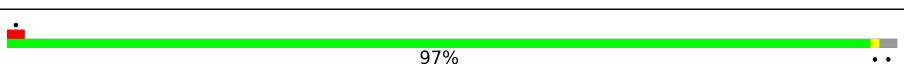
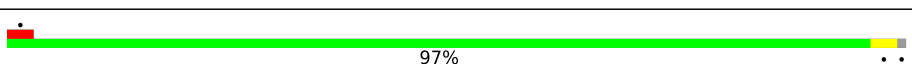
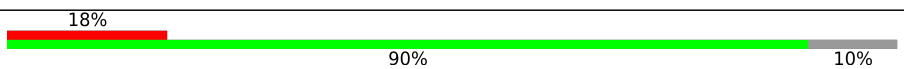
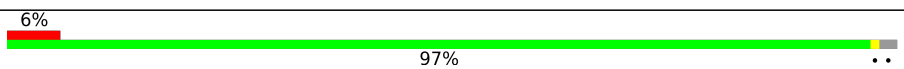
Mol	Chain	Length	Quality of chain
10	Y	143	
11	c	76	
12	d	120	
13	e	106	
14	f	57	
15	g	151	
16	h	189	
17	i	128	
18	j	105	
19	k	104	
20	l	186	
21	m	129	
22	n	179	
23	o	137	
24	p	176	

2 Entry composition (i)

There are 28 unique types of molecules in this entry. The entry contains 31948 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 dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	42	Total	C	N	O	S	0	0
			350	227	58	64	1		

- Molecule 2 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	163	Total	C	N	O	S	0	0
			1229	828	175	211	15		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	116	LEU	ASN	conflict	UNP P03925
J	117	GLY	LEU	conflict	UNP P03925

- Molecule 3 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	97	Total	C	N	O	S	0	0
			729	473	111	135	10		

- Molecule 4 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	606	Total	C	N	O	S	0	0
			4798	3181	746	826	45		

- Molecule 5 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	459	Total	C	N	O	S	0	0
			3630	2407	567	616	40		

- Molecule 6 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	344	Total	C	N	O	S	0	0
			2694	1790	416	451	37		

- Molecule 7 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	319	Total	C	N	O	S	0	0
			2599	1668	430	491	10		

- Molecule 8 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	U	89	Total	C	N	O	S	0	0
			718	462	105	146	5		

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	X	27	Total	C	N	O	0	0
			221	146	39	36		

- Molecule 10 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Y	139	Total	C	N	O	S	0	0
			1030	657	174	191	8		

- Molecule 11 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	47	Total	C	N	O	S	0	0
			389	255	67	66	1		

- Molecule 12 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	120	Total	C	N	O	S	0	0
			996	651	171	165	9		

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	e	105	Total	C	N	O	S	0	0
			877	555	162	152	8		

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	f	51	Total	C	N	O	S	0	0
			439	284	79	74	2		

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	102	Total	C	N	O	S	0	0
			858	553	137	164	4		

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	138	Total	C	N	O	S	0	0
			1162	762	194	203	3		

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	i	95	Total	C	N	O	S	0	0
			802	523	140	136	3		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	j	65	Total	C	N	O	S	0	0
			563	369	93	100	1		

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	k	73	Total	C	N	O	S	0	0
			582	383	102	95	2		

- Molecule 20 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	l	156	Total	C	N	O	S	0	0
			1312	846	219	236	11		

- Molecule 21 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	m	126	Total	C	N	O	0	0
			1050	676	189	185		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	n	178	Total	C	N	O	S	0	0
			1541	985	276	269	11		

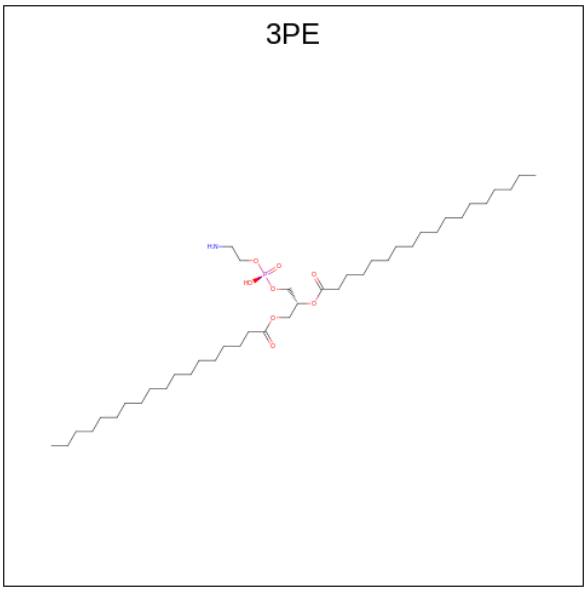
- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	o	123	Total	C	N	O	S	0	0
			1050	661	198	182	9		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

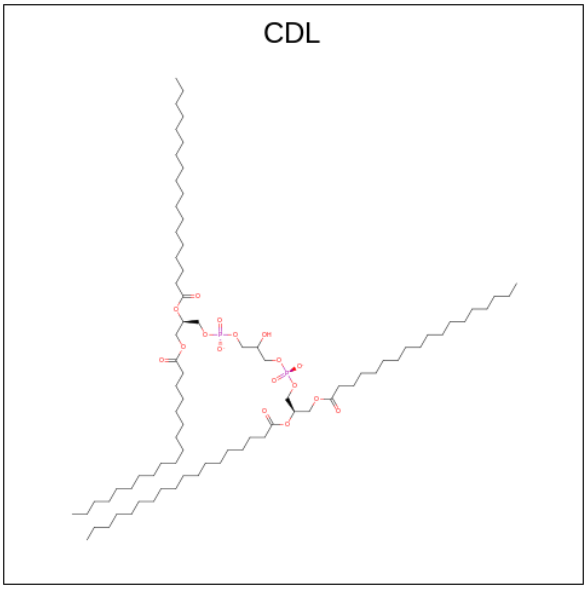
Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	172	Total	C	N	O	S	0	0
			1452	911	260	273	8		

- Molecule 25 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (three-letter code: 3PE) (formula: $C_{41}H_{82}NO_8P$) (labeled as "Ligand of Interest" by depositor).



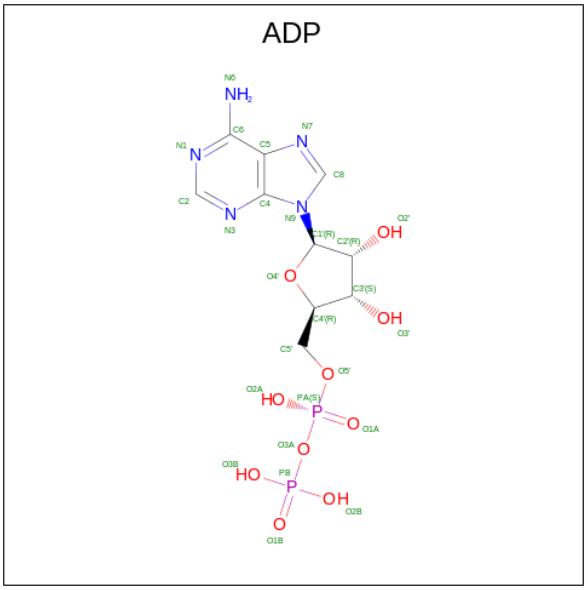
Mol	Chain	Residues	Atoms					AltConf
25	K	1	Total	C	N	O	P	0
			46	36	1	8	1	
25	L	1	Total	C	N	O	P	0
			40	30	1	8	1	
25	L	1	Total	C	N	O	P	0
			49	39	1	8	1	
25	L	1	Total	C	N	O	P	0
			40	30	1	8	1	
25	L	1	Total	C	N	O	P	0
			38	28	1	8	1	
25	M	1	Total	C	N	O	P	0
			37	27	1	8	1	
25	M	1	Total	C	N	O	P	0
			51	41	1	8	1	
25	N	1	Total	C	N	O	P	0
			51	41	1	8	1	
25	Y	1	Total	C	N	O	P	0
			41	31	1	8	1	
25	d	1	Total	C	N	O	P	0
			31	21	1	8	1	
25	i	1	Total	C	N	O	P	0
			40	30	1	8	1	
25	m	1	Total	C	N	O	P	0
			47	37	1	8	1	
25	m	1	Total	C	N	O	P	0
			51	41	1	8	1	
25	m	1	Total	C	N	O	P	0
			41	31	1	8	1	

- Molecule 26 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled as "Ligand of Interest" by depositor).



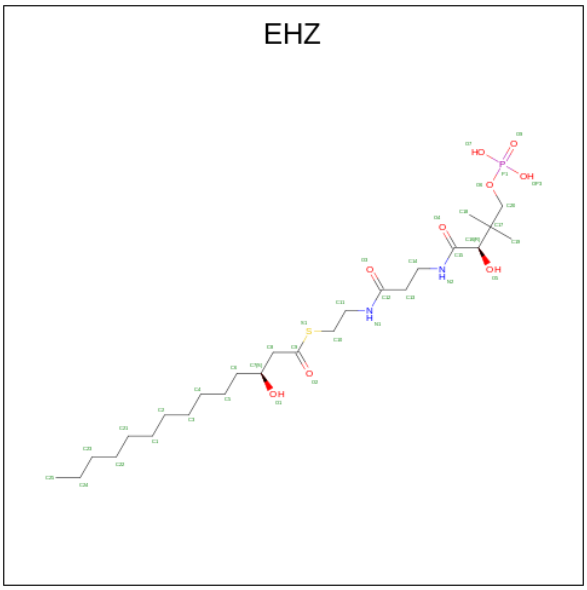
Mol	Chain	Residues	Atoms				AltConf
26	L	1	Total	C	O	P	0
			78	59	17	2	
26	X	1	Total	C	O	P	0
			67	48	17	2	
26	h	1	Total	C	O	P	0
			70	51	17	2	

- Molecule 27 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
27	O	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 28 is {S}-[2-[3-[[(2 {R})-3,3-dimethyl-2-oxidanyl-4-phosphonooxy-butanoyl]amino]propanoylamino]ethyl] (3 {S})-3-oxidanyltetradecanethioate (three-letter code: EHZ) (formula: $C_{25}H_{49}N_2O_9PS$) (labeled as "Ligand of Interest" by depositor).



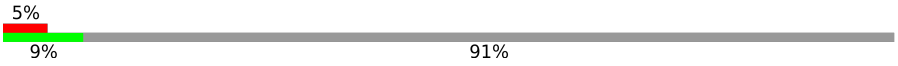
Mol	Chain	Residues	Atoms						AltConf
28	n	1	Total	C	N	O	P	S	0
			32	19	2	9	1	1	

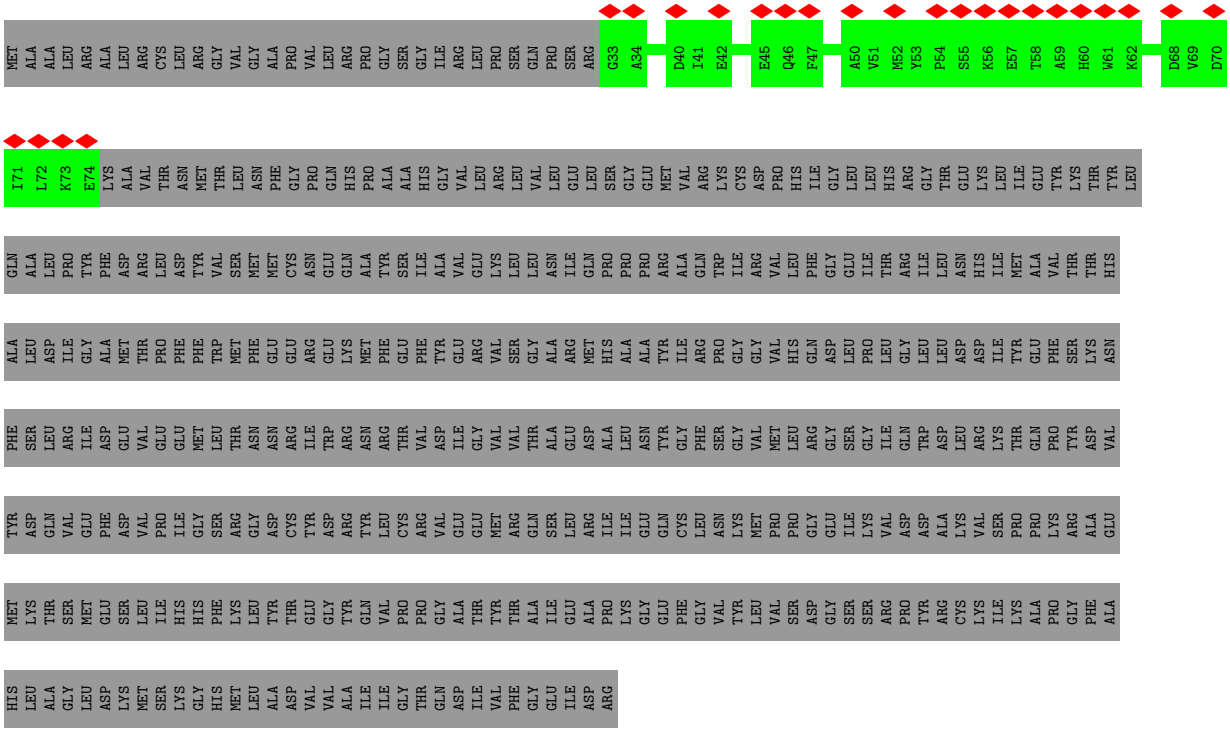
3 Residue-property plots (i)

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 dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial

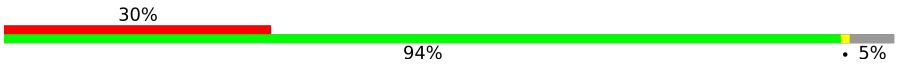
Chain D:

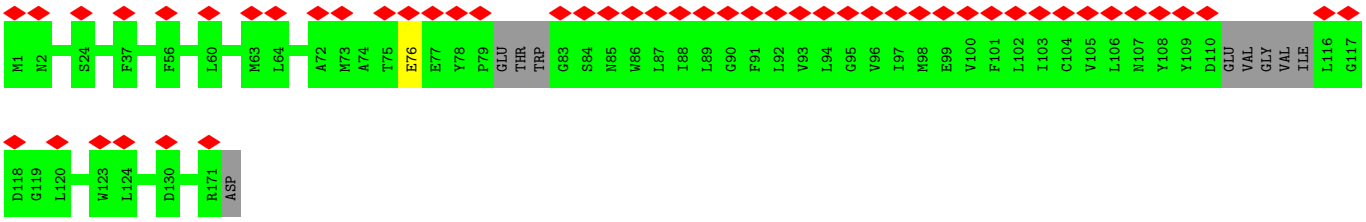




• Molecule 2: NADH-ubiquinone oxidoreductase chain 6

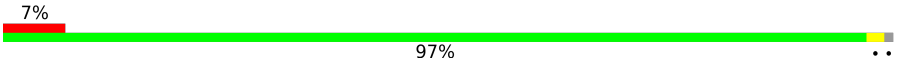
Chain J:

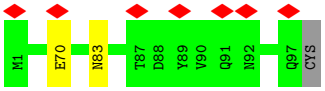




• Molecule 3: NADH-ubiquinone oxidoreductase chain 4L

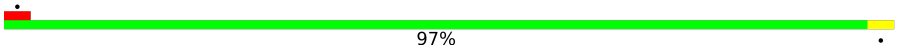
Chain K:





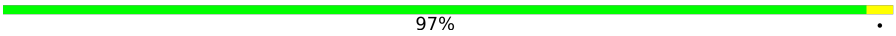
• Molecule 4: NADH-ubiquinone oxidoreductase chain 5

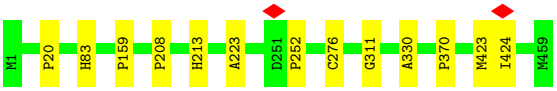
Chain L:



• Molecule 5: NADH-ubiquinone oxidoreductase chain 4

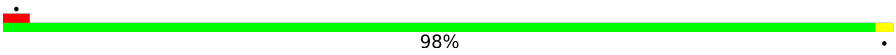
Chain M:

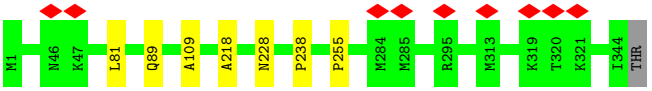




• Molecule 6: NADH-ubiquinone oxidoreductase chain 2

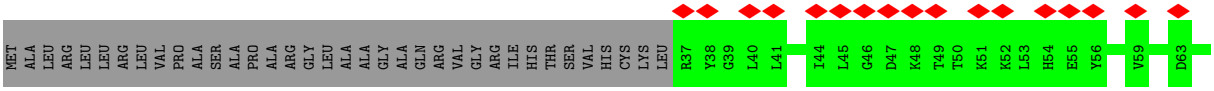
Chain N:

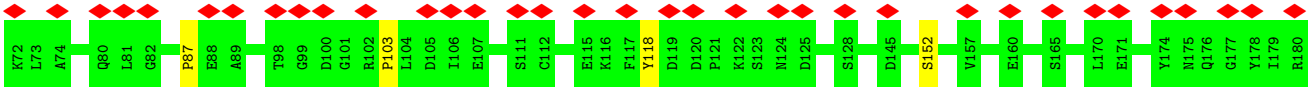


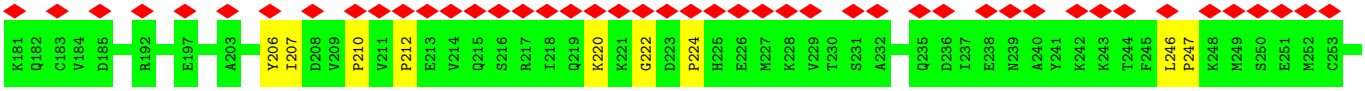


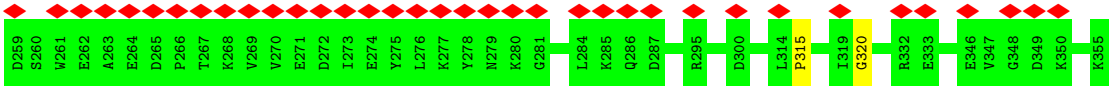
• Molecule 7: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

Chain O:



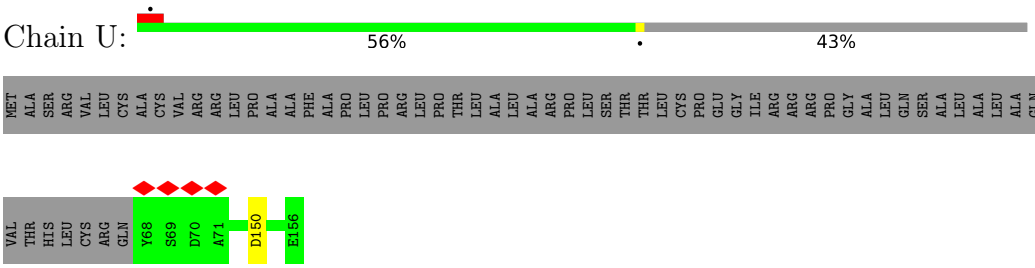






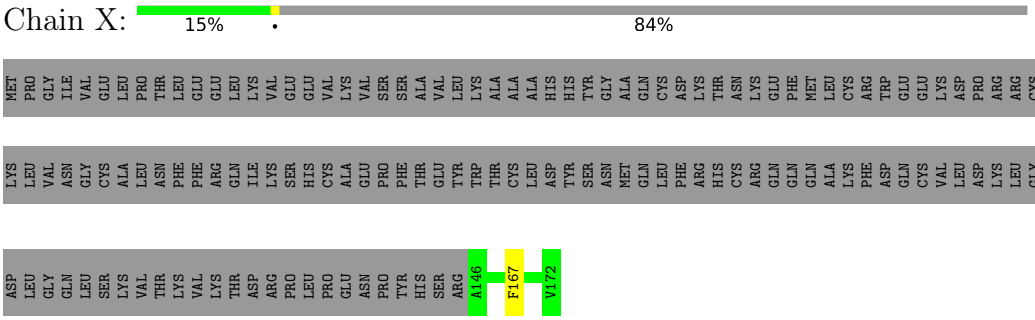
• Molecule 8: Acyl carrier protein, mitochondrial

