



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 28, 2026 – 04:06 PM JST

PDB ID : 9WZW / pdb_00009wzw
Title : Crystal structure of CTB10-PEC5.0-1n complex
Authors : Fu, K.; Rao, Y.J.
Deposited on : 2025-09-29
Resolution : 1.75 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.2
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.2
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

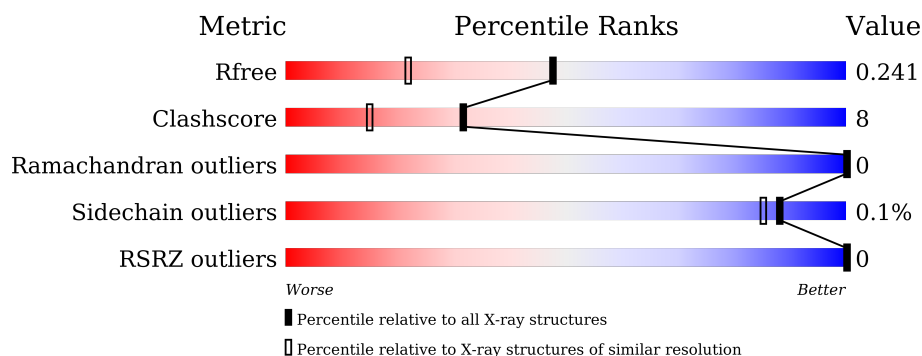
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	141	74% 18% 9%
1	B	141	74% 16% 11%
1	C	141	72% 16% 12%
1	D	141	78% 11% 11%
1	E	141	77% 14% 9%
1	F	141	72% 18% 10%

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Mol	Chain	Length	Quality of chain
1	G	141	 72% 15% 12%
1	H	141	 76% 13% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9352 atoms, of which 144 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 CTB10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			1059	680	177	195	7			
1	B	126	Total	C	N	O	S	0	0	0
			1030	663	170	190	7			
1	C	124	Total	C	N	O	S	0	0	0
			1017	654	168	188	7			
1	D	125	Total	C	N	O	S	0	0	0
			1025	658	170	190	7			
1	E	129	Total	C	N	O	S	0	0	0
			1059	680	177	195	7			
1	F	127	Total	C	N	O	S	0	0	0
			1039	668	171	193	7			
1	G	124	Total	C	N	O	S	0	0	0
			1017	654	168	188	7			
1	H	126	Total	C	N	O	S	0	0	0
			1026	660	169	190	7			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	PBF	TRP	conflict	UNP A0A977K7H6
A	76	VAL	ASN	conflict	UNP A0A977K7H6
A	107	VAL	THR	conflict	UNP A0A977K7H6
A	114	MET	PHE	conflict	UNP A0A977K7H6
A	115	GLY	ALA	conflict	UNP A0A977K7H6
A	117	LYS	MET	conflict	UNP A0A977K7H6
A	133	ALA	-	expression tag	UNP A0A977K7H6
A	134	LEU	-	expression tag	UNP A0A977K7H6
A	135	GLU	-	expression tag	UNP A0A977K7H6
A	136	HIS	-	expression tag	UNP A0A977K7H6
A	137	HIS	-	expression tag	UNP A0A977K7H6
A	138	HIS	-	expression tag	UNP A0A977K7H6
A	139	HIS	-	expression tag	UNP A0A977K7H6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	140	HIS	-	expression tag	UNP A0A977K7H6
A	141	HIS	-	expression tag	UNP A0A977K7H6
B	13	PBF	TRP	conflict	UNP A0A977K7H6
B	76	VAL	ASN	conflict	UNP A0A977K7H6
B	107	VAL	THR	conflict	UNP A0A977K7H6
B	114	MET	PHE	conflict	UNP A0A977K7H6
B	115	GLY	ALA	conflict	UNP A0A977K7H6
B	117	LYS	MET	conflict	UNP A0A977K7H6
B	133	ALA	-	expression tag	UNP A0A977K7H6
B	134	LEU	-	expression tag	UNP A0A977K7H6
B	135	GLU	-	expression tag	UNP A0A977K7H6
B	136	HIS	-	expression tag	UNP A0A977K7H6
B	137	HIS	-	expression tag	UNP A0A977K7H6
B	138	HIS	-	expression tag	UNP A0A977K7H6
B	139	HIS	-	expression tag	UNP A0A977K7H6
B	140	HIS	-	expression tag	UNP A0A977K7H6
B	141	HIS	-	expression tag	UNP A0A977K7H6
C	13	PBF	TRP	conflict	UNP A0A977K7H6
C	76	VAL	ASN	conflict	UNP A0A977K7H6
C	107	VAL	THR	conflict	UNP A0A977K7H6
C	114	MET	PHE	conflict	UNP A0A977K7H6
C	115	GLY	ALA	conflict	UNP A0A977K7H6
C	117	LYS	MET	conflict	UNP A0A977K7H6
C	133	ALA	-	expression tag	UNP A0A977K7H6
C	134	LEU	-	expression tag	UNP A0A977K7H6
C	135	GLU	-	expression tag	UNP A0A977K7H6
C	136	HIS	-	expression tag	UNP A0A977K7H6
C	137	HIS	-	expression tag	UNP A0A977K7H6
C	138	HIS	-	expression tag	UNP A0A977K7H6
C	139	HIS	-	expression tag	UNP A0A977K7H6
C	140	HIS	-	expression tag	UNP A0A977K7H6
C	141	HIS	-	expression tag	UNP A0A977K7H6
D	13	PBF	TRP	conflict	UNP A0A977K7H6
D	76	VAL	ASN	conflict	UNP A0A977K7H6
D	107	VAL	THR	conflict	UNP A0A977K7H6
D	114	MET	PHE	conflict	UNP A0A977K7H6
D	115	GLY	ALA	conflict	UNP A0A977K7H6
D	117	LYS	MET	conflict	UNP A0A977K7H6
D	133	ALA	-	expression tag	UNP A0A977K7H6
D	134	LEU	-	expression tag	UNP A0A977K7H6
D	135	GLU	-	expression tag	UNP A0A977K7H6
D	136	HIS	-	expression tag	UNP A0A977K7H6

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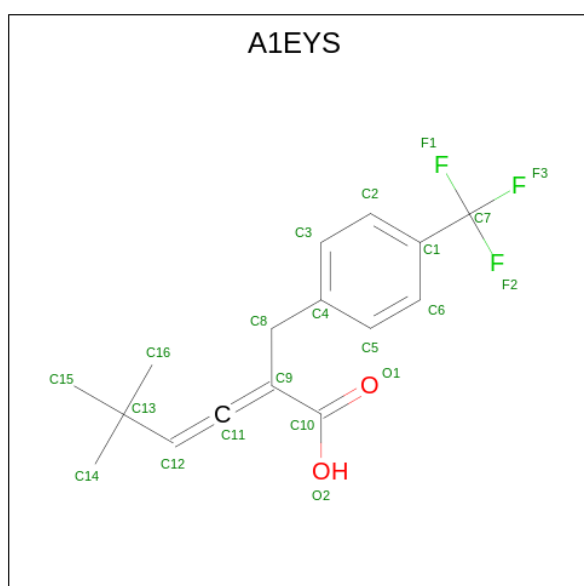
Chain	Residue	Modelled	Actual	Comment	Reference
D	137	HIS	-	expression tag	UNP A0A977K7H6
D	138	HIS	-	expression tag	UNP A0A977K7H6
D	139	HIS	-	expression tag	UNP A0A977K7H6
D	140	HIS	-	expression tag	UNP A0A977K7H6
D	141	HIS	-	expression tag	UNP A0A977K7H6
E	13	PBF	TRP	conflict	UNP A0A977K7H6
E	76	VAL	ASN	conflict	UNP A0A977K7H6
E	107	VAL	THR	conflict	UNP A0A977K7H6
E	114	MET	PHE	conflict	UNP A0A977K7H6
E	115	GLY	ALA	conflict	UNP A0A977K7H6
E	117	LYS	MET	conflict	UNP A0A977K7H6
E	133	ALA	-	expression tag	UNP A0A977K7H6
E	134	LEU	-	expression tag	UNP A0A977K7H6
E	135	GLU	-	expression tag	UNP A0A977K7H6
E	136	HIS	-	expression tag	UNP A0A977K7H6
E	137	HIS	-	expression tag	UNP A0A977K7H6
E	138	HIS	-	expression tag	UNP A0A977K7H6
E	139	HIS	-	expression tag	UNP A0A977K7H6
E	140	HIS	-	expression tag	UNP A0A977K7H6
E	141	HIS	-	expression tag	UNP A0A977K7H6
F	13	PBF	TRP	conflict	UNP A0A977K7H6
F	76	VAL	ASN	conflict	UNP A0A977K7H6
F	107	VAL	THR	conflict	UNP A0A977K7H6
F	114	MET	PHE	conflict	UNP A0A977K7H6
F	115	GLY	ALA	conflict	UNP A0A977K7H6
F	117	LYS	MET	conflict	UNP A0A977K7H6
F	133	ALA	-	expression tag	UNP A0A977K7H6
F	134	LEU	-	expression tag	UNP A0A977K7H6
F	135	GLU	-	expression tag	UNP A0A977K7H6
F	136	HIS	-	expression tag	UNP A0A977K7H6
F	137	HIS	-	expression tag	UNP A0A977K7H6
F	138	HIS	-	expression tag	UNP A0A977K7H6
F	139	HIS	-	expression tag	UNP A0A977K7H6
F	140	HIS	-	expression tag	UNP A0A977K7H6
F	141	HIS	-	expression tag	UNP A0A977K7H6
G	13	PBF	TRP	conflict	UNP A0A977K7H6
G	76	VAL	ASN	conflict	UNP A0A977K7H6
G	107	VAL	THR	conflict	UNP A0A977K7H6
G	114	MET	PHE	conflict	UNP A0A977K7H6
G	115	GLY	ALA	conflict	UNP A0A977K7H6
G	117	LYS	MET	conflict	UNP A0A977K7H6
G	133	ALA	-	expression tag	UNP A0A977K7H6

