



# Full wwPDB X-ray Structure Validation Report

May 14, 2020 – 10:25 pm BST

PDB ID : 6H4M  
Title : TarP-UDP-GlcNAc-3RboP  
Authors : Guo, Y.; Stehle, T.  
Deposited on : 2018-07-22  
Resolution : 2.73 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

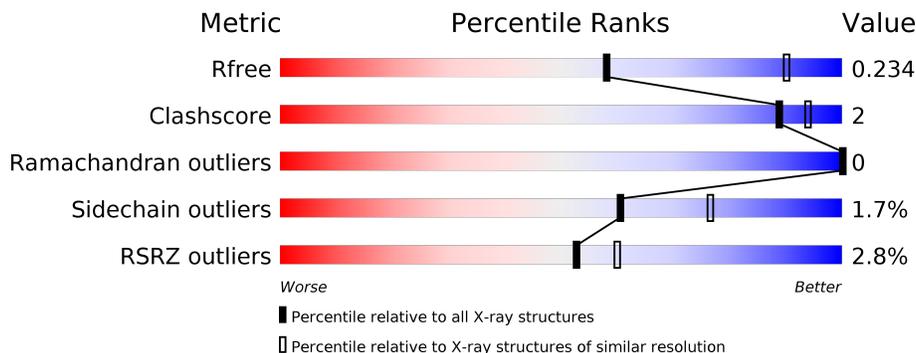
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.73 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.



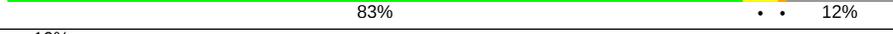
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	345	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 88%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">88% <span style="float: right;">8%</span></p>
1	B	345	<div style="display: flex; align-items: center;"> <div style="width: 88%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">88% <span style="float: right;">8%</span></p>
1	C	345	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 87%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">87% <span style="float: right;">9%</span></p>
1	D	345	<div style="display: flex; align-items: center;"> <div style="width: 87%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 10%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">87% <span style="float: right;">10%</span></p>
1	E	345	<div style="display: flex; align-items: center;"> <div style="width: 88%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">88% <span style="float: right;">8%</span></p>
1	F	345	<div style="display: flex; align-items: center;"> <div style="width: 87%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">87% <span style="float: right;">8%</span></p>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	G	345	 88% 9%
1	H	345	 88% 8%
1	I	345	 86% 5% 9%
1	O	345	 88% 8%
1	P	345	 83% 12%
1	Q	345	 83% 7% 9%

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 30905 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 Probable ss-1,3-N-acetylglucosaminyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	317	Total 2496	C 1606	N 412	O 470	S 8	0	0	0
1	C	314	Total 2431	C 1564	N 400	O 459	S 8	0	0	0
1	F	316	Total 2440	C 1574	N 395	O 463	S 8	0	0	0
1	O	316	Total 2464	C 1582	N 406	O 468	S 8	0	0	0
1	P	305	Total 2121	C 1355	N 359	O 401	S 6	0	0	0
1	E	317	Total 2476	C 1600	N 406	O 462	S 8	0	0	0
1	G	314	Total 2423	C 1562	N 398	O 455	S 8	0	0	0
1	Q	314	Total 2217	C 1413	N 377	O 421	S 6	0	0	0
1	A	317	Total 2488	C 1604	N 410	O 466	S 8	0	0	0
1	D	312	Total 2401	C 1549	N 398	O 446	S 8	0	0	0
1	H	318	Total 2522	C 1621	N 415	O 478	S 8	0	0	0
1	I	315	Total 2427	C 1558	N 400	O 461	S 8	0	0	0

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
B	-16	ARG	-	expression tag	UNP A0A0H3JNB0
B	-15	GLY	-	expression tag	UNP A0A0H3JNB0
B	-14	SER	-	expression tag	UNP A0A0H3JNB0
B	-13	HIS	-	expression tag	UNP A0A0H3JNB0

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP A0A0H3JNB0
B	-11	HIS	-	expression tag	UNP A0A0H3JNB0
B	-10	HIS	-	expression tag	UNP A0A0H3JNB0
B	-9	HIS	-	expression tag	UNP A0A0H3JNB0
B	-8	HIS	-	expression tag	UNP A0A0H3JNB0
B	-7	GLY	-	expression tag	UNP A0A0H3JNB0
B	-6	SER	-	expression tag	UNP A0A0H3JNB0
B	-5	LEU	-	expression tag	UNP A0A0H3JNB0
B	-4	VAL	-	expression tag	UNP A0A0H3JNB0
B	-3	PRO	-	expression tag	UNP A0A0H3JNB0
B	-2	ARG	-	expression tag	UNP A0A0H3JNB0
B	-1	GLY	-	expression tag	UNP A0A0H3JNB0
B	0	SER	-	expression tag	UNP A0A0H3JNB0
C	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
C	-16	ARG	-	expression tag	UNP A0A0H3JNB0
C	-15	GLY	-	expression tag	UNP A0A0H3JNB0
C	-14	SER	-	expression tag	UNP A0A0H3JNB0
C	-13	HIS	-	expression tag	UNP A0A0H3JNB0
C	-12	HIS	-	expression tag	UNP A0A0H3JNB0
C	-11	HIS	-	expression tag	UNP A0A0H3JNB0
C	-10	HIS	-	expression tag	UNP A0A0H3JNB0
C	-9	HIS	-	expression tag	UNP A0A0H3JNB0
C	-8	HIS	-	expression tag	UNP A0A0H3JNB0
C	-7	GLY	-	expression tag	UNP A0A0H3JNB0
C	-6	SER	-	expression tag	UNP A0A0H3JNB0
C	-5	LEU	-	expression tag	UNP A0A0H3JNB0
C	-4	VAL	-	expression tag	UNP A0A0H3JNB0
C	-3	PRO	-	expression tag	UNP A0A0H3JNB0
C	-2	ARG	-	expression tag	UNP A0A0H3JNB0
C	-1	GLY	-	expression tag	UNP A0A0H3JNB0
C	0	SER	-	expression tag	UNP A0A0H3JNB0
F	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
F	-16	ARG	-	expression tag	UNP A0A0H3JNB0
F	-15	GLY	-	expression tag	UNP A0A0H3JNB0
F	-14	SER	-	expression tag	UNP A0A0H3JNB0
F	-13	HIS	-	expression tag	UNP A0A0H3JNB0
F	-12	HIS	-	expression tag	UNP A0A0H3JNB0
F	-11	HIS	-	expression tag	UNP A0A0H3JNB0
F	-10	HIS	-	expression tag	UNP A0A0H3JNB0
F	-9	HIS	-	expression tag	UNP A0A0H3JNB0
F	-8	HIS	-	expression tag	UNP A0A0H3JNB0
F	-7	GLY	-	expression tag	UNP A0A0H3JNB0

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
F	-6	SER	-	expression tag	UNP A0A0H3JNB0
F	-5	LEU	-	expression tag	UNP A0A0H3JNB0
F	-4	VAL	-	expression tag	UNP A0A0H3JNB0
F	-3	PRO	-	expression tag	UNP A0A0H3JNB0
F	-2	ARG	-	expression tag	UNP A0A0H3JNB0
F	-1	GLY	-	expression tag	UNP A0A0H3JNB0
F	0	SER	-	expression tag	UNP A0A0H3JNB0
O	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
O	-16	ARG	-	expression tag	UNP A0A0H3JNB0
O	-15	GLY	-	expression tag	UNP A0A0H3JNB0
O	-14	SER	-	expression tag	UNP A0A0H3JNB0
O	-13	HIS	-	expression tag	UNP A0A0H3JNB0
O	-12	HIS	-	expression tag	UNP A0A0H3JNB0
O	-11	HIS	-	expression tag	UNP A0A0H3JNB0
O	-10	HIS	-	expression tag	UNP A0A0H3JNB0
O	-9	HIS	-	expression tag	UNP A0A0H3JNB0
O	-8	HIS	-	expression tag	UNP A0A0H3JNB0
O	-7	GLY	-	expression tag	UNP A0A0H3JNB0
O	-6	SER	-	expression tag	UNP A0A0H3JNB0
O	-5	LEU	-	expression tag	UNP A0A0H3JNB0
O	-4	VAL	-	expression tag	UNP A0A0H3JNB0
O	-3	PRO	-	expression tag	UNP A0A0H3JNB0
O	-2	ARG	-	expression tag	UNP A0A0H3JNB0
O	-1	GLY	-	expression tag	UNP A0A0H3JNB0
O	0	SER	-	expression tag	UNP A0A0H3JNB0
P	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
P	-16	ARG	-	expression tag	UNP A0A0H3JNB0
P	-15	GLY	-	expression tag	UNP A0A0H3JNB0
P	-14	SER	-	expression tag	UNP A0A0H3JNB0
P	-13	HIS	-	expression tag	UNP A0A0H3JNB0
P	-12	HIS	-	expression tag	UNP A0A0H3JNB0
P	-11	HIS	-	expression tag	UNP A0A0H3JNB0
P	-10	HIS	-	expression tag	UNP A0A0H3JNB0
P	-9	HIS	-	expression tag	UNP A0A0H3JNB0
P	-8	HIS	-	expression tag	UNP A0A0H3JNB0
P	-7	GLY	-	expression tag	UNP A0A0H3JNB0
P	-6	SER	-	expression tag	UNP A0A0H3JNB0
P	-5	LEU	-	expression tag	UNP A0A0H3JNB0
P	-4	VAL	-	expression tag	UNP A0A0H3JNB0
P	-3	PRO	-	expression tag	UNP A0A0H3JNB0
P	-2	ARG	-	expression tag	UNP A0A0H3JNB0
P	-1	GLY	-	expression tag	UNP A0A0H3JNB0

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
P	0	SER	-	expression tag	UNP A0A0H3JNB0
E	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
E	-16	ARG	-	expression tag	UNP A0A0H3JNB0
E	-15	GLY	-	expression tag	UNP A0A0H3JNB0
E	-14	SER	-	expression tag	UNP A0A0H3JNB0
E	-13	HIS	-	expression tag	UNP A0A0H3JNB0
E	-12	HIS	-	expression tag	UNP A0A0H3JNB0
E	-11	HIS	-	expression tag	UNP A0A0H3JNB0
E	-10	HIS	-	expression tag	UNP A0A0H3JNB0
E	-9	HIS	-	expression tag	UNP A0A0H3JNB0
E	-8	HIS	-	expression tag	UNP A0A0H3JNB0
E	-7	GLY	-	expression tag	UNP A0A0H3JNB0
E	-6	SER	-	expression tag	UNP A0A0H3JNB0
E	-5	LEU	-	expression tag	UNP A0A0H3JNB0
E	-4	VAL	-	expression tag	UNP A0A0H3JNB0
E	-3	PRO	-	expression tag	UNP A0A0H3JNB0
E	-2	ARG	-	expression tag	UNP A0A0H3JNB0
E	-1	GLY	-	expression tag	UNP A0A0H3JNB0
E	0	SER	-	expression tag	UNP A0A0H3JNB0
G	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
G	-16	ARG	-	expression tag	UNP A0A0H3JNB0
G	-15	GLY	-	expression tag	UNP A0A0H3JNB0
G	-14	SER	-	expression tag	UNP A0A0H3JNB0
G	-13	HIS	-	expression tag	UNP A0A0H3JNB0
G	-12	HIS	-	expression tag	UNP A0A0H3JNB0
G	-11	HIS	-	expression tag	UNP A0A0H3JNB0
G	-10	HIS	-	expression tag	UNP A0A0H3JNB0
G	-9	HIS	-	expression tag	UNP A0A0H3JNB0
G	-8	HIS	-	expression tag	UNP A0A0H3JNB0
G	-7	GLY	-	expression tag	UNP A0A0H3JNB0
G	-6	SER	-	expression tag	UNP A0A0H3JNB0
G	-5	LEU	-	expression tag	UNP A0A0H3JNB0
G	-4	VAL	-	expression tag	UNP A0A0H3JNB0
G	-3	PRO	-	expression tag	UNP A0A0H3JNB0
G	-2	ARG	-	expression tag	UNP A0A0H3JNB0
G	-1	GLY	-	expression tag	UNP A0A0H3JNB0
G	0	SER	-	expression tag	UNP A0A0H3JNB0
Q	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
Q	-16	ARG	-	expression tag	UNP A0A0H3JNB0
Q	-15	GLY	-	expression tag	UNP A0A0H3JNB0
Q	-14	SER	-	expression tag	UNP A0A0H3JNB0
Q	-13	HIS	-	expression tag	UNP A0A0H3JNB0

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
Q	-12	HIS	-	expression tag	UNP A0A0H3JNB0
Q	-11	HIS	-	expression tag	UNP A0A0H3JNB0
Q	-10	HIS	-	expression tag	UNP A0A0H3JNB0
Q	-9	HIS	-	expression tag	UNP A0A0H3JNB0
Q	-8	HIS	-	expression tag	UNP A0A0H3JNB0
Q	-7	GLY	-	expression tag	UNP A0A0H3JNB0
Q	-6	SER	-	expression tag	UNP A0A0H3JNB0
Q	-5	LEU	-	expression tag	UNP A0A0H3JNB0
Q	-4	VAL	-	expression tag	UNP A0A0H3JNB0
Q	-3	PRO	-	expression tag	UNP A0A0H3JNB0
Q	-2	ARG	-	expression tag	UNP A0A0H3JNB0
Q	-1	GLY	-	expression tag	UNP A0A0H3JNB0
Q	0	SER	-	expression tag	UNP A0A0H3JNB0
A	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
A	-16	ARG	-	expression tag	UNP A0A0H3JNB0
A	-15	GLY	-	expression tag	UNP A0A0H3JNB0
A	-14	SER	-	expression tag	UNP A0A0H3JNB0
A	-13	HIS	-	expression tag	UNP A0A0H3JNB0
A	-12	HIS	-	expression tag	UNP A0A0H3JNB0
A	-11	HIS	-	expression tag	UNP A0A0H3JNB0
A	-10	HIS	-	expression tag	UNP A0A0H3JNB0
A	-9	HIS	-	expression tag	UNP A0A0H3JNB0
A	-8	HIS	-	expression tag	UNP A0A0H3JNB0
A	-7	GLY	-	expression tag	UNP A0A0H3JNB0
A	-6	SER	-	expression tag	UNP A0A0H3JNB0
A	-5	LEU	-	expression tag	UNP A0A0H3JNB0
A	-4	VAL	-	expression tag	UNP A0A0H3JNB0
A	-3	PRO	-	expression tag	UNP A0A0H3JNB0
A	-2	ARG	-	expression tag	UNP A0A0H3JNB0
A	-1	GLY	-	expression tag	UNP A0A0H3JNB0
A	0	SER	-	expression tag	UNP A0A0H3JNB0
D	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
D	-16	ARG	-	expression tag	UNP A0A0H3JNB0
D	-15	GLY	-	expression tag	UNP A0A0H3JNB0
D	-14	SER	-	expression tag	UNP A0A0H3JNB0
D	-13	HIS	-	expression tag	UNP A0A0H3JNB0
D	-12	HIS	-	expression tag	UNP A0A0H3JNB0
D	-11	HIS	-	expression tag	UNP A0A0H3JNB0
D	-10	HIS	-	expression tag	UNP A0A0H3JNB0
D	-9	HIS	-	expression tag	UNP A0A0H3JNB0
D	-8	HIS	-	expression tag	UNP A0A0H3JNB0
D	-7	GLY	-	expression tag	UNP A0A0H3JNB0

*Continued on next page...*

*Continued from previous page...*

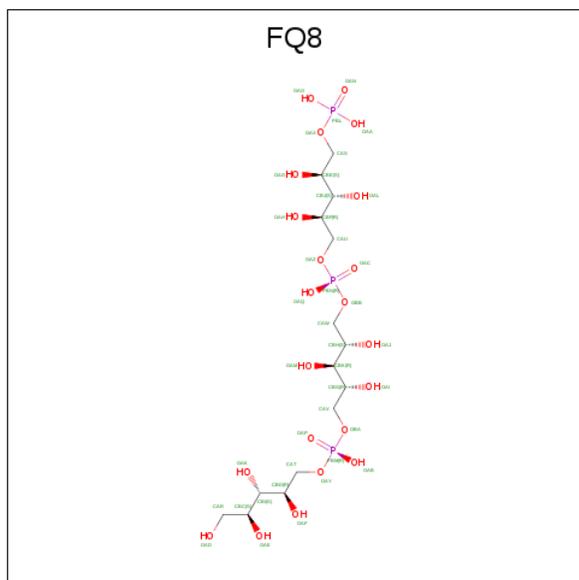
Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	SER	-	expression tag	UNP A0A0H3JNB0
D	-5	LEU	-	expression tag	UNP A0A0H3JNB0
D	-4	VAL	-	expression tag	UNP A0A0H3JNB0
D	-3	PRO	-	expression tag	UNP A0A0H3JNB0
D	-2	ARG	-	expression tag	UNP A0A0H3JNB0
D	-1	GLY	-	expression tag	UNP A0A0H3JNB0
D	0	SER	-	expression tag	UNP A0A0H3JNB0
H	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
H	-16	ARG	-	expression tag	UNP A0A0H3JNB0
H	-15	GLY	-	expression tag	UNP A0A0H3JNB0
H	-14	SER	-	expression tag	UNP A0A0H3JNB0
H	-13	HIS	-	expression tag	UNP A0A0H3JNB0
H	-12	HIS	-	expression tag	UNP A0A0H3JNB0
H	-11	HIS	-	expression tag	UNP A0A0H3JNB0
H	-10	HIS	-	expression tag	UNP A0A0H3JNB0
H	-9	HIS	-	expression tag	UNP A0A0H3JNB0
H	-8	HIS	-	expression tag	UNP A0A0H3JNB0
H	-7	GLY	-	expression tag	UNP A0A0H3JNB0
H	-6	SER	-	expression tag	UNP A0A0H3JNB0
H	-5	LEU	-	expression tag	UNP A0A0H3JNB0
H	-4	VAL	-	expression tag	UNP A0A0H3JNB0
H	-3	PRO	-	expression tag	UNP A0A0H3JNB0
H	-2	ARG	-	expression tag	UNP A0A0H3JNB0
H	-1	GLY	-	expression tag	UNP A0A0H3JNB0
H	0	SER	-	expression tag	UNP A0A0H3JNB0
I	-17	MET	-	initiating methionine	UNP A0A0H3JNB0
I	-16	ARG	-	expression tag	UNP A0A0H3JNB0
I	-15	GLY	-	expression tag	UNP A0A0H3JNB0
I	-14	SER	-	expression tag	UNP A0A0H3JNB0
I	-13	HIS	-	expression tag	UNP A0A0H3JNB0
I	-12	HIS	-	expression tag	UNP A0A0H3JNB0
I	-11	HIS	-	expression tag	UNP A0A0H3JNB0
I	-10	HIS	-	expression tag	UNP A0A0H3JNB0
I	-9	HIS	-	expression tag	UNP A0A0H3JNB0
I	-8	HIS	-	expression tag	UNP A0A0H3JNB0
I	-7	GLY	-	expression tag	UNP A0A0H3JNB0
I	-6	SER	-	expression tag	UNP A0A0H3JNB0
I	-5	LEU	-	expression tag	UNP A0A0H3JNB0
I	-4	VAL	-	expression tag	UNP A0A0H3JNB0
I	-3	PRO	-	expression tag	UNP A0A0H3JNB0
I	-2	ARG	-	expression tag	UNP A0A0H3JNB0
I	-1	GLY	-	expression tag	UNP A0A0H3JNB0

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	0	SER	-	expression tag	UNP A0A0H3JNB0

- Molecule 2 is [(2 {R},3 {S},4 {S})-2,3,4,5-tetrakis(oxidanyl)pentyl] [(2 {R},3 {R},4 {S})-2,3,4-tris(oxidanyl)-5-[oxidanyl-[(2 {R},3 {S},4 {S})-2,3,4-tris(oxidanyl)-5-phosphonooxy-pentoxyl]phosphoryl]oxy-pentyl] hydrogen phosphate (three-letter code: FQ8) (formula: C<sub>15</sub>H<sub>35</sub>O<sub>22</sub>P<sub>3</sub>).