Chain U:



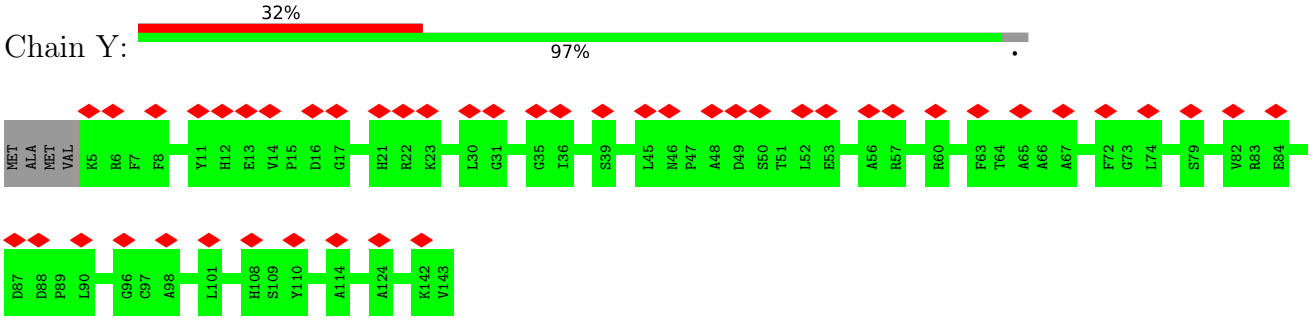
• Molecule 9: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

Chain X:



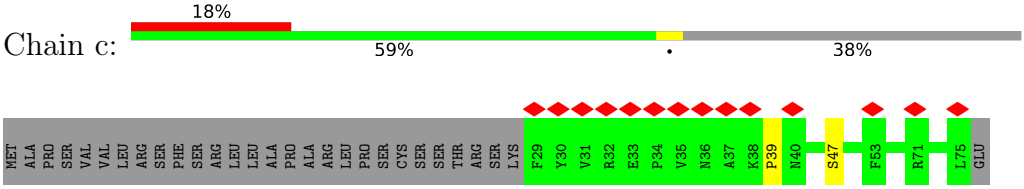
• Molecule 10: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

Chain Y:



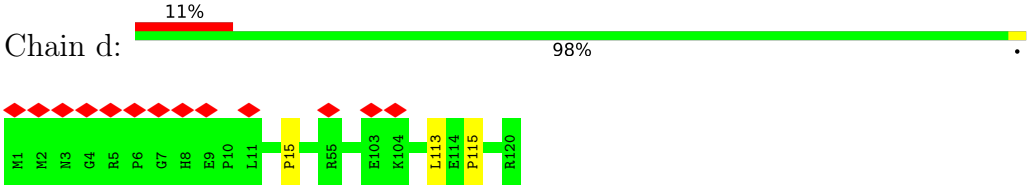
• Molecule 11: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

Chain c:



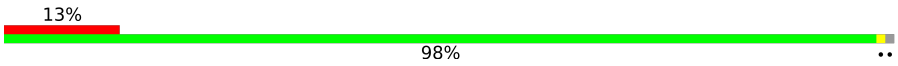
• Molecule 12: NADH dehydrogenase [ubiquinone] 1 subunit C2

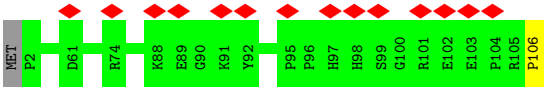
Chain d:



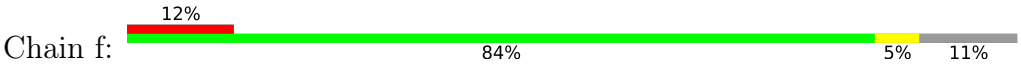
• Molecule 13: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

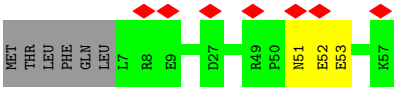
Chain e:



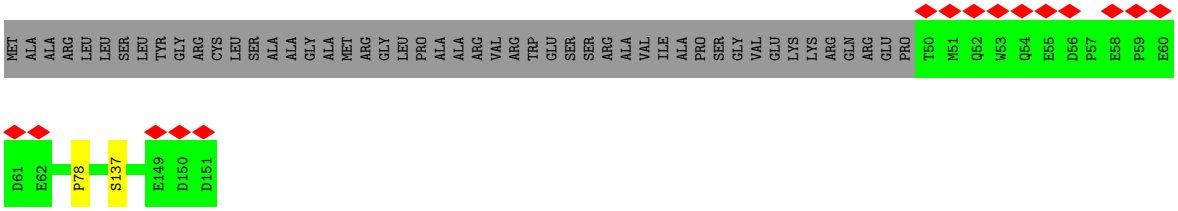


• Molecule 14: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1

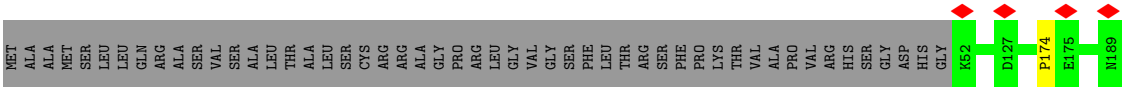




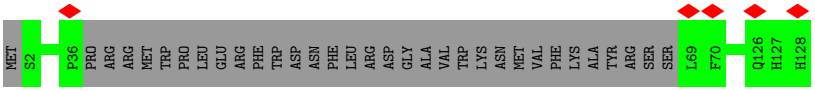
• Molecule 15: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



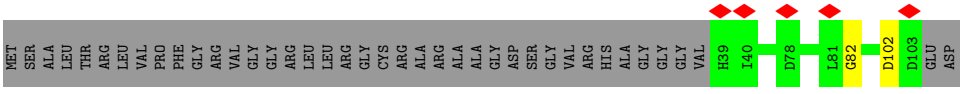
• Molecule 16: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



• Molecule 17: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6

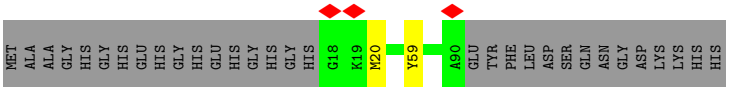


• Molecule 18: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



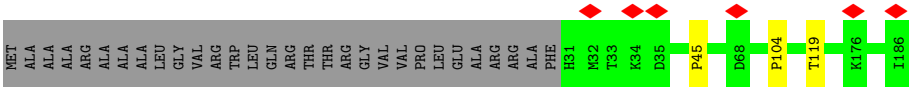
• Molecule 19: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3

Chain k:



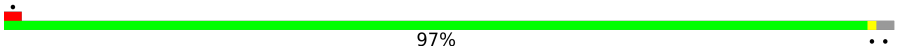
• Molecule 20: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

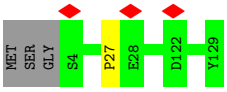
Chain l:



• Molecule 21: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4

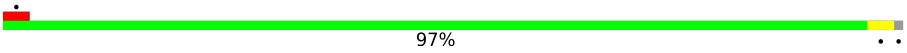
Chain m:

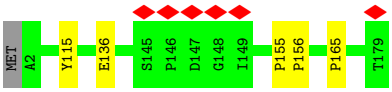




• Molecule 22: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

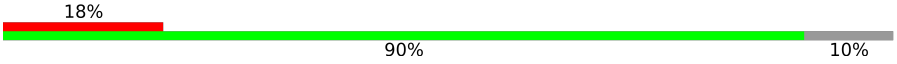
Chain n:

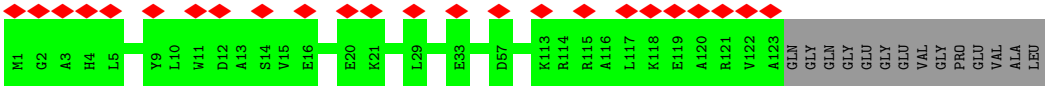




• Molecule 23: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

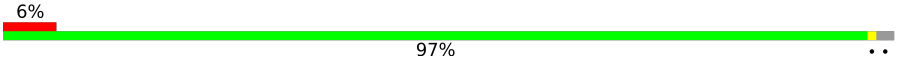
Chain o:

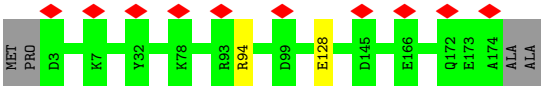




• Molecule 24: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10

Chain p:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	177076	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	46.1, 45.9	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k), GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.050	Depositor
Minimum map value	-1.895	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.085	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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: CDL, ADP, 3PE, EHZ

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	D	0.42	0/365	0.67	0/500
2	J	0.55	0/1257	0.72	1/1704 (0.1%)
3	K	0.59	0/740	0.83	2/1005 (0.2%)
4	L	0.69	6/4921 (0.1%)	0.90	18/6696 (0.3%)
5	M	0.69	5/3717 (0.1%)	0.90	10/5062 (0.2%)
6	N	0.67	2/2756 (0.1%)	0.86	7/3751 (0.2%)
7	O	0.77	7/2666 (0.3%)	0.89	19/3615 (0.5%)
8	U	0.62	0/731	0.79	1/988 (0.1%)
9	X	0.50	0/230	0.61	0/313
10	Y	0.52	0/1054	0.59	0/1429
11	c	0.81	1/400 (0.2%)	0.96	3/544 (0.6%)
12	d	0.77	2/1028 (0.2%)	0.75	5/1387 (0.4%)
13	e	0.50	1/900 (0.1%)	0.65	0/1199
14	f	0.62	0/451	0.85	3/607 (0.5%)
15	g	0.67	1/886 (0.1%)	0.92	3/1207 (0.2%)
16	h	0.55	1/1197 (0.1%)	0.78	0/1621
17	i	0.56	0/829	0.74	0/1127
18	j	0.55	0/588	0.82	2/805 (0.2%)
19	k	0.64	1/600 (0.2%)	0.83	1/810 (0.1%)
20	l	0.67	2/1367 (0.1%)	0.75	2/1866 (0.1%)
21	m	0.68	1/1079 (0.1%)	0.80	2/1463 (0.1%)
22	n	0.64	1/1596 (0.1%)	0.80	3/2162 (0.1%)
23	o	0.54	0/1075	0.63	0/1442
24	p	0.52	0/1485	0.73	3/2007 (0.1%)
All	All	0.65	31/31918 (0.1%)	0.82	85/43310 (0.2%)

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	O	247	PRO	N-CD	16.58	1.71	1.47
12	d	115	PRO	N-CD	-14.22	1.27	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	265	PRO	N-CD	13.77	1.67	1.47
6	N	255	PRO	N-CD	-13.72	1.28	1.47
11	c	39	PRO	N-CD	-13.29	1.29	1.47
21	m	27	PRO	N-CD	-13.01	1.29	1.47
7	O	315	PRO	N-CD	-12.11	1.30	1.47
4	L	234	PRO	N-CD	11.08	1.63	1.47
7	O	210	PRO	N-CD	-10.54	1.33	1.47
5	M	370	PRO	N-CD	-10.53	1.33	1.47
7	O	224	PRO	N-CD	-10.28	1.33	1.47
15	g	78	PRO	N-CD	-9.64	1.34	1.47
12	d	15	PRO	N-CD	-9.44	1.34	1.47
7	O	212	PRO	N-CD	-8.90	1.35	1.47
5	M	20	PRO	N-CD	8.54	1.59	1.47
4	L	212	PRO	N-CD	-8.33	1.36	1.47
22	n	155	PRO	N-CD	8.01	1.59	1.47
20	l	104	PRO	N-CD	-7.24	1.37	1.47
6	N	238	PRO	N-CD	-7.09	1.38	1.47
5	M	208	PRO	N-CD	7.08	1.57	1.47
13	e	106	PRO	N-CD	6.64	1.57	1.47
4	L	57	ASN	C-O	-6.22	1.11	1.23
4	L	384	PRO	N-CD	6.16	1.56	1.47
19	k	20	MET	C-N	5.92	1.47	1.34
4	L	112	PRO	N-CD	5.87	1.56	1.47
7	O	87	PRO	N-CD	-5.81	1.39	1.47
20	l	45	PRO	N-CD	-5.80	1.39	1.47
5	M	252	PRO	N-CD	-5.61	1.40	1.47
7	O	103	PRO	N-CD	-5.38	1.40	1.47
16	h	174	PRO	N-CD	-5.21	1.40	1.47
5	M	159	PRO	N-CD	5.01	1.54	1.47

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	N	255	PRO	CA-N-CD	9.94	125.61	111.70
7	O	206	TYR	N-CA-CB	-9.90	92.77	110.60
12	d	115	PRO	CA-N-CD	9.63	125.18	111.70
7	O	247	PRO	N-CA-CB	9.17	114.30	103.30
21	m	27	PRO	CA-N-CD	8.95	124.24	111.70
18	j	82	GLY	N-CA-C	-8.82	91.04	113.10
7	O	247	PRO	CA-N-CD	-8.76	99.23	111.50
7	O	315	PRO	CA-N-CD	8.73	123.93	111.70
11	c	39	PRO	CA-N-CD	8.13	123.08	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	O	210	PRO	CA-N-CD	7.40	122.06	111.70
4	L	265	PRO	CA-N-CD	-7.40	101.14	111.50
6	N	255	PRO	N-CA-CB	-7.25	94.61	103.30
7	O	220	LYS	CB-CA-C	-7.09	96.22	110.40
15	g	78	PRO	CA-N-CD	7.07	121.60	111.70
22	n	165	PRO	N-CA-C	7.04	130.41	112.10
4	L	265	PRO	N-CA-CB	6.93	111.62	103.30
12	d	115	PRO	N-CA-CB	-6.92	94.99	102.60
11	c	47	SER	N-CA-CB	6.90	120.84	110.50
7	O	224	PRO	CA-N-CD	6.87	121.32	111.70
5	M	213	HIS	CB-CA-C	-6.78	96.83	110.40
24	p	128	GLU	N-CA-CB	-6.70	98.54	110.60
7	O	222	GLY	N-CA-C	6.65	129.73	113.10
11	c	39	PRO	N-CA-CB	-6.61	95.33	102.60
21	m	27	PRO	N-CA-CB	-6.58	95.36	102.60
12	d	15	PRO	CA-N-CD	6.57	120.89	111.70
7	O	320	GLY	N-CA-C	-6.57	96.69	113.10
14	f	51	ASN	CB-CA-C	-6.54	97.33	110.40
19	k	59	TYR	N-CA-CB	-6.51	98.87	110.60
22	n	115	TYR	N-CA-CB	6.33	122.00	110.60
5	M	370	PRO	N-CA-C	6.30	128.48	112.10
5	M	424	ILE	N-CA-C	-6.30	93.99	111.00
6	N	255	PRO	N-CA-C	6.27	128.39	112.10
5	M	370	PRO	CA-N-CD	6.21	120.39	111.70
15	g	137	SER	N-CA-CB	-6.16	101.27	110.50
6	N	81	LEU	N-CA-C	-6.14	94.42	111.00
7	O	315	PRO	N-CA-CB	-6.01	95.99	102.60
4	L	231	PRO	N-CA-C	6.01	127.72	112.10
4	L	234	PRO	CA-N-CD	-6.00	103.10	111.50
4	L	276	THR	N-CA-CB	5.95	121.61	110.30
6	N	218	ALA	N-CA-CB	5.93	118.41	110.10
4	L	554	ASP	N-CA-CB	5.93	121.28	110.60
4	L	605	ASN	N-CA-CB	5.93	121.27	110.60
4	L	483	PRO	N-CA-C	-5.88	96.81	112.10
14	f	52	GLU	N-CA-CB	5.87	121.16	110.60
3	K	83	ASN	N-CA-CB	5.73	120.92	110.60
8	U	150	ASP	CB-CA-C	5.73	121.86	110.40
5	M	223	ALA	N-CA-CB	5.71	118.09	110.10
6	N	89	GLN	N-CA-CB	-5.65	100.43	110.60
20	l	119	THR	N-CA-C	-5.64	95.78	111.00
12	d	15	PRO	N-CA-CB	-5.63	96.40	102.60
4	L	415	ALA	N-CA-CB	5.63	117.98	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	O	118	TYR	N-CA-CB	-5.58	100.56	110.60
7	O	118	TYR	N-CA-C	5.51	125.88	111.00
5	M	311	GLY	N-CA-C	-5.51	99.33	113.10
22	n	136	GLU	CB-CA-C	5.46	121.31	110.40
7	O	212	PRO	N-CA-C	5.45	126.26	112.10
4	L	582	GLY	N-CA-C	-5.43	99.52	113.10
7	O	246	LEU	C-N-CD	5.40	139.74	128.40
7	O	152	SER	N-CA-CB	5.34	118.52	110.50
5	M	276	CYS	N-CA-CB	5.34	120.21	110.60
4	L	151	SER	N-CA-CB	5.33	118.50	110.50
4	L	194	ASN	N-CA-C	5.31	125.34	111.00
7	O	224	PRO	N-CA-CB	-5.31	96.76	102.60
4	L	234	PRO	N-CA-CB	5.26	109.61	103.30
4	L	212	PRO	N-CA-C	5.25	125.76	112.10
5	M	330	ALA	N-CA-CB	5.25	117.45	110.10
24	p	128	GLU	N-CA-C	5.25	125.17	111.00
4	L	248	HIS	CB-CA-C	5.24	120.88	110.40
3	K	70	GLU	N-CA-CB	5.24	120.03	110.60
12	d	113	LEU	N-CA-CB	-5.23	99.93	110.40
24	p	94	ARG	NE-CZ-NH1	5.23	122.92	120.30
5	M	423	MET	N-CA-C	-5.23	96.89	111.00
4	L	277	MET	CB-CA-C	-5.21	99.97	110.40
4	L	212	PRO	CA-N-CD	5.21	118.99	111.70
18	j	102	ASP	CB-CG-OD2	5.20	122.98	118.30
7	O	212	PRO	CA-N-CD	5.20	118.98	111.70
7	O	220	LYS	N-CA-C	5.15	124.92	111.00
2	J	76	GLU	N-CA-C	-5.15	97.09	111.00
20	l	104	PRO	CA-N-CD	5.14	118.89	111.70
14	f	53	GLU	N-CA-CB	-5.13	101.37	110.60
15	g	78	PRO	N-CA-CB	-5.11	96.98	102.60
4	L	247	LEU	N-CA-CB	5.10	120.61	110.40
5	M	83	HIS	N-CA-C	-5.09	97.25	111.00
7	O	207	ILE	N-CA-C	-5.09	97.27	111.00
6	N	228	ASN	N-CA-CB	5.06	119.71	110.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	D	40/463 (9%)	38 (95%)	2 (5%)	0	100	100
2	J	157/172 (91%)	148 (94%)	9 (6%)	0	100	100
3	K	95/98 (97%)	90 (95%)	5 (5%)	0	100	100
4	L	604/607 (100%)	573 (95%)	31 (5%)	0	100	100
5	M	457/459 (100%)	440 (96%)	17 (4%)	0	100	100
6	N	342/345 (99%)	331 (97%)	10 (3%)	1 (0%)	37	66
7	O	317/355 (89%)	309 (98%)	8 (2%)	0	100	100
8	U	87/156 (56%)	81 (93%)	6 (7%)	0	100	100
9	X	25/172 (14%)	21 (84%)	4 (16%)	0	100	100
10	Y	137/143 (96%)	132 (96%)	5 (4%)	0	100	100
11	c	45/76 (59%)	44 (98%)	1 (2%)	0	100	100
12	d	118/120 (98%)	116 (98%)	2 (2%)	0	100	100
13	e	103/106 (97%)	96 (93%)	7 (7%)	0	100	100
14	f	49/57 (86%)	48 (98%)	1 (2%)	0	100	100
15	g	100/151 (66%)	93 (93%)	7 (7%)	0	100	100
16	h	136/189 (72%)	131 (96%)	5 (4%)	0	100	100
17	i	91/128 (71%)	81 (89%)	10 (11%)	0	100	100
18	j	63/105 (60%)	58 (92%)	5 (8%)	0	100	100
19	k	71/104 (68%)	68 (96%)	3 (4%)	0	100	100
20	l	154/186 (83%)	140 (91%)	14 (9%)	0	100	100
21	m	124/129 (96%)	117 (94%)	7 (6%)	0	100	100
22	n	176/179 (98%)	165 (94%)	10 (6%)	1 (1%)	22	53
23	o	121/137 (88%)	117 (97%)	4 (3%)	0	100	100
24	p	170/176 (97%)	153 (90%)	17 (10%)	0	100	100
All	All	3782/4813 (79%)	3590 (95%)	190 (5%)	2 (0%)	50	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	N	109	ALA
22	n	156	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	36/395 (9%)	36 (100%)	0	100	100
2	J	129/137 (94%)	129 (100%)	0	100	100
3	K	87/88 (99%)	87 (100%)	0	100	100
4	L	549/550 (100%)	549 (100%)	0	100	100
5	M	415/415 (100%)	415 (100%)	0	100	100
6	N	307/308 (100%)	307 (100%)	0	100	100
7	O	283/309 (92%)	283 (100%)	0	100	100
8	U	82/135 (61%)	82 (100%)	0	100	100
9	X	23/154 (15%)	22 (96%)	1 (4%)	25	53
10	Y	104/107 (97%)	104 (100%)	0	100	100
11	c	41/67 (61%)	41 (100%)	0	100	100
12	d	107/107 (100%)	107 (100%)	0	100	100
13	e	93/94 (99%)	93 (100%)	0	100	100
14	f	47/53 (89%)	47 (100%)	0	100	100
15	g	93/129 (72%)	93 (100%)	0	100	100
16	h	123/162 (76%)	123 (100%)	0	100	100
17	i	90/120 (75%)	90 (100%)	0	100	100
18	j	61/87 (70%)	61 (100%)	0	100	100
19	k	55/78 (70%)	55 (100%)	0	100	100
20	l	141/161 (88%)	141 (100%)	0	100	100
21	m	112/114 (98%)	112 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	n	163/164 (99%)	163 (100%)	0	100	100
23	o	112/121 (93%)	112 (100%)	0	100	100
24	p	156/158 (99%)	156 (100%)	0	100	100
All	All	3409/4213 (81%)	3408 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	X	167	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (83) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	36	GLN
3	K	7	ASN
4	L	2	ASN
4	L	25	ASN
4	L	56	HIS
4	L	58	ASN
4	L	135	ASN
4	L	136	ASN
4	L	139	GLN
4	L	199	GLN
4	L	209	ASN
4	L	264	HIS
4	L	296	ASN
4	L	321	GLN
4	L	328	HIS
4	L	332	HIS
4	L	354	GLN
4	L	400	ASN
4	L	446	ASN
4	L	452	ASN
4	L	505	ASN
4	L	579	ASN
5	M	26	ASN
5	M	51	ASN
5	M	81	GLN
5	M	92	GLN
5	M	168	GLN

