wwPDB EM Validation Summary Report (i)

Dec 10, 2022 – 01:27 pm GMT

PDB ID	:	6QTI
EMDB ID	:	EMD-4635
Title	:	Structure of ovine transhydrogenase in the presence of NADP+ in a "double face-down" conformation
Authors	:	Kampjut, D.; Sazanov, L.A.
Deposited on	:	2019-02-25
Resolution	:	2.90 Å(reported)
Based on initial model	:	1D4O

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

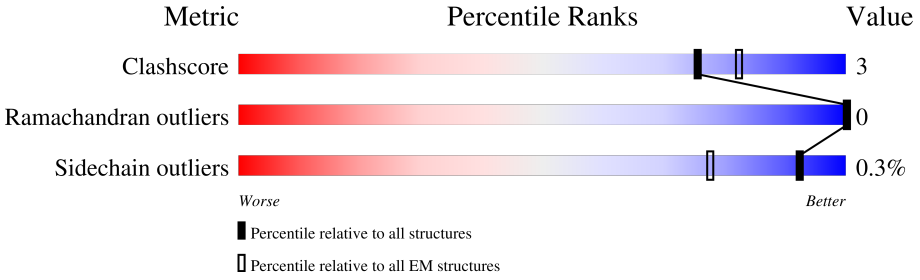
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.90 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	1086	6% 87% 8% •
1	B	1086	6% 87% 8% •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 15996 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 Nicotinamide nucleotide transhydrogenase.

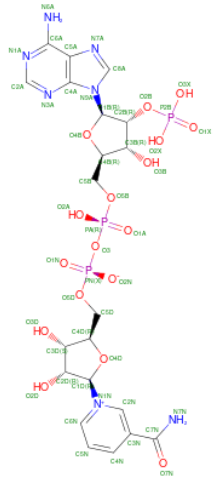
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1038	7620	4880	1264	1431	45	0	0
1	B	1038	7620	4880	1264	1431	45	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	THR	ALA	conflict	UNP W5PFI3
A	822	ILE	-	insertion	UNP W5PFI3
A	823	GLY	-	insertion	UNP W5PFI3
A	824	SER	-	insertion	UNP W5PFI3
A	825	SER	-	insertion	UNP W5PFI3
B	-8	THR	ALA	conflict	UNP W5PFI3
B	822	ILE	-	insertion	UNP W5PFI3
B	823	GLY	-	insertion	UNP W5PFI3
B	824	SER	-	insertion	UNP W5PFI3
B	825	SER	-	insertion	UNP W5PFI3

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).

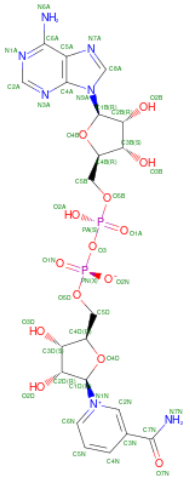
NAP



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
2	A	1	48	21	7	17	3	0
			Total	C	N	O	P	
2	B	1	48	21	7	17	3	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).

NAD



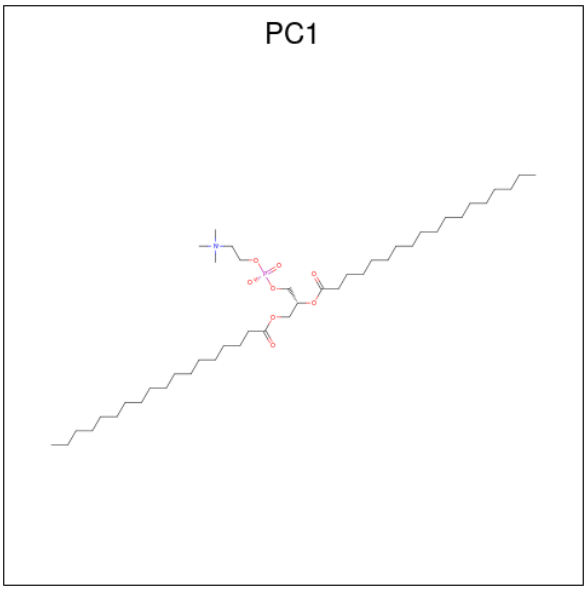
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	A	1	44	21	7	14	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	B	1	44	21	7	14	2	0

- Molecule 4 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: $C_{44}H_{88}NO_8P$).



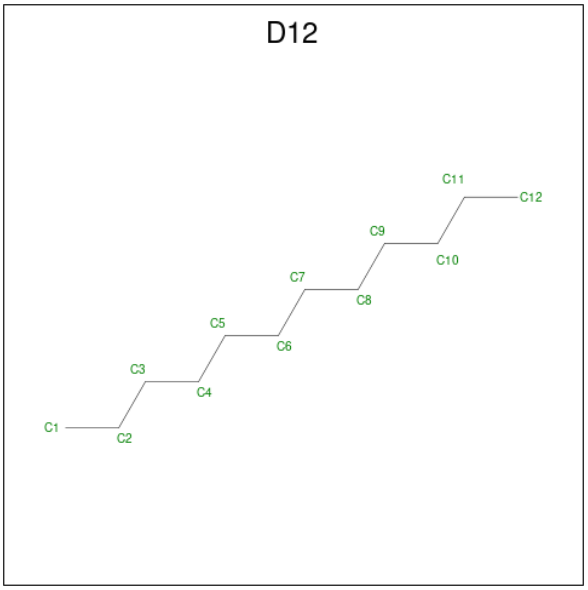
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	A	1	258	198	6	48	6	0
4	A	1	258	198	6	48	6	0
4	A	1	258	198	6	48	6	0
4	A	1	258	198	6	48	6	0
4	A	1	258	198	6	48	6	0
4	A	1	258	198	6	48	6	0
4	B	1	278	218	6	48	6	0
4	B	1	278	218	6	48	6	0
4	B	1	278	218	6	48	6	0
4	B	1	278	218	6	48	6	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	B	1	278	218	6	48	6	0
4	B	1	278	218	6	48	6	0

- Molecule 5 is DODECANE (three-letter code: D12) (formula: $C_{12}H_{26}$).



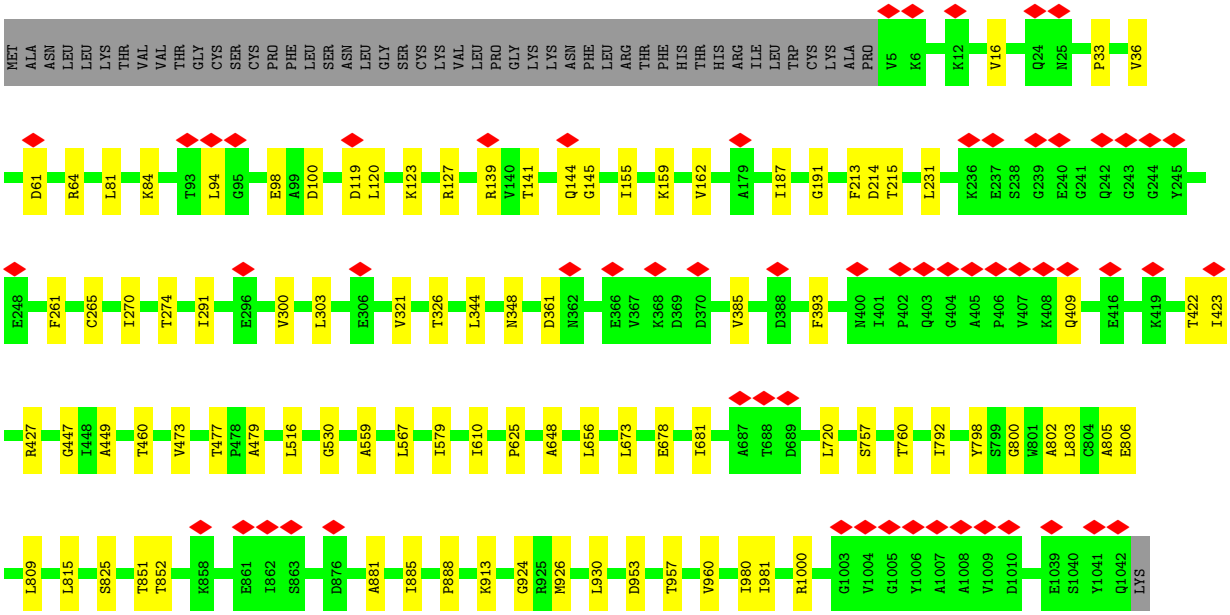
Mol	Chain	Residues	Atoms		AltConf
			Total	C	
5	A	1	12	12	0
5	B	1	24	24	0
5	B	1	24	24	0

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.

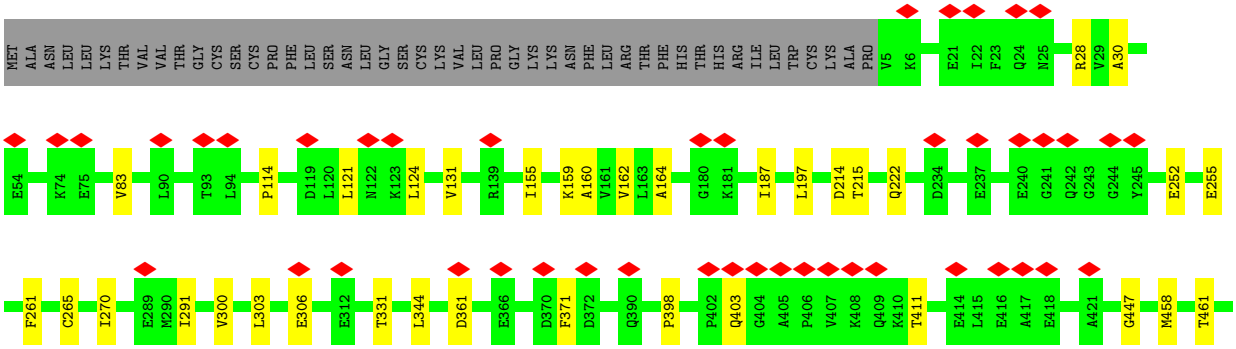
• Molecule 1: Nicotinamide nucleotide transhydrogenase