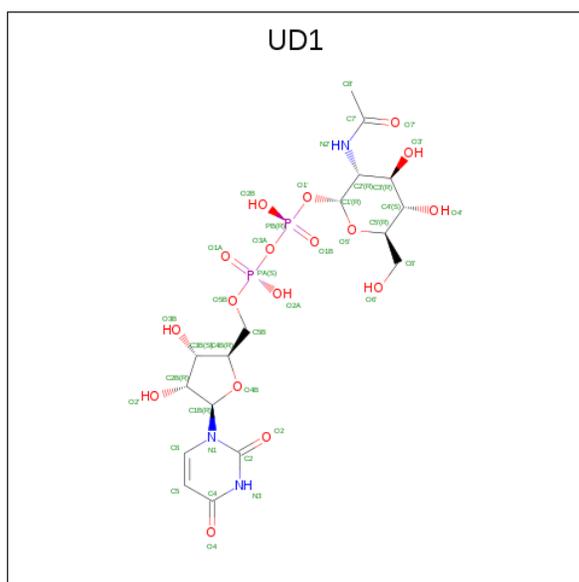
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
2	B	1	Total	C	O	P	0	0
			40	15	22	3		
2	C	1	Total	C	O	P	0	0
			40	15	22	3		
2	F	1	Total	C	O	P	0	0
			40	15	22	3		
2	O	1	Total	C	O	P	0	0
			40	15	22	3		
2	P	1	Total	C	O	P	0	0
			40	15	22	3		
2	E	1	Total	C	O	P	0	0
			40	15	22	3		
2	G	1	Total	C	O	P	0	0
			40	15	22	3		
2	Q	1	Total	C	O	P	0	0
			40	15	22	3		
2	A	1	Total	C	O	P	0	0
			40	15	22	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	D	1	Total	C	O	P	0	0
			40	15	22	3		
2	H	1	Total	C	O	P	0	0
			40	15	22	3		
2	I	1	Total	C	O	P	0	0
			40	15	22	3		

- Molecule 3 is URIDINE-DIPHOSPHATE-N-ACETYLGLUCOSAMINE (three-letter code: UD1) (formula: C<sub>17</sub>H<sub>27</sub>N<sub>3</sub>O<sub>17</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	C	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	F	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	O	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	E	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	G	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	Q	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	A	1	Total	C	N	O	P	0	0
			39	17	3	17	2		

Continued on next page...

*Continued from previous page...*

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	D	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	H	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
3	I	1	Total	C	N	O	P	0	0
			39	17	3	17	2		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	1	Total	Mg	0	0
			1	1		
4	G	1	Total	Mg	0	0
			1	1		
4	Q	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		
4	H	2	Total	Mg	0	0
			2	2		
4	B	2	Total	Mg	0	0
			2	2		
4	I	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	A	2	Total	Mg	0	0
			2	2		
4	O	1	Total	Mg	0	0
			1	1		
4	F	1	Total	Mg	0	0
			1	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

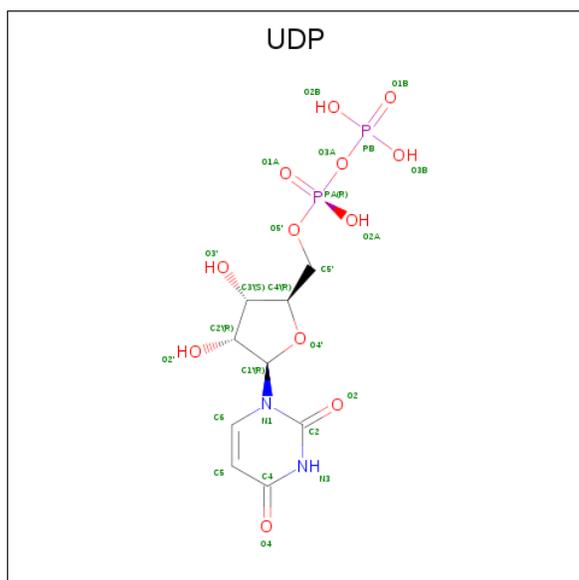
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	P	1	Total	Cl	0	0
			1	1		
5	D	1	Total	Cl	0	0
			1	1		

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	1	Total Cl 1 1	0	0
5	H	2	Total Cl 2 2	0	0
5	B	2	Total Cl 2 2	0	0
5	I	1	Total Cl 1 1	0	0
5	C	1	Total Cl 1 1	0	0
5	A	1	Total Cl 1 1	0	0
5	O	1	Total Cl 1 1	0	0
5	F	1	Total Cl 1 1	0	0

- Molecule 6 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C<sub>9</sub>H<sub>14</sub>N<sub>2</sub>O<sub>12</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	P	1	Total C N O P 25 9 2 12 2	0	0

- Molecule 7 is water.

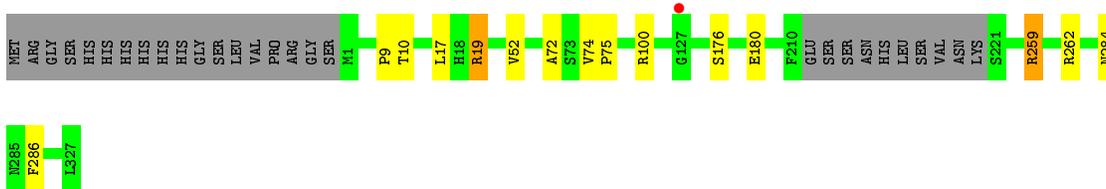
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	125	Total O 125 125	0	0
7	C	86	Total O 86 86	0	0
7	F	80	Total O 80 80	0	0
7	O	93	Total O 93 93	0	0
7	P	53	Total O 53 53	0	0
7	E	103	Total O 103 103	0	0
7	G	79	Total O 79 79	0	0
7	Q	48	Total O 48 48	0	0
7	A	108	Total O 108 108	0	0
7	D	89	Total O 89 89	0	0
7	H	105	Total O 105 105	0	0
7	I	69	Total O 69 69	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

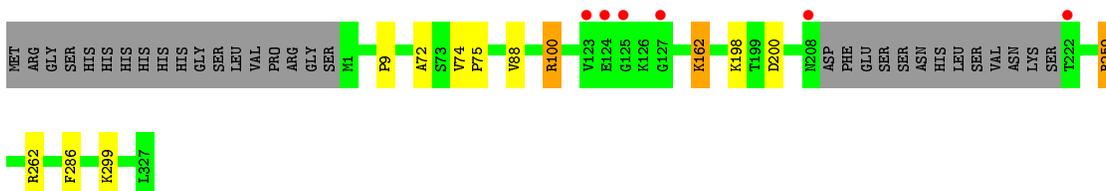
- Molecule 1: Probable ss-1,3-N-acetylglucosaminyltransferase

Chain B:  88% 8%



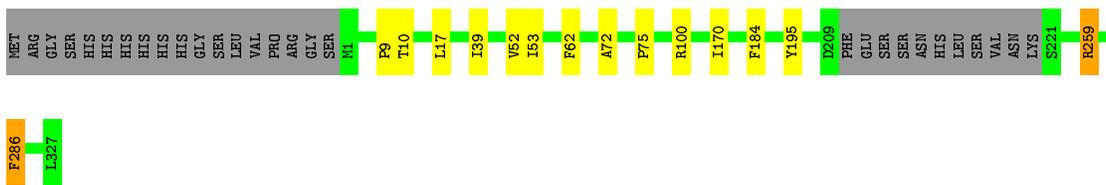
- Molecule 1: Probable ss-1,3-N-acetylglucosaminyltransferase

Chain C:  87% 2% 9%



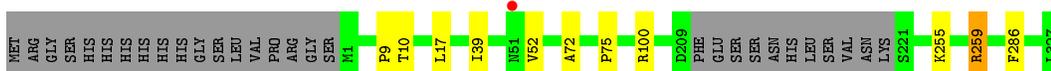
- Molecule 1: Probable ss-1,3-N-acetylglucosaminyltransferase

Chain F:  87% 8%



- Molecule 1: Probable ss-1,3-N-acetylglucosaminyltransferase

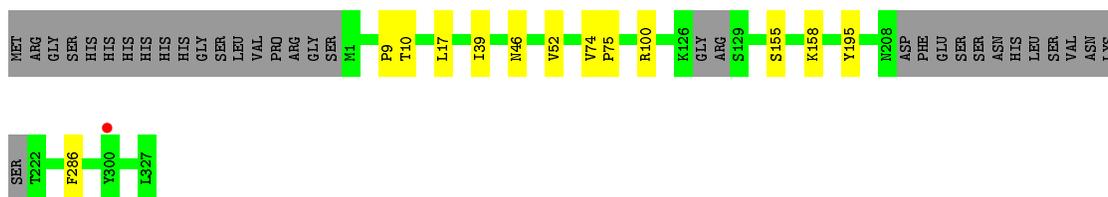
Chain O:  88% 8%





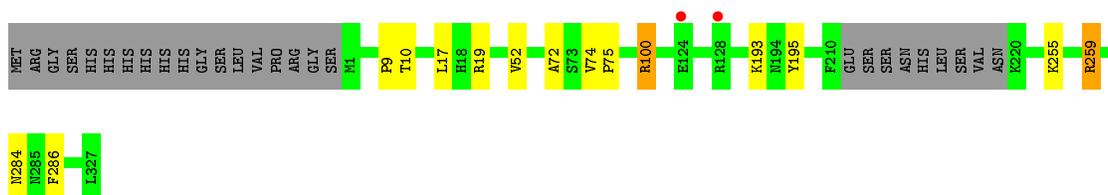
- Molecule 1: Probable ss-1,3-N-acetylglucosaminyltransferase

Chain D:  87% • 10%



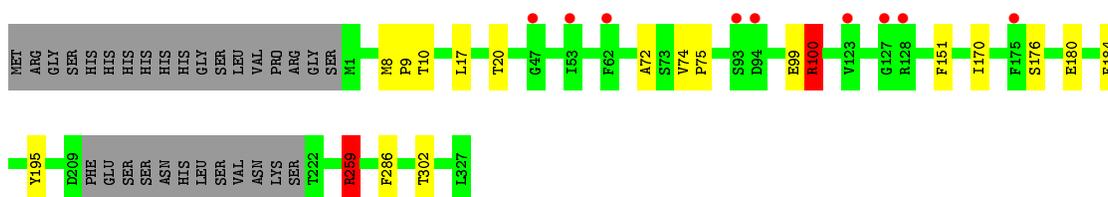
- Molecule 1: Probable ss-1,3-N-acetylglucosaminyltransferase

Chain H:  88% • • 8%



- Molecule 1: Probable ss-1,3-N-acetylglucosaminyltransferase

Chain I:  86% 5% • 9%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.17Å 210.75Å 123.20Å 90.00° 91.92° 90.00°	Depositor
Resolution (Å)	48.44 – 2.73 48.44 – 2.73	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.44-2.73) 99.9 (48.44-2.73)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.61 (at 2.73Å)	Xtrriage
Refinement program	REFMAC 5.8.0230	Depositor
R, $R_{free}$	0.189 , 0.233 0.191 , 0.234	Depositor DCC
$R_{free}$ test set	6412 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.3	Xtrriage
Anisotropy	0.472	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 61.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.037 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	30905	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: FQ8, MG, UD1, UDP, CL

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	0.41	0/2532	0.55	0/3417
1	B	0.40	0/2538	0.56	0/3423
1	C	0.38	0/2472	0.53	0/3341
1	D	0.40	0/2442	0.55	0/3303
1	E	0.41	0/2519	0.55	0/3399
1	F	0.39	0/2481	0.54	0/3354
1	G	0.39	0/2464	0.55	0/3332
1	H	0.41	0/2565	0.59	0/3456
1	I	0.38	0/2468	0.54	0/3338
1	O	0.39	0/2506	0.54	0/3384
1	P	0.39	0/2152	0.55	1/2922 (0.0%)
1	Q	0.42	0/2250	0.56	0/3060
All	All	0.40	0/29389	0.55	1/39729 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	3
1	C	0	2
1	D	0	1
1	F	0	2
1	G	0	2
1	H	0	2
1	I	0	2
1	O	0	2
1	P	0	1
1	Q	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	19

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	P	144	ASP	CB-CG-OD1	5.42	123.18	118.30

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	259	ARG	Sidechain
1	B	100	ARG	Sidechain
1	B	19	ARG	Sidechain
1	B	259	ARG	Sidechain
1	C	100	ARG	Sidechain
1	C	259	ARG	Sidechain
1	D	100	ARG	Sidechain
1	F	100	ARG	Sidechain
1	F	259	ARG	Sidechain
1	G	100	ARG	Sidechain
1	G	259	ARG	Sidechain
1	H	19	ARG	Sidechain
1	H	259	ARG	Sidechain
1	I	100	ARG	Sidechain
1	I	259	ARG	Sidechain
1	O	100	ARG	Sidechain
1	O	259	ARG	Sidechain
1	P	262	ARG	Sidechain
1	Q	262	ARG	Sidechain

## 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	2488	0	2398	7	0
1	B	2496	0	2423	8	0
1	C	2431	0	2308	7	0
1	D	2401	0	2274	7	0
1	E	2476	0	2387	7	0
1	F	2440	0	2303	8	0
1	G	2423	0	2299	5	0
1	H	2522	0	2459	8	0
1	I	2427	0	2288	13	0
1	O	2464	0	2360	6	0
1	P	2121	0	1726	13	0
1	Q	2217	0	1853	17	0
2	A	40	0	0	1	0
2	B	40	0	0	1	0
2	C	40	0	0	2	0
2	D	40	0	0	0	0
2	E	40	0	0	0	0
2	F	40	0	0	1	0
2	G	40	0	0	1	0
2	H	40	0	0	0	0
2	I	40	0	0	3	0
2	O	40	0	0	1	0
2	P	40	0	0	3	0
2	Q	40	0	0	1	0
3	A	39	0	25	1	0
3	B	39	0	25	1	0
3	C	39	0	25	1	0
3	D	39	0	25	0	0
3	E	39	0	25	1	0
3	F	39	0	25	1	0
3	G	39	0	25	0	0
3	H	39	0	25	1	0
3	I	39	0	25	1	0
3	O	39	0	25	1	0
3	Q	39	0	25	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	2	0	0	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	1	0	0	0	0
4	O	1	0	0	0	0
4	P	1	0	0	0	0
4	Q	1	0	0	0	0
5	A	1	0	0	0	0
5	B	2	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	H	2	0	0	0	0
5	I	1	0	0	0	0
5	O	1	0	0	0	0
5	P	1	0	0	0	0
6	P	25	0	11	1	0
7	A	108	0	0	0	0
7	B	125	0	0	0	0
7	C	86	0	0	0	0
7	D	89	0	0	0	0
7	E	103	0	0	0	0
7	F	80	0	0	0	0
7	G	79	0	0	0	0
7	H	105	0	0	0	0
7	I	69	0	0	0	0
7	O	93	0	0	0	0
7	P	53	0	0	0	0
7	Q	48	0	0	0	0
All	All	30905	0	27364	108	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 2.

All (108) 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:P:9:PRO:O	6:P:402:UDP:O2'	2.02	0.78
1:B:262:ARG:NH1	2:B:401:FQ8:OAO	2.23	0.70
2:C:401:FQ8:OAP	2:C:401:FQ8:OAF	2.09	0.69
1:Q:302:THR:HG22	1:Q:304:ILE:HG22	1.76	0.68
1:P:259:ARG:NH2	2:P:401:FQ8:OAP	2.27	0.67
1:Q:122:GLY:O	1:Q:205:ILE:HA	1.96	0.65

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:176:SER:HB3	1:B:180:GLU:OE2	1.97	0.64
1:I:72:ALA:HB2	3:I:402:UD1:O4B	1.97	0.64
1:Q:303:GLN:NE2	1:Q:303:GLN:HA	2.11	0.64
1:Q:302:THR:OG1	2:Q:401:FQ8:OAN	2.17	0.63
1:E:9:PRO:HB3	1:E:75:PRO:HB2	1.82	0.62
1:H:9:PRO:HB3	1:H:75:PRO:HB2	1.82	0.62
1:A:9:PRO:HB3	1:A:75:PRO:HB2	1.81	0.62
1:Q:9:PRO:HB3	1:Q:75:PRO:HB2	1.81	0.61
1:P:9:PRO:HB3	1:P:75:PRO:HB2	1.82	0.61
1:B:9:PRO:HB3	1:B:75:PRO:HB2	1.83	0.61
1:C:9:PRO:HB3	1:C:75:PRO:HB2	1.82	0.60
1:D:9:PRO:HB3	1:D:75:PRO:HB2	1.83	0.60
1:G:9:PRO:HB3	1:G:75:PRO:HB2	1.82	0.60
1:O:9:PRO:HB3	1:O:75:PRO:HB2	1.82	0.60
1:I:9:PRO:HB3	1:I:75:PRO:HB2	1.82	0.60
1:F:9:PRO:HB3	1:F:75:PRO:HB2	1.83	0.59
1:C:88:VAL:HG13	1:C:162:LYS:HG2	1.87	0.57
1:I:176:SER:HB3	1:I:180:GLU:OE2	2.05	0.57
2:I:401:FQ8:OBA	2:I:401:FQ8:OAF	2.23	0.56
1:P:262:ARG:HG2	1:P:305:PHE:CZ	2.42	0.54
1:Q:12:ASN:HD21	1:Q:44:ASN:CG	2.11	0.53
1:A:128:ARG:CB	3:A:402:UD1:H8'1	2.37	0.53
1:D:46:ASN:OD1	1:H:193:LYS:CD	2.57	0.52
1:C:198:LYS:HE3	1:C:200:ASP:OD1	2.10	0.52
1:P:286:PHE:O	1:P:286:PHE:HD1	1.93	0.52
1:Q:128:ARG:CB	1:Q:208:ASN:CG	2.79	0.52
1:Q:303:GLN:NE2	1:Q:303:GLN:CA	2.73	0.51
1:C:262:ARG:NH2	2:C:401:FQ8:OAN	2.40	0.50
1:H:72:ALA:HB2	3:H:402:UD1:O4B	2.12	0.49
1:O:72:ALA:HB2	3:O:402:UD1:O4B	2.11	0.49
1:E:10:THR:HG21	1:E:17:LEU:HD21	1.95	0.49
1:G:17:LEU:HB3	1:G:52:VAL:HG11	1.94	0.49
1:H:100:ARG:HB3	1:H:100:ARG:HH11	1.78	0.49
1:A:10:THR:HG21	1:A:17:LEU:HD21	1.96	0.48
1:P:258:THR:O	1:P:262:ARG:HG3	2.13	0.48
1:B:72:ALA:HB2	3:B:402:UD1:O4B	2.13	0.47
1:E:72:ALA:HB2	3:E:402:UD1:O4B	2.15	0.47
1:P:10:THR:O	1:P:40:ASP:HA	2.15	0.46
1:D:74:VAL:HB	1:D:75:PRO:HD3	1.98	0.46
1:B:74:VAL:HB	1:B:75:PRO:HD3	1.98	0.45
1:B:10:THR:HG21	1:B:17:LEU:HD21	1.99	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:17:LEU:HB3	1:O:52:VAL:HG11	1.98	0.45
1:Q:238:TYR:HE1	1:Q:253:ALA:HB2	1.80	0.45
1:E:286:PHE:HD1	1:E:286:PHE:O	2.00	0.45
1:H:74:VAL:HB	1:H:75:PRO:HD3	1.98	0.45
1:Q:146:ILE:HD13	1:Q:255:LYS:HG2	1.99	0.45
1:I:170:ILE:HG22	1:I:184:PHE:CE1	2.52	0.45
1:Q:175:PHE:HE1	1:Q:229:THR:HG1	1.62	0.45
1:P:11:PHE:CE1	1:P:68:ASN:ND2	2.85	0.44
1:F:17:LEU:HB3	1:F:52:VAL:HG11	2.00	0.44
1:G:74:VAL:HB	1:G:75:PRO:HD3	1.99	0.44
1:H:17:LEU:HB3	1:H:52:VAL:HG11	1.99	0.44
1:D:10:THR:HG21	1:D:17:LEU:HD21	1.99	0.44
1:I:302:THR:OG1	2:I:401:FQ8:OAN	2.24	0.44
1:Q:170:ILE:HG22	1:Q:184:PHE:CE1	2.52	0.44
1:F:286:PHE:HD1	1:F:286:PHE:O	2.00	0.44
1:P:11:PHE:CD1	1:P:68:ASN:ND2	2.86	0.44
1:Q:302:THR:CG2	1:Q:304:ILE:HG22	2.46	0.44
1:I:10:THR:HG21	1:I:17:LEU:HD21	1.98	0.44
1:F:10:THR:HG21	1:F:17:LEU:HD21	1.99	0.44
1:P:154:LEU:N	2:P:401:FQ8:OAB	2.50	0.44
1:G:259:ARG:NH2	2:G:401:FQ8:OAY	2.48	0.43
1:C:74:VAL:HB	1:C:75:PRO:HD3	2.00	0.43
1:E:170:ILE:HG22	1:E:184:PHE:CE1	2.53	0.43
1:F:170:ILE:HG22	1:F:184:PHE:CE1	2.53	0.43
1:C:72:ALA:HB2	3:C:402:UD1:O4B	2.18	0.43
1:A:170:ILE:HG22	1:A:184:PHE:CE1	2.53	0.43
1:A:74:VAL:HB	1:A:75:PRO:HD3	2.01	0.43
1:G:76:ARG:NH1	1:G:181:ASP:OD1	2.52	0.43
1:H:10:THR:HG21	1:H:17:LEU:HD21	2.01	0.43
1:O:10:THR:HG21	1:O:17:LEU:HD21	1.99	0.43
1:I:74:VAL:HB	1:I:75:PRO:HD3	2.00	0.42
1:A:99:GLU:HG3	1:A:100:ARG:HG2	2.00	0.42
1:P:170:ILE:HG22	1:P:184:PHE:CE1	2.54	0.42
1:I:259:ARG:NH1	2:I:401:FQ8:OAP	2.52	0.42
1:I:99:GLU:HG3	1:I:100:ARG:HG2	2.02	0.42
1:H:100:ARG:HG2	1:H:100:ARG:H	1.73	0.42
1:I:151:PHE:O	1:I:259:ARG:HD2	2.19	0.42
1:F:72:ALA:HB2	3:F:402:UD1:O4B	2.20	0.42
1:B:17:LEU:HB3	1:B:52:VAL:HG11	2.01	0.42
1:E:74:VAL:HB	1:E:75:PRO:HD3	2.02	0.42
1:Q:126:LYS:H	1:Q:208:ASN:HB2	1.85	0.42