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Mol	Chain	Res	Type
5	M	170	HIS
5	M	175	ASN
5	M	184	HIS
5	M	192	ASN
5	M	213	HIS
5	M	279	GLN
5	M	293	HIS
5	M	304	GLN
5	M	349	GLN
5	M	374	ASN
5	M	390	ASN
5	M	415	GLN
6	N	120	GLN
6	N	134	GLN
6	N	204	ASN
6	N	273	ASN
6	N	310	ASN
7	O	54	HIS
7	O	80	GLN
7	O	155	GLN
7	O	175	ASN
7	O	235	GLN
7	O	286	GLN
7	O	292	HIS
7	O	306	ASN
7	O	323	GLN
8	U	101	ASN
9	X	151	ASN
10	Y	19	GLN
10	Y	91	ASN
12	d	59	HIS
13	e	98	HIS
14	f	13	HIS
16	h	170	GLN
16	h	181	HIS
17	i	83	HIS
17	i	127	HIS
17	i	128	HIS
18	j	83	HIS
19	k	39	GLN
19	k	66	ASN
20	l	91	GLN

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Mol	Chain	Res	Type
20	l	106	HIS
20	l	115	ASN
21	m	75	ASN
21	m	79	ASN
22	n	12	HIS
22	n	13	GLN
22	n	14	GLN
22	n	33	HIS
22	n	53	ASN
23	o	61	HIS
24	p	67	GLN
24	p	91	GLN
24	p	100	GLN
24	p	124	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

19 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	$\#\|Z\|>2$
25	3PE	K	101	-	45,45,50	0.96	2 (4%)	48,50,55	1.10	4 (8%)
25	3PE	L	703	-	39,39,50	1.02	2 (5%)	42,44,55	1.15	3 (7%)
25	3PE	M	502	-	50,50,50	0.90	2 (4%)	53,55,55	1.15	4 (7%)
25	3PE	L	702	-	48,48,50	0.92	2 (4%)	51,53,55	1.13	4 (7%)
26	CDL	L	704	-	77,77,99	1.01	4 (5%)	83,89,111	1.13	6 (7%)
25	3PE	i	201	-	39,39,50	1.02	2 (5%)	42,44,55	1.05	2 (4%)
25	3PE	d	201	-	30,30,50	1.14	2 (6%)	33,35,55	1.31	5 (15%)
25	3PE	m	203	-	40,40,50	1.00	2 (5%)	43,45,55	1.12	3 (6%)
26	CDL	X	201	-	66,66,99	1.10	4 (6%)	72,78,111	1.27	7 (9%)
25	3PE	Y	201	-	40,40,50	1.02	2 (5%)	43,45,55	1.17	5 (11%)
25	3PE	L	705	-	37,37,50	1.03	2 (5%)	40,42,55	1.13	3 (7%)
25	3PE	m	201	-	46,46,50	0.96	2 (4%)	49,51,55	1.11	3 (6%)
25	3PE	M	501	-	36,36,50	1.09	2 (5%)	39,41,55	1.20	3 (7%)
25	3PE	m	202	-	50,50,50	0.91	2 (4%)	53,55,55	1.14	4 (7%)
25	3PE	N	401	-	50,50,50	0.91	2 (4%)	53,55,55	1.06	4 (7%)
27	ADP	O	401	-	24,29,29	0.93	1 (4%)	29,45,45	1.44	4 (13%)
28	EHZ	n	201	-	27,31,37	1.87	7 (25%)	37,41,47	1.58	6 (16%)
26	CDL	h	201	-	69,69,99	1.08	4 (5%)	75,81,111	1.21	6 (8%)
25	3PE	L	701	-	39,39,50	1.03	2 (5%)	42,44,55	1.14	3 (7%)

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
25	3PE	K	101	-	-	17/49/49/54	-
25	3PE	L	703	-	-	7/43/43/54	-
25	3PE	M	502	-	-	13/54/54/54	-
25	3PE	L	702	-	-	13/52/52/54	-
26	CDL	L	704	-	-	28/88/88/110	-
25	3PE	i	201	-	-	16/43/43/54	-
25	3PE	d	201	-	-	8/34/34/54	-
25	3PE	m	203	-	-	7/44/44/54	-
26	CDL	X	201	-	-	25/77/77/110	-
25	3PE	Y	201	-	-	10/44/44/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	3PE	L	705	-	-	14/41/41/54	-
25	3PE	m	201	-	-	10/50/50/54	-
25	3PE	M	501	-	-	14/40/40/54	-
25	3PE	m	202	-	-	8/54/54/54	-
25	3PE	N	401	-	-	11/54/54/54	-
27	ADP	O	401	-	-	2/12/32/32	0/3/3/3
28	EHZ	n	201	-	-	13/39/39/45	-
26	CDL	h	201	-	-	23/80/80/110	-
25	3PE	L	701	-	-	5/43/43/54	-

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	n	201	EHZ	C15-N2	5.24	1.45	1.33
28	n	201	EHZ	C12-N1	5.13	1.45	1.33
26	X	201	CDL	OB8-CB7	4.27	1.45	1.33
25	K	101	3PE	O31-C31	4.24	1.45	1.33
25	m	202	3PE	O31-C31	4.23	1.45	1.33
25	N	401	3PE	O31-C31	4.23	1.45	1.33
25	m	201	3PE	O31-C31	4.22	1.45	1.33
25	m	201	3PE	O21-C21	4.21	1.46	1.34
25	i	201	3PE	O31-C31	4.21	1.45	1.33
26	X	201	CDL	OA8-CA7	4.20	1.45	1.33
25	M	501	3PE	O21-C21	4.20	1.46	1.34
25	M	501	3PE	O31-C31	4.19	1.45	1.33
25	L	703	3PE	O31-C31	4.19	1.45	1.33
26	L	704	CDL	OB8-CB7	4.18	1.45	1.33
25	L	701	3PE	O31-C31	4.17	1.45	1.33
25	Y	201	3PE	O21-C21	4.17	1.46	1.34
25	m	203	3PE	O31-C31	4.17	1.45	1.33
25	L	705	3PE	O31-C31	4.15	1.45	1.33
25	Y	201	3PE	O31-C31	4.13	1.45	1.33
25	M	502	3PE	O31-C31	4.13	1.45	1.33
25	L	701	3PE	O21-C21	4.13	1.45	1.34
26	h	201	CDL	OA8-CA7	4.13	1.45	1.33
26	h	201	CDL	OB8-CB7	4.11	1.45	1.33
26	L	704	CDL	OB6-CB5	4.11	1.45	1.34
25	i	201	3PE	O21-C21	4.11	1.45	1.34
26	h	201	CDL	OB6-CB5	4.07	1.45	1.34
25	d	201	3PE	O31-C31	4.05	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	h	201	CDL	OA6-CA5	4.03	1.45	1.34
25	L	702	3PE	O31-C31	4.03	1.45	1.33
26	L	704	CDL	OA8-CA7	3.99	1.45	1.33
25	m	202	3PE	O21-C21	3.98	1.45	1.34
26	X	201	CDL	OB6-CB5	3.97	1.45	1.34
25	L	703	3PE	O21-C21	3.97	1.45	1.34
25	K	101	3PE	O21-C21	3.96	1.45	1.34
25	d	201	3PE	O21-C21	3.96	1.45	1.34
25	L	702	3PE	O21-C21	3.95	1.45	1.34
26	X	201	CDL	OA6-CA5	3.93	1.45	1.34
25	N	401	3PE	O21-C21	3.93	1.45	1.34
25	m	203	3PE	O21-C21	3.92	1.45	1.34
25	M	502	3PE	O21-C21	3.91	1.45	1.34
25	L	705	3PE	O21-C21	3.88	1.45	1.34
26	L	704	CDL	OA6-CA5	3.81	1.45	1.34
28	n	201	EHZ	P1-O7	2.60	1.64	1.54
28	n	201	EHZ	O4-C15	-2.45	1.18	1.23
28	n	201	EHZ	C9-S1	2.45	1.82	1.76
28	n	201	EHZ	P1-OP3	-2.30	1.46	1.54
28	n	201	EHZ	O3-C12	-2.28	1.18	1.23
27	O	401	ADP	C5-C4	2.24	1.46	1.40

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	n	201	EHZ	C8-C9-S1	5.01	119.83	113.63
25	m	201	3PE	O21-C21-C22	4.69	121.62	111.50
25	M	501	3PE	O21-C21-C22	4.65	121.52	111.50
25	m	202	3PE	O21-C21-C22	4.44	121.07	111.50
26	h	201	CDL	OB6-CB5-C51	4.43	121.06	111.50
26	X	201	CDL	OB6-CB5-C51	4.35	120.88	111.50
25	M	502	3PE	O21-C21-C22	4.28	120.72	111.50
26	L	704	CDL	OA6-CA5-C11	4.27	120.69	111.50
26	X	201	CDL	OA6-CA5-C11	4.22	120.60	111.50
25	Y	201	3PE	O21-C21-C22	4.16	120.46	111.50
25	K	101	3PE	O21-C21-C22	4.12	120.38	111.50
25	L	703	3PE	O21-C21-C22	4.05	120.22	111.50
25	L	702	3PE	O21-C21-C22	4.00	120.13	111.50
26	h	201	CDL	OA6-CA5-C11	3.96	120.04	111.50
25	d	201	3PE	O21-C21-C22	3.92	119.94	111.50
25	L	701	3PE	O21-C21-C22	3.88	119.86	111.50
25	N	401	3PE	O21-C21-C22	3.78	119.64	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	i	201	3PE	O21-C21-C22	3.77	119.62	111.50
26	L	704	CDL	OB6-CB5-C51	3.77	119.62	111.50
25	L	705	3PE	O21-C21-C22	3.71	119.50	111.50
25	m	203	3PE	O21-C21-C22	3.63	119.33	111.50
27	O	401	ADP	PA-O3A-PB	-3.52	120.75	132.83
27	O	401	ADP	N3-C2-N1	-3.42	123.34	128.68
25	M	502	3PE	C2-O21-C21	-3.15	110.04	117.79
25	d	201	3PE	O31-C31-C32	3.09	121.60	111.91
28	n	201	EHZ	C10-S1-C9	3.08	111.46	101.87
25	m	202	3PE	C2-O21-C21	-3.08	110.22	117.79
25	d	201	3PE	C2-O21-C21	-3.07	110.24	117.79
26	X	201	CDL	CA4-OA6-CA5	-3.06	110.26	117.79
25	m	203	3PE	C2-O21-C21	-3.02	110.35	117.79
25	M	502	3PE	O31-C31-C32	3.00	121.32	111.91
25	K	101	3PE	C2-O21-C21	-2.90	110.64	117.79
25	Y	201	3PE	O31-C31-C32	2.87	120.93	111.91
25	m	202	3PE	O31-C31-C32	2.84	120.81	111.91
25	i	201	3PE	O31-C31-C32	2.84	120.81	111.91
27	O	401	ADP	C3'-C2'-C1'	2.80	105.20	100.98
26	h	201	CDL	OB8-CB7-C71	2.80	120.70	111.91
25	m	201	3PE	O31-C31-C32	2.79	120.67	111.91
25	N	401	3PE	C2-O21-C21	-2.78	110.95	117.79
26	L	704	CDL	CA4-OA6-CA5	-2.75	111.03	117.79
26	X	201	CDL	OB8-CB7-C71	2.69	120.34	111.91
26	L	704	CDL	OB8-CB7-C71	2.67	120.30	111.91
25	m	203	3PE	O31-C31-C32	2.66	120.27	111.91
25	L	702	3PE	O31-C31-C32	2.65	120.23	111.91
25	K	101	3PE	O31-C31-C32	2.65	120.22	111.91
26	L	704	CDL	OA8-CA7-C31	2.65	120.22	111.91
25	L	703	3PE	O31-C31-C32	2.62	120.13	111.91
25	L	701	3PE	O31-C31-C32	2.62	120.12	111.91
26	h	201	CDL	CA4-OA6-CA5	-2.60	111.38	117.79
25	N	401	3PE	O31-C31-C32	2.59	120.03	111.91
27	O	401	ADP	C4-C5-N7	-2.59	106.70	109.40
26	X	201	CDL	OA8-CA7-C31	2.58	120.00	111.91
25	L	703	3PE	C2-O21-C21	-2.57	111.47	117.79
25	Y	201	3PE	C2-O21-C21	-2.49	111.67	117.79
26	h	201	CDL	OA8-CA7-C31	2.48	119.70	111.91
28	n	201	EHZ	OP3-P1-O9	-2.48	100.97	110.68
26	h	201	CDL	CB4-OB6-CB5	-2.47	111.70	117.79
25	L	702	3PE	C2-O21-C21	-2.45	111.77	117.79
25	L	705	3PE	C2-O21-C21	-2.43	111.80	117.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	M	501	3PE	C2-O21-C21	-2.41	111.86	117.79
25	L	705	3PE	O31-C31-C32	2.31	119.17	111.91
28	n	201	EHZ	C10-C11-N1	-2.30	107.58	112.42
25	K	101	3PE	O21-C21-O22	-2.29	118.17	123.70
25	d	201	3PE	O31-C31-O32	-2.25	117.92	123.59
25	M	502	3PE	O21-C21-O22	-2.21	118.36	123.70
25	Y	201	3PE	O21-C21-O22	-2.21	118.37	123.70
25	m	202	3PE	O21-C21-O22	-2.21	118.37	123.70
25	N	401	3PE	O21-C21-O22	-2.18	118.44	123.70
25	M	501	3PE	O31-C31-C32	2.14	118.62	111.91
28	n	201	EHZ	C5-C6-C7	-2.14	108.69	114.85
26	X	201	CDL	CB6-CB4-CB3	-2.12	106.78	111.79
25	d	201	3PE	O21-C21-O22	-2.12	118.59	123.70
25	L	702	3PE	O21-C21-O22	-2.06	118.71	123.70
25	Y	201	3PE	O31-C31-O32	-2.06	118.41	123.59
26	X	201	CDL	OB6-CB5-OB7	-2.05	118.74	123.70
25	L	701	3PE	C2-O21-C21	-2.02	112.83	117.79
26	L	704	CDL	OA6-CA5-OA7	-2.01	118.84	123.70
25	m	201	3PE	O21-C21-O22	-2.01	118.84	123.70
28	n	201	EHZ	C14-C13-C12	-2.00	109.02	112.36

There are no chirality outliers.