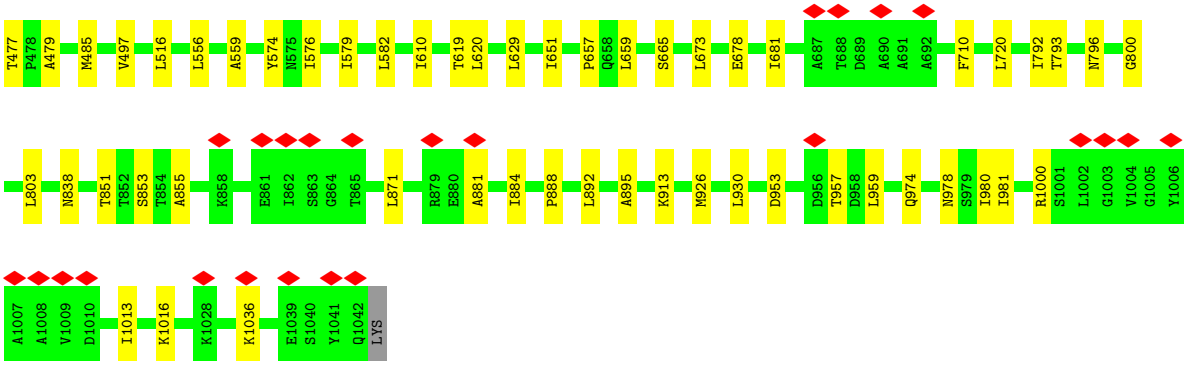
Chain A:



• Molecule 1: Nicotinamide nucleotide transhydrogenase

Chain B:




T477 P478 A479 M485 V497 L516 L556 A559 Y574 N575 I576 I579 L582 I610 T619 L620 L629 I651 P657 Q658 L659 S665 L673 E678 I681 A687 T688 D689 A690 A691 A692 F710 L720 I792 T793 N796 G800
L803 N838 T851 T852 S853 T854 A855 K858 E861 I862 S863 G864 T865 L871 R879 E880 A881 I884 P888 L892 A895 K913 M926 L930 D953 D956 T957 D958 L959 Q974 N978 S979 I980 I981 R1000 S1001 L1002 G1003 V1004 G1005 Y1006
A1007 A1008 V1009 D1010 I1013 K1016 K1028 K1036 E1039 S1040 Y1041 Q1042 LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98294	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	72	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.197	Depositor
Minimum map value	-0.096	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	136.32, 126.73501, 124.605	wwPDB
Map dimensions	117, 119, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	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: D12, NAD, NAP, PC1

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.31	0/7759	0.55	1/10538 (0.0%)
1	B	0.32	0/7759	0.57	2/10538 (0.0%)
All	All	0.32	0/15518	0.56	3/21076 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	94	LEU	CA-CB-CG	5.41	127.73	115.30
1	B	629	LEU	CA-CB-CG	5.36	127.62	115.30
1	B	361	ASP	CB-CG-OD1	5.30	123.07	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7620	0	7827	51	0
1	B	7620	0	7827	47	0
2	A	48	0	25	1	0
2	B	48	0	25	1	0
3	A	44	0	26	1	0
3	B	44	0	26	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	258	0	366	7	0
4	B	278	0	412	7	0
5	A	12	0	26	0	0
5	B	24	0	52	0	0
All	All	15996	0	16612	102	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 3.

The worst 5 of 102 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)
1:B:261:PHE:O	1:B:265:CYS:HB2	1.93	0.68
1:A:261:PHE:O	1:A:265:CYS:HB2	1.95	0.67
1:A:119:ASP:OD2	1:A:123:LYS:NZ	2.32	0.63
1:B:155:ILE:HD11	1:B:344:LEU:HD12	1.82	0.61
1:A:477:THR:HG22	1:A:479:ALA:H	1.66	0.60

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1036/1086 (95%)	974 (94%)	62 (6%)	0	100	100
1	B	1036/1086 (95%)	962 (93%)	74 (7%)	0	100	100
All	All	2072/2172 (95%)	1936 (93%)	136 (7%)	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	A	801/844 (95%)	799 (100%)	2 (0%)	93	98
1	B	801/844 (95%)	798 (100%)	3 (0%)	91	97
All	All	1602/1688 (95%)	1597 (100%)	5 (0%)	92	98

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	409	GLN
1	A	1000	ARG
1	B	28	ARG
1	B	403	GLN
1	B	1000	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	796	ASN
1	A	994	GLN
1	B	813	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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	$\#\|Z\| > 2$
5	D12	A	1106	-	11,11,11	0.11	0	10,10,10	0.15	0
4	PC1	A	1107	-	50,50,53	0.28	0	56,58,61	0.28	0
2	NAP	B	1102	-	45,52,52	0.57	0	56,80,80	0.57	1 (1%)
5	D12	B	1108	-	11,11,11	0.12	0	10,10,10	0.13	0
4	PC1	A	1108	-	34,34,53	0.36	0	40,42,61	0.34	0
4	PC1	A	1105	-	49,49,53	0.29	0	55,57,61	0.30	0
4	PC1	B	1105	-	53,53,53	0.27	0	59,61,61	0.30	0
4	PC1	A	1103	-	39,39,53	0.33	0	45,47,61	0.34	0
4	PC1	B	1110	-	34,34,53	0.34	0	40,42,61	0.34	0
4	PC1	B	1101	-	44,44,53	0.32	0	50,52,61	0.36	0
3	NAD	A	1102	-	42,48,48	0.55	0	50,73,73	0.59	1 (2%)
4	PC1	A	1109	-	36,36,53	0.36	0	42,44,61	0.51	1 (2%)
5	D12	B	1107	-	11,11,11	0.10	0	10,10,10	0.13	0
4	PC1	B	1104	-	45,45,53	0.31	0	51,53,61	0.32	0
4	PC1	B	1106	-	43,43,53	0.33	0	49,51,61	0.32	0
4	PC1	A	1104	-	44,44,53	0.31	0	50,52,61	0.30	0
2	NAP	A	1101	-	45,52,52	0.57	0	56,80,80	0.63	1 (1%)
4	PC1	B	1109	-	53,53,53	0.28	0	59,61,61	0.27	0
3	NAD	B	1103	-	42,48,48	0.55	0	50,73,73	0.61	1 (2%)

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
5	D12	A	1106	-	-	2/9/9/9	-
4	PC1	A	1107	-	-	15/54/54/57	-
2	NAP	B	1102	-	-	6/31/67/67	0/5/5/5
5	D12	B	1108	-	-	1/9/9/9	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PC1	A	1108	-	-	13/38/38/57	-
4	PC1	A	1105	-	-	19/53/53/57	-
4	PC1	B	1105	-	-	13/57/57/57	-
4	PC1	A	1103	-	-	12/43/43/57	-
4	PC1	B	1110	-	-	13/38/38/57	-
4	PC1	B	1101	-	-	9/48/48/57	-
3	NAD	A	1102	-	-	8/26/62/62	0/5/5/5
4	PC1	A	1109	-	-	13/40/40/57	-
5	D12	B	1107	-	-	0/9/9/9	-
4	PC1	B	1104	-	-	14/49/49/57	-
4	PC1	B	1106	-	-	13/47/47/57	-
4	PC1	A	1104	-	-	9/48/48/57	-
2	NAP	A	1101	-	-	12/31/67/67	0/5/5/5
4	PC1	B	1109	-	-	13/57/57/57	-
3	NAD	B	1103	-	-	8/26/62/62	0/5/5/5

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1103	NAD	C5A-C6A-N6A	2.35	123.92	120.35
3	A	1102	NAD	C5A-C6A-N6A	2.33	123.89	120.35
2	A	1101	NAP	C5A-C6A-N6A	2.30	123.84	120.35
2	B	1102	NAP	C5A-C6A-N6A	2.24	123.75	120.35
4	A	1109	PC1	O31-C3-C2	2.02	114.33	108.43

There are no chirality outliers.

5 of 193 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	NAP	C5B-O5B-PA-O3
2	A	1101	NAP	C5D-O5D-PN-O2N
2	A	1101	NAP	O4D-C1D-N1N-C6N
3	A	1102	NAD	C5B-O5B-PA-O3
3	A	1102	NAD	C5D-O5D-PN-O3

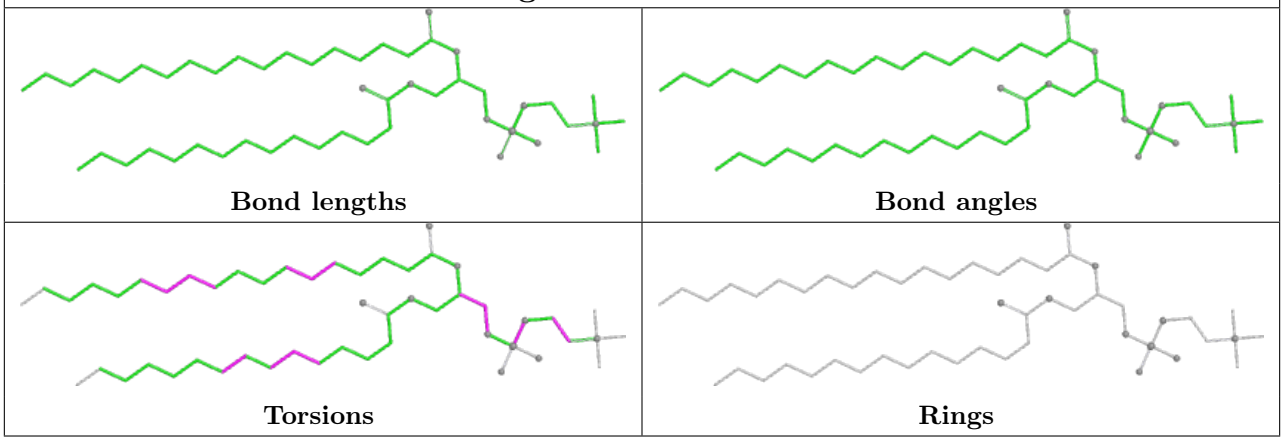
There are no ring outliers.