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:401:FQ8:CAV	2:F:401:FQ8:OAJ	2.68	0.41
1:O:255:LYS:NZ	2:O:401:FQ8:OAO	2.47	0.41
1:Q:238:TYR:CE2	1:Q:294:PRO:HG2	2.55	0.41
1:A:262:ARG:NH2	2:A:401:FQ8:OAN	2.52	0.41
1:D:17:LEU:HB3	1:D:52:VAL:HG11	2.01	0.41
1:B:17:LEU:HD12	1:B:17:LEU:HA	1.94	0.41
1:I:9:PRO:HB3	1:I:75:PRO:CB	2.51	0.41
1:C:9:PRO:HB3	1:C:75:PRO:CB	2.51	0.41
1:D:9:PRO:HA	1:D:39:ILE:O	2.21	0.41
1:F:9:PRO:HA	1:F:39:ILE:O	2.21	0.41
1:P:262:ARG:NH2	2:P:401:FQ8:OAN	2.54	0.40
1:Q:255:LYS:HD3	1:Q:255:LYS:HA	1.78	0.40
1:Q:261:LEU:HD13	1:Q:305:PHE:HB3	2.03	0.40
1:D:155:SER:O	1:D:158:LYS:CE	2.69	0.40
1:I:8:MET:SD	1:I:20:THR:HG21	2.62	0.40
1:E:9:PRO:HA	1:E:39:ILE:O	2.21	0.40
1:F:53:ILE:HG21	1:F:62:PHE:CD1	2.57	0.40
1:O:9:PRO:HA	1:O:39:ILE:O	2.22	0.40
1:P:9:PRO:HA	1:P:39:ILE:O	2.22	0.40
1:I:17:LEU:HA	1:I:17:LEU:HD12	1.96	0.40

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	313/345 (91%)	304 (97%)	9 (3%)	0	100	100
1	B	313/345 (91%)	306 (98%)	7 (2%)	0	100	100
1	C	310/345 (90%)	302 (97%)	8 (3%)	0	100	100
1	D	306/345 (89%)	298 (97%)	8 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	313/345 (91%)	304 (97%)	9 (3%)	0	100	100
1	F	312/345 (90%)	305 (98%)	7 (2%)	0	100	100
1	G	310/345 (90%)	302 (97%)	8 (3%)	0	100	100
1	H	314/345 (91%)	306 (98%)	8 (2%)	0	100	100
1	I	311/345 (90%)	303 (97%)	8 (3%)	0	100	100
1	O	312/345 (90%)	304 (97%)	8 (3%)	0	100	100
1	P	293/345 (85%)	283 (97%)	10 (3%)	0	100	100
1	Q	308/345 (89%)	300 (97%)	8 (3%)	0	100	100
All	All	3715/4140 (90%)	3617 (97%)	98 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	250/313 (80%)	247 (99%)	3 (1%)	71	83
1	B	253/313 (81%)	249 (98%)	4 (2%)	62	78
1	C	238/313 (76%)	233 (98%)	5 (2%)	53	72
1	D	233/313 (74%)	231 (99%)	2 (1%)	78	87
1	E	246/313 (79%)	241 (98%)	5 (2%)	55	72
1	F	235/313 (75%)	232 (99%)	3 (1%)	69	82
1	G	235/313 (75%)	232 (99%)	3 (1%)	69	82
1	H	260/313 (83%)	254 (98%)	6 (2%)	50	70
1	I	236/313 (75%)	232 (98%)	4 (2%)	60	76
1	O	248/313 (79%)	246 (99%)	2 (1%)	81	89
1	P	154/313 (49%)	151 (98%)	3 (2%)	57	74
1	Q	169/313 (54%)	163 (96%)	6 (4%)	35	55
All	All	2757/3756 (73%)	2711 (98%)	46 (2%)	60	76

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	19	ARG
1	B	259	ARG
1	B	284	ASN
1	B	286	PHE
1	C	100	ARG
1	C	162	LYS
1	C	259	ARG
1	C	286	PHE
1	C	299	LYS
1	F	195	TYR
1	F	259	ARG
1	F	286	PHE
1	O	259	ARG
1	O	286	PHE
1	P	195	TYR
1	P	259	ARG
1	P	286	PHE
1	E	100	ARG
1	E	110	LYS
1	E	195	TYR
1	E	259	ARG
1	E	286	PHE
1	G	195	TYR
1	G	259	ARG
1	G	286	PHE
1	Q	175	PHE
1	Q	195	TYR
1	Q	255	LYS
1	Q	259	ARG
1	Q	286	PHE
1	Q	303	GLN
1	A	100	ARG
1	A	259	ARG
1	A	286	PHE
1	D	195	TYR
1	D	286	PHE
1	H	100	ARG
1	H	195	TYR
1	H	255	LYS
1	H	259	ARG
1	H	284	ASN
1	H	286	PHE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	I	100	ARG
1	I	195	TYR
1	I	259	ARG
1	I	286	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	Q	303	GLN

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 51 ligands modelled in this entry, 27 are monoatomic - leaving 24 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FQ8	B	401	-	39,39,39	1.03	2 (5%)	54,56,56	0.86	1 (1%)
3	UD1	Q	402	-	34,41,41	0.74	1 (2%)	45,62,62	1.11	4 (8%)
2	FQ8	G	401	-	39,39,39	1.17	4 (10%)	54,56,56	1.02	3 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FQ8	E	401	-	39,39,39	1.21	3 (7%)	54,56,56	0.95	1 (1%)
2	FQ8	C	401	-	39,39,39	1.00	2 (5%)	54,56,56	0.82	1 (1%)
2	FQ8	D	401	-	39,39,39	1.01	2 (5%)	54,56,56	0.83	1 (1%)
3	UD1	B	402	4	34,41,41	0.66	1 (2%)	45,62,62	1.01	2 (4%)
2	FQ8	Q	401	-	39,39,39	1.04	2 (5%)	54,56,56	0.85	3 (5%)
2	FQ8	I	401	-	39,39,39	1.08	2 (5%)	54,56,56	1.02	3 (5%)
3	UD1	G	402	4	34,41,41	0.70	1 (2%)	45,62,62	1.03	3 (6%)
2	FQ8	P	401	-	39,39,39	1.11	4 (10%)	54,56,56	0.97	2 (3%)
2	FQ8	A	401	-	39,39,39	1.03	2 (5%)	54,56,56	0.85	1 (1%)
3	UD1	D	402	4	34,41,41	0.66	0	45,62,62	1.07	3 (6%)
3	UD1	I	402	4	34,41,41	0.61	1 (2%)	45,62,62	1.06	2 (4%)
3	UD1	F	402	4	34,41,41	0.64	0	45,62,62	1.42	5 (11%)
2	FQ8	F	401	-	39,39,39	1.34	5 (12%)	54,56,56	1.02	3 (5%)
3	UD1	O	402	4	34,41,41	0.64	1 (2%)	45,62,62	1.10	2 (4%)
3	UD1	E	402	4	34,41,41	0.65	1 (2%)	45,62,62	1.12	5 (11%)
3	UD1	H	402	4	34,41,41	0.63	0	45,62,62	1.28	5 (11%)
3	UD1	C	402	4	34,41,41	0.60	0	45,62,62	0.97	1 (2%)
3	UD1	A	402	4	34,41,41	0.63	1 (2%)	45,62,62	0.98	1 (2%)
2	FQ8	H	401	-	39,39,39	1.04	2 (5%)	54,56,56	0.84	2 (3%)
6	UDP	P	402	-	20,26,26	0.90	1 (5%)	25,40,40	1.29	2 (8%)
2	FQ8	O	401	-	39,39,39	1.11	2 (5%)	54,56,56	1.30	9 (16%)

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	FQ8	B	401	-	-	31/56/56/56	-
3	UD1	Q	402	-	-	7/24/63/63	0/3/3/3
2	FQ8	G	401	-	-	31/56/56/56	-
2	FQ8	E	401	-	-	34/56/56/56	-
2	FQ8	C	401	-	-	34/56/56/56	-
2	FQ8	D	401	-	-	30/56/56/56	-
3	UD1	B	402	4	-	10/24/63/63	0/3/3/3
2	FQ8	Q	401	-	-	34/56/56/56	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FQ8	I	401	-	-	34/56/56/56	-
3	UD1	G	402	4	-	10/24/63/63	0/3/3/3
2	FQ8	P	401	-	-	34/56/56/56	-
2	FQ8	A	401	-	-	35/56/56/56	-
3	UD1	D	402	4	-	10/24/63/63	0/3/3/3
3	UD1	I	402	4	-	9/24/63/63	0/3/3/3
3	UD1	F	402	4	-	10/24/63/63	0/3/3/3
2	FQ8	F	401	-	-	28/56/56/56	-
3	UD1	O	402	4	-	9/24/63/63	0/3/3/3
3	UD1	E	402	4	-	6/24/63/63	0/3/3/3
3	UD1	H	402	4	-	7/24/63/63	0/3/3/3
3	UD1	C	402	4	-	10/24/63/63	0/3/3/3
3	UD1	A	402	4	-	8/24/63/63	0/3/3/3
2	FQ8	H	401	-	-	36/56/56/56	-
6	UDP	P	402	-	-	7/14/32/32	0/2/2/2
2	FQ8	O	401	-	-	21/56/56/56	-

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	FQ8	PBL-OAN	4.43	1.64	1.50
2	E	401	FQ8	PBL-OAN	4.27	1.64	1.50
2	G	401	FQ8	PBL-OAN	3.71	1.62	1.50
2	F	401	FQ8	PBM-OAP	3.67	1.63	1.50
2	A	401	FQ8	PBL-OAN	3.53	1.61	1.50
2	B	401	FQ8	PBL-OAN	3.51	1.61	1.50
2	Q	401	FQ8	PBL-OAN	3.49	1.61	1.50
2	H	401	FQ8	PBL-OAN	3.46	1.61	1.50
2	O	401	FQ8	PBL-OAN	3.44	1.61	1.50
2	E	401	FQ8	PBM-OAP	3.41	1.63	1.50
2	I	401	FQ8	PBM-OAP	3.39	1.62	1.50
2	C	401	FQ8	PBL-OAN	3.35	1.61	1.50
2	P	401	FQ8	PBL-OAN	3.34	1.61	1.50
2	I	401	FQ8	PBL-OAN	3.31	1.61	1.50
2	D	401	FQ8	PBL-OAN	3.30	1.61	1.50
2	P	401	FQ8	PBM-OAP	3.25	1.62	1.50
2	D	401	FQ8	PBM-OAP	3.15	1.62	1.50
2	H	401	FQ8	PBM-OAP	3.13	1.62	1.50
2	A	401	FQ8	PBM-OAP	3.13	1.62	1.50

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Q	401	FQ8	PBM-OAP	3.09	1.61	1.50
2	C	401	FQ8	PBM-OAP	3.07	1.61	1.50
2	O	401	FQ8	PBM-OAP	3.06	1.61	1.50
2	B	401	FQ8	PBM-OAP	3.02	1.61	1.50
2	P	401	FQ8	PBL-OAO	2.66	1.65	1.54
2	G	401	FQ8	PBM-OAP	2.57	1.60	1.50
2	G	401	FQ8	CAW-CBH	2.45	1.55	1.51
2	G	401	FQ8	PBL-OAO	2.32	1.63	1.54
2	F	401	FQ8	PBL-OAO	2.28	1.63	1.54
3	Q	402	UD1	C2-N3	-2.25	1.33	1.38
3	G	402	UD1	C2-N3	-2.23	1.33	1.38
3	I	402	UD1	C2-N3	-2.20	1.33	1.38
2	F	401	FQ8	CAT-CBD	2.17	1.54	1.51
2	F	401	FQ8	CBC-CBI	2.14	1.57	1.53
2	E	401	FQ8	PBL-OAO	2.13	1.63	1.54
2	P	401	FQ8	PBN-OAQ	2.11	1.65	1.55
6	P	402	UDP	C2-N3	-2.10	1.34	1.38
3	B	402	UD1	C2-N3	-2.08	1.34	1.38
3	O	402	UD1	C2-N3	-2.08	1.34	1.38
3	A	402	UD1	C2-N3	-2.02	1.34	1.38
3	E	402	UD1	C2-N3	-2.02	1.34	1.38

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	402	UD1	C8'-C7'-N2'	-4.28	108.84	116.10
3	H	402	UD1	C8'-C7'-N2'	-3.81	109.65	116.10
3	C	402	UD1	PB-O3A-PA	-3.79	119.83	132.83
6	P	402	UDP	PA-O3A-PB	-3.78	119.87	132.83
3	I	402	UD1	PB-O3A-PA	-3.54	120.69	132.83
3	D	402	UD1	C4'-C3'-C2'	-3.34	105.45	110.34
2	O	401	FQ8	OAZ-CAU-CBF	-3.32	100.49	109.36
3	H	402	UD1	C1'-C2'-N2'	-3.32	105.29	111.00
2	E	401	FQ8	OAD-CAR-CBC	-3.27	103.94	111.07
3	Q	402	UD1	PB-O3A-PA	-3.26	121.62	132.83
3	F	402	UD1	PB-O3A-PA	-3.23	121.75	132.83
3	F	402	UD1	C1'-C2'-N2'	-3.17	105.54	111.00
2	O	401	FQ8	OAD-CAR-CBC	-3.01	104.51	111.07
3	O	402	UD1	PB-O3A-PA	-3.00	122.53	132.83
3	B	402	UD1	PB-O3A-PA	-2.97	122.63	132.83
3	A	402	UD1	PB-O3A-PA	-2.96	122.68	132.83
3	G	402	UD1	PB-O3A-PA	-2.95	122.69	132.83

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	402	UD1	PB-O3A-PA	-2.89	122.89	132.83
6	P	402	UDP	C3'-C2'-C1'	2.87	105.31	100.98
3	O	402	UD1	C4'-C3'-C2'	-2.84	106.18	110.34
2	O	401	FQ8	OAX-PBL-OAN	2.82	114.39	106.47
2	I	401	FQ8	OAA-PBL-OAX	2.79	114.17	106.73
3	F	402	UD1	O5'-C1'-O1'	-2.79	107.72	111.36
3	D	402	UD1	PB-O3A-PA	-2.79	123.27	132.83
2	G	401	FQ8	OAD-CAR-CBC	-2.76	105.06	111.07
2	P	401	FQ8	OAA-PBL-OAX	2.72	113.97	106.73
2	C	401	FQ8	OAA-PBL-OAX	2.69	113.89	106.73
2	D	401	FQ8	OAA-PBL-OAX	2.69	113.89	106.73
2	B	401	FQ8	OAA-PBL-OAX	2.69	113.89	106.73
3	H	402	UD1	PB-O3A-PA	-2.68	123.64	132.83
3	B	402	UD1	C1'-C2'-N2'	-2.64	106.45	111.00
2	P	401	FQ8	CAV-CBG-CBK	-2.64	107.10	112.20
2	A	401	FQ8	OAA-PBL-OAX	2.64	113.75	106.73
3	H	402	UD1	O7'-C7'-N2'	2.63	126.79	121.95
3	Q	402	UD1	C1'-C2'-N2'	-2.61	106.52	111.00
2	Q	401	FQ8	OAA-PBL-OAX	2.60	113.66	106.73
2	G	401	FQ8	CBC-CBI-CBD	-2.57	108.01	113.36
2	H	401	FQ8	OAA-PBL-OAX	2.57	113.57	106.73
2	F	401	FQ8	OAE-CBC-CAR	-2.54	103.17	109.14
3	I	402	UD1	C3B-C2B-C1B	2.50	104.75	100.98
3	E	402	UD1	C1'-C2'-N2'	-2.47	106.76	111.00
2	G	401	FQ8	OAA-PBL-OAX	2.46	113.29	106.73
2	F	401	FQ8	CAU-CBF-CBJ	-2.46	107.45	112.20
3	E	402	UD1	C3'-C2'-N2'	2.44	115.22	110.62
2	O	401	FQ8	OAO-PBL-OAX	-2.42	100.28	106.73
2	O	401	FQ8	OBA-CAV-CBG	-2.42	102.90	109.36
2	I	401	FQ8	OAD-CAR-CBC	-2.41	105.81	111.07
3	E	402	UD1	C4'-C3'-C2'	-2.39	106.84	110.34
3	G	402	UD1	C3'-C2'-N2'	2.37	115.08	110.62
3	H	402	UD1	O5'-C1'-O1'	-2.35	108.30	111.36
3	G	402	UD1	C4'-C3'-C2'	-2.35	106.91	110.34
3	Q	402	UD1	O1'-C1'-C2'	2.31	112.57	108.40
3	F	402	UD1	O2B-PB-O1B	2.28	123.52	112.24
2	O	401	FQ8	OAA-PBL-OAX	2.27	112.77	106.73
2	O	401	FQ8	OAA-PBL-OAO	2.25	116.23	107.64
3	D	402	UD1	C3'-C2'-N2'	2.24	114.86	110.62
2	O	401	FQ8	CAW-CBH-CBK	-2.24	107.88	112.20
2	H	401	FQ8	CBC-CBI-CBD	-2.15	108.88	113.36
2	F	401	FQ8	OAH-CBF-CBJ	2.14	114.31	109.10

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	401	FQ8	OA0-PBL-OAN	-2.13	102.33	110.68
2	Q	401	FQ8	CBC-CBI-CBD	-2.08	109.03	113.36
2	I	401	FQ8	CAU-CBF-CBJ	-2.07	108.21	112.20
3	E	402	UD1	C8'-C7'-N2'	-2.03	112.67	116.10
3	Q	402	UD1	O2B-PB-O1B	2.02	122.24	112.24
2	Q	401	FQ8	CBF-CBJ-CBE	-2.01	109.18	113.36

There are no chirality outliers.

All (485) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	FQ8	CAU-OAZ-PBN-OAQ
2	B	401	FQ8	CAU-OAZ-PBN-OBB
2	B	401	FQ8	OBB-CAW-CBH-OAJ
2	B	401	FQ8	OBB-CAW-CBH-CBK
2	B	401	FQ8	OBA-CAV-CBG-CBK
2	B	401	FQ8	OBA-CAV-CBG-OAI
2	B	401	FQ8	CAT-CBD-CBI-OAK
2	B	401	FQ8	CAT-CBD-CBI-CBC
2	B	401	FQ8	OAE-CBC-CBI-CBD
2	B	401	FQ8	CAR-CBC-CBI-CBD
2	B	401	FQ8	OAE-CBC-CBI-OAK
2	B	401	FQ8	CAR-CBC-CBI-OAK
2	B	401	FQ8	OAD-CAR-CBC-CBI
2	B	401	FQ8	OAD-CAR-CBC-OAE
3	Q	402	UD1	C5B-O5B-PA-O1A
3	Q	402	UD1	C5B-O5B-PA-O2A
3	Q	402	UD1	C5B-O5B-PA-O3A
2	G	401	FQ8	OAZ-CAU-CBF-CBJ
2	G	401	FQ8	CAU-OAZ-PBN-OAQ
2	G	401	FQ8	CAU-OAZ-PBN-OAC
2	G	401	FQ8	CAU-OAZ-PBN-OBB
2	G	401	FQ8	CAW-OBB-PBN-OAZ
2	G	401	FQ8	OBA-CAV-CBG-CBK
2	G	401	FQ8	CAV-OBA-PBM-OAP
2	G	401	FQ8	CAV-OBA-PBM-OAB
2	G	401	FQ8	CAT-OAY-PBM-OBA
2	G	401	FQ8	CAT-OAY-PBM-OAP
2	G	401	FQ8	CAT-OAY-PBM-OAB
2	G	401	FQ8	CAT-CBD-CBI-OAK
2	G	401	FQ8	OAF-CBD-CBI-OAK
2	G	401	FQ8	OAF-CBD-CBI-CBC

