



wwPDB EM Validation Summary Report ⓘ

Oct 14, 2024 – 03:31 PM JST

PDB ID : 7E2H
EMDB ID : EMD-30957
Title : Cryo-EM structure of hDisp1NNN-3C-Cleavage
Authors : Li, W.; Wang, L.; Gong, X.
Deposited on : 2021-02-05
Resolution : 3.68 Å(reported)

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 ⓘ 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.dev113
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) : 2.39

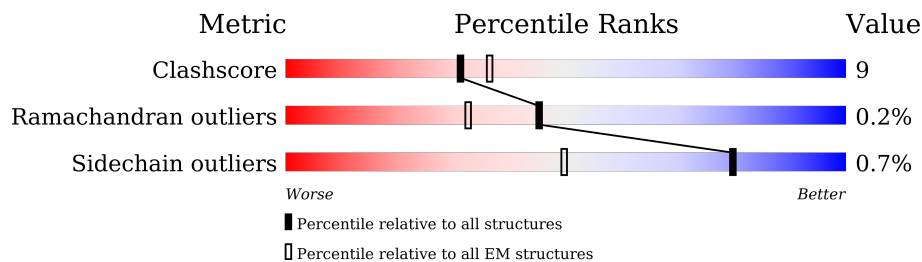
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.68 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	210492	15764
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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	D	270	 28% . 69%
2	E	1248	 52% 14% 34%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7274 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 Protein dispatched homolog 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	D	83	615	403	98	109	5	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	263	SER	-	linker	UNP Q96F81
D	264	SER	-	linker	UNP Q96F81
D	271	LEU	-	linker	UNP Q96F81
D	272	GLU	-	linker	UNP Q96F81
D	273	VAL	-	linker	UNP Q96F81
D	274	LEU	-	linker	UNP Q96F81
D	275	PHE	-	linker	UNP Q96F81
D	276	GLN	-	linker	UNP Q96F81

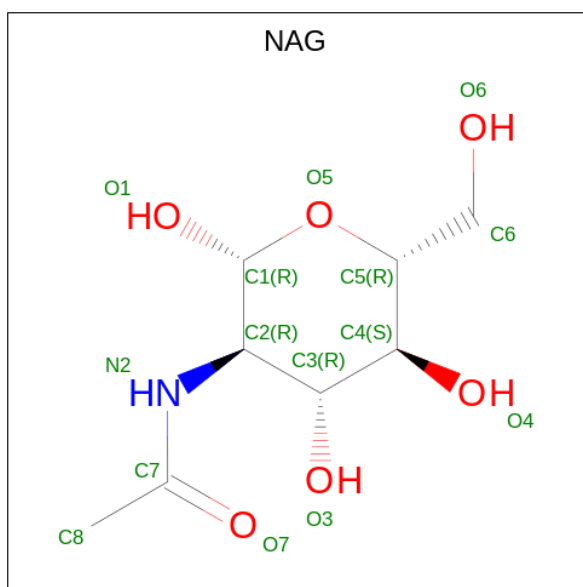
- Molecule 2 is a protein called Protein dispatched homolog 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	824	6323	4117	1018	1134	54	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	277	GLY	-	linker	UNP Q96F81
E	278	PRO	-	linker	UNP Q96F81
E	279	GLY	-	linker	UNP Q96F81
E	280	SER	-	linker	UNP Q96F81
E	572	ASN	ASP	engineered mutation	UNP Q96F81
E	573	ASN	ASP	engineered mutation	UNP Q96F81
E	1051	ASN	ASP	engineered mutation	UNP Q96F81

- Molecule 3 is CHOLESTEROL HEMISUCCINATE (three-letter code: Y01) (formula: C₃₁H₅₀O₄).

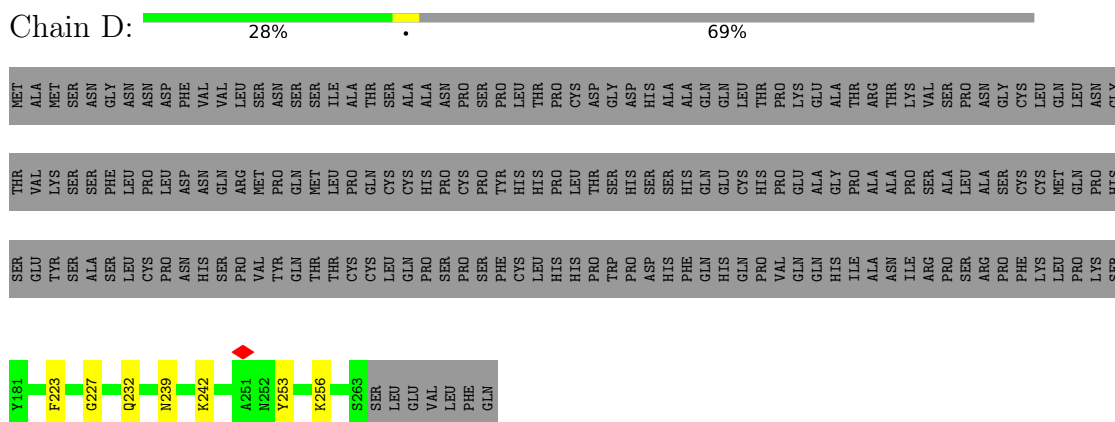


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	

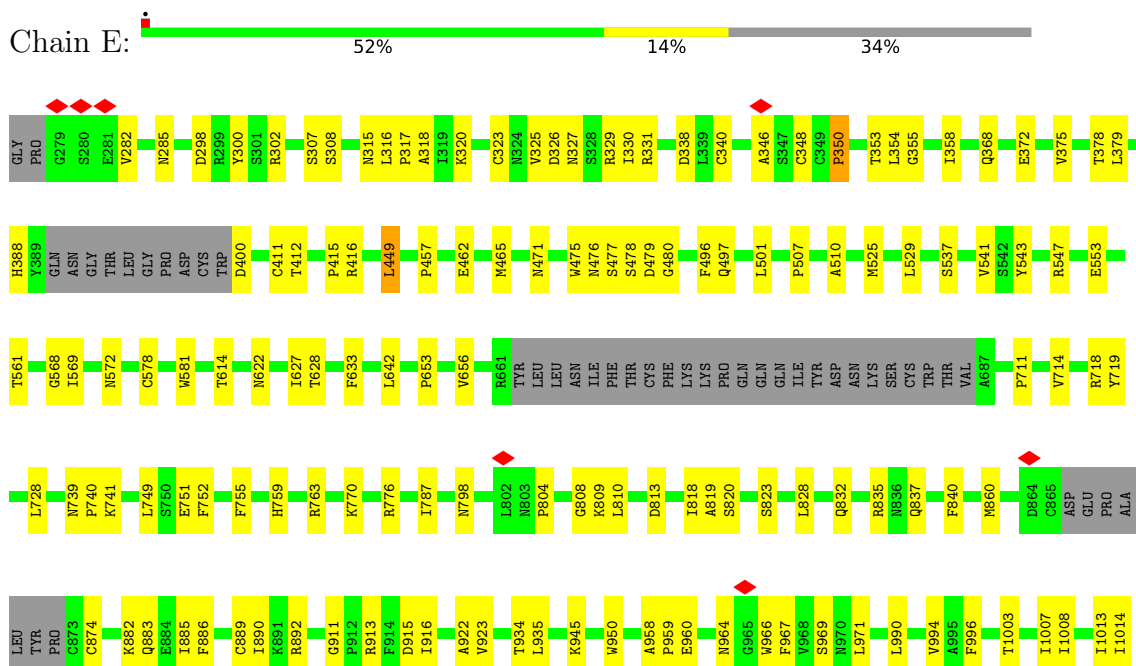
3 Residue-property plots

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: Protein dispatched homolog 1



- Molecule 2: Protein dispatched homolog 1



L1029	L1030	G1031	W1032	V1036	L1037	E1038	S1039	V1040	T1041	V1050	V1054	V1058	A1059	Y1060	R1061	L1062	E1069	I1073	F1074	S1075	L1076	V1079	T1090	M1097	L1108	C1117	T1124	F1125	F1126	F1127	Q1128	R1132	C1133	L1134	G1135	P1136	P1144	LEU	PRO	PRO	LYS	LYS	LEU	GLN	CYS						
SER	ALA	PHE	SER	HIS	ALA	LEU	SER	PRO	ASP	LYS	GLY	SER	THR	THR	HIS	THR	ALA	TYR	HIS	LEU	ASP	PRO	GLY	PRO	LYS	SER	LEU	GLU	TYR	GLU	LEU	PRO	LEU	LEU	ALA	SER	HIS	HIS	SER	CYS	THR	ALA	PRO	GLU	LYS	LYS	LEU	THR	TYR	GLU	
GLU	THR	HIS	ILE	CYS	SER	GLU	PHE	ASN	ASN	GLN	ASP	GLY	MET	PRO	VAL	HIS	ALA	TYR	ASN	SER	GLU	LEU	LYS	THR	THR	GLU	ASP	VAL	ALA	GLY	SER	ALA	LEU	VAL	GLN	ASN	HIS	THR	VAL	CYS	HIS	PHE	VAL	SER	LEU	ASN	GLN	ARG	CYS		
SER	CYS	PRO	ASP	ALA	TYR	LYS	HIS	LEU	GLY	LEU	TYR	ASN	GLY	PRO	ALA	HIS	SER	ASN	CYS	GLN	GLY	MET	ASN	GLN	GLY	ASP	VAL	ALA	GLN	ASN	ALA	LEU	CYS	GLN	THR	ASN	GLN	VAL	PRO	GLY	LEU	ALA	THR	GLN	GLY	GLY	THR	PRO	ILE	HIS	
ILE	HIS	HIS	CYS	PRO	CYS	LEU	GLN	GLY	ARG	VAL	LYS	PRO	ALA	PRO	PHE	LEU	HIS	LEU	HIS	PRO	VAL	ASN	ARG	GLN	GLY	ASN	GLY	GLY	THR	THR	ASN	VAL	VAL	HIS	SER	ILE	GLU	GLU	GLU	HIS	LEU	LEU	THR	PRO	LYS	MET	ALA	VAL	ASN		
SER	SER	VAL	ASN	ARG	SER	THR	GLY	LEU	LEU	LYS	THR	CYS	GLY	PRO	ASN	GLY	LYS	CYS	ASN	ASN	ARG	GLN	GLY	VAL	SER	ASN	GLY	THR	GLU	VAL	LYS	ALA	GLY	GLY	THR	GLU	VAL	LYS	ASN	GLU	LEU	THR	THR	ASP	ALA	VAL	VAL	VAL	ASN		
SER	GLU	HIS	PHE	GLN	ASN	GLU	PRO	LYS	VAL	PHE	ASN	HIS	LEU	GLY	GLY	GLY	PRO	ASN	ASN	ASN	SER	GLN	SER	CYS	GLY	ARG	ILE	VAL	ARG	VAL	VAL	VAL	CYS	GLN	MET	PRO	ASN	ASN	MET	GLU	ALA	ALA	VAL	VAL	GLU	THR	THR	HIS			
SER	GLU	LEU	SER	GLY	GLU	SER	LEU	ILE	THR	LEU	ASN	HIS	LEU	VAL	VAL	VAL	LYS	CYS	ASN	ASN	ARG	ILE	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63043	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	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	0.204	Depositor
Minimum map value	-0.135	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	198.72, 198.72, 198.72	wwPDB
Map dimensions	184, 184, 184	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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: Y01, NAG

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	0.27	0/631	0.47	0/866
2	E	0.29	0/6487	0.45	0/8839
All	All	0.29	0/7118	0.45	0/9705

There are no bond length outliers.

