



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:50 AM UTC

PDB ID : 9H38 / pdb_00009h38
Title : C-terminal domain of the F-ENA tip fibrillum F-BclA from *Bacillus thuringiensis*
Authors : Sogues, A.; Sleutel, M.; Remaut, H.
Deposited on : 2024-10-16
Resolution : 2.29 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:

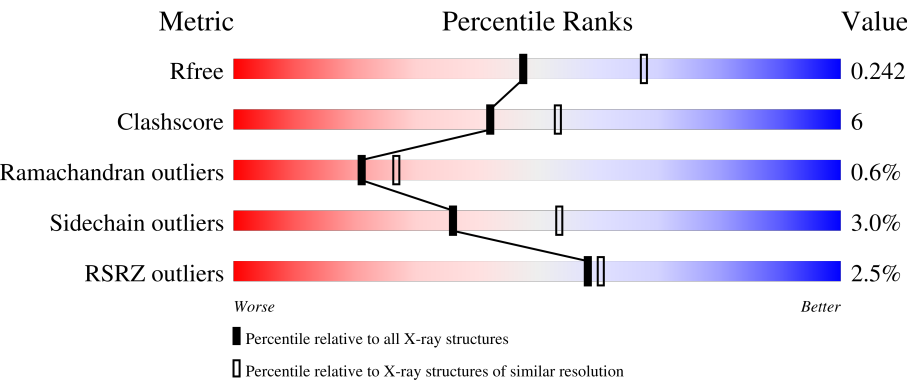
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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.



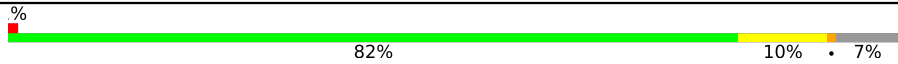
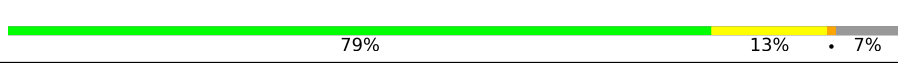
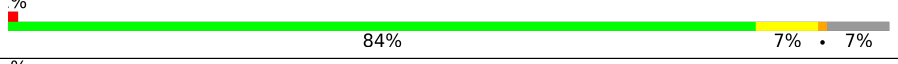
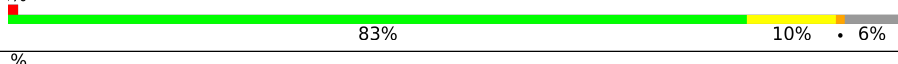
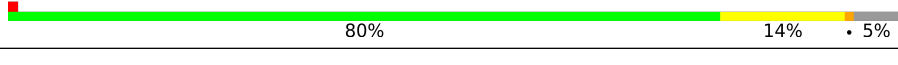
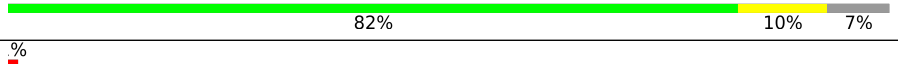
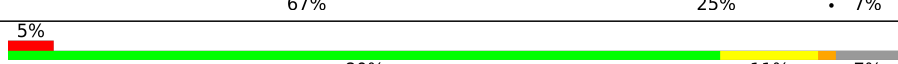
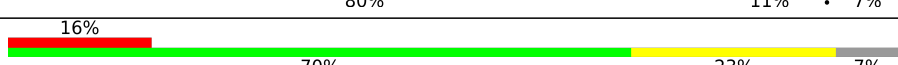
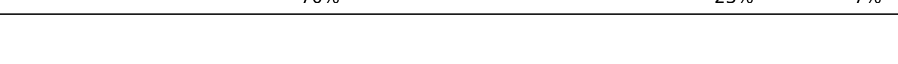
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	148	2% 82% 12% • 5%
1	B	148	% 88% • • 7%
1	C	148	77% 13% • 7%
1	D	148	84% 9% 7%
1	E	148	81% 11% 7%

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Mol	Chain	Length	Quality of chain
1	F	148	
1	G	148	
1	H	148	
1	I	148	
1	J	148	
1	K	148	
1	L	148	
1	M	148	
1	N	148	
1	O	148	
1	P	148	
1	Q	148	
1	R	148	
1	S	148	
1	T	148	
1	U	148	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	A	201	-	X	-	-
2	GOL	G	201	-	X	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 22780 atoms, of which 0 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 Flagellar hook-length control protein FliK.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	140	Total	C	N	O	0	1	0
			1014	632	170	212			
1	B	137	Total	C	N	O	0	0	0
			990	616	166	208			
1	C	137	Total	C	N	O	0	0	0
			990	616	166	208			
1	D	137	Total	C	N	O	0	0	0
			990	616	166	208			
1	E	137	Total	C	N	O	0	0	0
			986	614	166	206			
1	F	137	Total	C	N	O	0	0	0
			990	616	166	208			
1	G	137	Total	C	N	O	0	0	0
			990	616	166	208			
1	H	137	Total	C	N	O	0	0	0
			990	616	166	208			
1	I	137	Total	C	N	O	0	0	0
			990	616	166	208			
1	J	140	Total	C	N	O	0	0	0
			1009	629	169	211			
1	K	139	Total	C	N	O	0	1	0
			1007	627	169	211			
1	L	140	Total	C	N	O	0	0	0
			1008	629	169	210			
1	M	135	Total	C	N	O	0	0	0
			979	610	164	205			
1	N	137	Total	C	N	O	0	0	0
			990	616	166	208			
1	O	137	Total	C	N	O	0	1	0
			995	619	167	209			
1	P	140	Total	C	N	O	0	0	0
			1009	629	169	211			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	Q	139	Total	C	N	O	0	0	0
			1002	624	168	210			
1	R	141	Total	C	N	O	0	0	0
			1006	627	167	212			
1	S	138	Total	C	N	O	0	0	0
			997	622	167	208			
1	T	138	Total	C	N	O	0	0	0
			994	620	167	207			
1	U	138	Total	C	N	O	0	0	0
			992	619	164	209			