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	E	401	FQ8	CAS-OAX-PBL-OAO
2	E	401	FQ8	OAZ-CAU-CBF-CBJ
2	E	401	FQ8	OAZ-CAU-CBF-OAH
2	E	401	FQ8	CAU-OAZ-PBN-OAQ
2	E	401	FQ8	CAU-OAZ-PBN-OAC
2	E	401	FQ8	CAU-OAZ-PBN-OBB
2	E	401	FQ8	OBA-CAV-CBG-OAI
2	E	401	FQ8	CAV-OBA-PBM-OAP
2	E	401	FQ8	CAV-OBA-PBM-OAY
2	E	401	FQ8	CAT-OAY-PBM-OAP
2	E	401	FQ8	CAT-OAY-PBM-OAB
2	E	401	FQ8	OAY-CAT-CBD-OAF
2	E	401	FQ8	OAY-CAT-CBD-CBI
2	C	401	FQ8	CAS-OAX-PBL-OAN
2	C	401	FQ8	CAS-OAX-PBL-OAO
2	C	401	FQ8	CAS-OAX-PBL-OAA
2	C	401	FQ8	CAU-OAZ-PBN-OAQ
2	C	401	FQ8	CAU-OAZ-PBN-OAC
2	C	401	FQ8	CAU-OAZ-PBN-OBB
2	C	401	FQ8	OBA-CAV-CBG-CBK
2	C	401	FQ8	CAV-OBA-PBM-OAP
2	C	401	FQ8	CAV-OBA-PBM-OAB
2	C	401	FQ8	CAT-OAY-PBM-OAB
2	C	401	FQ8	OAY-CAT-CBD-OAF
2	C	401	FQ8	OAY-CAT-CBD-CBI
2	D	401	FQ8	CAU-OAZ-PBN-OAC
2	D	401	FQ8	CAW-OBB-PBN-OAQ
2	D	401	FQ8	OBB-CAW-CBH-OAJ
2	D	401	FQ8	OBB-CAW-CBH-CBK
2	D	401	FQ8	CAW-CBH-CBK-OAM
2	D	401	FQ8	CAV-OBA-PBM-OAP
2	D	401	FQ8	CAV-OBA-PBM-OAY
2	D	401	FQ8	CAT-OAY-PBM-OBA
2	D	401	FQ8	CAT-OAY-PBM-OAB
3	B	402	UD1	C2B-C1B-N1-C6
3	B	402	UD1	O4B-C1B-N1-C6
3	B	402	UD1	C5B-O5B-PA-O2A
2	Q	401	FQ8	CAS-OAX-PBL-OAO
2	Q	401	FQ8	CAS-OAX-PBL-OAA
2	Q	401	FQ8	OAX-CAS-CBE-OAG
2	Q	401	FQ8	OAX-CAS-CBE-CBJ
2	Q	401	FQ8	OBB-CAW-CBH-OAJ

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	Q	401	FQ8	OBB-CAW-CBH-CBK
2	Q	401	FQ8	OAY-CAT-CBD-OAF
2	Q	401	FQ8	OAY-CAT-CBD-CBI
2	Q	401	FQ8	CAT-CBD-CBI-OAK
2	Q	401	FQ8	OAF-CBD-CBI-OAK
2	Q	401	FQ8	OAF-CBD-CBI-CBC
2	I	401	FQ8	CAS-OAX-PBL-OAN
2	I	401	FQ8	CAS-OAX-PBL-OAO
2	I	401	FQ8	CAS-OAX-PBL-OAA
2	I	401	FQ8	OAX-CAS-CBE-OAG
2	I	401	FQ8	OAX-CAS-CBE-CBJ
2	I	401	FQ8	OAZ-CAU-CBF-OAH
2	I	401	FQ8	OBB-CAW-CBH-OAJ
2	I	401	FQ8	OBB-CAW-CBH-CBK
2	I	401	FQ8	OBA-CAV-CBG-CBK
2	I	401	FQ8	OBA-CAV-CBG-OAI
2	I	401	FQ8	CAT-OAY-PBM-OAP
2	I	401	FQ8	CAT-OAY-PBM-OAB
2	I	401	FQ8	CAR-CBC-CBI-OAK
3	G	402	UD1	C2B-C1B-N1-C6
3	G	402	UD1	O4B-C1B-N1-C6
3	G	402	UD1	C5B-O5B-PA-O2A
2	P	401	FQ8	CAS-OAX-PBL-OAN
2	P	401	FQ8	CAU-OAZ-PBN-OAQ
2	P	401	FQ8	CAU-OAZ-PBN-OAC
2	P	401	FQ8	CAU-OAZ-PBN-OBB
2	P	401	FQ8	CAT-OAY-PBM-OAB
2	P	401	FQ8	CAT-CBD-CBI-OAK
2	P	401	FQ8	CAT-CBD-CBI-CBC
2	P	401	FQ8	OAF-CBD-CBI-OAK
2	P	401	FQ8	OAF-CBD-CBI-CBC
2	P	401	FQ8	OAD-CAR-CBC-OAE
2	A	401	FQ8	CAS-OAX-PBL-OAO
2	A	401	FQ8	CAS-OAX-PBL-OAA
2	A	401	FQ8	OAG-CBE-CBJ-OAL
2	A	401	FQ8	OAG-CBE-CBJ-CBF
2	A	401	FQ8	CAU-OAZ-PBN-OAQ
2	A	401	FQ8	CAU-OAZ-PBN-OBB
2	A	401	FQ8	CAW-OBB-PBN-OAC
2	A	401	FQ8	OBB-CAW-CBH-OAJ
2	A	401	FQ8	OBB-CAW-CBH-CBK
2	A	401	FQ8	CAV-OBA-PBM-OAP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	A	401	FQ8	CAT-OAY-PBM-OAP
2	A	401	FQ8	CAT-OAY-PBM-OAB
2	A	401	FQ8	OAD-CAR-CBC-OAE
3	D	402	UD1	C2B-C1B-N1-C6
3	D	402	UD1	O4B-C1B-N1-C6
3	D	402	UD1	C5B-O5B-PA-O1A
3	D	402	UD1	C5B-O5B-PA-O2A
3	I	402	UD1	C2B-C1B-N1-C6
3	I	402	UD1	O4B-C1B-N1-C6
3	I	402	UD1	C5B-O5B-PA-O2A
3	F	402	UD1	C2B-C1B-N1-C6
3	F	402	UD1	O4B-C1B-N1-C6
2	F	401	FQ8	CAS-OAX-PBL-OAA
2	F	401	FQ8	OBA-CAV-CBG-CBK
2	F	401	FQ8	OBA-CAV-CBG-OAI
2	F	401	FQ8	CAV-OBA-PBM-OAP
2	F	401	FQ8	CAV-OBA-PBM-OAB
2	F	401	FQ8	CAV-OBA-PBM-OAY
2	F	401	FQ8	CAT-OAY-PBM-OAB
2	F	401	FQ8	OAY-CAT-CBD-OAF
2	F	401	FQ8	OAY-CAT-CBD-CBI
2	F	401	FQ8	OAE-CBC-CBI-CBD
2	F	401	FQ8	OAE-CBC-CBI-OAK
2	F	401	FQ8	OAD-CAR-CBC-CBI
3	O	402	UD1	O4B-C1B-N1-C6
3	E	402	UD1	C2B-C1B-N1-C6
3	E	402	UD1	O4B-C1B-N1-C6
3	H	402	UD1	C2B-C1B-N1-C6
3	H	402	UD1	O4B-C1B-N1-C6
3	C	402	UD1	C2B-C1B-N1-C6
3	C	402	UD1	O4B-C1B-N1-C6
3	A	402	UD1	O5'-C1'-O1'-PB
3	A	402	UD1	C2B-C1B-N1-C6
3	A	402	UD1	O4B-C1B-N1-C6
2	H	401	FQ8	CAS-OAX-PBL-OAO
2	H	401	FQ8	CAS-OAX-PBL-OAA
2	H	401	FQ8	CAS-CBE-CBJ-CBF
2	H	401	FQ8	OAG-CBE-CBJ-CBF
2	H	401	FQ8	OAZ-CAU-CBF-CBJ
2	H	401	FQ8	OAZ-CAU-CBF-OAH
2	H	401	FQ8	CAW-OBB-PBN-OAZ
2	H	401	FQ8	CAW-OBB-PBN-OAC

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	H	401	FQ8	OBB-CAW-CBH-OAJ
2	H	401	FQ8	OBA-CAV-CBG-CBK
2	H	401	FQ8	CAV-OBA-PBM-OAP
2	H	401	FQ8	CAT-OAY-PBM-OAB
2	H	401	FQ8	OAY-CAT-CBD-OAF
2	H	401	FQ8	OAY-CAT-CBD-CBI
6	P	402	UDP	C5'-O5'-PA-O1A
6	P	402	UDP	C5'-O5'-PA-O2A
6	P	402	UDP	PB-O3A-PA-O5'
2	O	401	FQ8	OAZ-CAU-CBF-CBJ
2	O	401	FQ8	OAZ-CAU-CBF-OAH
2	O	401	FQ8	CAW-OBB-PBN-OAC
2	O	401	FQ8	OBB-CAW-CBH-OAJ
2	O	401	FQ8	OBB-CAW-CBH-CBK
2	O	401	FQ8	CAV-OBA-PBM-OAP
2	O	401	FQ8	CAT-OAY-PBM-OAP
2	O	401	FQ8	CAT-OAY-PBM-OAB
2	O	401	FQ8	OAY-CAT-CBD-OAF
2	O	401	FQ8	OAY-CAT-CBD-CBI
2	O	401	FQ8	CAT-CBD-CBI-CBC
2	F	401	FQ8	OAD-CAR-CBC-OAE
2	D	401	FQ8	OAD-CAR-CBC-CBI
2	P	401	FQ8	OAD-CAR-CBC-CBI
2	A	401	FQ8	OAD-CAR-CBC-CBI
2	B	401	FQ8	OAF-CBD-CBI-OAK
2	D	401	FQ8	OAJ-CBH-CBK-OAM
2	P	401	FQ8	OAH-CBF-CBJ-OAL
2	H	401	FQ8	OAG-CBE-CBJ-OAL
6	P	402	UDP	C3'-C4'-C5'-O5'
6	P	402	UDP	O4'-C4'-C5'-O5'
2	B	401	FQ8	OAG-CBE-CBJ-CBF
2	B	401	FQ8	OAF-CBD-CBI-CBC
2	E	401	FQ8	OAG-CBE-CBJ-CBF
2	E	401	FQ8	OAI-CBG-CBK-CBH
2	D	401	FQ8	OAG-CBE-CBJ-CBF
2	D	401	FQ8	OAJ-CBH-CBK-CBG
2	I	401	FQ8	OAG-CBE-CBJ-CBF
2	P	401	FQ8	OAH-CBF-CBJ-CBE
2	O	401	FQ8	OAF-CBD-CBI-CBC
2	B	401	FQ8	CAS-CBE-CBJ-OAL
2	E	401	FQ8	CAV-CBG-CBK-OAM
2	D	401	FQ8	CAS-CBE-CBJ-OAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	I	401	FQ8	CAS-CBE-CBJ-OAL
2	P	401	FQ8	CAU-CBF-CBJ-OAL
2	A	401	FQ8	CAS-CBE-CBJ-OAL
2	F	401	FQ8	CAR-CBC-CBI-OAK
2	H	401	FQ8	CAS-CBE-CBJ-OAL
2	O	401	FQ8	CAT-CBD-CBI-OAK
2	B	401	FQ8	CAS-CBE-CBJ-CBF
2	G	401	FQ8	CAT-CBD-CBI-CBC
2	E	401	FQ8	CAV-CBG-CBK-CBH
2	D	401	FQ8	CAS-CBE-CBJ-CBF
2	D	401	FQ8	CAW-CBH-CBK-CBG
2	Q	401	FQ8	CAT-CBD-CBI-CBC
2	I	401	FQ8	CAS-CBE-CBJ-CBF
2	I	401	FQ8	CAR-CBC-CBI-CBD
2	A	401	FQ8	CAS-CBE-CBJ-CBF
2	D	401	FQ8	OAD-CAR-CBC-OAE
3	H	402	UD1	C1'-O1'-PB-O3A
3	Q	402	UD1	C8'-C7'-N2'-C2'
3	F	402	UD1	C8'-C7'-N2'-C2'
2	G	401	FQ8	OAE-CBC-CBI-OAK
2	A	401	FQ8	OAF-CBD-CBI-OAK
2	I	401	FQ8	OAE-CBC-CBI-CBD
2	C	401	FQ8	CBD-CAT-OAY-PBM
2	G	401	FQ8	CAR-CBC-CBI-OAK
2	E	401	FQ8	CAU-CBF-CBJ-OAL
2	C	401	FQ8	CAT-CBD-CBI-OAK
2	Q	401	FQ8	CAV-CBG-CBK-OAM
2	P	401	FQ8	CAS-CBE-CBJ-OAL
2	P	401	FQ8	CAW-CBH-CBK-OAM
2	A	401	FQ8	CAT-CBD-CBI-OAK
2	H	401	FQ8	CAW-CBH-CBK-OAM
2	E	401	FQ8	CAS-CBE-CBJ-CBF
2	Q	401	FQ8	CAV-CBG-CBK-CBH
2	P	401	FQ8	CAU-CBF-CBJ-CBE
2	P	401	FQ8	CAW-CBH-CBK-CBG
2	A	401	FQ8	CAT-CBD-CBI-CBC
2	F	401	FQ8	CAT-CBD-CBI-CBC
2	F	401	FQ8	CAR-CBC-CBI-CBD
2	B	401	FQ8	CAV-OBA-PBM-OAY
2	G	401	FQ8	CAV-OBA-PBM-OAY
2	E	401	FQ8	CAT-OAY-PBM-OBA
2	C	401	FQ8	CAW-OBB-PBN-OAZ

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	C	401	FQ8	CAV-OBA-PBM-OAY
2	C	401	FQ8	CAT-OAY-PBM-OBA
2	D	401	FQ8	CAU-OAZ-PBN-OBB
2	Q	401	FQ8	CAV-OBA-PBM-OAY
2	I	401	FQ8	CAV-OBA-PBM-OAY
2	I	401	FQ8	CAT-OAY-PBM-OBA
2	A	401	FQ8	CAT-OAY-PBM-OBA
2	F	401	FQ8	CAU-OAZ-PBN-OBB
2	F	401	FQ8	CAT-OAY-PBM-OBA
2	H	401	FQ8	CAT-OAY-PBM-OBA
2	O	401	FQ8	CAW-OBB-PBN-OAZ
2	O	401	FQ8	CAT-OAY-PBM-OBA
3	B	402	UD1	C1'-O1'-PB-O3A
3	D	402	UD1	C1'-O1'-PB-O3A
3	A	402	UD1	C1'-O1'-PB-O3A
2	B	401	FQ8	OAG-CBE-CBJ-OAL
2	E	401	FQ8	OAG-CBE-CBJ-OAL
2	E	401	FQ8	OAH-CBF-CBJ-OAL
2	E	401	FQ8	OAI-CBG-CBK-OAM
2	D	401	FQ8	OAG-CBE-CBJ-OAL
2	Q	401	FQ8	OAI-CBG-CBK-OAM
2	I	401	FQ8	OAG-CBE-CBJ-OAL
2	I	401	FQ8	OAE-CBC-CBI-OAK
2	P	401	FQ8	OAG-CBE-CBJ-OAL
2	P	401	FQ8	OAJ-CBH-CBK-OAM
2	O	401	FQ8	OAF-CBD-CBI-OAK
2	G	401	FQ8	OAD-CAR-CBC-CBI
3	H	402	UD1	C8'-C7'-N2'-C2'
2	E	401	FQ8	OAH-CBF-CBJ-CBE
2	C	401	FQ8	OAF-CBD-CBI-CBC
2	Q	401	FQ8	OAI-CBG-CBK-CBH
2	P	401	FQ8	OAG-CBE-CBJ-CBF
2	P	401	FQ8	OAJ-CBH-CBK-CBG
2	A	401	FQ8	OAF-CBD-CBI-CBC
2	F	401	FQ8	OAF-CBD-CBI-CBC
2	I	401	FQ8	CBD-CAT-OAY-PBM
2	G	401	FQ8	OAZ-CAU-CBF-OAH
2	C	401	FQ8	OBB-CAW-CBH-OAJ
2	A	401	FQ8	OAY-CAT-CBD-OAF
2	H	401	FQ8	OBA-CAV-CBG-OAI
2	O	401	FQ8	OBA-CAV-CBG-OAI
2	G	401	FQ8	CAR-CBC-CBI-CBD

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	E	401	FQ8	CAU-CBF-CBJ-CBE
2	C	401	FQ8	CAR-CBC-CBI-CBD
2	Q	401	FQ8	OAD-CAR-CBC-OAE
2	C	401	FQ8	OAF-CBD-CBI-OAK
2	D	401	FQ8	OAF-CBD-CBI-OAK
2	C	401	FQ8	OAE-CBC-CBI-CBD
3	G	402	UD1	C1'-O1'-PB-O3A
2	G	401	FQ8	OAD-CAR-CBC-OAE
2	G	401	FQ8	OAG-CBE-CBJ-OAL
2	C	401	FQ8	OAG-CBE-CBJ-OAL
2	P	401	FQ8	OAI-CBG-CBK-OAM
2	E	401	FQ8	CAS-CBE-CBJ-OAL
2	D	401	FQ8	CAT-CBD-CBI-OAK
2	I	401	FQ8	CAU-CBF-CBJ-OAL
2	I	401	FQ8	CAT-CBD-CBI-OAK
3	E	402	UD1	O4B-C4B-C5B-O5B
3	C	402	UD1	O4B-C4B-C5B-O5B
2	G	401	FQ8	OAE-CBC-CBI-CBD
2	C	401	FQ8	OAG-CBE-CBJ-CBF
2	D	401	FQ8	OAF-CBD-CBI-CBC
2	H	401	FQ8	OAJ-CBH-CBK-CBG
2	P	401	FQ8	CAW-OBB-PBN-OAZ
2	P	401	FQ8	CAT-OAY-PBM-OBA
2	H	401	FQ8	CAV-OBA-PBM-OAY
2	O	401	FQ8	CBD-CAT-OAY-PBM
2	C	401	FQ8	OBB-CAW-CBH-CBK
2	P	401	FQ8	OAY-CAT-CBD-CBI
2	A	401	FQ8	OAY-CAT-CBD-CBI
2	H	401	FQ8	OBB-CAW-CBH-CBK
2	O	401	FQ8	OBA-CAV-CBG-CBK
3	O	402	UD1	C4'-C5'-C6'-O6'
2	C	401	FQ8	OAE-CBC-CBI-OAK
2	A	401	FQ8	OAH-CBF-CBJ-OAL
3	E	402	UD1	C3B-C4B-C5B-O5B
2	Q	401	FQ8	CAU-CBF-CBJ-OAL
2	H	401	FQ8	OAE-CBC-CBI-CBD
2	G	401	FQ8	CBD-CAT-OAY-PBM
2	E	401	FQ8	CAS-OAX-PBL-OAN
2	Q	401	FQ8	CAS-OAX-PBL-OAN
2	G	401	FQ8	CAS-CBE-CBJ-CBF
2	C	401	FQ8	CAS-CBE-CBJ-CBF
2	D	401	FQ8	CAT-CBD-CBI-CBC

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	P	401	FQ8	CAS-CBE-CBJ-CBF
3	A	402	UD1	C4'-C5'-C6'-O6'
3	D	402	UD1	C1'-O1'-PB-O2B
3	H	402	UD1	C1'-O1'-PB-O2B
2	G	401	FQ8	OAG-CBE-CBJ-CBF
2	Q	401	FQ8	OAG-CBE-CBJ-CBF
2	Q	401	FQ8	CBD-CAT-OAY-PBM
2	P	401	FQ8	CBE-CAS-OAX-PBL
2	C	401	FQ8	OBA-CAV-CBG-OAI
2	G	401	FQ8	CAS-CBE-CBJ-OAL
2	C	401	FQ8	CAS-CBE-CBJ-OAL
2	C	401	FQ8	CAR-CBC-CBI-OAK
2	P	401	FQ8	CAV-CBG-CBK-OAM
2	A	401	FQ8	CAU-CBF-CBJ-OAL
2	F	401	FQ8	CAT-CBD-CBI-OAK
2	H	401	FQ8	CAR-CBC-CBI-OAK
2	C	401	FQ8	CAT-CBD-CBI-CBC
2	Q	401	FQ8	CAS-CBE-CBJ-CBF
2	Q	401	FQ8	CAU-CBF-CBJ-CBE
2	I	401	FQ8	CAU-CBF-CBJ-CBE
2	P	401	FQ8	CAV-CBG-CBK-CBH
2	A	401	FQ8	CAU-CBF-CBJ-CBE
2	H	401	FQ8	CAW-CBH-CBK-CBG
2	H	401	FQ8	CAR-CBC-CBI-CBD
2	P	401	FQ8	CAV-OBA-PBM-OAY
2	Q	401	FQ8	OAG-CBE-CBJ-OAL
2	F	401	FQ8	OAF-CBD-CBI-OAK
2	H	401	FQ8	OAE-CBC-CBI-OAK
3	C	402	UD1	C3B-C4B-C5B-O5B
2	E	401	FQ8	OAF-CBD-CBI-CBC
2	A	401	FQ8	OAH-CBF-CBJ-CBE
2	E	401	FQ8	CBD-CAT-OAY-PBM
2	A	401	FQ8	CBD-CAT-OAY-PBM
3	I	402	UD1	C4B-C5B-O5B-PA
2	Q	401	FQ8	CAS-CBE-CBJ-OAL
2	Q	401	FQ8	OAH-CBF-CBJ-OAL
2	H	401	FQ8	OAJ-CBH-CBK-OAM
2	D	401	FQ8	CAV-CBG-CBK-CBH
2	E	401	FQ8	CAS-OAX-PBL-OAA
3	A	402	UD1	O5'-C5'-C6'-O6'
3	O	402	UD1	O5'-C5'-C6'-O6'
2	E	401	FQ8	CBF-CAU-OAZ-PBN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	B	402	UD1	C5B-O5B-PA-O3A
3	G	402	UD1	C5B-O5B-PA-O3A
3	D	402	UD1	C5B-O5B-PA-O3A
3	I	402	UD1	C5B-O5B-PA-O3A
3	F	402	UD1	C5B-O5B-PA-O3A
3	O	402	UD1	C5B-O5B-PA-O3A
3	B	402	UD1	PB-O3A-PA-O2A
3	G	402	UD1	PB-O3A-PA-O2A
3	F	402	UD1	PB-O3A-PA-O2A
3	O	402	UD1	PB-O3A-PA-O2A
3	C	402	UD1	PB-O3A-PA-O2A
2	I	401	FQ8	CAT-CBD-CBI-CBC
2	D	401	FQ8	CAW-OBB-PBN-OAZ
2	Q	401	FQ8	CAW-OBB-PBN-OAZ
2	O	401	FQ8	CAV-OBA-PBM-OAY
2	B	401	FQ8	CAU-OAZ-PBN-OAC
2	B	401	FQ8	CAV-OBA-PBM-OAB
2	G	401	FQ8	CAW-OBB-PBN-OAQ
2	C	401	FQ8	CAW-OBB-PBN-OAC
2	D	401	FQ8	CAU-OAZ-PBN-OAQ
2	D	401	FQ8	CAW-OBB-PBN-OAC
2	D	401	FQ8	CAT-OAY-PBM-OAP
3	B	402	UD1	C5B-O5B-PA-O1A
2	I	401	FQ8	CAV-OBA-PBM-OAB
3	G	402	UD1	C5B-O5B-PA-O1A
2	P	401	FQ8	CAT-OAY-PBM-OAP
2	A	401	FQ8	CAU-OAZ-PBN-OAC
3	I	402	UD1	C5B-O5B-PA-O1A
2	F	401	FQ8	CAU-OAZ-PBN-OAC
2	F	401	FQ8	CAT-OAY-PBM-OAP
3	O	402	UD1	C5B-O5B-PA-O2A
2	H	401	FQ8	CAV-OBA-PBM-OAB
2	O	401	FQ8	CAW-OBB-PBN-OAQ
2	I	401	FQ8	OAF-CBD-CBI-OAK
2	G	401	FQ8	OBB-CAW-CBH-OAJ
3	I	402	UD1	C4'-C5'-C6'-O6'
2	Q	401	FQ8	OAH-CBF-CBJ-CBE
2	P	401	FQ8	OAI-CBG-CBK-CBH
2	F	401	FQ8	OAJ-CBH-CBK-CBG
2	H	401	FQ8	OAF-CBD-CBI-CBC
2	A	401	FQ8	CAV-CBG-CBK-CBH
3	G	402	UD1	C4B-C5B-O5B-PA