There are no bond angle outliers.

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	D	615	0	599	6	0
2	E	6323	0	6088	117	0
3	E	280	0	392	10	0
4	E	56	0	52	0	0
All	All	7274	0	7131	123	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 9.

The worst 5 of 123 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1054:VAL:O	2:E:1058:VAL:HG12	1.76	0.85
2:E:1132:ARG:NH1	2:E:1133:CYS:SG	2.55	0.79
1:D:253:TYR:OH	2:E:813:ASP:OD1	2.05	0.74
2:E:329:ARG:HH22	2:E:475:TRP:HB2	1.57	0.69
2:E:543:TYR:OH	2:E:547:ARG:NH1	2.27	0.68

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	D	81/270 (30%)	72 (89%)	8 (10%)	1 (1%)	11	41
2	E	816/1248 (65%)	747 (92%)	68 (8%)	1 (0%)	48	78
All	All	897/1518 (59%)	819 (91%)	76 (8%)	2 (0%)	45	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	256	LYS
2	E	350	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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	62/236 (26%)	62 (100%)	0	100	100
2	E	666/1106 (60%)	661 (99%)	5 (1%)	79	85
All	All	728/1342 (54%)	723 (99%)	5 (1%)	80	88

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

Mol	Chain	Res	Type
2	E	449	LEU
2	E	1058	VAL
2	E	1061	ARG
2	E	1062	LEU
2	E	1132	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	977	GLN
2	E	1035	ASN
2	E	622	ASN
2	E	832	GLN
2	E	862	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

12 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
3	Y01	E	1606	-	38,38,38	0.43	0	57,57,57	0.62	0
4	NAG	E	1612	2	14,14,15	0.21	0	17,19,21	0.36	0
3	Y01	E	1603	-	38,38,38	0.44	0	57,57,57	0.55	0
3	Y01	E	1607	-	38,38,38	0.44	0	57,57,57	0.65	0
3	Y01	E	1602	-	38,38,38	0.42	0	57,57,57	0.60	0
4	NAG	E	1610	2	14,14,15	0.25	0	17,19,21	0.32	0
3	Y01	E	1608	-	38,38,38	0.44	0	57,57,57	0.49	0
3	Y01	E	1601	-	38,38,38	0.45	0	57,57,57	0.63	0
3	Y01	E	1605	-	38,38,38	0.44	0	57,57,57	0.50	0
3	Y01	E	1604	-	38,38,38	0.43	0	57,57,57	0.59	0
4	NAG	E	1609	2	14,14,15	1.15	1 (7%)	17,19,21	1.30	1 (5%)
4	NAG	E	1611	2	14,14,15	0.25	0	17,19,21	0.44	0

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
3	Y01	E	1606	-	-	5/19/77/77	0/4/4/4
4	NAG	E	1612	2	-	1/6/23/26	0/1/1/1
3	Y01	E	1603	-	-	10/19/77/77	0/4/4/4
3	Y01	E	1607	-	-	13/19/77/77	0/4/4/4
3	Y01	E	1602	-	-	6/19/77/77	0/4/4/4
4	NAG	E	1610	2	-	0/6/23/26	0/1/1/1
3	Y01	E	1608	-	-	7/19/77/77	0/4/4/4
3	Y01	E	1601	-	-	10/19/77/77	0/4/4/4
3	Y01	E	1605	-	-	3/19/77/77	0/4/4/4
3	Y01	E	1604	-	-	3/19/77/77	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	1609	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1611	2	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1609	NAG	O5-C1	3.92	1.50	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1609	NAG	C1-O5-C5	5.17	119.20	112.19

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	1607	Y01	OAG-CAY-OAW-CBC
3	E	1607	Y01	CAM-CAY-OAW-CBC
3	E	1608	Y01	CAR-CBC-OAW-CAY
3	E	1607	Y01	CAC-CBB-CBE-CAP
3	E	1607	Y01	CAC-CBB-CBE-CBI

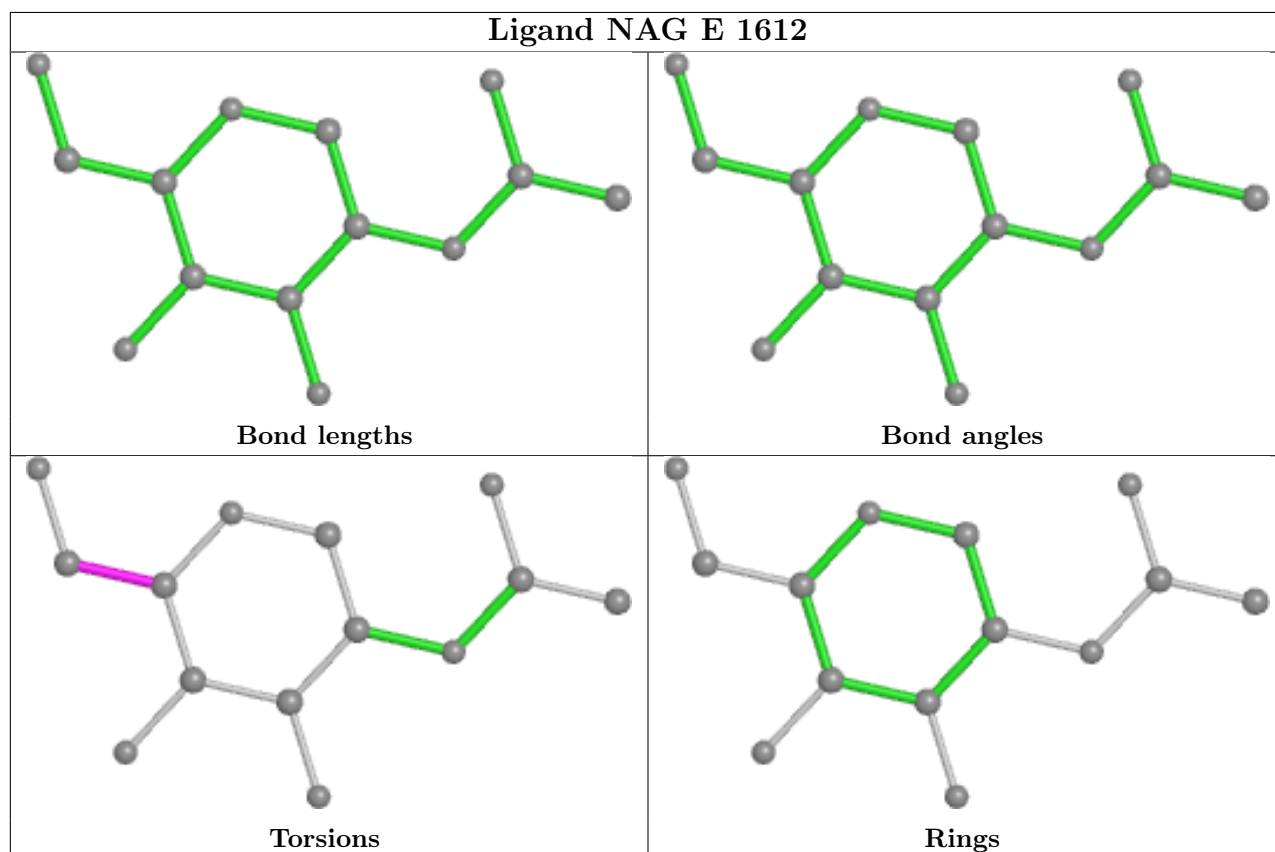
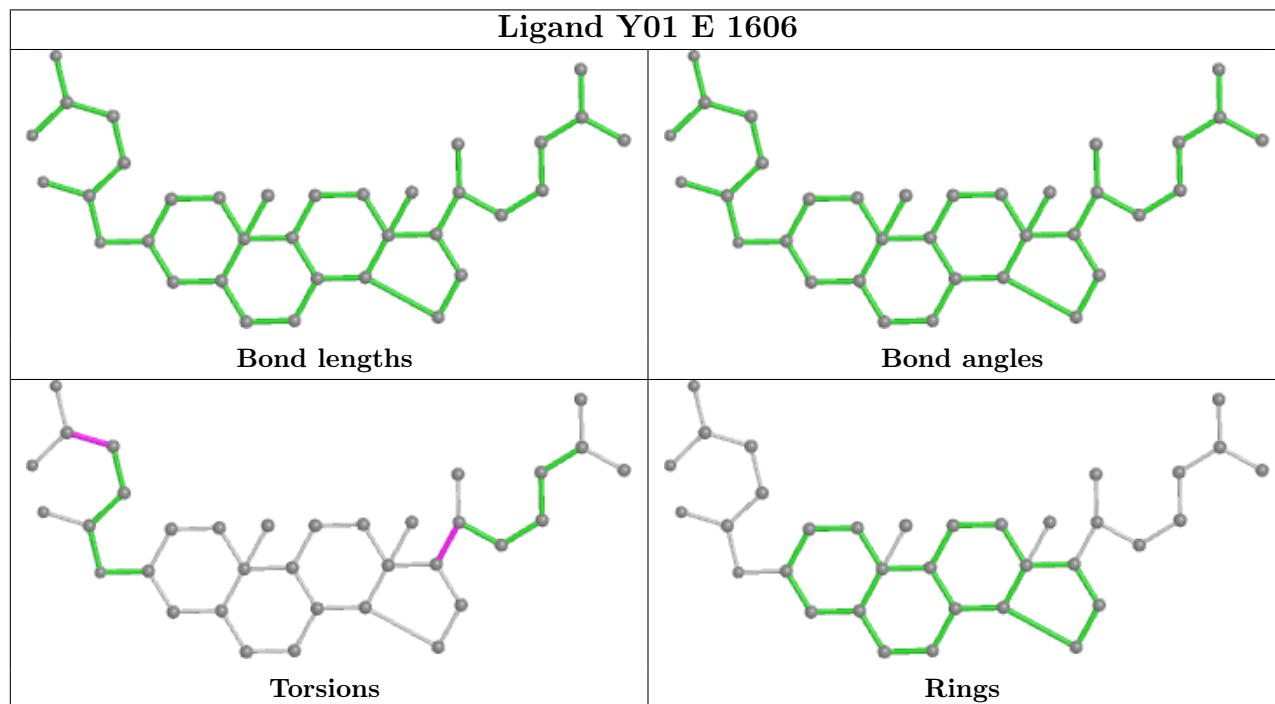
There are no ring outliers.