There are 147 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	MET	-	initiating methionine	UNP A0A9X6QBI1
A	33	HIS	-	expression tag	UNP A0A9X6QBI1
A	34	HIS	-	expression tag	UNP A0A9X6QBI1
A	35	HIS	-	expression tag	UNP A0A9X6QBI1
A	36	HIS	-	expression tag	UNP A0A9X6QBI1
A	37	HIS	-	expression tag	UNP A0A9X6QBI1
A	38	HIS	-	expression tag	UNP A0A9X6QBI1
B	32	MET	-	initiating methionine	UNP A0A9X6QBI1
B	33	HIS	-	expression tag	UNP A0A9X6QBI1
B	34	HIS	-	expression tag	UNP A0A9X6QBI1
B	35	HIS	-	expression tag	UNP A0A9X6QBI1
B	36	HIS	-	expression tag	UNP A0A9X6QBI1
B	37	HIS	-	expression tag	UNP A0A9X6QBI1
B	38	HIS	-	expression tag	UNP A0A9X6QBI1
C	32	MET	-	initiating methionine	UNP A0A9X6QBI1
C	33	HIS	-	expression tag	UNP A0A9X6QBI1
C	34	HIS	-	expression tag	UNP A0A9X6QBI1
C	35	HIS	-	expression tag	UNP A0A9X6QBI1
C	36	HIS	-	expression tag	UNP A0A9X6QBI1
C	37	HIS	-	expression tag	UNP A0A9X6QBI1
C	38	HIS	-	expression tag	UNP A0A9X6QBI1
D	32	MET	-	initiating methionine	UNP A0A9X6QBI1
D	33	HIS	-	expression tag	UNP A0A9X6QBI1
D	34	HIS	-	expression tag	UNP A0A9X6QBI1
D	35	HIS	-	expression tag	UNP A0A9X6QBI1
D	36	HIS	-	expression tag	UNP A0A9X6QBI1
D	37	HIS	-	expression tag	UNP A0A9X6QBI1
D	38	HIS	-	expression tag	UNP A0A9X6QBI1
E	32	MET	-	initiating methionine	UNP A0A9X6QBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	33	HIS	-	expression tag	UNP A0A9X6QBI1
E	34	HIS	-	expression tag	UNP A0A9X6QBI1
E	35	HIS	-	expression tag	UNP A0A9X6QBI1
E	36	HIS	-	expression tag	UNP A0A9X6QBI1
E	37	HIS	-	expression tag	UNP A0A9X6QBI1
E	38	HIS	-	expression tag	UNP A0A9X6QBI1
F	32	MET	-	initiating methionine	UNP A0A9X6QBI1
F	33	HIS	-	expression tag	UNP A0A9X6QBI1
F	34	HIS	-	expression tag	UNP A0A9X6QBI1
F	35	HIS	-	expression tag	UNP A0A9X6QBI1
F	36	HIS	-	expression tag	UNP A0A9X6QBI1
F	37	HIS	-	expression tag	UNP A0A9X6QBI1
F	38	HIS	-	expression tag	UNP A0A9X6QBI1
G	32	MET	-	initiating methionine	UNP A0A9X6QBI1
G	33	HIS	-	expression tag	UNP A0A9X6QBI1
G	34	HIS	-	expression tag	UNP A0A9X6QBI1
G	35	HIS	-	expression tag	UNP A0A9X6QBI1
G	36	HIS	-	expression tag	UNP A0A9X6QBI1
G	37	HIS	-	expression tag	UNP A0A9X6QBI1
G	38	HIS	-	expression tag	UNP A0A9X6QBI1
H	32	MET	-	initiating methionine	UNP A0A9X6QBI1
H	33	HIS	-	expression tag	UNP A0A9X6QBI1
H	34	HIS	-	expression tag	UNP A0A9X6QBI1
H	35	HIS	-	expression tag	UNP A0A9X6QBI1
H	36	HIS	-	expression tag	UNP A0A9X6QBI1
H	37	HIS	-	expression tag	UNP A0A9X6QBI1
H	38	HIS	-	expression tag	UNP A0A9X6QBI1
I	32	MET	-	initiating methionine	UNP A0A9X6QBI1
I	33	HIS	-	expression tag	UNP A0A9X6QBI1
I	34	HIS	-	expression tag	UNP A0A9X6QBI1
I	35	HIS	-	expression tag	UNP A0A9X6QBI1
I	36	HIS	-	expression tag	UNP A0A9X6QBI1
I	37	HIS	-	expression tag	UNP A0A9X6QBI1
I	38	HIS	-	expression tag	UNP A0A9X6QBI1
J	32	MET	-	initiating methionine	UNP A0A9X6QBI1
J	33	HIS	-	expression tag	UNP A0A9X6QBI1
J	34	HIS	-	expression tag	UNP A0A9X6QBI1
J	35	HIS	-	expression tag	UNP A0A9X6QBI1
J	36	HIS	-	expression tag	UNP A0A9X6QBI1
J	37	HIS	-	expression tag	UNP A0A9X6QBI1
J	38	HIS	-	expression tag	UNP A0A9X6QBI1
K	32	MET	-	initiating methionine	UNP A0A9X6QBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
K	33	HIS	-	expression tag	UNP A0A9X6QBI1
K	34	HIS	-	expression tag	UNP A0A9X6QBI1
K	35	HIS	-	expression tag	UNP A0A9X6QBI1
K	36	HIS	-	expression tag	UNP A0A9X6QBI1
K	37	HIS	-	expression tag	UNP A0A9X6QBI1
K	38	HIS	-	expression tag	UNP A0A9X6QBI1
L	32	MET	-	initiating methionine	UNP A0A9X6QBI1
L	33	HIS	-	expression tag	UNP A0A9X6QBI1
L	34	HIS	-	expression tag	UNP A0A9X6QBI1
L	35	HIS	-	expression tag	UNP A0A9X6QBI1
L	36	HIS	-	expression tag	UNP A0A9X6QBI1
L	37	HIS	-	expression tag	UNP A0A9X6QBI1
L	38	HIS	-	expression tag	UNP A0A9X6QBI1
M	32	MET	-	initiating methionine	UNP A0A9X6QBI1
M	33	HIS	-	expression tag	UNP A0A9X6QBI1
M	34	HIS	-	expression tag	UNP A0A9X6QBI1
M	35	HIS	-	expression tag	UNP A0A9X6QBI1
M	36	HIS	-	expression tag	UNP A0A9X6QBI1
M	37	HIS	-	expression tag	UNP A0A9X6QBI1
M	38	HIS	-	expression tag	UNP A0A9X6QBI1
N	32	MET	-	initiating methionine	UNP A0A9X6QBI1
N	33	HIS	-	expression tag	UNP A0A9X6QBI1
N	34	HIS	-	expression tag	UNP A0A9X6QBI1
N	35	HIS	-	expression tag	UNP A0A9X6QBI1
N	36	HIS	-	expression tag	UNP A0A9X6QBI1
N	37	HIS	-	expression tag	UNP A0A9X6QBI1
N	38	HIS	-	expression tag	UNP A0A9X6QBI1
O	32	MET	-	initiating methionine	UNP A0A9X6QBI1
O	33	HIS	-	expression tag	UNP A0A9X6QBI1
O	34	HIS	-	expression tag	UNP A0A9X6QBI1
O	35	HIS	-	expression tag	UNP A0A9X6QBI1
O	36	HIS	-	expression tag	UNP A0A9X6QBI1
O	37	HIS	-	expression tag	UNP A0A9X6QBI1
O	38	HIS	-	expression tag	UNP A0A9X6QBI1
P	32	MET	-	initiating methionine	UNP A0A9X6QBI1
P	33	HIS	-	expression tag	UNP A0A9X6QBI1
P	34	HIS	-	expression tag	UNP A0A9X6QBI1
P	35	HIS	-	expression tag	UNP A0A9X6QBI1
P	36	HIS	-	expression tag	UNP A0A9X6QBI1
P	37	HIS	-	expression tag	UNP A0A9X6QBI1
P	38	HIS	-	expression tag	UNP A0A9X6QBI1
Q	32	MET	-	initiating methionine	UNP A0A9X6QBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	33	HIS	-	expression tag	UNP A0A9X6QBI1
Q	34	HIS	-	expression tag	UNP A0A9X6QBI1
Q	35	HIS	-	expression tag	UNP A0A9X6QBI1
Q	36	HIS	-	expression tag	UNP A0A9X6QBI1
Q	37	HIS	-	expression tag	UNP A0A9X6QBI1
Q	38	HIS	-	expression tag	UNP A0A9X6QBI1
R	32	MET	-	initiating methionine	UNP A0A9X6QBI1
R	33	HIS	-	expression tag	UNP A0A9X6QBI1
R	34	HIS	-	expression tag	UNP A0A9X6QBI1
R	35	HIS	-	expression tag	UNP A0A9X6QBI1
R	36	HIS	-	expression tag	UNP A0A9X6QBI1
R	37	HIS	-	expression tag	UNP A0A9X6QBI1
R	38	HIS	-	expression tag	UNP A0A9X6QBI1
S	32	MET	-	initiating methionine	UNP A0A9X6QBI1
S	33	HIS	-	expression tag	UNP A0A9X6QBI1
S	34	HIS	-	expression tag	UNP A0A9X6QBI1
S	35	HIS	-	expression tag	UNP A0A9X6QBI1
S	36	HIS	-	expression tag	UNP A0A9X6QBI1
S	37	HIS	-	expression tag	UNP A0A9X6QBI1
S	38	HIS	-	expression tag	UNP A0A9X6QBI1
T	32	MET	-	initiating methionine	UNP A0A9X6QBI1
T	33	HIS	-	expression tag	UNP A0A9X6QBI1
T	34	HIS	-	expression tag	UNP A0A9X6QBI1
T	35	HIS	-	expression tag	UNP A0A9X6QBI1
T	36	HIS	-	expression tag	UNP A0A9X6QBI1
T	37	HIS	-	expression tag	UNP A0A9X6QBI1
T	38	HIS	-	expression tag	UNP A0A9X6QBI1
U	32	MET	-	initiating methionine	UNP A0A9X6QBI1
U	33	HIS	-	expression tag	UNP A0A9X6QBI1
U	34	HIS	-	expression tag	UNP A0A9X6QBI1
U	35	HIS	-	expression tag	UNP A0A9X6QBI1
U	36	HIS	-	expression tag	UNP A0A9X6QBI1
U	37	HIS	-	expression tag	UNP A0A9X6QBI1
U	38	HIS	-	expression tag	UNP A0A9X6QBI1

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		
2	J	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		
3	N	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	122	Total	O	0	0
			122	122		
4	B	110	Total	O	0	0
			110	110		
4	C	104	Total	O	0	0
			104	104		
4	D	94	Total	O	0	0
			94	94		
4	E	110	Total	O	0	0
			110	110		
4	F	89	Total	O	0	0
			89	89		
4	G	124	Total	O	0	0
			124	124		
4	H	93	Total	O	0	0
			93	93		

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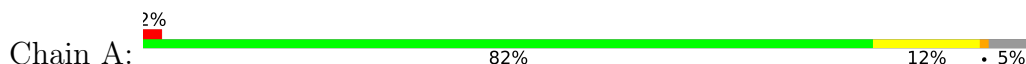
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	99	Total 99	O 99	0	0
4	J	100	Total 100	O 100	0	0
4	K	88	Total 88	O 88	0	0
4	L	103	Total 103	O 103	0	0
4	M	113	Total 113	O 113	0	0
4	N	98	Total 98	O 98	0	0
4	O	60	Total 60	O 60	0	0
4	P	77	Total 77	O 77	0	0
4	Q	52	Total 52	O 52	0	0
4	R	59	Total 59	O 59	0	0
4	S	33	Total 33	O 33	0	0
4	T	64	Total 64	O 64	0	0
4	U	24	Total 24	O 24	0	0

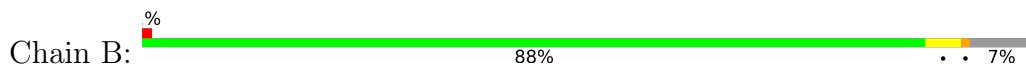
3 Residue-property plots [i](#)

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.

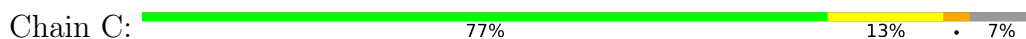
- Molecule 1: Flagellar hook-length control protein FliK



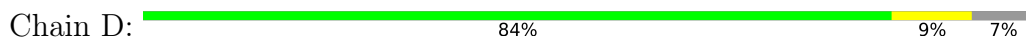
- Molecule 1: Flagellar hook-length control protein FliK



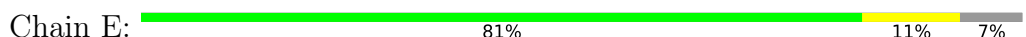
- Molecule 1: Flagellar hook-length control protein FliK



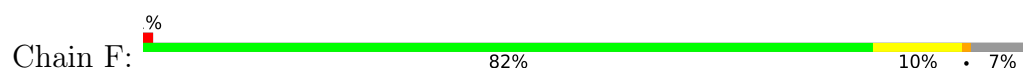
- Molecule 1: Flagellar hook-length control protein FliK



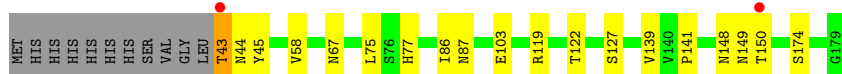
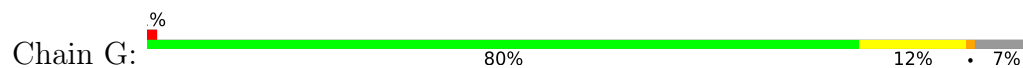
- Molecule 1: Flagellar hook-length control protein FliK



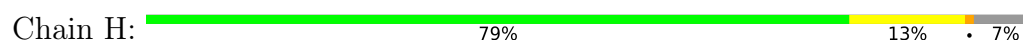
- Molecule 1: Flagellar hook-length control protein FliK



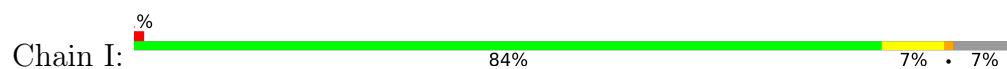
- Molecule 1: Flagellar hook-length control protein FliK



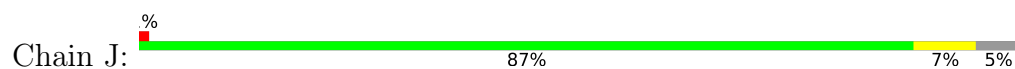
- Molecule 1: Flagellar hook-length control protein FliK



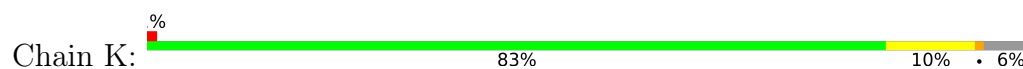
- Molecule 1: Flagellar hook-length control protein FliK



