



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 21, 2021 – 06:09 am BST

PDB ID : 7P76
Title : Re-engineered 2-deoxy-D-ribose-5-phosphate aldolase catalysing asymmetric Michael addition reactions, Schiff base complex with cinnamaldehyde
Authors : Thunnissen, A.M.W.H.; Rozeboom, H.J.; Kunzendorf, A.; Poelarends, G.J.
Deposited on : 2021-07-19
Resolution : 1.90 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

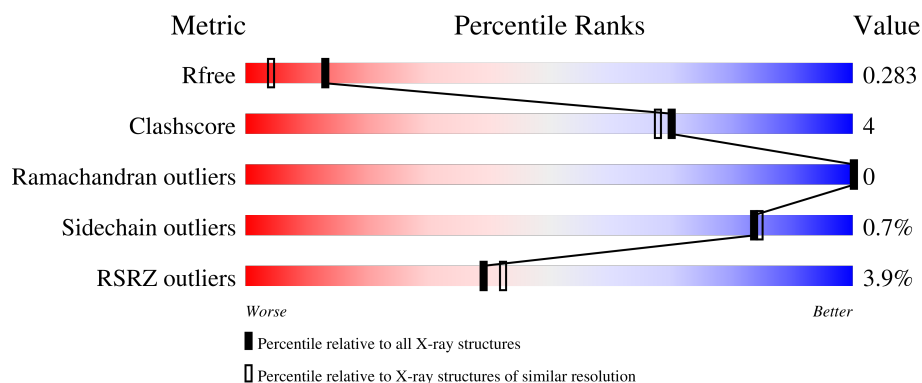
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	267	<div> <div>4%</div> <div>84%</div> <div>9%</div> <div>7%</div> </div>
1	B	267	<div> <div>2%</div> <div>84%</div> <div>9%</div> <div>7%</div> </div>
1	C	267	<div> <div>4%</div> <div>86%</div> <div>7%</div> <div>7%</div> </div>
1	D	267	<div> <div>3%</div> <div>85%</div> <div>8%</div> <div>7%</div> </div>
1	E	267	<div> <div>2%</div> <div>84%</div> <div>9%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	267	
1	G	267	
1	H	267	
1	I	267	
1	J	267	
1	K	267	
1	L	267	

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
3	GOL	I	302	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 23612 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 Deoxyribose-phosphate aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	247	Total	C	N	O	S	0	0	0
			1851	1168	320	355	8			
1	B	247	Total	C	N	O	S	0	0	0
			1850	1166	319	357	8			
1	C	248	Total	C	N	O	S	0	0	0
			1859	1172	321	358	8			
1	D	247	Total	C	N	O	S	0	1	0
			1855	1168	321	358	8			
1	E	248	Total	C	N	O	S	0	0	0
			1855	1170	321	356	8			
1	F	248	Total	C	N	O	S	0	1	0
			1870	1178	325	359	8			
1	G	248	Total	C	N	O	S	0	0	0
			1859	1172	321	358	8			
1	H	246	Total	C	N	O	S	0	0	0
			1843	1162	318	355	8			
1	I	246	Total	C	N	O	S	0	0	0
			1843	1162	318	355	8			
1	J	246	Total	C	N	O	S	0	0	0
			1846	1164	318	356	8			
1	K	247	Total	C	N	O	S	0	0	0
			1849	1166	318	357	8			
1	L	246	Total	C	N	O	S	0	0	0
			1843	1161	318	356	8			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	SER	THR	engineered mutation	UNP V0AAC4
A	22	GLY	ASP	engineered mutation	UNP V0AAC4
A	24	TYR	ASP	engineered mutation	UNP V0AAC4
A	47	SER	CYS	engineered mutation	UNP V0AAC4
A	52	SER	PHE	engineered mutation	UNP V0AAC4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	142	SER	THR	engineered mutation	UNP V0AAC4
A	172	LEU	LYS	engineered mutation	UNP V0AAC4
A	197	SER	THR	engineered mutation	UNP V0AAC4
A	202	VAL	PRO	engineered mutation	UNP V0AAC4
A	203	THR	ALA	engineered mutation	UNP V0AAC4
A	206	ALA	VAL	engineered mutation	UNP V0AAC4
A	239	GLY	SER	engineered mutation	UNP V0AAC4
A	260	LEU	-	expression tag	UNP V0AAC4
A	261	GLU	-	expression tag	UNP V0AAC4
A	262	HIS	-	expression tag	UNP V0AAC4
A	263	HIS	-	expression tag	UNP V0AAC4
A	264	HIS	-	expression tag	UNP V0AAC4
A	265	HIS	-	expression tag	UNP V0AAC4
A	266	HIS	-	expression tag	UNP V0AAC4
A	267	HIS	-	expression tag	UNP V0AAC4
B	18	SER	THR	engineered mutation	UNP V0AAC4
B	22	GLY	ASP	engineered mutation	UNP V0AAC4
B	24	TYR	ASP	engineered mutation	UNP V0AAC4
B	47	SER	CYS	engineered mutation	UNP V0AAC4
B	52	SER	PHE	engineered mutation	UNP V0AAC4
B	142	SER	THR	engineered mutation	UNP V0AAC4
B	172	LEU	LYS	engineered mutation	UNP V0AAC4
B	197	SER	THR	engineered mutation	UNP V0AAC4
B	202	VAL	PRO	engineered mutation	UNP V0AAC4
B	203	THR	ALA	engineered mutation	UNP V0AAC4
B	206	ALA	VAL	engineered mutation	UNP V0AAC4
B	239	GLY	SER	engineered mutation	UNP V0AAC4
B	260	LEU	-	expression tag	UNP V0AAC4
B	261	GLU	-	expression tag	UNP V0AAC4
B	262	HIS	-	expression tag	UNP V0AAC4
B	263	HIS	-	expression tag	UNP V0AAC4
B	264	HIS	-	expression tag	UNP V0AAC4
B	265	HIS	-	expression tag	UNP V0AAC4
B	266	HIS	-	expression tag	UNP V0AAC4
B	267	HIS	-	expression tag	UNP V0AAC4
C	18	SER	THR	engineered mutation	UNP V0AAC4
C	22	GLY	ASP	engineered mutation	UNP V0AAC4
C	24	TYR	ASP	engineered mutation	UNP V0AAC4
C	47	SER	CYS	engineered mutation	UNP V0AAC4
C	52	SER	PHE	engineered mutation	UNP V0AAC4
C	142	SER	THR	engineered mutation	UNP V0AAC4
C	172	LEU	LYS	engineered mutation	UNP V0AAC4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	197	SER	THR	engineered mutation	UNP V0AAC4
C	202	VAL	PRO	engineered mutation	UNP V0AAC4
C	203	THR	ALA	engineered mutation	UNP V0AAC4
C	206	ALA	VAL	engineered mutation	UNP V0AAC4
C	239	GLY	SER	engineered mutation	UNP V0AAC4
C	260	LEU	-	expression tag	UNP V0AAC4
C	261	GLU	-	expression tag	UNP V0AAC4
C	262	HIS	-	expression tag	UNP V0AAC4
C	263	HIS	-	expression tag	UNP V0AAC4
C	264	HIS	-	expression tag	UNP V0AAC4
C	265	HIS	-	expression tag	UNP V0AAC4
C	266	HIS	-	expression tag	UNP V0AAC4
C	267	HIS	-	expression tag	UNP V0AAC4
D	18	SER	THR	engineered mutation	UNP V0AAC4
D	22	GLY	ASP	engineered mutation	UNP V0AAC4
D	24	TYR	ASP	engineered mutation	UNP V0AAC4
D	47	SER	CYS	engineered mutation	UNP V0AAC4
D	52	SER	PHE	engineered mutation	UNP V0AAC4
D	142	SER	THR	engineered mutation	UNP V0AAC4
D	172	LEU	LYS	engineered mutation	UNP V0AAC4
D	197	SER	THR	engineered mutation	UNP V0AAC4
D	202	VAL	PRO	engineered mutation	UNP V0AAC4
D	203	THR	ALA	engineered mutation	UNP V0AAC4
D	206	ALA	VAL	engineered mutation	UNP V0AAC4
D	239	GLY	SER	engineered mutation	UNP V0AAC4
D	260	LEU	-	expression tag	UNP V0AAC4
D	261	GLU	-	expression tag	UNP V0AAC4
D	262	HIS	-	expression tag	UNP V0AAC4
D	263	HIS	-	expression tag	UNP V0AAC4
D	264	HIS	-	expression tag	UNP V0AAC4
D	265	HIS	-	expression tag	UNP V0AAC4
D	266	HIS	-	expression tag	UNP V0AAC4
D	267	HIS	-	expression tag	UNP V0AAC4
E	18	SER	THR	engineered mutation	UNP V0AAC4
E	22	GLY	ASP	engineered mutation	UNP V0AAC4
E	24	TYR	ASP	engineered mutation	UNP V0AAC4
E	47	SER	CYS	engineered mutation	UNP V0AAC4
E	52	SER	PHE	engineered mutation	UNP V0AAC4
E	142	SER	THR	engineered mutation	UNP V0AAC4
E	172	LEU	LYS	engineered mutation	UNP V0AAC4
E	197	SER	THR	engineered mutation	UNP V0AAC4
E	202	VAL	PRO	engineered mutation	UNP V0AAC4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	203	THR	ALA	engineered mutation	UNP V0AAC4
E	206	ALA	VAL	engineered mutation	UNP V0AAC4
E	239	GLY	SER	engineered mutation	UNP V0AAC4
E	260	LEU	-	expression tag	UNP V0AAC4
E	261	GLU	-	expression tag	UNP V0AAC4
E	262	HIS	-	expression tag	UNP V0AAC4
E	263	HIS	-	expression tag	UNP V0AAC4
E	264	HIS	-	expression tag	UNP V0AAC4
E	265	HIS	-	expression tag	UNP V0AAC4
E	266	HIS	-	expression tag	UNP V0AAC4
E	267	HIS	-	expression tag	UNP V0AAC4
F	18	SER	THR	engineered mutation	UNP V0AAC4
F	22	GLY	ASP	engineered mutation	UNP V0AAC4
F	24	TYR	ASP	engineered mutation	UNP V0AAC4
F	47	SER	CYS	engineered mutation	UNP V0AAC4
F	52	SER	PHE	engineered mutation	UNP V0AAC4
F	142	SER	THR	engineered mutation	UNP V0AAC4
F	172	LEU	LYS	engineered mutation	UNP V0AAC4
F	197	SER	THR	engineered mutation	UNP V0AAC4
F	202	VAL	PRO	engineered mutation	UNP V0AAC4
F	203	THR	ALA	engineered mutation	UNP V0AAC4
F	206	ALA	VAL	engineered mutation	UNP V0AAC4
F	239	GLY	SER	engineered mutation	UNP V0AAC4
F	260	LEU	-	expression tag	UNP V0AAC4
F	261	GLU	-	expression tag	UNP V0AAC4
F	262	HIS	-	expression tag	UNP V0AAC4
F	263	HIS	-	expression tag	UNP V0AAC4
F	264	HIS	-	expression tag	UNP V0AAC4
F	265	HIS	-	expression tag	UNP V0AAC4
F	266	HIS	-	expression tag	UNP V0AAC4
F	267	HIS	-	expression tag	UNP V0AAC4
G	18	SER	THR	engineered mutation	UNP V0AAC4
G	22	GLY	ASP	engineered mutation	UNP V0AAC4
G	24	TYR	ASP	engineered mutation	UNP V0AAC4
G	47	SER	CYS	engineered mutation	UNP V0AAC4
G	52	SER	PHE	engineered mutation	UNP V0AAC4
G	142	SER	THR	engineered mutation	UNP V0AAC4
G	172	LEU	LYS	engineered mutation	UNP V0AAC4
G	197	SER	THR	engineered mutation	UNP V0AAC4
G	202	VAL	PRO	engineered mutation	UNP V0AAC4
G	203	THR	ALA	engineered mutation	UNP V0AAC4
G	206	ALA	VAL	engineered mutation	UNP V0AAC4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	239	GLY	SER	engineered mutation	UNP V0AAC4
G	260	LEU	-	expression tag	UNP V0AAC4
G	261	GLU	-	expression tag	UNP V0AAC4
G	262	HIS	-	expression tag	UNP V0AAC4
G	263	HIS	-	expression tag	UNP V0AAC4
G	264	HIS	-	expression tag	UNP V0AAC4
G	265	HIS	-	expression tag	UNP V0AAC4
G	266	HIS	-	expression tag	UNP V0AAC4
G	267	HIS	-	expression tag	UNP V0AAC4
H	18	SER	THR	engineered mutation	UNP V0AAC4
H	22	GLY	ASP	engineered mutation	UNP V0AAC4
H	24	TYR	ASP	engineered mutation	UNP V0AAC4
H	47	SER	CYS	engineered mutation	UNP V0AAC4
H	52	SER	PHE	engineered mutation	UNP V0AAC4
H	142	SER	THR	engineered mutation	UNP V0AAC4
H	172	LEU	LYS	engineered mutation	UNP V0AAC4
H	197	SER	THR	engineered mutation	UNP V0AAC4
H	202	VAL	PRO	engineered mutation	UNP V0AAC4
H	203	THR	ALA	engineered mutation	UNP V0AAC4
H	206	ALA	VAL	engineered mutation	UNP V0AAC4
H	239	GLY	SER	engineered mutation	UNP V0AAC4
H	260	LEU	-	expression tag	UNP V0AAC4
H	261	GLU	-	expression tag	UNP V0AAC4
H	262	HIS	-	expression tag	UNP V0AAC4
H	263	HIS	-	expression tag	UNP V0AAC4
H	264	HIS	-	expression tag	UNP V0AAC4
H	265	HIS	-	expression tag	UNP V0AAC4
H	266	HIS	-	expression tag	UNP V0AAC4
H	267	HIS	-	expression tag	UNP V0AAC4
I	18	SER	THR	engineered mutation	UNP V0AAC4
I	22	GLY	ASP	engineered mutation	UNP V0AAC4
I	24	TYR	ASP	engineered mutation	UNP V0AAC4
I	47	SER	CYS	engineered mutation	UNP V0AAC4
I	52	SER	PHE	engineered mutation	UNP V0AAC4
I	142	SER	THR	engineered mutation	UNP V0AAC4
I	172	LEU	LYS	engineered mutation	UNP V0AAC4
I	197	SER	THR	engineered mutation	UNP V0AAC4
I	202	VAL	PRO	engineered mutation	UNP V0AAC4
I	203	THR	ALA	engineered mutation	UNP V0AAC4
I	206	ALA	VAL	engineered mutation	UNP V0AAC4
I	239	GLY	SER	engineered mutation	UNP V0AAC4
I	260	LEU	-	expression tag	UNP V0AAC4