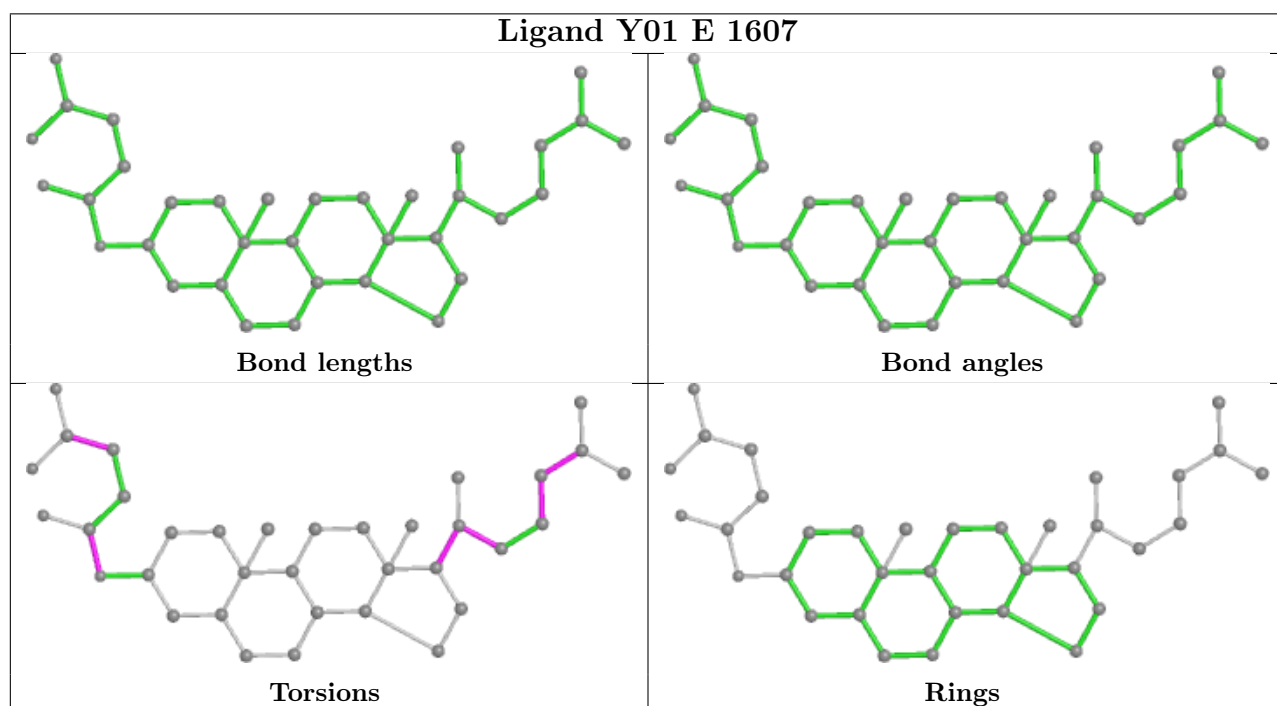
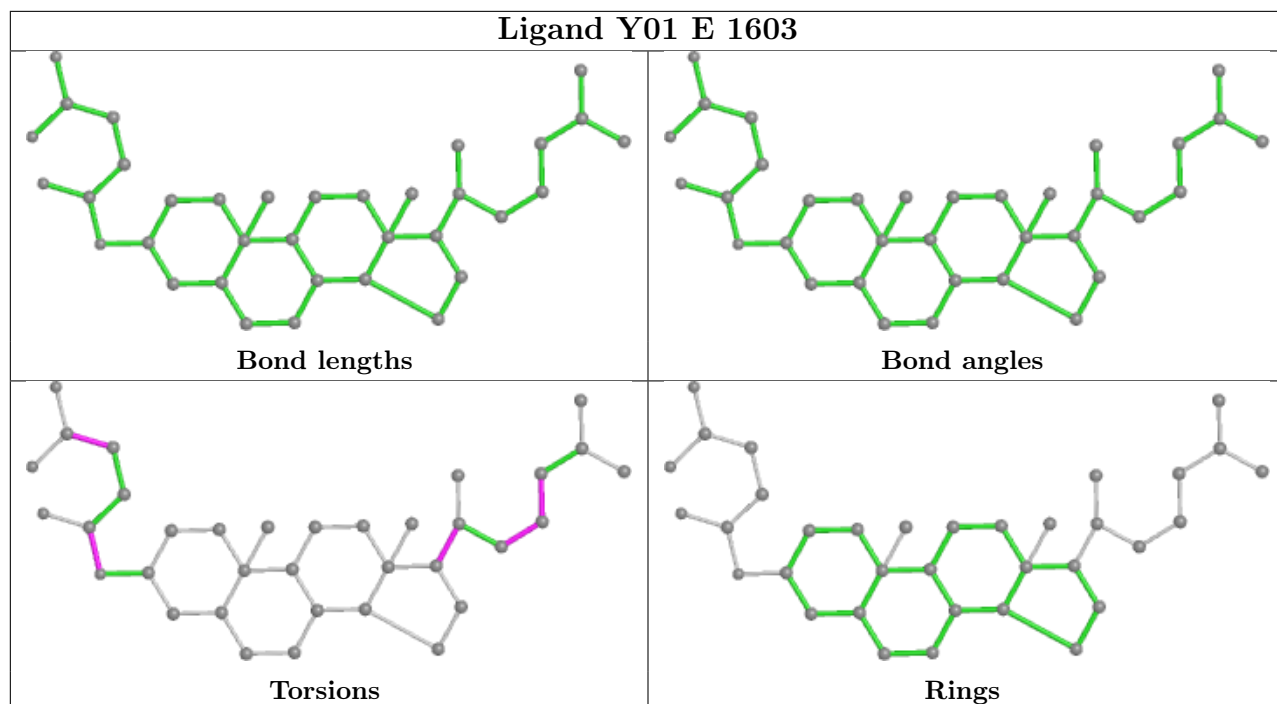
5 monomers are involved in 10 short contacts:

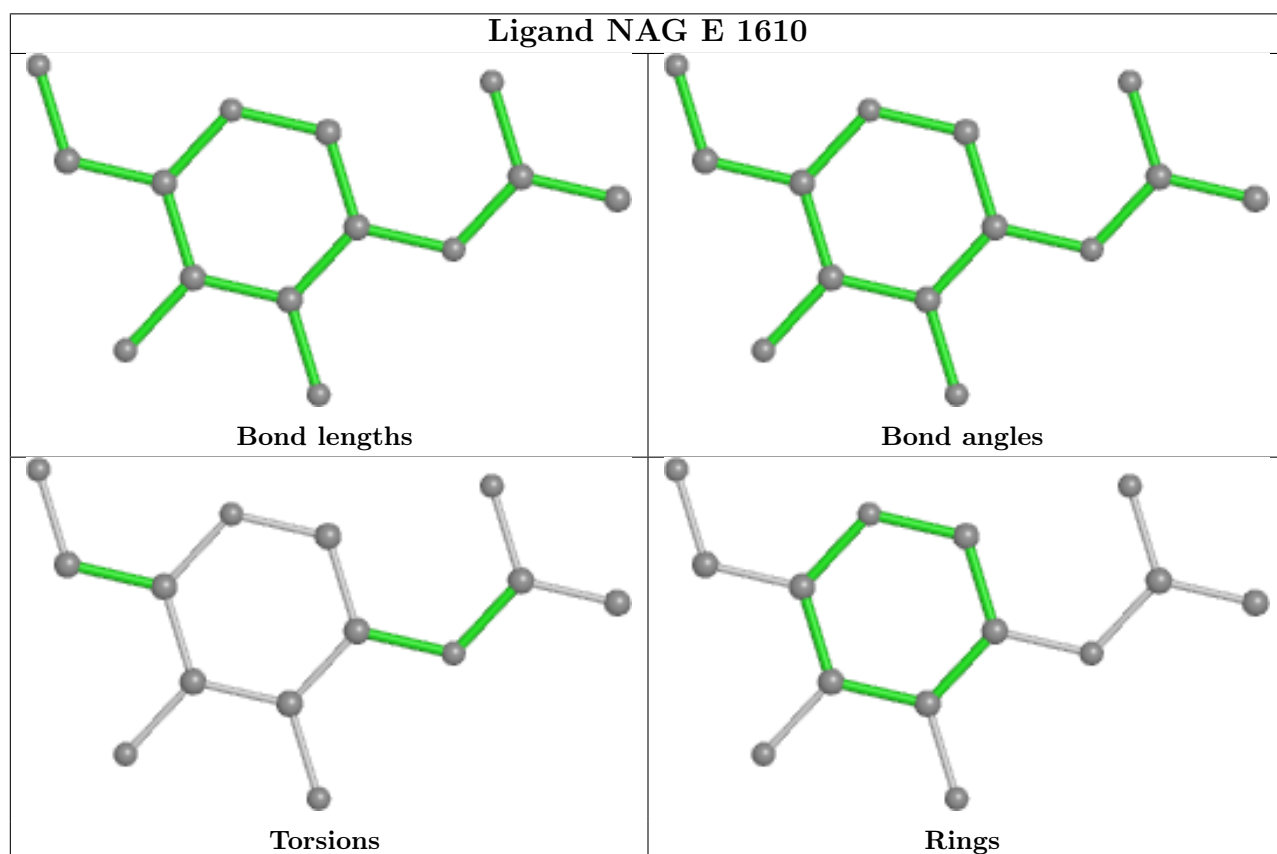
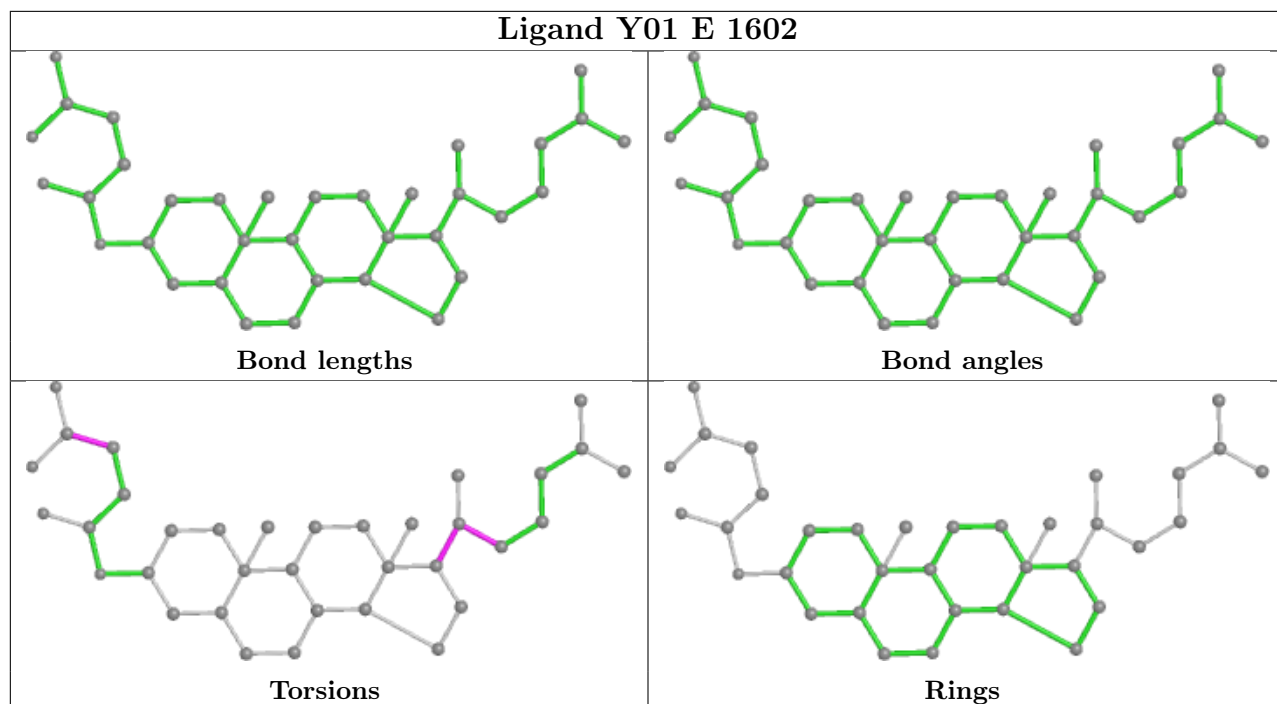
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	1607	Y01	5	0
3	E	1602	Y01	1	0
3	E	1608	Y01	2	0
3	E	1601	Y01	1	0
3	E	1604	Y01	3	0

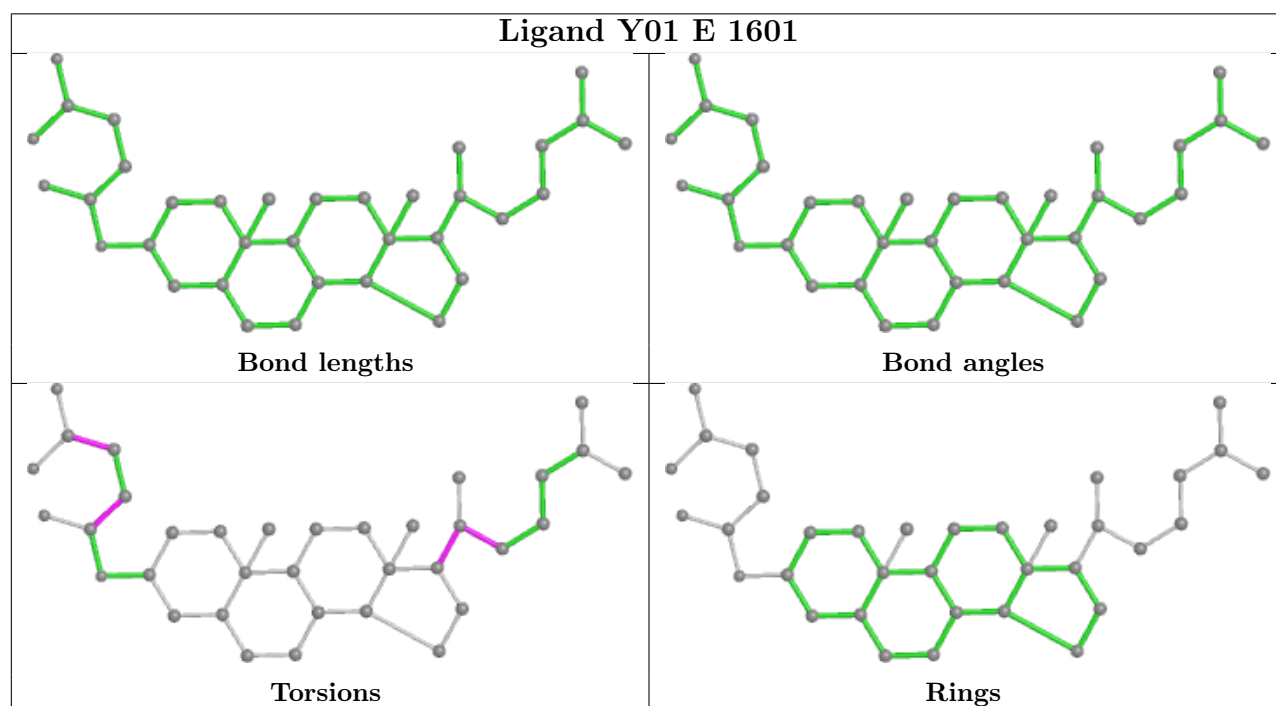
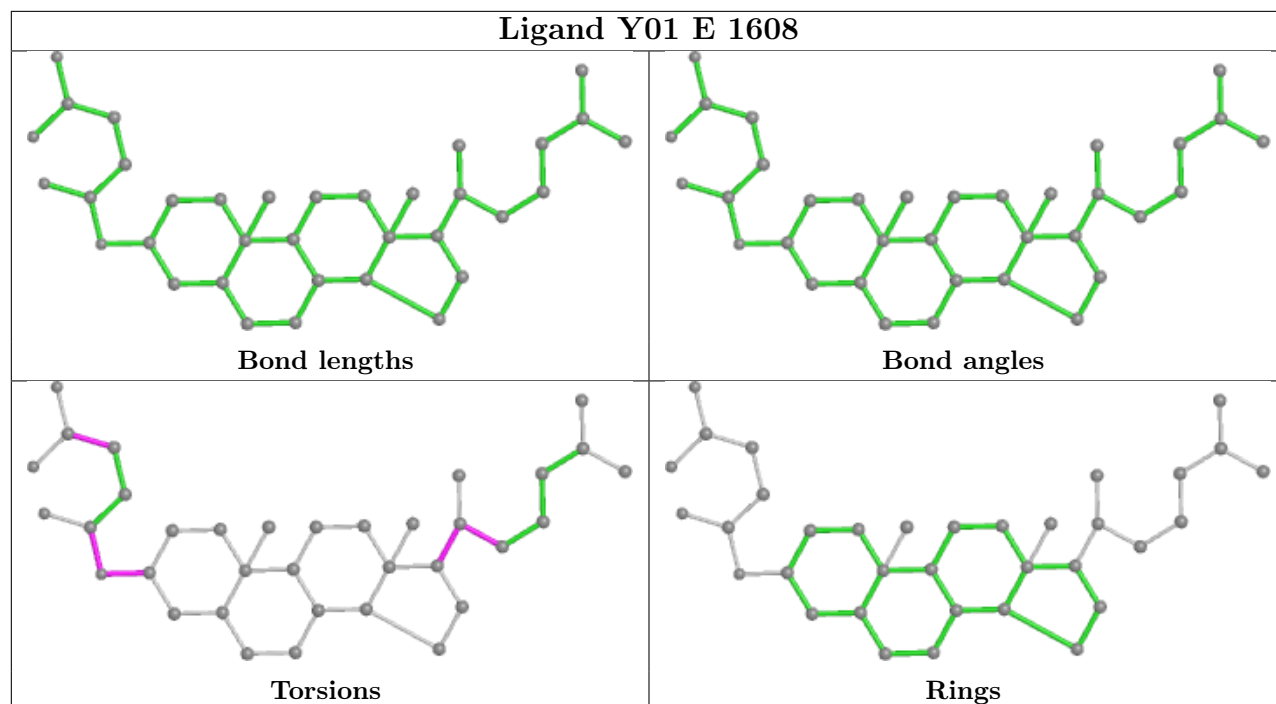
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