All (244) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	K	101	3PE	C11-O13-P-O12
25	L	701	3PE	C1-O11-P-O13
25	L	701	3PE	C2-C1-O11-P
25	L	702	3PE	C1-O11-P-O12
25	L	702	3PE	O22-C21-O21-C2
25	L	702	3PE	C22-C21-O21-C2
25	L	703	3PE	C11-O13-P-O11
25	L	703	3PE	C11-O13-P-O12
25	L	703	3PE	C11-O13-P-O14
25	L	705	3PE	C1-O11-P-O12
25	L	705	3PE	C1-O11-P-O14
25	L	705	3PE	C11-O13-P-O12
25	L	705	3PE	C11-O13-P-O14
25	M	501	3PE	C1-O11-P-O12
25	M	501	3PE	C1-O11-P-O13
25	M	501	3PE	C1-O11-P-O14
25	M	501	3PE	C11-O13-P-O11

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Mol	Chain	Res	Type	Atoms
25	M	501	3PE	C11-O13-P-O12
25	M	501	3PE	C11-O13-P-O14
25	M	502	3PE	C1-O11-P-O12
25	M	502	3PE	C11-O13-P-O14
25	N	401	3PE	C11-O13-P-O11
25	N	401	3PE	C11-O13-P-O12
25	Y	201	3PE	C1-O11-P-O12
25	d	201	3PE	O22-C21-O21-C2
25	i	201	3PE	C1-O11-P-O12
25	i	201	3PE	C1-O11-P-O13
25	i	201	3PE	C1-O11-P-O14
25	i	201	3PE	C11-O13-P-O12
25	m	201	3PE	C1-O11-P-O14
25	m	201	3PE	C22-C21-O21-C2
25	m	202	3PE	C22-C21-O21-C2
25	m	203	3PE	C1-O11-P-O12
25	m	203	3PE	C1-O11-P-O14
25	m	203	3PE	C22-C21-O21-C2
26	L	704	CDL	CA2-OA2-PA1-OA3
26	L	704	CDL	CB2-OB2-PB2-OB4
26	L	704	CDL	CB3-OB5-PB2-OB3
26	L	704	CDL	CB3-OB5-PB2-OB4
26	L	704	CDL	C51-CB5-OB6-CB4
26	X	201	CDL	CA3-OA5-PA1-OA2
26	X	201	CDL	CA3-OA5-PA1-OA3
26	X	201	CDL	CA3-OA5-PA1-OA4
26	X	201	CDL	CB2-OB2-PB2-OB3
26	X	201	CDL	CB2-OB2-PB2-OB5
26	X	201	CDL	CB3-OB5-PB2-OB3
26	X	201	CDL	C51-CB5-OB6-CB4
26	h	201	CDL	CA2-OA2-PA1-OA3
26	h	201	CDL	CA2-OA2-PA1-OA4
26	h	201	CDL	CA3-OA5-PA1-OA4
26	h	201	CDL	CB2-OB2-PB2-OB3
26	h	201	CDL	CB3-OB5-PB2-OB3
26	h	201	CDL	C51-CB5-OB6-CB4
28	n	201	EHZ	C12-C13-C14-N2
28	n	201	EHZ	N2-C15-C16-O5
28	n	201	EHZ	C15-C16-C17-C18
28	n	201	EHZ	C15-C16-C17-C19
28	n	201	EHZ	C15-C16-C17-C20
28	n	201	EHZ	O5-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
28	n	201	EHZ	O5-C16-C17-C19
28	n	201	EHZ	O5-C16-C17-C20
26	L	704	CDL	OA9-CA7-OA8-CA6
25	m	202	3PE	O22-C21-O21-C2
25	m	203	3PE	O22-C21-O21-C2
26	L	704	CDL	OB7-CB5-OB6-CB4
26	X	201	CDL	OB7-CB5-OB6-CB4
26	h	201	CDL	OB7-CB5-OB6-CB4
25	K	101	3PE	C32-C31-O31-C3
25	d	201	3PE	C22-C21-O21-C2
25	N	401	3PE	C32-C31-O31-C3
26	L	704	CDL	C31-CA7-OA8-CA6
25	m	201	3PE	O22-C21-O21-C2
25	N	401	3PE	O32-C31-O31-C3
25	m	203	3PE	O32-C31-O31-C3
26	X	201	CDL	O1-C1-CB2-OB2
25	K	101	3PE	O32-C31-O31-C3
25	L	705	3PE	C22-C21-O21-C2
26	L	704	CDL	C11-CA5-OA6-CA4
25	m	203	3PE	C32-C31-O31-C3
26	h	201	CDL	CA4-CA3-OA5-PA1
25	L	705	3PE	O22-C21-O21-C2
25	i	201	3PE	C32-C31-O31-C3
26	X	201	CDL	C31-CA7-OA8-CA6
25	M	501	3PE	C32-C33-C34-C35
25	m	202	3PE	C32-C31-O31-C3
26	h	201	CDL	C71-CB7-OB8-CB6
26	X	201	CDL	OA9-CA7-OA8-CA6
26	L	704	CDL	OA7-CA5-OA6-CA4
25	i	201	3PE	O32-C31-O31-C3
25	m	202	3PE	O32-C31-O31-C3
25	K	101	3PE	C1-O11-P-O13
25	L	702	3PE	C1-O11-P-O13
25	L	705	3PE	C1-O11-P-O13
25	L	705	3PE	C11-O13-P-O11
25	M	502	3PE	C11-O13-P-O11
25	Y	201	3PE	C1-O11-P-O13
25	Y	201	3PE	C11-O13-P-O11
25	i	201	3PE	C11-O13-P-O11
25	m	203	3PE	C1-O11-P-O13
26	L	704	CDL	CA2-OA2-PA1-OA5
26	L	704	CDL	CB2-OB2-PB2-OB5

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Mol	Chain	Res	Type	Atoms
26	L	704	CDL	CB3-OB5-PB2-OB2
26	h	201	CDL	CA2-OA2-PA1-OA5
26	h	201	CDL	CA3-OA5-PA1-OA2
26	X	201	CDL	CA2-C1-CB2-OB2
25	M	502	3PE	C22-C21-O21-C2
26	h	201	CDL	C18-C19-C20-C21
25	d	201	3PE	C32-C31-O31-C3
25	M	502	3PE	O22-C21-O21-C2
25	L	703	3PE	C25-C26-C27-C28
26	X	201	CDL	C1-CB2-OB2-PB2
26	h	201	CDL	OB9-CB7-OB8-CB6
25	K	101	3PE	C22-C23-C24-C25
26	X	201	CDL	C71-CB7-OB8-CB6
25	m	201	3PE	C26-C27-C28-C29
25	M	501	3PE	C32-C31-O31-C3
25	d	201	3PE	O32-C31-O31-C3
25	m	201	3PE	C32-C31-O31-C3
25	M	502	3PE	C23-C24-C25-C26
26	L	704	CDL	C55-C56-C57-C58
25	m	201	3PE	O32-C31-O31-C3
26	X	201	CDL	OB9-CB7-OB8-CB6
25	M	501	3PE	O32-C31-O31-C3
25	M	502	3PE	C3C-C3D-C3E-C3F
25	d	201	3PE	C11-O13-P-O11
26	h	201	CDL	CB3-OB5-PB2-OB2
25	Y	201	3PE	C2-C1-O11-P
25	K	101	3PE	C33-C34-C35-C36
25	N	401	3PE	C24-C25-C26-C27
25	L	702	3PE	C24-C25-C26-C27
28	n	201	EHZ	O4-C15-C16-O5
25	L	703	3PE	C32-C31-O31-C3
26	L	704	CDL	CB6-CB4-OB6-CB5
26	L	704	CDL	OB5-CB3-CB4-OB6
25	L	702	3PE	C32-C31-O31-C3
26	L	704	CDL	C71-CB7-OB8-CB6
25	L	705	3PE	C32-C31-O31-C3
25	m	201	3PE	C27-C28-C29-C2A
25	K	101	3PE	C36-C37-C38-C39
25	L	703	3PE	O32-C31-O31-C3
25	i	201	3PE	C22-C21-O21-C2
26	X	201	CDL	CA3-CA4-CA6-OA8
25	M	501	3PE	C2-C3-O31-C31

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Mol	Chain	Res	Type	Atoms
26	h	201	CDL	CB2-OB2-PB2-OB5
26	L	704	CDL	C32-C33-C34-C35
25	K	101	3PE	O11-C1-C2-O21
28	n	201	EHZ	C3-C4-C5-C6
26	L	704	CDL	OB9-CB7-OB8-CB6
26	X	201	CDL	OA6-CA4-CA6-OA8
25	i	201	3PE	O22-C21-O21-C2
25	i	201	3PE	C2-C1-O11-P
26	X	201	CDL	C1-CA2-OA2-PA1
26	h	201	CDL	C14-C15-C16-C17
28	n	201	EHZ	O2-C9-S1-C10
25	L	705	3PE	O32-C31-O31-C3
26	L	704	CDL	C12-C13-C14-C15
25	Y	201	3PE	C22-C21-O21-C2
26	X	201	CDL	C11-CA5-OA6-CA4
25	Y	201	3PE	C32-C31-O31-C3
25	i	201	3PE	C1-C2-O21-C21
26	h	201	CDL	CB3-CB4-OB6-CB5
28	n	201	EHZ	C8-C9-S1-C10
26	h	201	CDL	CB4-CB3-OB5-PB2
25	L	702	3PE	O32-C31-O31-C3
25	M	501	3PE	O11-C1-C2-O21
27	O	401	ADP	PA-O3A-PB-O3B
25	L	702	3PE	C28-C29-C2A-C2B
25	Y	201	3PE	O22-C21-O21-C2
26	X	201	CDL	OA7-CA5-OA6-CA4
25	M	502	3PE	C1-O11-P-O13
26	L	704	CDL	CA3-OA5-PA1-OA2
25	K	101	3PE	C2-C1-O11-P
25	K	101	3PE	C1-O11-P-O12
25	K	101	3PE	C1-O11-P-O14
25	L	701	3PE	C1-O11-P-O12
25	M	502	3PE	C11-O13-P-O12
25	N	401	3PE	C11-O13-P-O14
25	Y	201	3PE	C11-O13-P-O12
25	Y	201	3PE	C11-O13-P-O14
25	i	201	3PE	C11-O13-P-O14
26	L	704	CDL	CA2-OA2-PA1-OA4
26	h	201	CDL	CA3-OA5-PA1-OA3
26	h	201	CDL	CB3-OB5-PB2-OB4
25	Y	201	3PE	O32-C31-O31-C3
25	N	401	3PE	C12-C11-O13-P

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Mol	Chain	Res	Type	Atoms
25	d	201	3PE	C12-C11-O13-P
25	L	702	3PE	C25-C26-C27-C28
26	X	201	CDL	C52-C53-C54-C55
28	n	201	EHZ	C2-C3-C4-C5
25	m	201	3PE	C1-C2-O21-C21
26	X	201	CDL	CB6-CB4-OB6-CB5
25	M	501	3PE	O11-C1-C2-C3
26	L	704	CDL	OB5-CB3-CB4-CB6
25	L	701	3PE	C26-C27-C28-C29
25	K	101	3PE	C11-O13-P-O11
25	N	401	3PE	C1-O11-P-O13
26	X	201	CDL	CA2-OA2-PA1-OA5
26	X	201	CDL	CB3-OB5-PB2-OB2
25	m	202	3PE	C32-C33-C34-C35
25	L	702	3PE	C33-C34-C35-C36
25	N	401	3PE	C34-C35-C36-C37
25	d	201	3PE	C24-C25-C26-C27
25	L	705	3PE	C2-C1-O11-P
26	L	704	CDL	CA4-CA3-OA5-PA1
26	L	704	CDL	C1-CB2-OB2-PB2
25	m	202	3PE	C23-C24-C25-C26
25	N	401	3PE	C28-C29-C2A-C2B
25	M	501	3PE	O13-C11-C12-N
26	L	704	CDL	C34-C35-C36-C37
25	i	201	3PE	C24-C25-C26-C27
25	i	201	3PE	C2B-C2C-C2D-C2E
25	L	705	3PE	C24-C25-C26-C27
25	M	502	3PE	C2B-C2C-C2D-C2E
25	m	201	3PE	C1-O11-P-O13
26	h	201	CDL	C31-CA7-OA8-CA6
26	h	201	CDL	OA9-CA7-OA8-CA6
25	K	101	3PE	C26-C27-C28-C29
25	M	502	3PE	C39-C3A-C3B-C3C
25	K	101	3PE	O11-C1-C2-C3
25	L	705	3PE	C34-C35-C36-C37
26	X	201	CDL	C59-C60-C61-C62
25	N	401	3PE	C23-C24-C25-C26
25	m	202	3PE	O11-C1-C2-O21
27	O	401	ADP	PA-O3A-PB-O2B
25	L	702	3PE	C39-C3A-C3B-C3C
25	M	502	3PE	C3A-C3B-C3C-C3D
25	L	705	3PE	C33-C34-C35-C36

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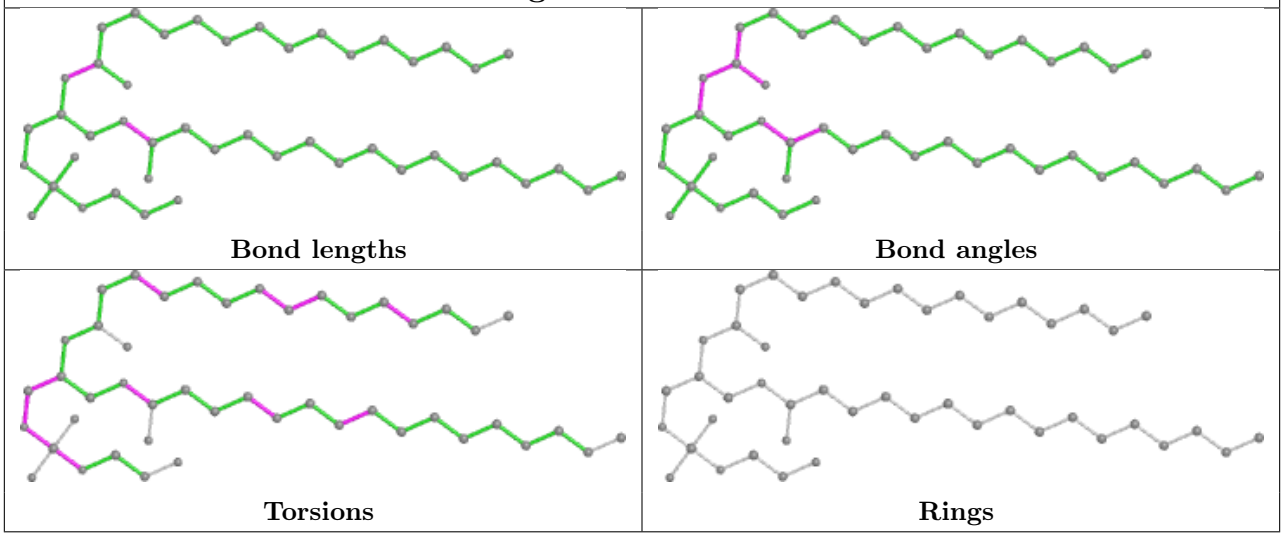
Mol	Chain	Res	Type	Atoms
26	L	704	CDL	C11-C12-C13-C14
25	L	702	3PE	C34-C35-C36-C37
26	L	704	CDL	C77-C78-C79-C80
25	i	201	3PE	O21-C21-C22-C23
25	K	101	3PE	C2A-C2B-C2C-C2D
25	L	701	3PE	C38-C39-C3A-C3B
25	K	101	3PE	C11-O13-P-O14
25	M	502	3PE	C1-O11-P-O14
25	d	201	3PE	C11-O13-P-O14
25	m	201	3PE	C1-O11-P-O12
25	m	202	3PE	C1-O11-P-O14
25	L	702	3PE	C2B-C2C-C2D-C2E
25	M	501	3PE	C12-C11-O13-P
25	i	201	3PE	O22-C21-C22-C23
25	K	101	3PE	C27-C28-C29-C2A
26	h	201	CDL	C72-C71-CB7-OB8
25	L	703	3PE	C22-C23-C24-C25

There are no ring outliers.

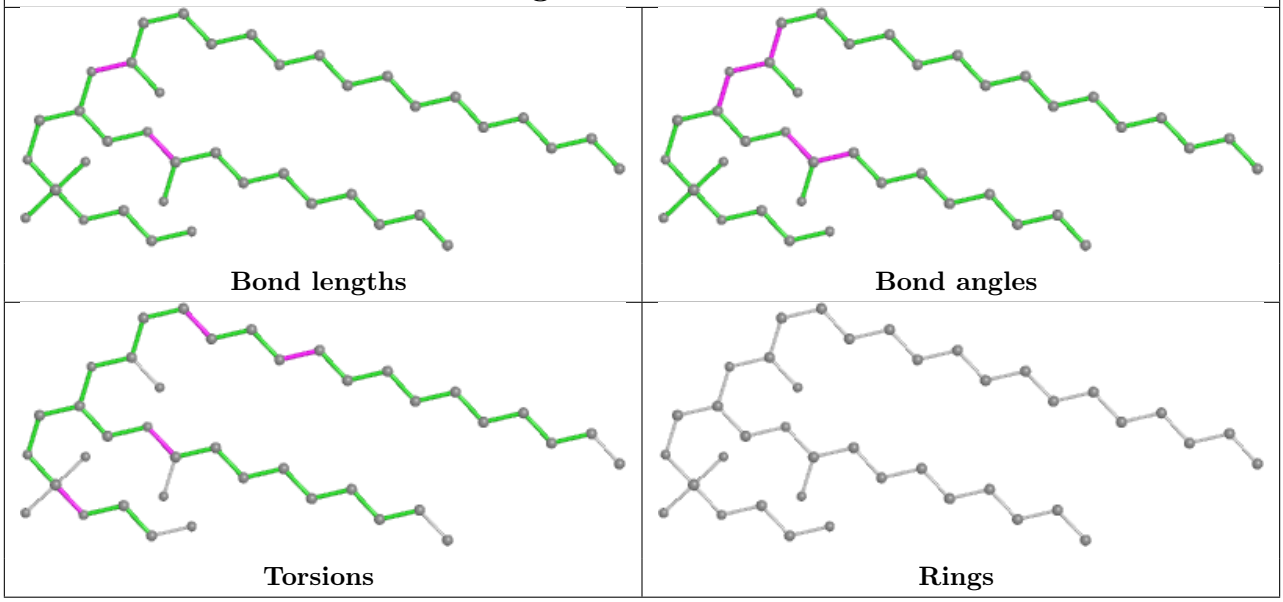
No monomer is involved in short contacts.

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.