13 monomers are involved in 16 short contacts:

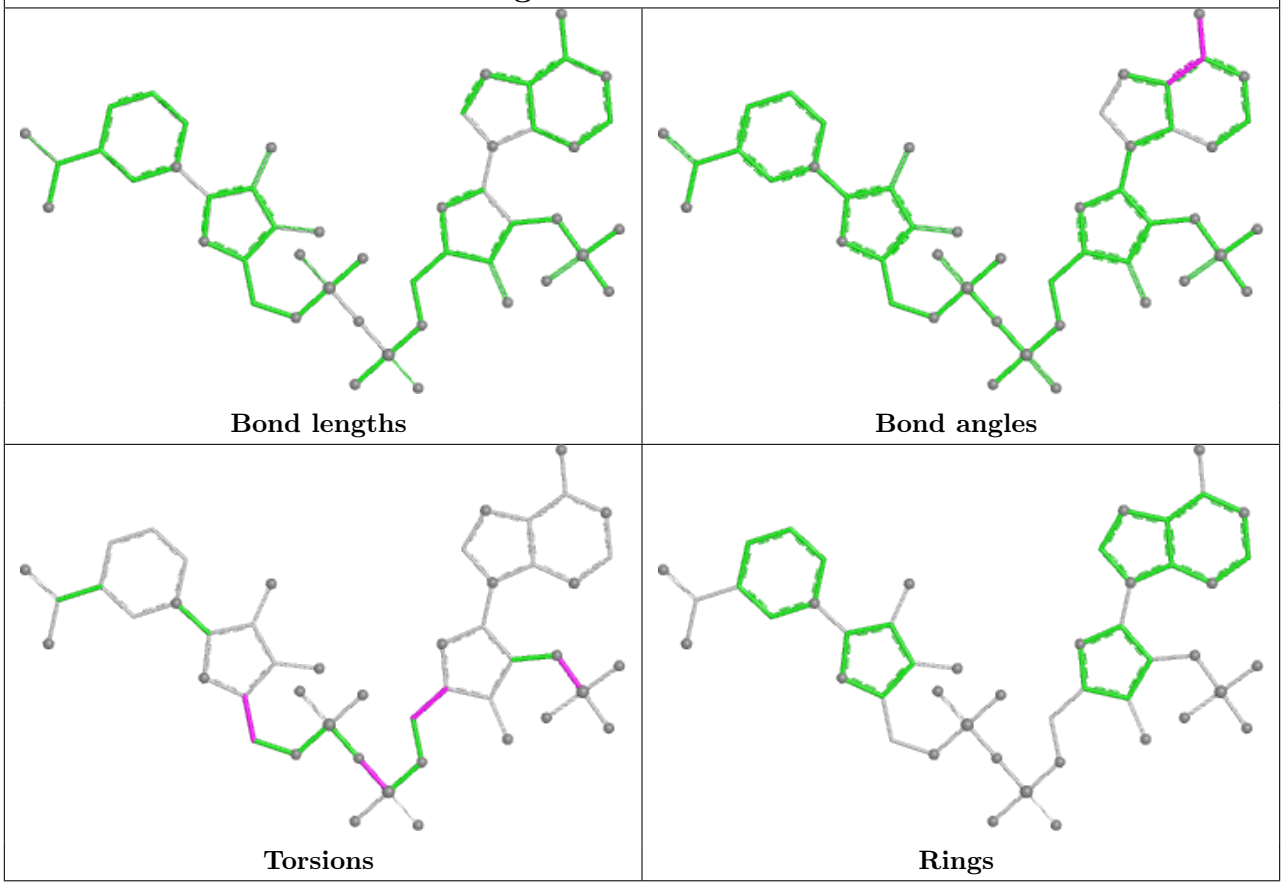
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1102	NAP	1	0
4	A	1108	PC1	2	0
4	A	1105	PC1	1	0
4	B	1105	PC1	1	0
4	A	1103	PC1	1	0
4	B	1110	PC1	1	0
4	B	1101	PC1	3	0
3	A	1102	NAD	1	0
4	A	1109	PC1	1	0
4	B	1104	PC1	1	0
4	A	1104	PC1	3	0
2	A	1101	NAP	1	0
4	B	1109	PC1	1	0

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

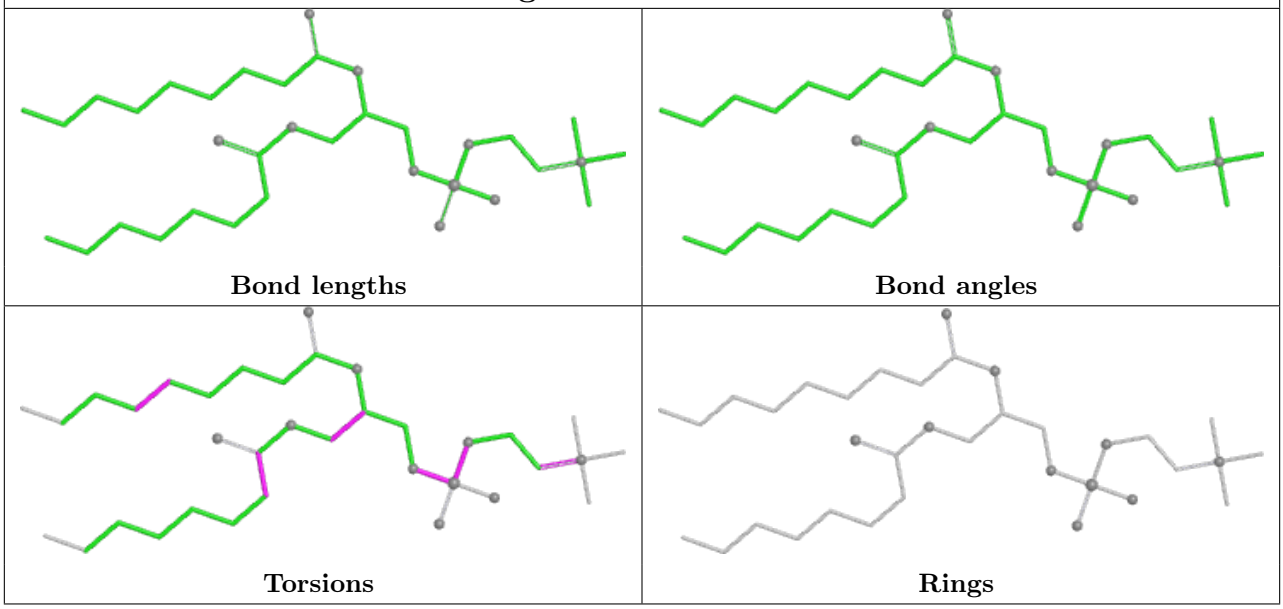
Ligand PC1 A 1107

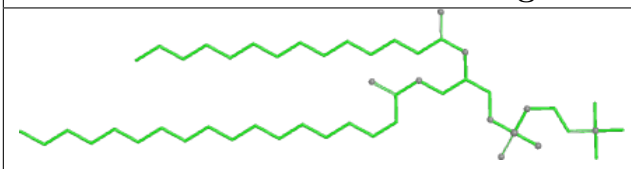
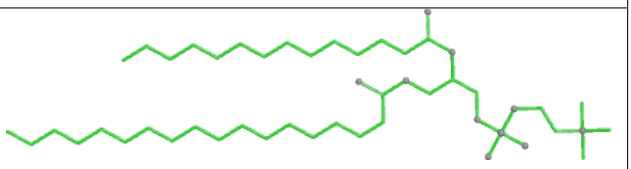
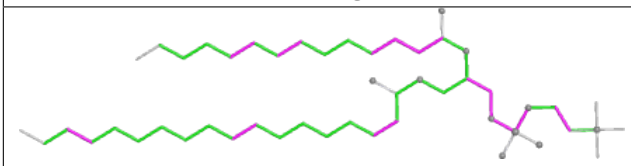
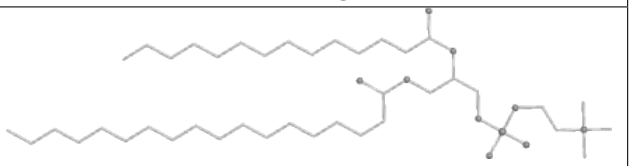


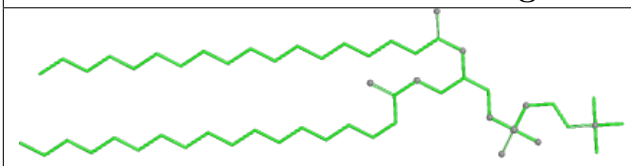
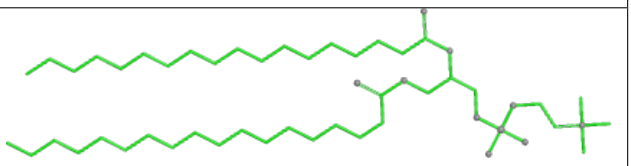
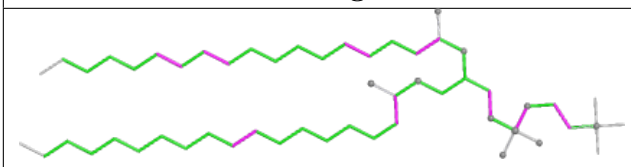
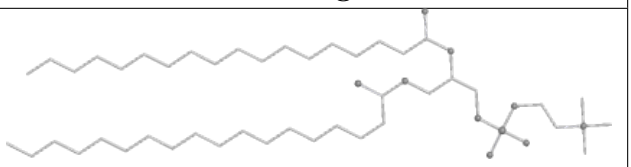
Ligand NAP B 1102

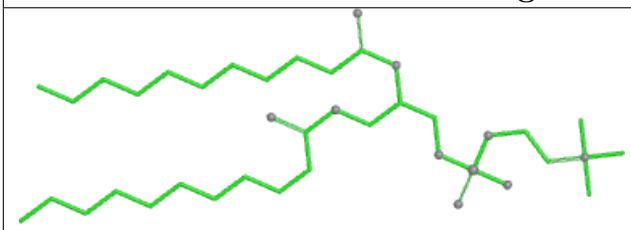
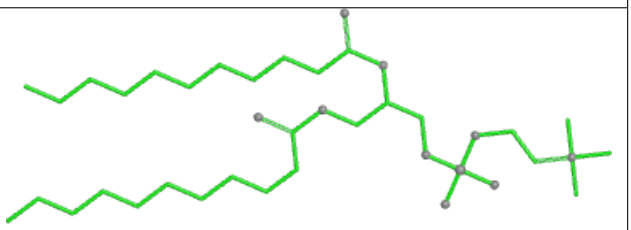
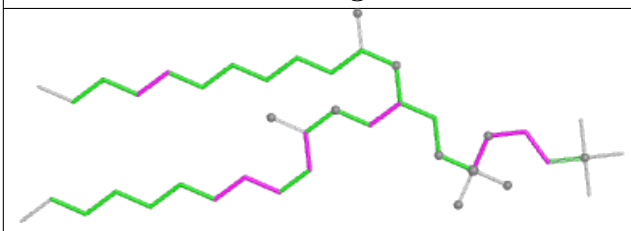
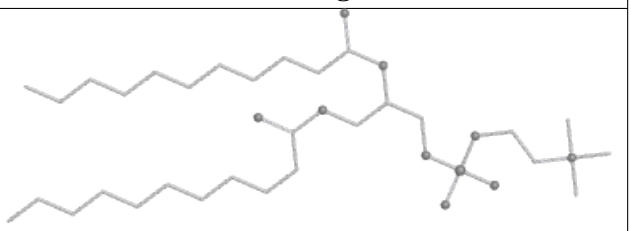