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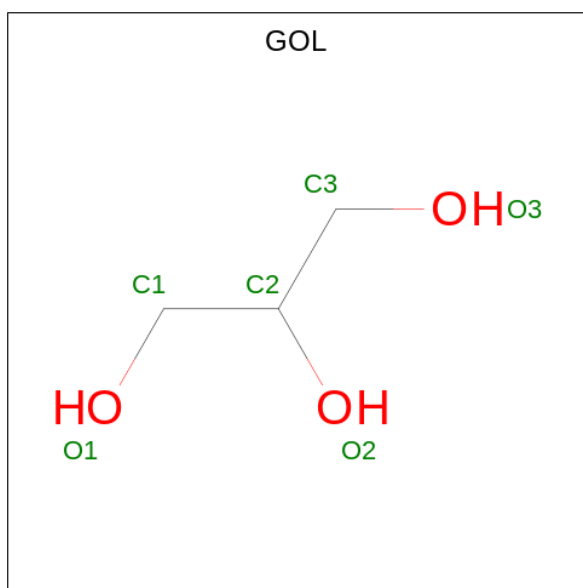
Chain	Residue	Modelled	Actual	Comment	Reference
G	134	LEU	-	expression tag	UNP A0A977K7H6
G	135	GLU	-	expression tag	UNP A0A977K7H6
G	136	HIS	-	expression tag	UNP A0A977K7H6
G	137	HIS	-	expression tag	UNP A0A977K7H6
G	138	HIS	-	expression tag	UNP A0A977K7H6
G	139	HIS	-	expression tag	UNP A0A977K7H6
G	140	HIS	-	expression tag	UNP A0A977K7H6
G	141	HIS	-	expression tag	UNP A0A977K7H6
H	13	PBF	TRP	conflict	UNP A0A977K7H6
H	76	VAL	ASN	conflict	UNP A0A977K7H6
H	107	VAL	THR	conflict	UNP A0A977K7H6
H	114	MET	PHE	conflict	UNP A0A977K7H6
H	115	GLY	ALA	conflict	UNP A0A977K7H6
H	117	LYS	MET	conflict	UNP A0A977K7H6
H	133	ALA	-	expression tag	UNP A0A977K7H6
H	134	LEU	-	expression tag	UNP A0A977K7H6
H	135	GLU	-	expression tag	UNP A0A977K7H6
H	136	HIS	-	expression tag	UNP A0A977K7H6
H	137	HIS	-	expression tag	UNP A0A977K7H6
H	138	HIS	-	expression tag	UNP A0A977K7H6
H	139	HIS	-	expression tag	UNP A0A977K7H6
H	140	HIS	-	expression tag	UNP A0A977K7H6
H	141	HIS	-	expression tag	UNP A0A977K7H6

- Molecule 2 is 5,5-dimethyl-2-[[4-(trifluoromethyl)phenyl]methyl]hexa-2,3-dienoic acid (CCD ID: A1EYS) (formula: C₁₆H₁₇F₃O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	H	O	0	0
			37	16	3	16	2		
2	B	1	Total	C	F	H	O	0	0
			37	16	3	16	2		
2	C	1	Total	C	F	H	O	0	0
			37	16	3	16	2		
2	D	1	Total	C	F	H	O	0	0
			37	16	3	16	2		
2	E	1	Total	C	F	H	O	0	0
			37	16	3	16	2		
2	F	1	Total	C	F	H	O	0	0
			37	16	3	16	2		
2	G	1	Total	C	F	H	O	0	0
			37	16	3	16	2		
2	H	1	Total	C	F	H	O	0	0
			37	16	3	16	2		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	H	O	0	0
			14	3	8	3		
3	E	1	Total	C	H	O	0	0
			14	3	8	3		

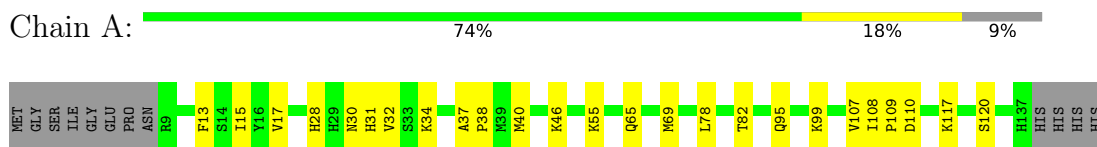
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	88	Total 88	O 88	0	0
4	B	107	Total 107	O 107	0	0
4	C	89	Total 89	O 89	0	0
4	D	128	Total 128	O 128	0	0
4	E	87	Total 87	O 87	0	0
4	F	84	Total 84	O 84	0	0
4	G	90	Total 90	O 90	0	0
4	H	83	Total 83	O 83	0	0

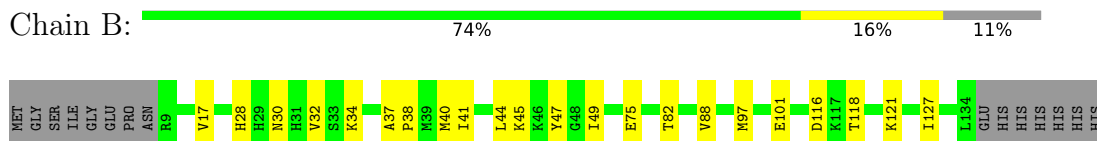
3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

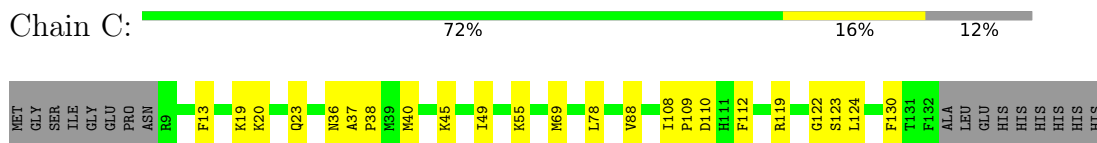
- Molecule 1: CTB10



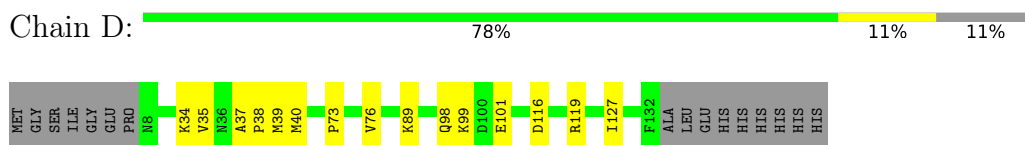
- Molecule 1: CTB10



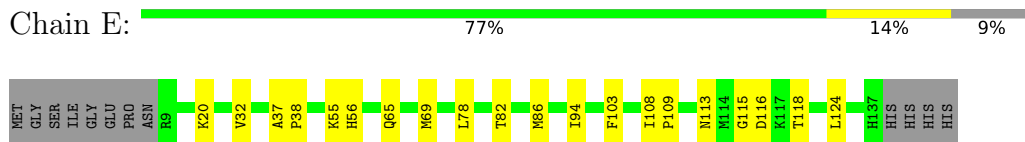
- Molecule 1: CTB10



- Molecule 1: CTB10



- Molecule 1: CTB10



- Molecule 1: CTB10





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	325.04Å 54.87Å 68.85Å 90.00° 100.08° 90.00°	Depositor
Resolution (Å)	48.79 – 1.75 48.79 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.79-1.75) 99.2 (48.79-1.75)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.02 (at 1.75Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.205 , 0.240 0.205 , 0.241	Depositor DCC
R_{free} test set	5838 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 27.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.069 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9352	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: PBF, GOL, A1EYS

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	0.34	0/1064	0.59	0/1435
1	B	0.33	0/1033	0.55	0/1393
1	C	0.36	0/1020	0.60	0/1375
1	D	0.42	0/1028	0.63	0/1386
1	E	0.34	0/1064	0.56	0/1435
1	F	0.34	0/1042	0.59	0/1405
1	G	0.35	0/1020	0.59	0/1375
1	H	0.31	0/1029	0.57	0/1389
All	All	0.35	0/8300	0.59	0/11193

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	1059	0	1037	21	0
1	B	1030	0	1017	17	0
1	C	1017	0	1001	22	0
1	D	1025	0	1007	11	0
1	E	1059	0	1037	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1039	0	1023	20	0
1	G	1017	0	1001	22	0
1	H	1026	0	1006	16	0
2	A	21	16	0	1	0
2	B	21	16	0	0	0
2	C	21	16	0	1	0
2	D	21	16	0	0	0
2	E	21	16	0	1	0
2	F	21	16	0	0	0
2	G	21	16	0	0	0
2	H	21	16	0	0	0
3	D	6	8	8	0	0
3	E	6	8	8	0	0
4	A	88	0	0	6	0
4	B	107	0	0	0	0
4	C	89	0	0	3	0
4	D	128	0	0	3	0
4	E	87	0	0	3	0
4	F	84	0	0	4	0
4	G	90	0	0	2	0
4	H	83	0	0	4	0
All	All	9208	144	8145	134	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 8.