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	F	402	UD1	C1'-O1'-PB-O3A
3	E	402	UD1	C1'-O1'-PB-O3A
2	B	401	FQ8	CAS-OAX-PBL-OAN
3	D	402	UD1	C4B-C5B-O5B-PA
3	F	402	UD1	O7'-C7'-N2'-C2'
2	Q	401	FQ8	CAU-OAZ-PBN-OBB
2	I	401	FQ8	CAU-OAZ-PBN-OBB
2	A	401	FQ8	CAW-OBB-PBN-OAZ
2	A	401	FQ8	CAV-OBA-PBM-OAY
3	O	402	UD1	O5'-C1'-O1'-PB
3	C	402	UD1	O5'-C1'-O1'-PB
3	G	402	UD1	PB-O3A-PA-O1A
3	D	402	UD1	PB-O3A-PA-O1A
3	A	402	UD1	PB-O3A-PA-O2A
2	I	401	FQ8	OAF-CBD-CBI-CBC
2	Q	401	FQ8	OAD-CAR-CBC-CBI
2	P	401	FQ8	CBD-CAT-OAY-PBM
2	H	401	FQ8	CBD-CAT-OAY-PBM
2	D	401	FQ8	OAI-CBG-CBK-OAM
2	F	401	FQ8	CAW-CBH-CBK-CBG
3	G	402	UD1	C1'-O1'-PB-O2B
3	F	402	UD1	C1'-O1'-PB-O2B
3	E	402	UD1	C1'-O1'-PB-O2B
2	B	401	FQ8	CBD-CAT-OAY-PBM
3	B	402	UD1	C4B-C5B-O5B-PA
2	A	401	FQ8	OAI-CBG-CBK-OAM
2	H	401	FQ8	OAF-CBD-CBI-OAK
2	F	401	FQ8	CAW-CBH-CBK-OAM
2	E	401	FQ8	CAT-CBD-CBI-CBC
2	B	401	FQ8	CBE-CAS-OAX-PBL
2	D	401	FQ8	CAV-CBG-CBK-OAM
3	Q	402	UD1	PB-O3A-PA-O1A
3	D	402	UD1	PB-O3A-PA-O2A
3	H	402	UD1	PB-O3A-PA-O2A
3	Q	402	UD1	O7'-C7'-N2'-C2'
2	E	401	FQ8	CAT-CBD-CBI-OAK
2	H	401	FQ8	OAD-CAR-CBC-OAE
2	E	401	FQ8	OAF-CBD-CBI-OAK
2	I	401	FQ8	OAH-CBF-CBJ-OAL
2	F	401	FQ8	CBD-CAT-OAY-PBM
3	I	402	UD1	O4B-C4B-C5B-O5B
2	B	401	FQ8	CAS-OAX-PBL-OAA

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	G	401	FQ8	OAY-CAT-CBD-OAF
2	B	401	FQ8	CAW-CBH-CBK-OAM
2	C	401	FQ8	CAW-CBH-CBK-OAM
2	A	401	FQ8	CAV-CBG-CBK-OAM
2	A	401	FQ8	CAS-OAX-PBL-OAN
2	H	401	FQ8	CAS-OAX-PBL-OAN
3	A	402	UD1	O4B-C4B-C5B-O5B
6	P	402	UDP	PA-O3A-PB-O2B
3	C	402	UD1	C5B-O5B-PA-O3A
6	P	402	UDP	C5'-O5'-PA-O3A
2	I	401	FQ8	OAH-CBF-CBJ-CBE
3	Q	402	UD1	O4B-C4B-C5B-O5B
3	B	402	UD1	PB-O3A-PA-O1A
2	B	401	FQ8	CAW-CBH-CBK-CBG
2	F	401	FQ8	OAJ-CBH-CBK-OAM
2	B	401	FQ8	OAJ-CBH-CBK-CBG
3	H	402	UD1	O7'-C7'-N2'-C2'
2	B	401	FQ8	CAW-OBB-PBN-OAC
2	C	401	FQ8	OAZ-CAU-CBF-CBJ
2	Q	401	FQ8	CAU-OAZ-PBN-OAC
2	Q	401	FQ8	CAW-OBB-PBN-OAQ
2	Q	401	FQ8	OBA-CAV-CBG-CBK
2	I	401	FQ8	OAZ-CAU-CBF-CBJ
3	F	402	UD1	C5B-O5B-PA-O1A
3	F	402	UD1	C5B-O5B-PA-O2A
3	O	402	UD1	C5B-O5B-PA-O1A
3	C	402	UD1	C5B-O5B-PA-O1A
3	C	402	UD1	C5B-O5B-PA-O2A
3	I	402	UD1	O5'-C5'-C6'-O6'
3	B	402	UD1	C1'-O1'-PB-O2B
2	H	401	FQ8	OAI-CBG-CBK-OAM
3	O	402	UD1	C4B-C5B-O5B-PA
3	C	402	UD1	C4B-C5B-O5B-PA
2	H	401	FQ8	CAT-CBD-CBI-OAK

There are no ring outliers.

18 monomers are involved in 23 short contacts:

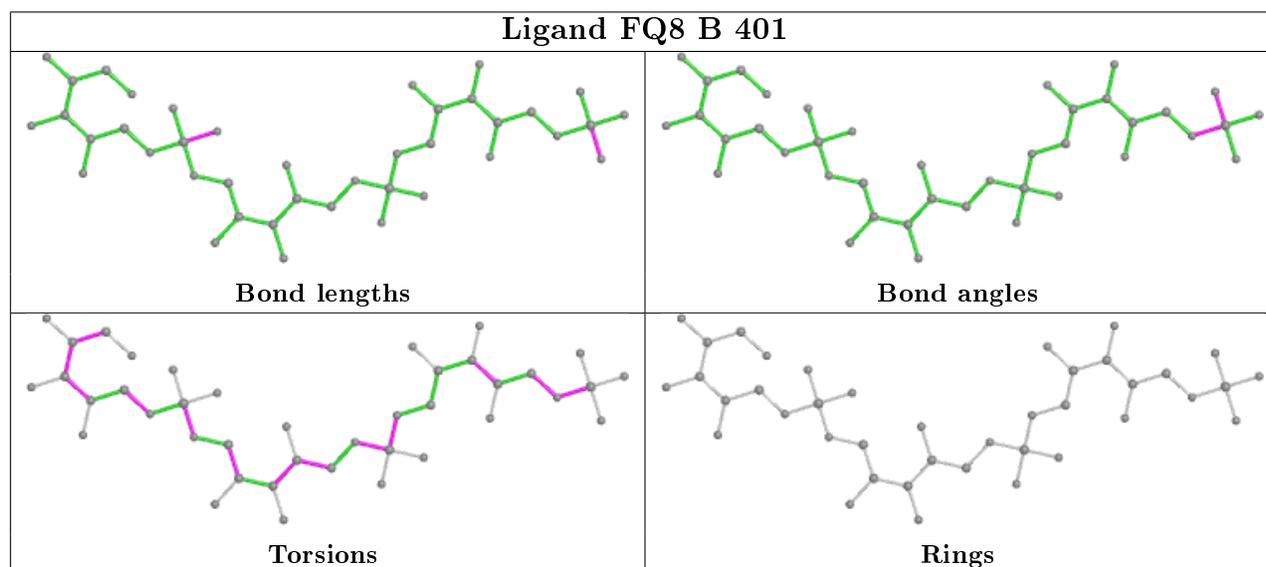
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	FQ8	1	0
2	G	401	FQ8	1	0
2	C	401	FQ8	2	0

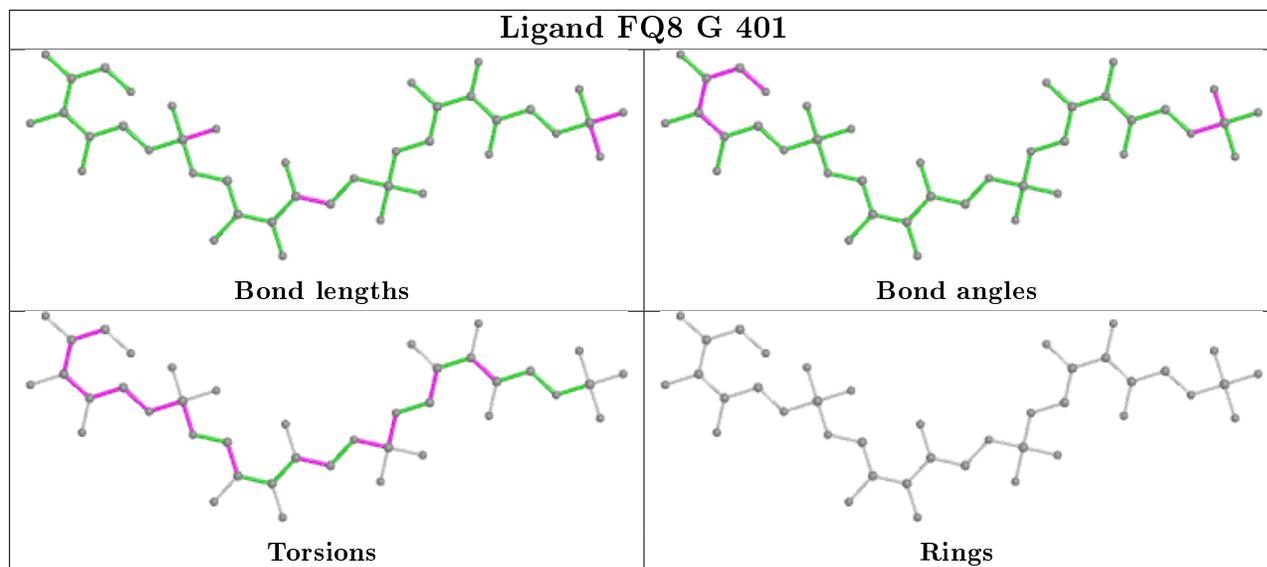
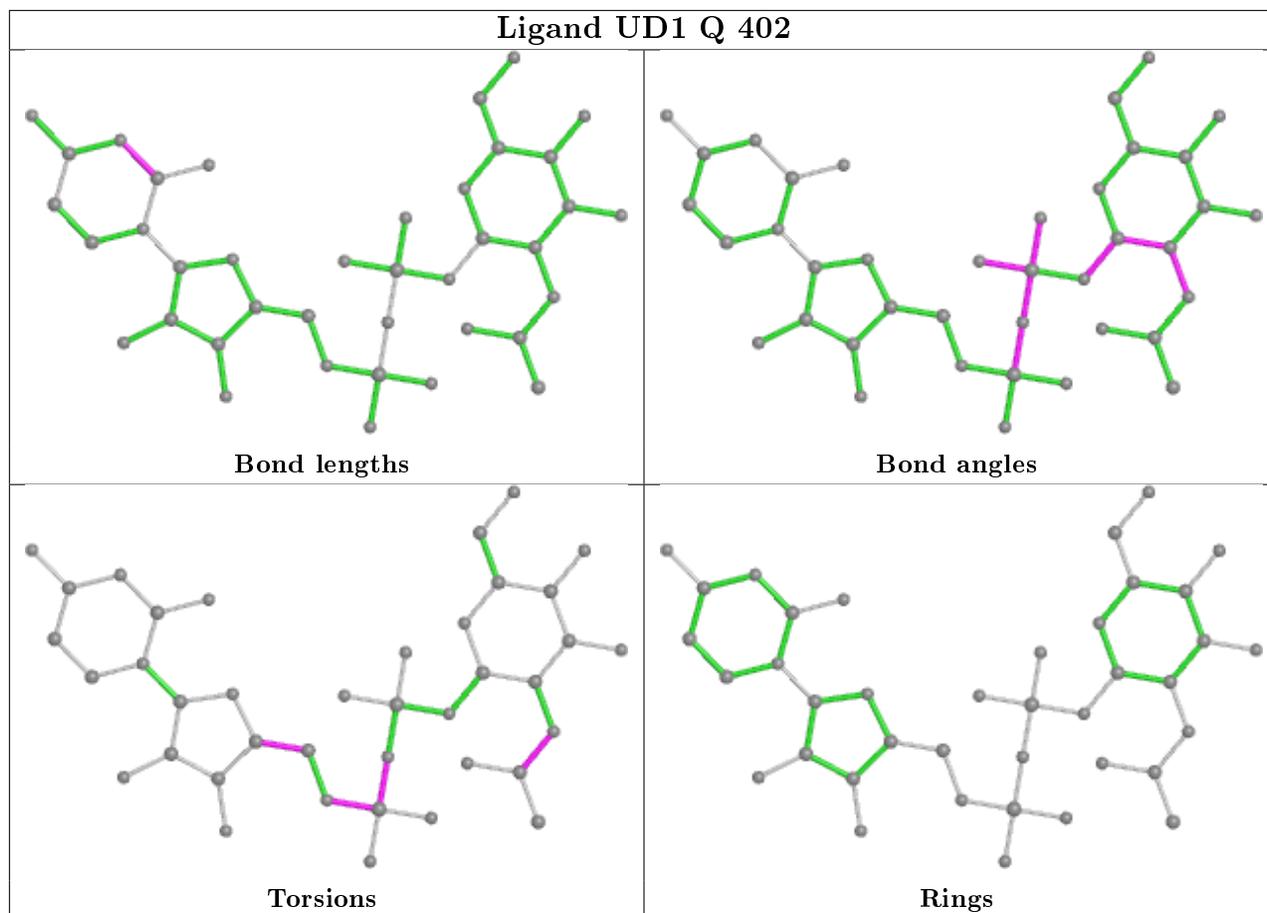
*Continued on next page...*

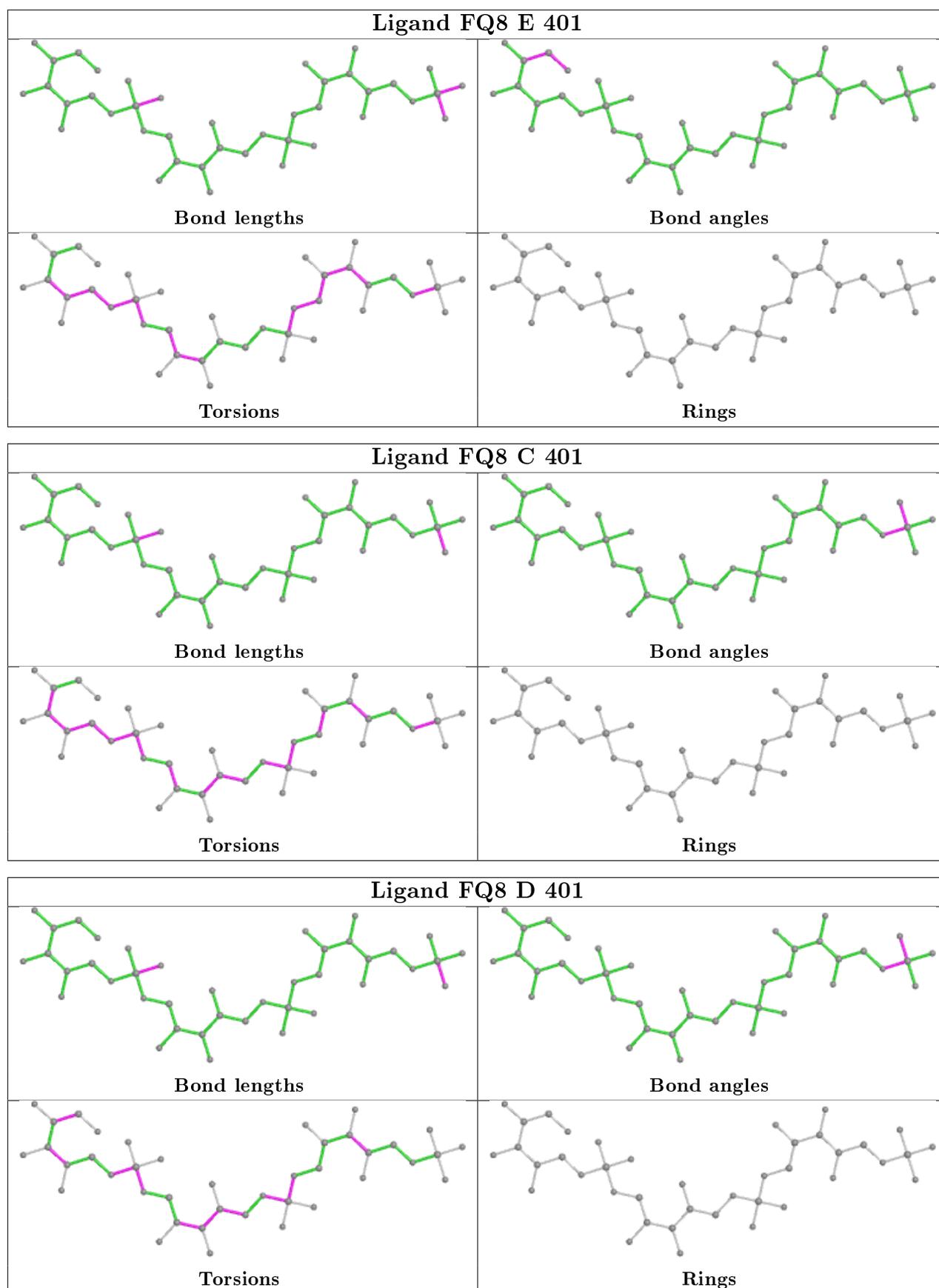
Continued from previous page...

