



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:13 PM UTC

PDB ID : 7WPQ / pdb_00007wpq
EMDB ID : EMD-32688
Title : Cryo-EM structure of VWF D'D3 dimer complexed with D1D2 at 3.27 angstrom resolution (2 units)
Authors : Zeng, J.W.; Shu, Z.M.; Zhou, A.W.
Deposited on : 2022-01-24
Resolution : 3.27 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:

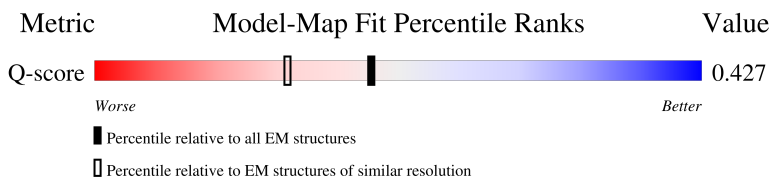
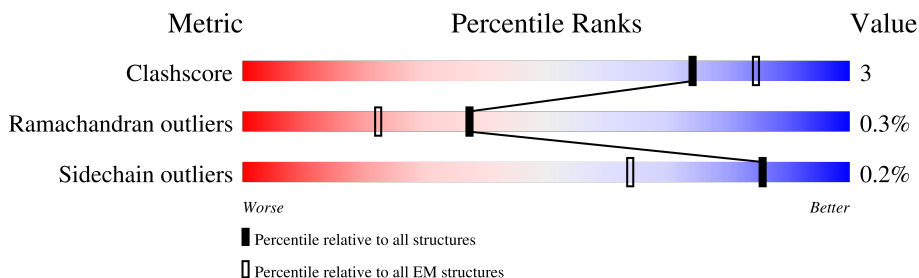
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.27 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14477 (2.77 - 3.76)

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	A	741	
1	B	741	
1	E	741	
1	G	741	

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Mol	Chain	Length	Quality of chain
2	C	490	5% 89% 9%
2	D	490	89% 8%
2	F	490	89% 9%
2	H	490	6% 90% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36576 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 von Willebrand antigen 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	B	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	E	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		
1	G	711	Total	C	N	O	S	0	0
			5421	3353	929	1061	78		

- Molecule 2 is a protein called von Willebrand factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	D	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	F	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		
2	H	478	Total	C	N	O	S	1	0
			3649	2247	631	711	60		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1242	GLY	-	expression tag	UNP P04275
C	1243	LEU	-	expression tag	UNP P04275
C	1244	VAL	-	expression tag	UNP P04275
C	1245	VAL	-	expression tag	UNP P04275
C	1246	PRO	-	expression tag	UNP P04275
C	1247	PRO	-	expression tag	UNP P04275
C	1248	HIS	-	expression tag	UNP P04275
C	1249	HIS	-	expression tag	UNP P04275
C	1250	HIS	-	expression tag	UNP P04275

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1251	HIS	-	expression tag	UNP P04275
C	1252	HIS	-	expression tag	UNP P04275
C	1253	HIS	-	expression tag	UNP P04275
D	1242	GLY	-	expression tag	UNP P04275
D	1243	LEU	-	expression tag	UNP P04275
D	1244	VAL	-	expression tag	UNP P04275
D	1245	VAL	-	expression tag	UNP P04275
D	1246	PRO	-	expression tag	UNP P04275
D	1247	PRO	-	expression tag	UNP P04275
D	1248	HIS	-	expression tag	UNP P04275
D	1249	HIS	-	expression tag	UNP P04275
D	1250	HIS	-	expression tag	UNP P04275
D	1251	HIS	-	expression tag	UNP P04275
D	1252	HIS	-	expression tag	UNP P04275
D	1253	HIS	-	expression tag	UNP P04275
F	1242	GLY	-	expression tag	UNP P04275
F	1243	LEU	-	expression tag	UNP P04275
F	1244	VAL	-	expression tag	UNP P04275
F	1245	VAL	-	expression tag	UNP P04275
F	1246	PRO	-	expression tag	UNP P04275
F	1247	PRO	-	expression tag	UNP P04275
F	1248	HIS	-	expression tag	UNP P04275
F	1249	HIS	-	expression tag	UNP P04275
F	1250	HIS	-	expression tag	UNP P04275
F	1251	HIS	-	expression tag	UNP P04275
F	1252	HIS	-	expression tag	UNP P04275
F	1253	HIS	-	expression tag	UNP P04275
H	1242	GLY	-	expression tag	UNP P04275
H	1243	LEU	-	expression tag	UNP P04275
H	1244	VAL	-	expression tag	UNP P04275
H	1245	VAL	-	expression tag	UNP P04275
H	1246	PRO	-	expression tag	UNP P04275
H	1247	PRO	-	expression tag	UNP P04275
H	1248	HIS	-	expression tag	UNP P04275
H	1249	HIS	-	expression tag	UNP P04275
H	1250	HIS	-	expression tag	UNP P04275
H	1251	HIS	-	expression tag	UNP P04275
H	1252	HIS	-	expression tag	UNP P04275
H	1253	HIS	-	expression tag	UNP P04275

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	
3	H	1	Total	C	N	O	0
			14	8	1	5	
3	H	1	Total	C	N	O	0
			14	8	1	5	
3	H	1	Total	C	N	O	0
			14	8	1	5	

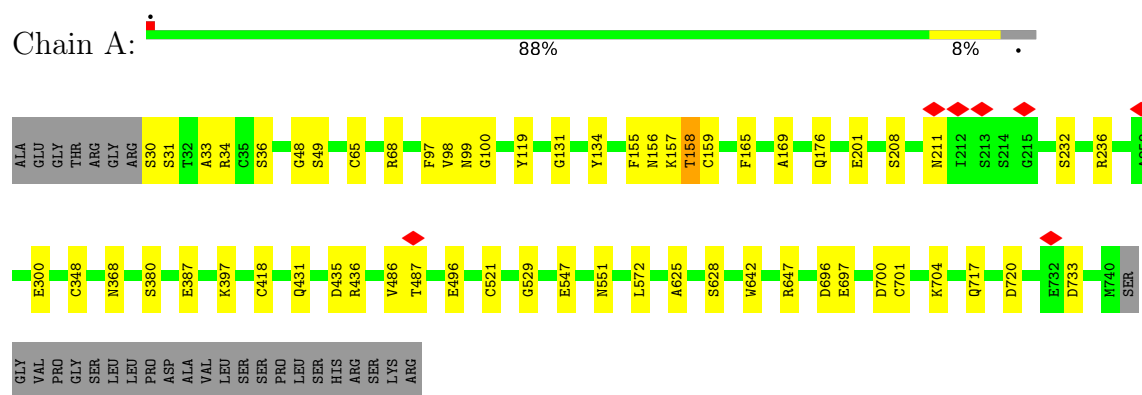
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total	Ca	0
			2	2	
4	B	2	Total	Ca	0
			2	2	
4	C	2	Total	Ca	0
			2	2	
4	D	2	Total	Ca	0
			2	2	
4	E	2	Total	Ca	0
			2	2	
4	F	2	Total	Ca	0
			2	2	
4	G	2	Total	Ca	0
			2	2	
4	H	2	Total	Ca	0
			2	2	

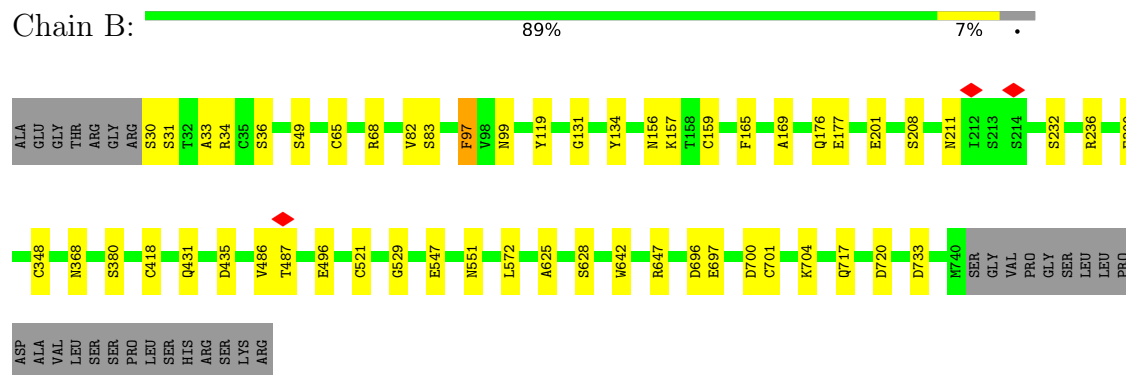
3 Residue-property plots

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.

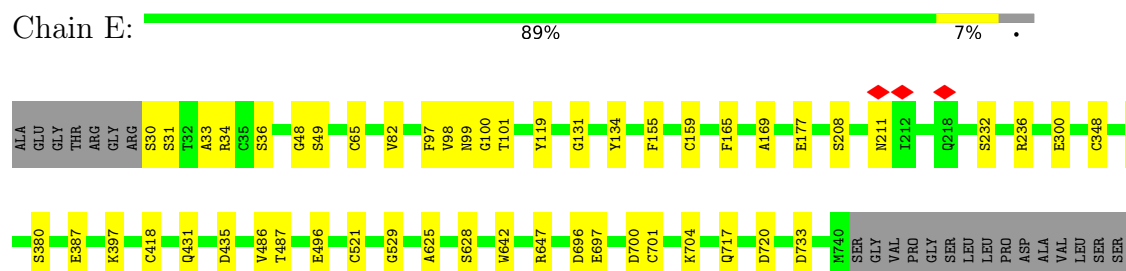
- Molecule 1: von Willebrand antigen 2



- Molecule 1: von Willebrand antigen 2



- Molecule 1: von Willebrand antigen 2



PRO
LEU
SER
HIS
ARG
SER
LYS
ARG

- Molecule 1: von Willebrand antigen 2

Chain G:  88% 8%

ALA GLU GLY THR ARG GLY ARG
S30 A33 R34 C35 S36 G48 S49 G63 G64 C65 S83 F97 V98 N99 T100 T101 Y119 G131 Y134 G135 L150 R153 Y154 F155 N156 T157 T158 C159 N164 F165 N166 A169 S208 N211 I212 S232 R236

G259 E300 C348 N368 S380 C418 Q431 D435 R436 V486 T487 E496 C521 N529 E547 N551 A625 S628 W642 R647 D696 E697 D700 C701 K704 Q717 D720 D733 N740 SER GLY VAL PRO GLY SER

LEU PRO ASP ALA VAL LEU SER PRO LEU HIS ARG SER LYS ARG

- Molecule 2: von Willebrand factor

Chain C:  5% 89% 9%

S764 L765 C776 D779 L786 T789 C792 C804 W805 S806 L824 V850 C851 Q852 D853 R854 R855 G880 C887 E888 N901 N911 G931 R945 K991 Q1003 N1004 S1009 S1010 N1011 E1016 V1019 N1023 F1068 S1093 V1118

C1130 N1134 E1143 W1144 R1145 Y1146 N1147 S1148 P1197 E1200 V1201 A1202 G1203 R1204 R1205 S1208 N1215 P1216 S1217 D1218 P1219 E1220 H1221 C1222 Q1223 L1232 T1233 C1234 E1235 A1236 C1237 E1238 E1239 P1240 G1241 GLY LEU VAL VAL PRO HIS HIS HIS HIS HIS HIS

- Molecule 2: von Willebrand factor

Chain D:  89% 8%

S764 C776 C792 C804 W805 S806 K834 Y836 V850 R854 N857 G880 G887 E888 N901 N911 G931 R945 K991 Q1003 N1004 S1009 S1010 N1011 E1016 V1019 D1020 F1021 G1022 S1024 Q1053 S1093 R1121 C1130 R1136

Y1146 N1147 S1148 E1171 P1197 E1200 V1201 A1202 E1203 R1204 R1205 S1208 V1212 T1213 L1214 M1215 P1216 S1217 D1218 P1219 E1220 H1221 L1232 A1236 C1237 Q1238 E1239 P1240 G1241 GLY LEU VAL VAL PRO HIS HIS HIS HIS HIS HIS

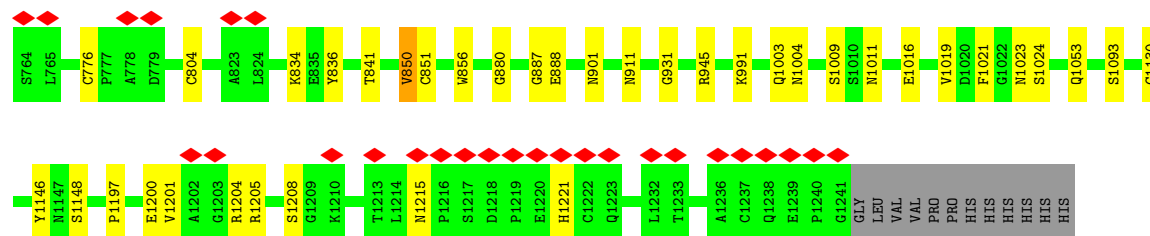
- Molecule 2: von Willebrand factor

Chain F:  89% 9%

S764 L765 C776 C792 C804 K834 E835 Y836 R854 N857 C858 G880 G887 E888 N901 N911 G931 R945 K991 Q1003 N1004 S1009 S1010 N1011 E1016 V1019 D1020 F1021 G1022 N1023 S1024 Q1053 F1068 S1093 V1118 R1121 C1130

Y1146 N1147 S1148 P1151 H1174 P1197 E1200 V1201 A1202 G1203 R1204 R1205 S1208 T1213 L1214 N1215 P1216 S1217 D1218 P1219 E1220 H1221 L1232 T1233 C1234 E1235 A1236 C1237 E1238 E1239 P1240 G1241 GLY LEU VAL VAL PRO HIS HIS HIS HIS HIS HIS

Chain H:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	539243	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)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.111	Depositor
Minimum map value	-0.054	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	189.15001, 290.03, 206.61	wwPDB
Map dimensions	195, 299, 213	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.97, 0.96999997, 0.97	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: NAG, CA