The worst 5 of 134 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:G:41:ILE:HG22	1:G:45:LYS:NZ	1.96	0.80
1:B:116:ASP:OD1	1:B:118:THR:HB	1.82	0.80
1:A:30:ASN:HB3	4:A:371:HOH:O	1.86	0.75
1:H:116:ASP:OD1	1:H:118:THR:HG22	1.85	0.75
1:A:120:SER:HA	4:A:308:HOH:O	1.87	0.74

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	126/141 (89%)	122 (97%)	4 (3%)	0	100	100
1	B	123/141 (87%)	120 (98%)	3 (2%)	0	100	100
1	C	121/141 (86%)	120 (99%)	1 (1%)	0	100	100
1	D	122/141 (86%)	120 (98%)	2 (2%)	0	100	100
1	E	126/141 (89%)	125 (99%)	1 (1%)	0	100	100
1	F	124/141 (88%)	121 (98%)	3 (2%)	0	100	100
1	G	121/141 (86%)	120 (99%)	1 (1%)	0	100	100
1	H	123/141 (87%)	120 (98%)	3 (2%)	0	100	100
All	All	986/1128 (87%)	968 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	115/127 (91%)	115 (100%)	0	100	100
1	B	112/127 (88%)	112 (100%)	0	100	100
1	C	111/127 (87%)	111 (100%)	0	100	100
1	D	112/127 (88%)	112 (100%)	0	100	100
1	E	115/127 (91%)	115 (100%)	0	100	100
1	F	113/127 (89%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	111/127 (87%)	110 (99%)	1 (1%)	70	60
1	H	111/127 (87%)	111 (100%)	0	100	100
All	All	900/1016 (89%)	899 (100%)	1 (0%)	88	85

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

Mol	Chain	Res	Type
1	G	90	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	8	ASN
1	D	72	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	PBF	F	13	1	19,20,21	0.25	0	23,26,28	0.64	0
1	PBF	H	13	1	19,20,21	0.16	0	23,26,28	0.69	0
1	PBF	D	13	1	19,20,21	0.19	0	23,26,28	0.82	0
1	PBF	C	13	1	19,20,21	0.13	0	23,26,28	0.54	0
1	PBF	B	13	1	19,20,21	0.19	0	23,26,28	0.53	0
1	PBF	G	13	1	19,20,21	0.26	0	23,26,28	0.68	0
1	PBF	E	13	1	19,20,21	0.15	0	23,26,28	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PBF	A	13	1	19,20,21	0.23	0	23,26,28	0.49	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
1	PBF	F	13	1	-	2/13/14/16	0/2/2/2
1	PBF	H	13	1	-	2/13/14/16	0/2/2/2
1	PBF	D	13	1	-	2/13/14/16	0/2/2/2
1	PBF	C	13	1	-	6/13/14/16	0/2/2/2
1	PBF	B	13	1	-	2/13/14/16	0/2/2/2
1	PBF	G	13	1	-	6/13/14/16	0/2/2/2
1	PBF	E	13	1	-	2/13/14/16	0/2/2/2
1	PBF	A	13	1	-	2/13/14/16	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	13	PBF	CA-CB-CG-CD2
1	D	13	PBF	CA-CB-CG-CD1
1	E	13	PBF	CA-CB-CG-CD1
1	A	13	PBF	CA-CB-CG-CD1
1	F	13	PBF	CA-CB-CG-CD1

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	F	13	PBF	1	0
1	C	13	PBF	4	0
1	A	13	PBF	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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
2	A1EYS	C	201	-	20,21,21	1.53	2 (10%)	26,31,31	1.57	3 (11%)
3	GOL	E	201	-	5,5,5	0.07	0	5,5,5	0.22	0
3	GOL	D	202	-	5,5,5	0.53	0	5,5,5	1.25	1 (20%)
2	A1EYS	G	201	-	20,21,21	1.53	1 (5%)	26,31,31	0.71	0
2	A1EYS	B	201	-	20,21,21	1.56	1 (5%)	26,31,31	0.67	0
2	A1EYS	D	201	-	20,21,21	1.40	1 (5%)	26,31,31	0.73	0
2	A1EYS	E	202	-	20,21,21	1.54	1 (5%)	26,31,31	0.84	0
2	A1EYS	F	201	-	20,21,21	1.49	1 (5%)	26,31,31	0.68	0
2	A1EYS	A	201	-	20,21,21	1.53	1 (5%)	26,31,31	1.12	2 (7%)
2	A1EYS	H	201	-	20,21,21	1.46	1 (5%)	26,31,31	0.86	1 (3%)

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
2	A1EYS	C	201	-	-	9/17/20/20	0/1/1/1
3	GOL	E	201	-	-	4/4/4/4	-
3	GOL	D	202	-	-	4/4/4/4	-
2	A1EYS	G	201	-	-	5/17/20/20	0/1/1/1
2	A1EYS	B	201	-	-	1/17/20/20	0/1/1/1
2	A1EYS	D	201	-	-	0/17/20/20	0/1/1/1
2	A1EYS	E	202	-	-	3/17/20/20	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A1EYS	F	201	-	-	1/17/20/20	0/1/1/1
2	A1EYS	A	201	-	-	1/17/20/20	0/1/1/1
2	A1EYS	H	201	-	-	0/17/20/20	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	201	A1EYS	C10-C9	-6.64	1.33	1.48
2	E	202	A1EYS	C10-C9	-6.56	1.33	1.48
2	A	201	A1EYS	C10-C9	-6.47	1.33	1.48
2	G	201	A1EYS	C10-C9	-6.47	1.33	1.48
2	C	201	A1EYS	C10-C9	-6.33	1.34	1.48

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	201	A1EYS	C8-C4-C3	5.19	128.33	120.89
2	C	201	A1EYS	C8-C4-C5	-5.08	113.63	120.89
2	A	201	A1EYS	C8-C4-C3	-3.27	116.20	120.89
2	A	201	A1EYS	C8-C4-C5	3.18	125.45	120.89
3	D	202	GOL	C3-C2-C1	-2.46	102.13	111.70

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	202	A1EYS	C11-C12-C13-C15
2	E	202	A1EYS	C11-C12-C13-C16
2	G	201	A1EYS	C4-C8-C9-C11
3	D	202	GOL	O1-C1-C2-C3
3	D	202	GOL	C1-C2-C3-O3

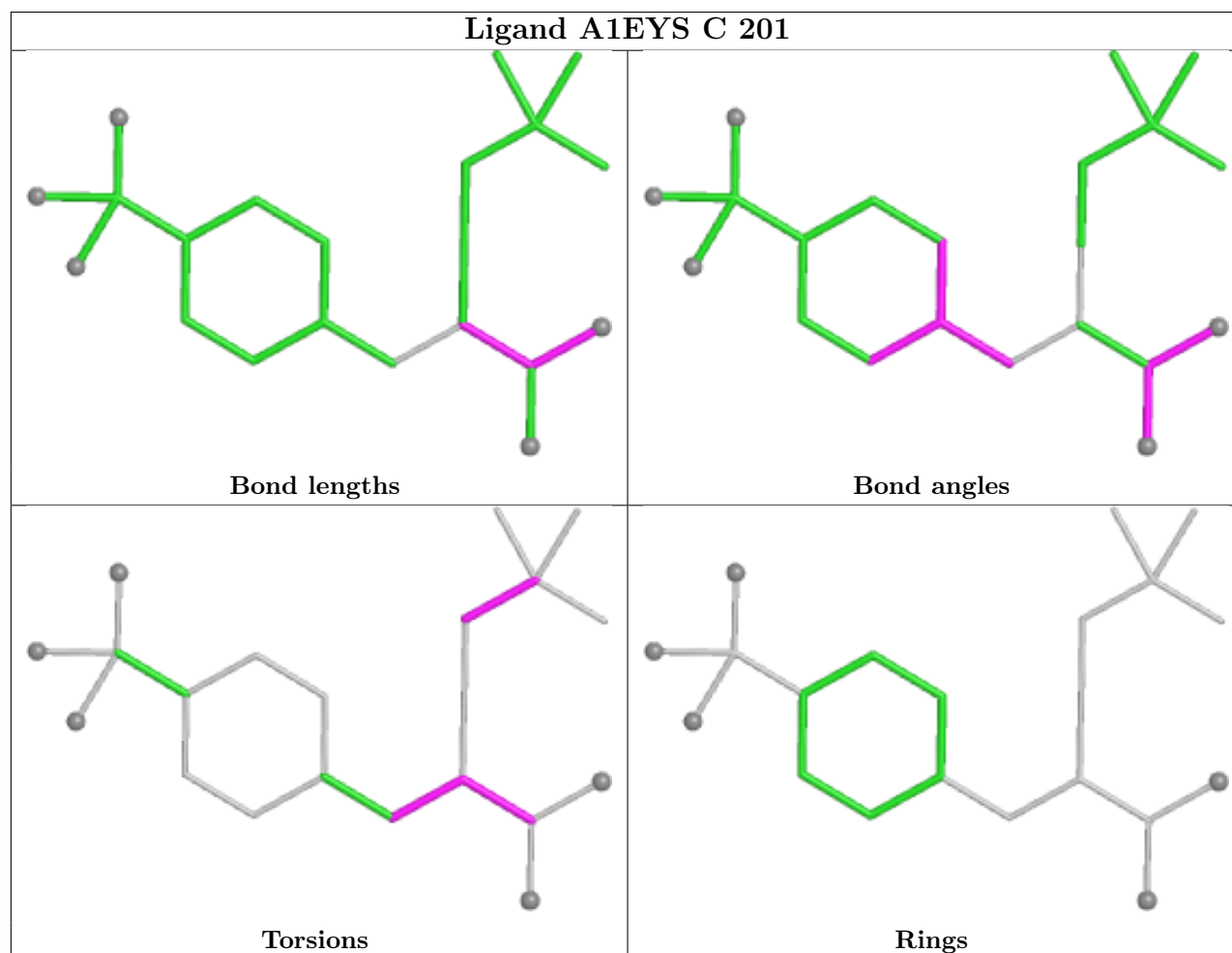
There are no ring outliers.