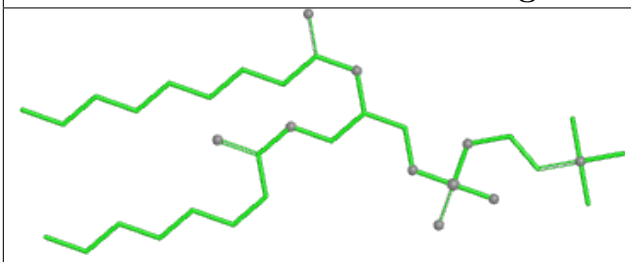
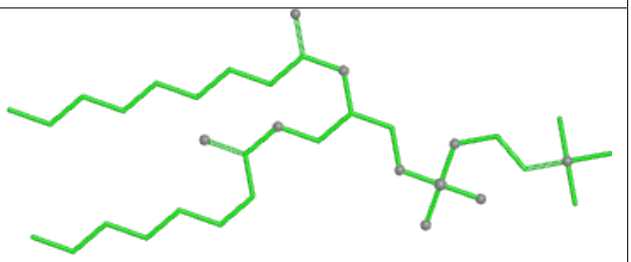
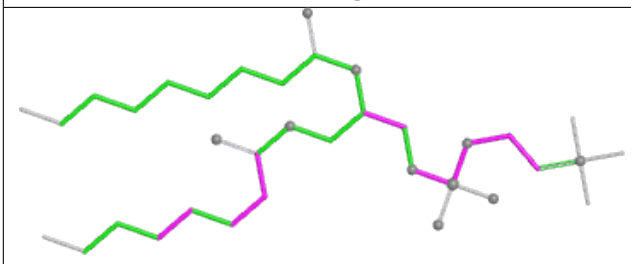
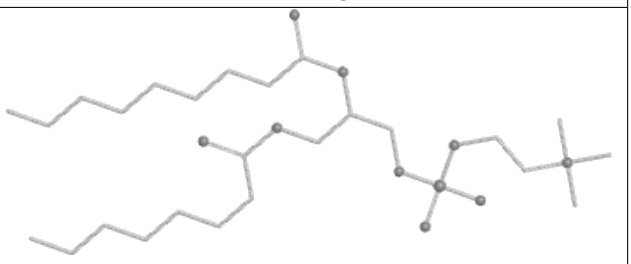
Ligand PC1 A 1108

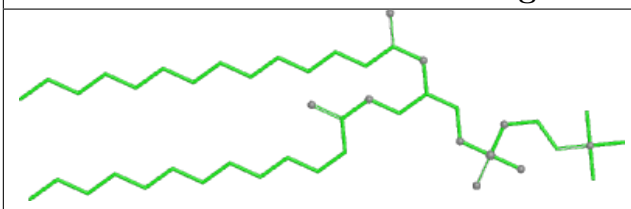
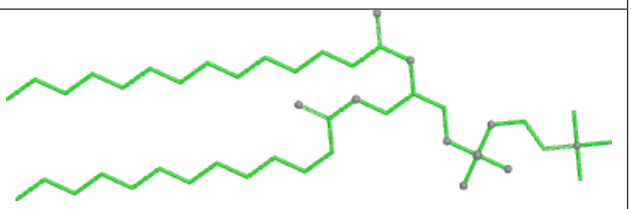
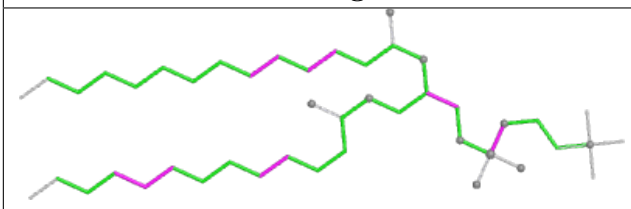
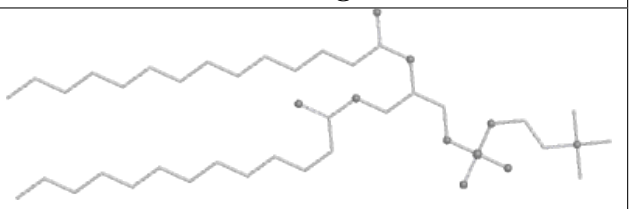


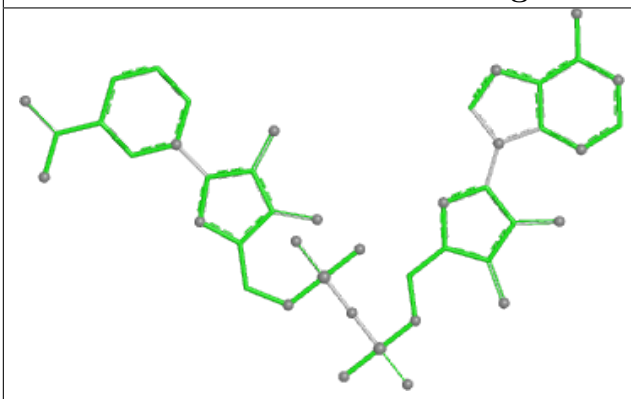
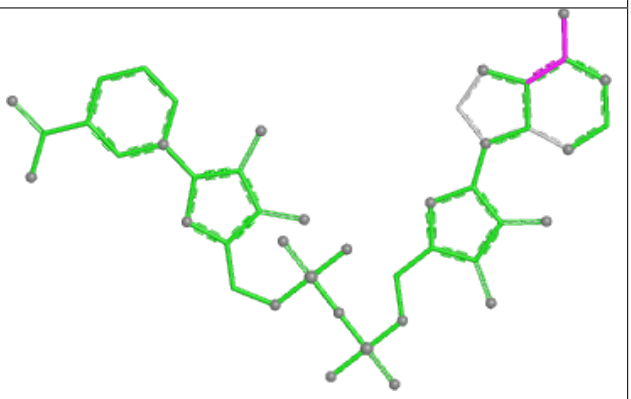
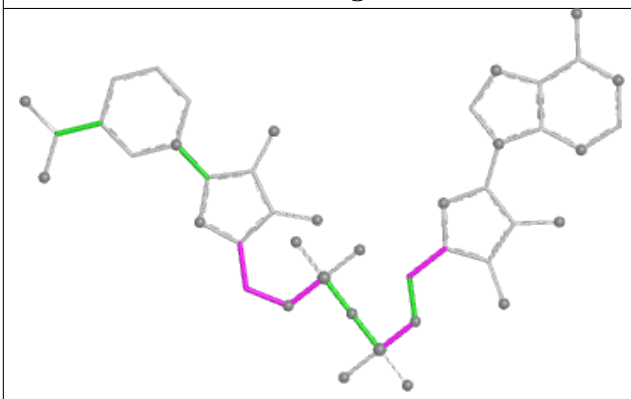
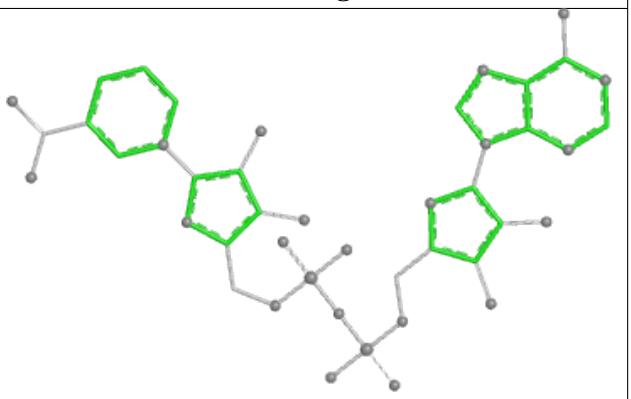
Ligand PC1 A 1105	
 Bond lengths	 Bond angles
 Torsions	 Rings

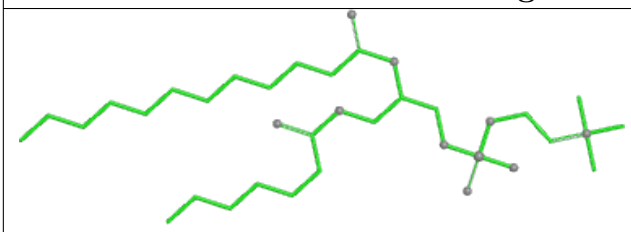
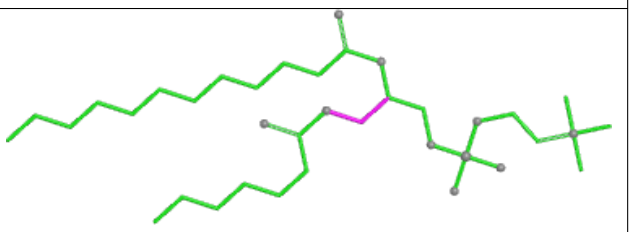
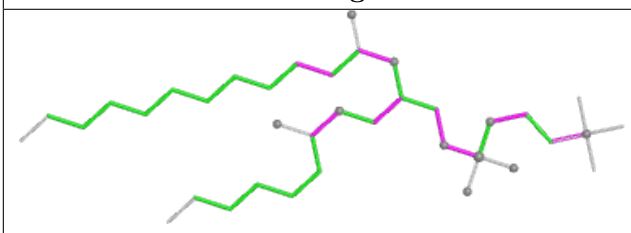
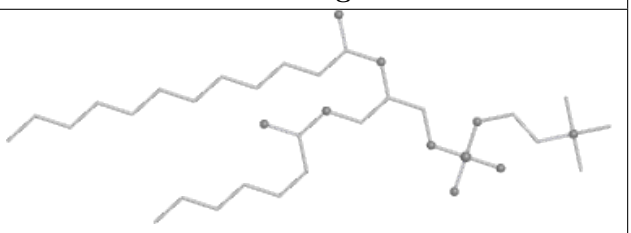
Ligand PC1 B 1105	
 Bond lengths	 Bond angles
 Torsions	 Rings