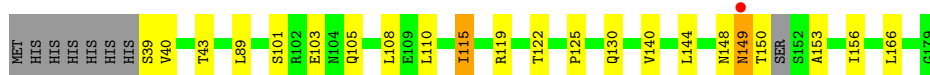
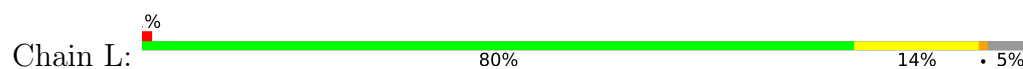
- Molecule 1: Flagellar hook-length control protein FliK



- Molecule 1: Flagellar hook-length control protein FliK



- Molecule 1: Flagellar hook-length control protein FliK



- Molecule 1: Flagellar hook-length control protein FliK

Chain M:  80% 11% 9%



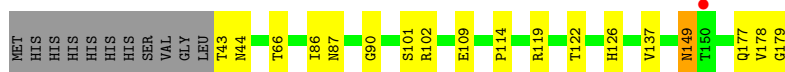
- Molecule 1: Flagellar hook-length control protein FliK

Chain N:  82% 10% 7%



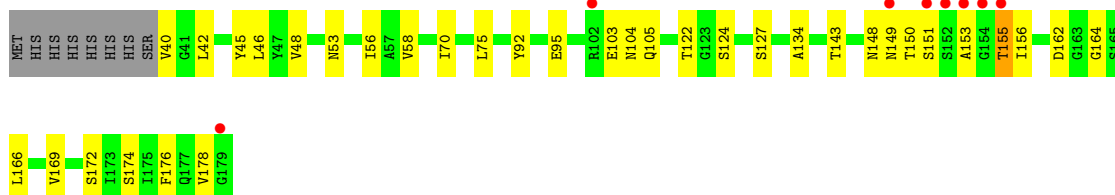
- Molecule 1: Flagellar hook-length control protein FliK

Chain O:  80% 11% 7%



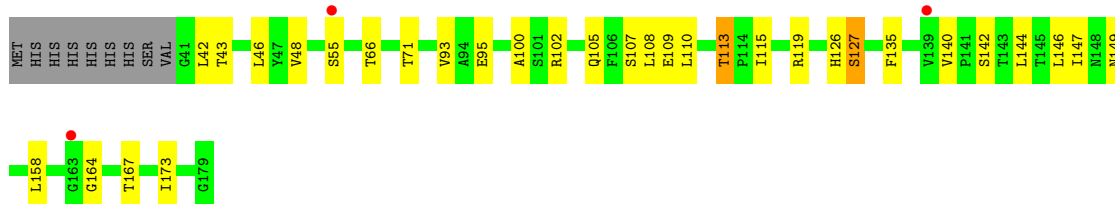
- Molecule 1: Flagellar hook-length control protein FliK

Chain P:  71% 23% 5%



- Molecule 1: Flagellar hook-length control protein FliK

Chain Q:  72% 20% 6%



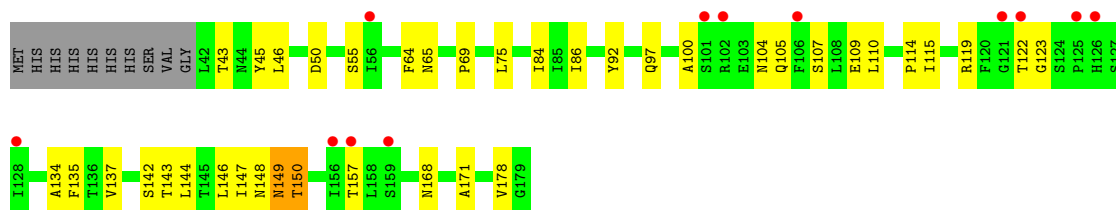
- Molecule 1: Flagellar hook-length control protein FliK

Chain R:  76% 18% 5%



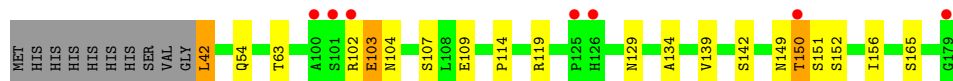
• Molecule 1: Flagellar hook-length control protein FliK

Chain S:  8% 67% 25% 7%



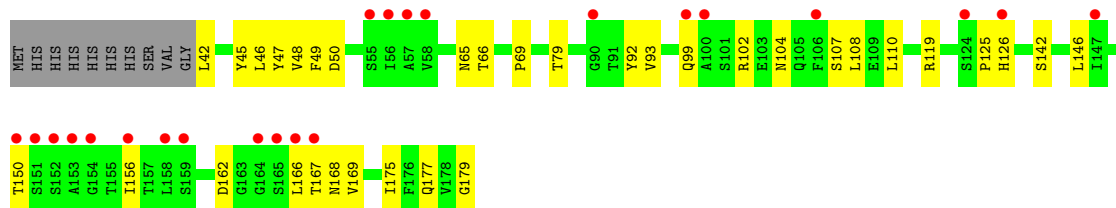
• Molecule 1: Flagellar hook-length control protein FliK

Chain T:  5% 80% 11% 7%



• Molecule 1: Flagellar hook-length control protein FliK

Chain U:  16% 70% 23% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.83Å 113.49Å 113.60Å 60.11° 89.19° 86.36°	Depositor
Resolution (Å)	49.24 – 2.29 49.24 – 2.29	Depositor EDS
% Data completeness (in resolution range)	92.3 (49.24-2.29) 92.3 (49.24-2.29)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
R, R_{free}	0.185 , 0.242 0.185 , 0.242	Depositor DCC
R_{free} test set	6372 reflections (4.57%)	wwPDB-VP
Wilson B-factor (Å ²)	12.2	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.033 for -h,-k+l,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	22780	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, GOL

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	0.35	0/1033	0.59	0/1415
1	B	0.36	0/1006	0.60	0/1378
1	C	0.38	0/1006	0.59	0/1378
1	D	0.36	0/1006	0.54	0/1378
1	E	0.37	0/1002	0.57	0/1373
1	F	0.34	0/1006	0.52	0/1378
1	G	0.36	0/1006	0.54	0/1378
1	H	0.35	0/1006	0.57	0/1378
1	I	0.34	0/1006	0.51	0/1378
1	J	0.37	0/1025	0.56	0/1404
1	K	0.32	0/1026	0.52	0/1405
1	L	0.36	0/1024	0.55	0/1403
1	M	0.34	0/995	0.53	0/1363
1	N	0.33	0/1006	0.56	0/1378
1	O	0.28	0/1014	0.48	0/1389
1	P	0.28	0/1025	0.50	0/1404
1	Q	0.27	0/1018	0.50	0/1394
1	R	0.26	0/1022	0.44	0/1401
1	S	0.24	0/1013	0.41	0/1387
1	T	0.26	0/1010	0.46	0/1384
1	U	0.20	0/1008	0.39	0/1382
All	All	0.32	0/21263	0.52	0/29128

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

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	1014	0	995	12	0
1	B	990	0	966	6	0
1	C	990	0	966	13	0
1	D	990	0	966	7	0
1	E	986	0	962	9	0
1	F	990	0	966	9	0
1	G	990	0	966	13	0
1	H	990	0	966	10	0
1	I	990	0	966	7	0
1	J	1009	0	989	9	0
1	K	1007	0	986	16	0
1	L	1008	0	986	19	0
1	M	979	0	956	10	0
1	N	990	0	966	8	0
1	O	995	0	972	11	0
1	P	1009	0	989	29	0
1	Q	1002	0	980	19	0
1	R	1006	0	973	19	0
1	S	997	0	977	27	0
1	T	994	0	973	15	0
1	U	992	0	966	21	0
2	A	6	0	7	3	0
2	C	6	0	8	0	0
2	G	6	0	8	0	0
2	H	6	0	6	0	0
2	J	6	0	8	1	0
3	D	4	0	6	0	0
3	E	4	0	6	1	0
3	F	4	0	6	0	0
3	N	4	0	6	1	0
4	A	122	0	0	5	0
4	B	110	0	0	2	0
4	C	104	0	0	4	0
4	D	94	0	0	1	0
4	E	110	0	0	2	0
4	F	89	0	0	0	0
4	G	124	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	93	0	0	2	0
4	I	99	0	0	2	0
4	J	100	0	0	1	0
4	K	88	0	0	3	0
4	L	103	0	0	4	0
4	M	113	0	0	2	0
4	N	98	0	0	3	0
4	O	60	0	0	2	0
4	P	77	0	0	5	0
4	Q	52	0	0	3	0
4	R	59	0	0	0	0
4	S	33	0	0	1	0
4	T	64	0	0	1	0
4	U	24	0	0	1	0
All	All	22780	0	20493	259	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 6.

The worst 5 of 259 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:L:150:THR:HG21	1:L:156:ILE:HD11	1.52	0.91
1:J:40:VAL:HA	1:J:71:THR:HG23	1.59	0.84
1:C:148:ASN:ND2	4:C:301:HOH:O	2.12	0.82
1:G:149:ASN:O	4:G:301:HOH:O	2.00	0.79
1:S:119:ARG:HE	1:S:149:ASN:HD22	1.31	0.78

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 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	139/148 (94%)	132 (95%)	6 (4%)	1 (1%)	18	23
1	B	135/148 (91%)	133 (98%)	2 (2%)	0	100	100
1	C	135/148 (91%)	132 (98%)	1 (1%)	2 (2%)	8	8
1	D	135/148 (91%)	132 (98%)	2 (2%)	1 (1%)	18	23
1	E	135/148 (91%)	132 (98%)	3 (2%)	0	100	100
1	F	135/148 (91%)	131 (97%)	4 (3%)	0	100	100
1	G	135/148 (91%)	131 (97%)	3 (2%)	1 (1%)	18	23
1	H	135/148 (91%)	130 (96%)	5 (4%)	0	100	100
1	I	135/148 (91%)	131 (97%)	3 (2%)	1 (1%)	18	23
1	J	138/148 (93%)	133 (96%)	4 (3%)	1 (1%)	18	23
1	K	138/148 (93%)	133 (96%)	5 (4%)	0	100	100
1	L	138/148 (93%)	136 (99%)	2 (1%)	0	100	100
1	M	133/148 (90%)	131 (98%)	1 (1%)	1 (1%)	16	20
1	N	135/148 (91%)	130 (96%)	4 (3%)	1 (1%)	18	23
1	O	136/148 (92%)	132 (97%)	4 (3%)	0	100	100
1	P	138/148 (93%)	133 (96%)	4 (3%)	1 (1%)	18	23
1	Q	137/148 (93%)	133 (97%)	3 (2%)	1 (1%)	18	23
1	R	139/148 (94%)	133 (96%)	5 (4%)	1 (1%)	18	23
1	S	136/148 (92%)	130 (96%)	4 (3%)	2 (2%)	8	8
1	T	136/148 (92%)	130 (96%)	4 (3%)	2 (2%)	8	8
1	U	136/148 (92%)	136 (100%)	0	0	100	100
All	All	2859/3108 (92%)	2774 (97%)	69 (2%)	16 (1%)	21	27