3 monomers are involved in 3 short contacts:

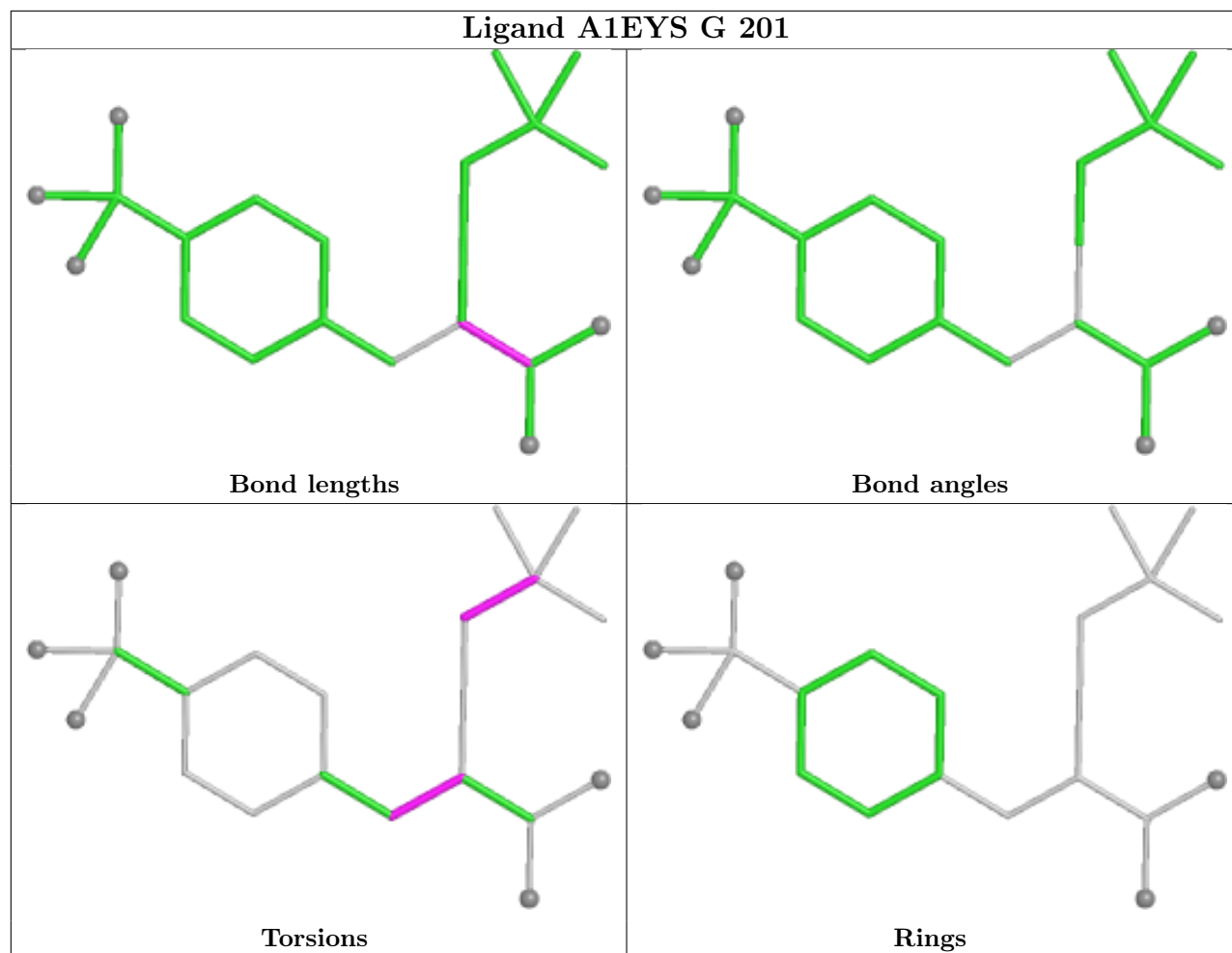
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	201	A1EYS	1	0
2	E	202	A1EYS	1	0
2	A	201	A1EYS	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

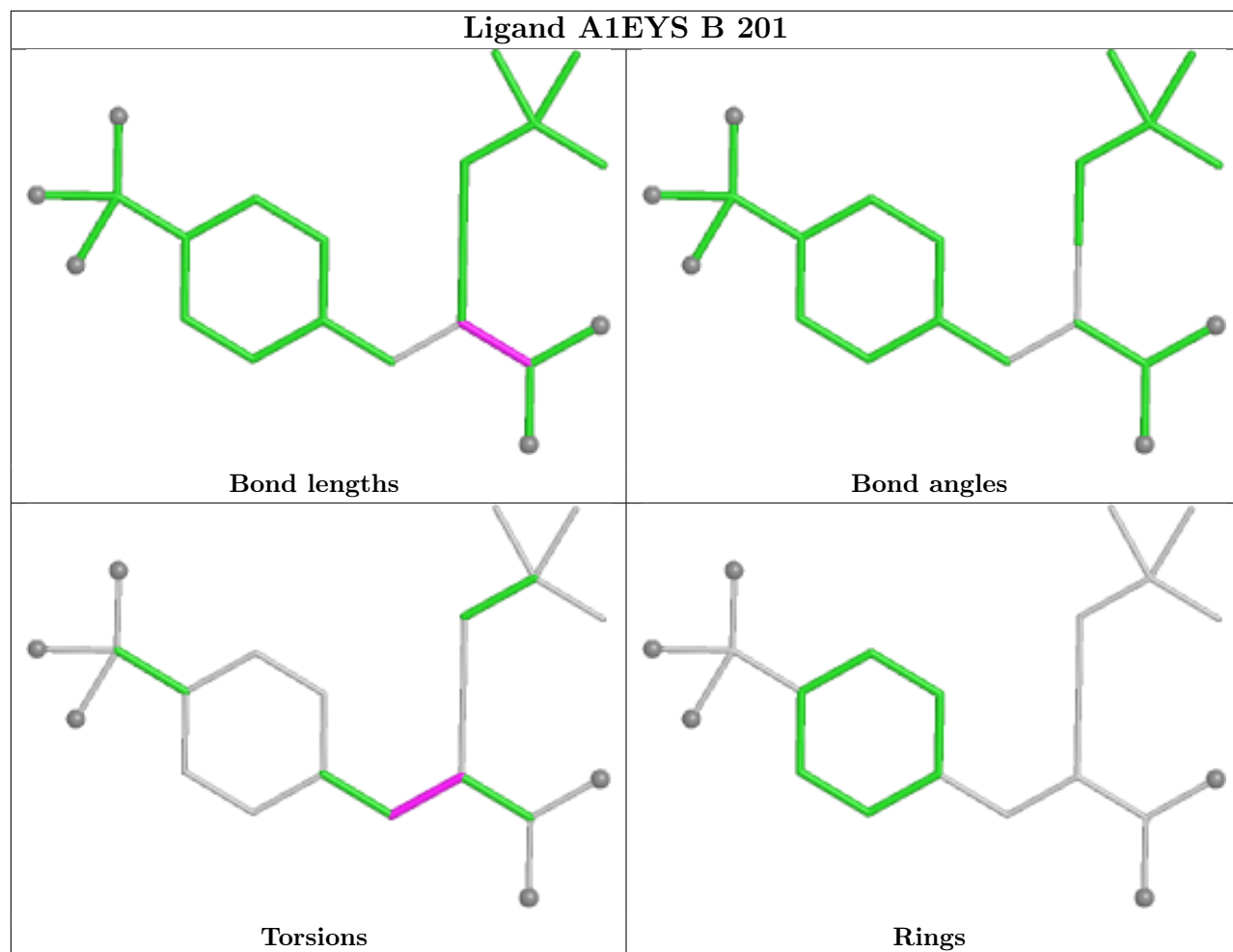
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.