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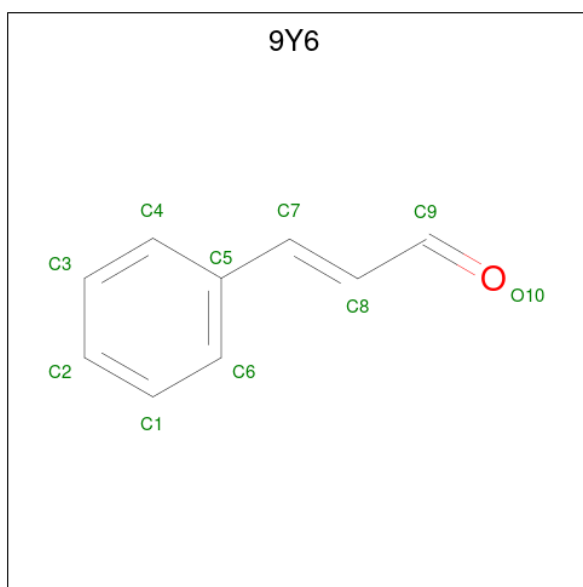
Chain	Residue	Modelled	Actual	Comment	Reference
I	261	GLU	-	expression tag	UNP V0AAC4
I	262	HIS	-	expression tag	UNP V0AAC4
I	263	HIS	-	expression tag	UNP V0AAC4
I	264	HIS	-	expression tag	UNP V0AAC4
I	265	HIS	-	expression tag	UNP V0AAC4
I	266	HIS	-	expression tag	UNP V0AAC4
I	267	HIS	-	expression tag	UNP V0AAC4
J	18	SER	THR	engineered mutation	UNP V0AAC4
J	22	GLY	ASP	engineered mutation	UNP V0AAC4
J	24	TYR	ASP	engineered mutation	UNP V0AAC4
J	47	SER	CYS	engineered mutation	UNP V0AAC4
J	52	SER	PHE	engineered mutation	UNP V0AAC4
J	142	SER	THR	engineered mutation	UNP V0AAC4
J	172	LEU	LYS	engineered mutation	UNP V0AAC4
J	197	SER	THR	engineered mutation	UNP V0AAC4
J	202	VAL	PRO	engineered mutation	UNP V0AAC4
J	203	THR	ALA	engineered mutation	UNP V0AAC4
J	206	ALA	VAL	engineered mutation	UNP V0AAC4
J	239	GLY	SER	engineered mutation	UNP V0AAC4
J	260	LEU	-	expression tag	UNP V0AAC4
J	261	GLU	-	expression tag	UNP V0AAC4
J	262	HIS	-	expression tag	UNP V0AAC4
J	263	HIS	-	expression tag	UNP V0AAC4
J	264	HIS	-	expression tag	UNP V0AAC4
J	265	HIS	-	expression tag	UNP V0AAC4
J	266	HIS	-	expression tag	UNP V0AAC4
J	267	HIS	-	expression tag	UNP V0AAC4
K	18	SER	THR	engineered mutation	UNP V0AAC4
K	22	GLY	ASP	engineered mutation	UNP V0AAC4
K	25	TYR	ASP	engineered mutation	UNP V0AAC4
K	47	SER	CYS	engineered mutation	UNP V0AAC4
K	52	SER	PHE	engineered mutation	UNP V0AAC4
K	142	SER	THR	engineered mutation	UNP V0AAC4
K	172	LEU	LYS	engineered mutation	UNP V0AAC4
K	197	SER	THR	engineered mutation	UNP V0AAC4
K	202	VAL	PRO	engineered mutation	UNP V0AAC4
K	203	THR	ALA	engineered mutation	UNP V0AAC4
K	206	ALA	VAL	engineered mutation	UNP V0AAC4
K	239	GLY	SER	engineered mutation	UNP V0AAC4
K	260	LEU	-	expression tag	UNP V0AAC4
K	261	GLU	-	expression tag	UNP V0AAC4
K	262	HIS	-	expression tag	UNP V0AAC4

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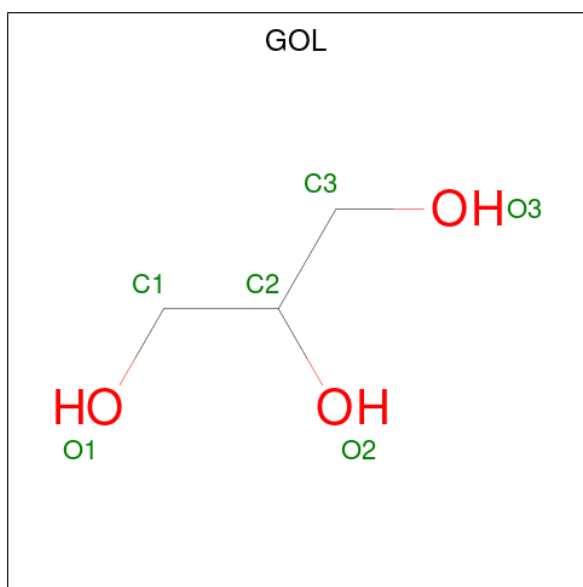
Chain	Residue	Modelled	Actual	Comment	Reference
K	263	HIS	-	expression tag	UNP V0AAC4
K	264	HIS	-	expression tag	UNP V0AAC4
K	265	HIS	-	expression tag	UNP V0AAC4
K	266	HIS	-	expression tag	UNP V0AAC4
K	267	HIS	-	expression tag	UNP V0AAC4
L	18	SER	THR	engineered mutation	UNP V0AAC4
L	22	GLY	ASP	engineered mutation	UNP V0AAC4
L	24	TYR	ASP	engineered mutation	UNP V0AAC4
L	47	SER	CYS	engineered mutation	UNP V0AAC4
L	52	SER	PHE	engineered mutation	UNP V0AAC4
L	142	SER	THR	engineered mutation	UNP V0AAC4
L	172	LEU	LYS	engineered mutation	UNP V0AAC4
L	197	SER	THR	engineered mutation	UNP V0AAC4
L	202	VAL	PRO	engineered mutation	UNP V0AAC4
L	203	THR	ALA	engineered mutation	UNP V0AAC4
L	206	ALA	VAL	engineered mutation	UNP V0AAC4
L	239	GLY	SER	engineered mutation	UNP V0AAC4
L	260	LEU	-	expression tag	UNP V0AAC4
L	261	GLU	-	expression tag	UNP V0AAC4
L	262	HIS	-	expression tag	UNP V0AAC4
L	263	HIS	-	expression tag	UNP V0AAC4
L	264	HIS	-	expression tag	UNP V0AAC4
L	265	HIS	-	expression tag	UNP V0AAC4
L	266	HIS	-	expression tag	UNP V0AAC4
L	267	HIS	-	expression tag	UNP V0AAC4

- Molecule 2 is (2E)-3-phenylprop-2-enal (three-letter code: 9Y6) (formula: C₉H₈O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C 9 9	0	0
2	B	1	Total C 9 9	0	0
2	C	1	Total C 9 9	0	0
2	D	1	Total C 9 9	0	0
2	E	1	Total C 9 9	0	0
2	F	1	Total C 9 9	0	0
2	G	1	Total C 9 9	0	0
2	H	1	Total C 9 9	0	0
2	I	1	Total C 9 9	0	0
2	J	1	Total C 9 9	0	0
2	K	1	Total C 9 9	0	0
2	L	1	Total C 9 9	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	I	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	114	Total	O	0	0
			114	114		
4	B	104	Total	O	0	0
			104	104		
4	C	121	Total	O	0	0
			121	121		
4	D	83	Total	O	0	0
			83	83		
4	E	126	Total	O	0	0
			126	126		
4	F	144	Total	O	0	0
			144	144		
4	G	117	Total	O	0	0
			117	117		
4	H	74	Total	O	0	0
			74	74		
4	I	85	Total	O	0	0
			85	85		
4	J	94	Total	O	0	0
			94	94		
4	K	116	Total	O	0	0
			116	116		

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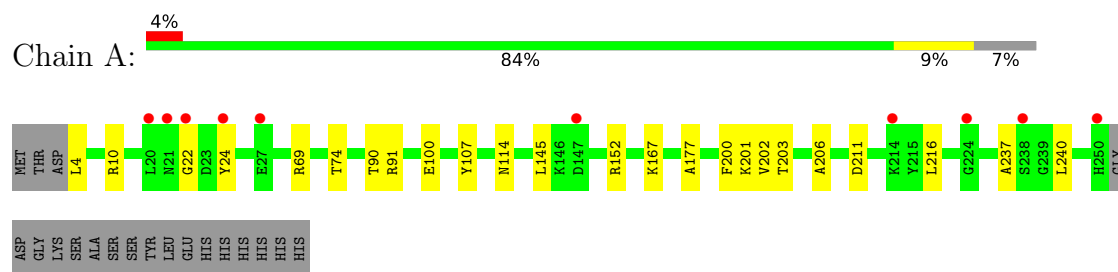
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	97	Total	O	0	0
			97	97		

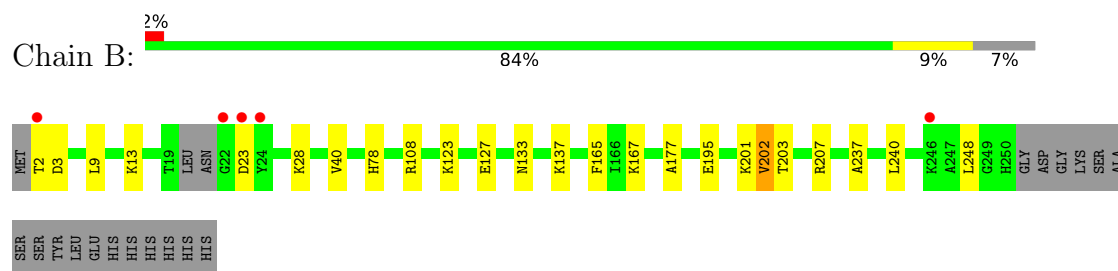
3 Residue-property plots [i](#)

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.