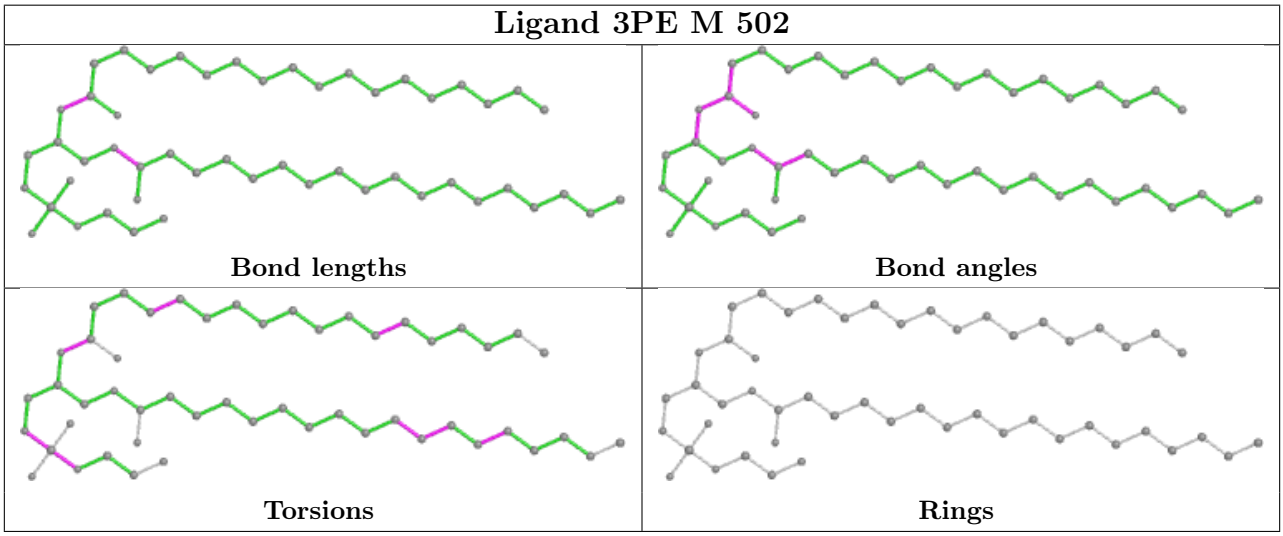
Ligand 3PE K 101



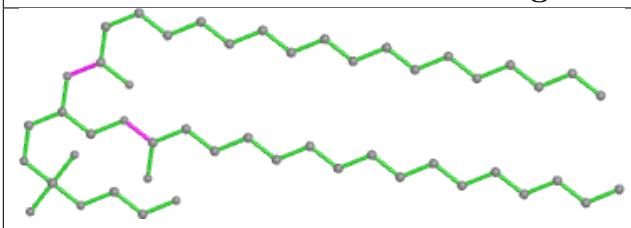
Ligand 3PE L 703



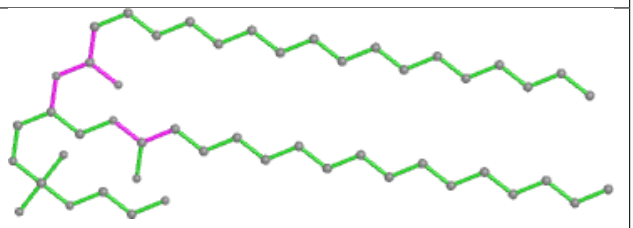
Ligand 3PE M 502



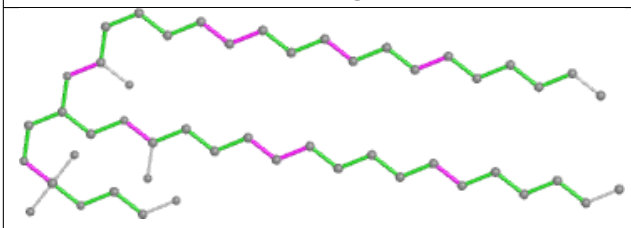
Ligand 3PE L 702



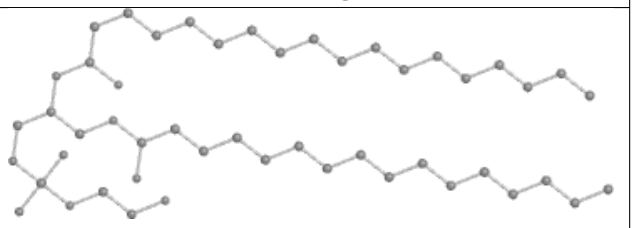
Bond lengths



Bond angles

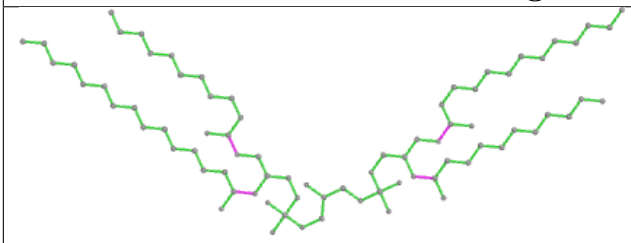


Torsions

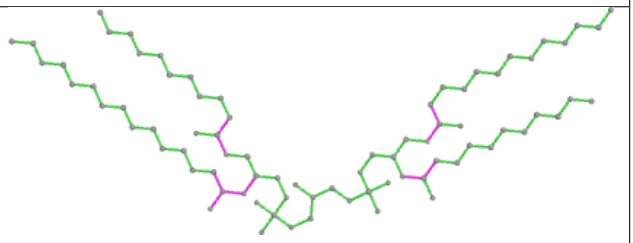


Rings

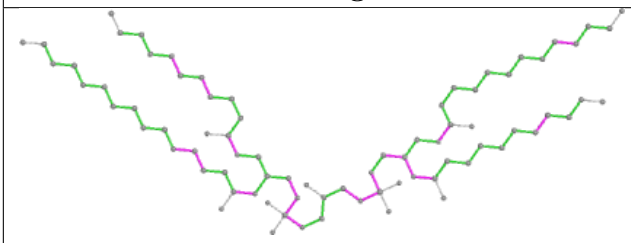
Ligand CDL L 704



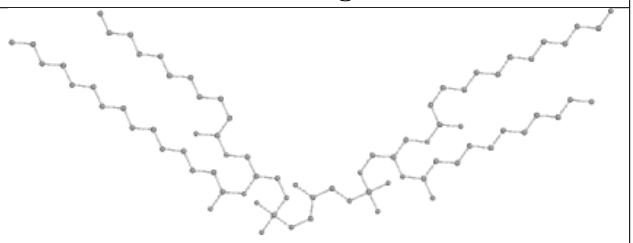
Bond lengths



Bond angles

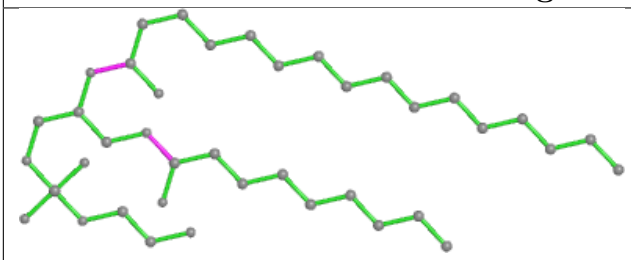


Torsions

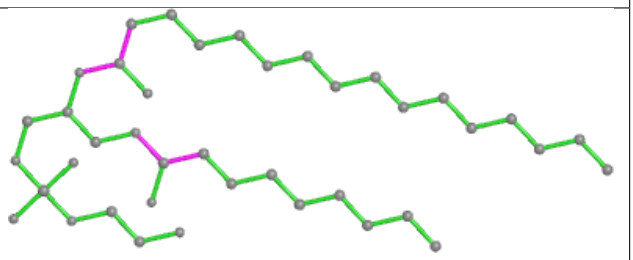


Rings

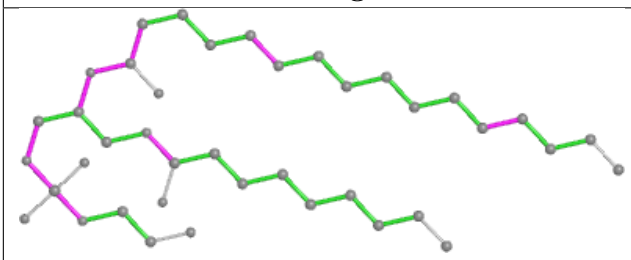
Ligand 3PE i 201



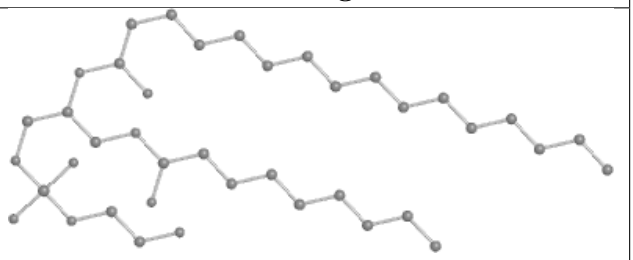
Bond lengths



Bond angles

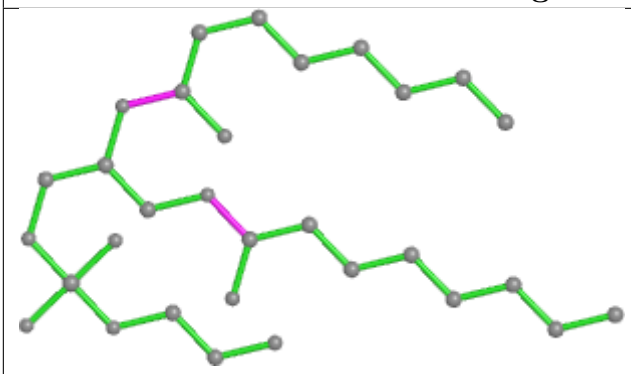


Torsions

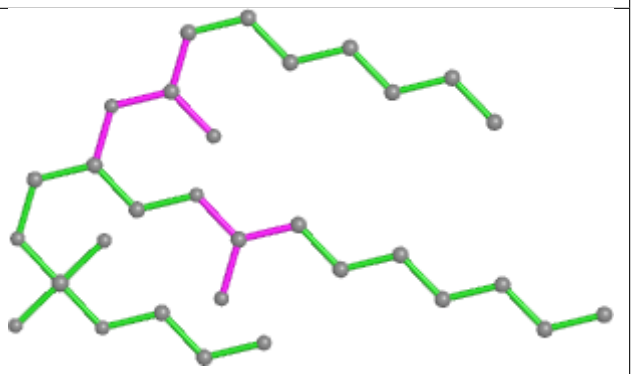


Rings

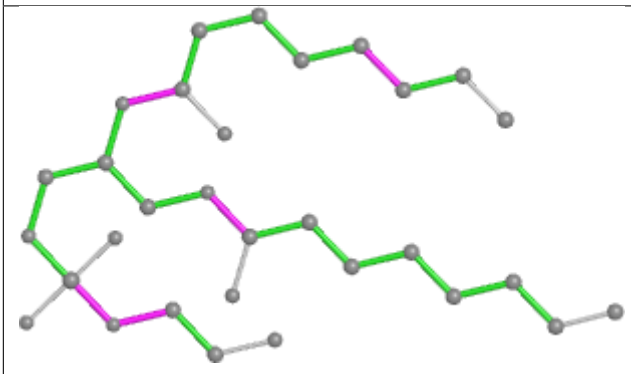
Ligand 3PE d 201



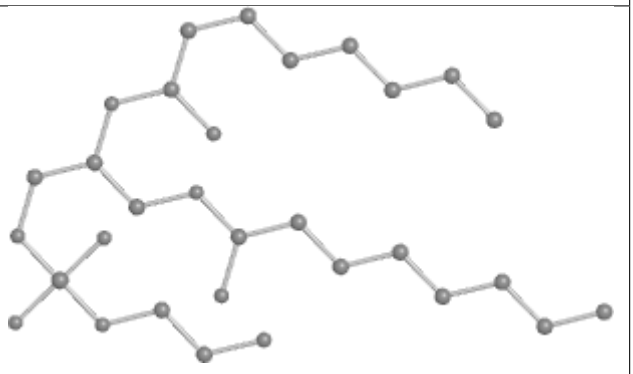
Bond lengths



Bond angles

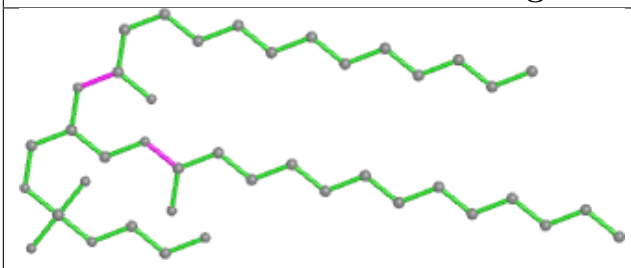


Torsions

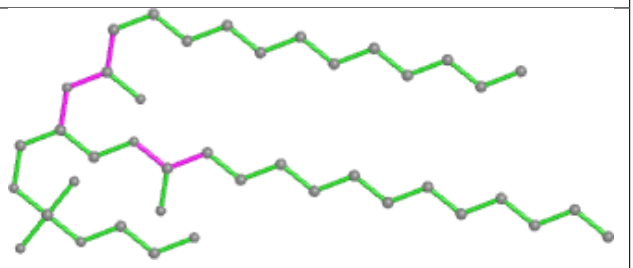


Rings

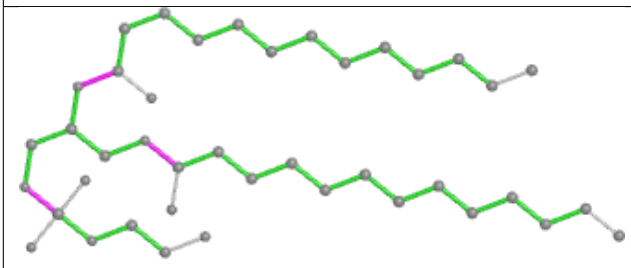
Ligand 3PE m 203



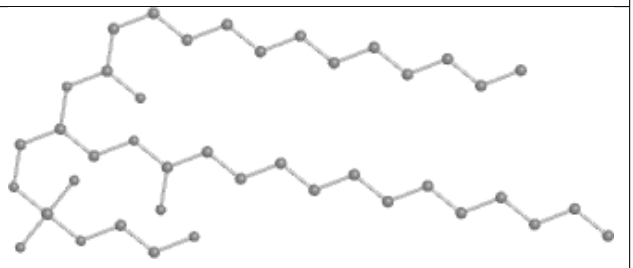
Bond lengths



Bond angles

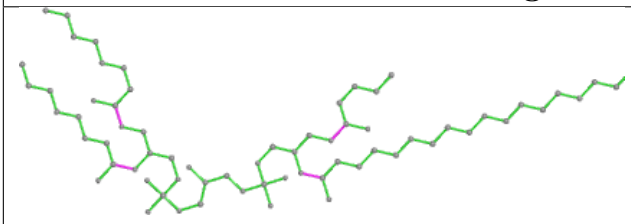


Torsions

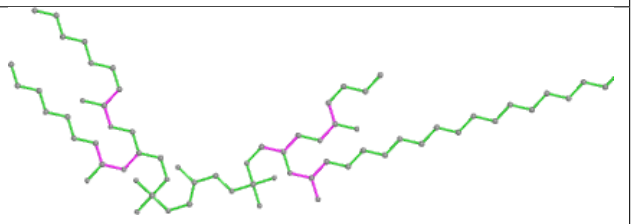


Rings

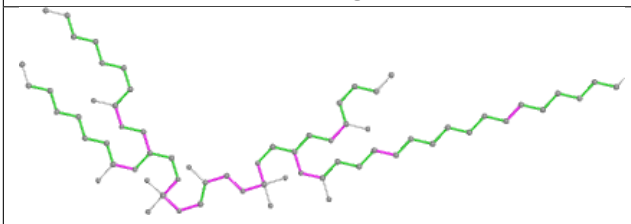
Ligand CDL X 201



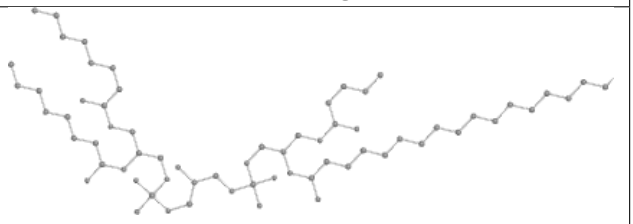
Bond lengths



Bond angles

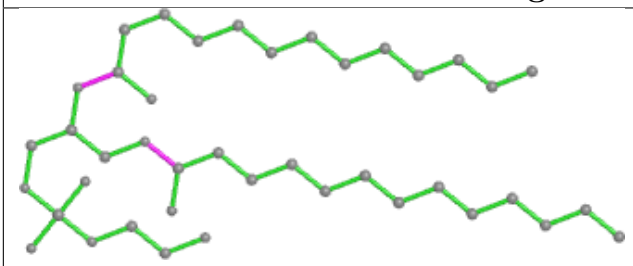


Torsions

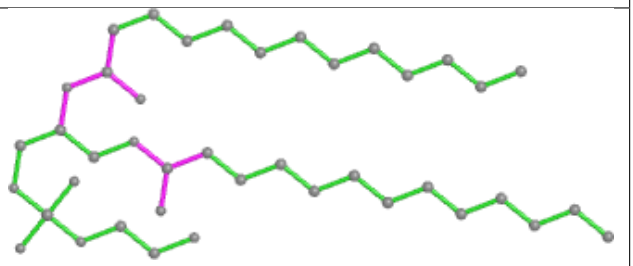


Rings

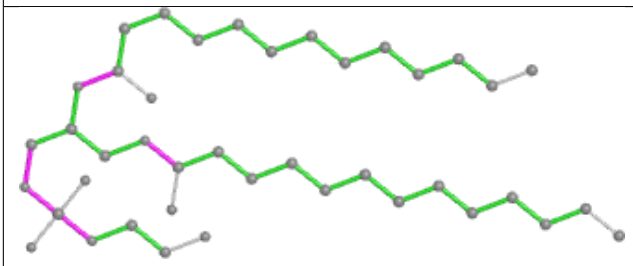
Ligand 3PE Y 201



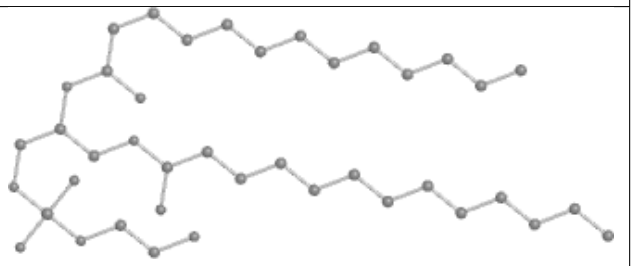