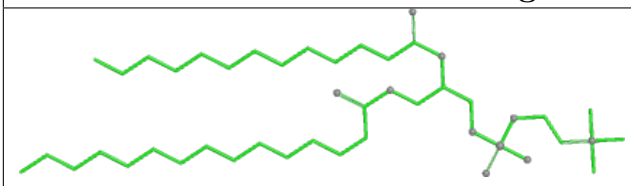
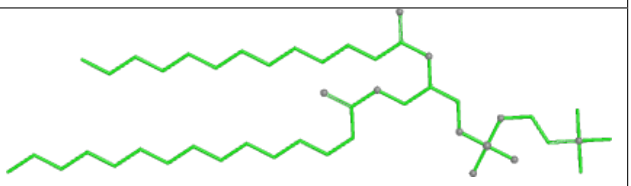
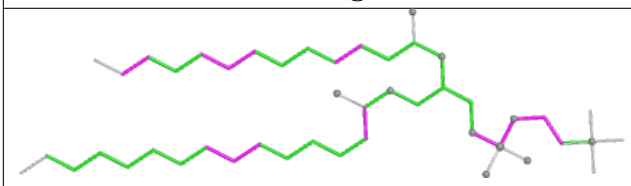
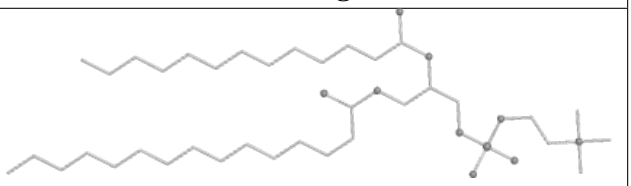
Ligand PC1 A 1103	
 Bond lengths	 Bond angles
 Torsions	 Rings

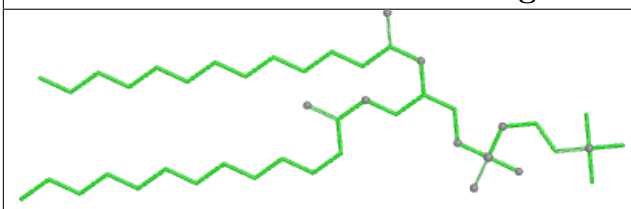
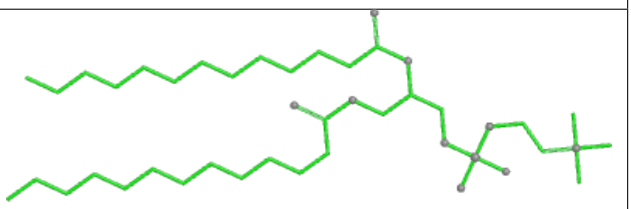
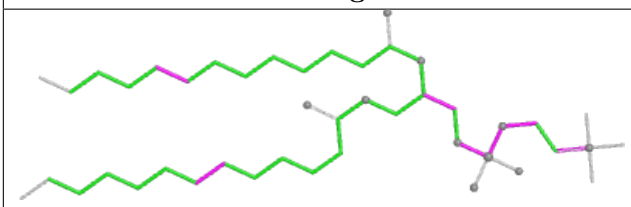
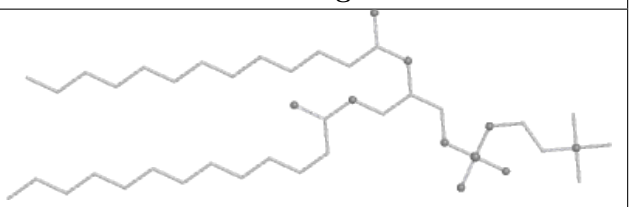
Ligand PC1 B 1110	
 Bond lengths	 Bond angles
 Torsions	 Rings

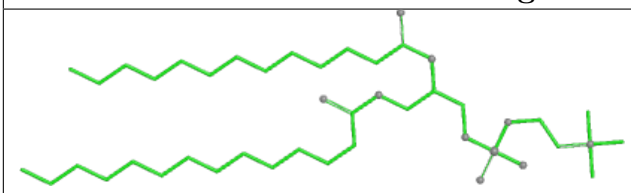
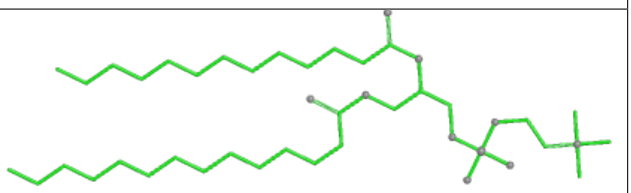
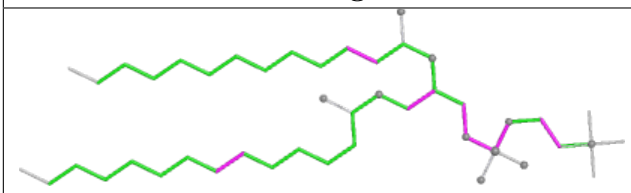
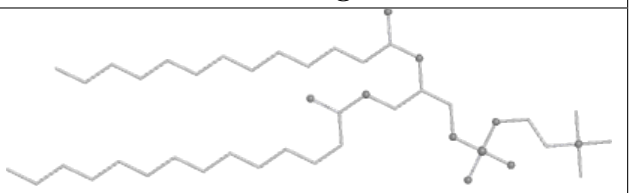
Ligand PC1 B 1101	
 Bond lengths	 Bond angles
 Torsions	 Rings

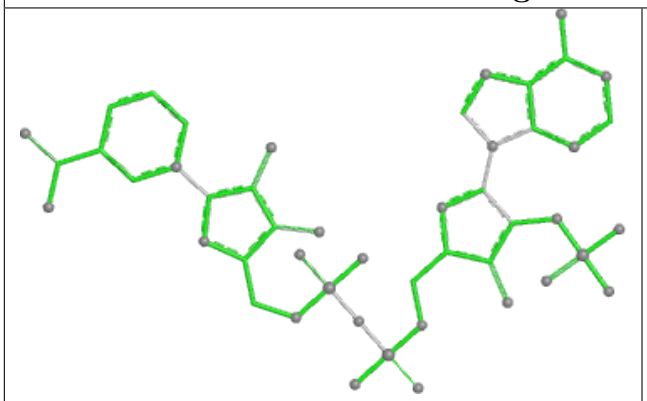
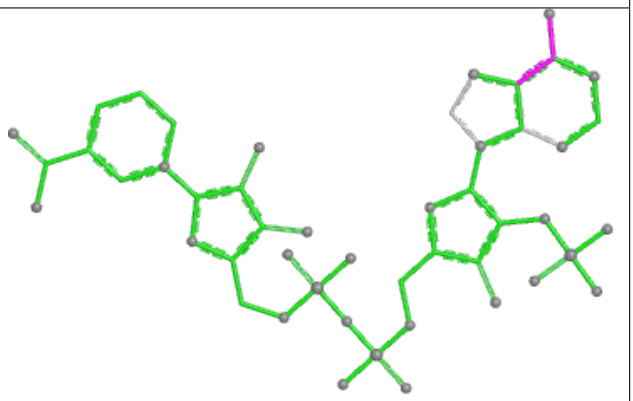
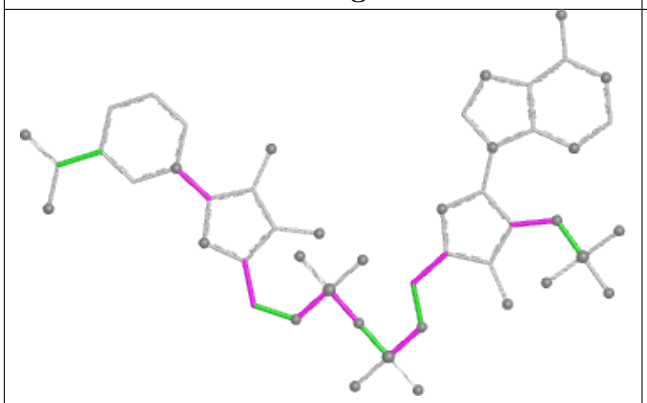
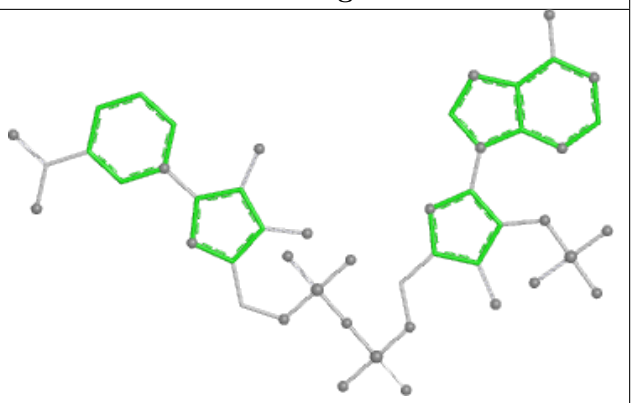
Ligand NAD A 1102	
 Bond lengths	 Bond angles
 Torsions	 Rings

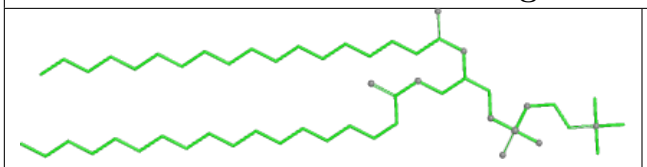
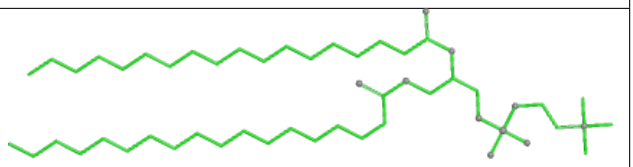
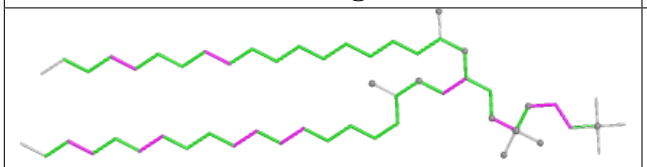
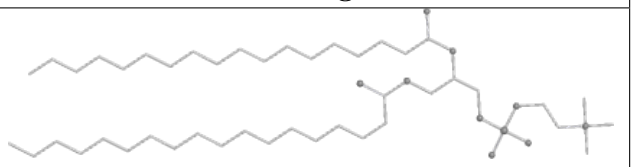
Ligand PC1 A 1109	
 Bond lengths	 Bond angles
 Torsions	 Rings