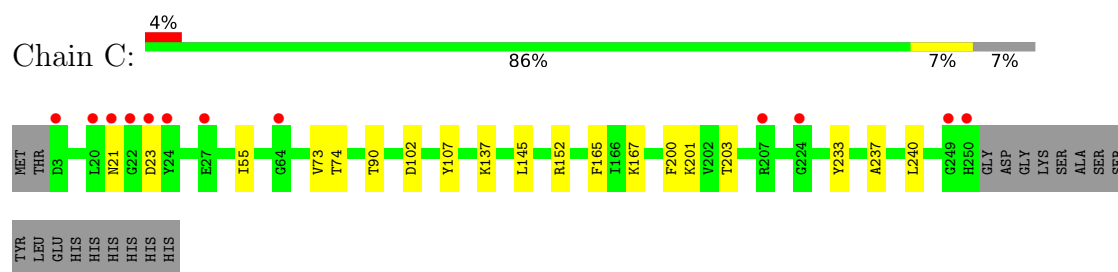
• Molecule 1: Deoxyribose-phosphate aldolase



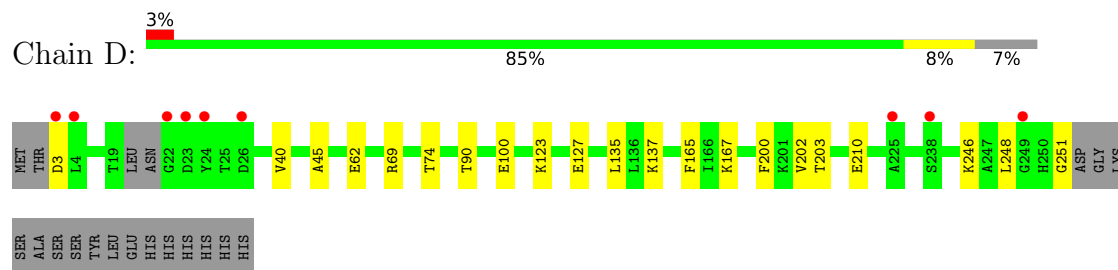
• Molecule 1: Deoxyribose-phosphate aldolase



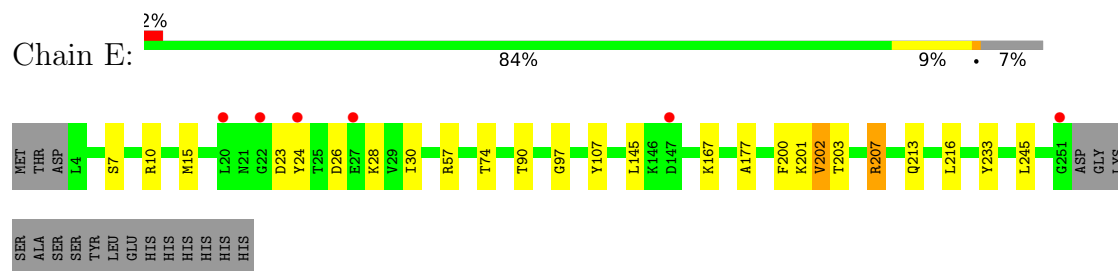
• Molecule 1: Deoxyribose-phosphate aldolase



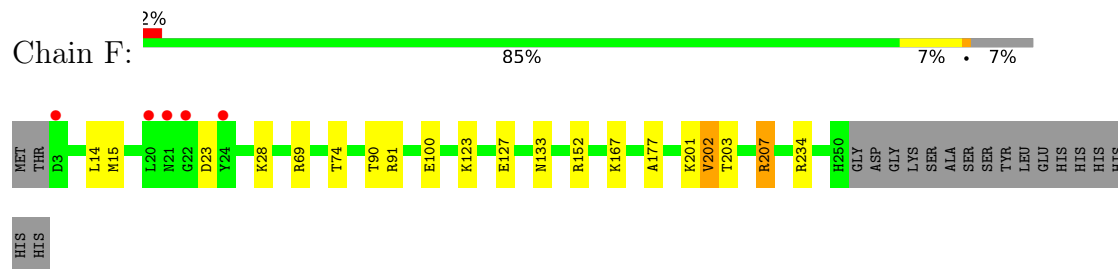
• Molecule 1: Deoxyribose-phosphate aldolase



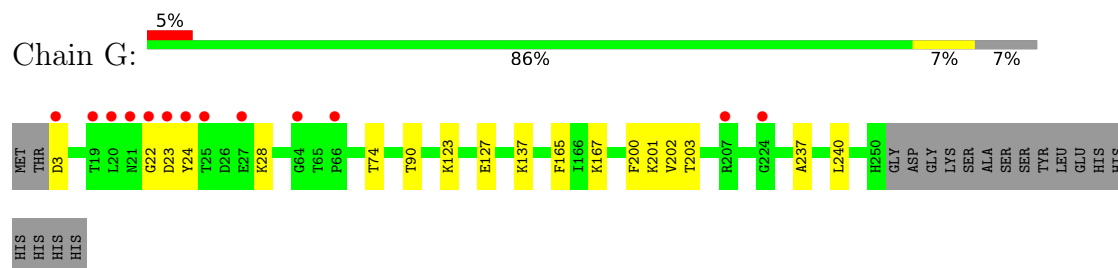
- Molecule 1: Deoxyribose-phosphate aldolase



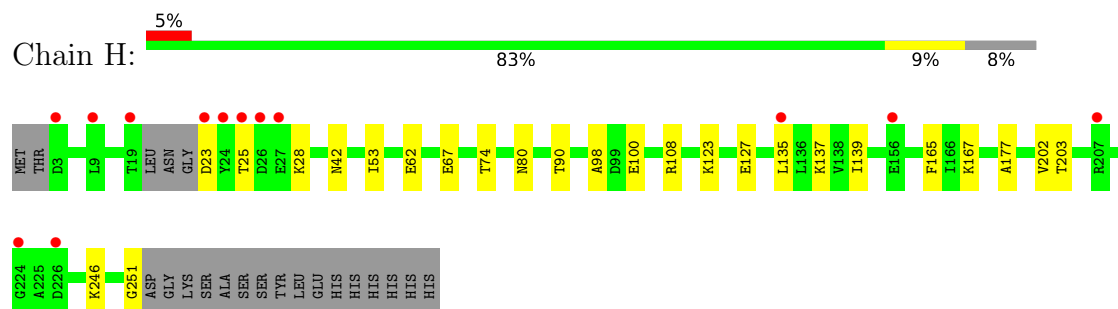
- Molecule 1: Deoxyribose-phosphate aldolase



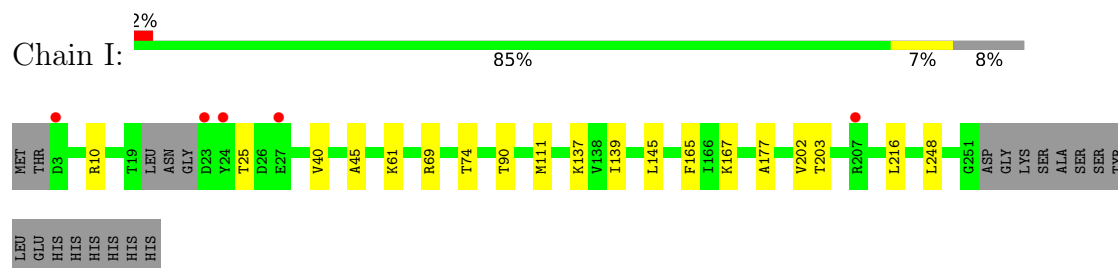
- Molecule 1: Deoxyribose-phosphate aldolase



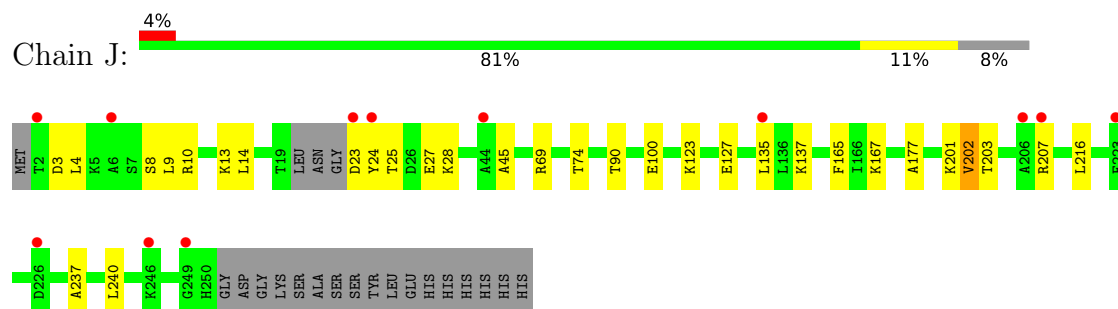
- Molecule 1: Deoxyribose-phosphate aldolase



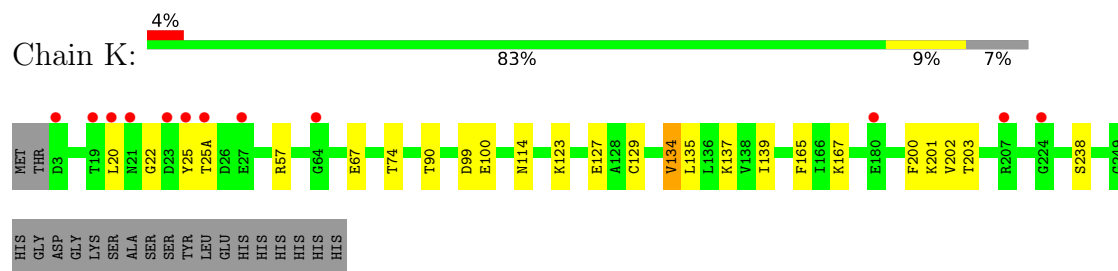
- Molecule 1: Deoxyribose-phosphate aldolase



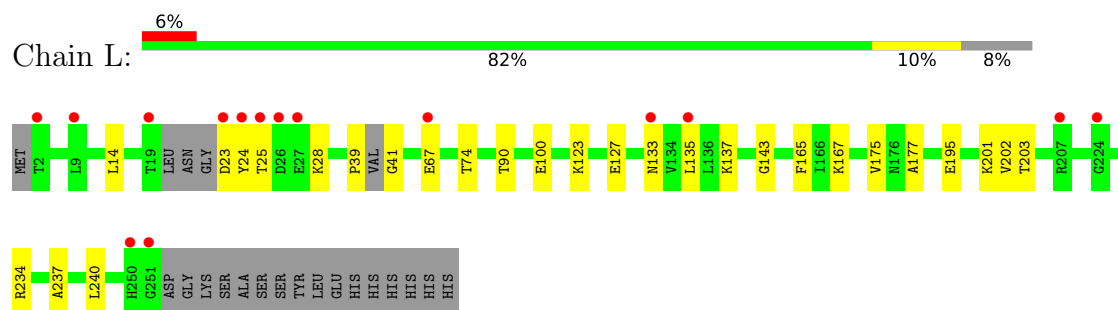
- Molecule 1: Deoxyribose-phosphate aldolase



- Molecule 1: Deoxyribose-phosphate aldolase



- Molecule 1: Deoxyribose-phosphate aldolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	80.27Å 92.79Å 106.89Å 88.96° 88.83° 89.08°	Depositor
Resolution (Å)	80.24 – 1.90 80.24 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.6 (80.24-1.90) 94.3 (80.24-1.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.19.2	Depositor
R, R_{free}	0.235 , 0.283 0.237 , 0.283	Depositor DCC
R_{free} test set	11336 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	14.7	Xtriage
Anisotropy	1.046	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-l 0.000 for -h,k,-l 0.000 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	23612	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 70.73 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9675e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GOL, 9Y6

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	0.46	0/1876	0.63	0/2536
1	B	0.40	0/1874	0.61	0/2532
1	C	0.41	0/1884	0.61	0/2547
1	D	0.39	0/1879	0.61	0/2538
1	E	0.41	0/1880	0.64	0/2541
1	F	0.38	0/1895	0.61	0/2561
1	G	0.42	0/1884	0.62	0/2547
1	H	0.42	0/1867	0.61	0/2522
1	I	0.39	0/1867	0.59	0/2522
1	J	0.41	0/1870	0.60	0/2527
1	K	0.44	0/1873	0.63	0/2532
1	L	0.44	0/1866	0.60	0/2519
All	All	0.41	0/22515	0.61	0/30424

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	1851	0	1892	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1850	0	1885	15	0
1	C	1859	0	1896	12	0
1	D	1855	0	1886	14	0
1	E	1855	0	1895	15	0
1	F	1870	0	1908	13	0
1	G	1859	0	1896	9	0
1	H	1843	0	1878	13	0
1	I	1843	0	1878	11	0
1	J	1846	0	1882	19	0
1	K	1849	0	1889	14	0
1	L	1843	0	1875	17	0
2	A	9	0	0	0	0
2	B	9	0	0	0	0
2	C	9	0	0	0	0
2	D	9	0	0	0	0
2	E	9	0	0	0	0
2	F	9	0	0	0	0
2	G	9	0	0	0	0
2	H	9	0	0	0	0
2	I	9	0	0	0	0
2	J	9	0	0	0	0
2	K	9	0	0	0	0
2	L	9	0	0	0	0
3	I	6	0	8	0	0
4	A	114	0	0	3	0
4	B	104	0	0	1	1
4	C	121	0	0	1	1
4	D	83	0	0	1	0
4	E	126	0	0	1	0
4	F	144	0	0	3	0
4	G	117	0	0	1	1
4	H	74	0	0	0	0
4	I	85	0	0	1	0
4	J	94	0	0	2	0
4	K	116	0	0	1	0
4	L	97	0	0	2	1
All	All	23612	0	22668	160	2

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 4.