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	0.32	0/5547	0.51	0/7520
1	B	0.31	0/5547	0.51	0/7520
1	E	0.31	0/5547	0.51	0/7520
1	G	0.32	0/5547	0.51	0/7520
2	C	0.31	0/3728	0.50	0/5066
2	D	0.29	0/3728	0.49	0/5066
2	F	0.29	0/3728	0.49	0/5066
2	H	0.30	0/3728	0.50	0/5066
All	All	0.31	0/37100	0.50	0/50344

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	A	5421	0	5000	38	0
1	B	5421	0	5000	34	0
1	E	5421	0	5001	32	0
1	G	5421	0	5001	35	0
2	C	3649	0	3441	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3649	0	3441	24	0
2	F	3649	0	3441	27	0
2	H	3649	0	3441	23	0
3	A	28	0	26	2	0
3	B	28	0	26	2	0
3	C	42	0	39	0	0
3	D	42	0	39	1	0
3	E	28	0	26	4	0
3	F	42	0	39	1	0
3	G	28	0	26	1	0
3	H	42	0	39	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
4	G	2	0	0	0	0
4	H	2	0	0	0	0
All	All	36576	0	34026	223	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 223 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:156:ASN:O	1:B:157:LYS:HD2	1.77	0.84
3:E:801:NAG:O7	3:E:801:NAG:H3	1.82	0.78
2:C:1009:SER:OG	2:C:1011:ASN:OD1	2.02	0.77
2:C:850:VAL:HG13	2:C:852:GLN:HE22	1.50	0.76
2:F:1009:SER:OG	2:F:1011:ASN:OD1	2.02	0.76

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	709/741 (96%)	641 (90%)	65 (9%)	3 (0%)	30	59
1	B	709/741 (96%)	639 (90%)	69 (10%)	1 (0%)	48	76
1	E	709/741 (96%)	642 (91%)	66 (9%)	1 (0%)	48	76
1	G	709/741 (96%)	643 (91%)	64 (9%)	2 (0%)	36	66
2	C	477/490 (97%)	423 (89%)	52 (11%)	2 (0%)	30	59
2	D	477/490 (97%)	423 (89%)	53 (11%)	1 (0%)	43	70
2	F	477/490 (97%)	422 (88%)	54 (11%)	1 (0%)	43	70
2	H	477/490 (97%)	425 (89%)	51 (11%)	1 (0%)	43	70
All	All	4744/4924 (96%)	4258 (90%)	474 (10%)	12 (0%)	37	66

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	156	ASN
1	A	158	THR
1	B	99	ASN
1	G	158	THR
2	C	854	ARG

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	599/628 (95%)	597 (100%)	2 (0%)	86	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	599/628 (95%)	597 (100%)	2 (0%)	86	86
1	E	599/628 (95%)	598 (100%)	1 (0%)	87	87
1	G	599/628 (95%)	598 (100%)	1 (0%)	87	87
2	C	423/436 (97%)	423 (100%)	0	100	100
2	D	423/436 (97%)	422 (100%)	1 (0%)	87	87
2	F	423/436 (97%)	423 (100%)	0	100	100
2	H	423/436 (97%)	422 (100%)	1 (0%)	87	87
All	All	4088/4256 (96%)	4080 (100%)	8 (0%)	85	87

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	850	VAL
1	G	348	CYS
2	D	857	ASN
1	B	348	CYS
1	E	348	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	1134	ASN
1	G	421	HIS
2	F	1176	HIS
1	G	566	HIS
2	D	952	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 16 are monoatomic - leaving 20 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	G	802	1	14,14,15	0.42	0	17,19,21	0.76	0
3	NAG	E	801	1	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	C	1302	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	G	801	1	14,14,15	0.39	0	17,19,21	0.76	0
3	NAG	A	801	1	14,14,15	0.28	0	17,19,21	0.87	1 (5%)
3	NAG	C	1301	2	14,14,15	0.39	0	17,19,21	0.53	0
3	NAG	F	1301	2	14,14,15	0.39	0	17,19,21	0.53	0
3	NAG	F	1302	2	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	H	1301	2	14,14,15	0.39	0	17,19,21	0.54	0
3	NAG	F	1303	2	14,14,15	0.41	0	17,19,21	0.76	0
3	NAG	H	1302	2	14,14,15	0.42	0	17,19,21	0.76	0
3	NAG	E	802	1	14,14,15	0.34	0	17,19,21	0.54	0
3	NAG	D	1301	2	14,14,15	0.38	0	17,19,21	0.53	0
3	NAG	D	1302	2	14,14,15	0.31	0	17,19,21	0.60	0
3	NAG	B	801	1	14,14,15	0.43	0	17,19,21	0.75	0
3	NAG	D	1303	2	14,14,15	0.40	0	17,19,21	0.76	0
3	NAG	B	802	1	14,14,15	0.40	0	17,19,21	0.75	0
3	NAG	H	1303	2	14,14,15	0.41	0	17,19,21	0.76	0
3	NAG	A	802	1	14,14,15	0.33	0	17,19,21	0.81	2 (11%)
3	NAG	C	1303	2	14,14,15	0.40	0	17,19,21	0.75	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	NAG	G	802	1	-	2/6/23/26	0/1/1/1
3	NAG	E	801	1	-	3/6/23/26	0/1/1/1
3	NAG	C	1302	2	-	0/6/23/26	0/1/1/1
3	NAG	G	801	1	-	1/6/23/26	0/1/1/1
3	NAG	A	801	1	-	3/6/23/26	0/1/1/1
3	NAG	C	1301	2	-	2/6/23/26	0/1/1/1
3	NAG	F	1301	2	-	2/6/23/26	0/1/1/1
3	NAG	F	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	H	1301	2	-	2/6/23/26	0/1/1/1
3	NAG	F	1303	2	-	1/6/23/26	0/1/1/1
3	NAG	H	1302	2	-	1/6/23/26	0/1/1/1
3	NAG	E	802	1	-	3/6/23/26	0/1/1/1
3	NAG	D	1301	2	-	2/6/23/26	0/1/1/1
3	NAG	D	1302	2	-	4/6/23/26	0/1/1/1
3	NAG	B	801	1	-	2/6/23/26	0/1/1/1
3	NAG	D	1303	2	-	3/6/23/26	0/1/1/1
3	NAG	B	802	1	-	1/6/23/26	0/1/1/1
3	NAG	H	1303	2	-	2/6/23/26	0/1/1/1
3	NAG	A	802	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1303	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	801	NAG	C1-O5-C5	2.78	115.91	112.19
3	A	802	NAG	C2-N2-C7	-2.06	120.14	122.90
3	A	802	NAG	C4-C3-C2	-2.04	108.03	111.02

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

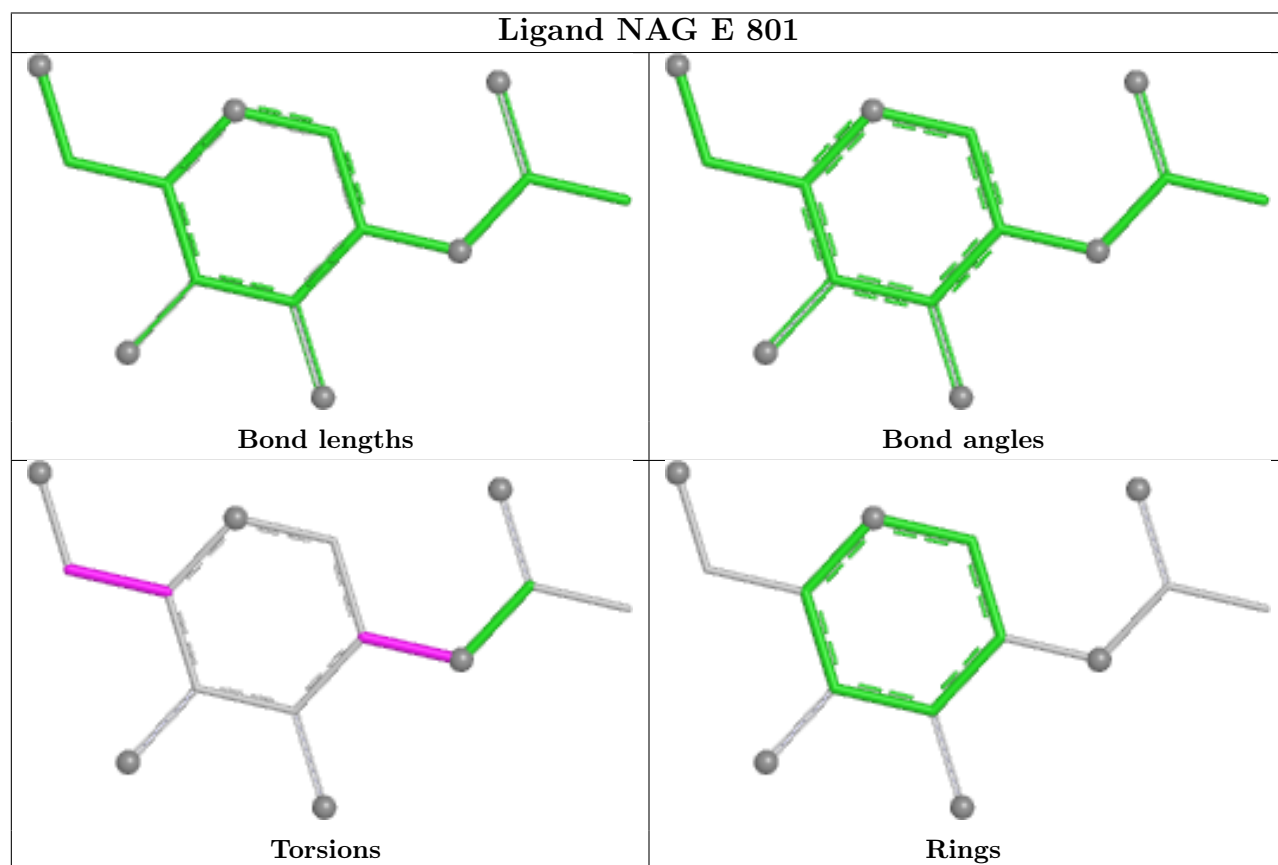
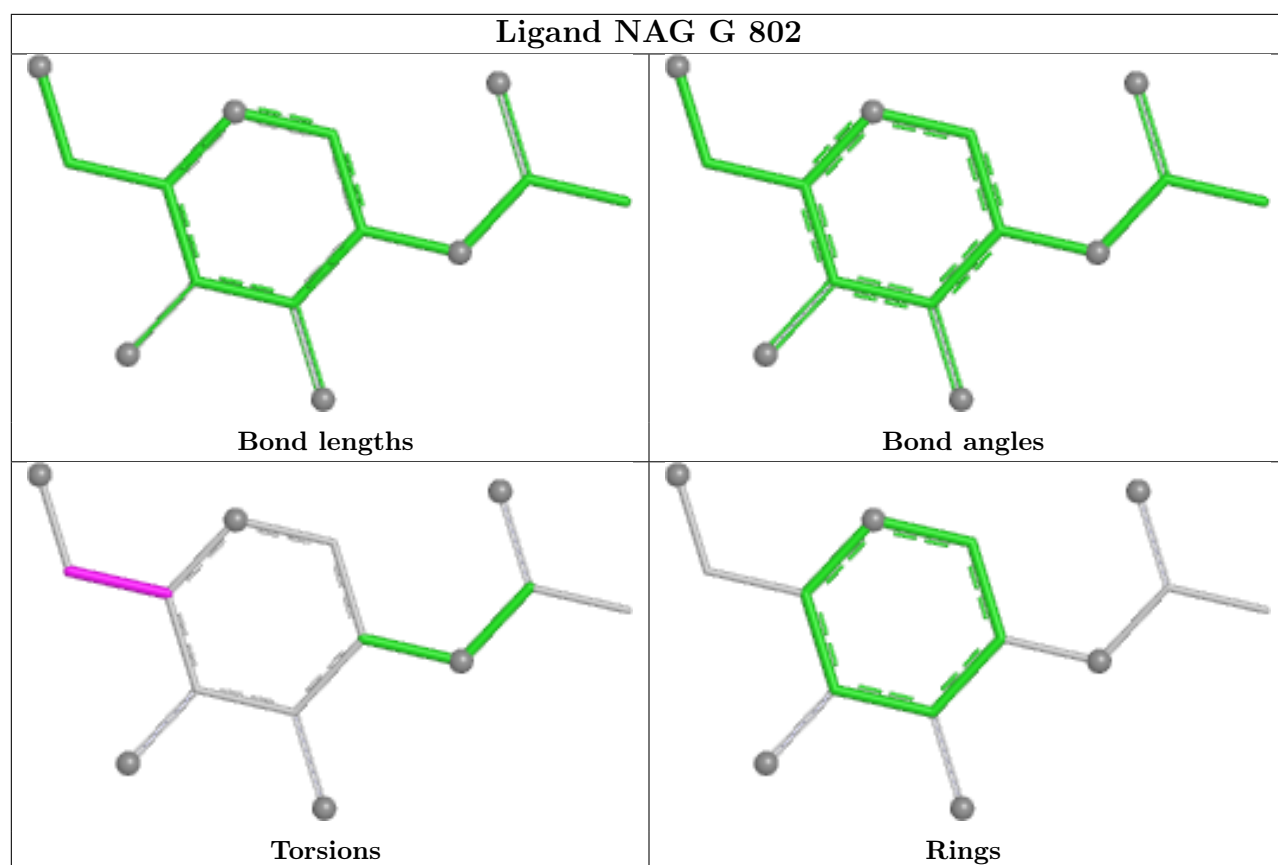
Mol	Chain	Res	Type	Atoms
3	A	801	NAG	C3-C2-N2-C7
3	A	802	NAG	C8-C7-N2-C2
3	A	802	NAG	O7-C7-N2-C2
3	D	1302	NAG	C1-C2-N2-C7
3	D	1302	NAG	O7-C7-N2-C2

There are no ring outliers.