Bond lengths



Bond angles

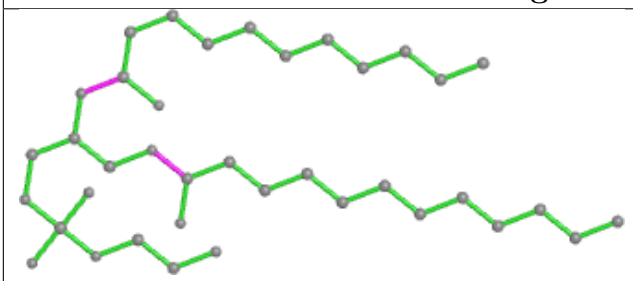


Torsions

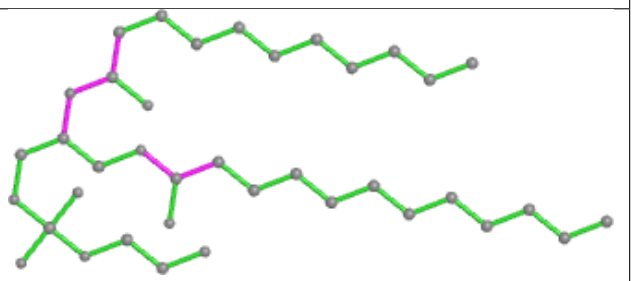


Rings

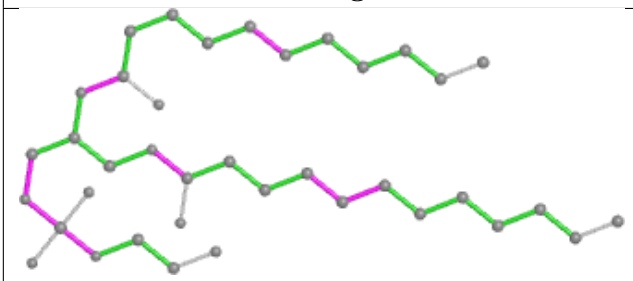
Ligand 3PE L 705



Bond lengths



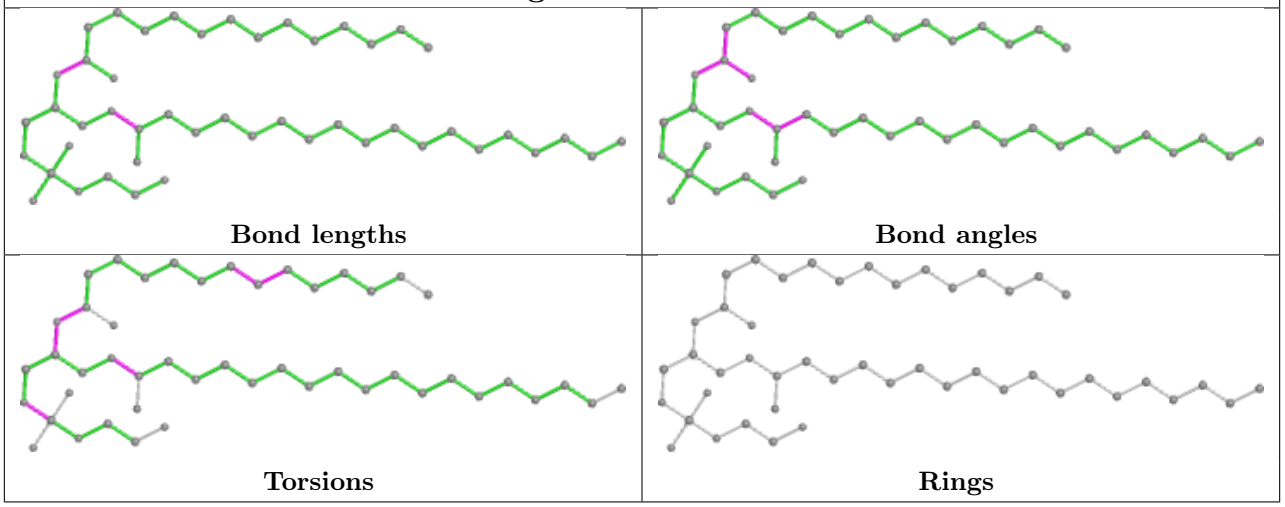
Bond angles



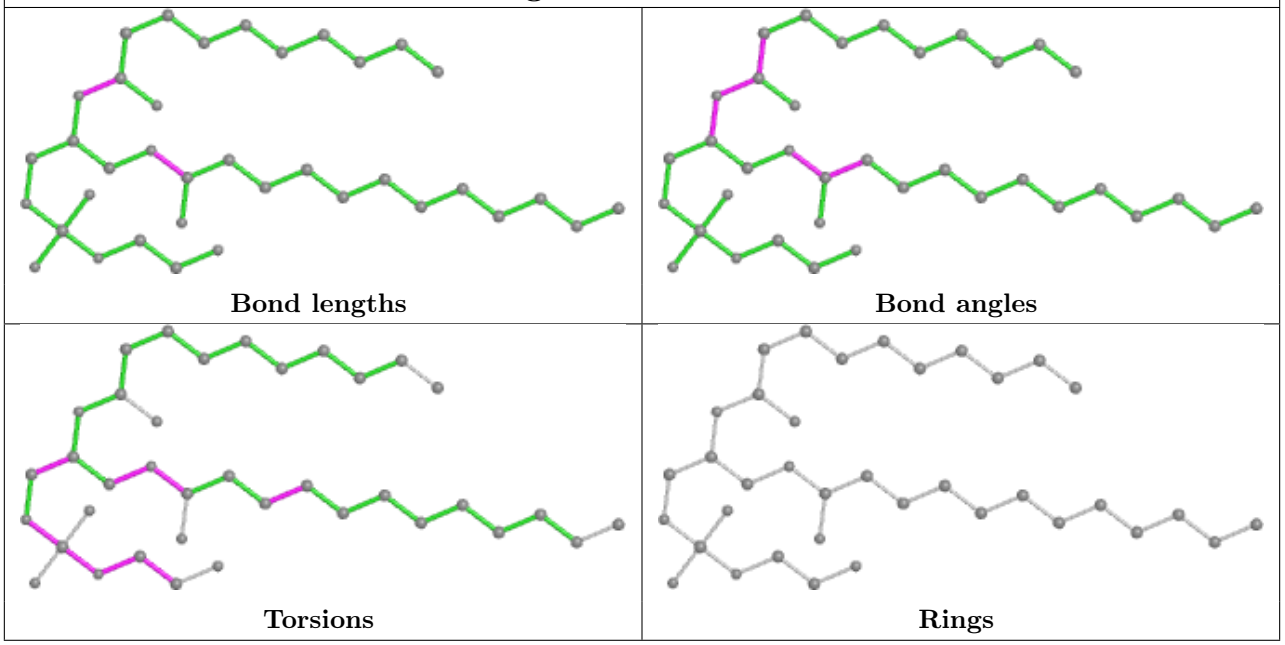
Torsions

Rings

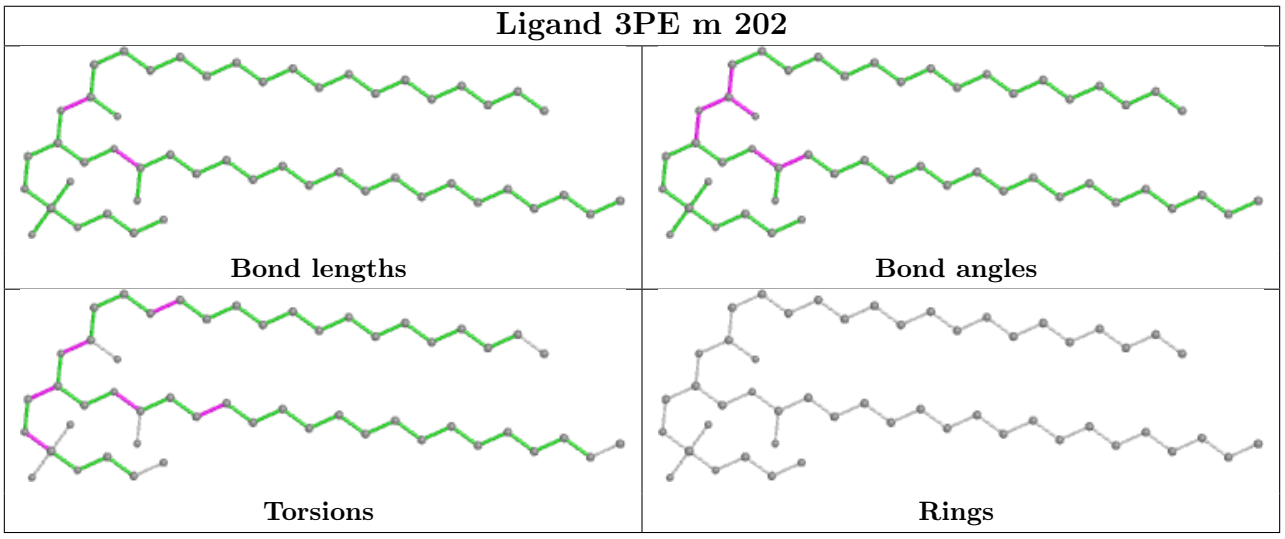
Ligand 3PE m 201



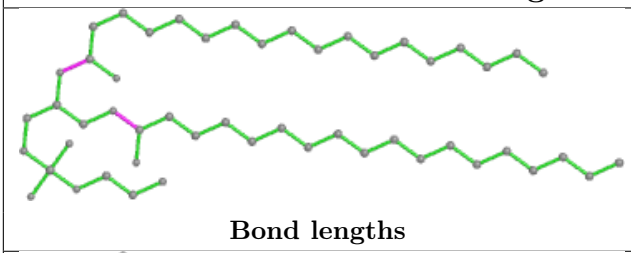
Ligand 3PE M 501



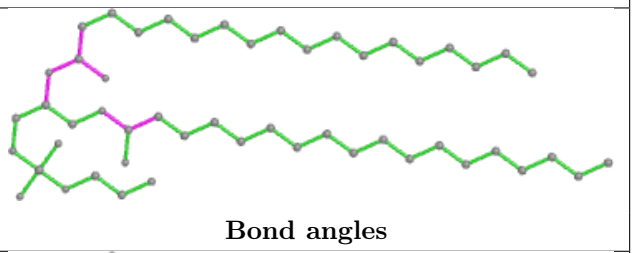
Ligand 3PE m 202



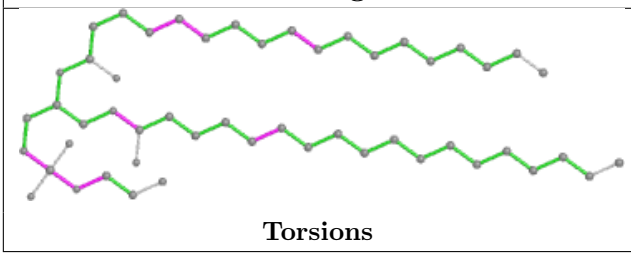
Ligand 3PE N 401



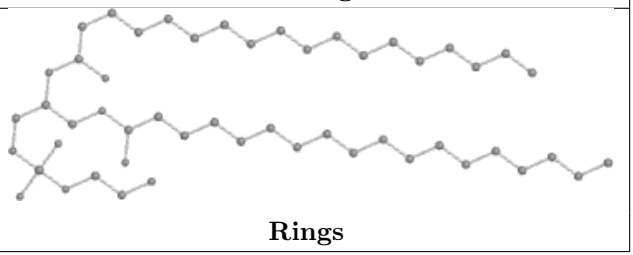
Bond lengths



Bond angles

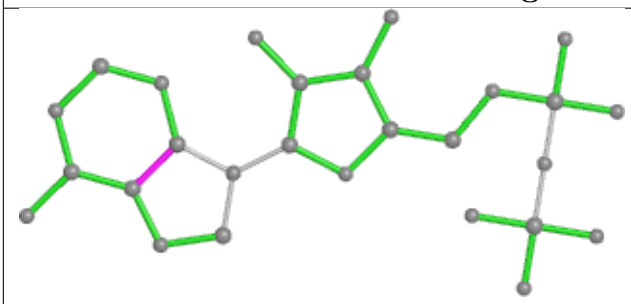


Torsions

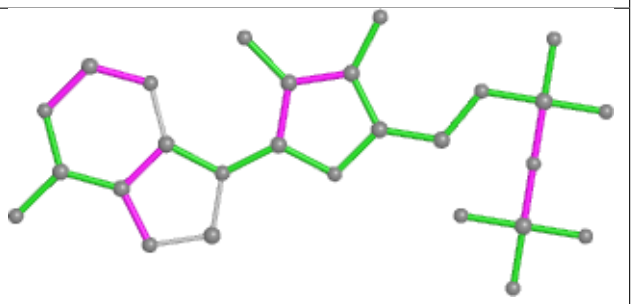


Rings

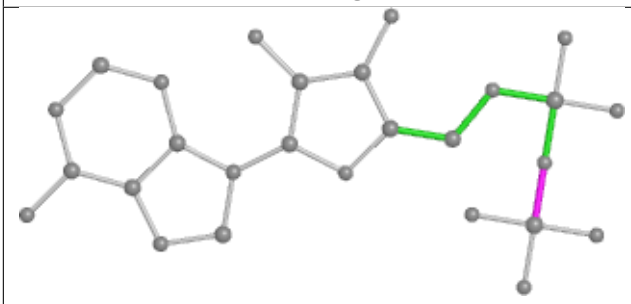
Ligand ADP O 401



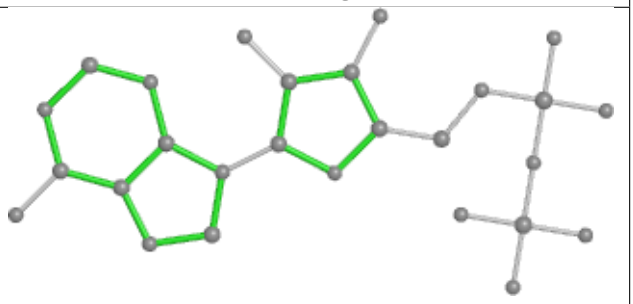
Bond lengths



Bond angles

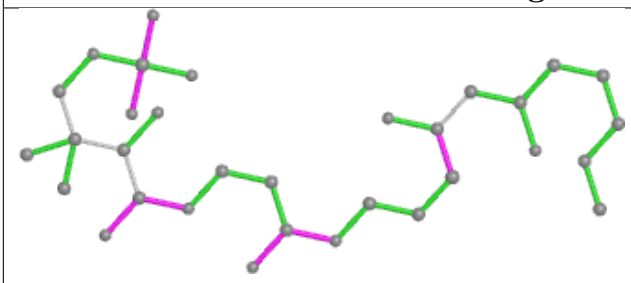


Torsions

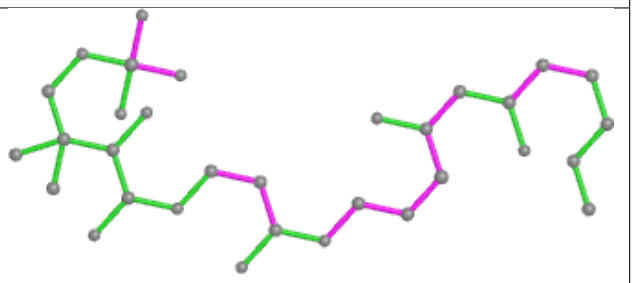


Rings

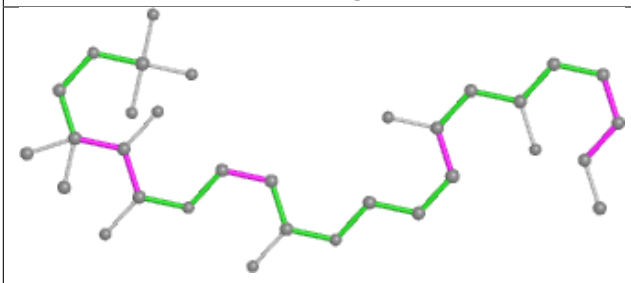
Ligand EHZ n 201



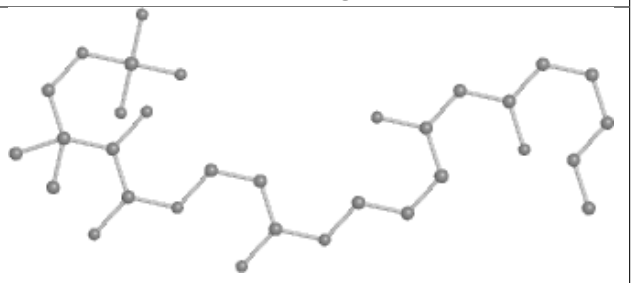
Bond lengths



Bond angles

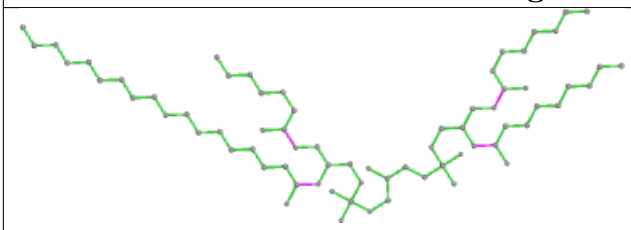


Torsions

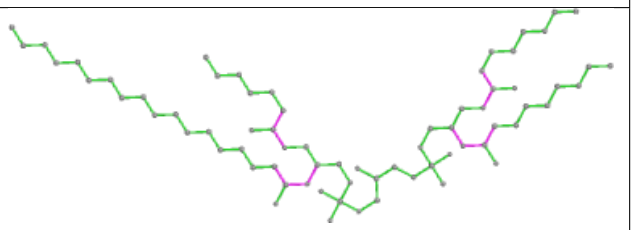


Rings

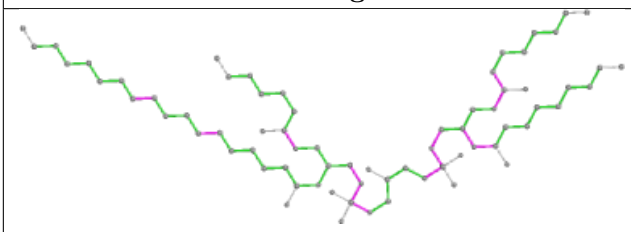
Ligand CDL h 201



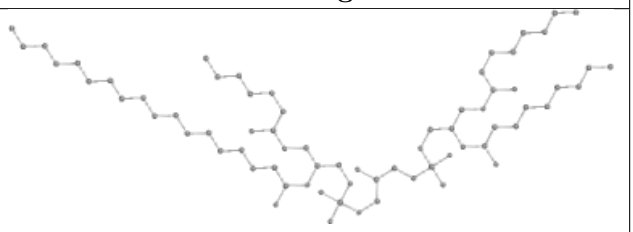
Bond lengths



Bond angles

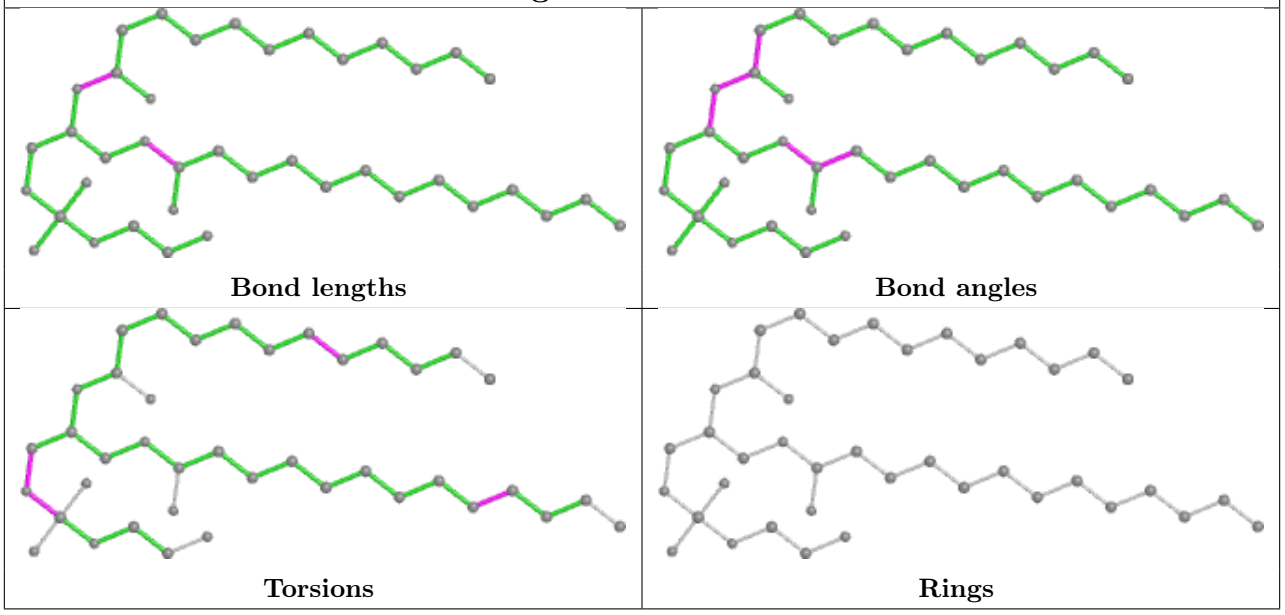


Torsions



Rings

Ligand 3PE L 701



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.

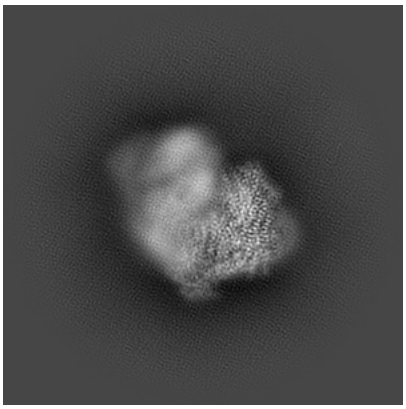
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-35342. These allow visual inspection of the internal detail of the map and identification of artifacts.