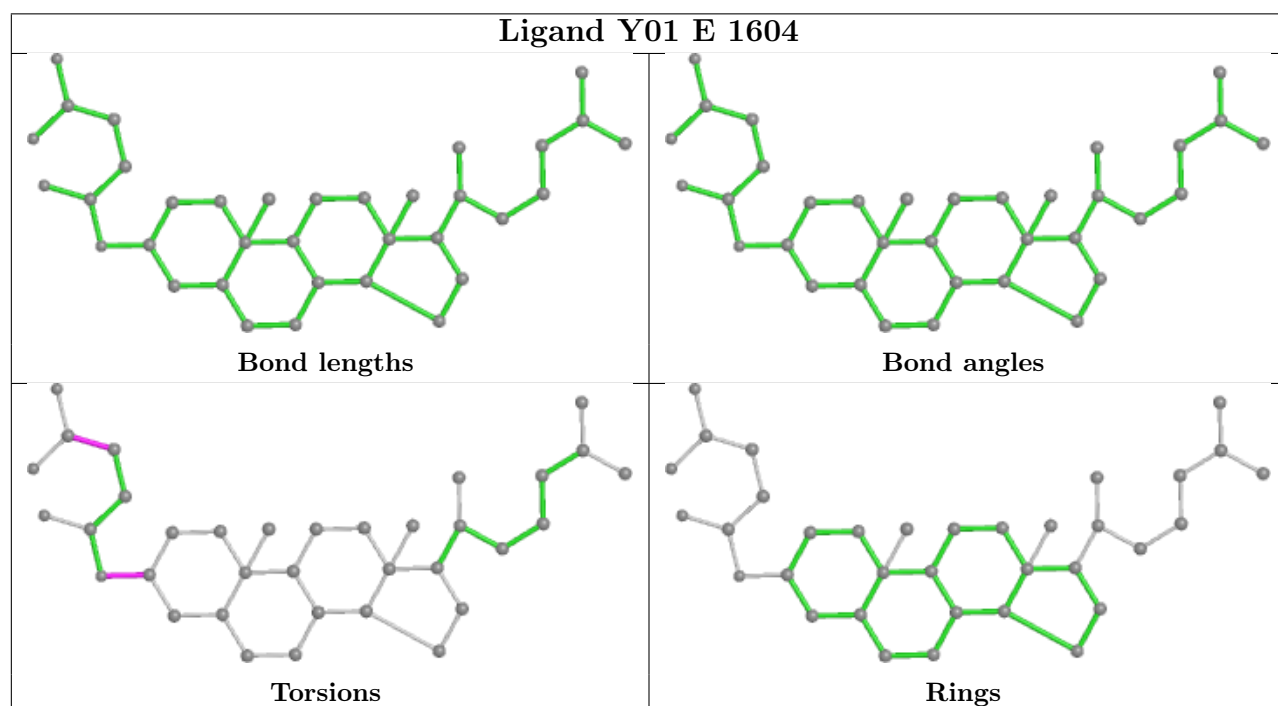
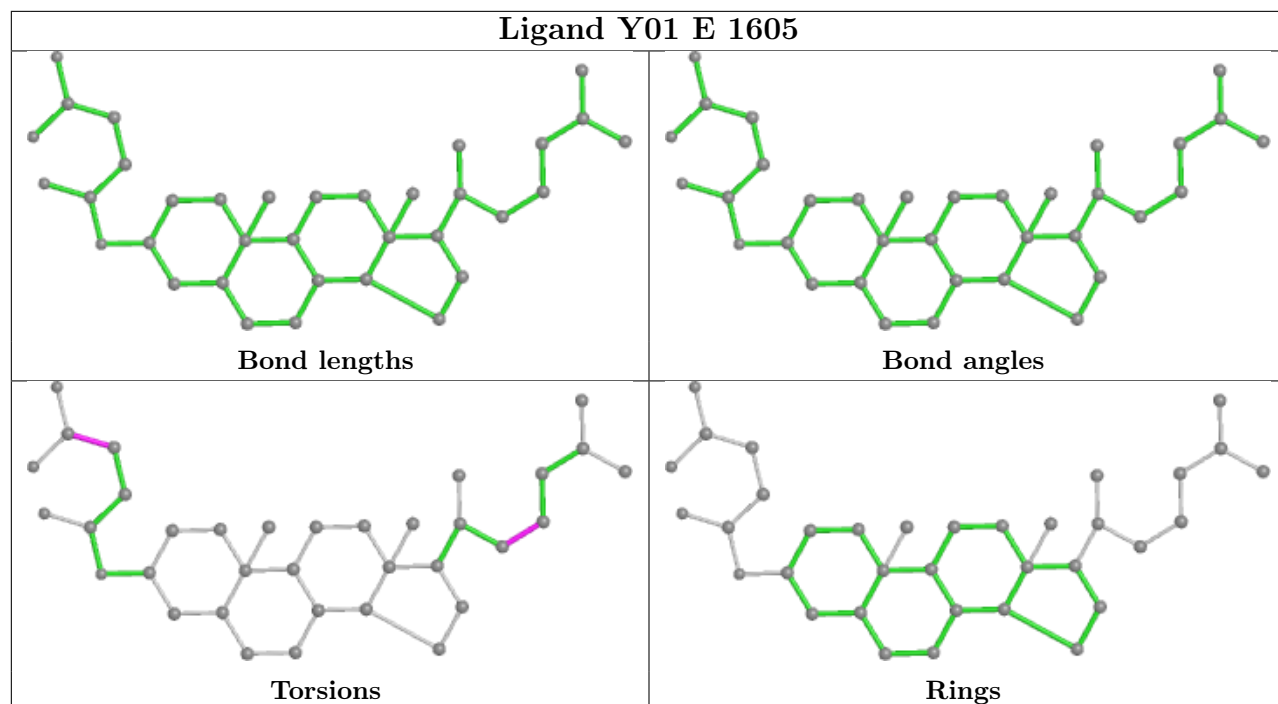
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

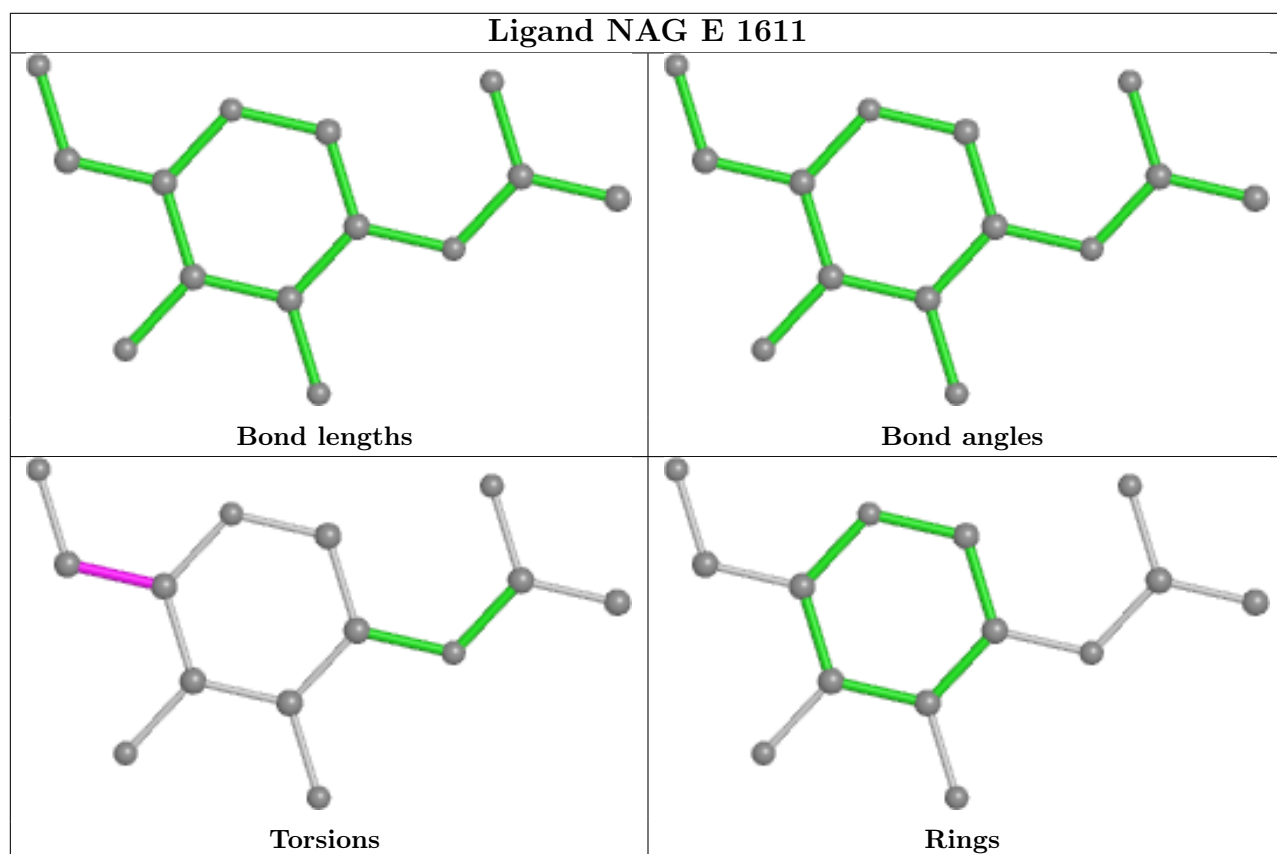
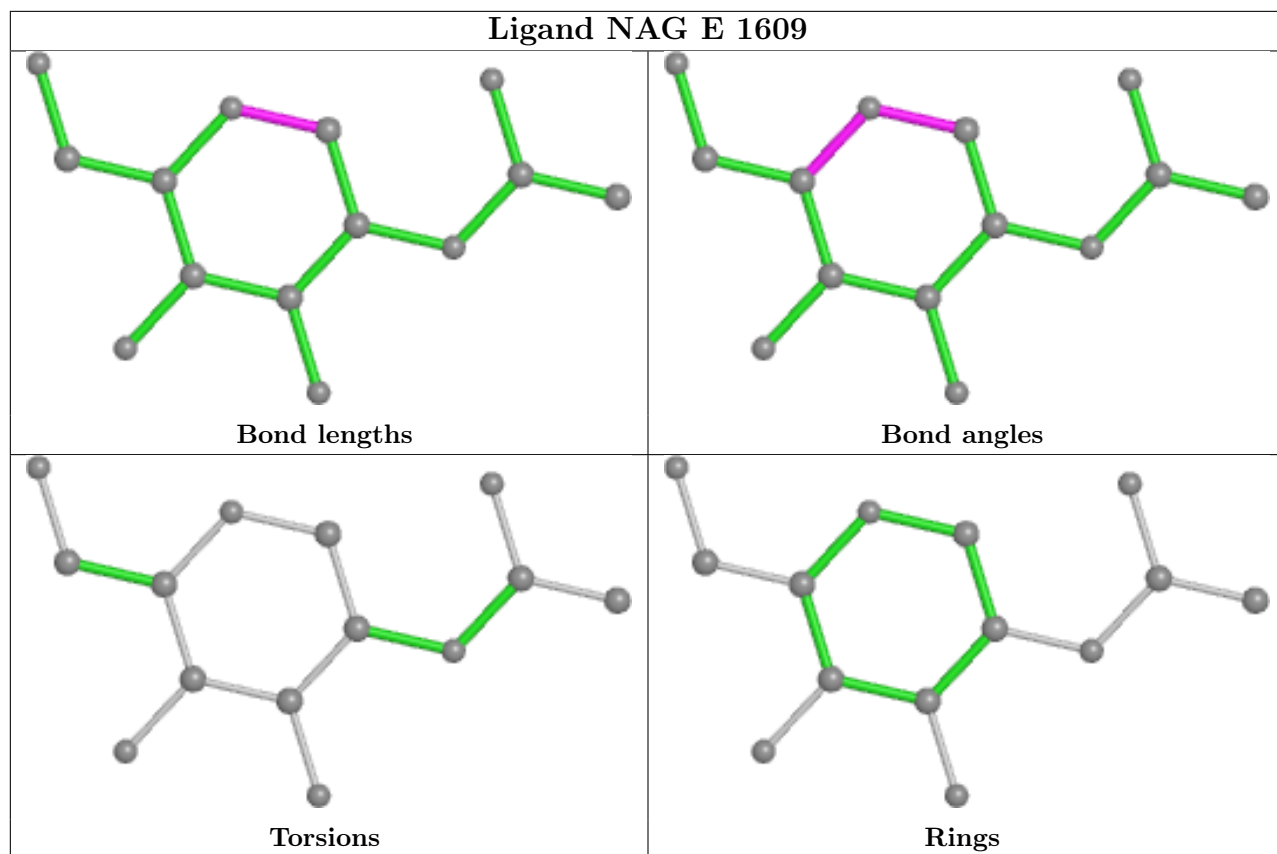