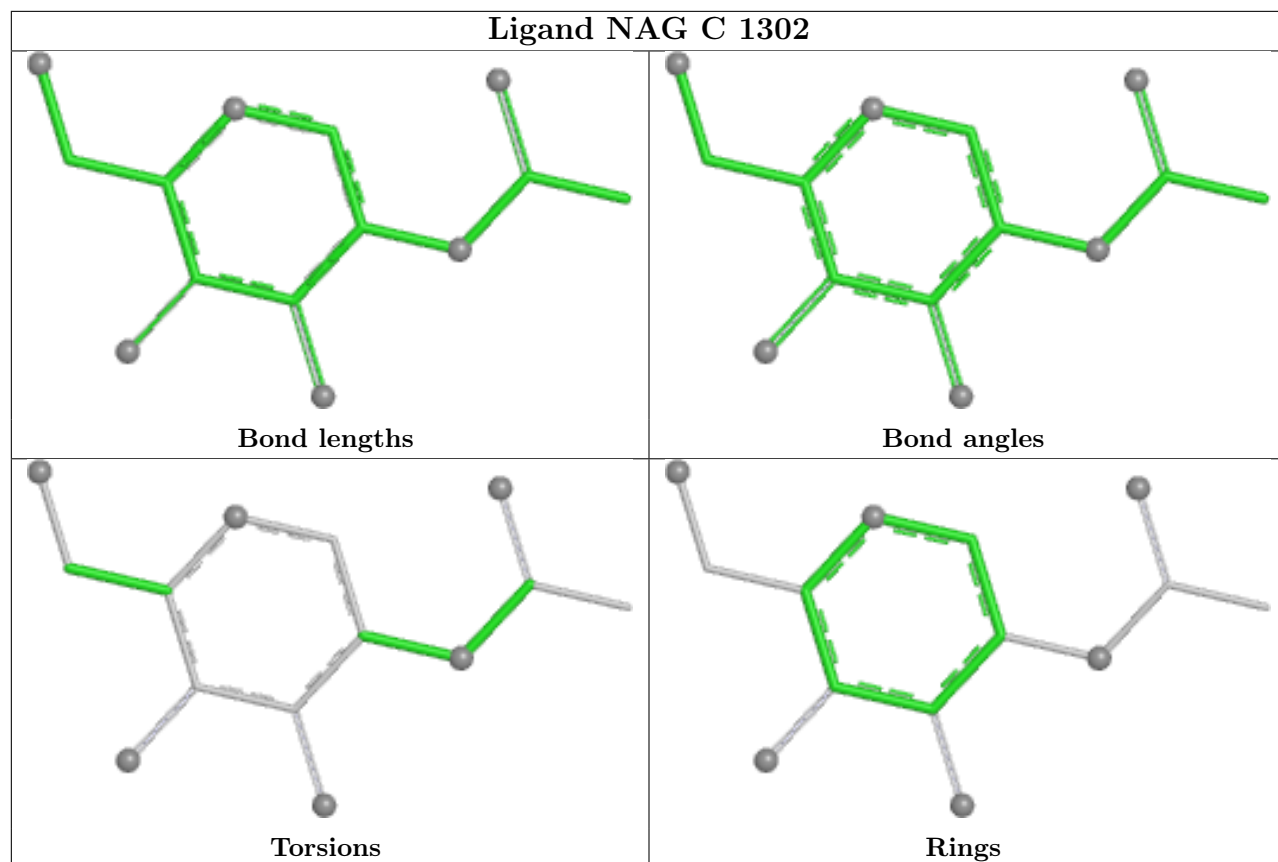
7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	802	NAG	1	0
3	E	801	NAG	2	0
3	F	1303	NAG	1	0
3	E	802	NAG	2	0
3	D	1303	NAG	1	0
3	B	802	NAG	2	0
3	A	802	NAG	2	0

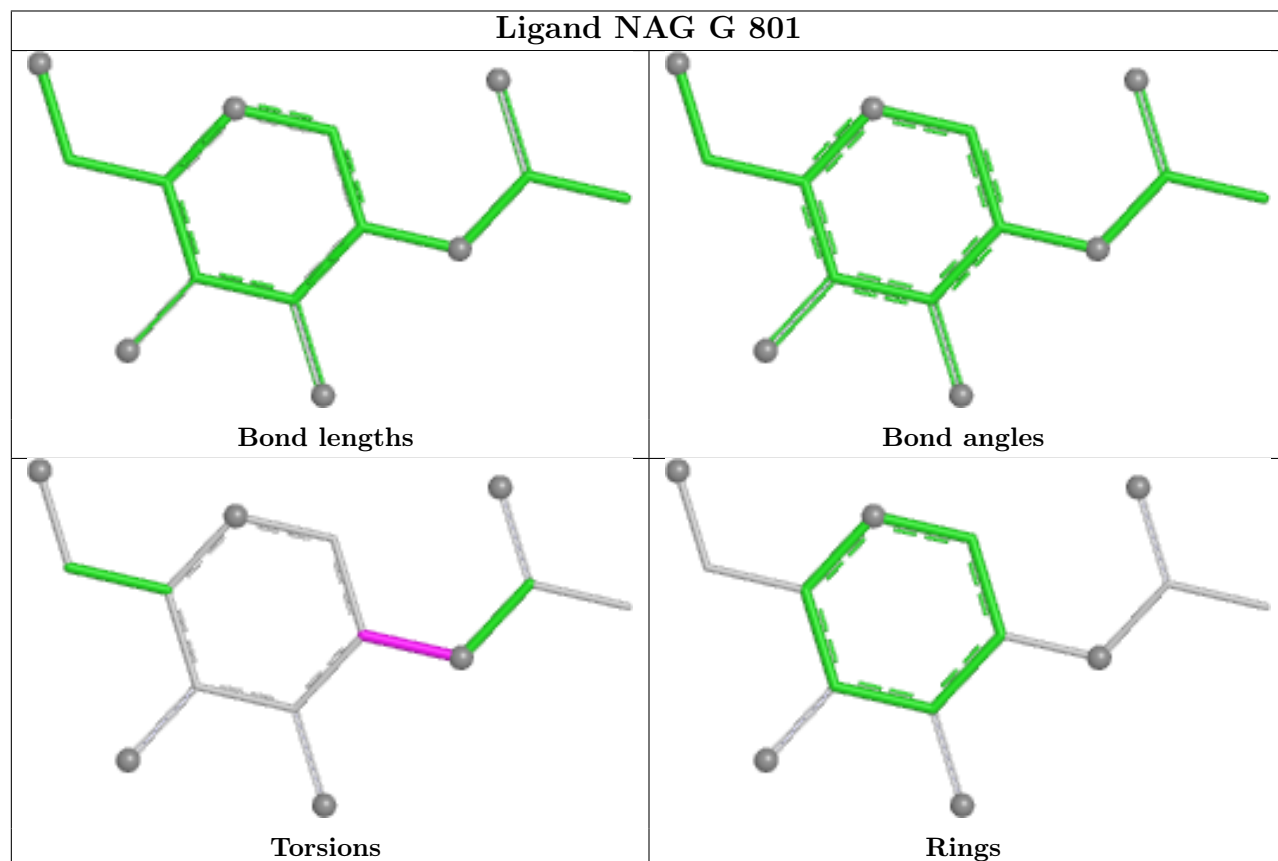
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

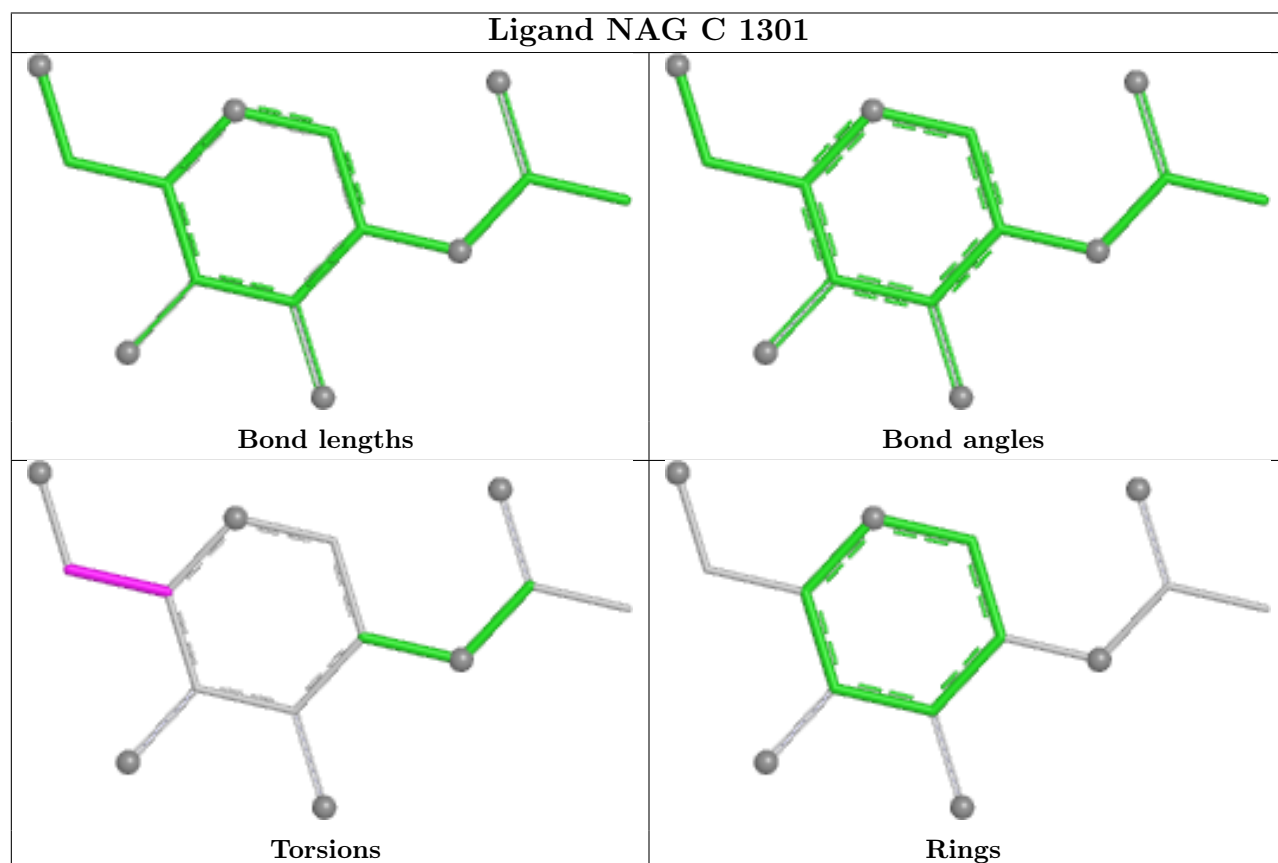
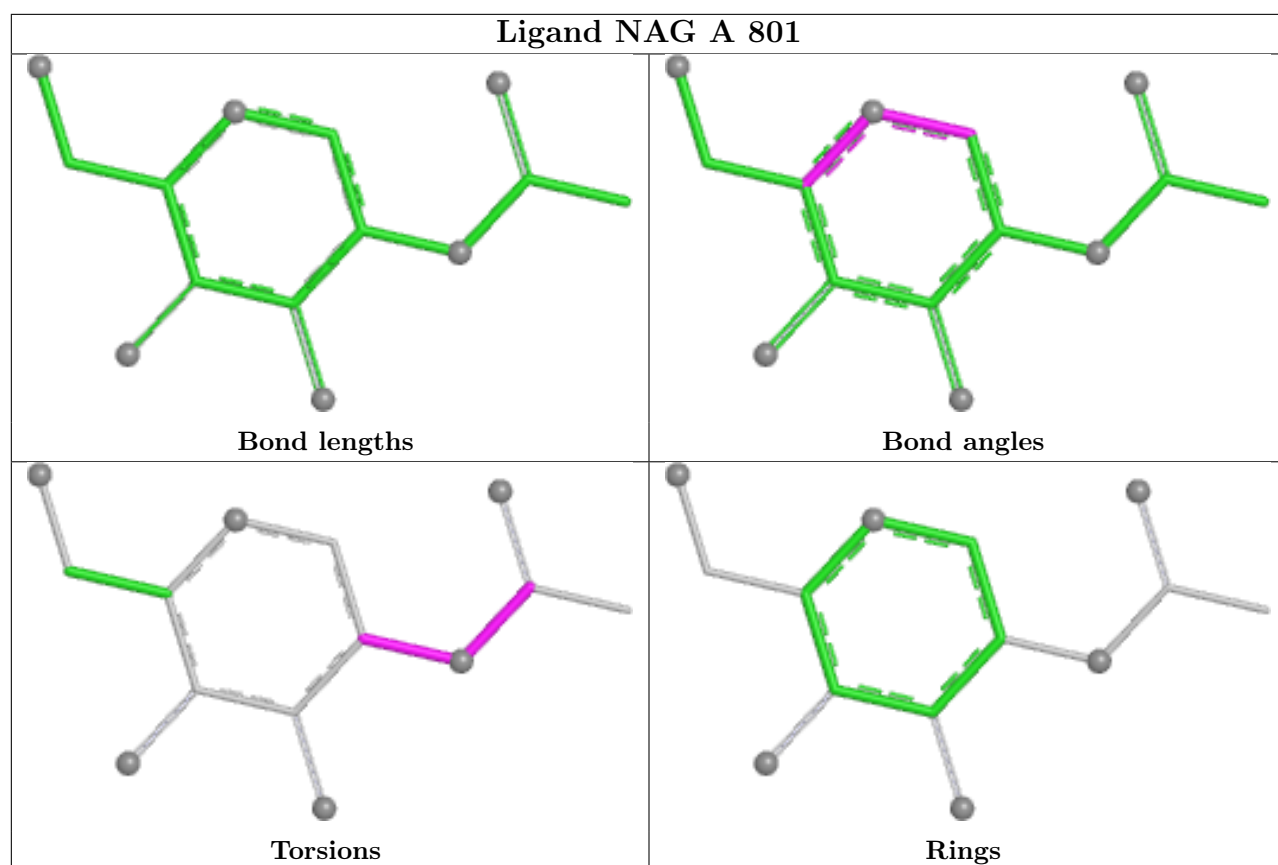