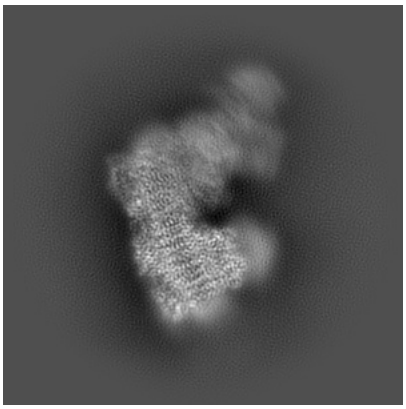
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

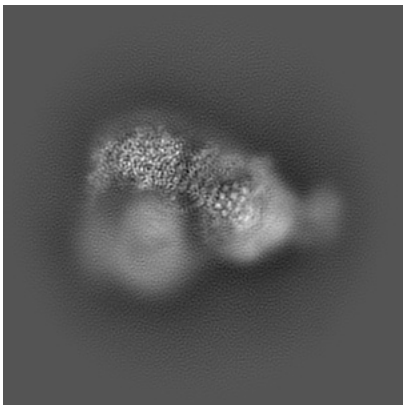
6.1.1 Primary map



X

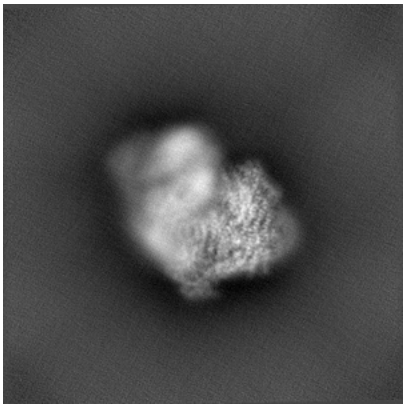


Y

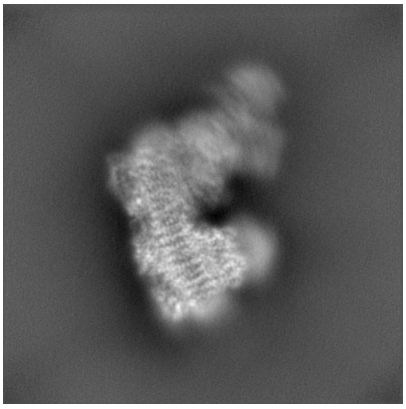


Z

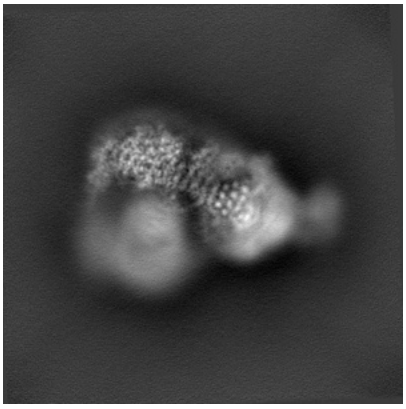
6.1.2 Raw map



X



Y

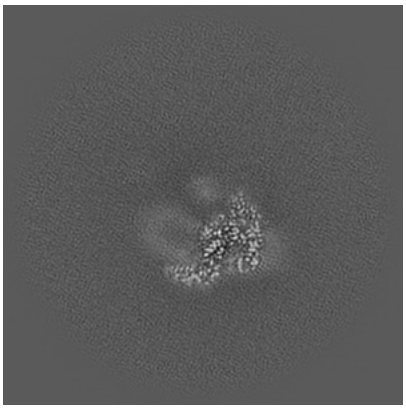


Z

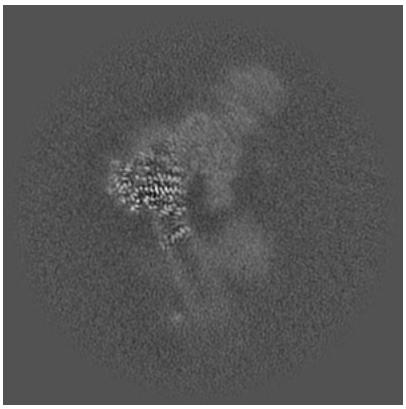
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

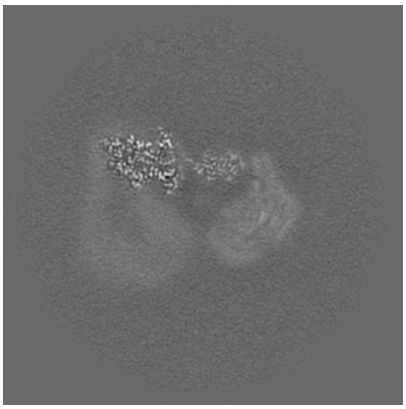
6.2.1 Primary map



X Index: 192

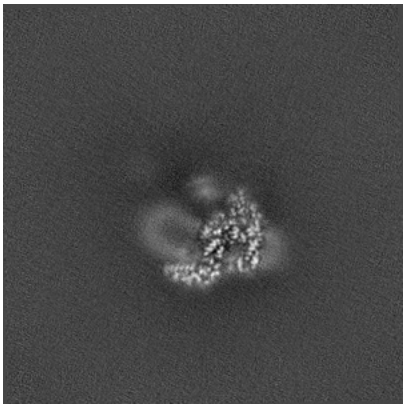


Y Index: 192

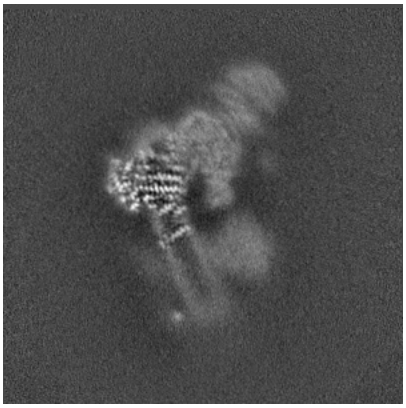


Z Index: 192

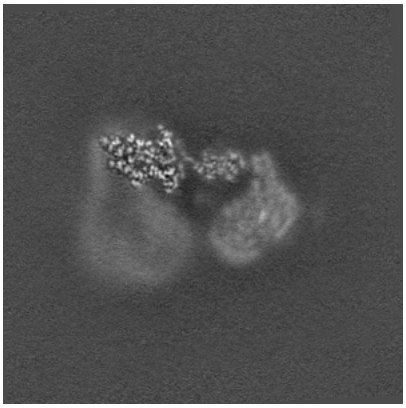
6.2.2 Raw map



X Index: 192



Y Index: 192

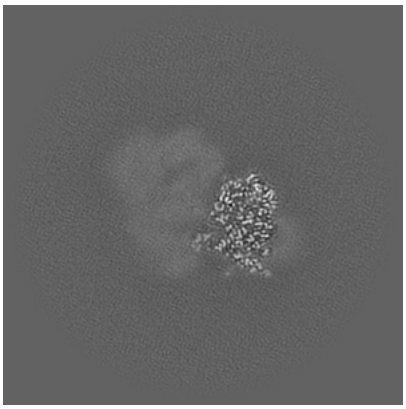


Z Index: 192

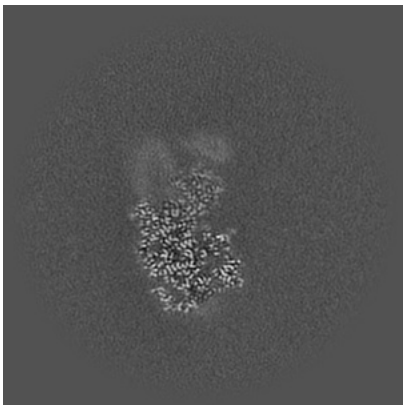
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

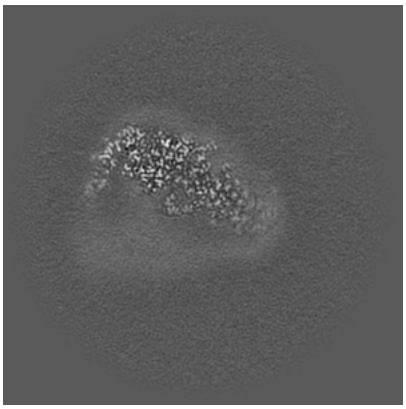
6.3.1 Primary map



X Index: 158

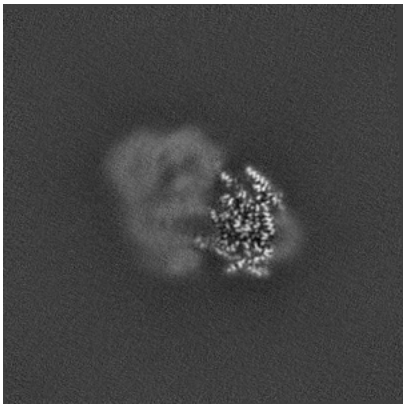


Y Index: 226

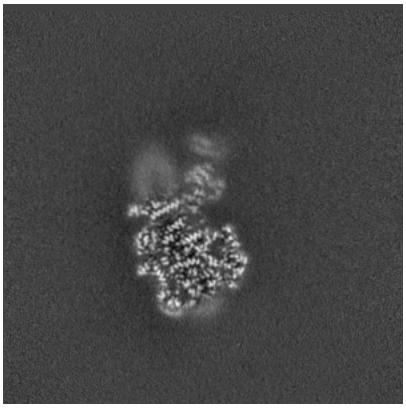


Z Index: 162

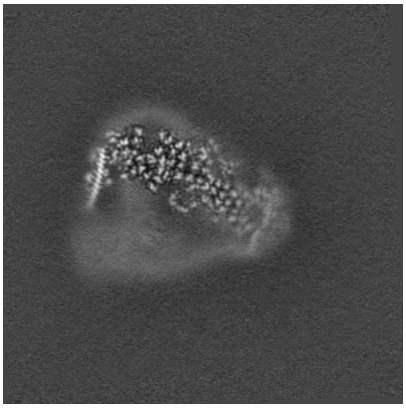
6.3.2 Raw map



X Index: 153



Y Index: 237

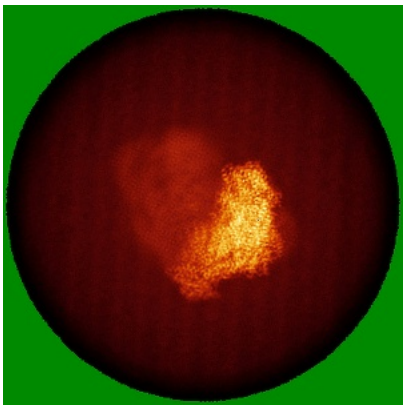


Z Index: 167

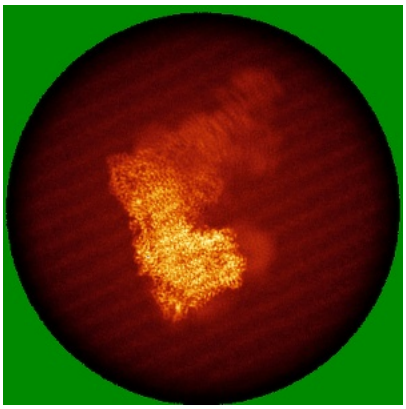
The images above show the largest variance slices of the map in three orthogonal directions.

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

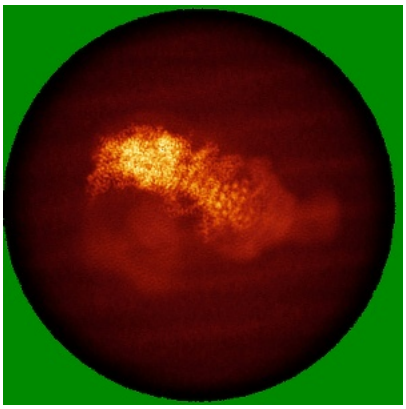
6.4.1 Primary map



X

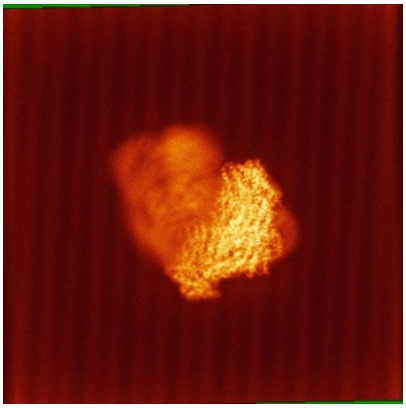


Y

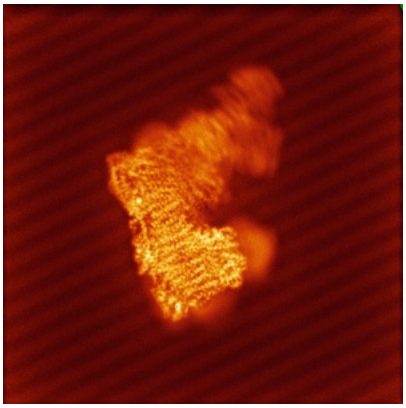


Z

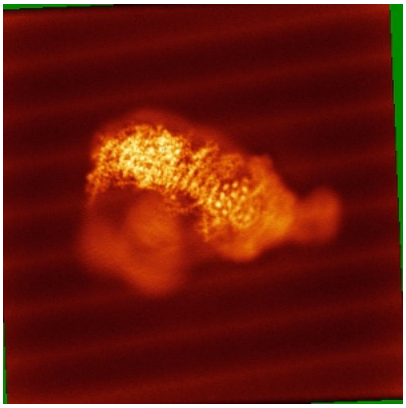
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.55. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

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

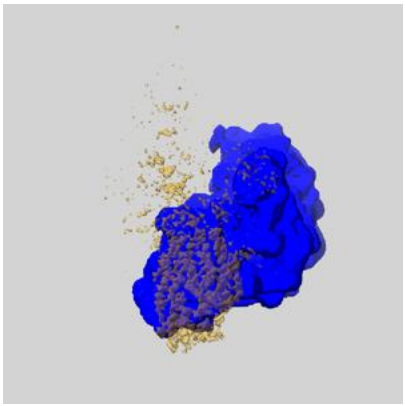
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

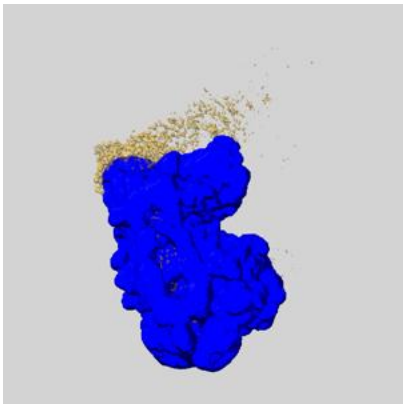
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

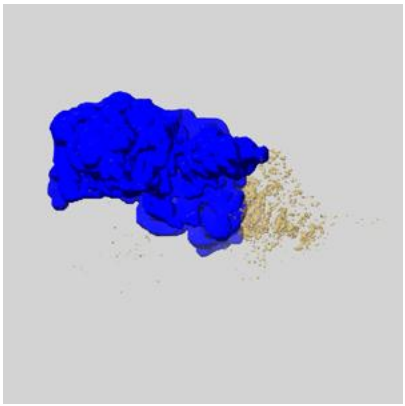
6.6.1 emd_35342_msk_1.map (i)



X



Y

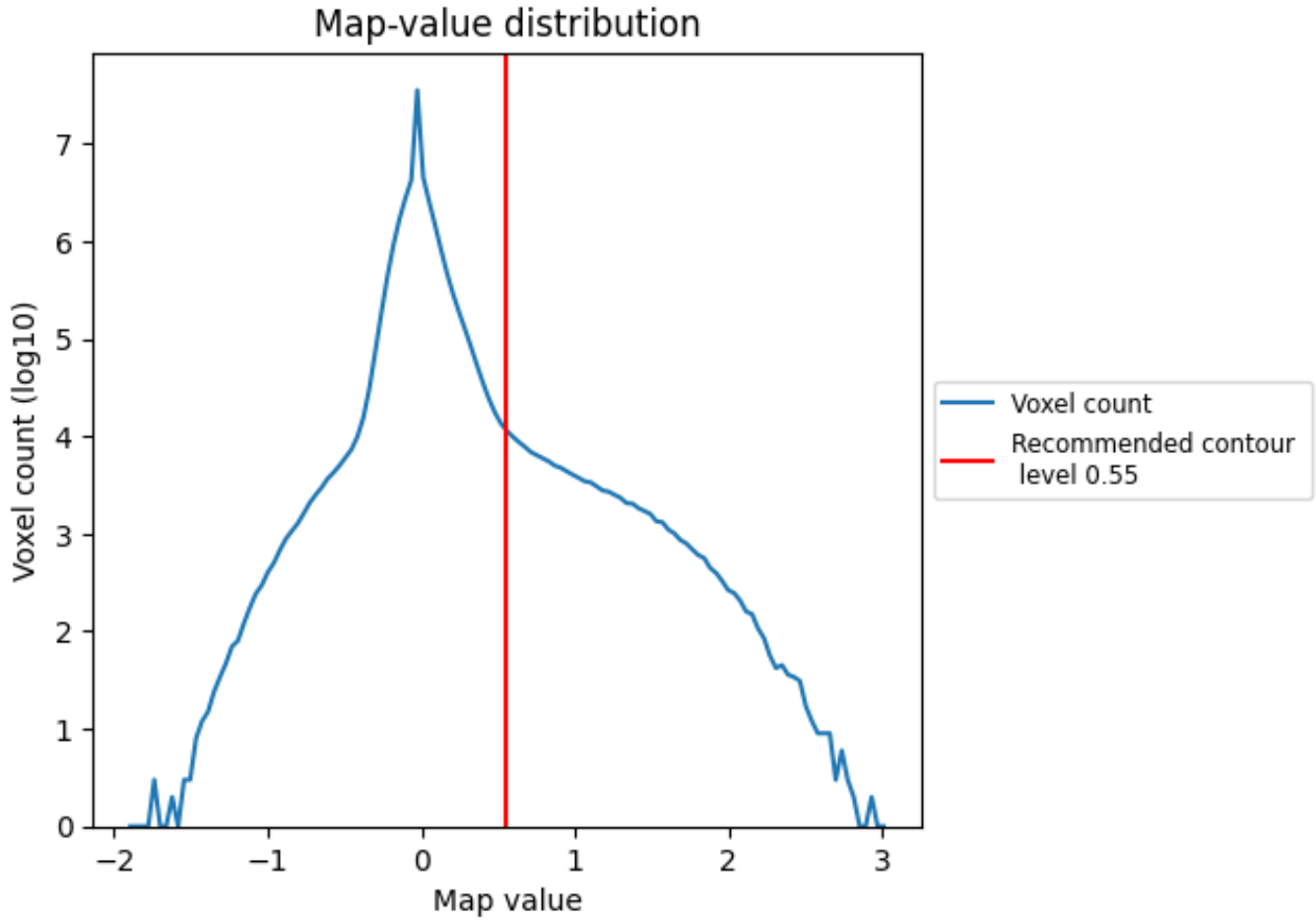


Z

7 Map analysis

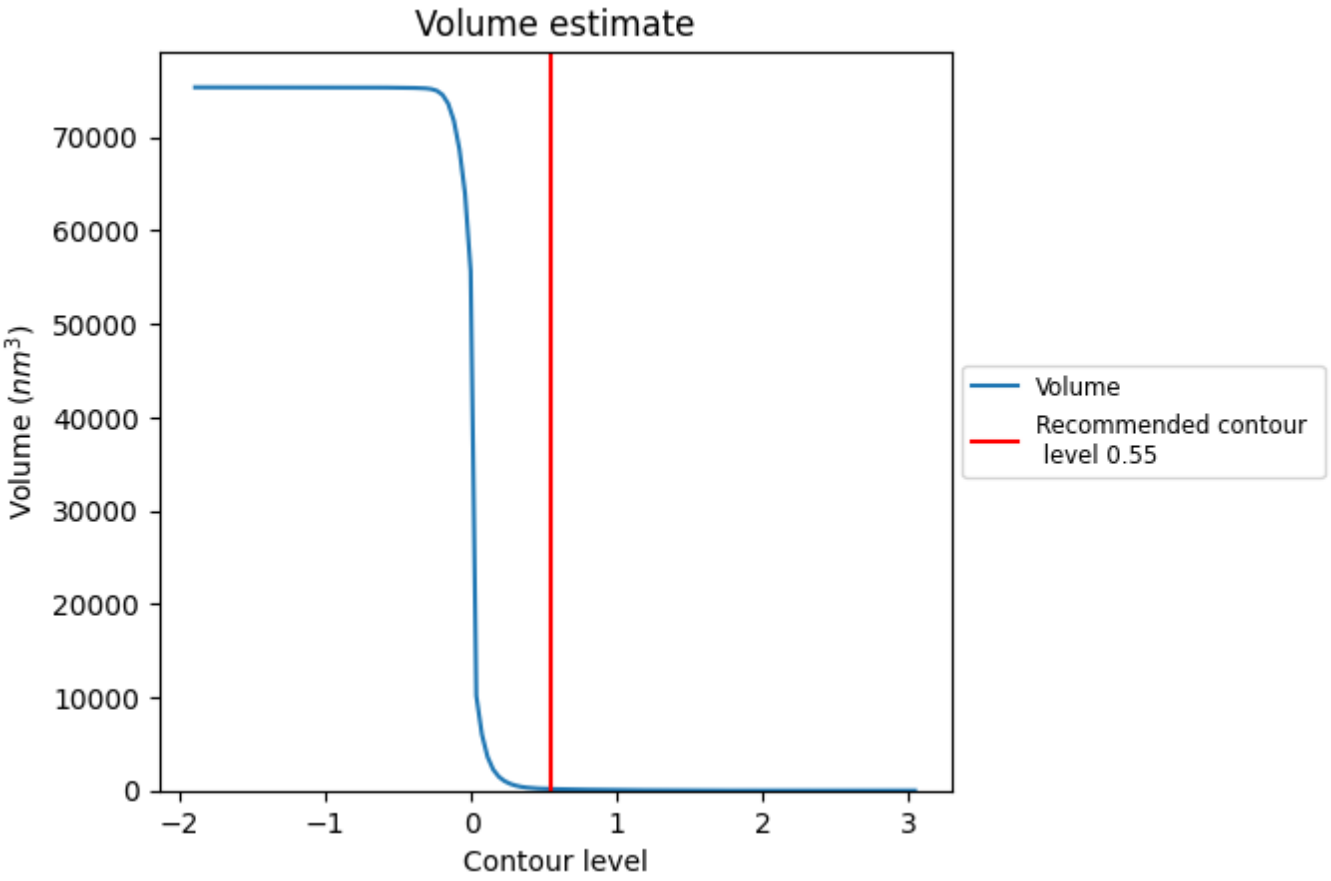
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