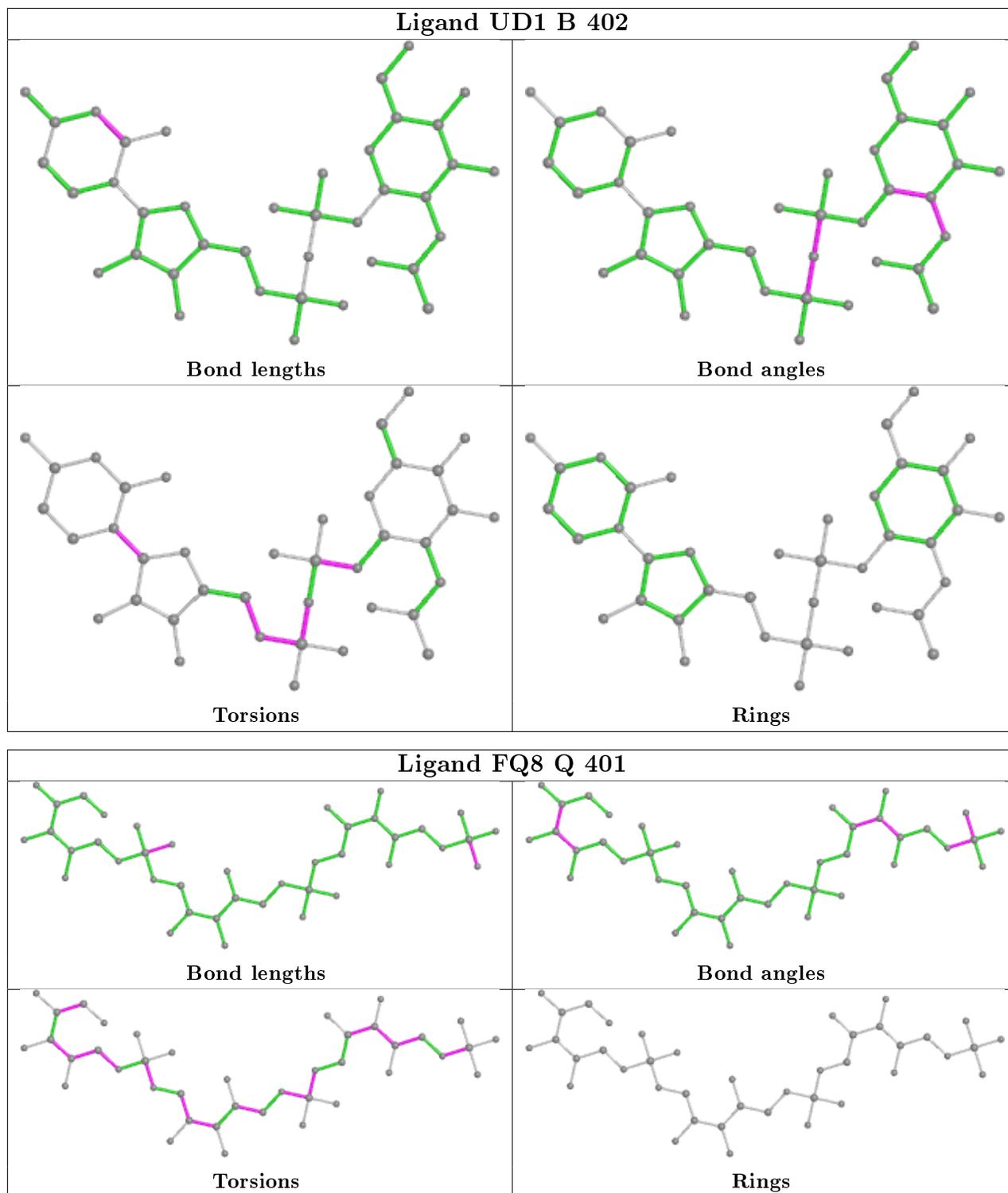
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	402	UD1	1	0
2	Q	401	FQ8	1	0
2	I	401	FQ8	3	0
2	P	401	FQ8	3	0
2	A	401	FQ8	1	0
3	I	402	UD1	1	0
3	F	402	UD1	1	0
2	F	401	FQ8	1	0
3	O	402	UD1	1	0
3	E	402	UD1	1	0
3	H	402	UD1	1	0
3	C	402	UD1	1	0
3	A	402	UD1	1	0
6	P	402	UDP	1	0
2	O	401	FQ8	1	0

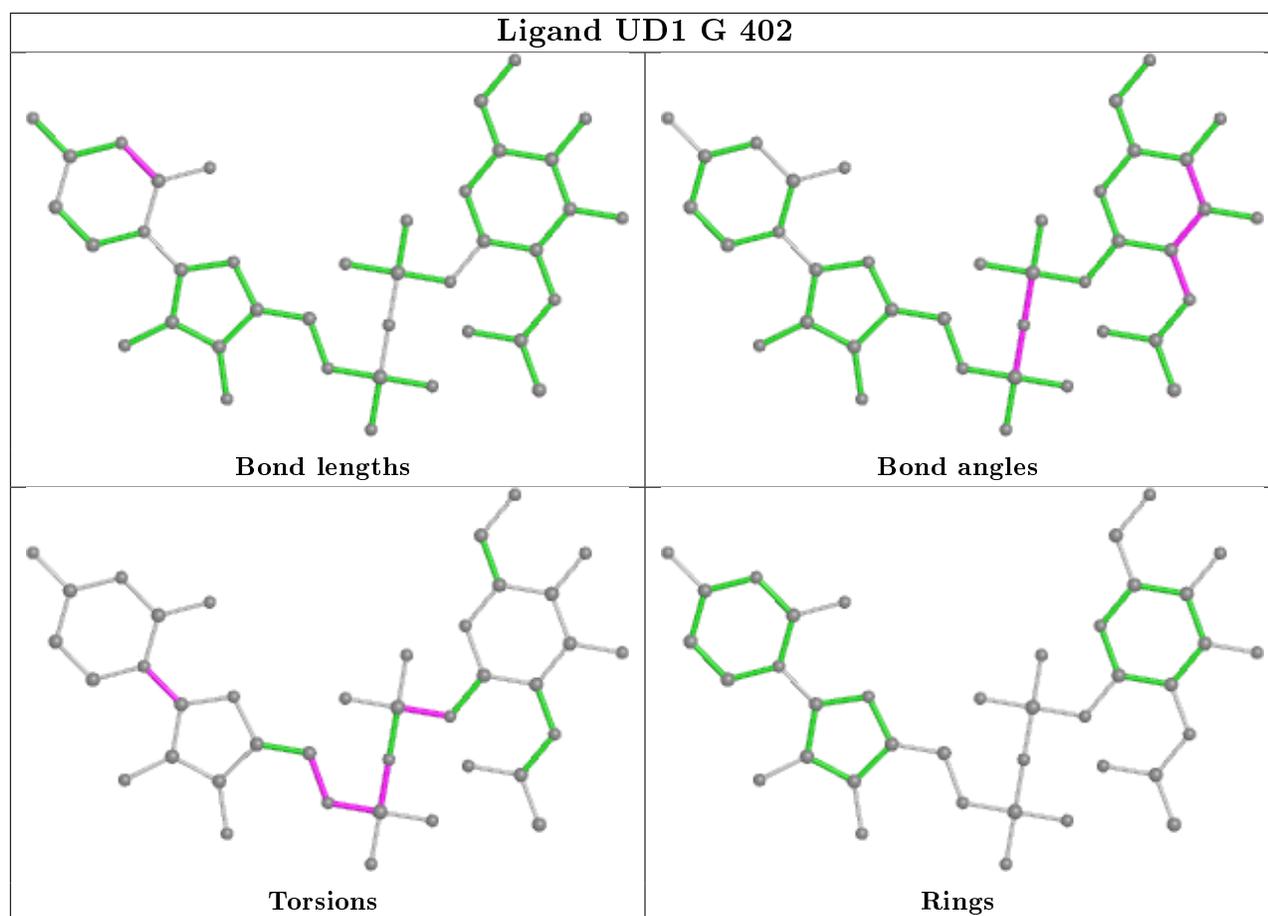
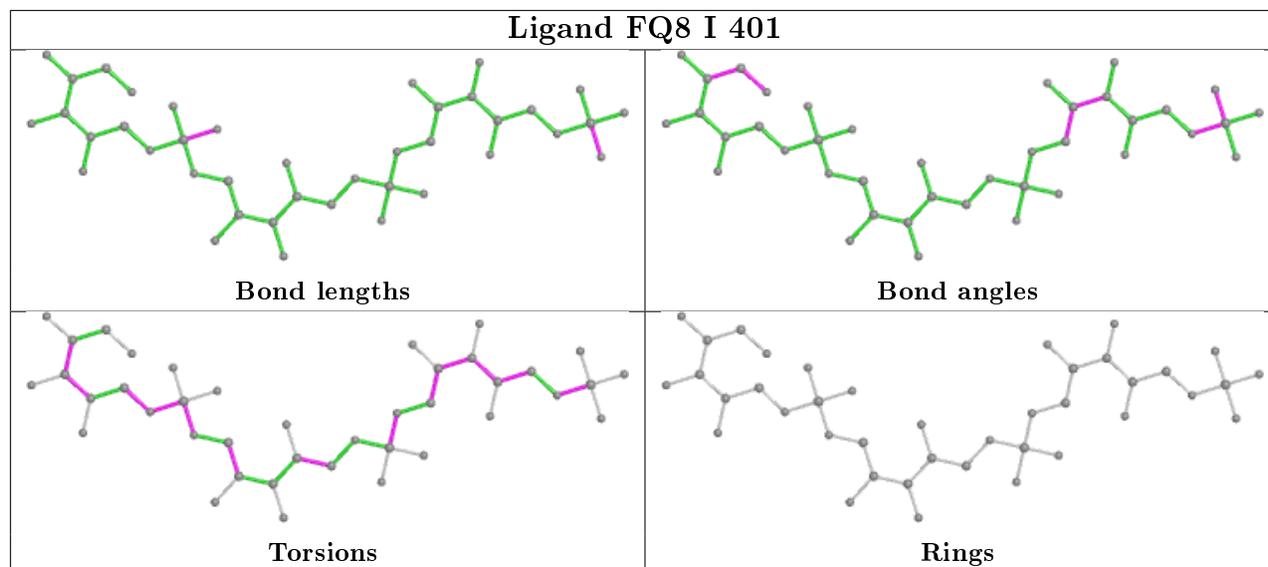
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

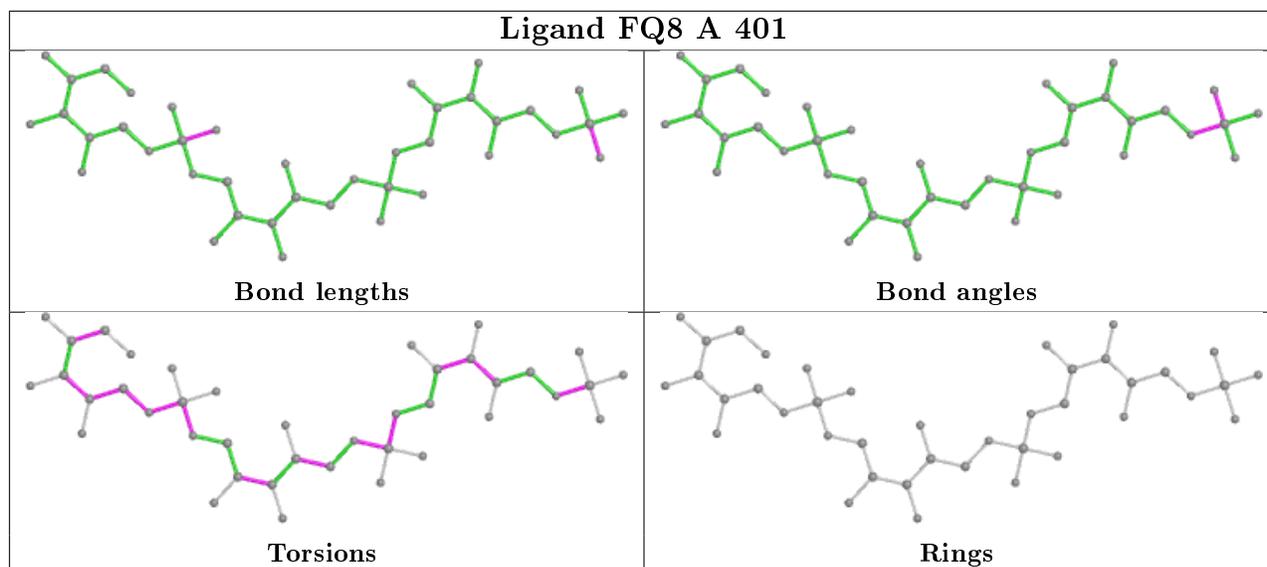
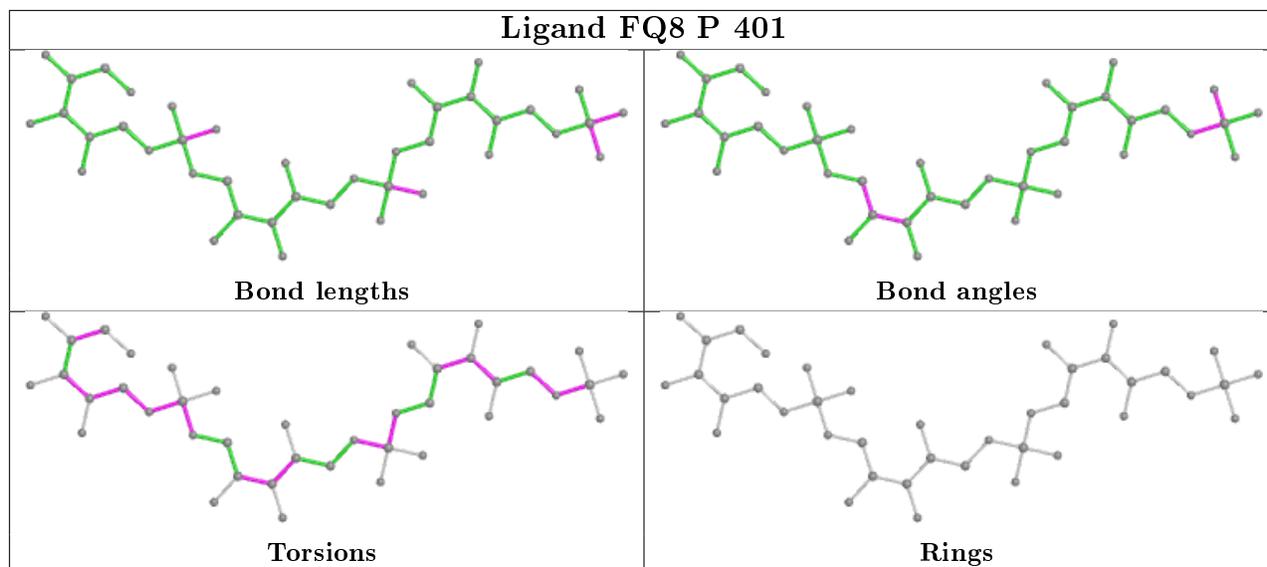