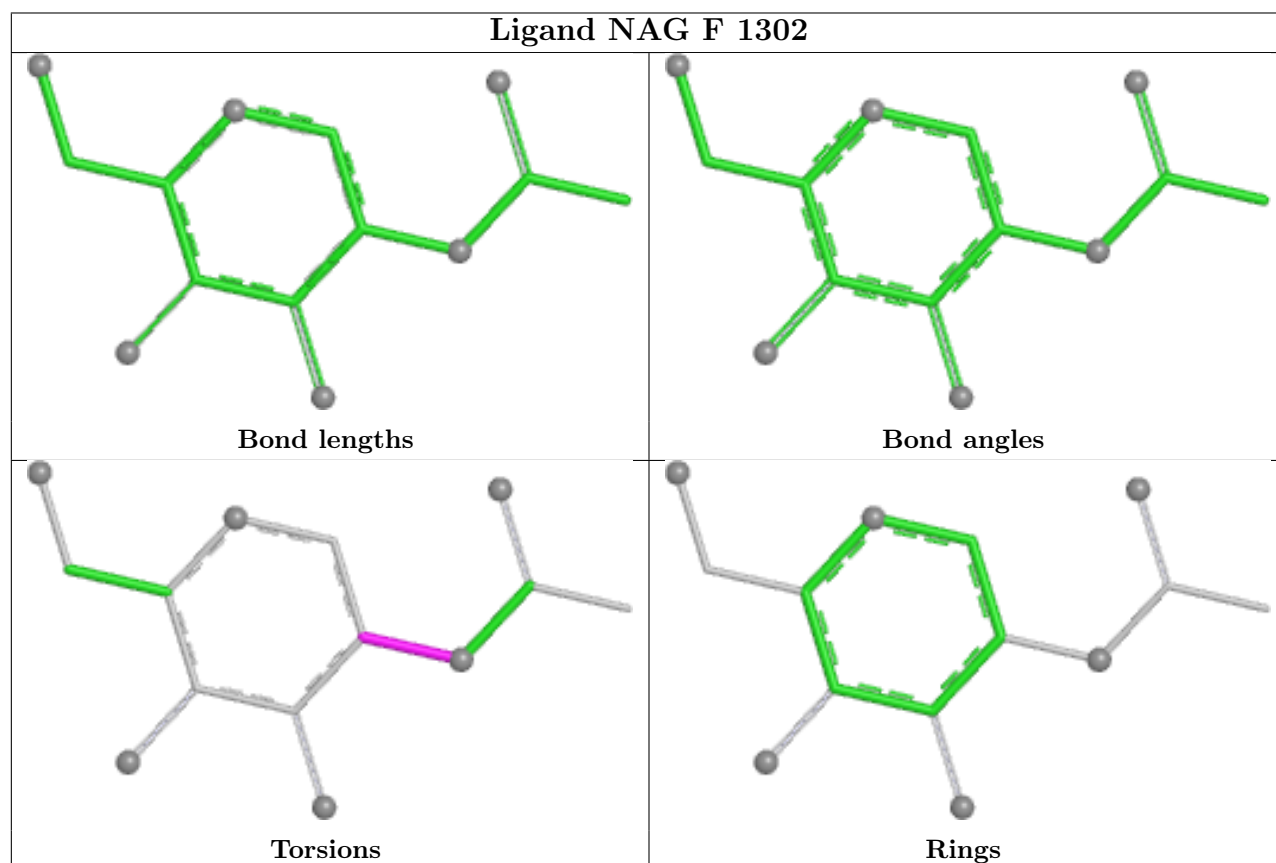
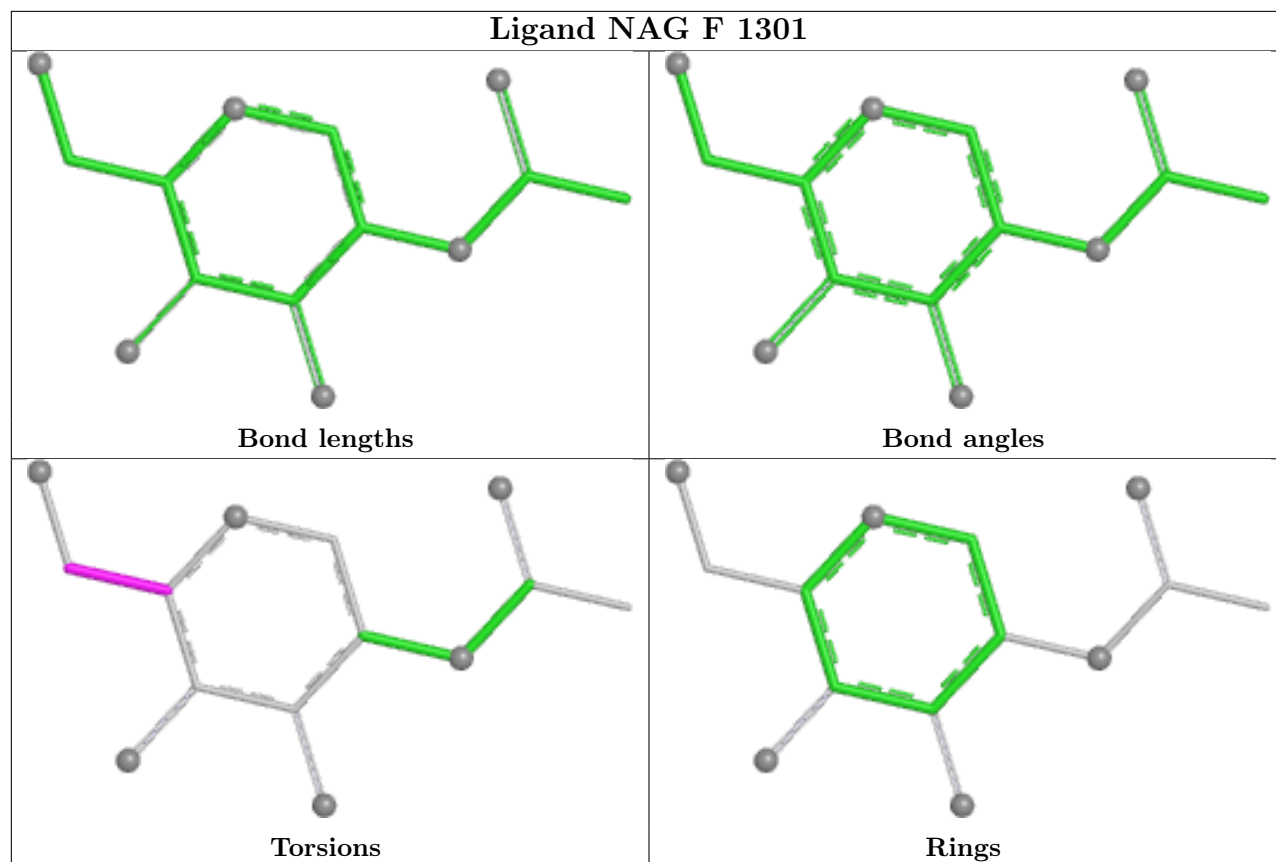
Ligand NAG C 1302