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	155	THR
1	Q	42	LEU
1	R	151	SER
1	A	148	ASN
1	I	148	ASN

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	116/123 (94%)	109 (94%)	7 (6%)	17	25
1	B	113/123 (92%)	111 (98%)	2 (2%)	51	70
1	C	113/123 (92%)	106 (94%)	7 (6%)	16	24
1	D	113/123 (92%)	110 (97%)	3 (3%)	39	58
1	E	112/123 (91%)	110 (98%)	2 (2%)	51	70
1	F	113/123 (92%)	111 (98%)	2 (2%)	51	70
1	G	113/123 (92%)	109 (96%)	4 (4%)	32	48
1	H	113/123 (92%)	110 (97%)	3 (3%)	39	58
1	I	113/123 (92%)	110 (97%)	3 (3%)	39	58
1	J	115/123 (94%)	115 (100%)	0	100	100
1	K	115/123 (94%)	111 (96%)	4 (4%)	32	48
1	L	114/123 (93%)	112 (98%)	2 (2%)	51	70
1	M	112/123 (91%)	109 (97%)	3 (3%)	39	58
1	N	113/123 (92%)	110 (97%)	3 (3%)	39	58
1	O	114/123 (93%)	108 (95%)	6 (5%)	20	30
1	P	115/123 (94%)	115 (100%)	0	100	100
1	Q	114/123 (93%)	107 (94%)	7 (6%)	17	24
1	R	113/123 (92%)	109 (96%)	4 (4%)	32	48
1	S	114/123 (93%)	108 (95%)	6 (5%)	20	30
1	T	113/123 (92%)	109 (96%)	4 (4%)	32	48
1	U	113/123 (92%)	110 (97%)	3 (3%)	39	58
All	All	2384/2583 (92%)	2309 (97%)	75 (3%)	36	52

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Q	140	VAL
1	T	165	SER

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Mol	Chain	Res	Type
1	R	127	SER
1	S	143	THR
1	G	127	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	104	ASN
1	N	104	ASN
1	U	168	ASN
1	L	129	ASN
1	M	87	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 [i](#)

9 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	GOL	C	201	-	5,5,5	1.11	0	5,5,5	1.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	N	201	-	3,3,3	0.46	0	2,2,2	0.35	0
2	GOL	J	201	-	5,5,5	1.82	2 (40%)	5,5,5	0.74	0
3	EDO	E	201	-	3,3,3	0.49	0	2,2,2	0.64	0
3	EDO	F	201	-	3,3,3	0.41	0	2,2,2	0.66	0
2	GOL	G	201	-	5,5,5	1.43	2 (40%)	5,5,5	0.91	0
2	GOL	H	201	-	5,5,5	1.44	1 (20%)	5,5,5	1.01	0
3	EDO	D	201	-	3,3,3	0.54	0	2,2,2	0.44	0
2	GOL	A	201	-	5,5,5	1.64	2 (40%)	5,5,5	0.96	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
2	GOL	C	201	-	-	2/4/4/4	-
3	EDO	N	201	-	-	0/1/1/1	-
2	GOL	J	201	-	-	2/4/4/4	-
3	EDO	E	201	-	-	1/1/1/1	-
3	EDO	F	201	-	-	0/1/1/1	-
2	GOL	G	201	-	-	4/4/4/4	-
2	GOL	H	201	-	-	0/4/4/4	-
3	EDO	D	201	-	-	0/1/1/1	-
2	GOL	A	201	-	-	4/4/4/4	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	201	GOL	C3-C2	2.86	1.62	1.51
2	H	201	GOL	O2-C2	-2.63	1.35	1.43
2	A	201	GOL	C3-C2	2.44	1.61	1.51
2	J	201	GOL	C1-C2	2.41	1.61	1.51
2	A	201	GOL	O2-C2	-2.40	1.36	1.43

There are no bond angle outliers.

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	201	GOL	O1-C1-C2-C3

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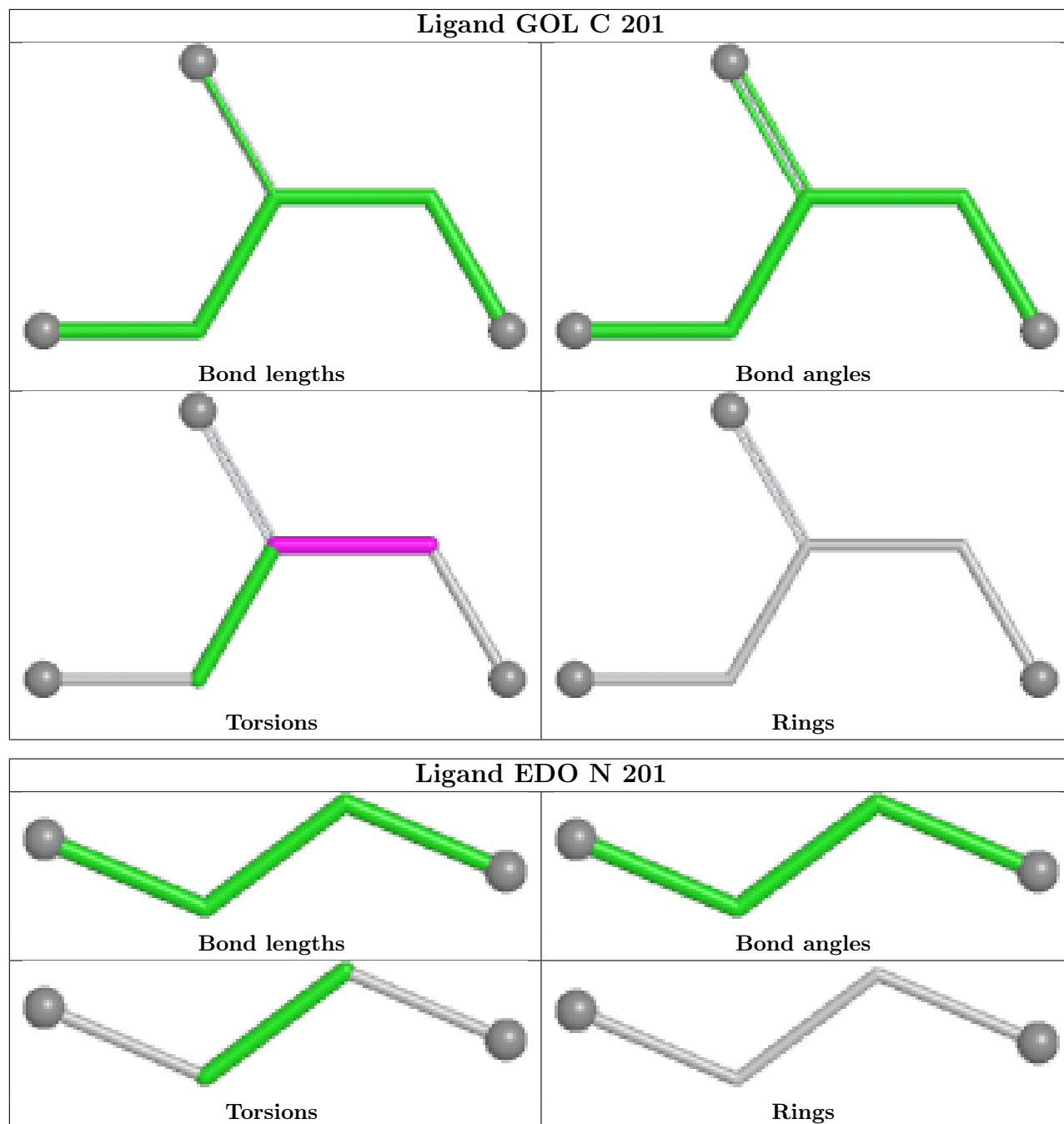
Mol	Chain	Res	Type	Atoms
2	G	201	GOL	O1-C1-C2-C3
2	G	201	GOL	C1-C2-C3-O3
2	J	201	GOL	O1-C1-C2-O2
2	A	201	GOL	O1-C1-C2-C3