The worst 5 of 160 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:H:123:LYS:NZ	1:H:127:GLU:OE2	2.18	0.77
1:L:123:LYS:NZ	1:L:127:GLU:OE2	2.19	0.76
1:B:123:LYS:NZ	1:B:127:GLU:OE2	2.19	0.74
1:G:123:LYS:NZ	1:G:127:GLU:OE2	2.20	0.70
1:I:111:MET:HE2	1:I:145:LEU:HA	1.75	0.69

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:481:HOH:O	4:C:476:HOH:O[1_655]	2.14	0.06
4:G:424:HOH:O	4:L:479:HOH:O[1_565]	2.19	0.01

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	245/267 (92%)	239 (98%)	6 (2%)	0	100	100
1	B	243/267 (91%)	238 (98%)	5 (2%)	0	100	100
1	C	246/267 (92%)	239 (97%)	7 (3%)	0	100	100
1	D	244/267 (91%)	239 (98%)	5 (2%)	0	100	100
1	E	246/267 (92%)	238 (97%)	8 (3%)	0	100	100
1	F	247/267 (92%)	241 (98%)	6 (2%)	0	100	100
1	G	246/267 (92%)	241 (98%)	5 (2%)	0	100	100
1	H	242/267 (91%)	237 (98%)	5 (2%)	0	100	100
1	I	242/267 (91%)	236 (98%)	6 (2%)	0	100	100
1	J	242/267 (91%)	237 (98%)	5 (2%)	0	100	100
1	K	245/267 (92%)	240 (98%)	5 (2%)	0	100	100
1	L	240/267 (90%)	235 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2928/3204 (91%)	2860 (98%)	68 (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	190/207 (92%)	190 (100%)	0	100	100
1	B	190/207 (92%)	188 (99%)	2 (1%)	73	73
1	C	191/207 (92%)	191 (100%)	0	100	100
1	D	190/207 (92%)	190 (100%)	0	100	100
1	E	190/207 (92%)	187 (98%)	3 (2%)	62	60
1	F	192/207 (93%)	189 (98%)	3 (2%)	62	60
1	G	191/207 (92%)	189 (99%)	2 (1%)	76	76
1	H	189/207 (91%)	188 (100%)	1 (0%)	88	89
1	I	189/207 (91%)	188 (100%)	1 (0%)	88	89
1	J	190/207 (92%)	188 (99%)	2 (1%)	73	73
1	K	190/207 (92%)	187 (98%)	3 (2%)	62	60
1	L	189/207 (91%)	189 (100%)	0	100	100
All	All	2281/2484 (92%)	2264 (99%)	17 (1%)	84	84

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	25	TYR
1	K	134	VAL
1	F	207[B]	ARG
1	G	3	ASP
1	G	24	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

13 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	9Y6	G	301	1	9,9,10	0.30	0	10,10,11	0.43	0
3	GOL	I	302	-	5,5,5	0.88	0	5,5,5	0.95	0
2	9Y6	C	301	1	9,9,10	0.36	0	10,10,11	0.43	0
2	9Y6	F	301	1	9,9,10	0.34	0	10,10,11	0.46	0
2	9Y6	B	301	1	9,9,10	0.34	0	10,10,11	0.45	0
2	9Y6	H	301	1	9,9,10	0.30	0	10,10,11	0.38	0
2	9Y6	D	301	1	9,9,10	0.30	0	10,10,11	0.43	0
2	9Y6	A	301	1	9,9,10	0.34	0	10,10,11	0.48	0
2	9Y6	K	301	1	9,9,10	0.35	0	10,10,11	0.42	0
2	9Y6	J	301	1	9,9,10	0.30	0	10,10,11	0.45	0
2	9Y6	L	301	1	9,9,10	0.28	0	10,10,11	0.49	0
2	9Y6	E	301	1	9,9,10	0.30	0	10,10,11	0.45	0
2	9Y6	I	301	1	9,9,10	0.29	0	10,10,11	0.41	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	9Y6	G	301	1	-	0/3/3/4	0/1/1/1
3	GOL	I	302	-	-	0/4/4/4	-
2	9Y6	C	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	F	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	B	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	H	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	D	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	A	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	K	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	J	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	L	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	E	301	1	-	0/3/3/4	0/1/1/1
2	9Y6	I	301	1	-	0/3/3/4	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

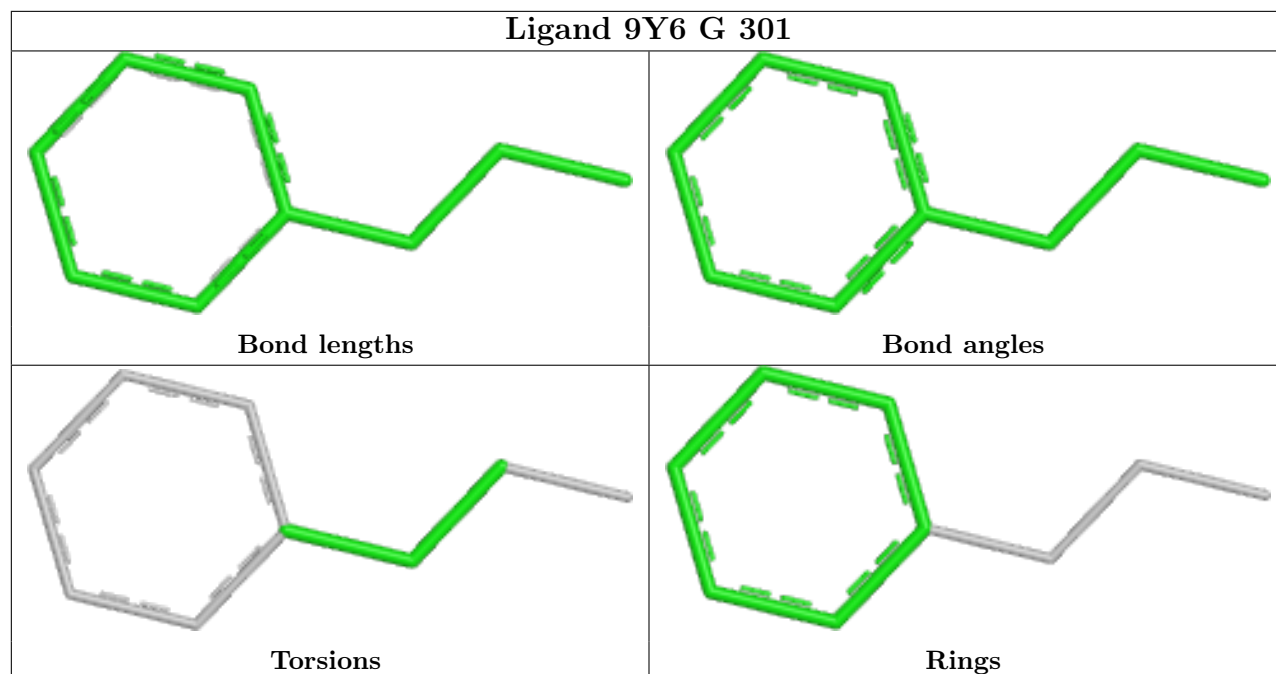
There are no torsion outliers.

There are no ring outliers.

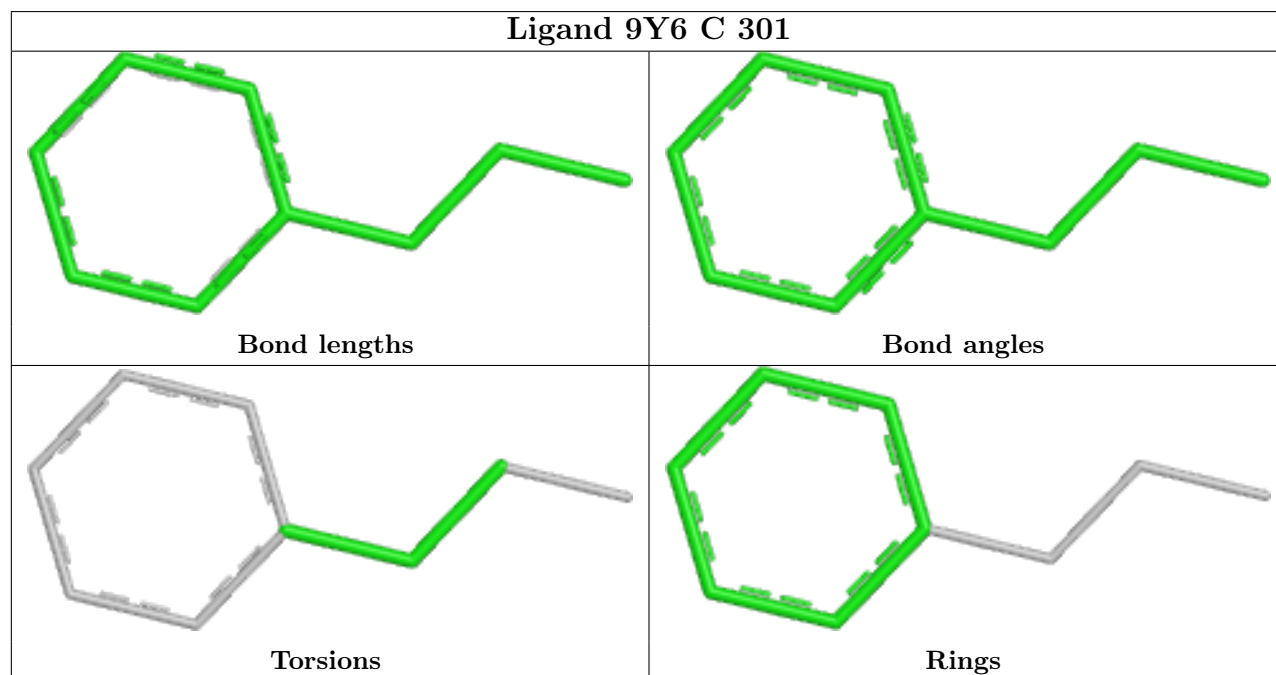
No monomer is involved in short contacts.

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.