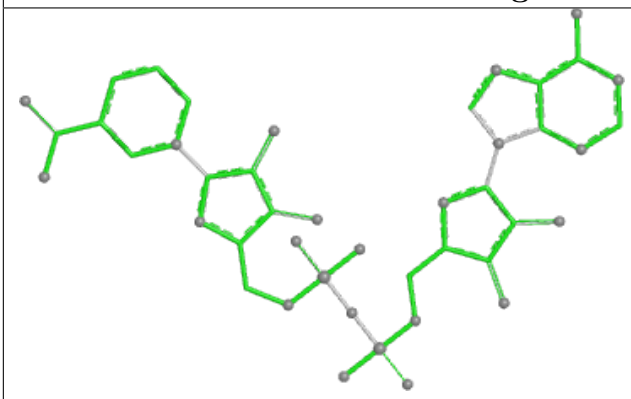
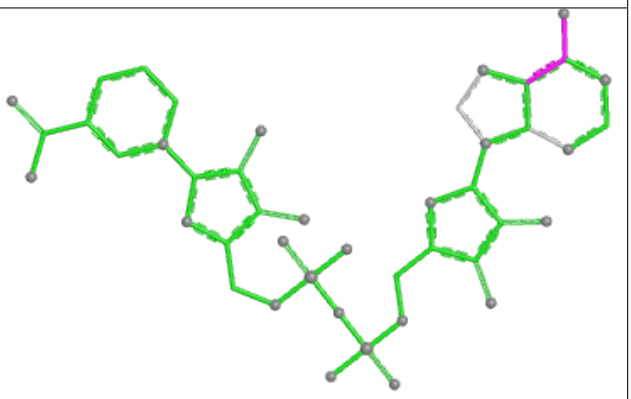
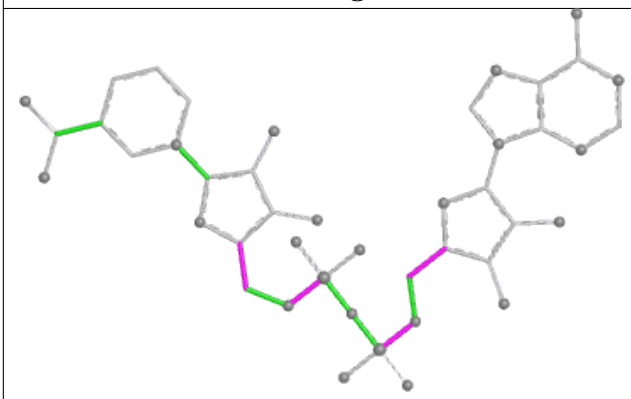
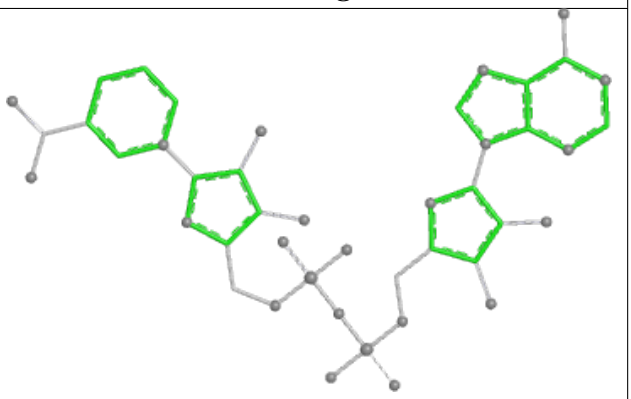
Ligand PC1 B 1104	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand PC1 B 1106	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand PC1 A 1104	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand NAP A 1101	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand PC1 B 1109	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand NAD B 1103	
 Bond lengths	 Bond angles
 Torsions	 Rings

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.

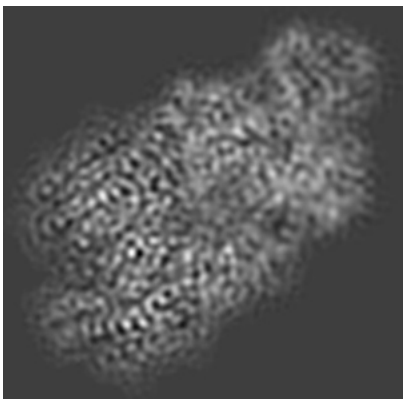
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-4635. These allow visual inspection of the internal detail of the map and identification of artifacts.

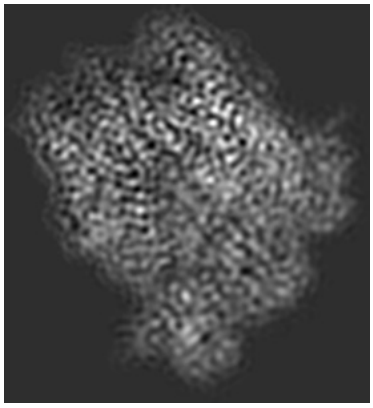
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

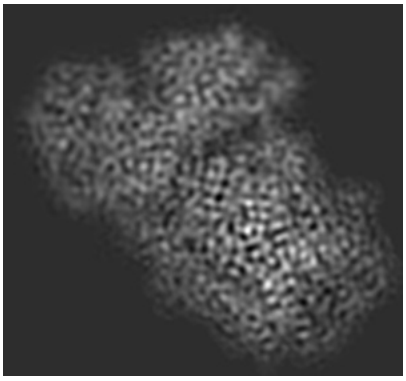
6.1.1 Primary map



X



Y

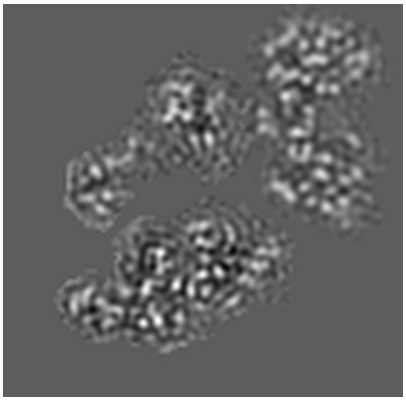


Z

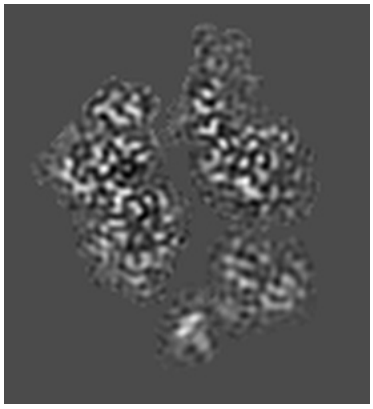
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

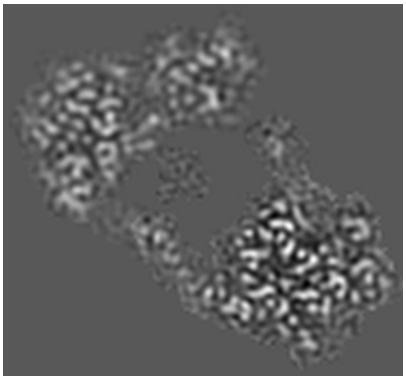
6.2.1 Primary map



X Index: 64



Y Index: 59

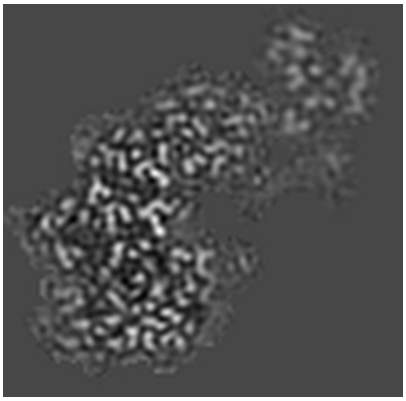


Z Index: 58

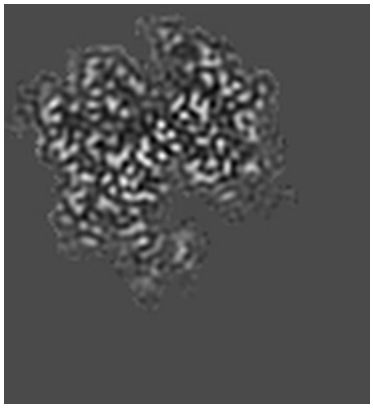
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

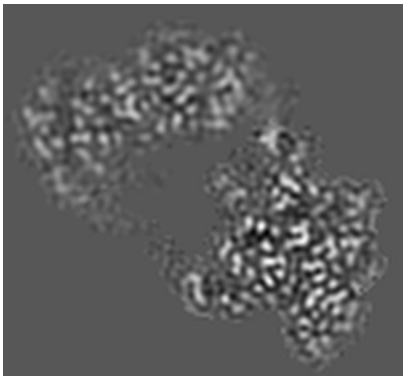
6.3.1 Primary map



X Index: 82



Y Index: 42



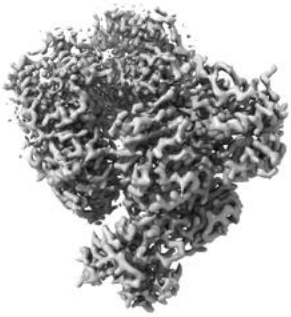
Z Index: 64

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

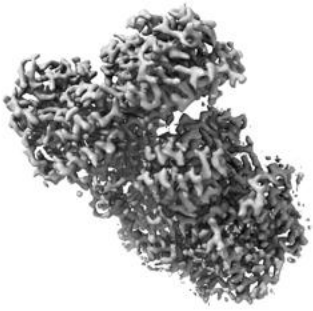
6.4 Orthogonal surface views (i)