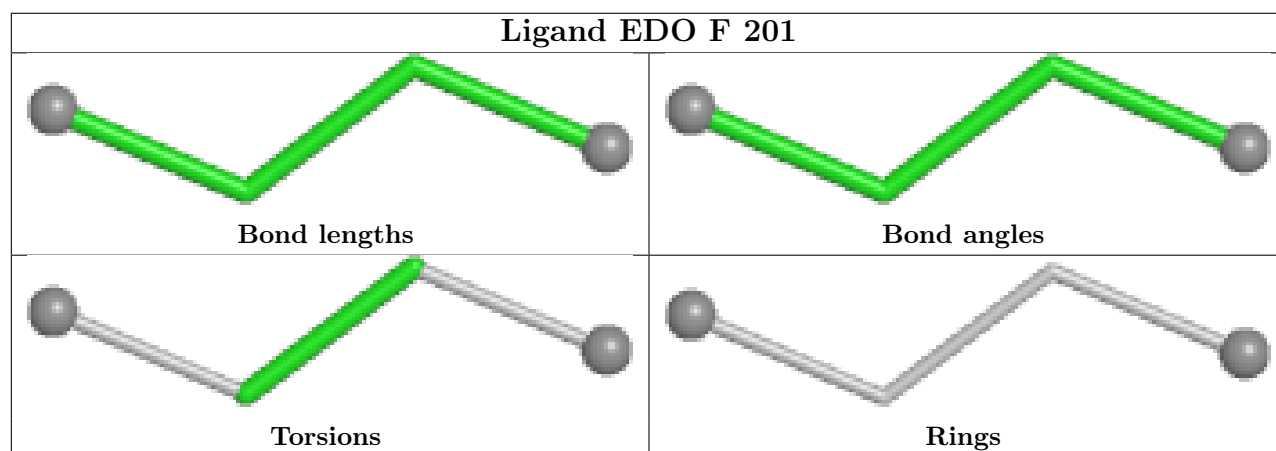
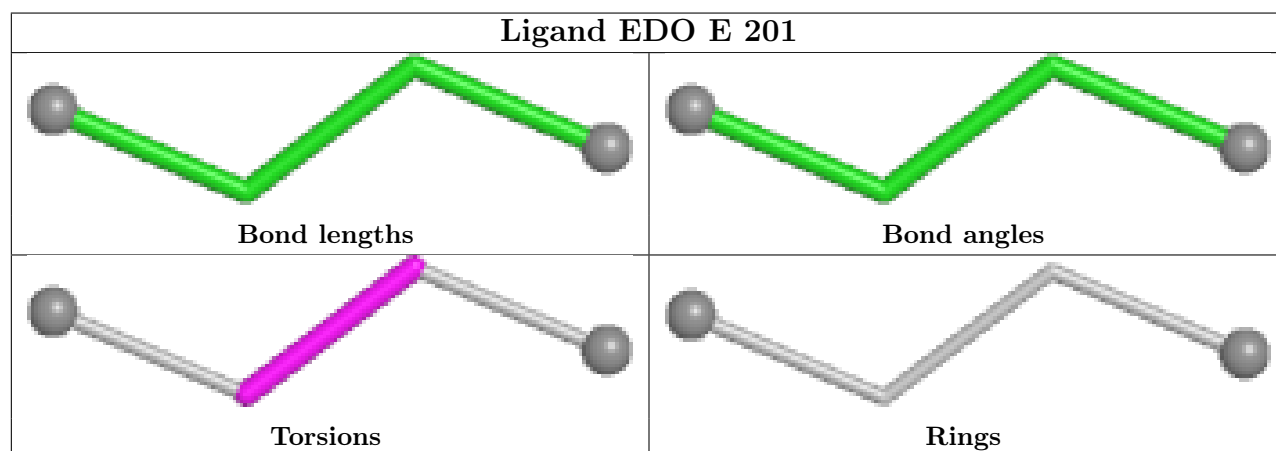
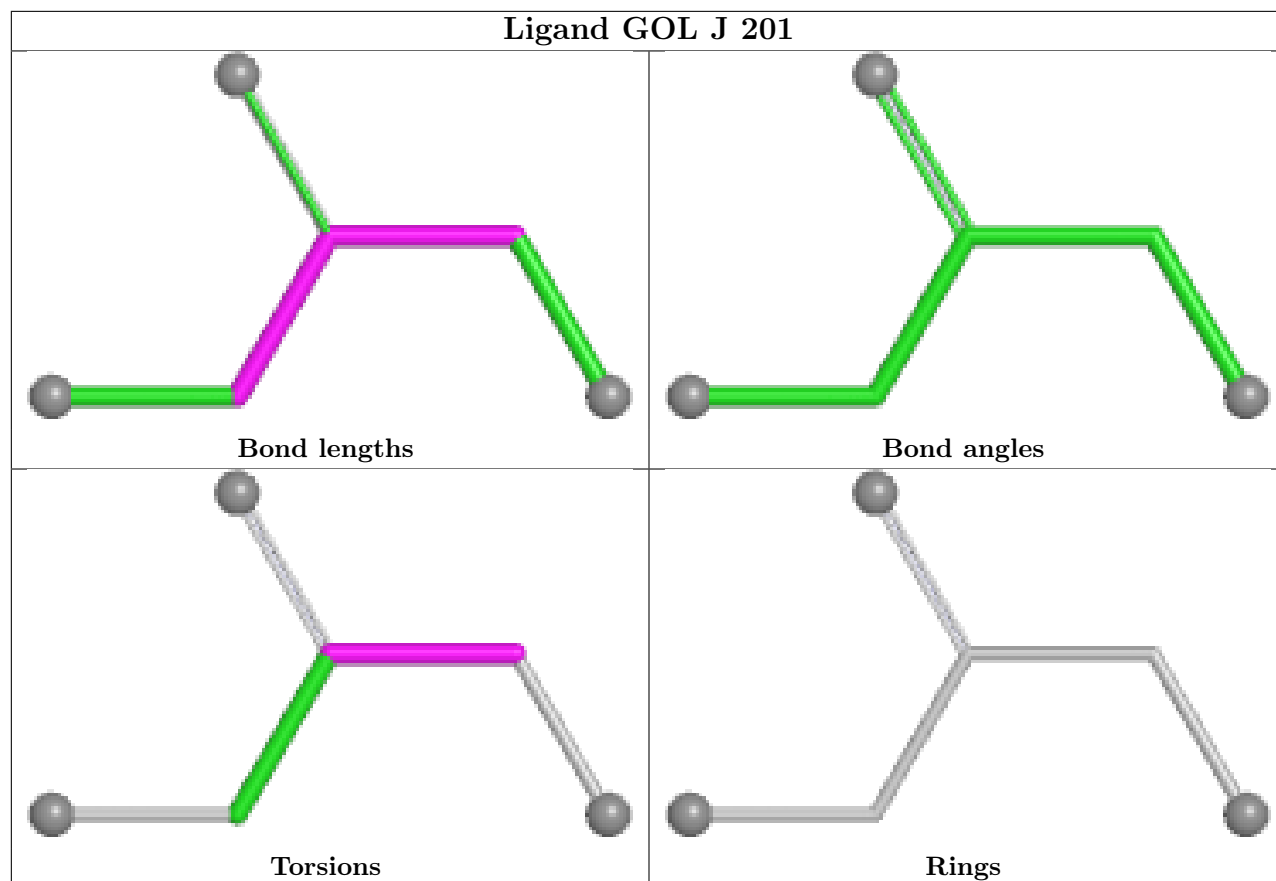
There are no ring outliers.

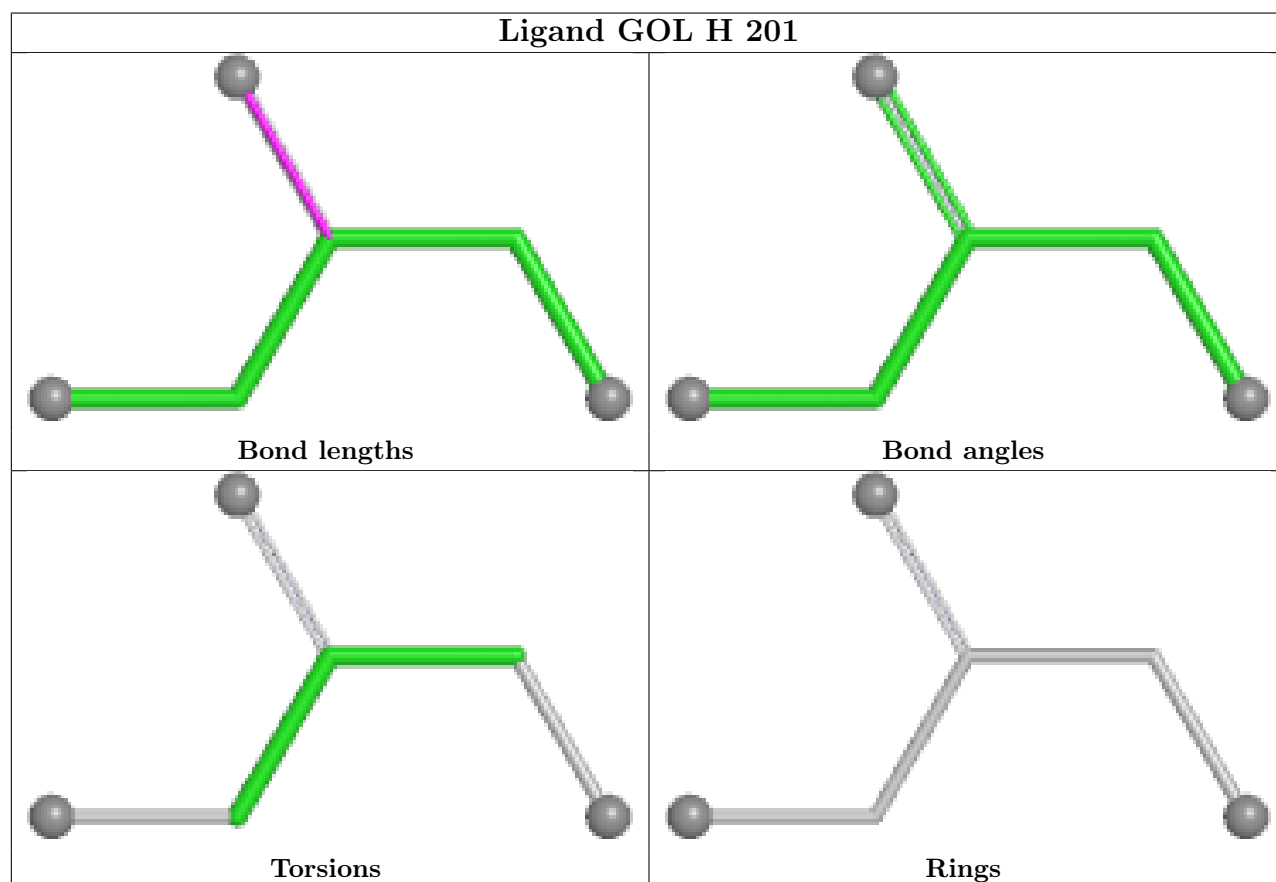
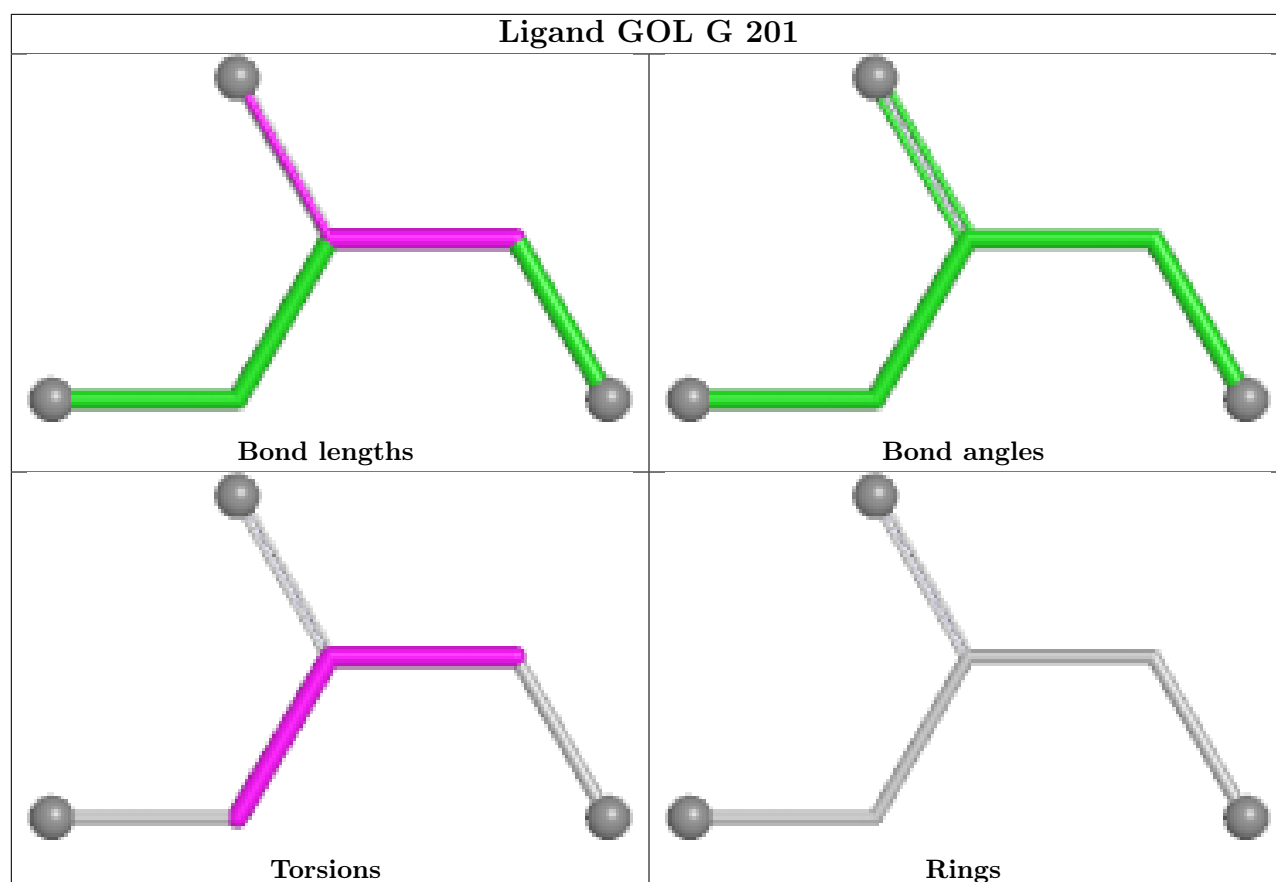
4 monomers are involved in 6 short contacts:

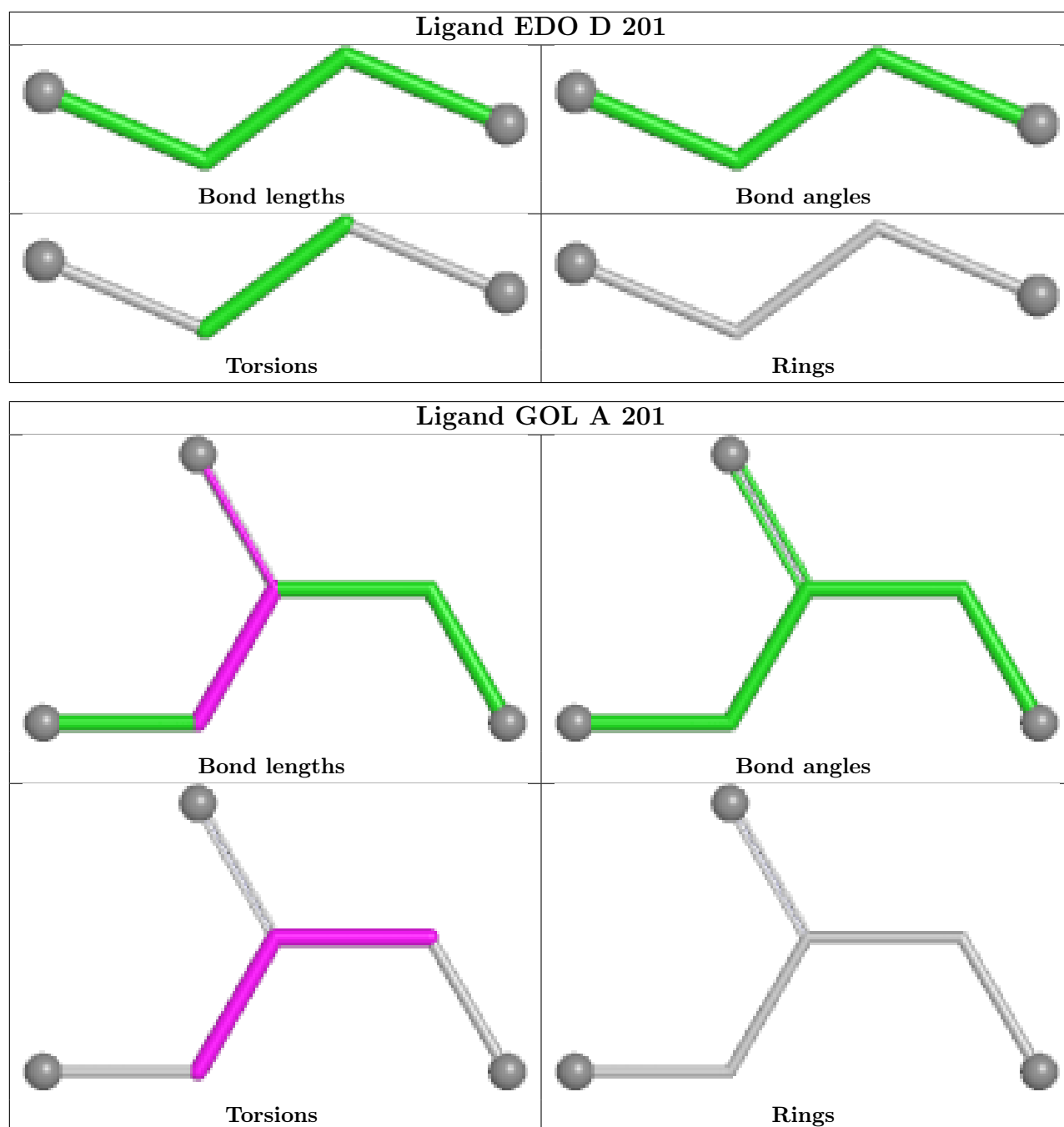
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	N	201	EDO	1	0
2	J	201	GOL	1	0
3	E	201	EDO	1	0
2	A	201	GOL	3	0

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 [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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	140/148 (94%)	-0.16	3 (2%) 63 65	4, 7, 16, 60	1 (0%)
1	B	137/148 (92%)	-0.40	1 (0%) 84 85	3, 6, 13, 22	0
1	C	137/148 (92%)	-0.24	0 100 100	5, 10, 16, 22	0
1	D	137/148 (92%)	-0.23	0 100 100	4, 10, 19, 26	0
1	E	137/148 (92%)	-0.36	0 100 100	5, 7, 13, 19	0
1	F	137/148 (92%)	-0.26	1 (0%) 84 85	6, 10, 18, 28	0
1	G	137/148 (92%)	-0.31	2 (1%) 72 73	4, 8, 16, 20	0
1	H	137/148 (92%)	-0.18	0 100 100	5, 10, 17, 27	0
1	I	137/148 (92%)	-0.23	1 (0%) 84 85	4, 10, 17, 25	0
1	J	140/148 (94%)	-0.27	1 (0%) 84 85	5, 8, 17, 24	0
1	K	139/148 (93%)	-0.25	2 (1%) 73 75	7, 12, 16, 20	1 (0%)
1	L	140/148 (94%)	-0.24	1 (0%) 84 85	5, 10, 17, 22	0
1	M	135/148 (91%)	-0.27	0 100 100	4, 10, 17, 23	0
1	N	137/148 (92%)	-0.12	0 100 100	7, 13, 22, 29	0
1	O	137/148 (92%)	0.14	1 (0%) 84 85	14, 20, 30, 36	1 (0%)
1	P	140/148 (94%)	0.52	8 (5%) 29 31	14, 24, 42, 60	0
1	Q	139/148 (93%)	0.66	3 (2%) 62 64	19, 31, 38, 44	0
1	R	141/148 (95%)	0.56	6 (4%) 40 41	15, 28, 42, 61	0
1	S	138/148 (93%)	0.99	12 (8%) 16 17	21, 38, 56, 63	0
1	T	138/148 (93%)	0.55	7 (5%) 33 35	15, 25, 53, 67	0
1	U	138/148 (93%)	1.29	23 (16%) 4 5	26, 47, 63, 75	0
All	All	2898/3108 (93%)	0.06	72 (2%) 58 60	3, 12, 45, 75	3 (0%)

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	152	SER	6.5
1	A	42	LEU	6.3
1	P	154	GLY	6.3
1	P	153	ALA	5.3
1	A	40	VAL	5.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

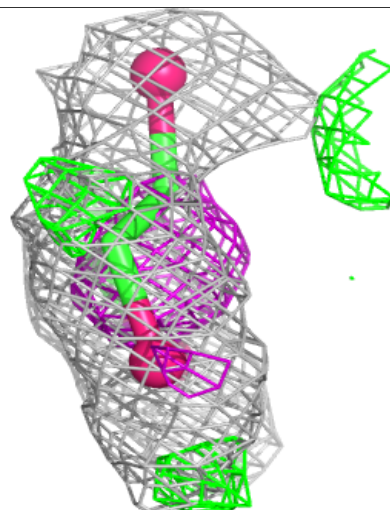
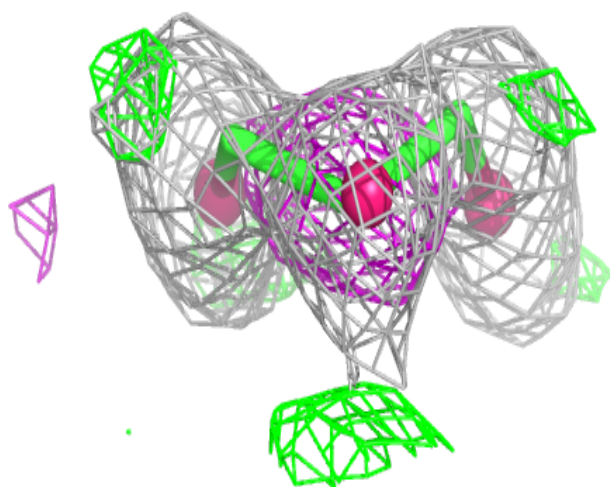
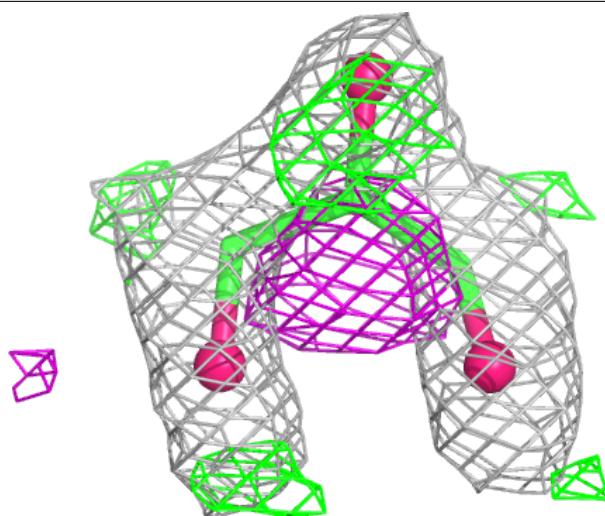
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	GOL	J	201	6/6	0.75	0.20	13,17,20,22	0
2	GOL	A	201	6/6	0.89	0.12	9,9,12,17	0
3	EDO	D	201	4/4	0.89	0.09	10,10,10,16	0
3	EDO	E	201	4/4	0.89	0.09	6,7,8,21	0
3	EDO	N	201	4/4	0.93	0.08	11,12,13,21	0
2	GOL	C	201	6/6	0.95	0.07	6,9,11,14	0
3	EDO	F	201	4/4	0.96	0.05	7,7,8,8	0
2	GOL	H	201	6/6	0.96	0.07	6,6,10,13	0
2	GOL	G	201	6/6	0.97	0.06	6,9,13,17	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.