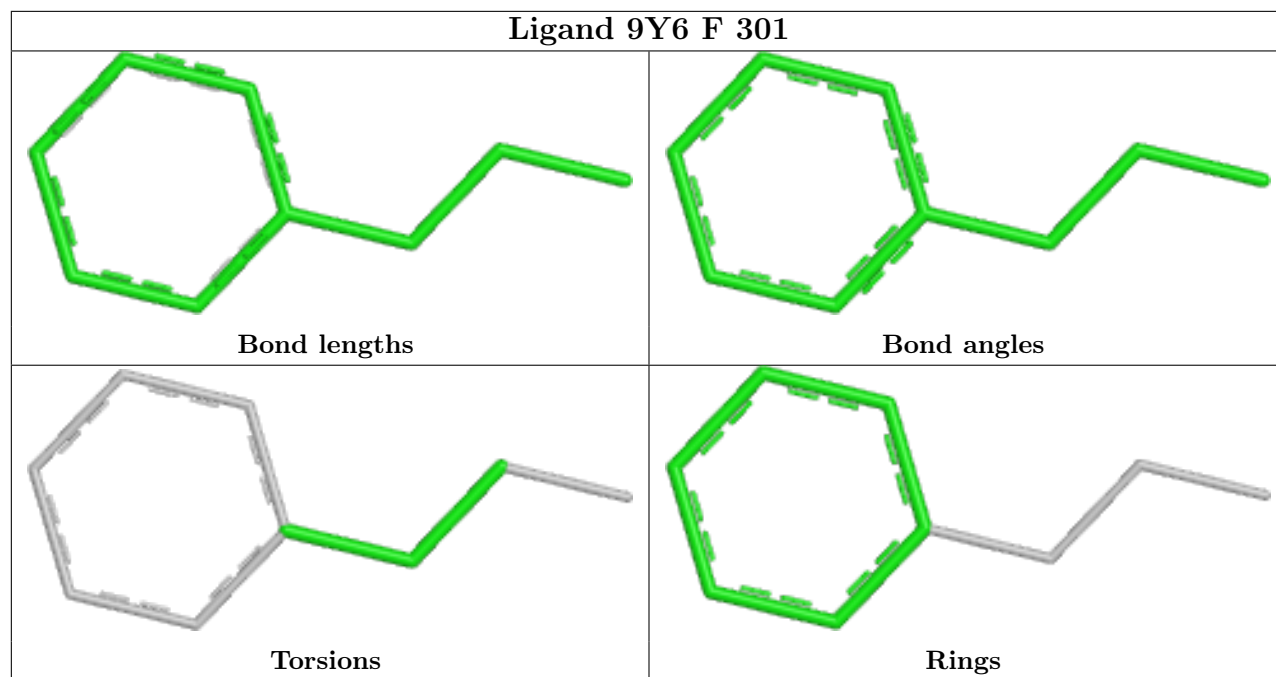
Ligand 9Y6 G 301



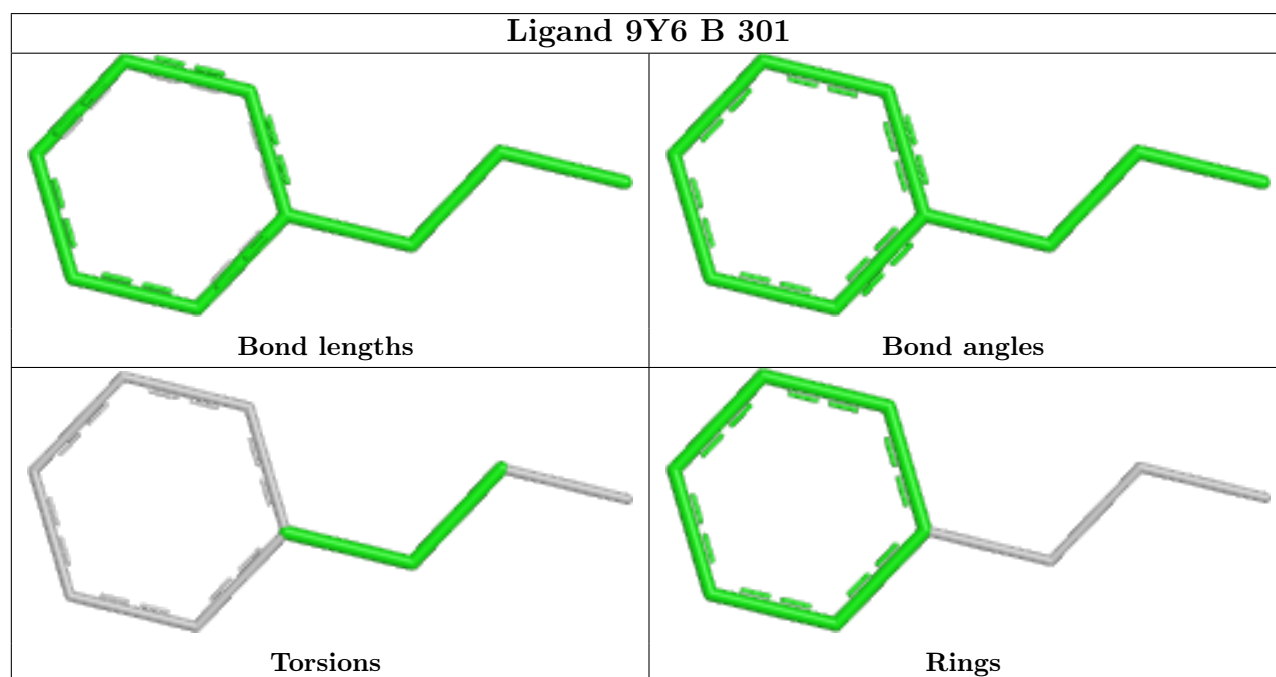
Ligand 9Y6 C 301



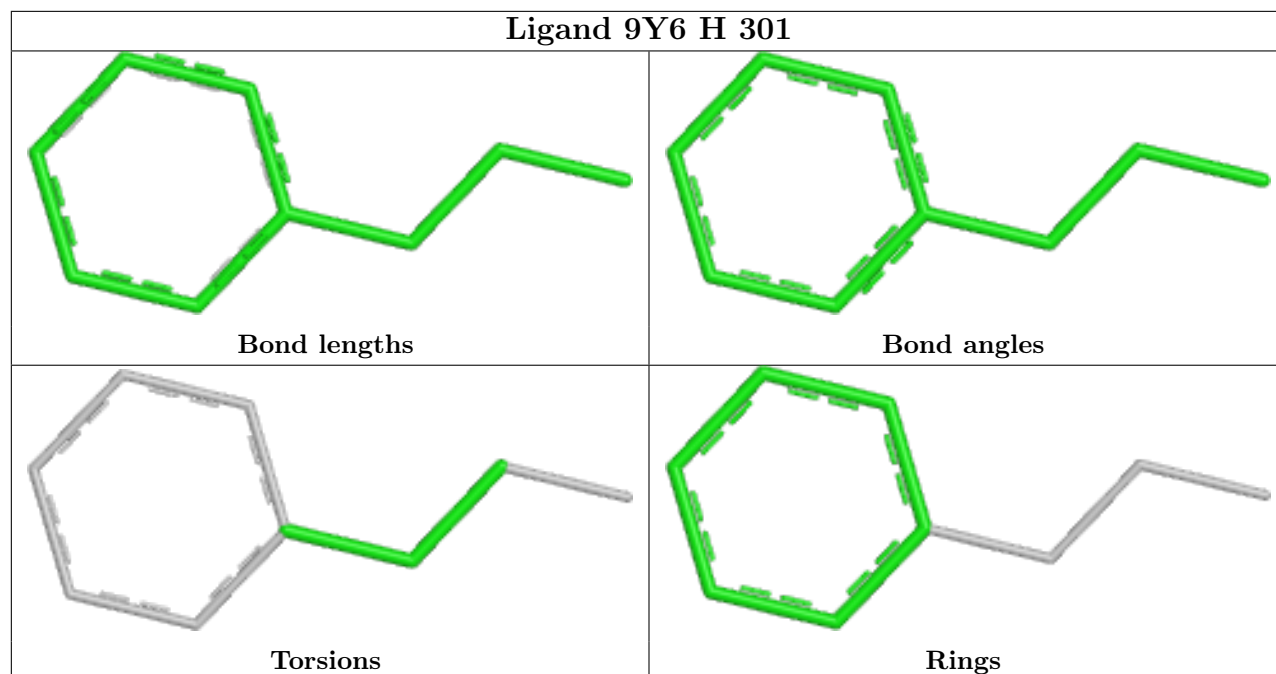
Ligand 9Y6 F 301



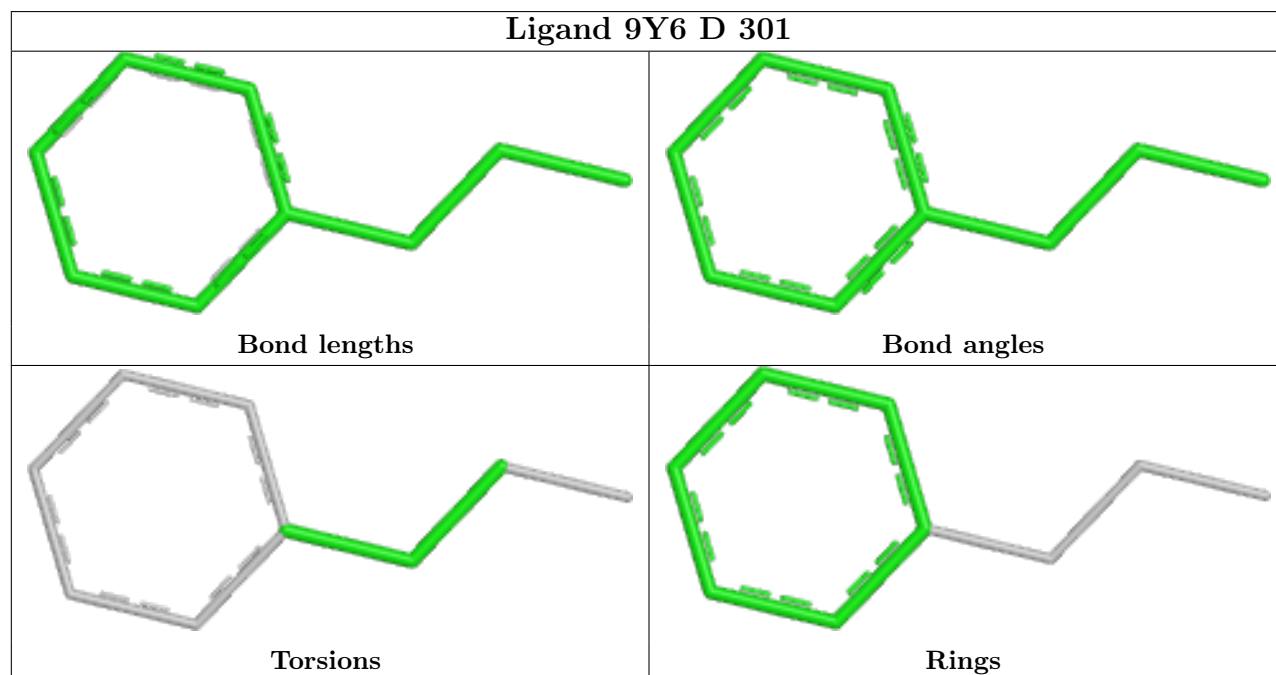