6.4.1 Primary map

X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

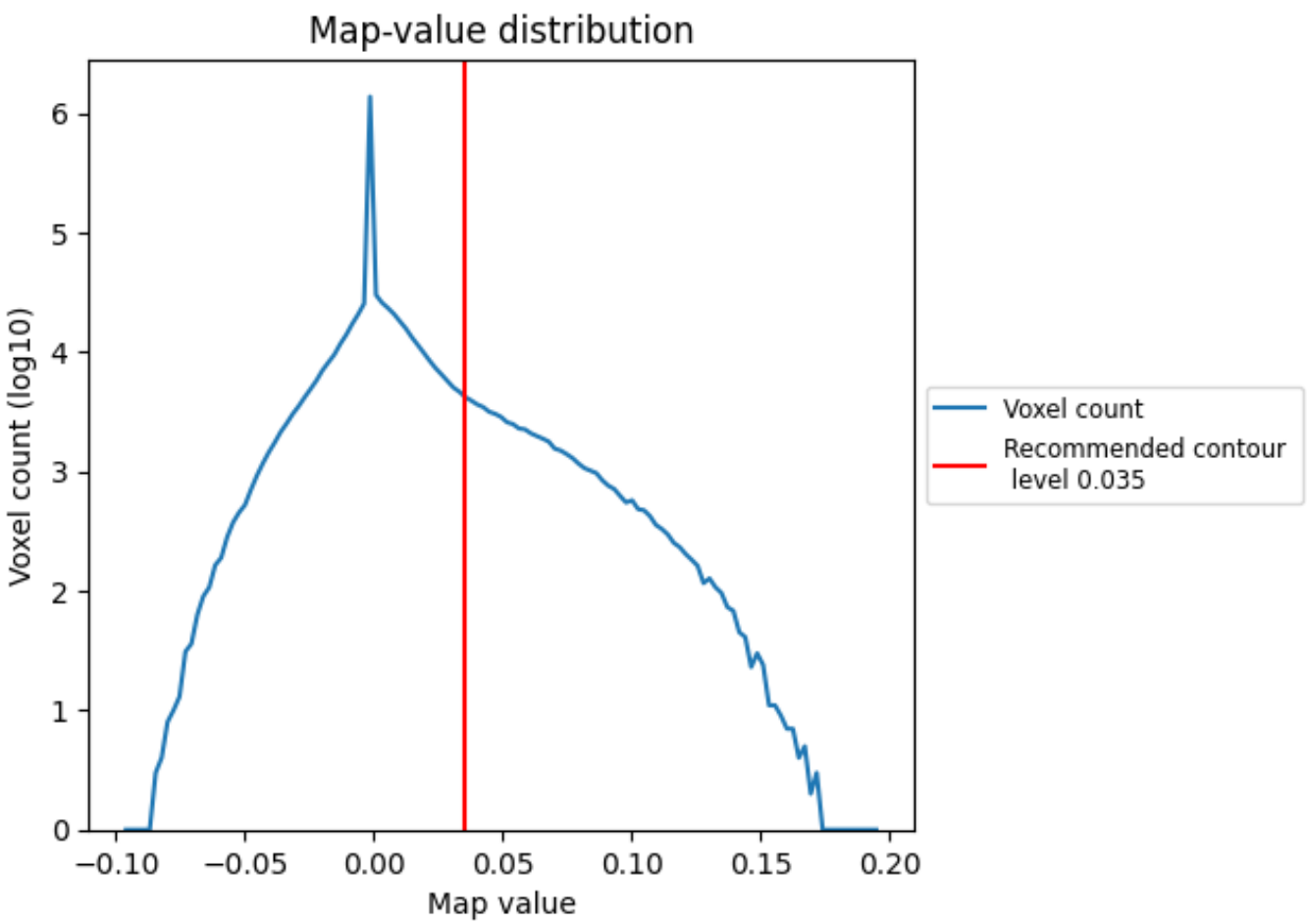
6.5 Mask visualisation (i)

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

7 Map analysis (i)

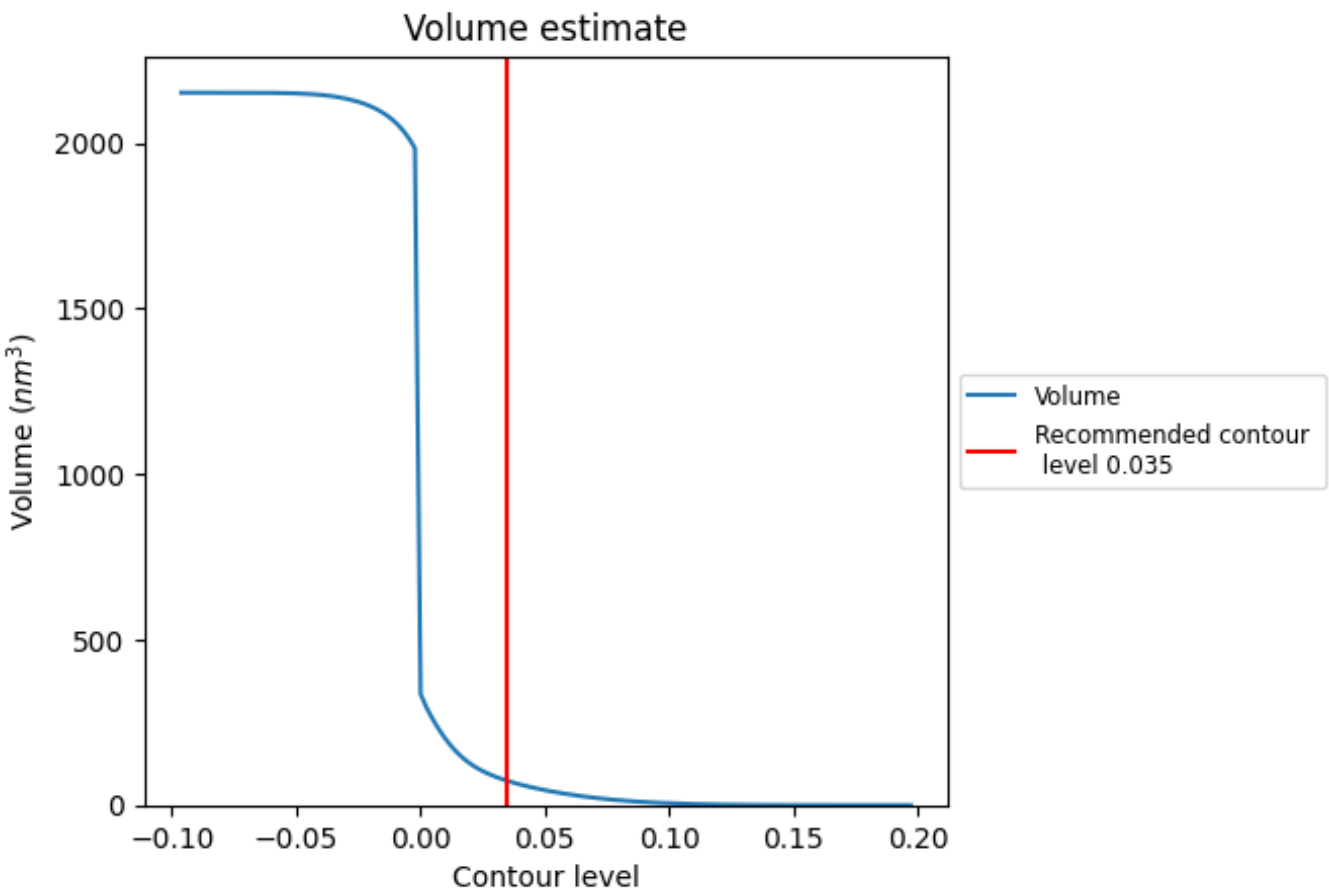
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

7.2 Volume estimate (i)



The volume at the recommended contour level is 73 nm^3; this corresponds to an approximate mass of 66 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.

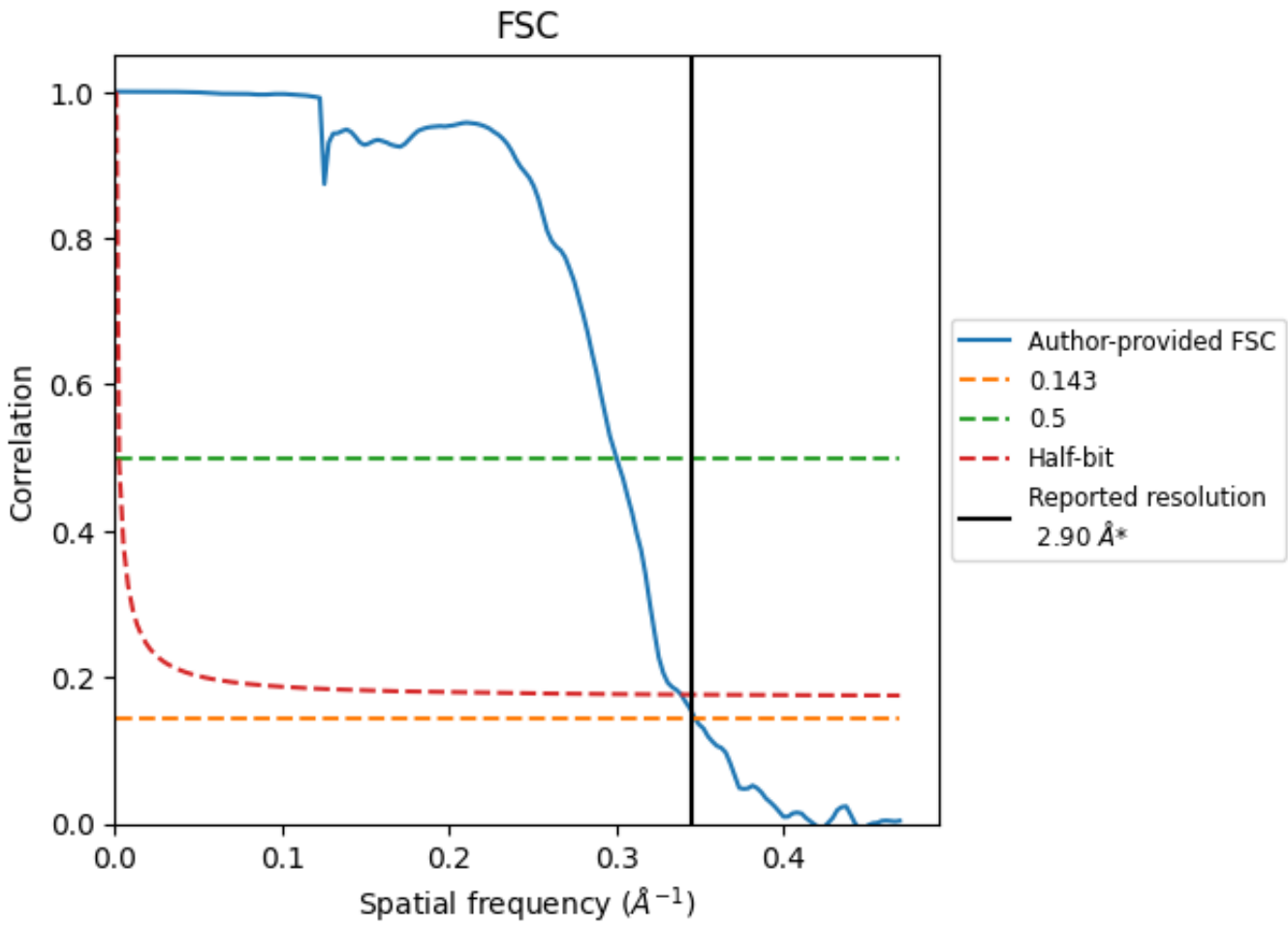
7.3 Rotationally averaged power spectrum (i)