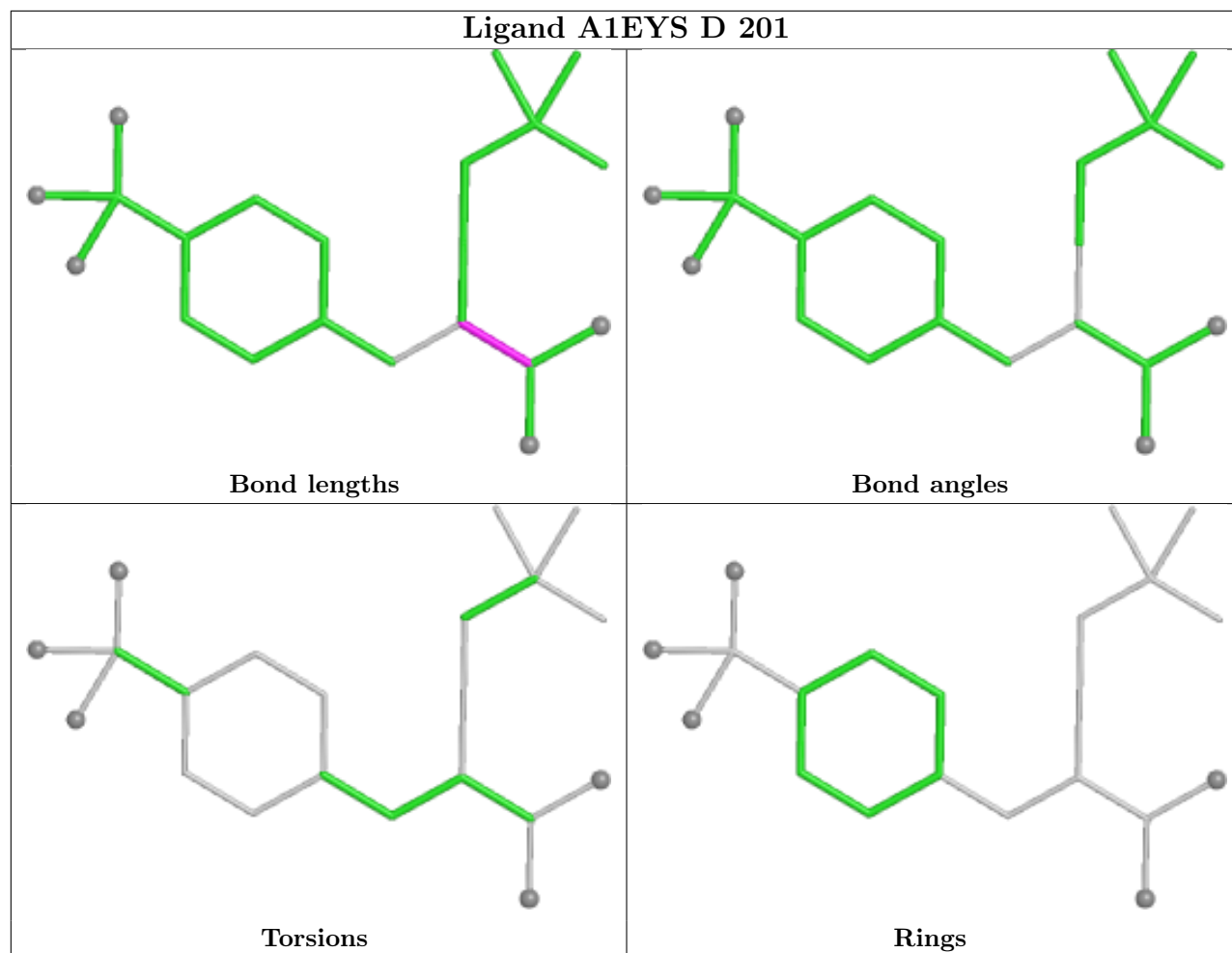
Ligand A1EYS G 201



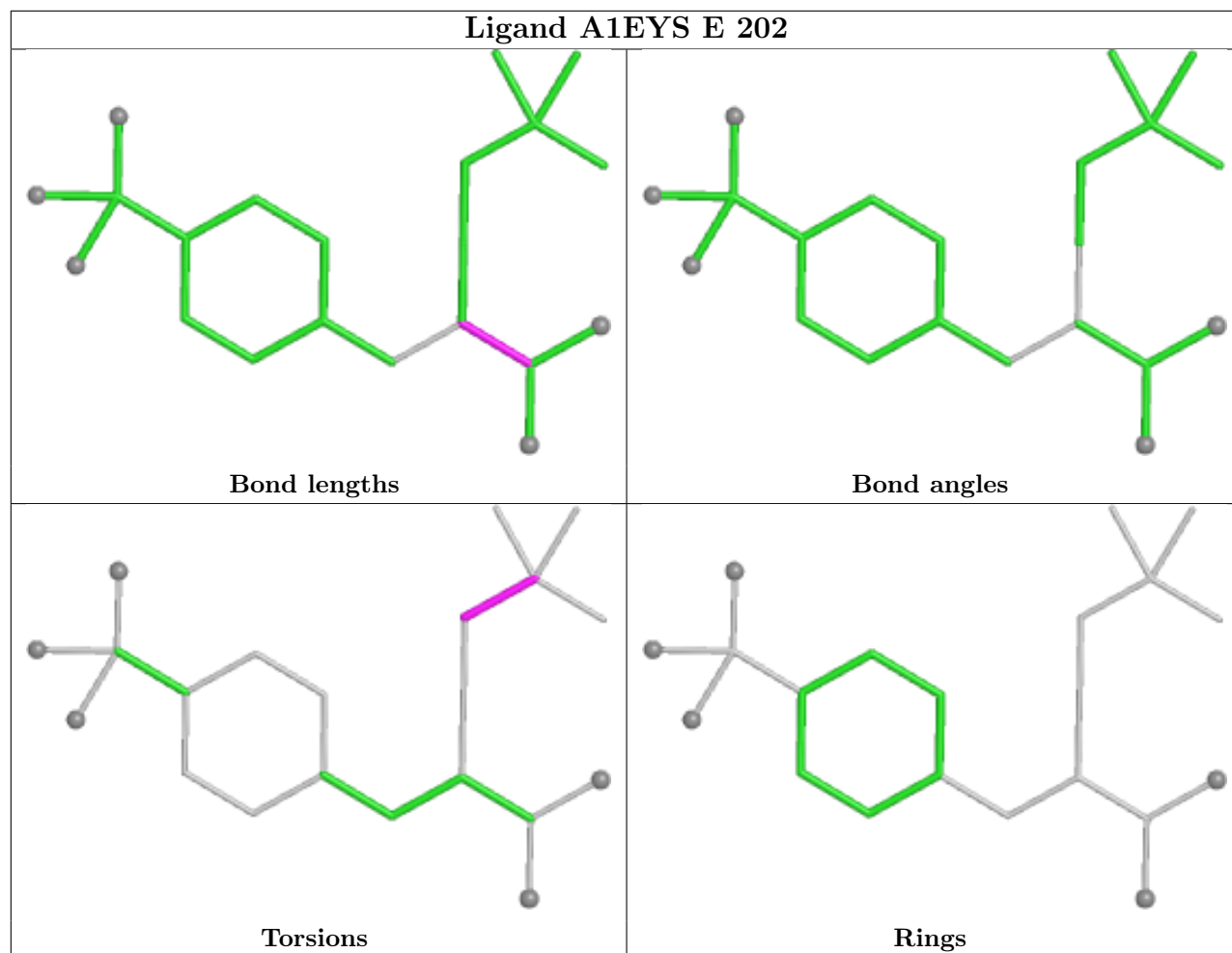
Ligand A1EYS B 201



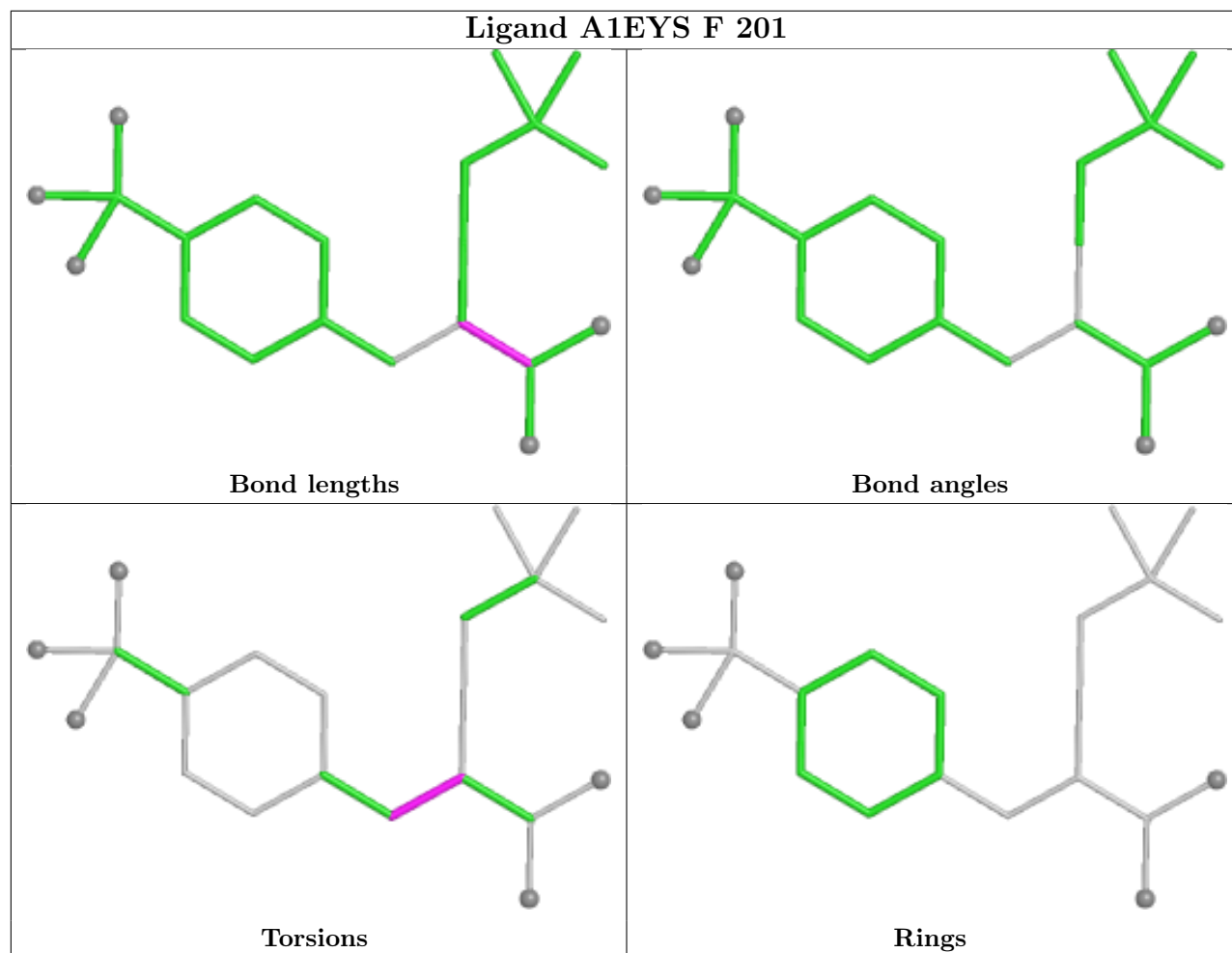
Ligand A1EYS D 201



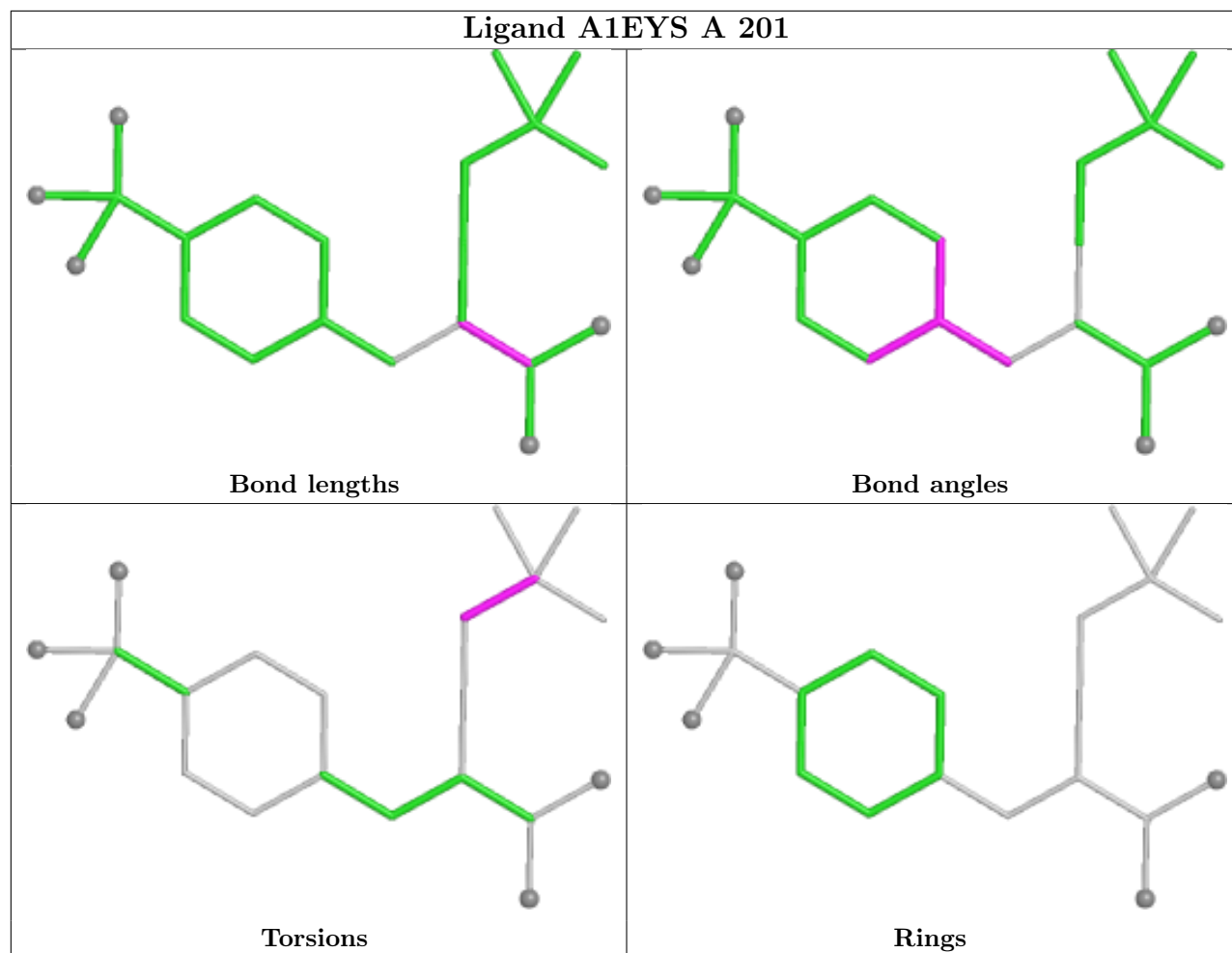
Ligand A1EYS E 202

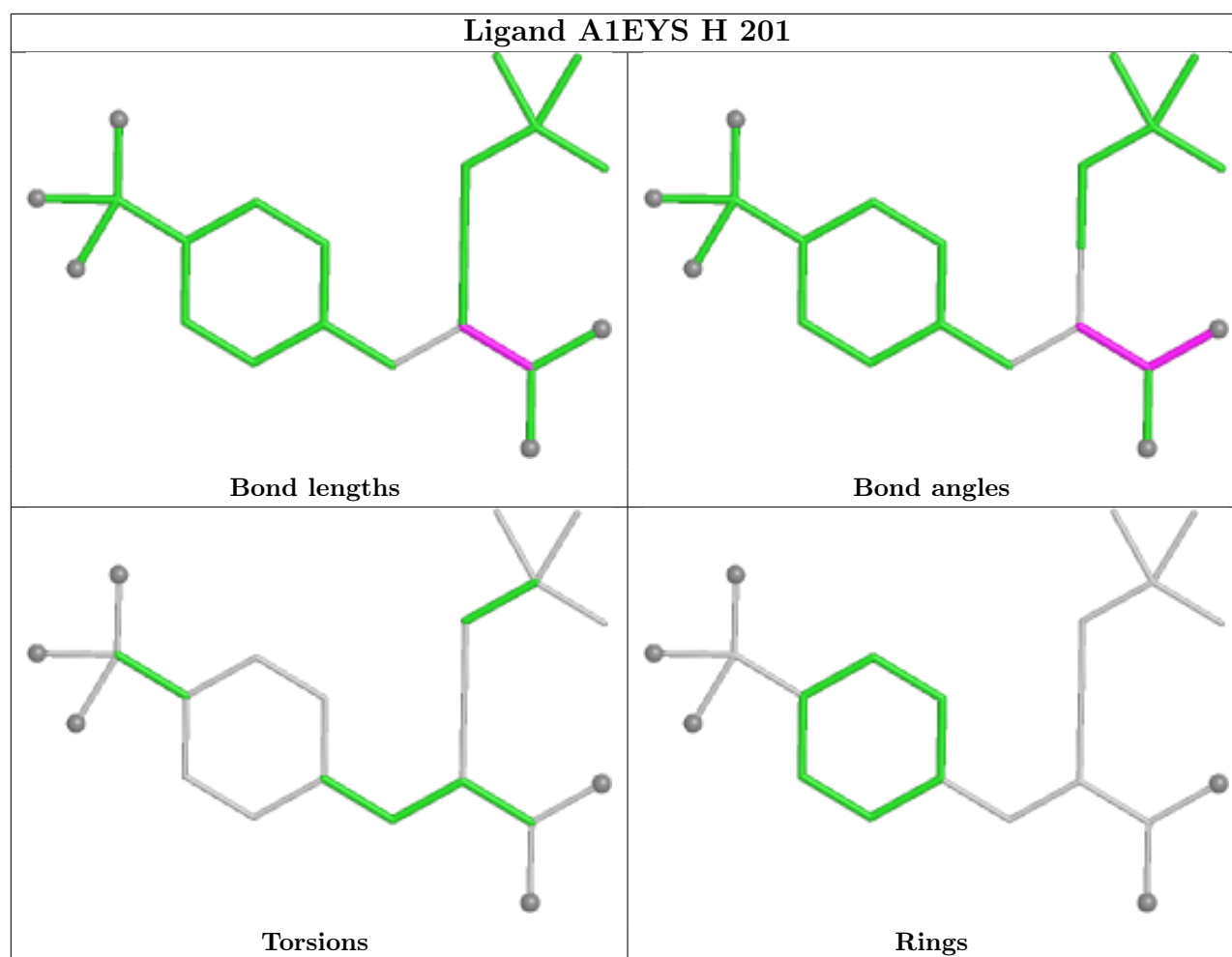


Ligand A1EYS F 201



Ligand A1EYS A 201





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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	128/141 (90%)	-1.22	0 100 100	11, 18, 30, 39	0
1	B	125/141 (88%)	-1.22	0 100 100	12, 18, 29, 40	0
1	C	123/141 (87%)	-1.26	0 100 100	12, 18, 29, 41	0
1	D	124/141 (87%)	-1.29	0 100 100	10, 16, 25, 30	0
1	E	128/141 (90%)	-1.16	0 100 100	9, 20, 32, 44	0
1	F	126/141 (89%)	-1.24	0 100 100	11, 19, 31, 40	0
1	G	123/141 (87%)	-1.13	0 100 100	11, 21, 33, 45	0