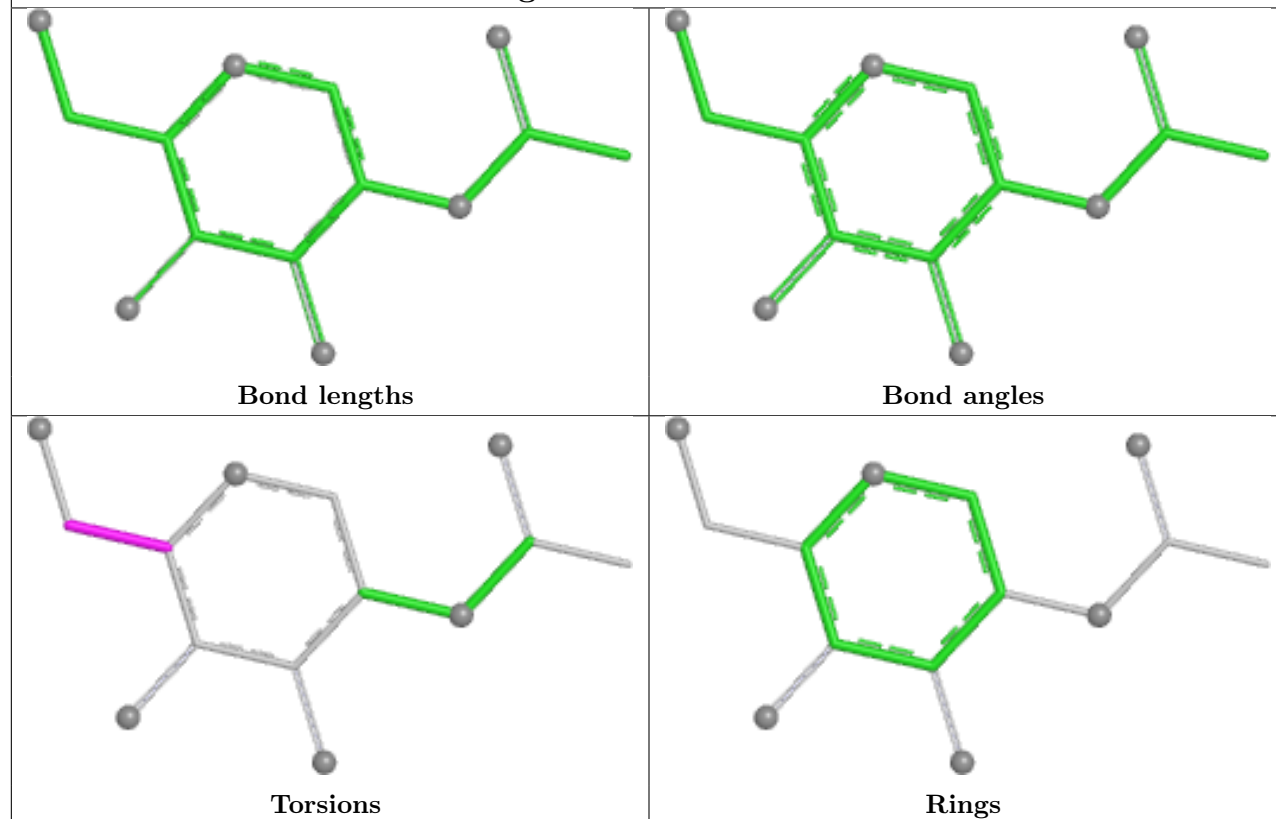
Ligand NAG G 801



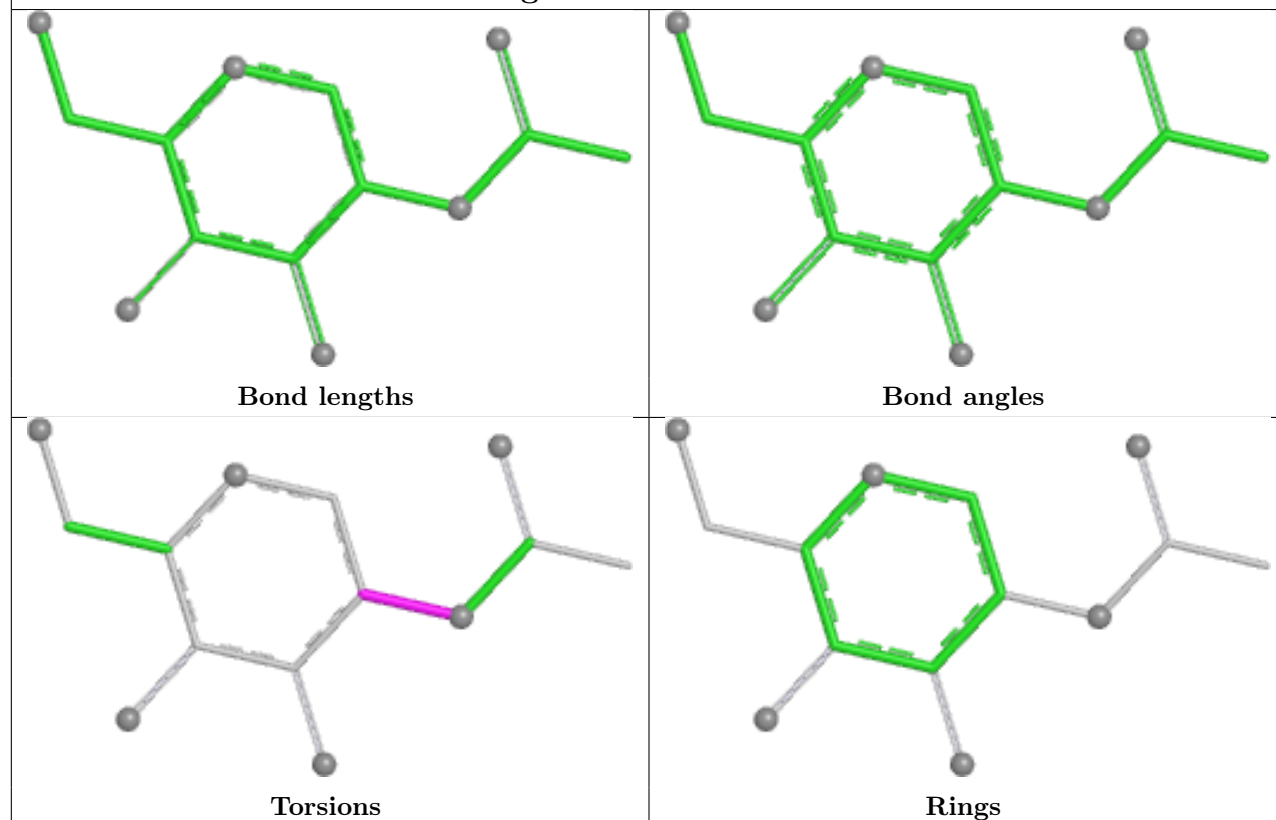




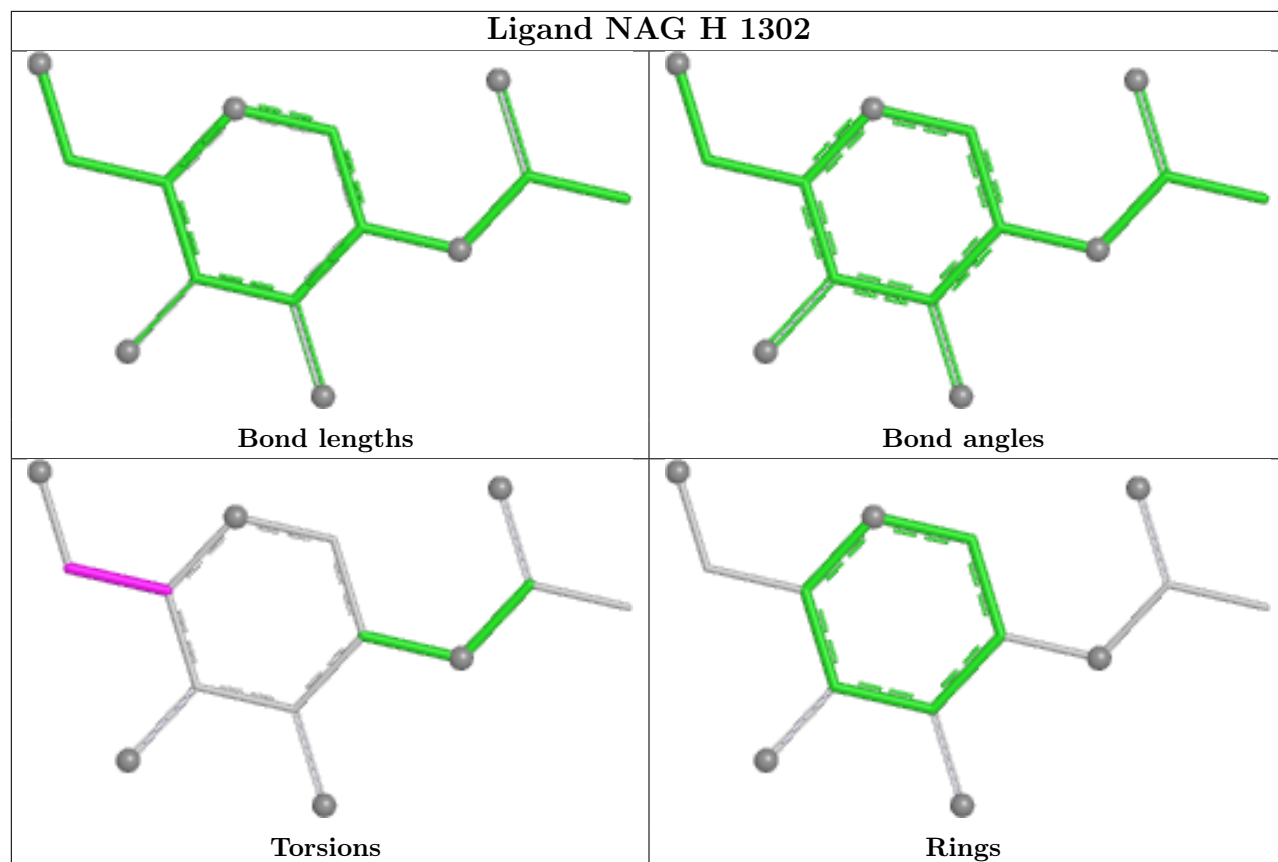
Ligand NAG H 1301



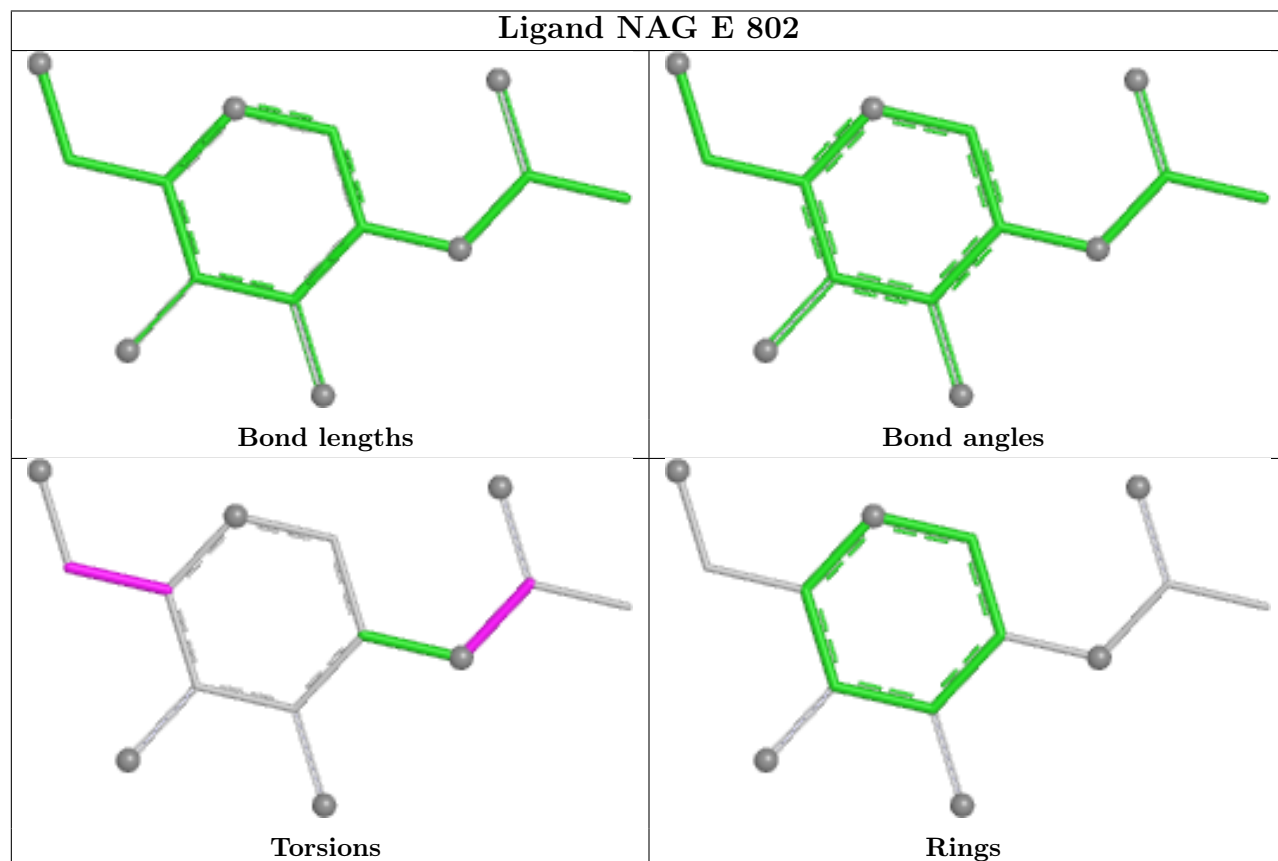
Ligand NAG F 1303

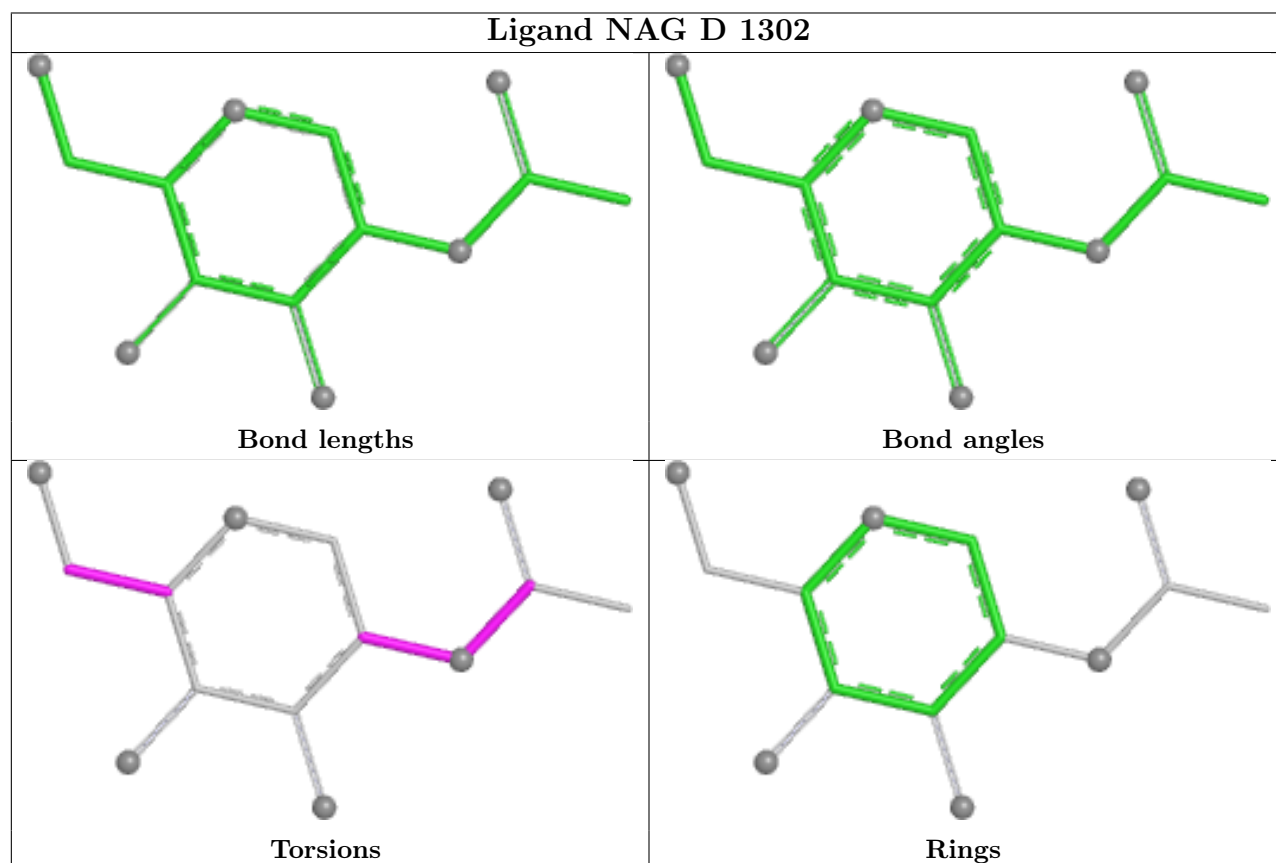
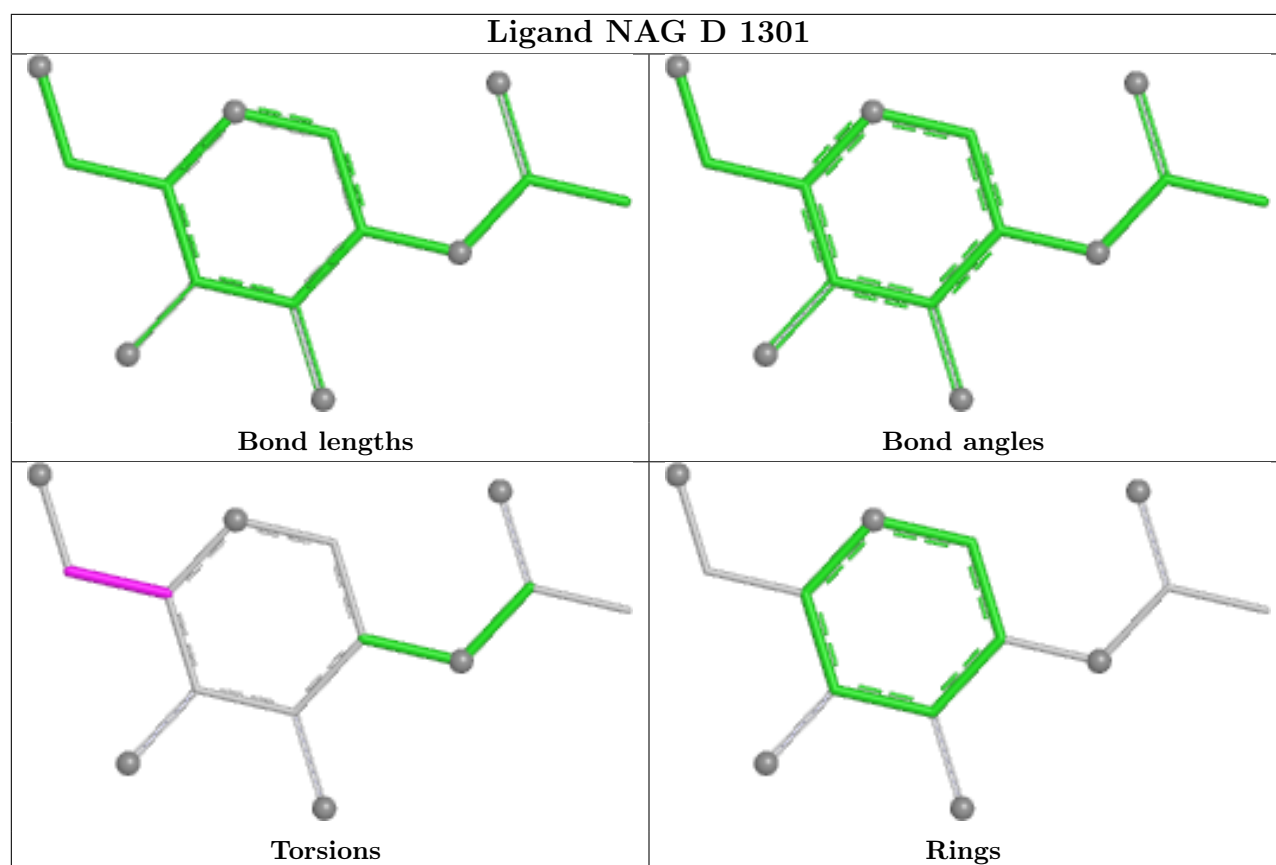