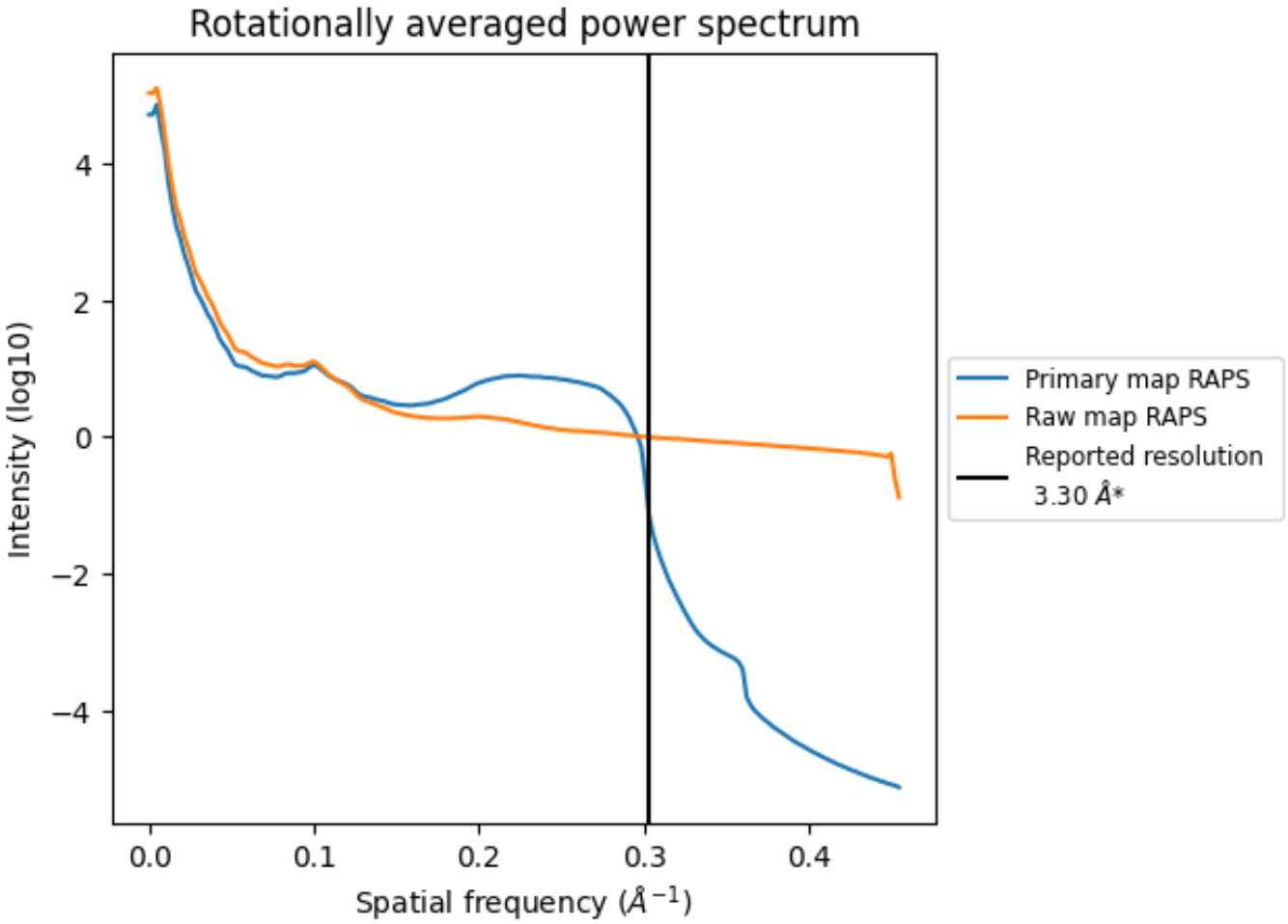
7.2 Volume estimate



The volume at the recommended contour level is 170 nm^3; this corresponds to an approximate mass of 154 kDa.

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

7.3 Rotationally averaged power spectrum (i)

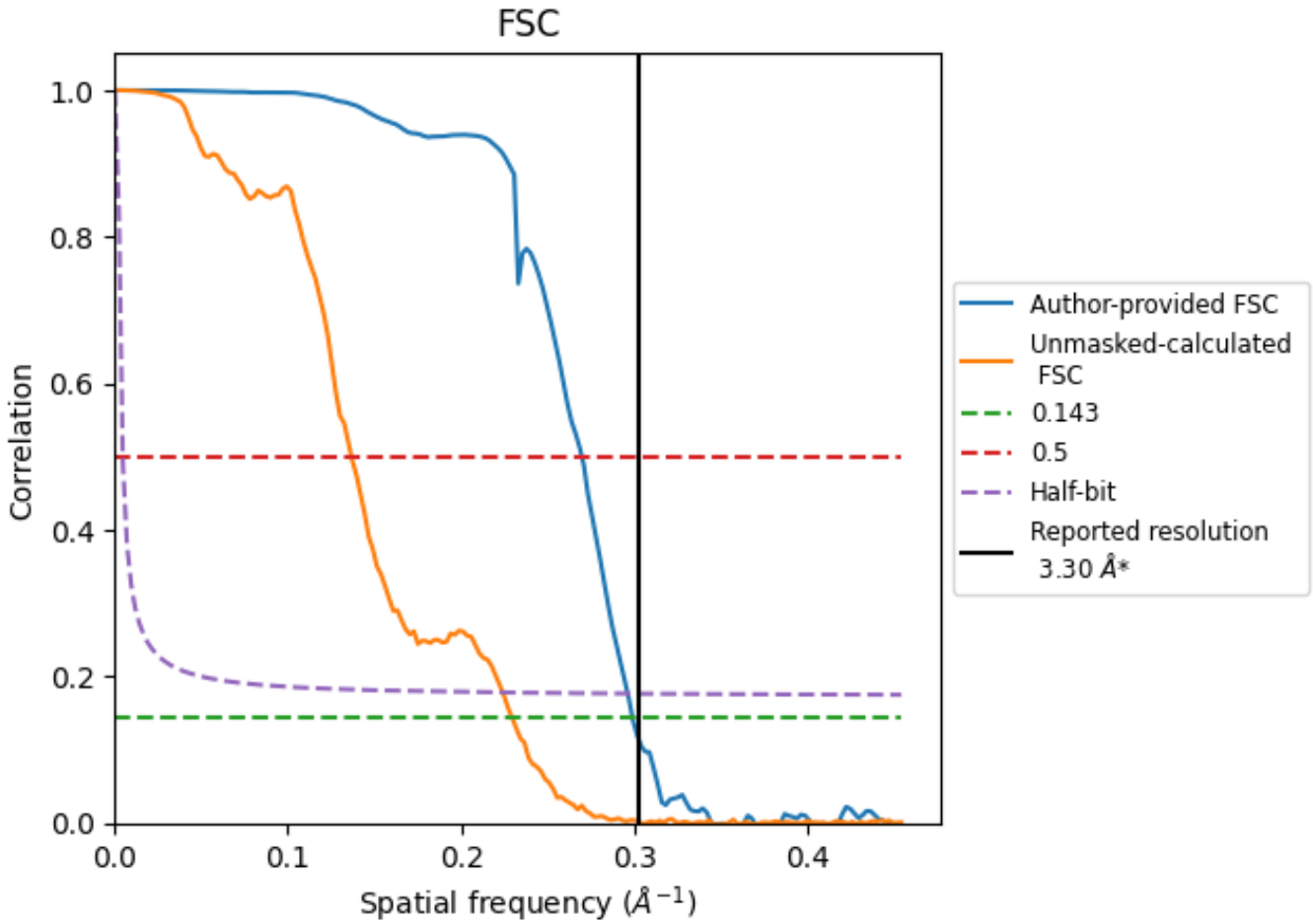


*Reported resolution corresponds to spatial frequency of 0.303 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8.2 Resolution estimates (i)

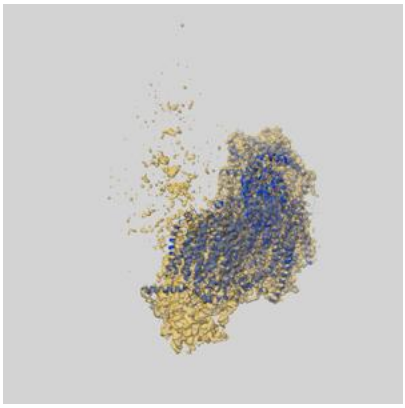
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.34	3.71	3.37
Unmasked-calculated*	4.35	7.31	4.46

*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 4.35 differs from the reported value 3.3 by more than 10 %

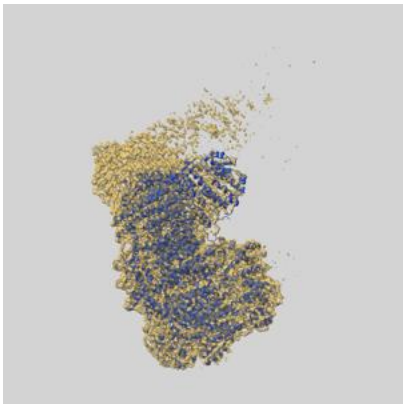
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-35342 and PDB model 8IBF. Per-residue inclusion information can be found in section 3 on page 11.

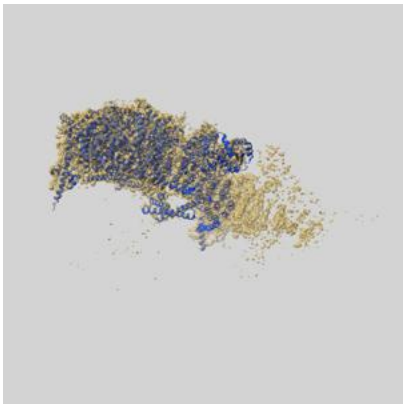
9.1 Map-model overlay



X



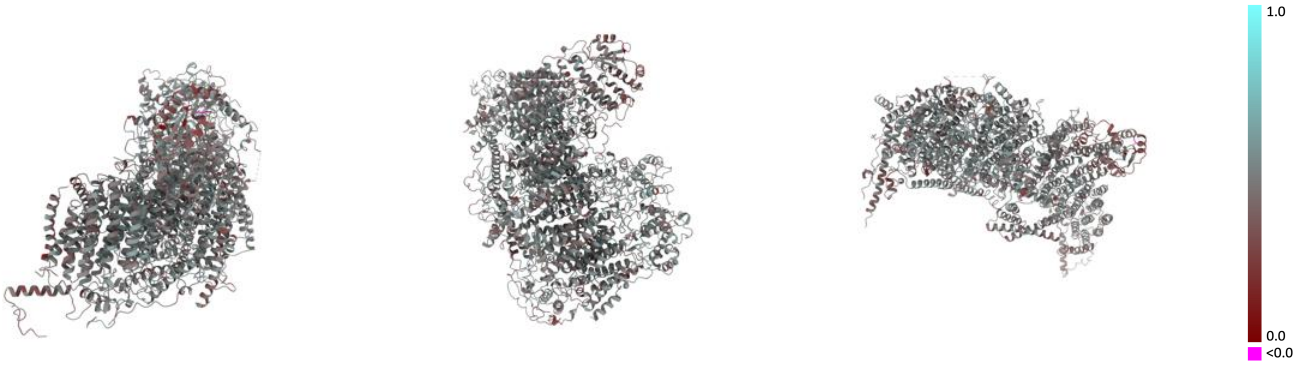
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.55 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.

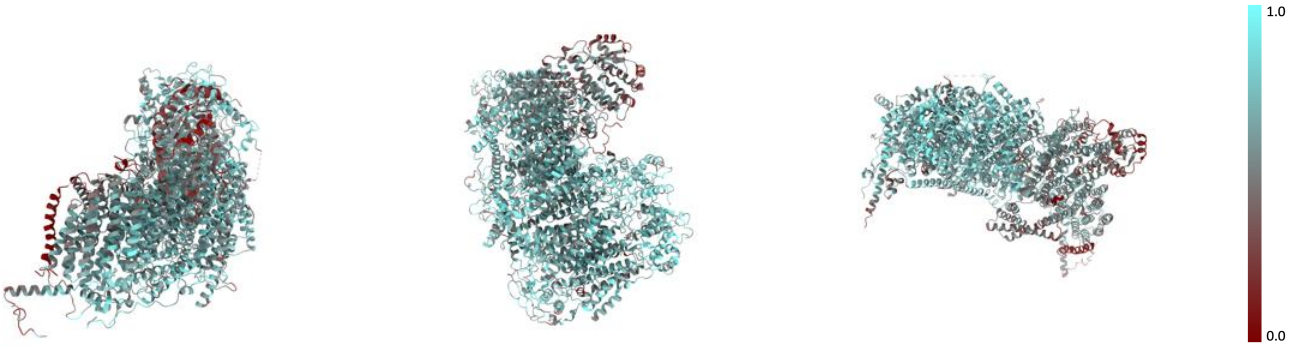
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

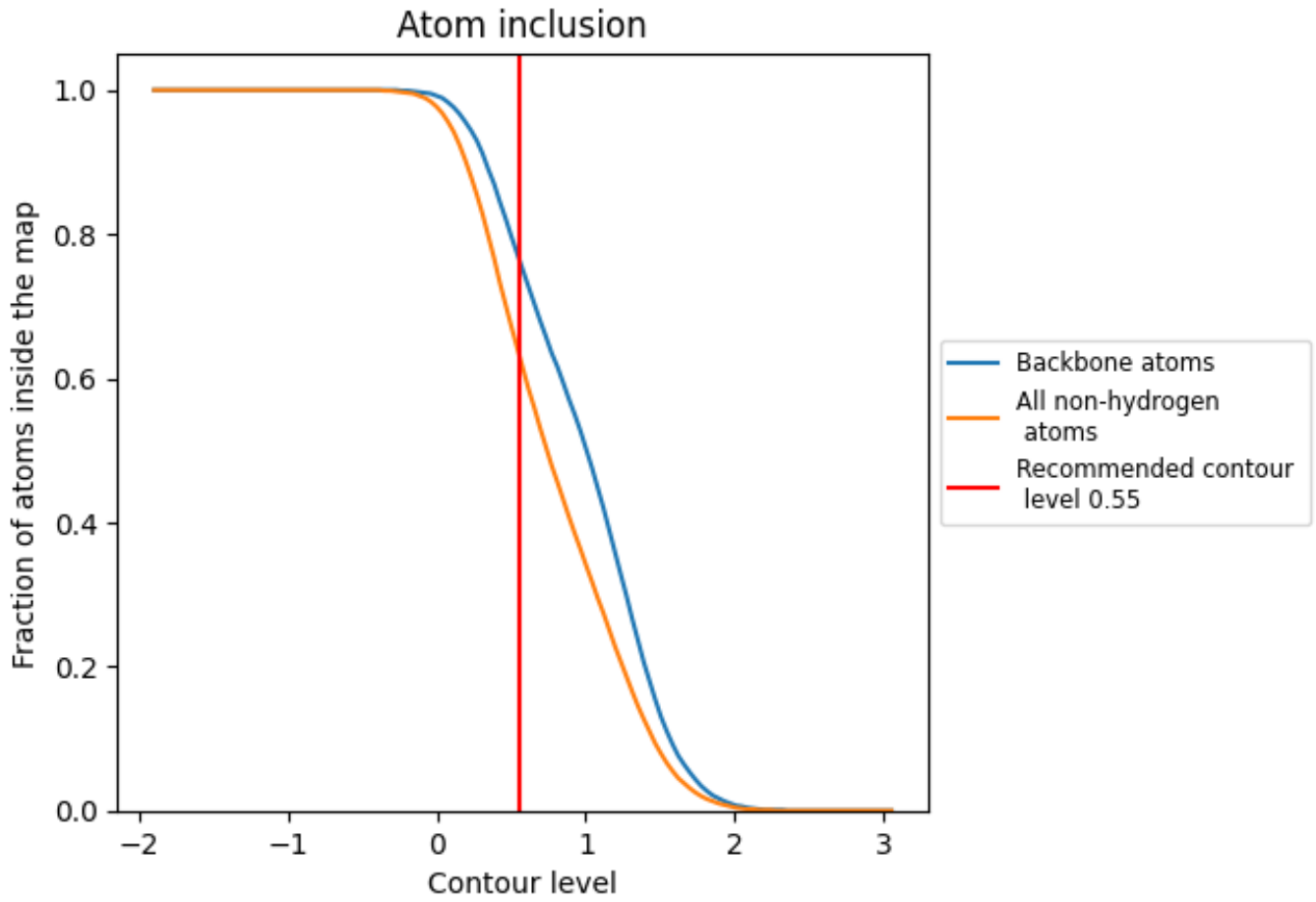
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.55).

9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 64% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6350	0.4710
D	0.3180	0.4700
J	0.4500	0.4350
K	0.5620	0.4800
L	0.6700	0.4800
M	0.6990	0.4960
N	0.6570	0.4930
O	0.4340	0.4140
U	0.7270	0.4810
X	0.6470	0.4890
Y	0.4580	0.4380
c	0.5160	0.4070
d	0.6720	0.4970
e	0.5930	0.4310
f	0.6290	0.4650
g	0.6610	0.4610
h	0.6960	0.4730
i	0.7010	0.4960
j	0.6930	0.4550
k	0.7190	0.4850
l	0.7340	0.4930
m	0.6250	0.4810
n	0.7600	0.5010
o	0.6480	0.4350
p	0.6780	0.4590