1	H	125/141 (88%)	-1.23	0 100 100	11, 19, 30, 34	0
All	All	1002/1128 (88%)	-1.22	0 100 100	9, 18, 31, 45	0

There are no RSRZ outliers to report.

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	PBF	A	13	19/20	0.99	0.03	9,16,23,25	0
1	PBF	B	13	19/20	0.99	0.03	9,14,19,19	0
1	PBF	C	13	19/20	0.99	0.04	11,21,33,34	0
1	PBF	D	13	19/20	0.99	0.03	8,12,19,20	0
1	PBF	F	13	19/20	0.99	0.03	8,14,22,24	0
1	PBF	G	13	19/20	0.99	0.03	10,21,25,26	0
1	PBF	H	13	19/20	0.99	0.03	9,11,16,16	0
1	PBF	E	13	19/20	1.00	0.02	8,13,21,24	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

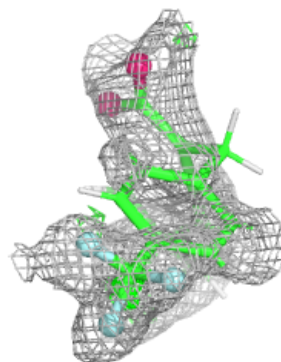
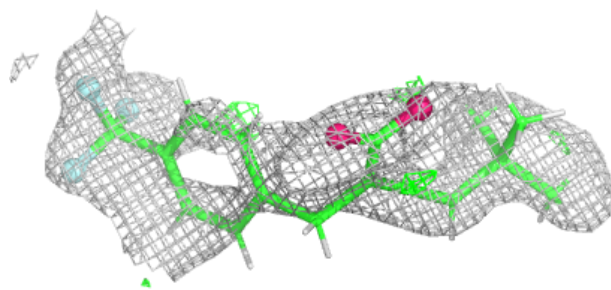
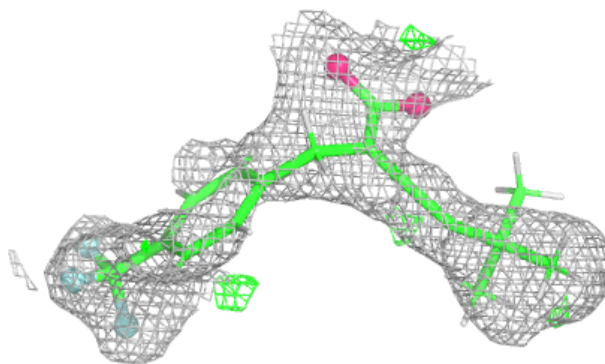
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	E	201	6/6	0.96	0.08	20,20,20,20	0
2	A1EYS	E	202	21/21	0.97	0.06	31,39,46,52	0