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 0.345 Å^{-1}

8.2 Resolution estimates (i)

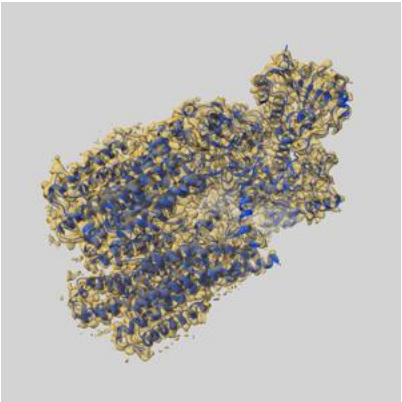
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.88	3.33	2.95
Unmasked-calculated*	-	-	-

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

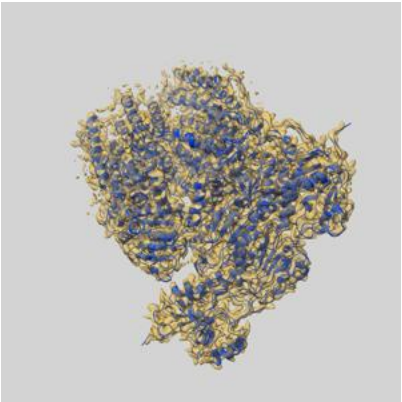
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-4635 and PDB model 6QTI. Per-residue inclusion information can be found in section 3 on page 7.

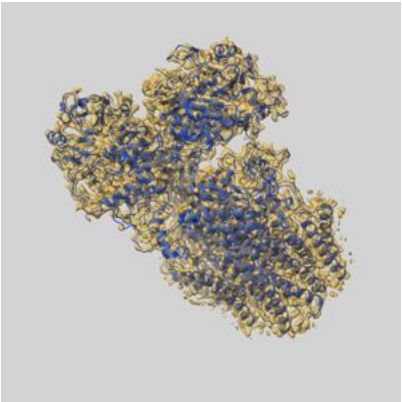
9.1 Map-model overlay (i)



X



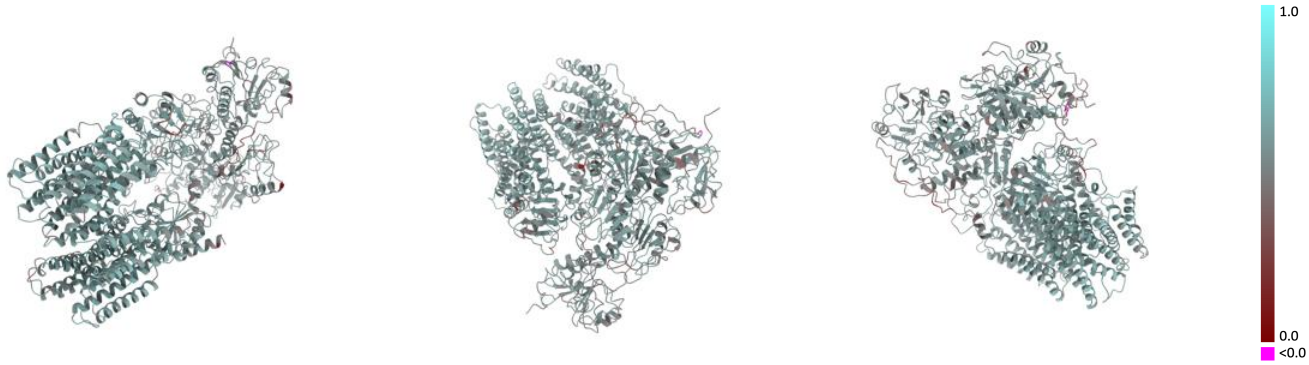
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035 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.

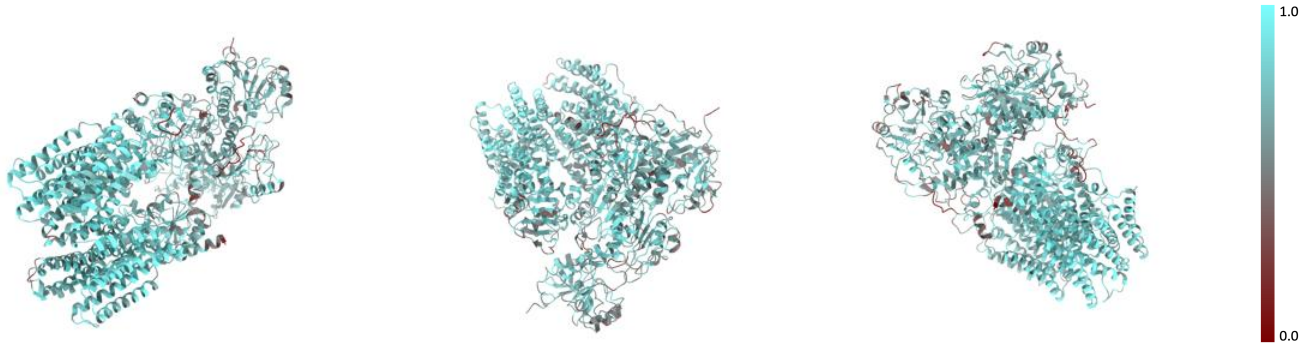
9.2 Q-score mapped to coordinate model (i)



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.

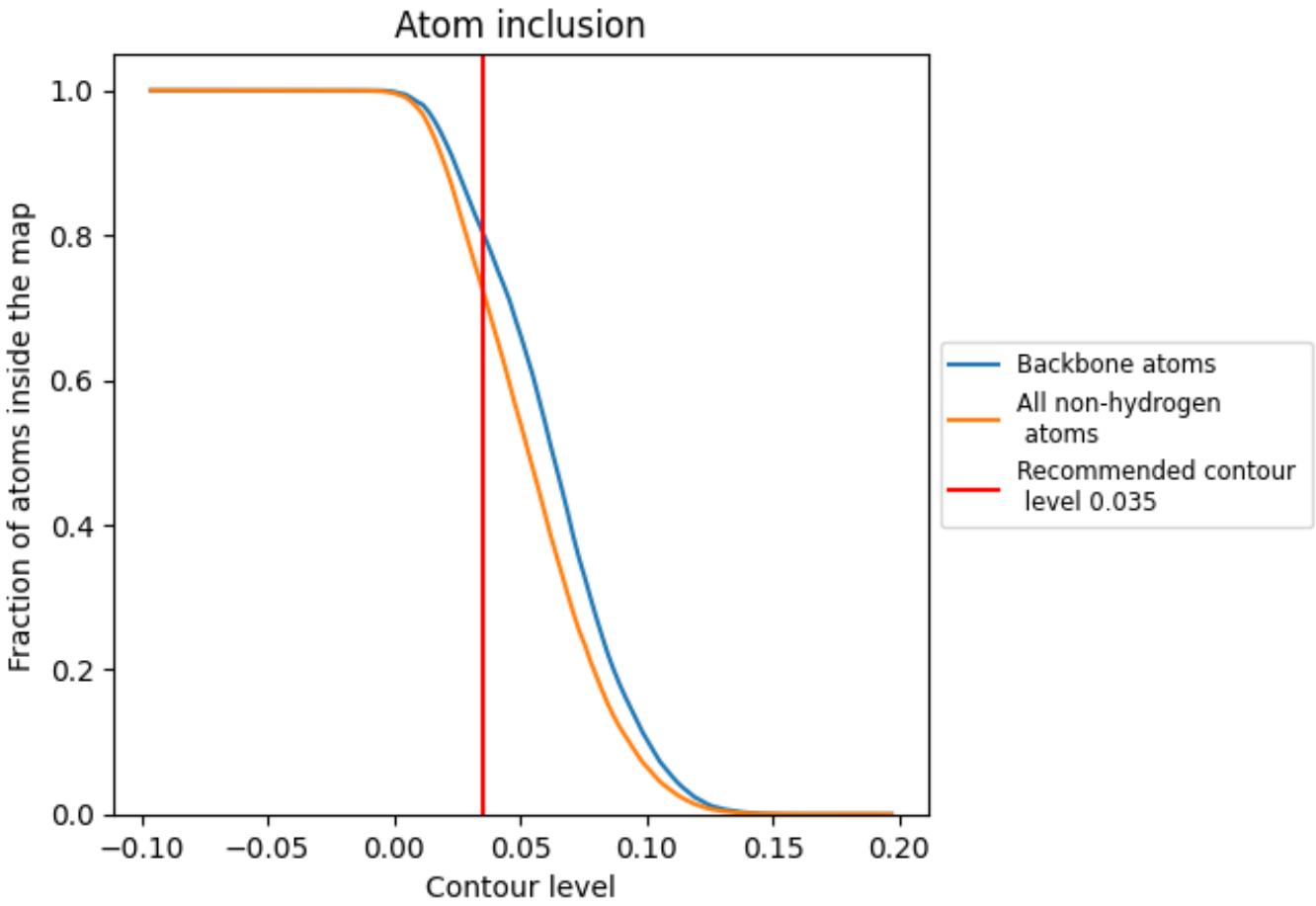
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.035).

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 73% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7271	0.5540
A	0.7305	0.5560
B	0.7237	0.5520