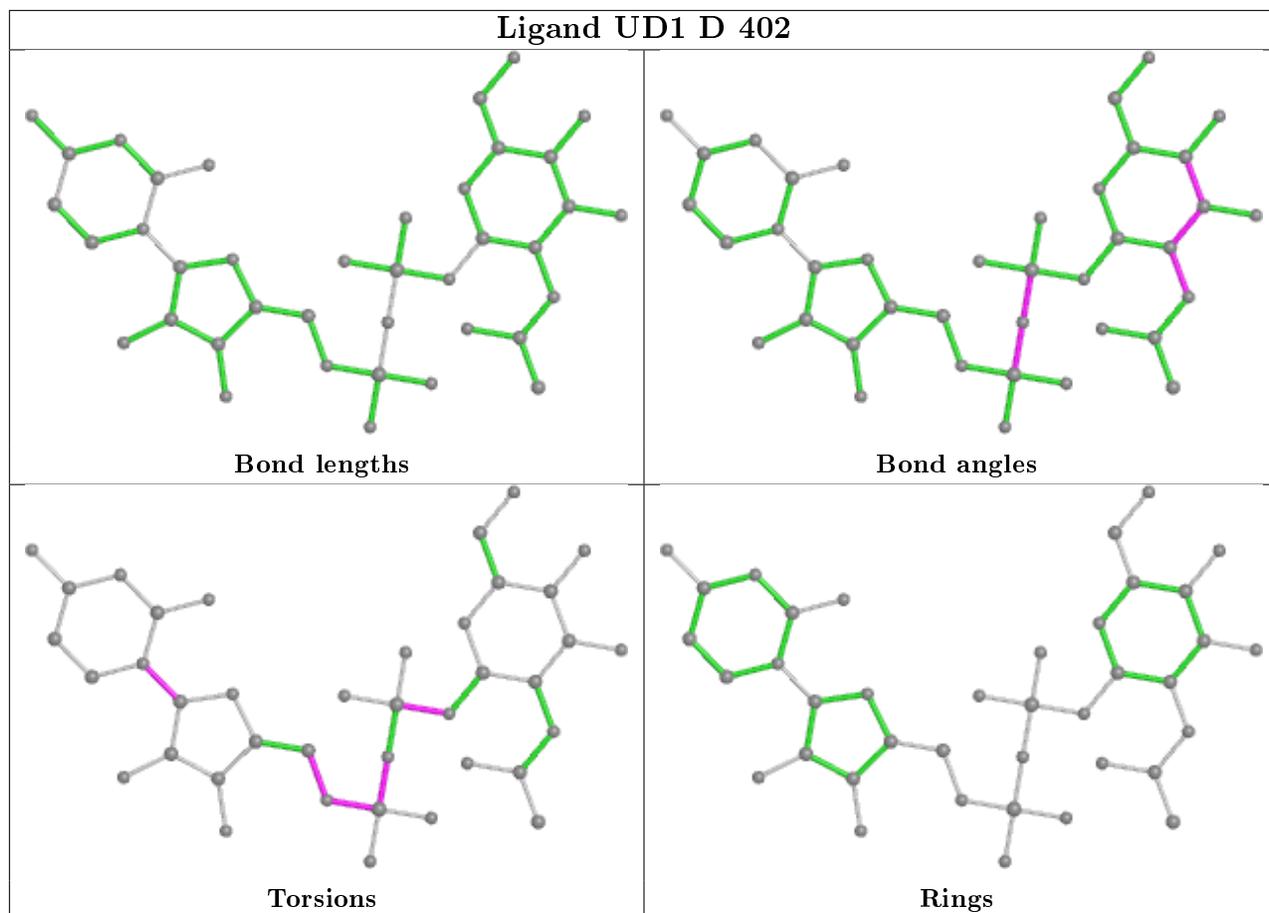


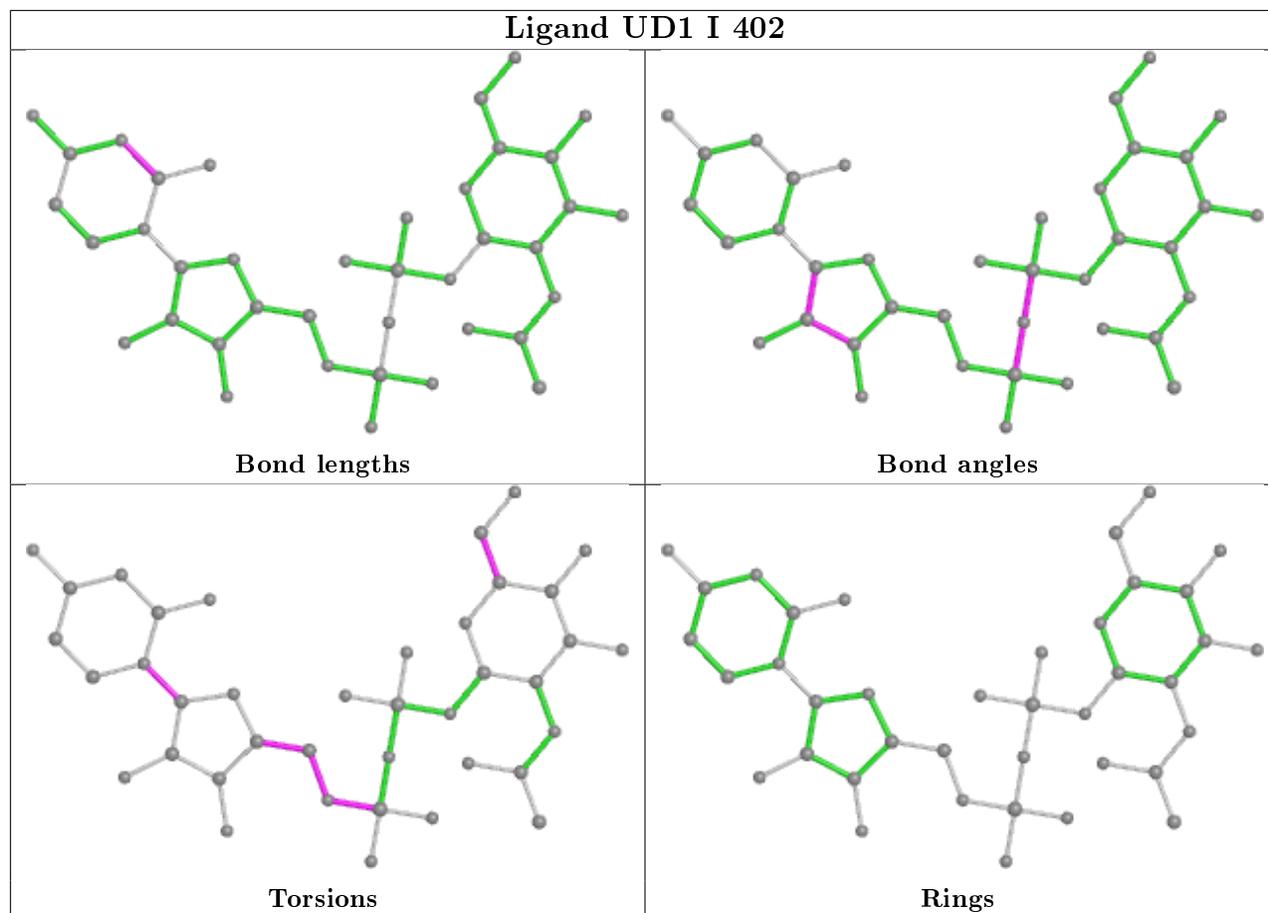


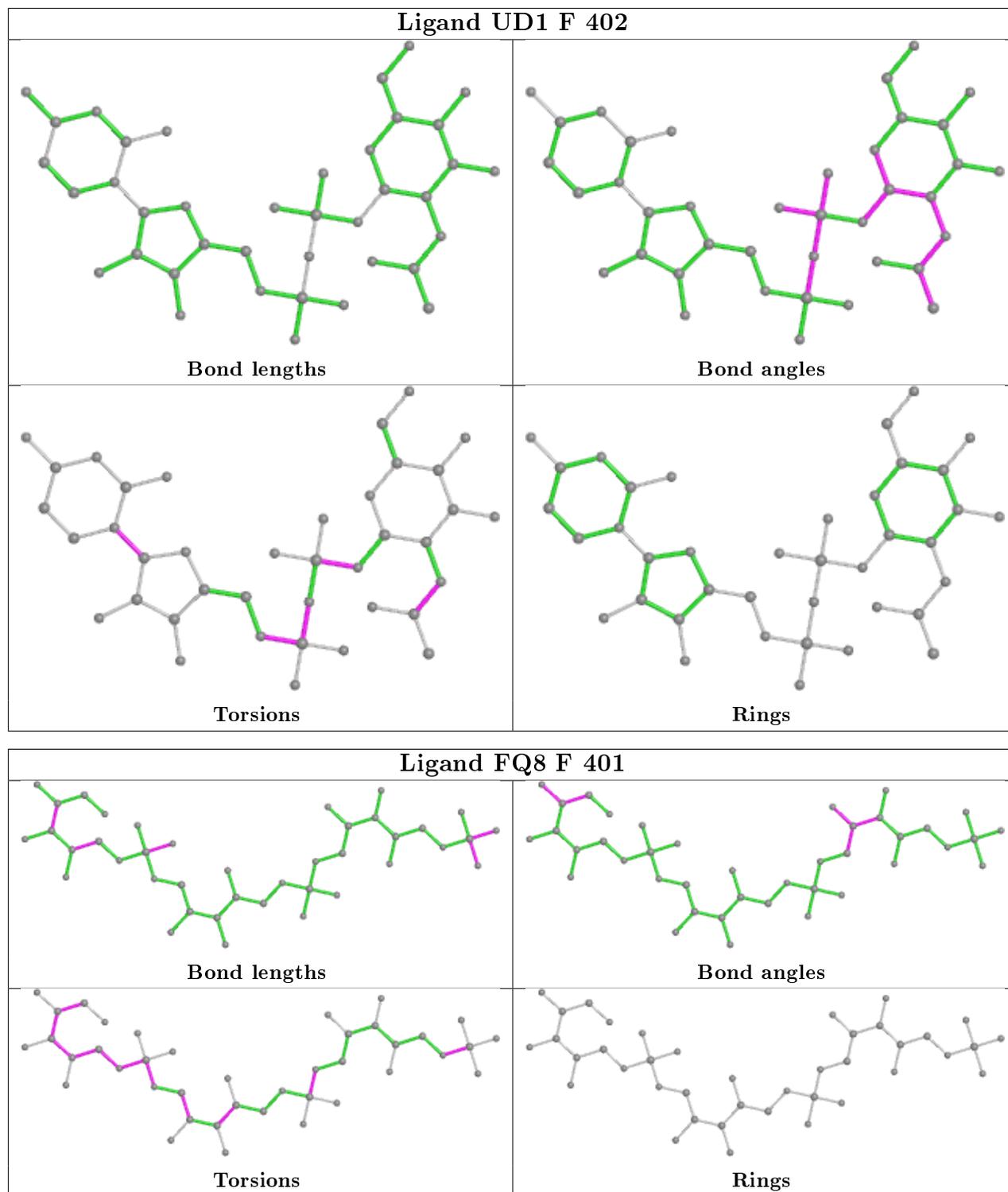


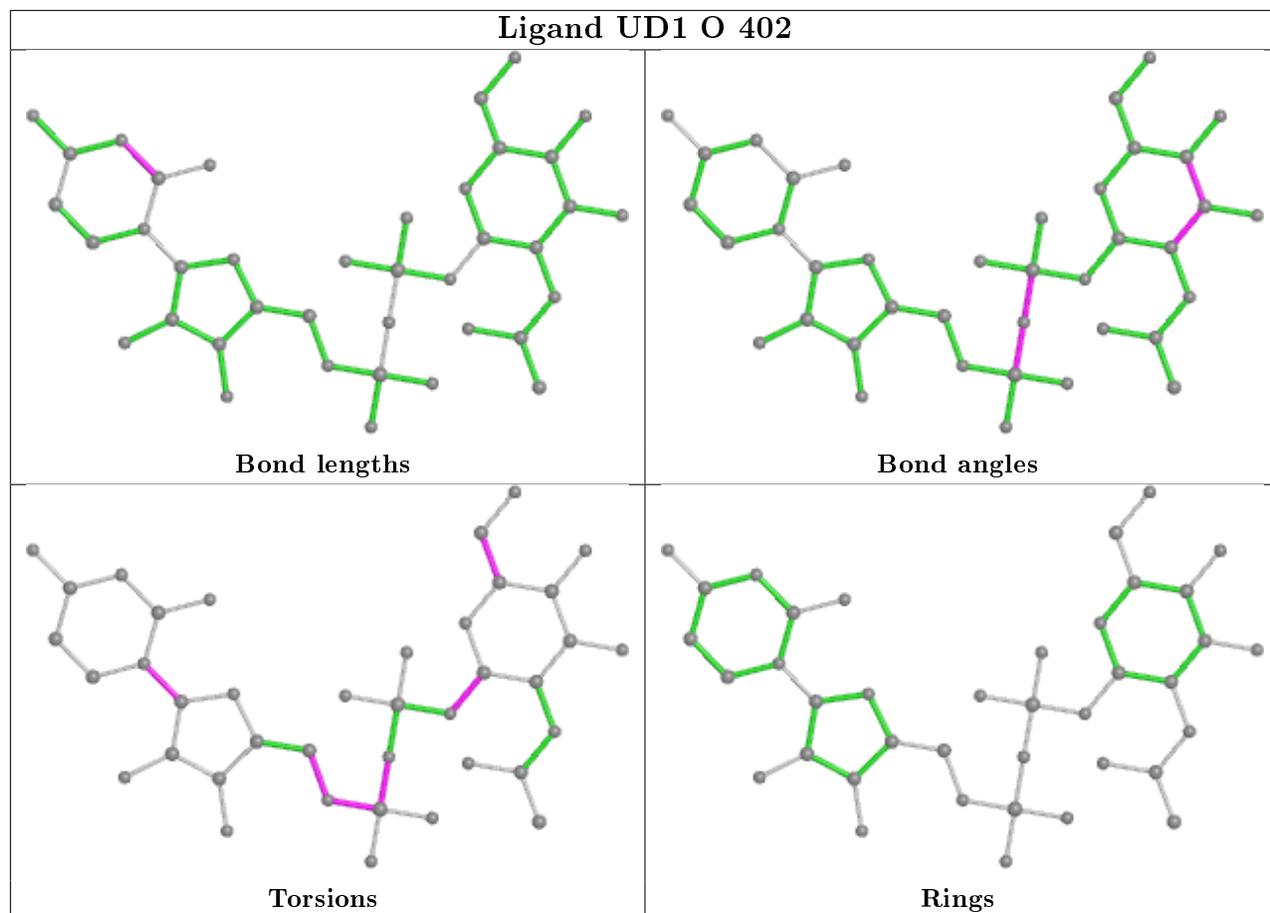


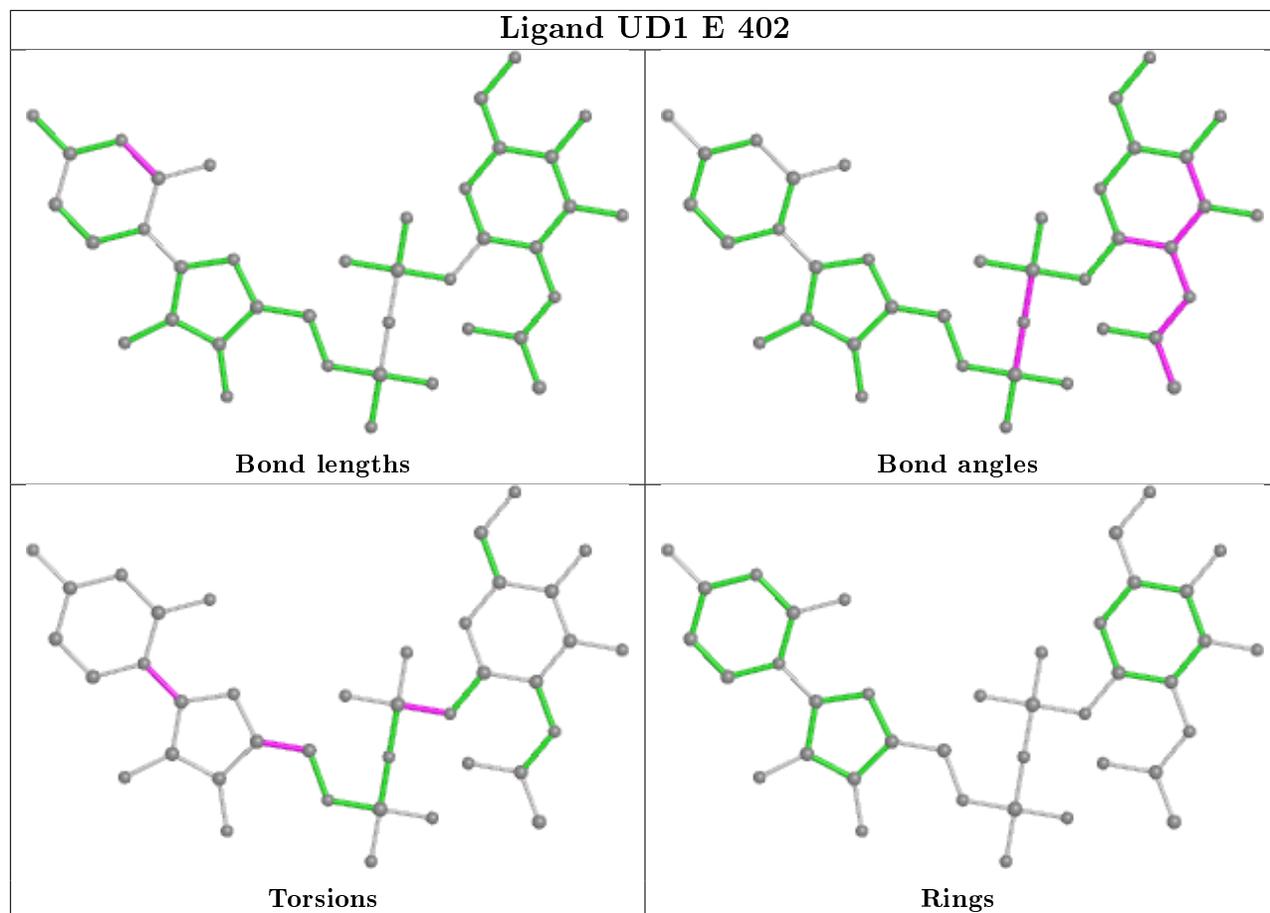


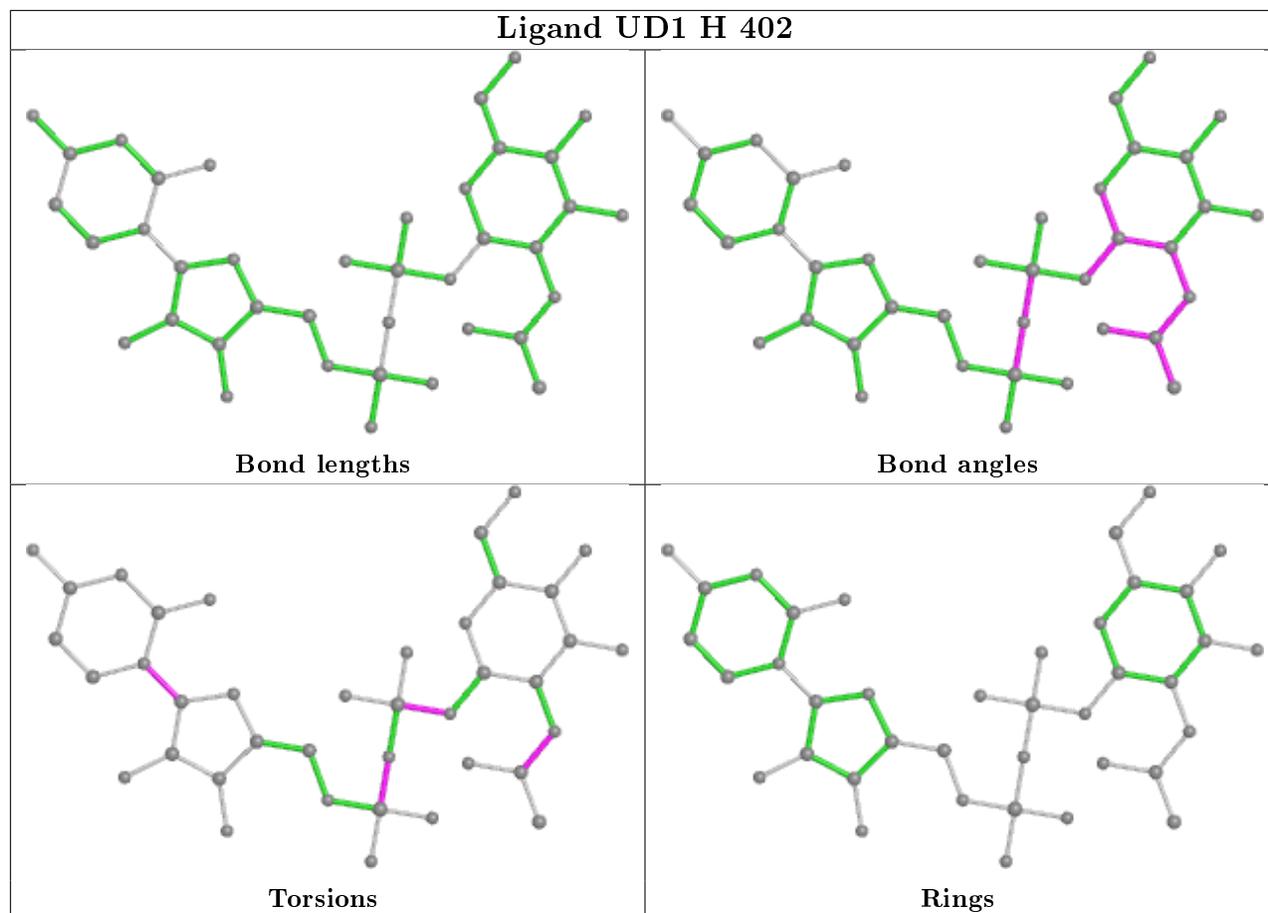


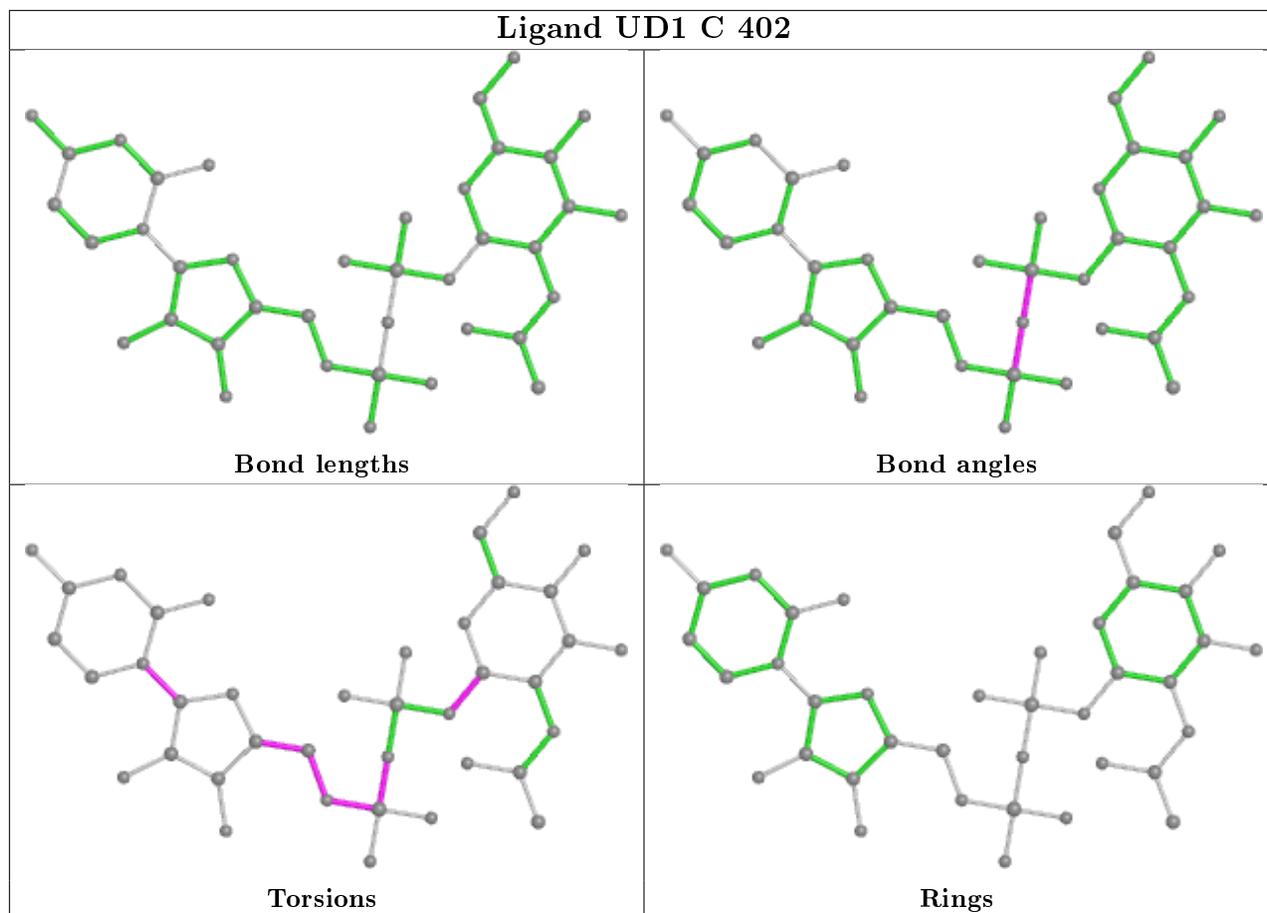


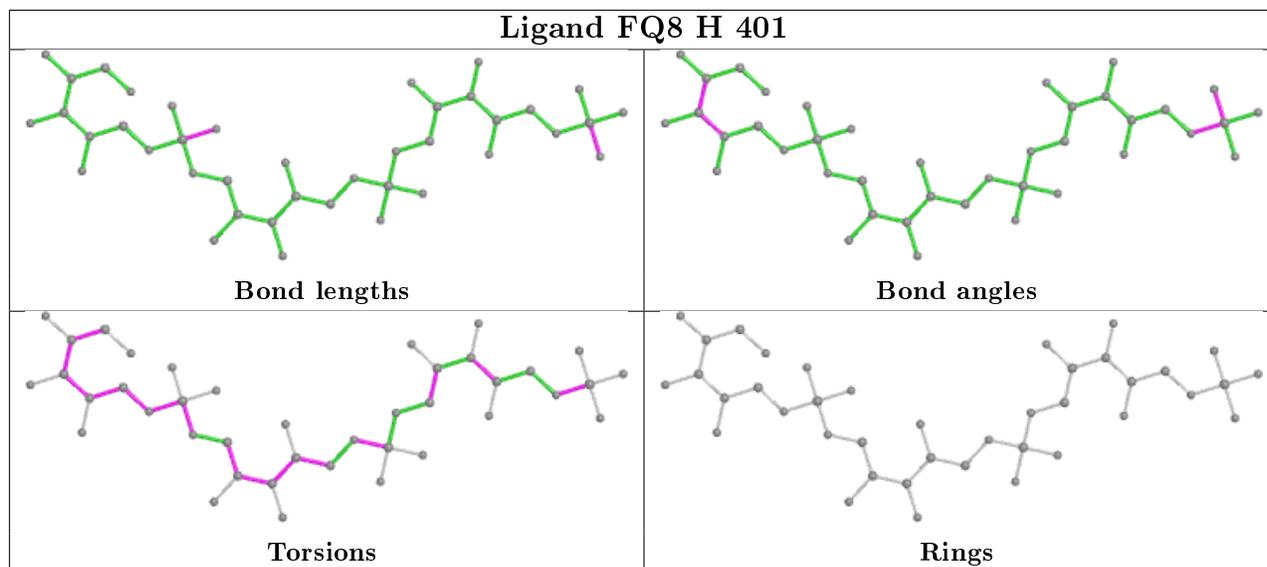
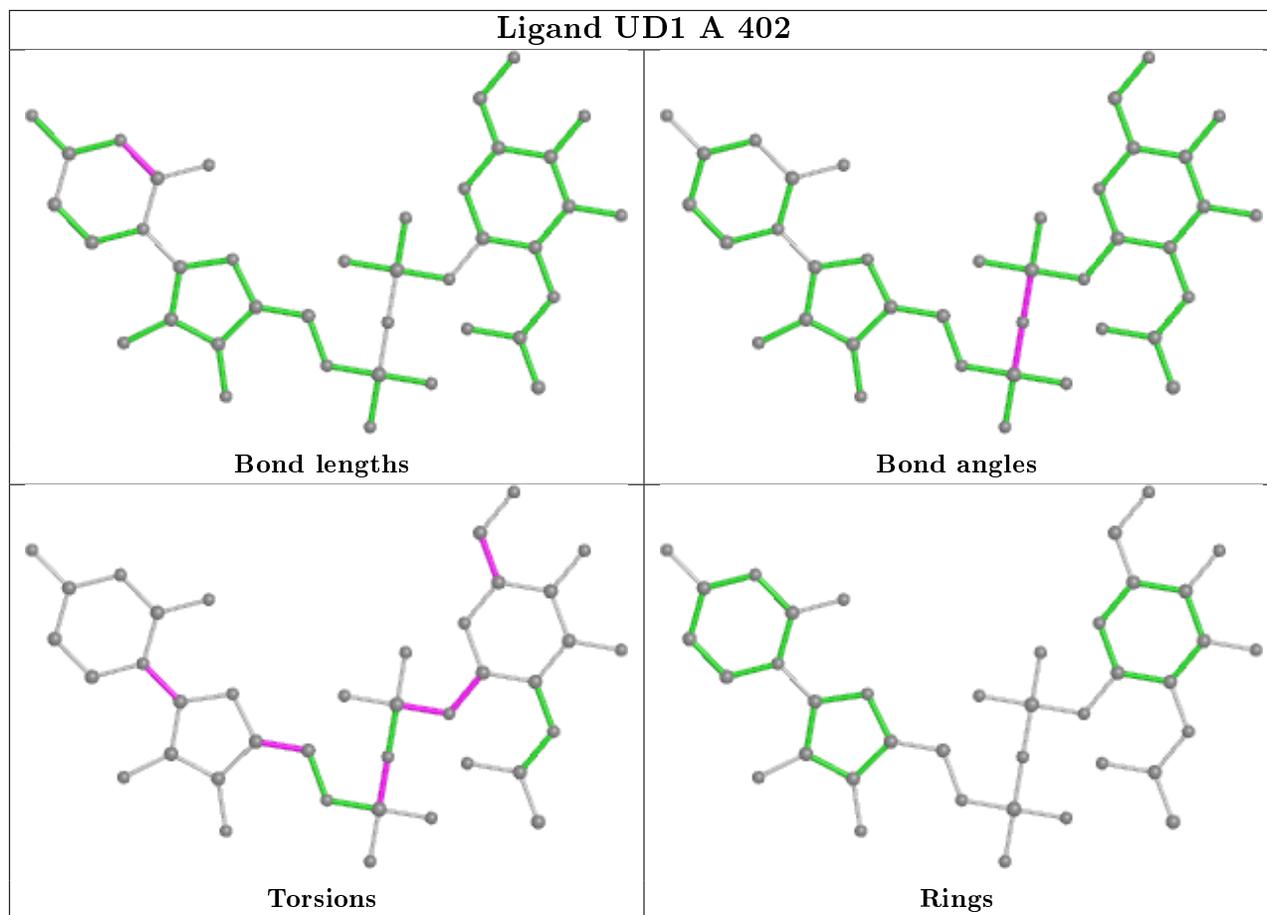