5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

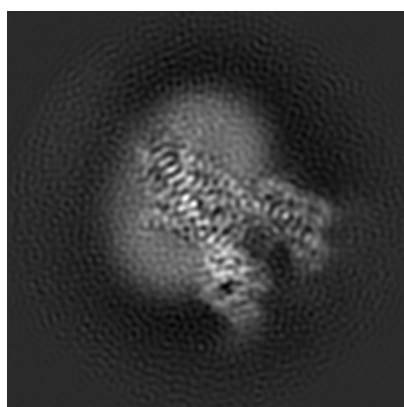
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30957. These allow visual inspection of the internal detail of the map and identification of artifacts.

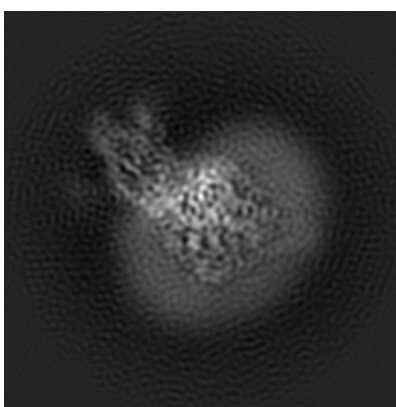
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

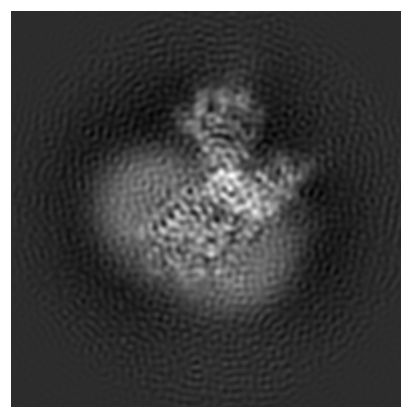
6.1.1 Primary map



X



Y

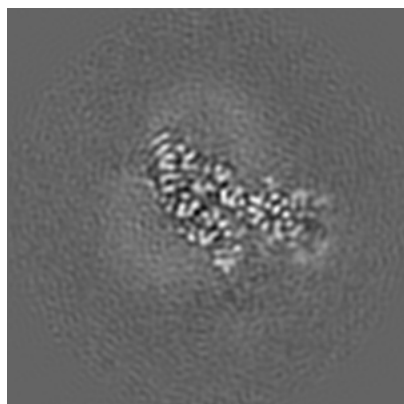


Z

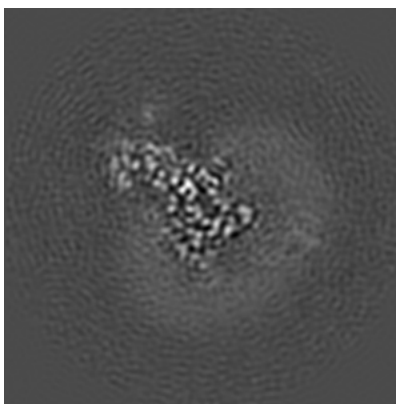
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

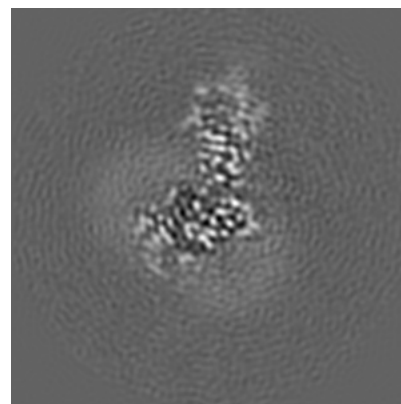
6.2.1 Primary map



X Index: 92



Y Index: 92

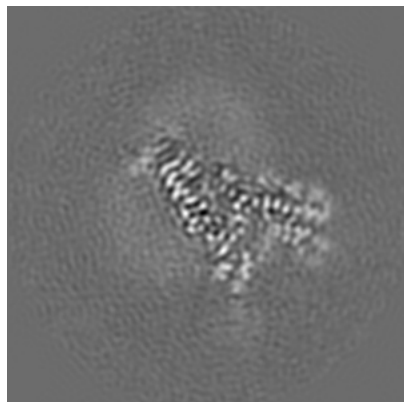


Z Index: 92

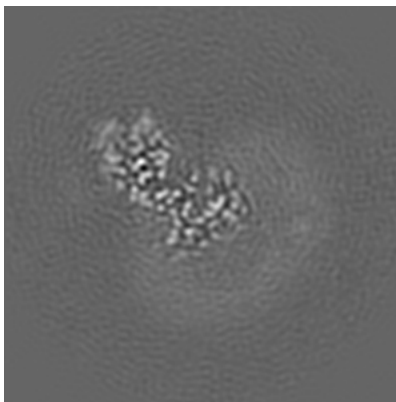
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

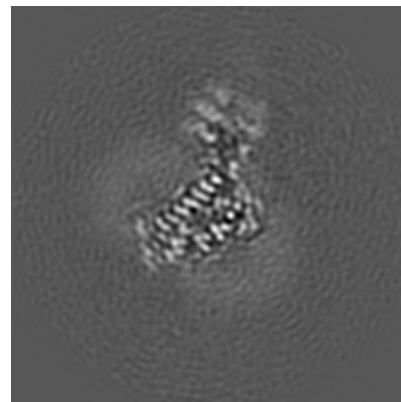
6.3.1 Primary map



X Index: 96



Y Index: 99

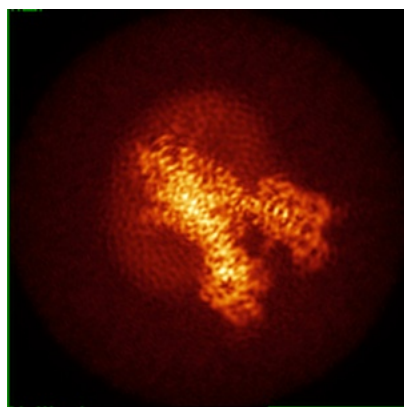


Z Index: 97

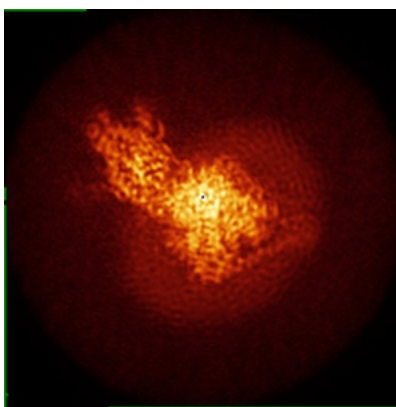
The images above show the largest variance slices of the map in three orthogonal directions.