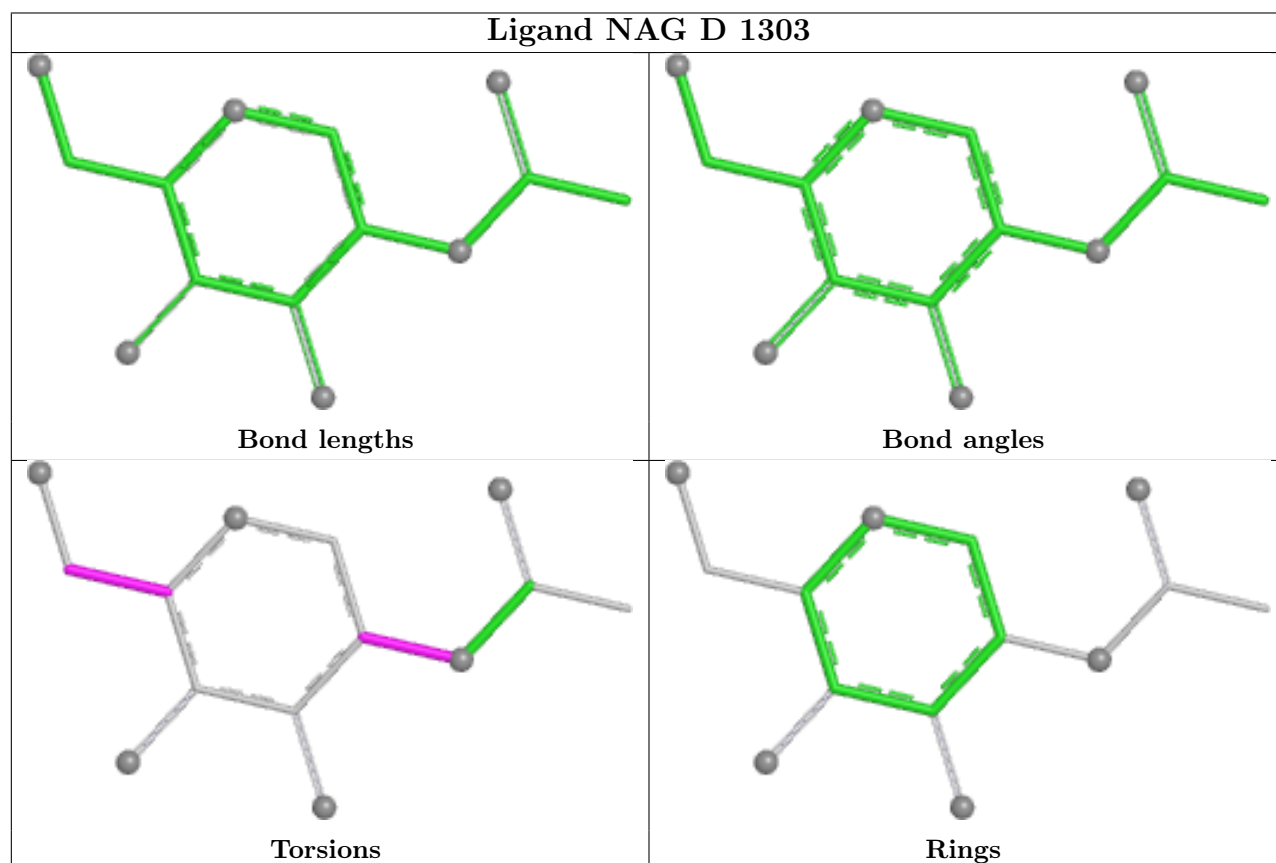
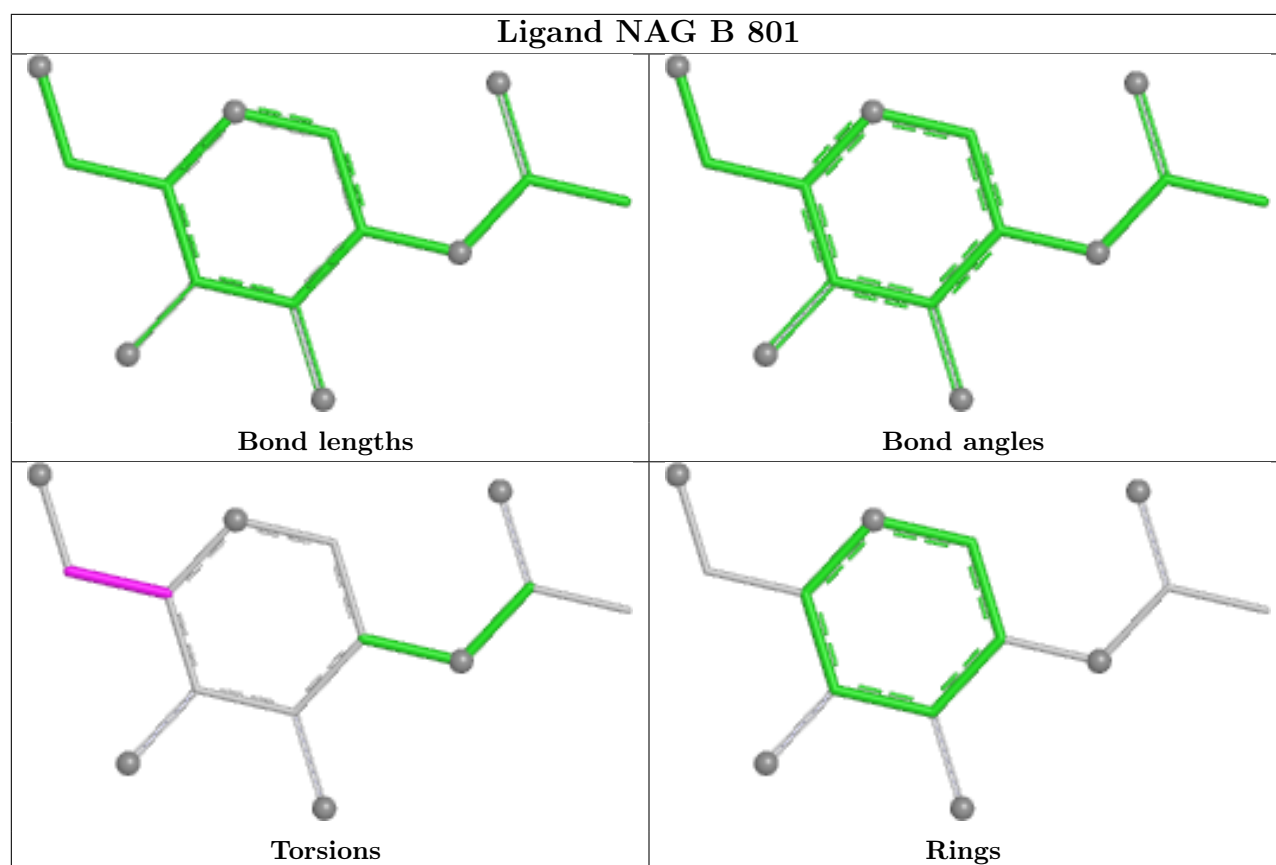
Ligand NAG H 1302

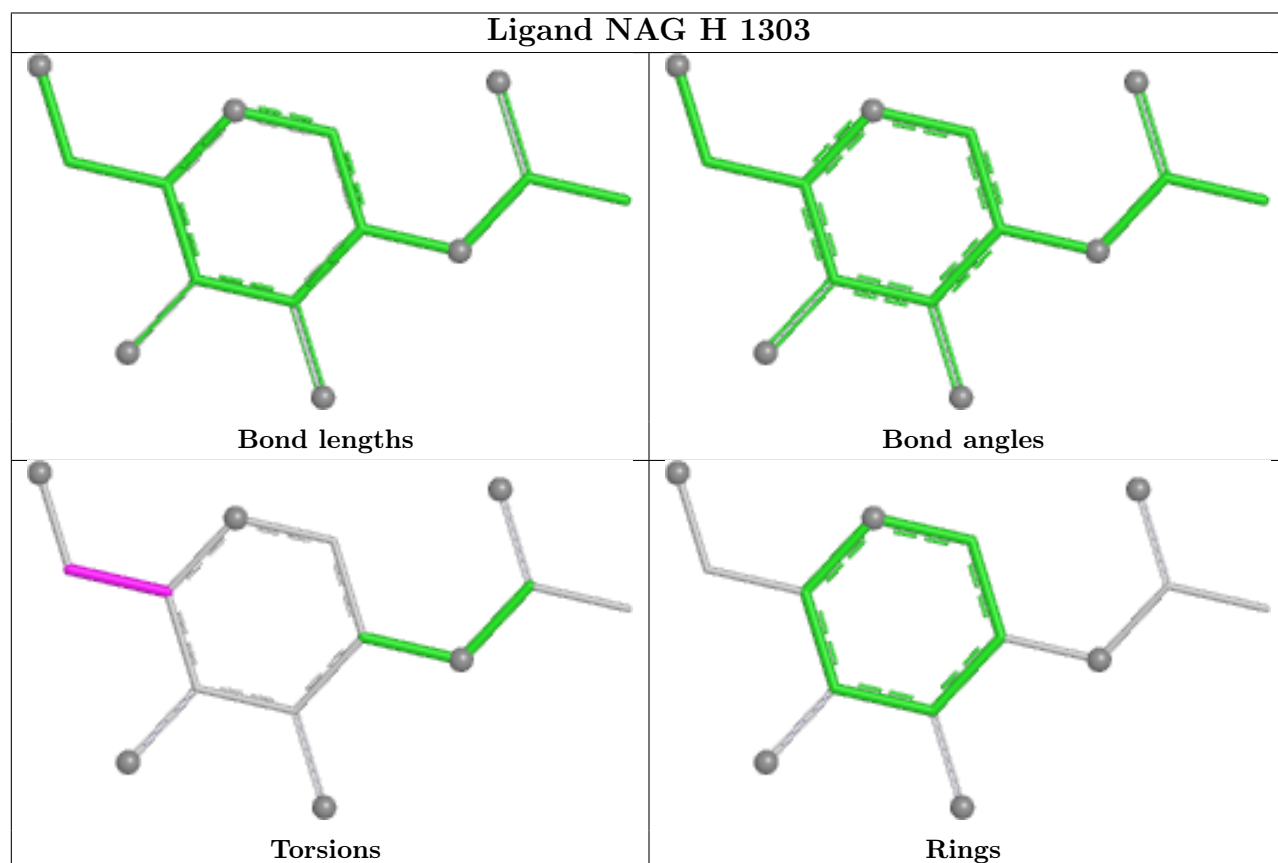
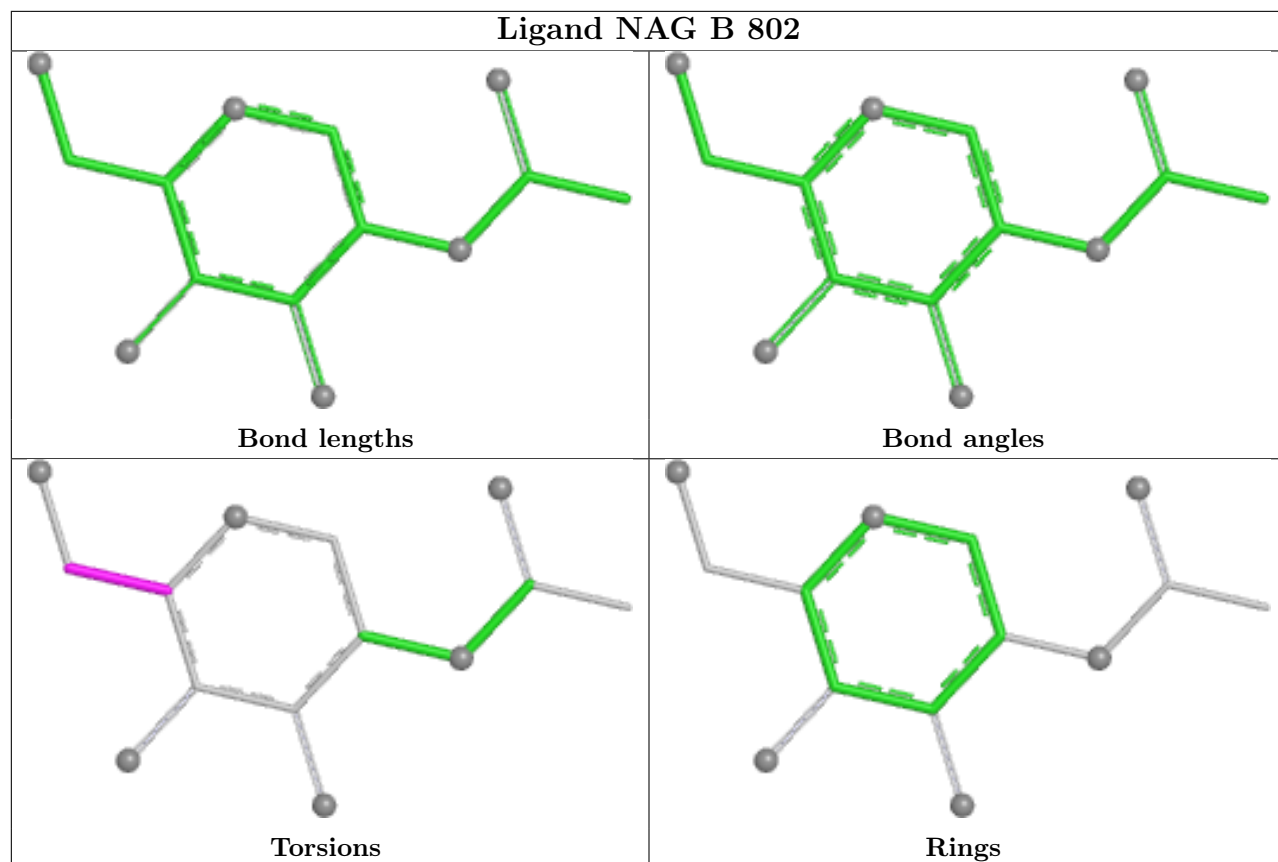