Ligand 9Y6 B 301



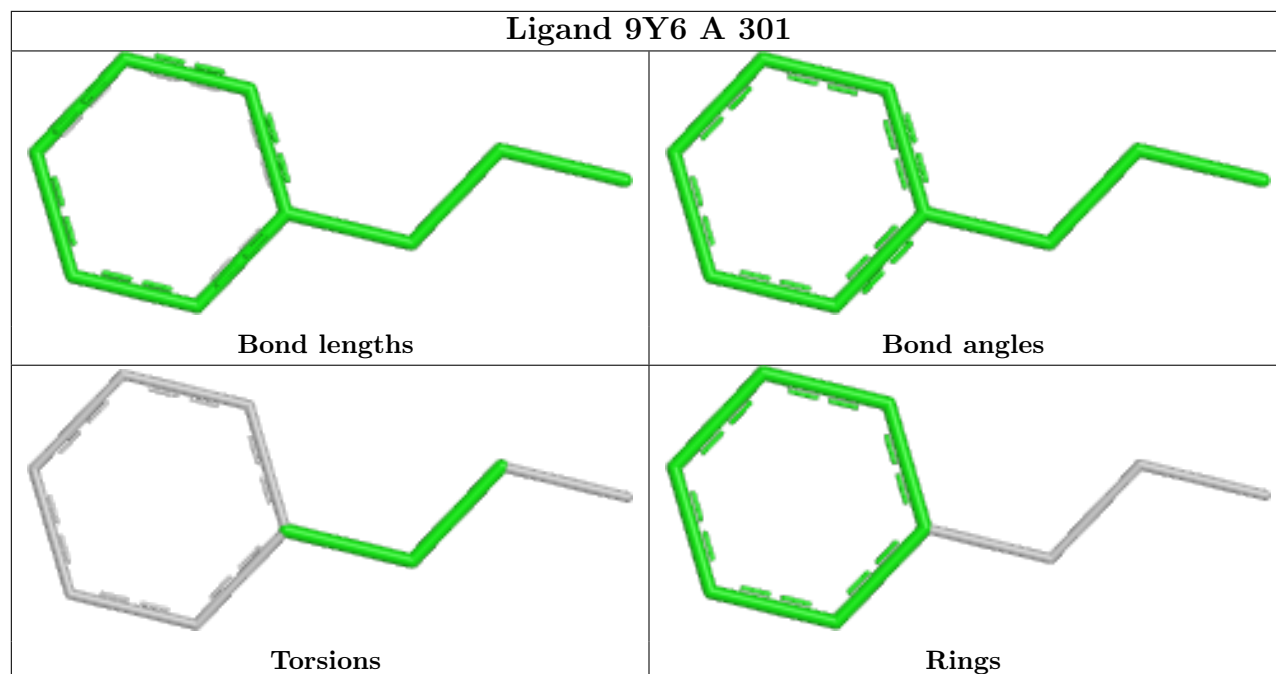
Ligand 9Y6 H 301



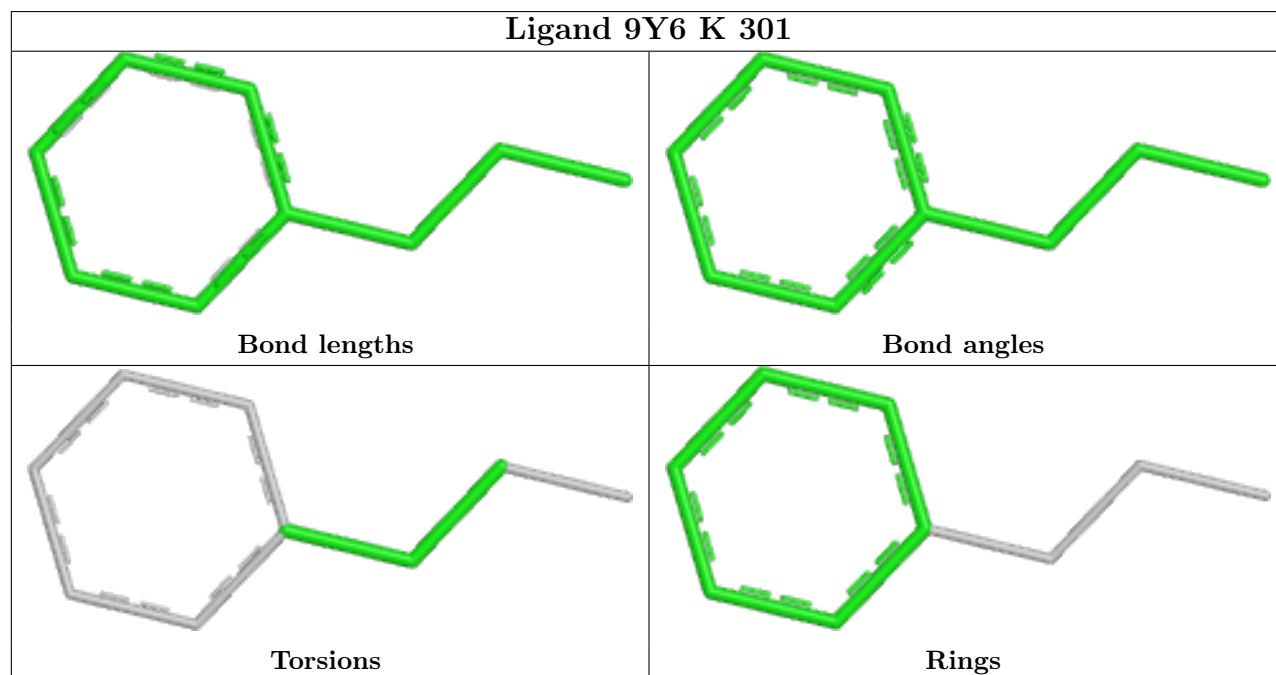
Ligand 9Y6 D 301

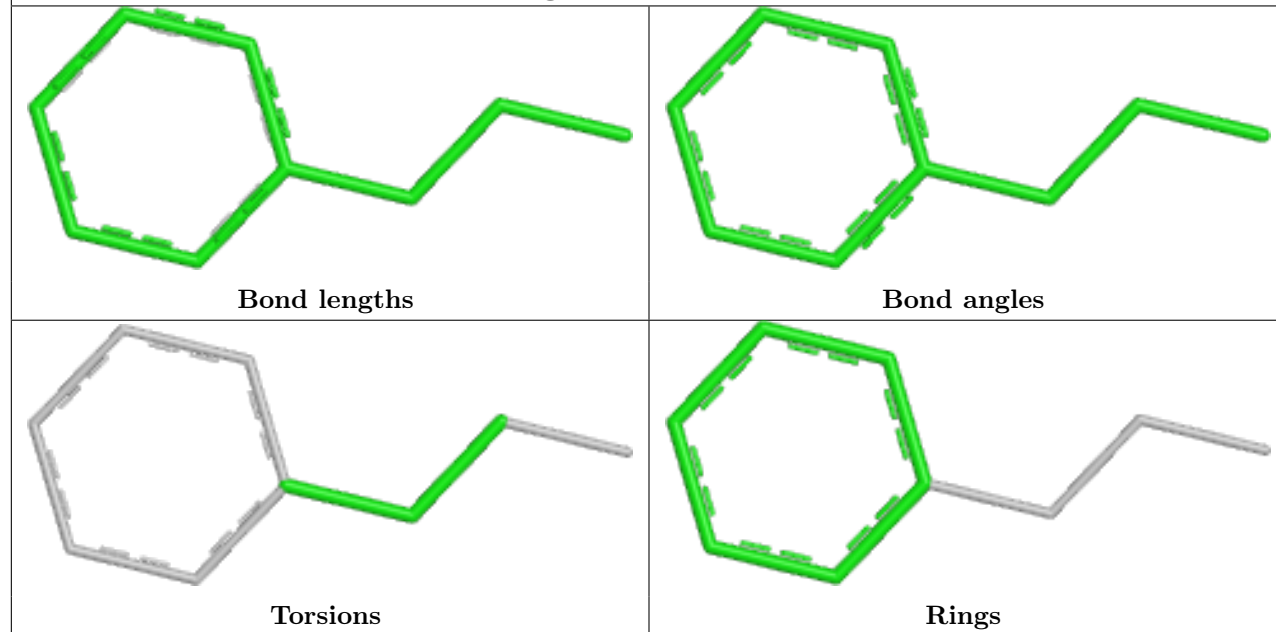
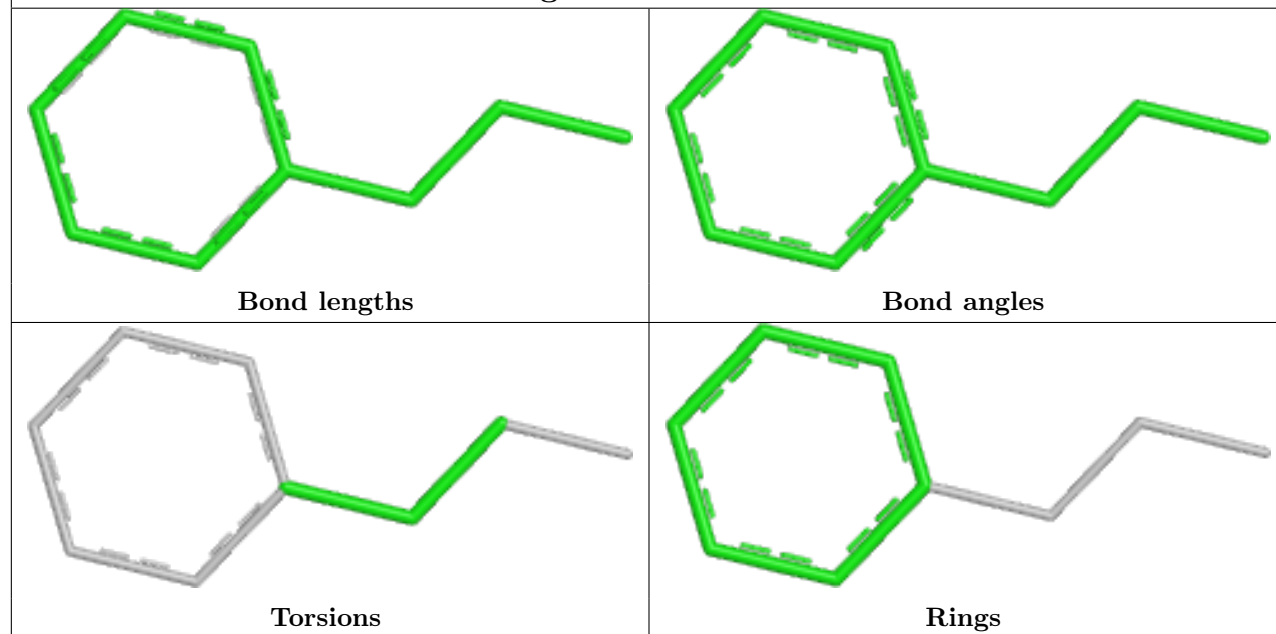