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

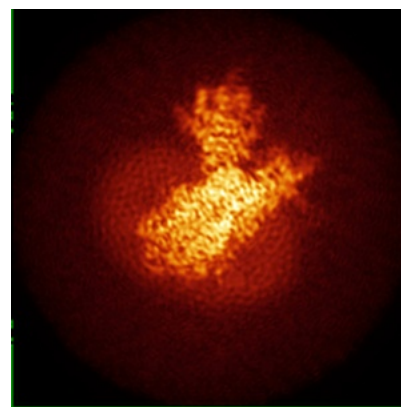
6.4.1 Primary map



X



Y

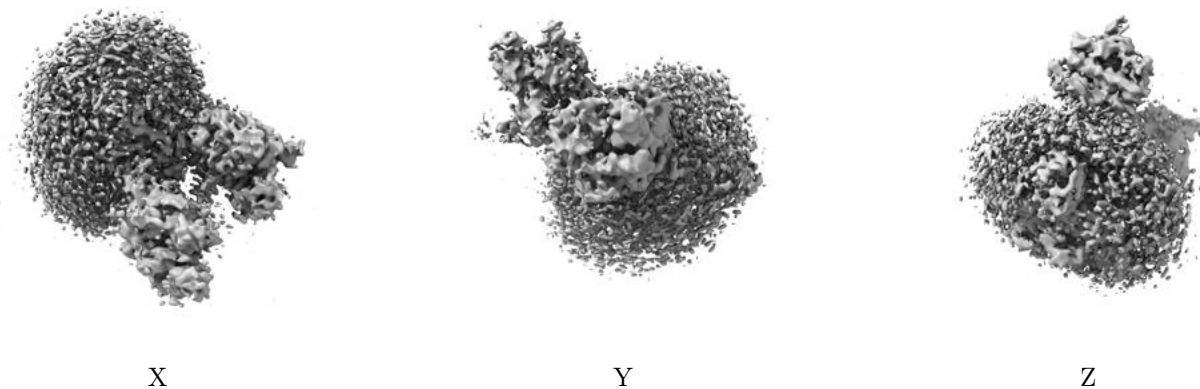


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

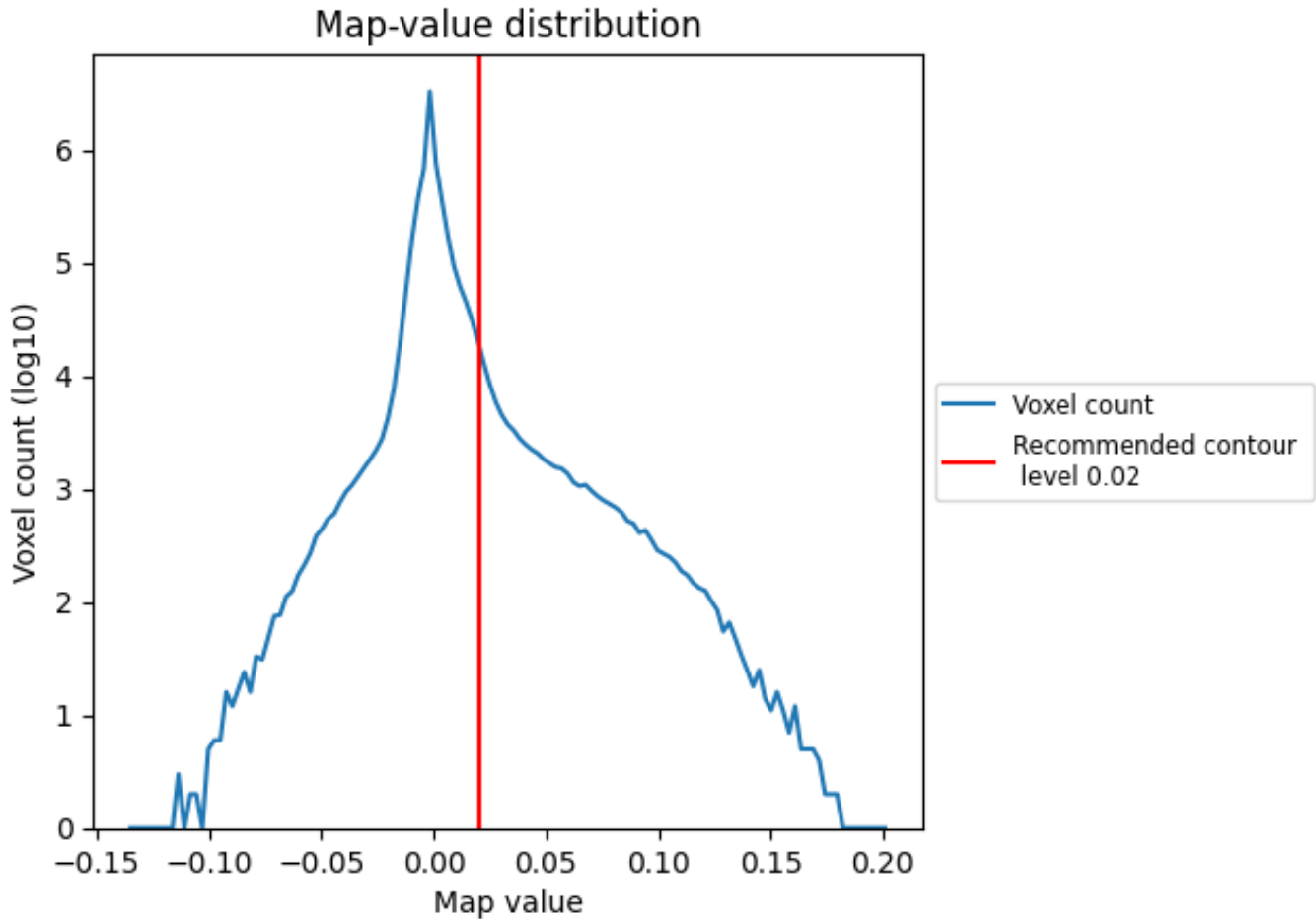
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

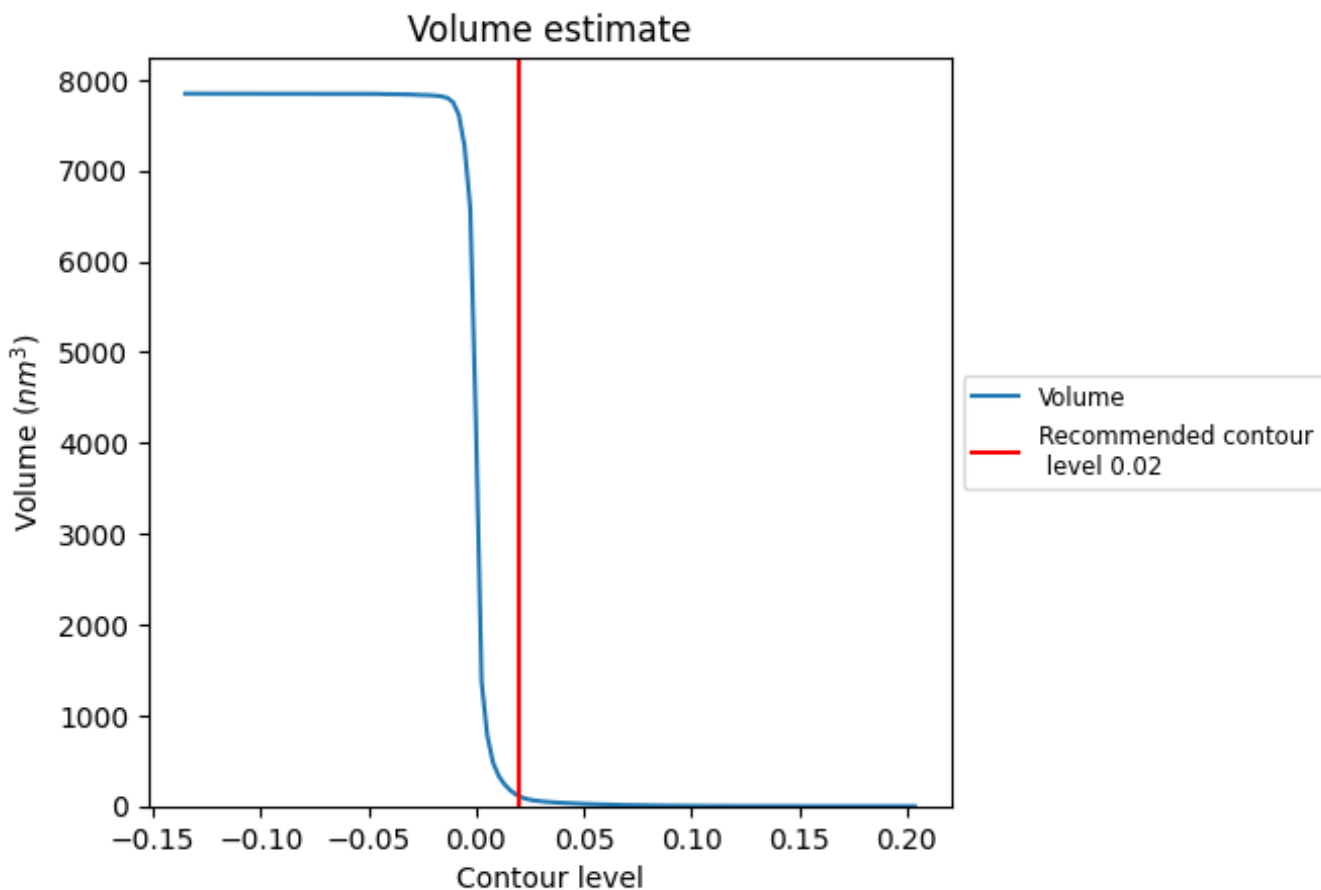
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

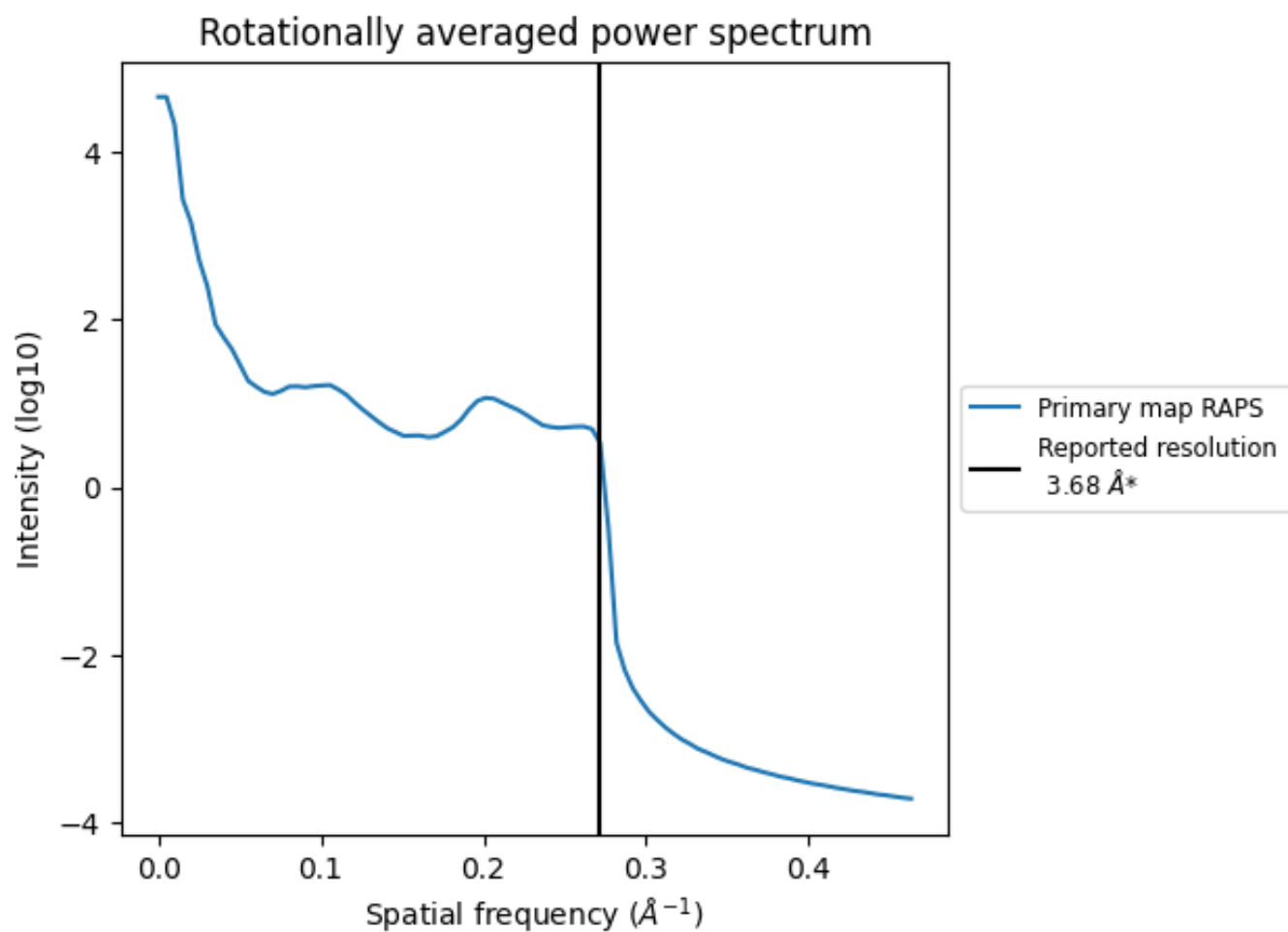
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 110 nm^3 ; this corresponds to an approximate mass of 100 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 0.272 Å⁻¹