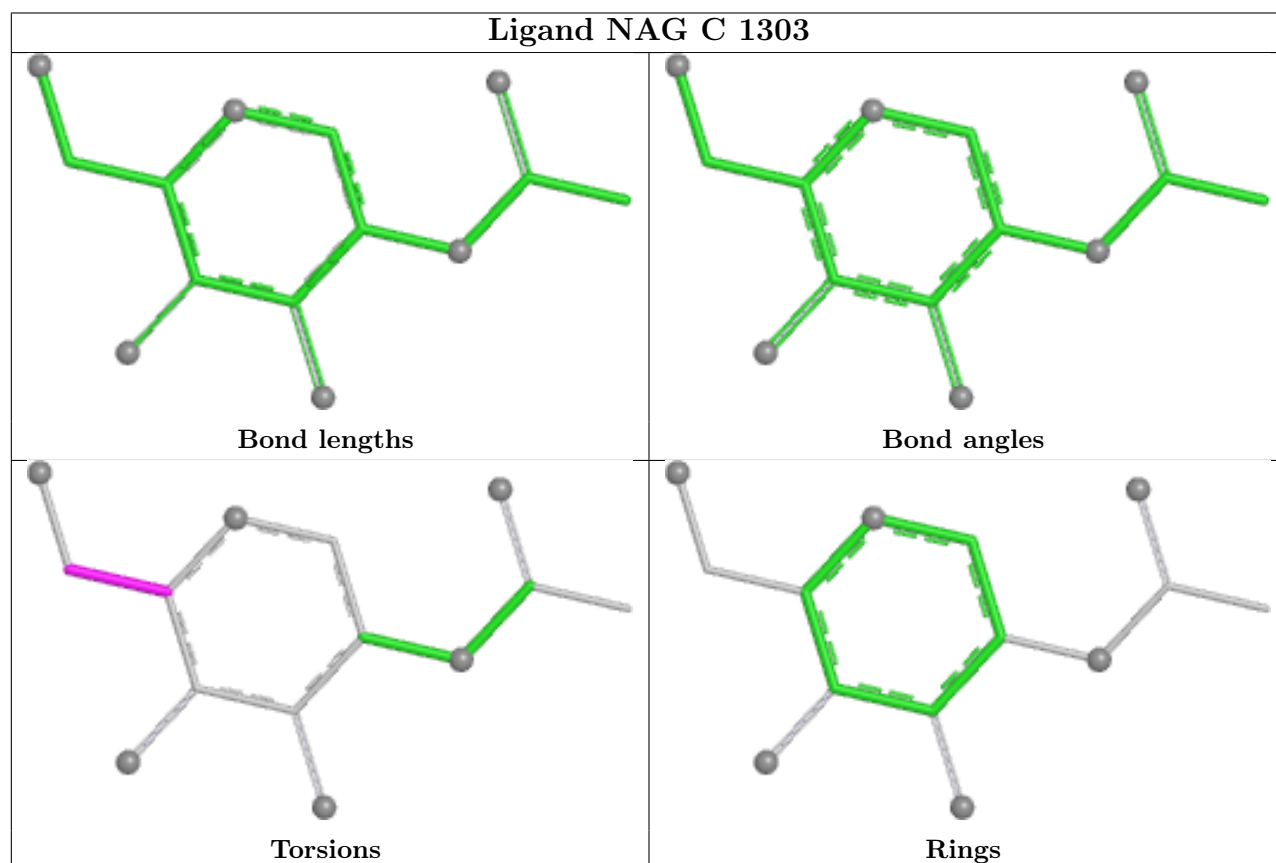
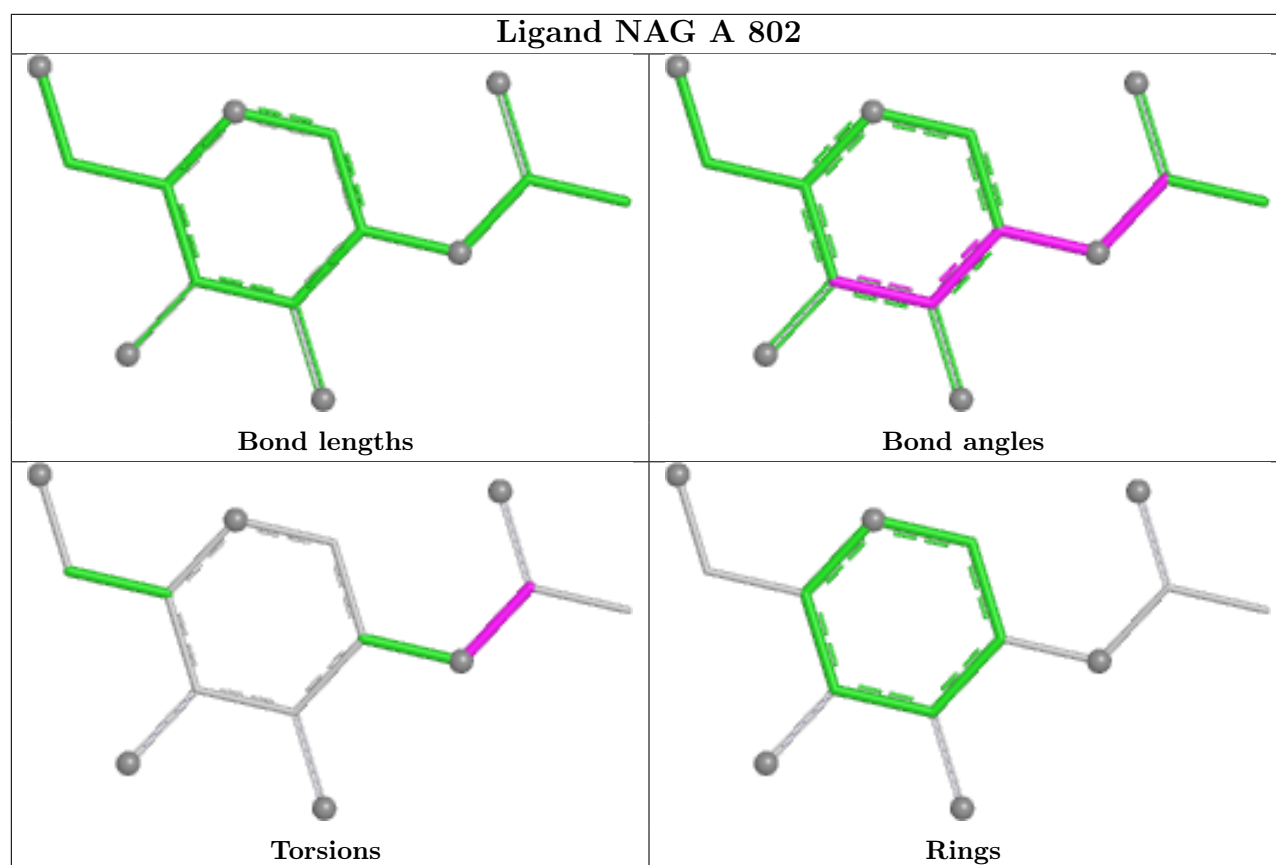
Ligand NAG E 802











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.

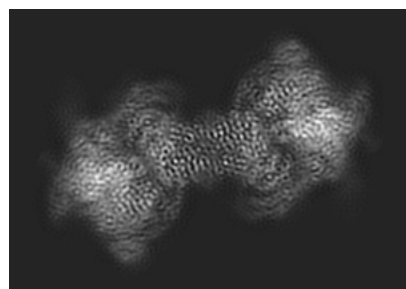
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32688. These allow visual inspection of the internal detail of the map and identification of artifacts.

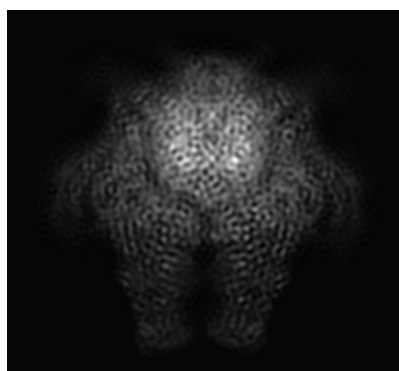
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

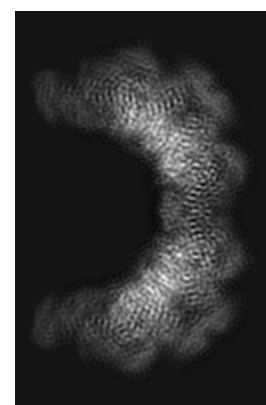
6.1.1 Primary map



X



Y

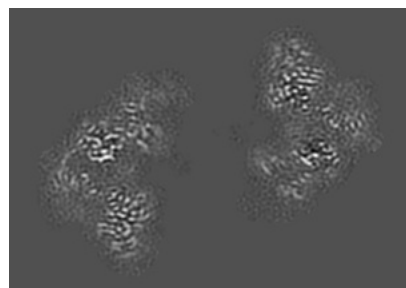


Z

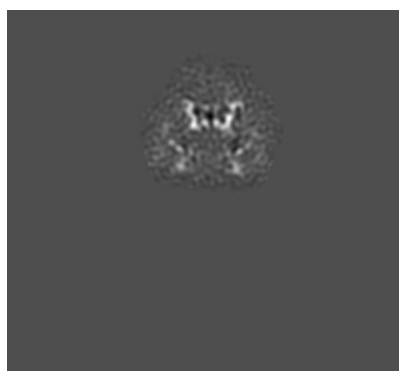
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

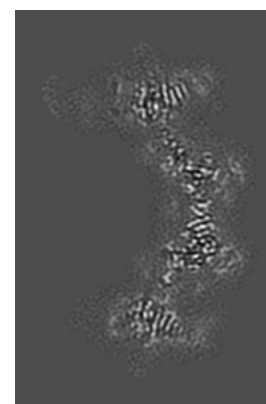
6.2.1 Primary map



X Index: 97



Y Index: 149

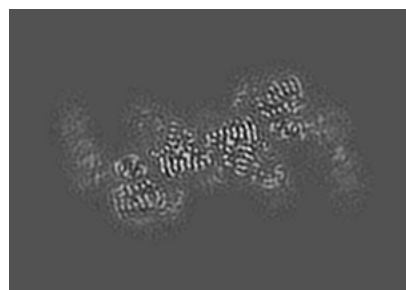


Z Index: 106

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: 133



Y Index: 230

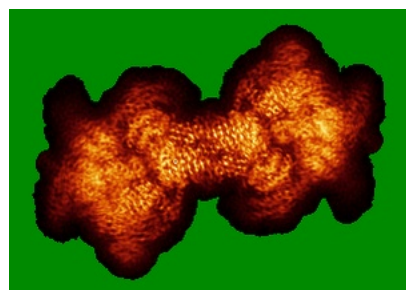


Z Index: 121

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

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

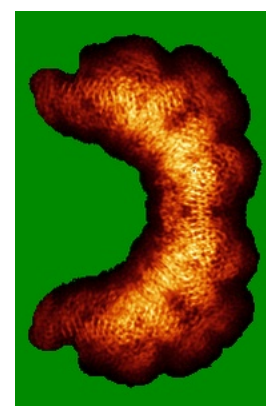
6.4.1 Primary map



X



Y

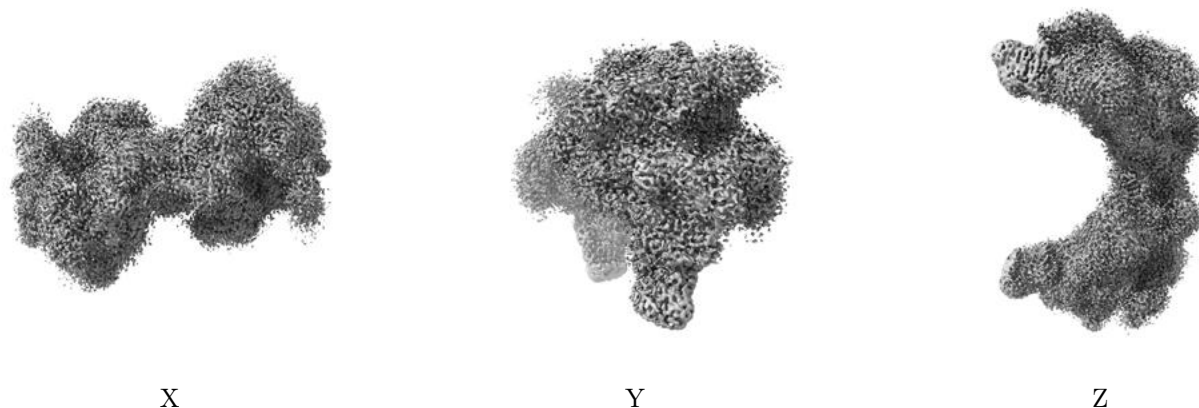


Z

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 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

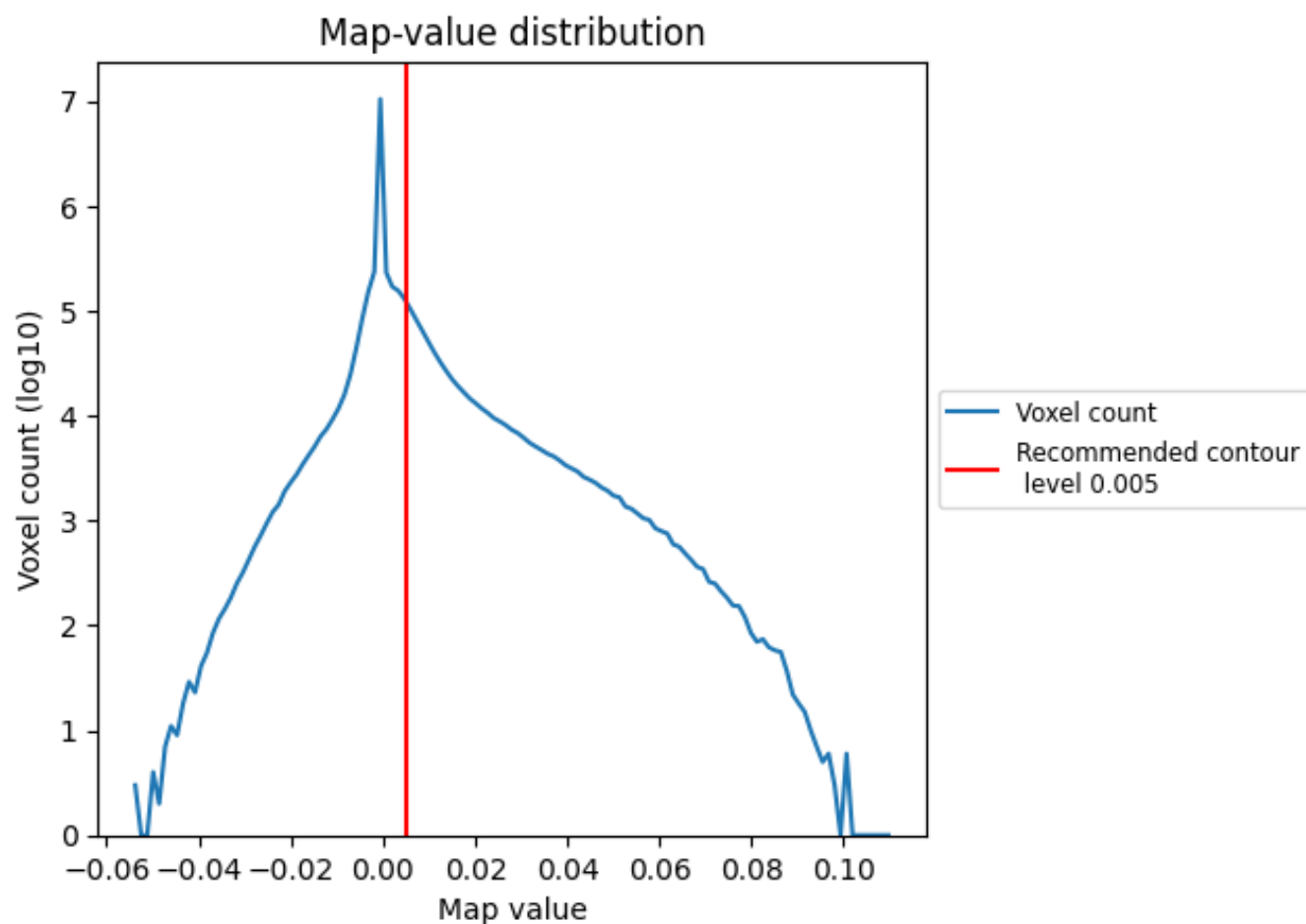
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