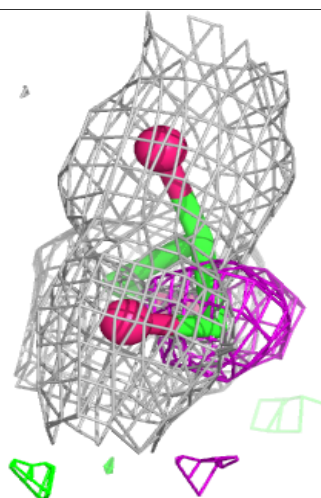
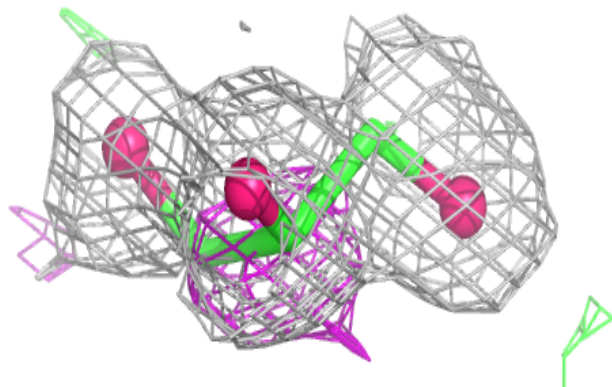
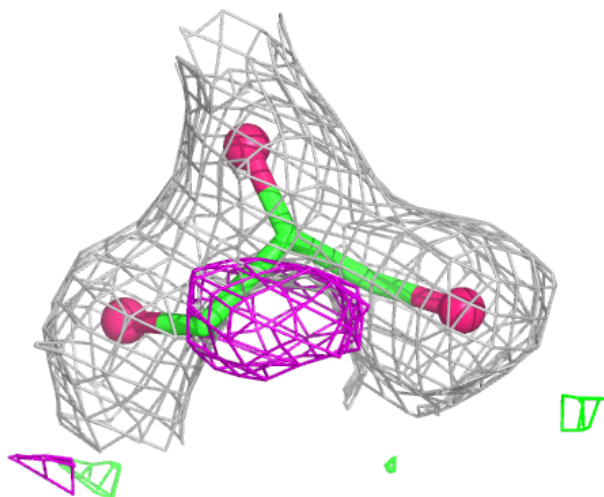
Electron density around GOL J 201:

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



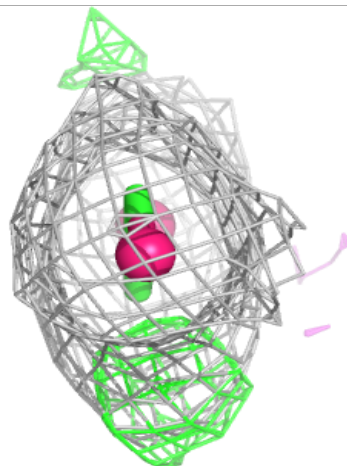
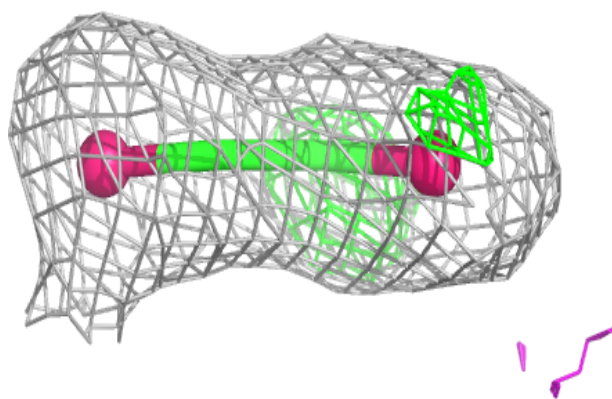
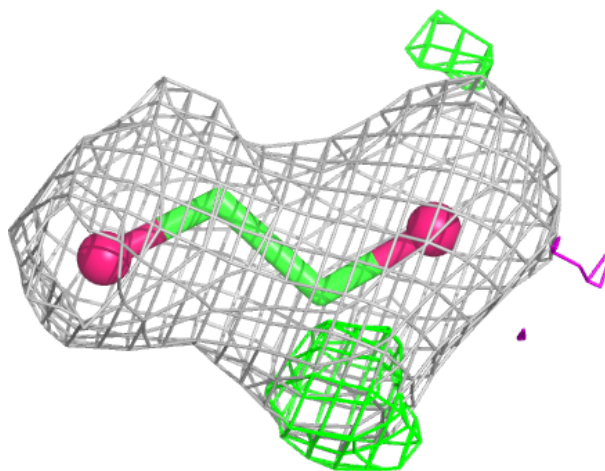
Electron density around GOL A 201:

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



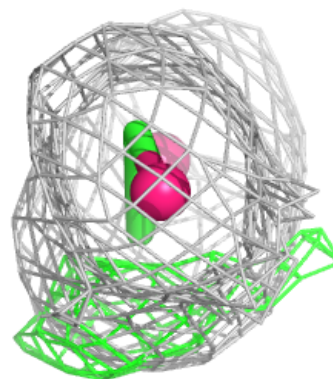
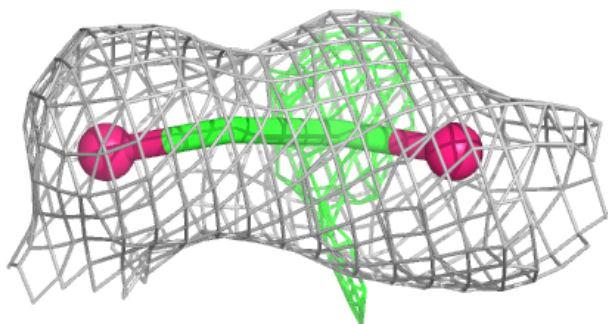
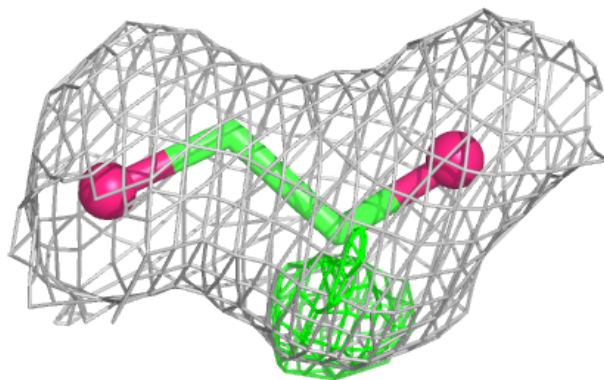
Electron density around EDO D 201:

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and green (positive)

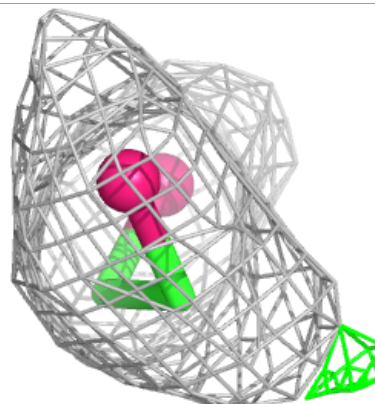
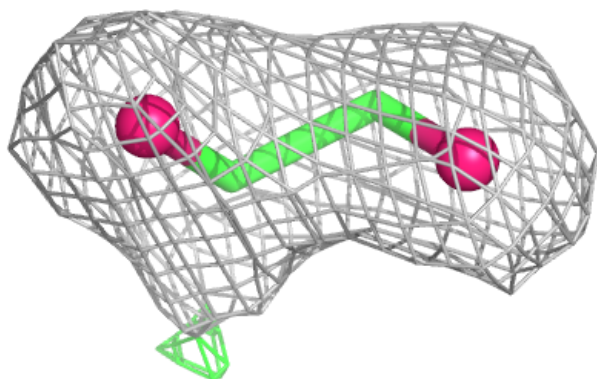
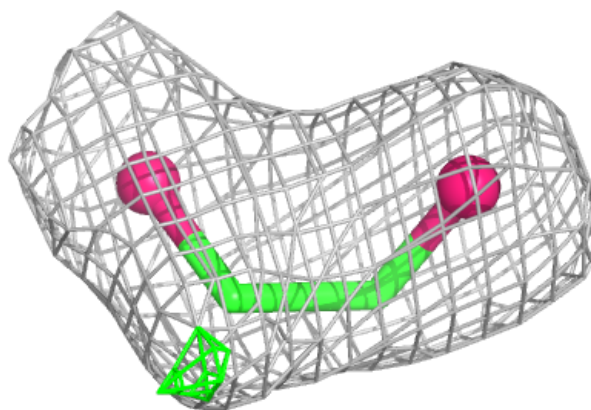


Electron density around EDO E 201:

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

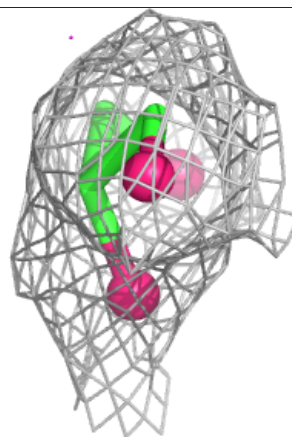
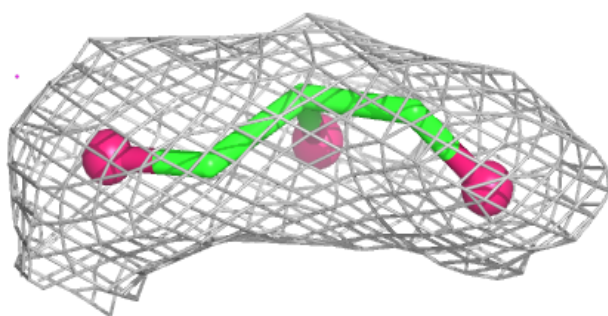
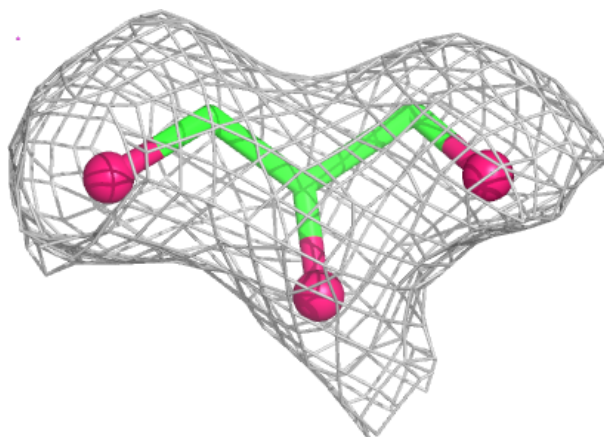
**Electron density around EDO N 201:**

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



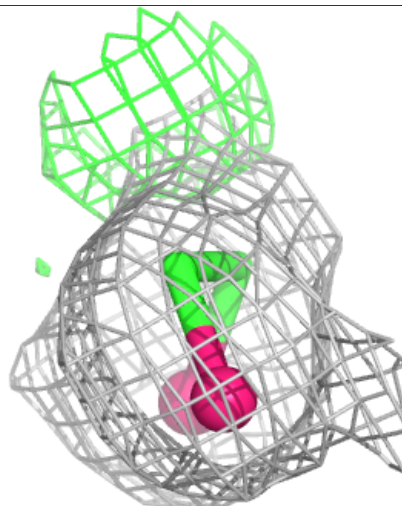
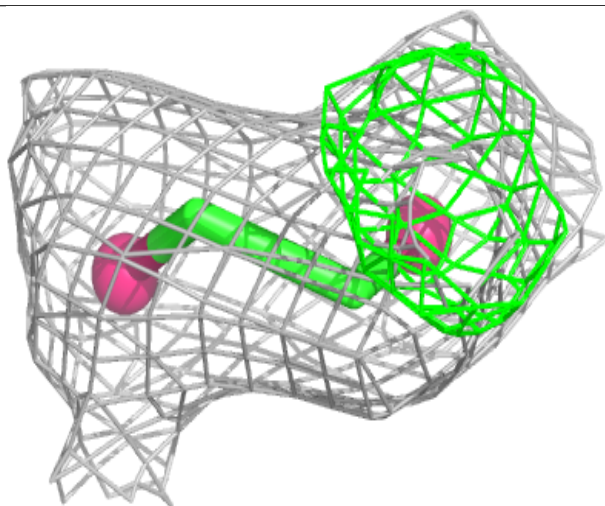
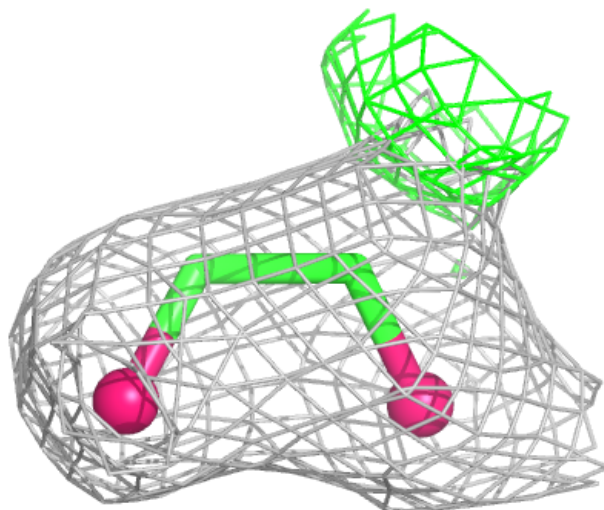
Electron density around GOL C 201:

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



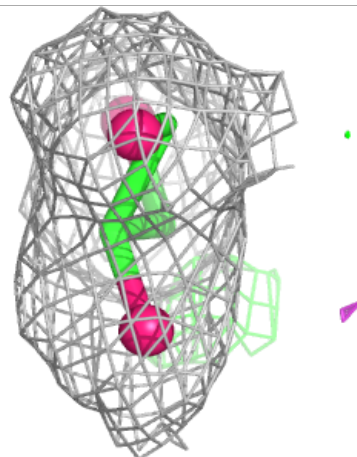
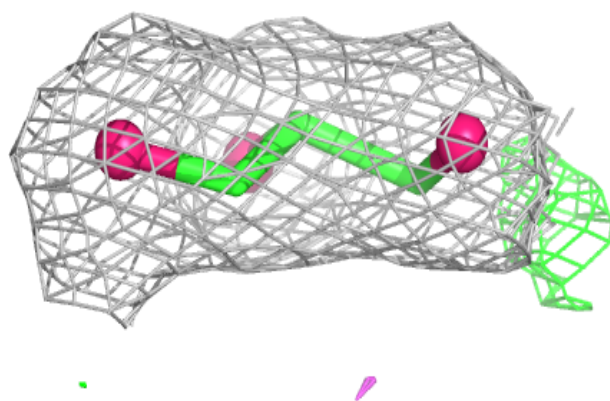
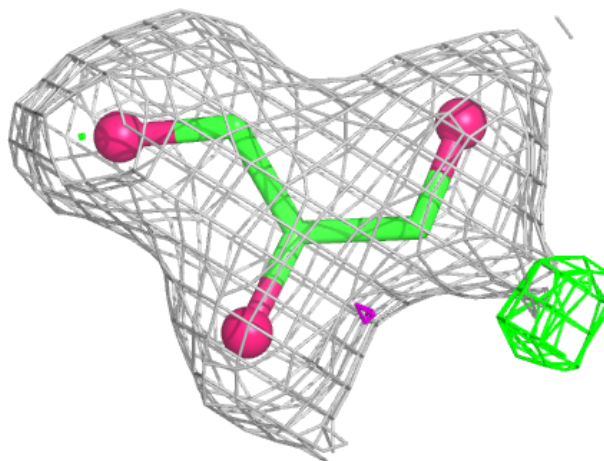
Electron density around EDO F 201:

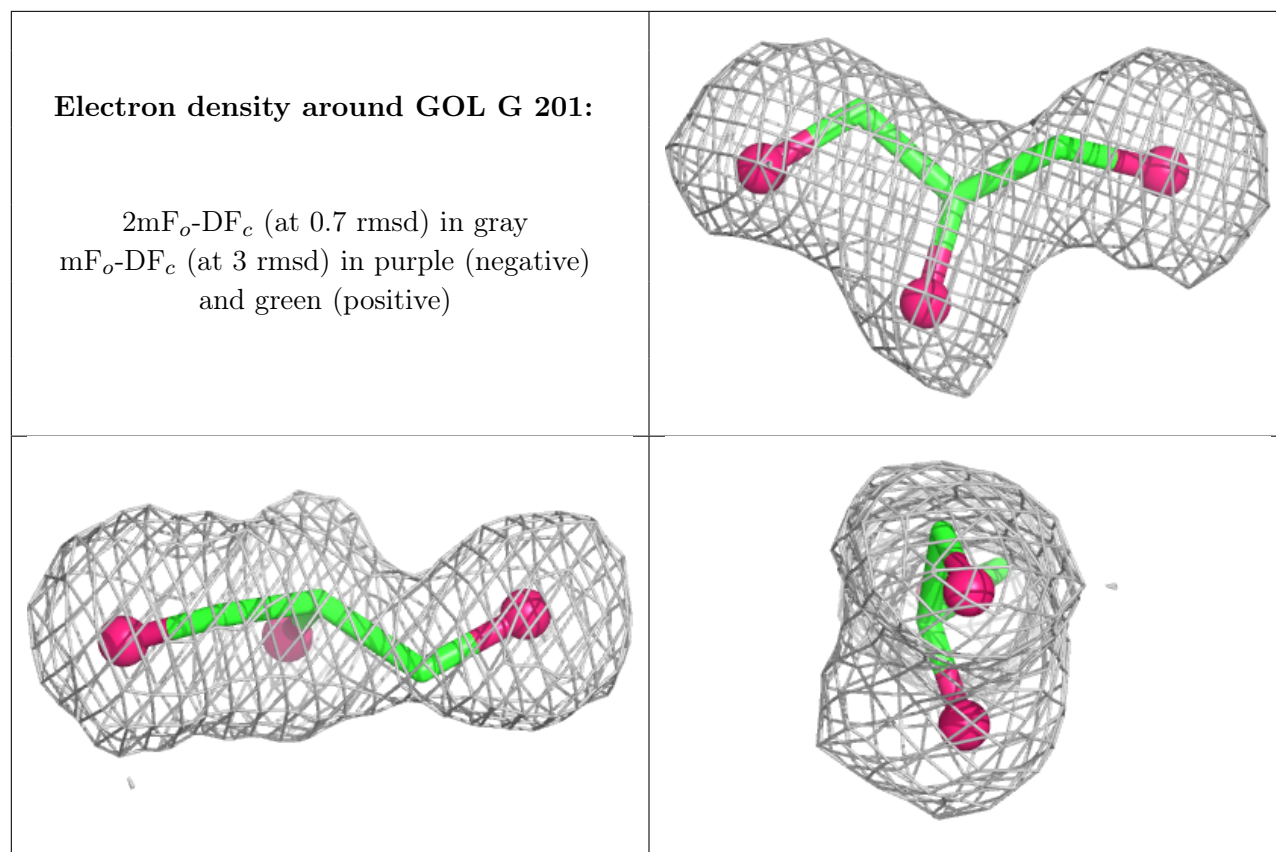
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GOL 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.