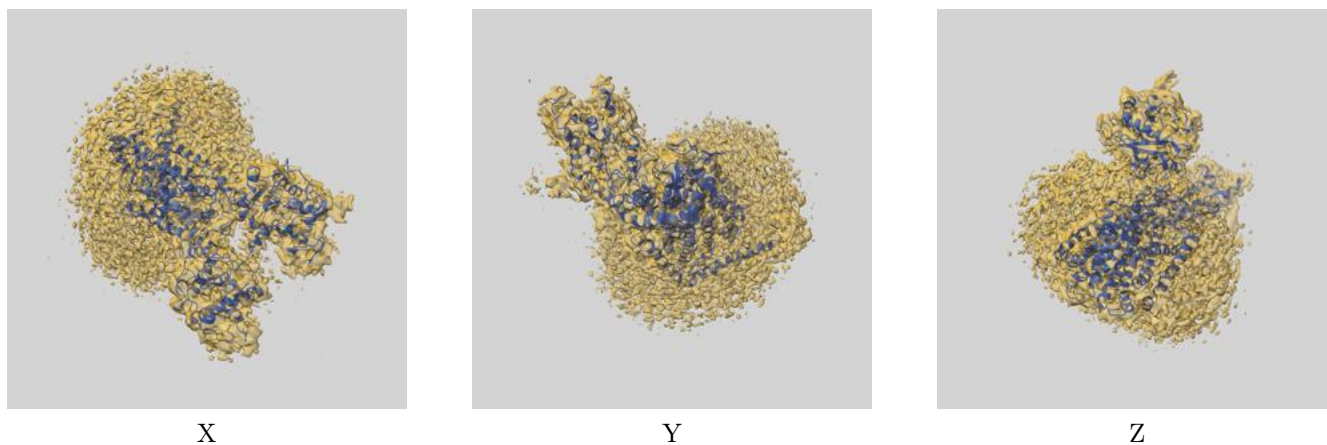
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

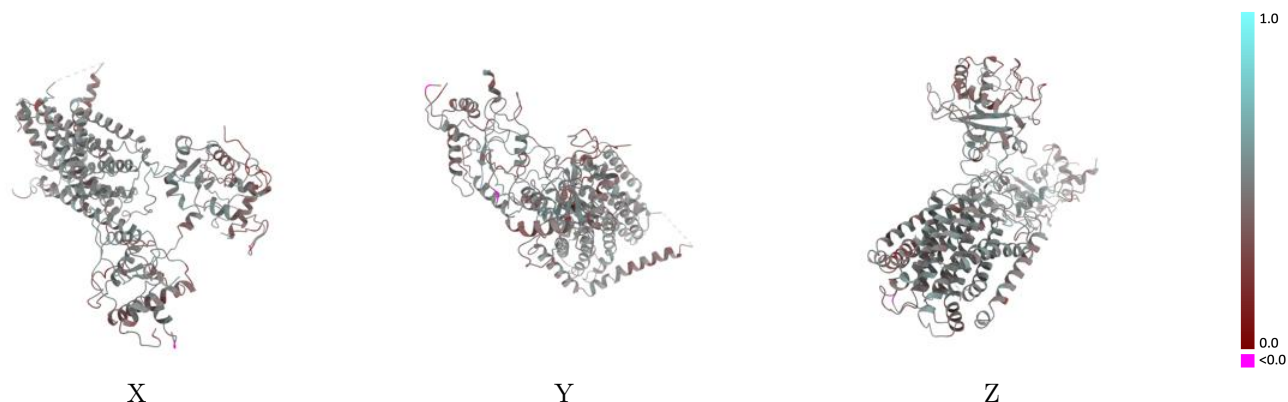
This section contains information regarding the fit between EMDB map EMD-30957 and PDB model 7E2H. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



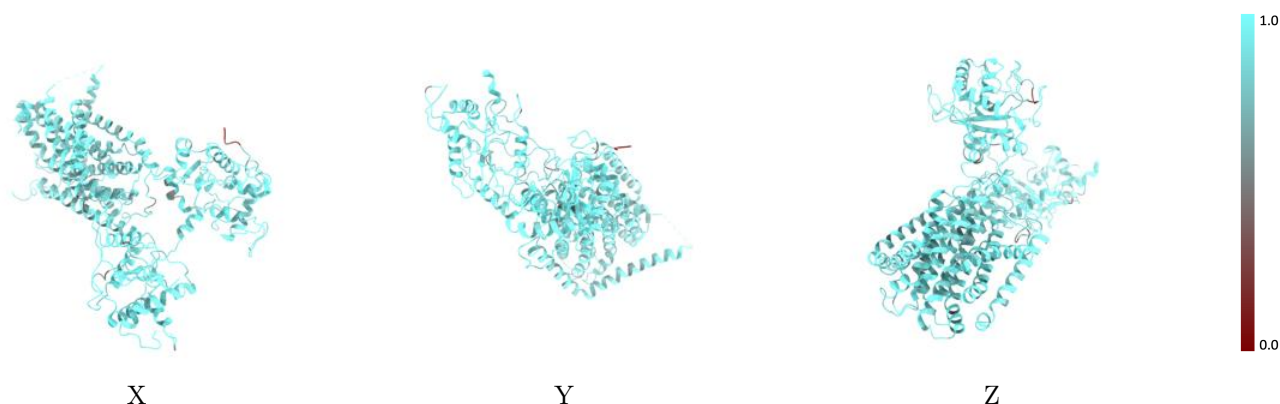
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



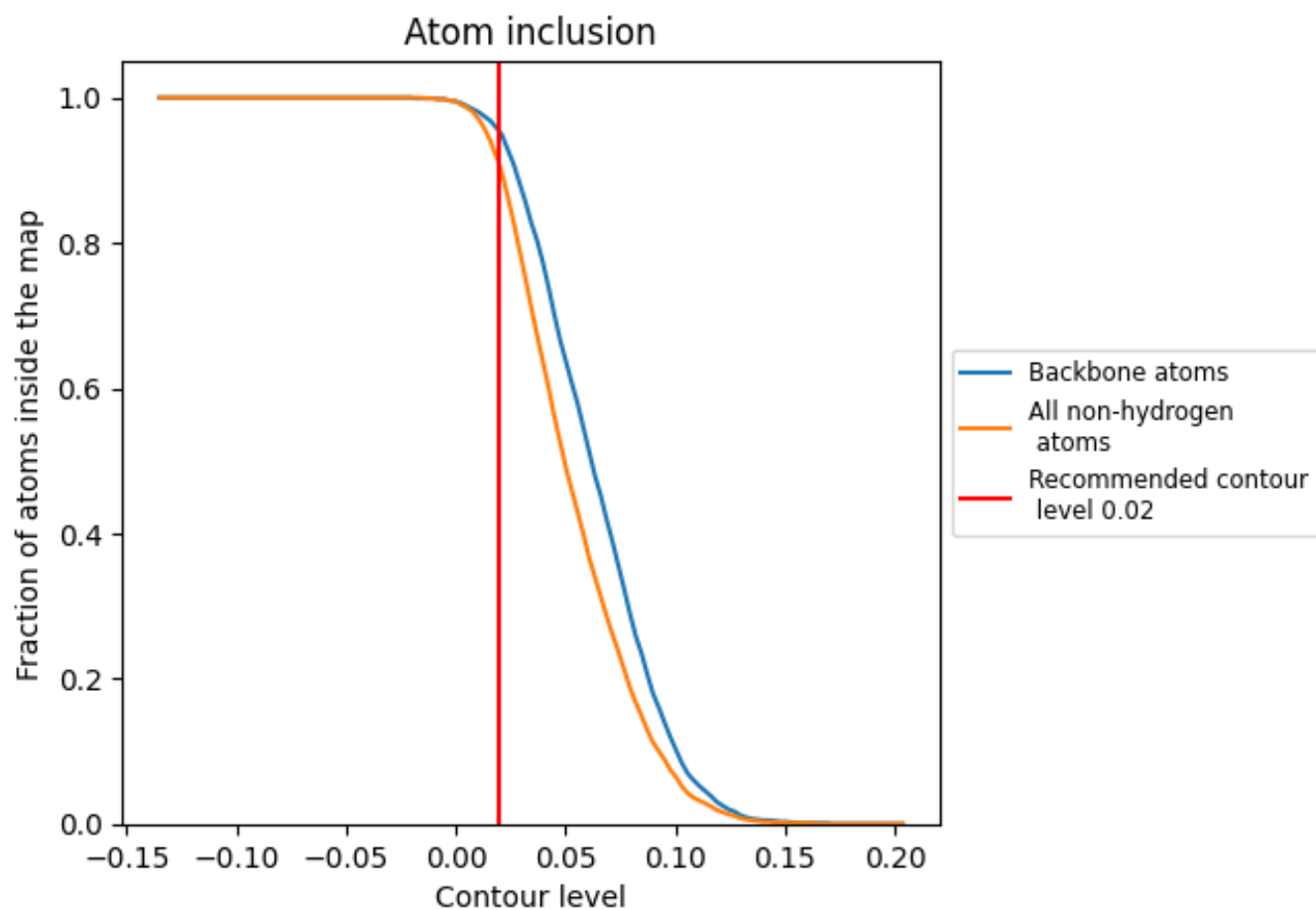
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).






9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9070	 0.4640
D	 0.9120	 0.4700
E	 0.9060	 0.4630