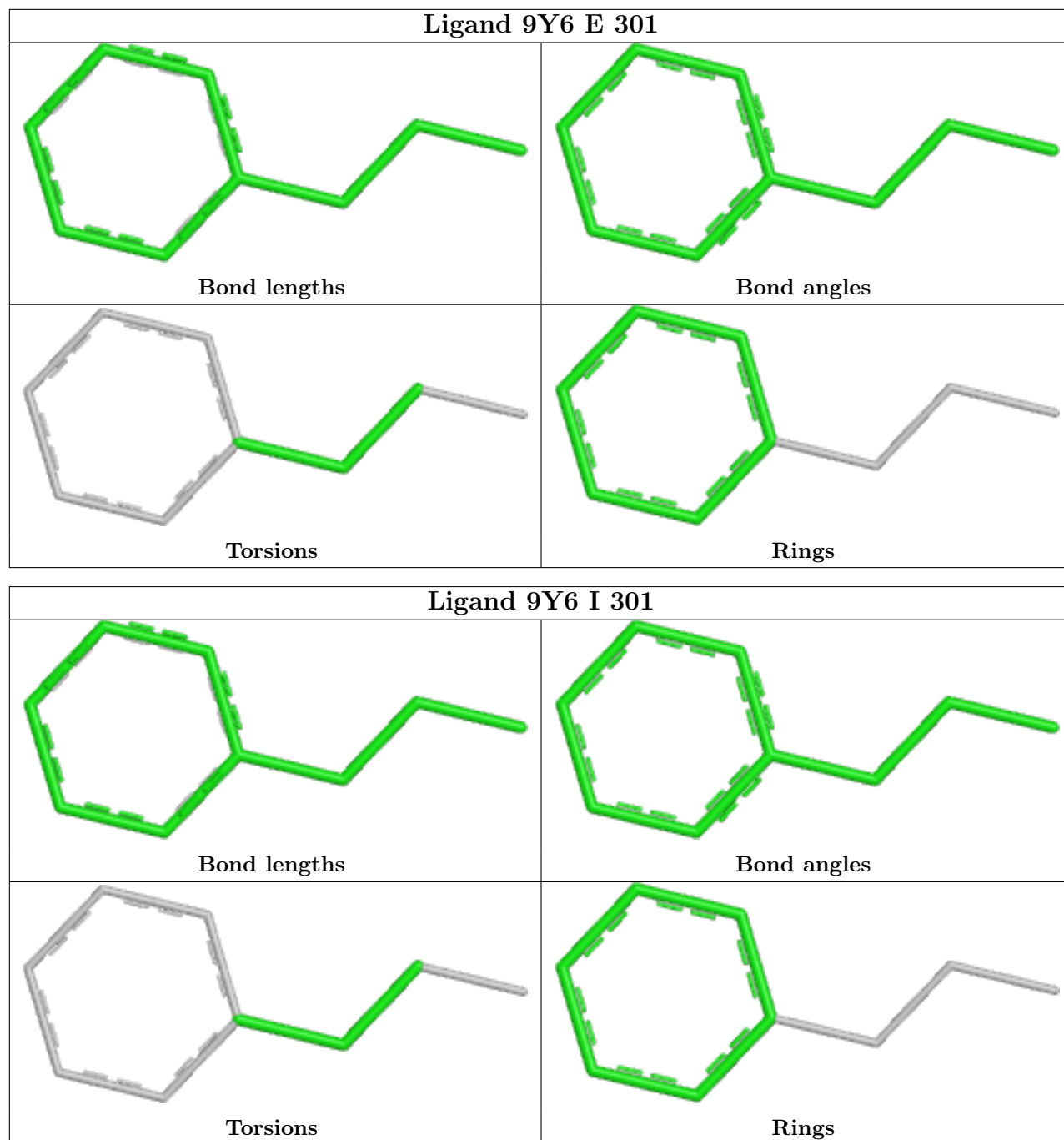
Ligand 9Y6 A 301



Ligand 9Y6 K 301



Ligand 9Y6 J 301**Ligand 9Y6 L 301**



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	247/267 (92%)	0.39	10 (4%) 38 41	7, 17, 33, 45	0
1	B	247/267 (92%)	0.02	5 (2%) 65 68	7, 16, 30, 44	0
1	C	248/267 (92%)	0.12	12 (4%) 30 33	7, 14, 31, 47	0
1	D	247/267 (92%)	0.56	9 (3%) 42 45	10, 22, 36, 48	0
1	E	248/267 (92%)	0.29	6 (2%) 59 62	7, 17, 32, 41	0
1	F	248/267 (92%)	0.05	5 (2%) 65 68	7, 14, 28, 42	0
1	G	248/267 (92%)	0.45	13 (5%) 27 30	7, 18, 35, 49	0
1	H	246/267 (92%)	0.49	13 (5%) 26 29	10, 22, 36, 50	0
1	I	246/267 (92%)	0.15	5 (2%) 65 68	7, 19, 33, 46	0
1	J	246/267 (92%)	0.45	12 (4%) 29 33	9, 20, 34, 44	0
1	K	247/267 (92%)	0.39	12 (4%) 29 33	7, 18, 35, 49	0
1	L	246/267 (92%)	0.45	15 (6%) 21 24	9, 20, 34, 50	0
All	All	2964/3204 (92%)	0.32	117 (3%) 39 42	7, 18, 34, 50	0

The worst 5 of 117 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	24	TYR	8.8
1	H	24	TYR	8.6
1	G	20	LEU	8.4
1	A	24	TYR	7.6
1	G	24	TYR	7.5

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

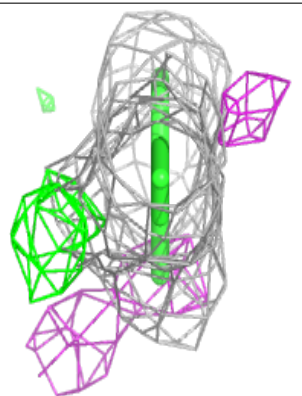
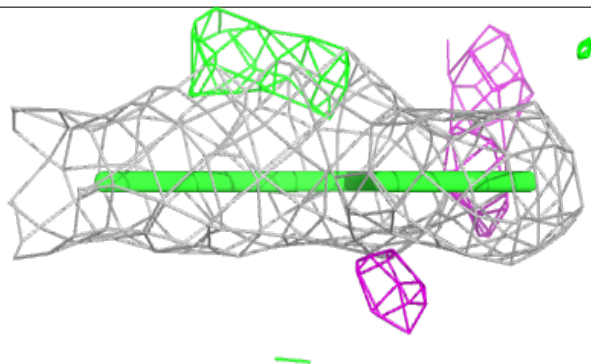
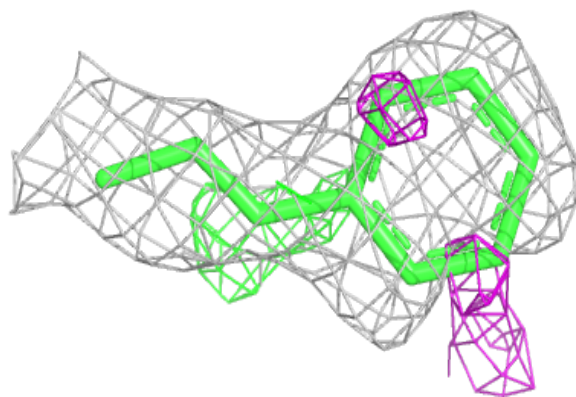
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GOL	I	302	6/6	0.71	0.45	44,45,46,47	0
2	9Y6	D	301	9/10	0.82	0.21	24,27,28,28	0
2	9Y6	J	301	9/10	0.85	0.17	22,22,24,25	0
2	9Y6	A	301	9/10	0.85	0.25	14,24,27,27	0
2	9Y6	K	301	9/10	0.86	0.18	18,22,23,23	0
2	9Y6	H	301	9/10	0.86	0.18	21,22,23,24	0
2	9Y6	G	301	9/10	0.87	0.12	21,28,30,30	0
2	9Y6	I	301	9/10	0.88	0.15	18,23,23,24	0
2	9Y6	L	301	9/10	0.88	0.16	18,21,22,22	0
2	9Y6	E	301	9/10	0.88	0.16	18,22,23,23	0
2	9Y6	B	301	9/10	0.90	0.14	16,17,17,17	0
2	9Y6	F	301	9/10	0.93	0.12	11,18,20,20	0
2	9Y6	C	301	9/10	0.94	0.13	13,19,20,20	0

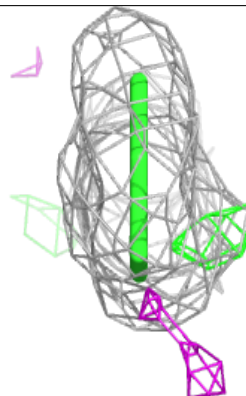
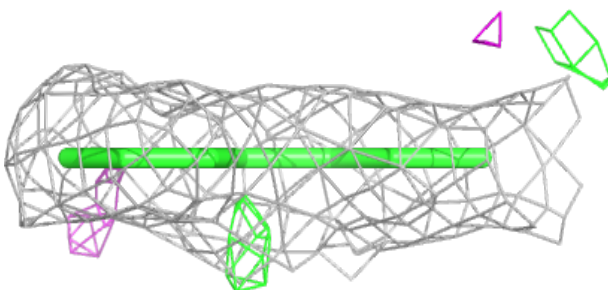
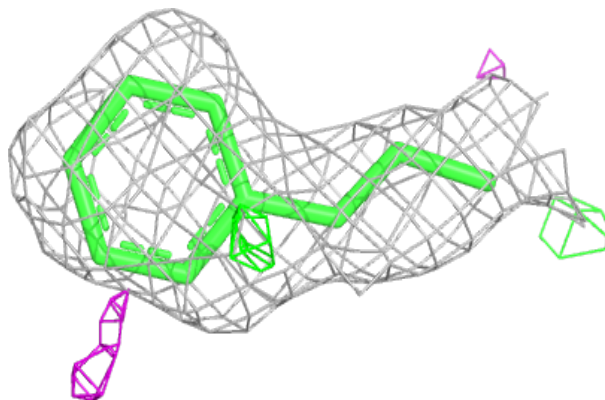
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 9Y6 D 301:

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

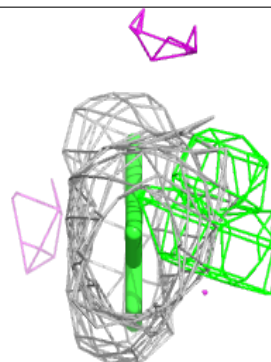
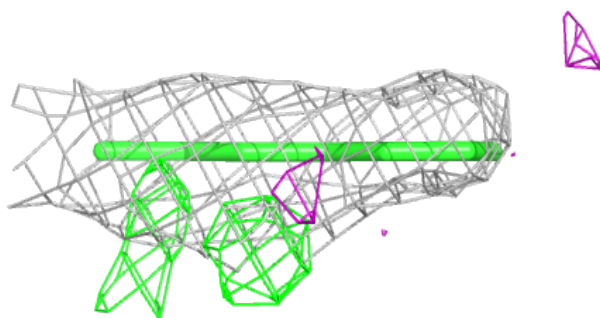
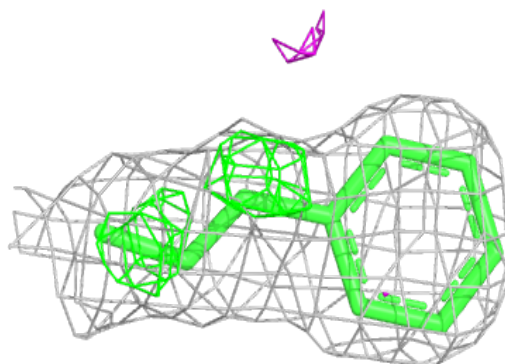
**Electron density around 9Y6 J 301:**

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

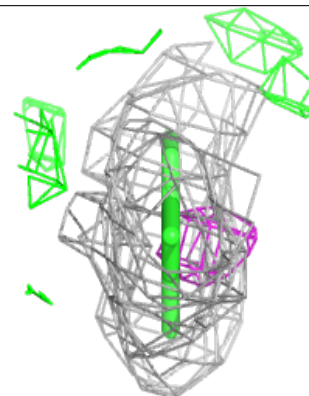
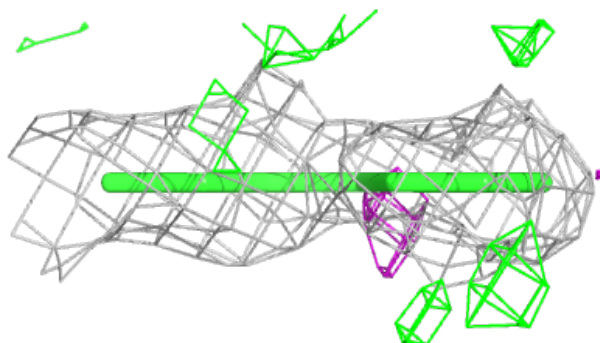
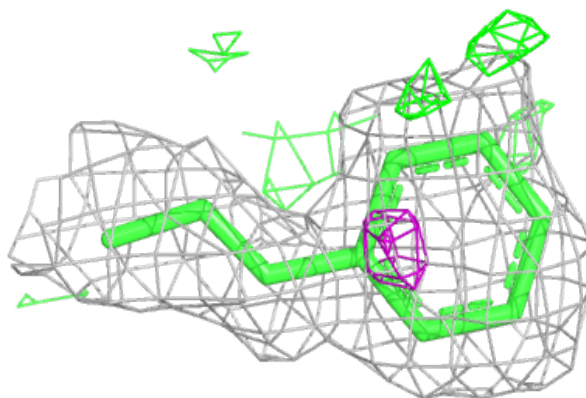


Electron density around 9Y6 A 301:

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

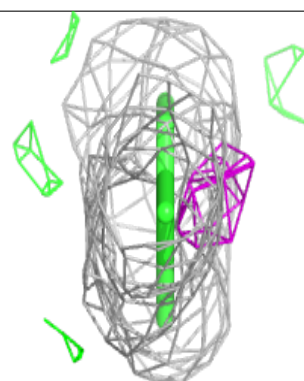
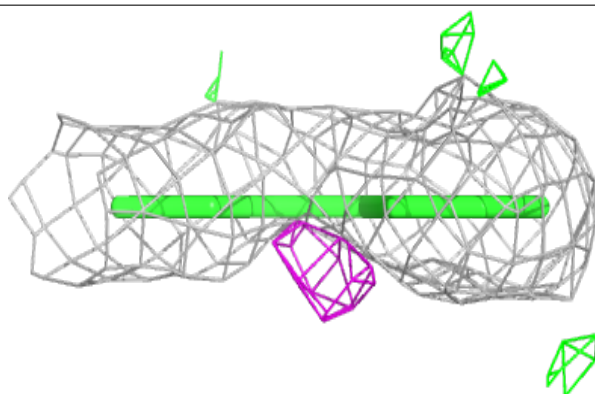
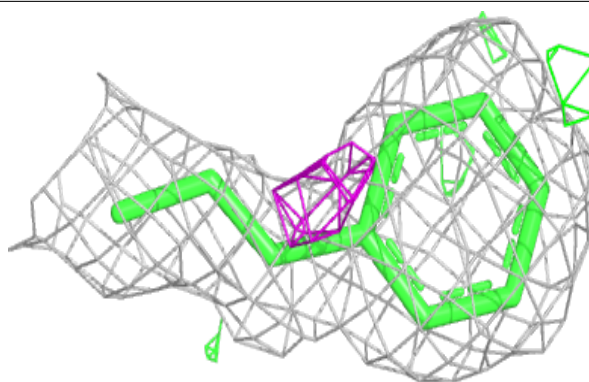
**Electron density around 9Y6 K 301:**