3	GOL	D	202	6/6	0.97	0.05	35,43,50,52	0
2	A1EYS	C	201	21/21	0.97	0.06	22,35,43,45	0
2	A1EYS	G	201	21/21	0.98	0.06	30,36,49,49	0
2	A1EYS	H	201	21/21	0.98	0.04	18,26,31,31	0
2	A1EYS	A	201	21/21	0.98	0.06	27,39,50,51	0
2	A1EYS	F	201	21/21	0.98	0.05	28,37,42,46	0
2	A1EYS	B	201	21/21	0.99	0.04	22,29,33,41	0
2	A1EYS	D	201	21/21	0.99	0.03	18,25,32,32	0

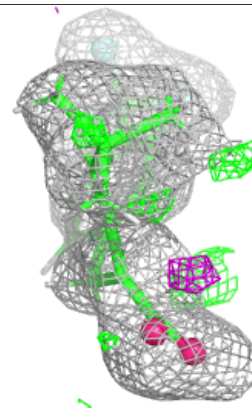
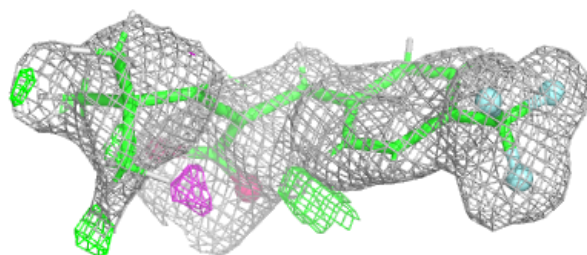
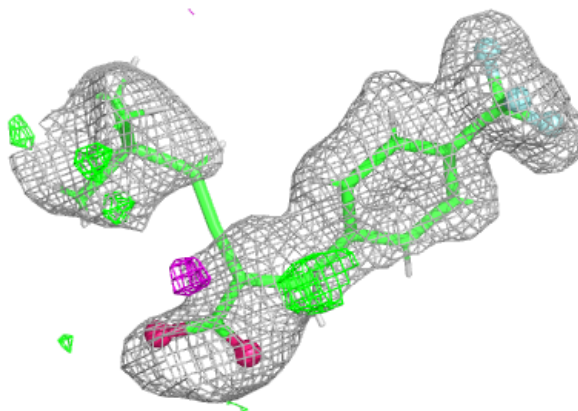
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around A1EYS E 202:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

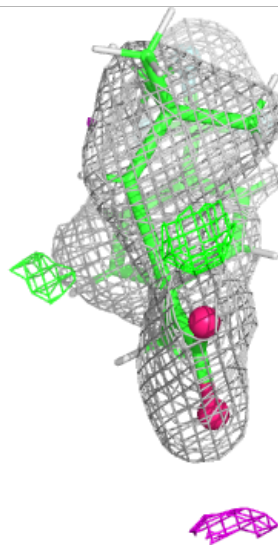
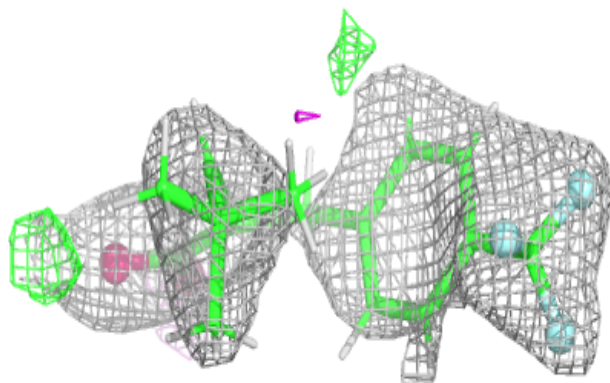
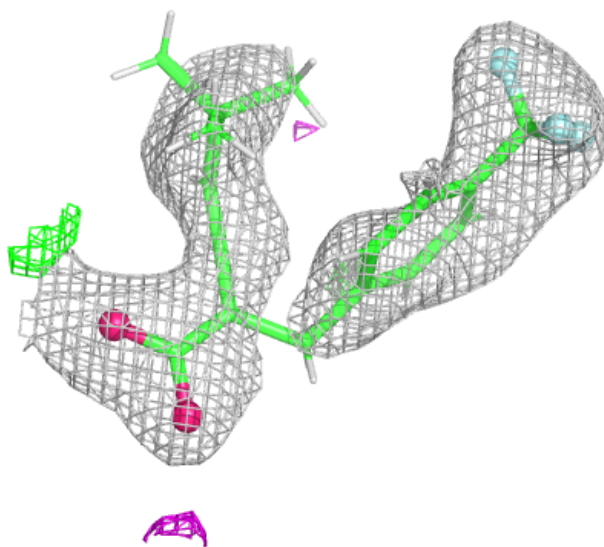
**Electron density around A1EYS C 201:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