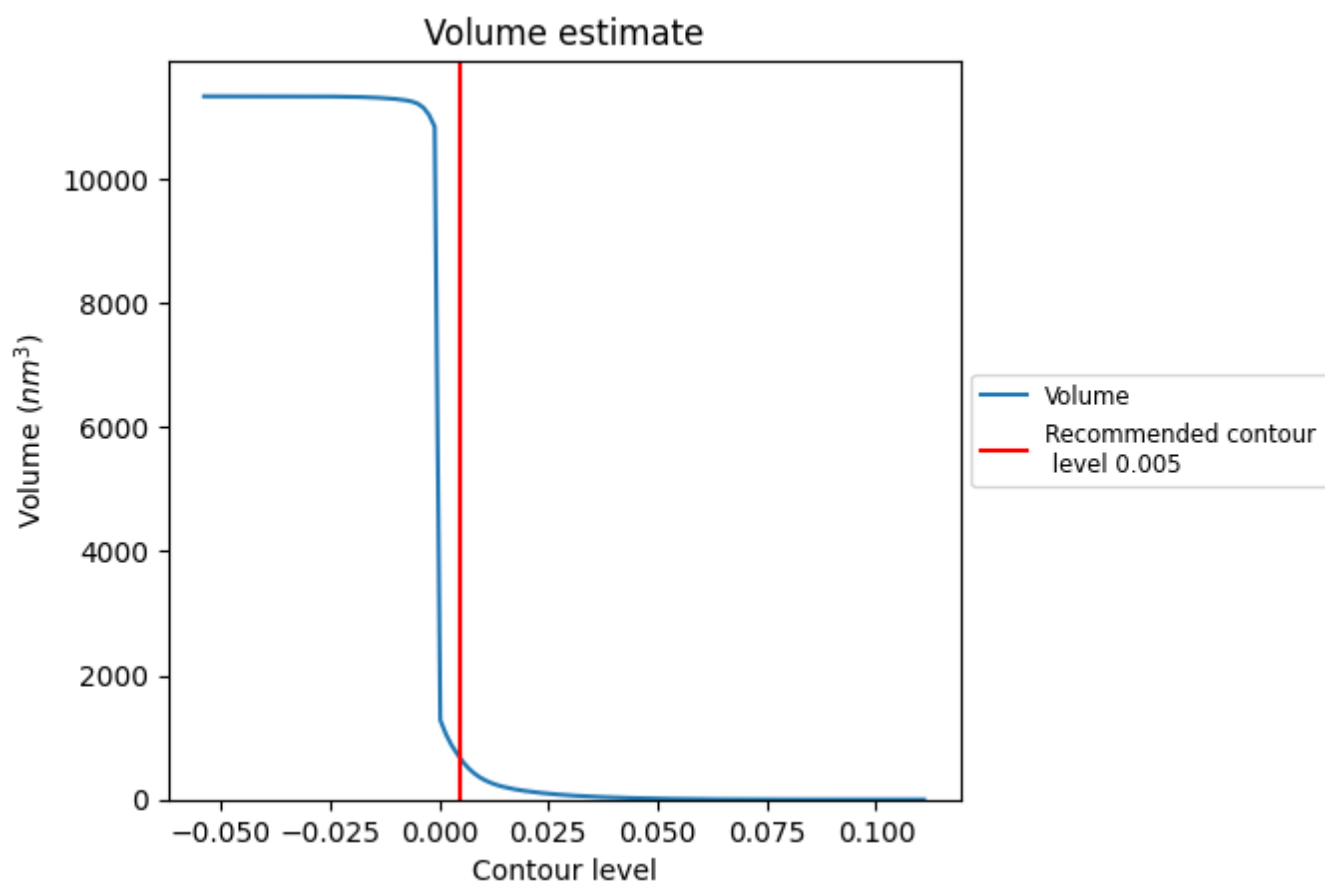
This section contains the results of statistical analysis of the map.

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 653 nm³; this corresponds to an approximate mass of 590 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.

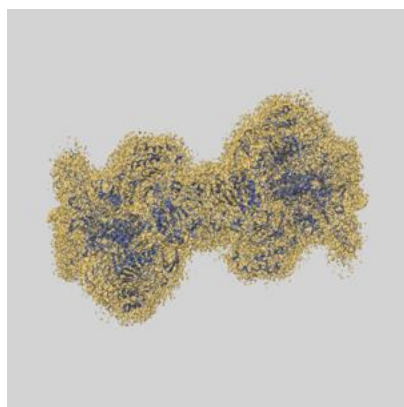
8 Fourier-Shell correlation ⓘ

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

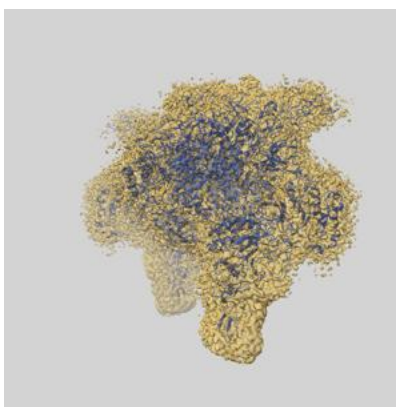
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32688 and PDB model 7WPQ. Per-residue inclusion information can be found in section [3](#) on page [8](#).

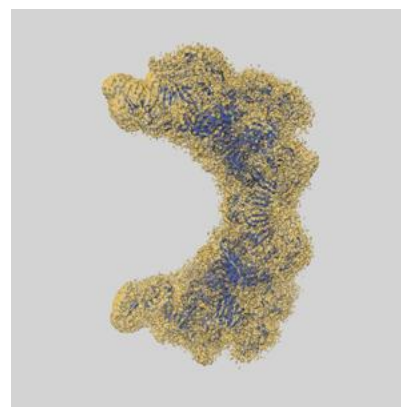
9.1 Map-model overlay [i](#)



X



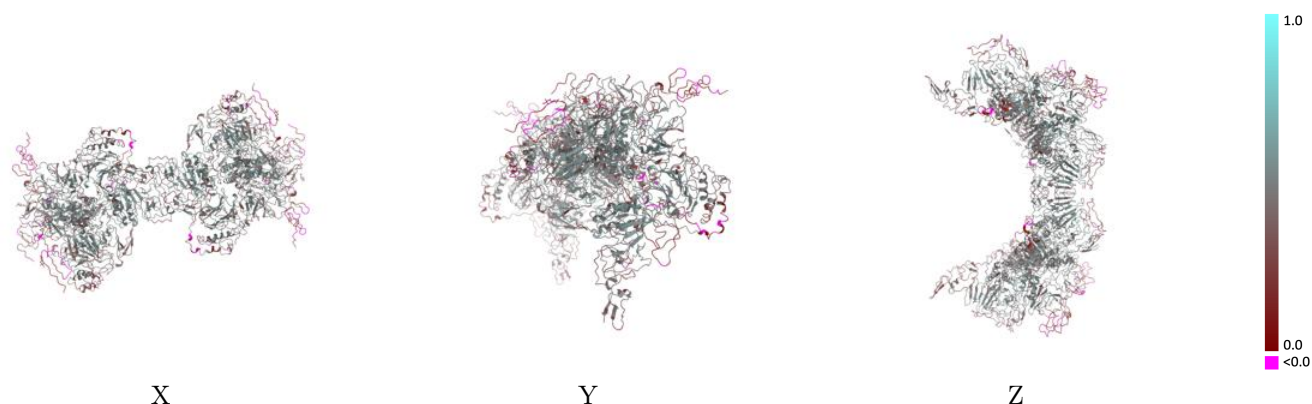
Y



Z

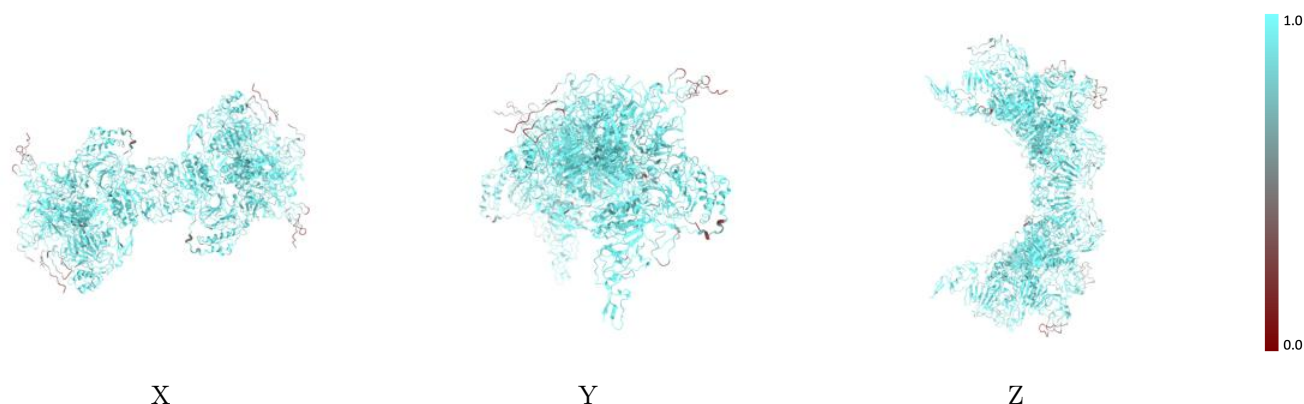
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



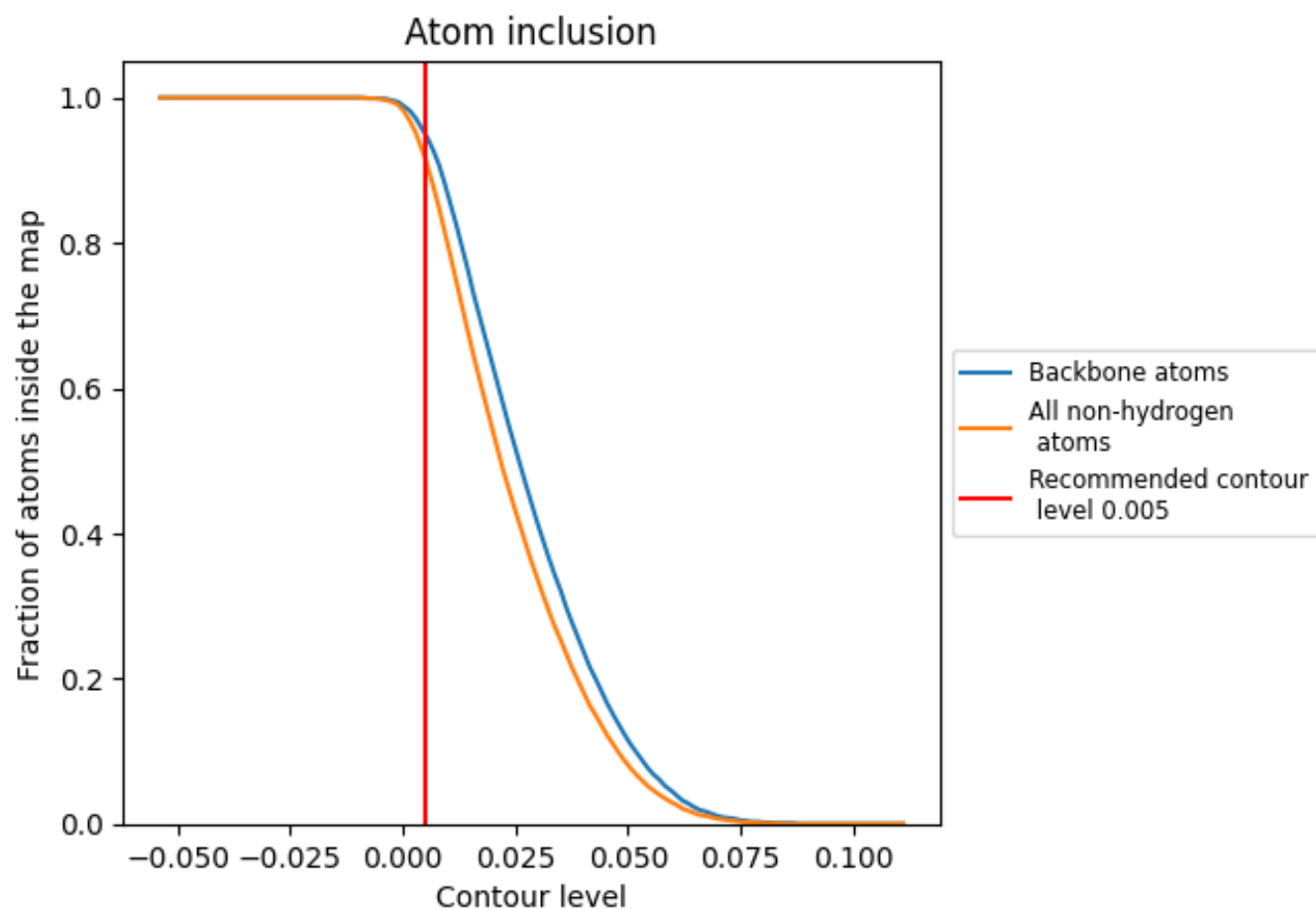
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9160	0.4270
A	0.9350	0.4370
B	0.9380	0.4570
C	0.8810	0.3880
D	0.8910	0.4000
E	0.9330	0.4550
F	0.8980	0.4070
G	0.9360	0.4430
H	0.8810	0.3860

1.0

0.0

<0.0