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

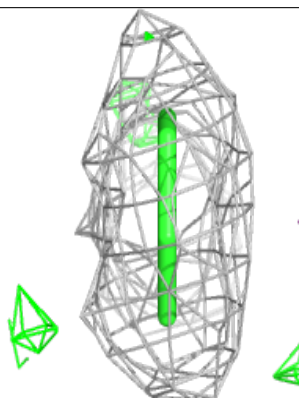
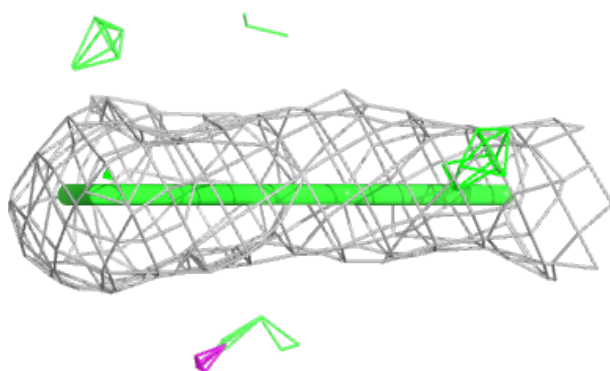
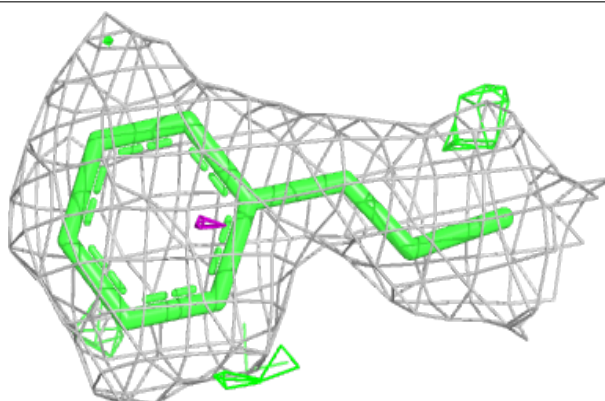


Electron density around 9Y6 H 301:

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

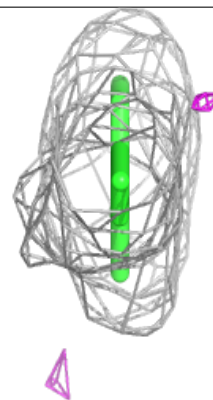
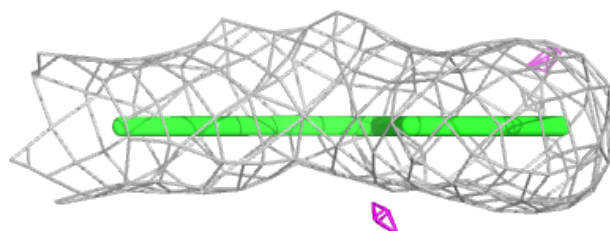
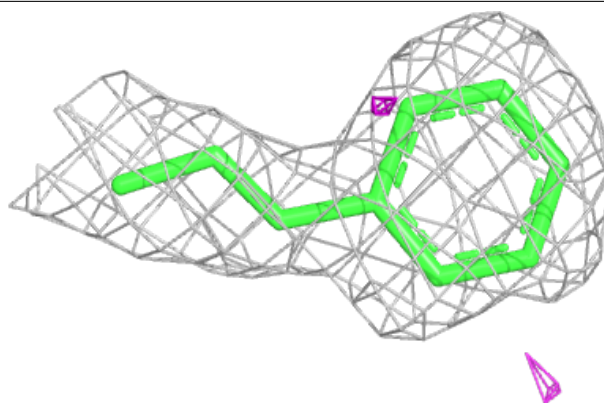
**Electron density around 9Y6 G 301:**

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

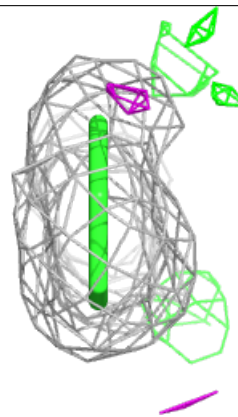
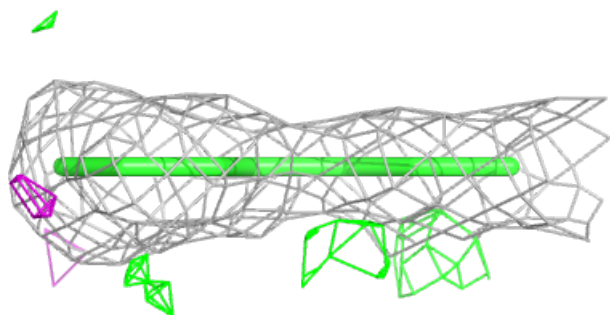
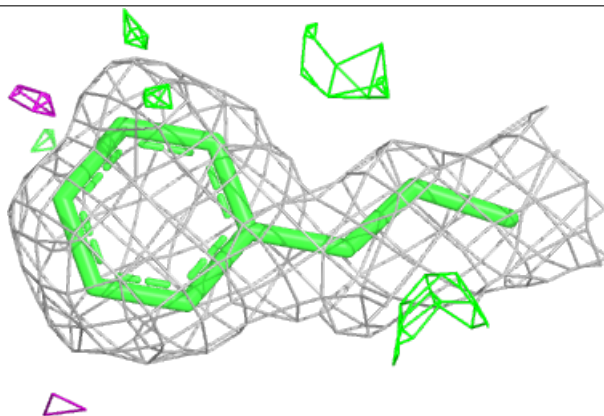


Electron density around 9Y6 I 301:

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

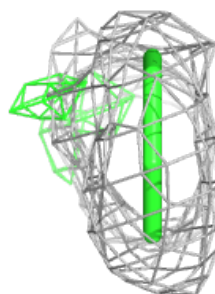
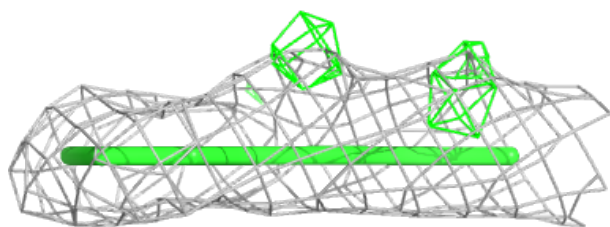
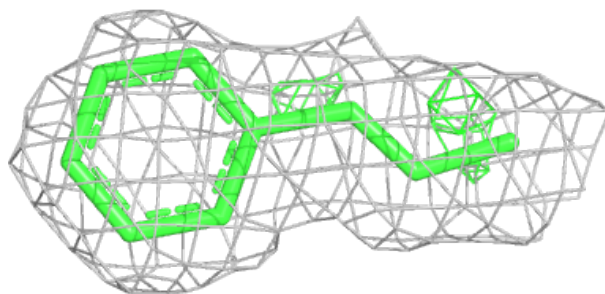
**Electron density around 9Y6 L 301:**

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

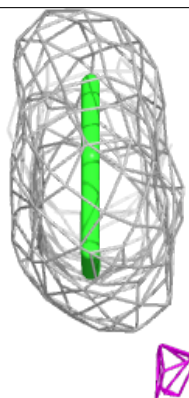
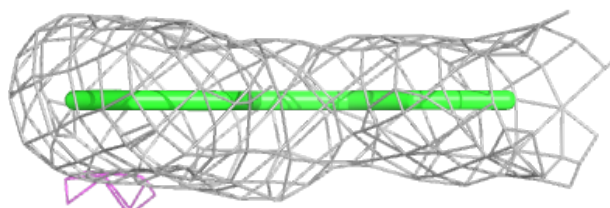
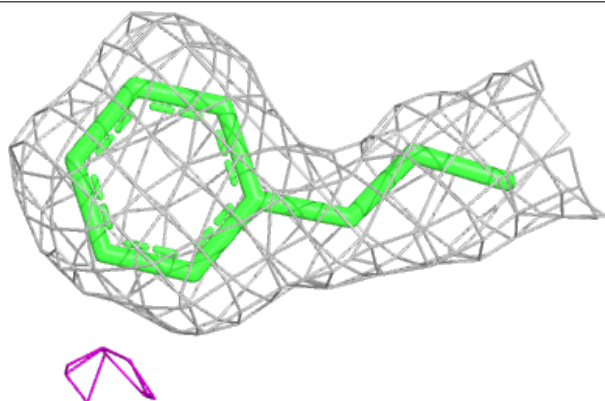


Electron density around 9Y6 E 301:

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

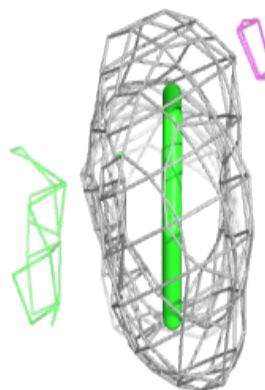
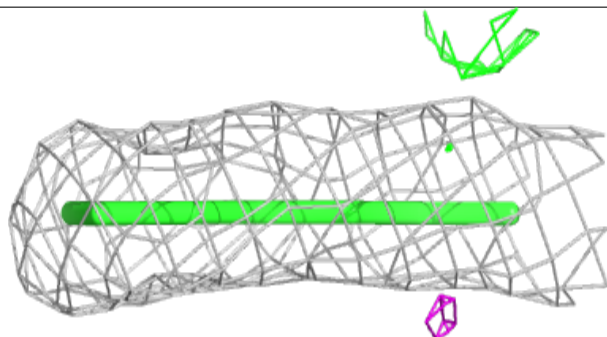
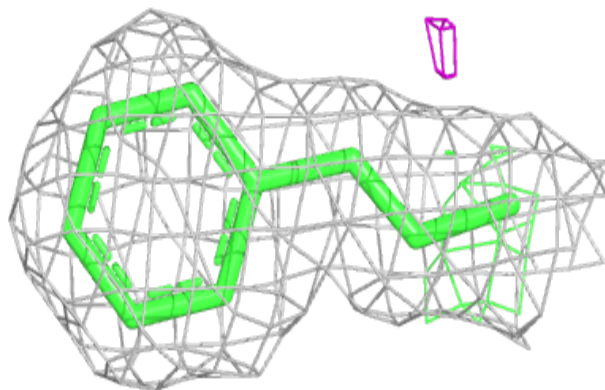
**Electron density around 9Y6 B 301:**

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

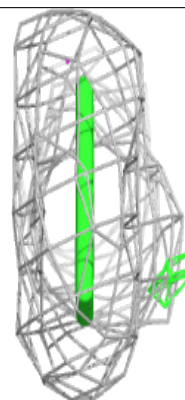
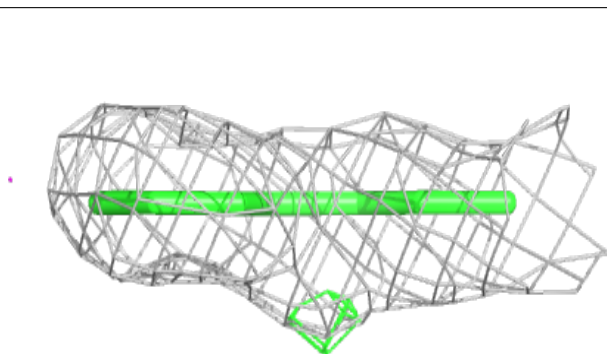
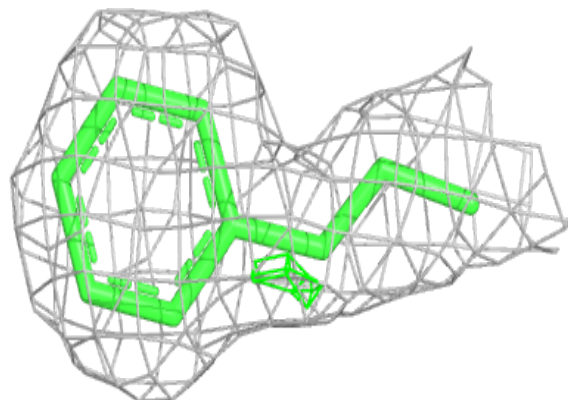


Electron density around 9Y6 F 301:

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

**Electron density around 9Y6 C 301:**

$2mF_o-DF_c$ (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.