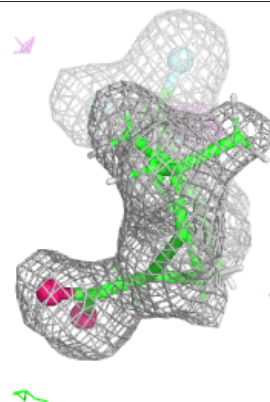
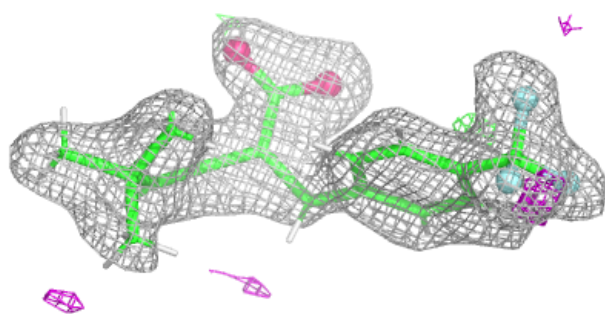
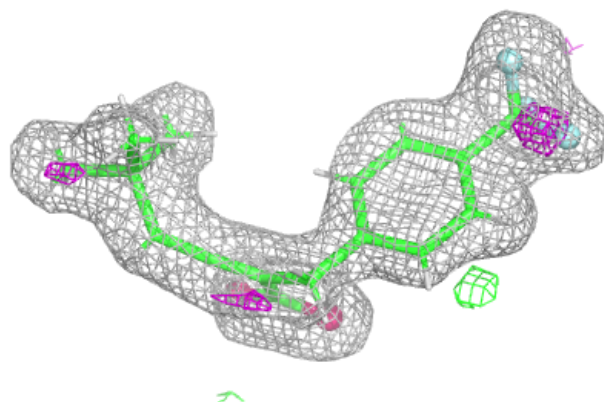
Electron density around A1EYS G 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

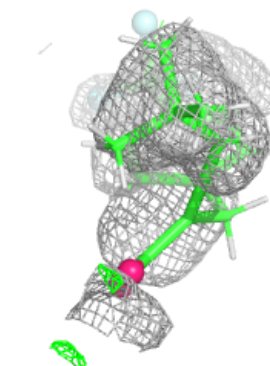
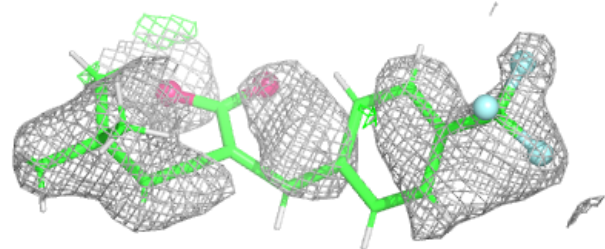
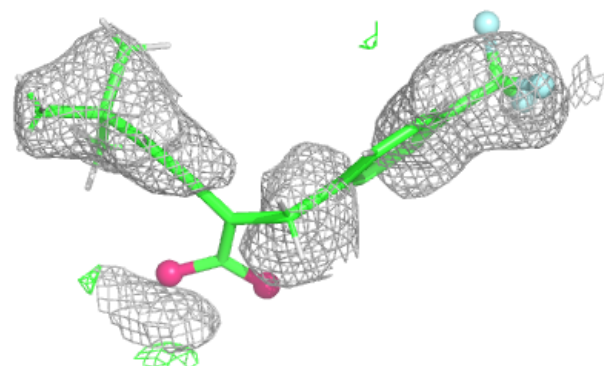


Electron density around A1EYS H 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

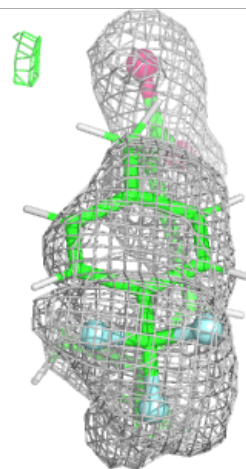
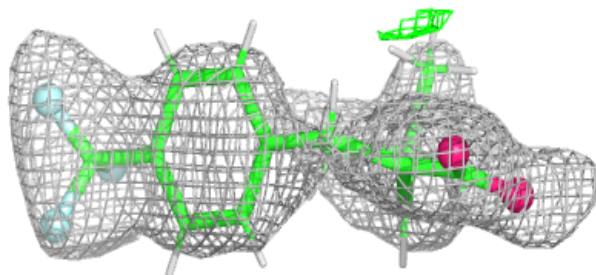
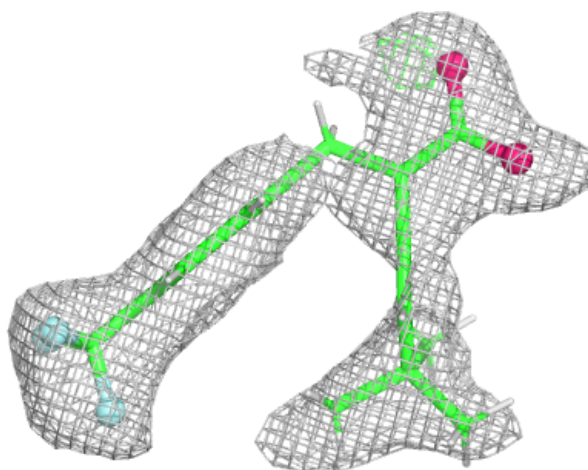
**Electron density around A1EYS A 201:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



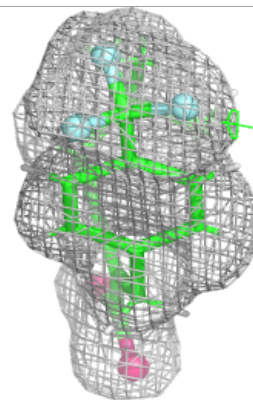
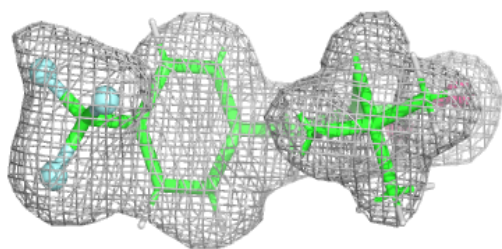
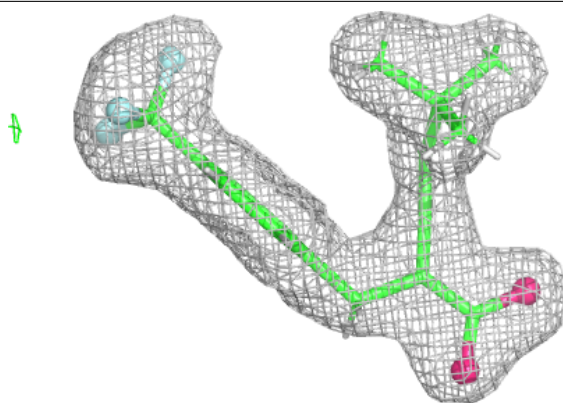
Electron density around A1EYS F 201:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

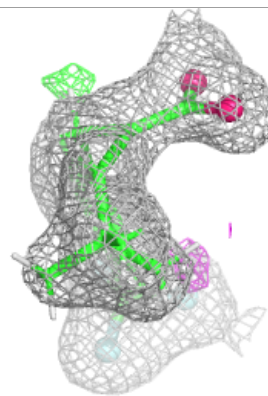
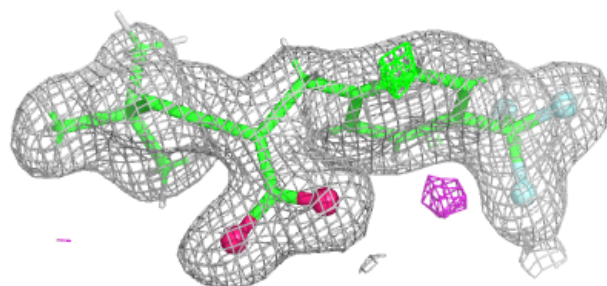
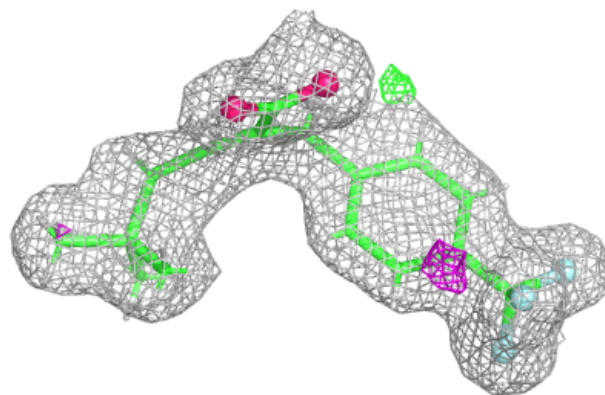


Electron density around A1EYS B 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around A1EYS D 201:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.