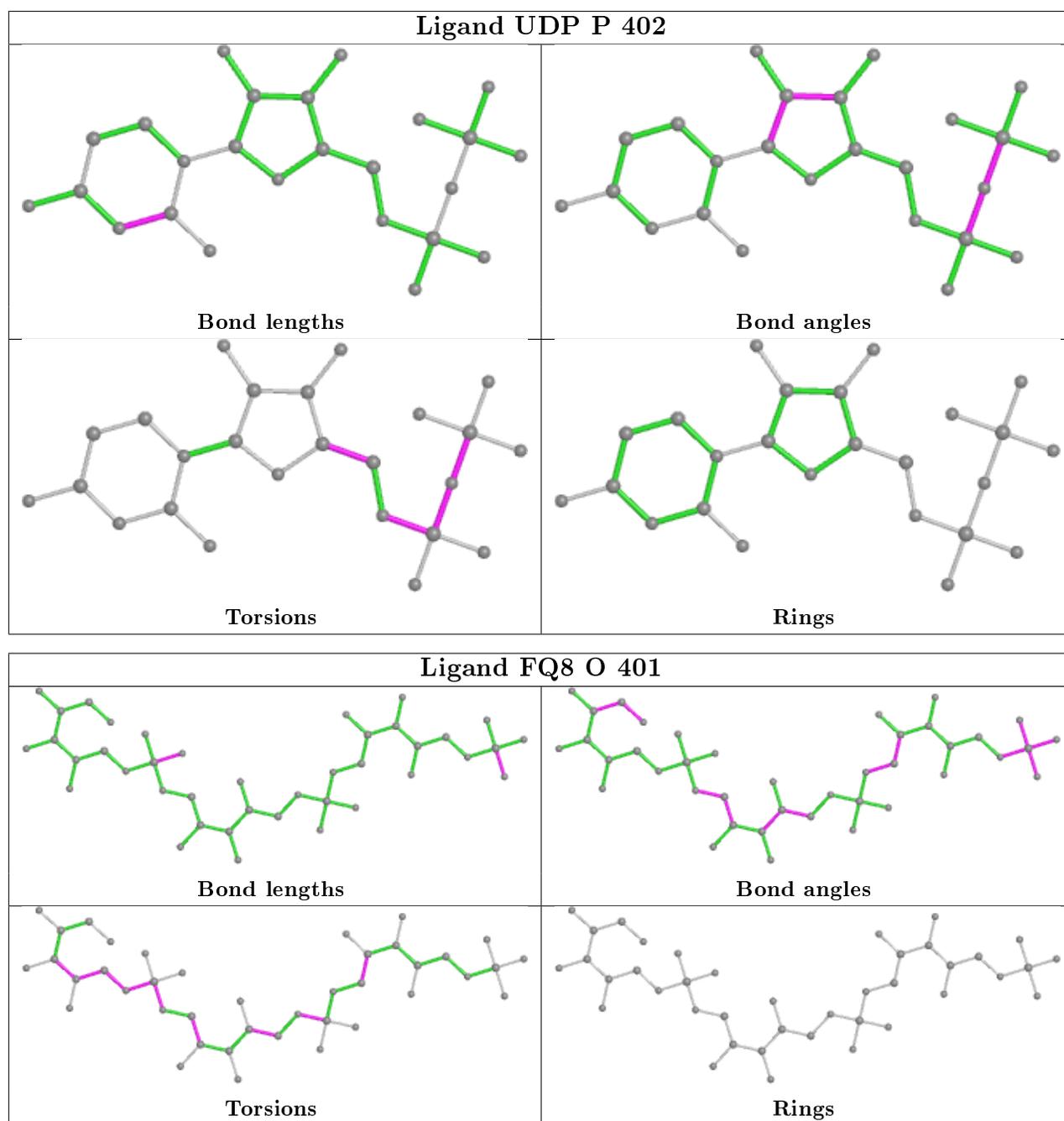












## 5.7 Other polymers [\(i\)](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	317/345 (91%)	-0.17	2 (0%) 89   91	25, 41, 66, 100	0
1	B	317/345 (91%)	-0.16	1 (0%) 94   96	27, 39, 65, 97	0
1	C	314/345 (91%)	-0.08	6 (1%) 66   73	29, 47, 80, 115	0
1	D	312/345 (90%)	-0.09	1 (0%) 94   96	33, 47, 68, 111	0
1	E	317/345 (91%)	-0.19	0 100   100	28, 42, 71, 107	0
1	F	316/345 (91%)	0.01	0 100   100	33, 45, 69, 92	0
1	G	314/345 (91%)	-0.05	1 (0%) 94   96	33, 48, 79, 104	0
1	H	318/345 (92%)	-0.17	2 (0%) 89   91	26, 39, 68, 105	0
1	I	315/345 (91%)	0.02	9 (2%) 51   58	32, 51, 83, 104	0
1	O	316/345 (91%)	0.01	1 (0%) 94   96	31, 44, 69, 98	0
1	P	305/345 (88%)	0.69	49 (16%) 1   1	39, 72, 118, 141	0
1	Q	314/345 (91%)	0.48	34 (10%) 5   5	34, 65, 113, 147	0
All	All	3775/4140 (91%)	0.02	106 (2%) 53   60	25, 47, 91, 147	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	98	HIS	5.1
1	P	136	GLU	5.0
1	P	62	PHE	4.8
1	C	127	GLY	4.8
1	P	34	TYR	4.7
1	Q	14	GLY	4.5
1	P	32	THR	4.5
1	P	59	LEU	4.5
1	Q	97	LEU	4.4
1	Q	202	GLU	4.4
1	P	25	LEU	4.4

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	I	127	GLY	4.3
1	Q	24	VAL	4.2
1	P	101	ALA	4.1
1	I	128	ARG	3.9
1	P	203	TYR	3.9
1	P	204	TYR	3.8
1	I	93	SER	3.7
1	P	24	VAL	3.7
1	Q	203	TYR	3.7
1	P	138	GLY	3.6
1	C	222	THR	3.6
1	P	11	PHE	3.5
1	Q	1	MET	3.5
1	I	53	ILE	3.5
1	B	127	GLY	3.4
1	Q	28	THR	3.3
1	P	122	GLY	3.3
1	P	93	SER	3.3
1	P	68	ASN	3.3
1	P	22	SER	3.2
1	Q	34	TYR	3.2
1	P	39	ILE	3.2
1	P	95	ASP	3.2
1	P	201	TYR	3.1
1	I	123	VAL	3.0
1	Q	32	THR	3.0
1	H	128	ARG	3.0
1	Q	123	VAL	3.0
1	P	30	LYS	3.0
1	Q	45	ASP	3.0
1	Q	29	MET	2.9
1	Q	99	GLU	2.9
1	Q	201	TYR	2.9
1	Q	13	ASN	2.9
1	P	112	ASN	2.8
1	P	9	PRO	2.8
1	Q	204	TYR	2.8
1	P	21	ILE	2.8
1	P	36	LEU	2.8
1	Q	49	THR	2.8
1	P	60	VAL	2.7
1	P	199	THR	2.7

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	I	47	GLY	2.6
1	P	202	GLU	2.6
1	C	125	GLY	2.5
1	P	99	GLU	2.5
1	P	131	PRO	2.5
1	I	62	PHE	2.5
1	P	20	THR	2.5
1	P	5	SER	2.5
1	Q	106	TYR	2.5
1	P	26	ASN	2.5
1	Q	135	PHE	2.4
1	P	135	PHE	2.4
1	P	100	ARG	2.4
1	C	124	GLU	2.4
1	Q	30	LYS	2.4
1	P	327	LEU	2.4
1	P	28	THR	2.4
1	I	94	ASP	2.3
1	Q	124	GLU	2.3
1	P	96	LEU	2.3
1	Q	10	THR	2.3
1	D	300	TYR	2.3
1	P	119	GLY	2.2
1	P	141	ALA	2.2
1	Q	121	TYR	2.2
1	O	51	ASN	2.2
1	Q	15	GLU	2.2
1	P	66	LYS	2.2
1	P	120	LYS	2.2
1	P	198	LYS	2.2
1	P	98	HIS	2.2
1	C	123	VAL	2.2
1	P	108	TYR	2.2
1	Q	122	GLY	2.2
1	A	175	PHE	2.1
1	P	139	ASN	2.1
1	Q	17	LEU	2.1
1	C	208	ASN	2.1
1	Q	44	ASN	2.1
1	I	175	PHE	2.1
1	Q	138	GLY	2.1
1	P	205	ILE	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	Q	119	GLY	2.1
1	H	124	GLU	2.1
1	A	128	ARG	2.1
1	Q	40	ASP	2.1
1	Q	7	ILE	2.0
1	P	35	GLU	2.0
1	P	97	LEU	2.0
1	P	10	THR	2.0
1	G	53	ILE	2.0
1	Q	51	ASN	2.0
1	Q	25	LEU	2.0

## 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 carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	FQ8	E	401	40/40	0.82	0.26	60,114,157,186	0
6	UDP	P	402	25/25	0.84	0.21	76,95,121,135	0
2	FQ8	A	401	40/40	0.86	0.25	65,110,158,175	0
4	MG	P	403	1/1	0.86	0.10	56,56,56,56	0
4	MG	O	403	1/1	0.86	0.26	45,45,45,45	0
3	UD1	Q	402	39/39	0.87	0.21	61,94,165,170	0
4	MG	G	403	1/1	0.88	0.22	46,46,46,46	0
2	FQ8	H	401	40/40	0.89	0.30	48,93,137,158	0
4	MG	A	403	1/1	0.90	0.17	52,52,52,52	0
2	FQ8	D	401	40/40	0.90	0.27	48,89,155,199	0
2	FQ8	Q	401	40/40	0.91	0.23	45,99,149,175	0
2	FQ8	B	401	40/40	0.91	0.28	49,92,149,166	0

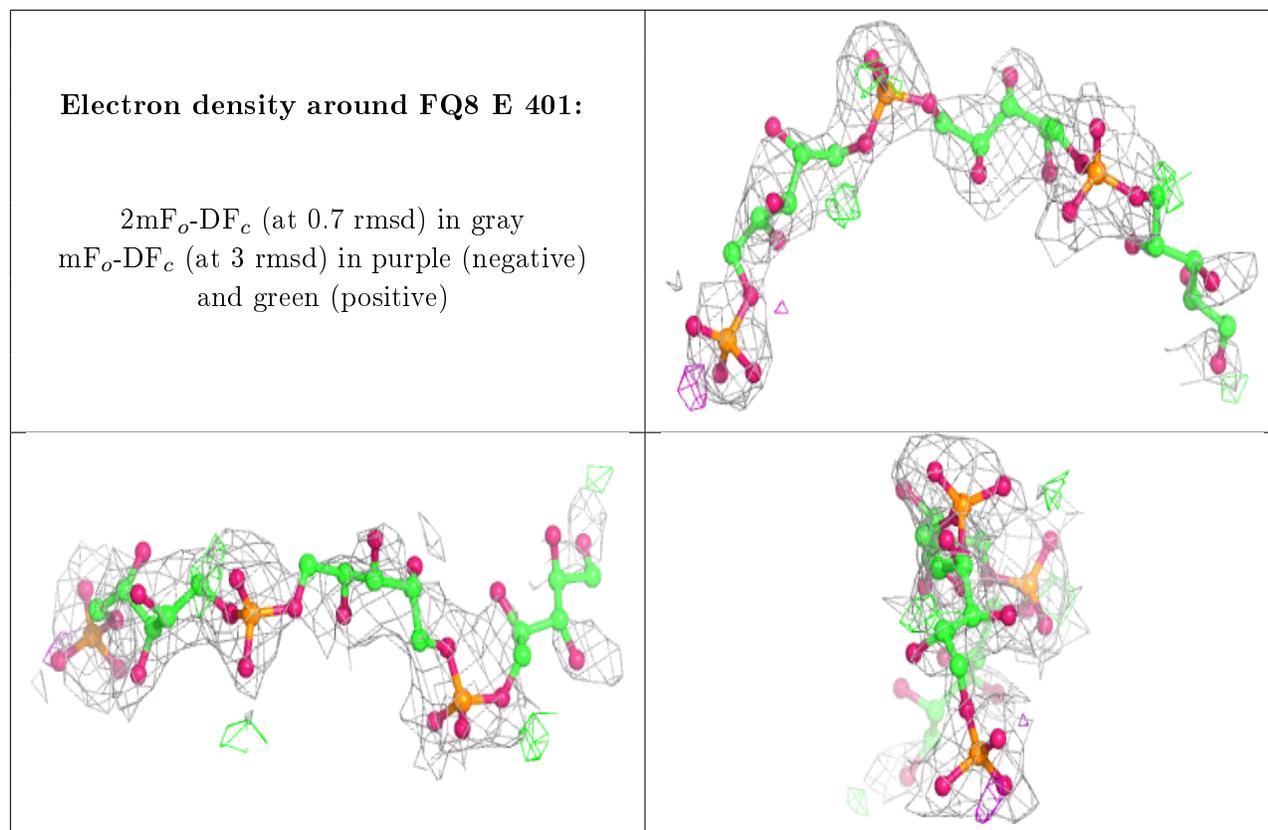
*Continued on next page...*

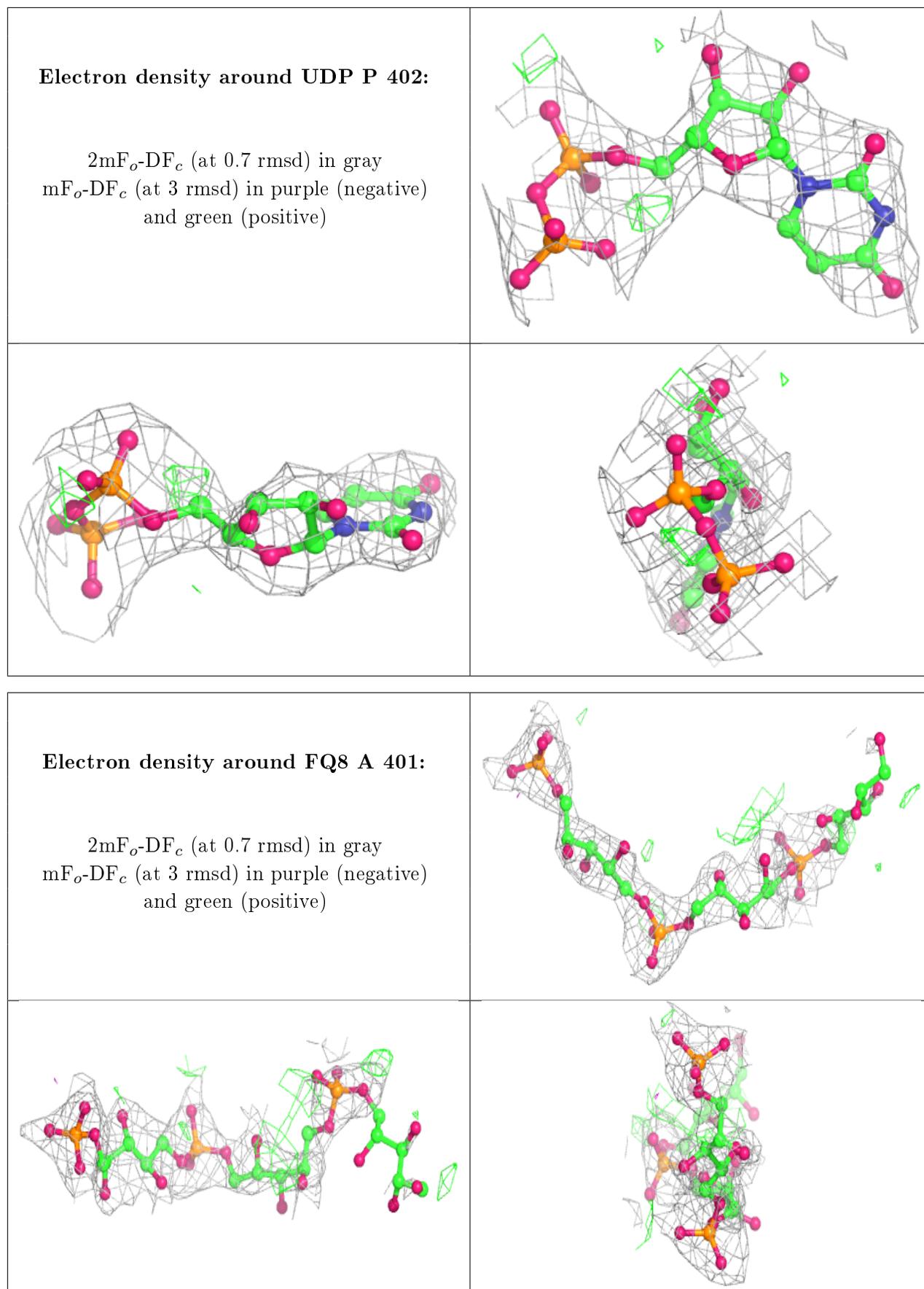
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	FQ8	P	401	40/40	0.91	0.22	55,92,144,173	0
5	CL	E	404	1/1	0.92	0.10	44,44,44,44	0
4	MG	H	403	1/1	0.92	0.16	45,45,45,45	0
4	MG	D	403	1/1	0.92	0.11	57,57,57,57	0
4	MG	A	404	1/1	0.93	0.20	56,56,56,56	0
3	UD1	G	402	39/39	0.94	0.19	39,77,129,138	0
2	FQ8	G	401	40/40	0.94	0.24	49,78,155,158	0
2	FQ8	C	401	40/40	0.94	0.21	44,75,128,177	0
4	MG	H	404	1/1	0.94	0.36	61,61,61,61	0
2	FQ8	I	401	40/40	0.94	0.24	51,82,128,135	0
3	UD1	C	402	39/39	0.94	0.21	58,73,123,135	0
3	UD1	I	402	39/39	0.94	0.22	55,80,117,133	0
3	UD1	O	402	39/39	0.94	0.26	42,72,120,125	0
5	CL	P	404	1/1	0.94	0.10	76,76,76,76	0
4	MG	B	403	1/1	0.95	0.39	55,55,55,55	0
2	FQ8	F	401	40/40	0.95	0.26	40,74,136,136	0
4	MG	I	403	1/1	0.95	0.11	49,49,49,49	0
5	CL	I	404	1/1	0.95	0.12	53,53,53,53	0
3	UD1	D	402	39/39	0.95	0.16	39,57,89,93	0
3	UD1	A	402	39/39	0.95	0.13	34,61,101,115	0
3	UD1	E	402	39/39	0.95	0.14	37,56,109,134	0
4	MG	B	404	1/1	0.95	0.17	40,40,40,40	0
3	UD1	F	402	39/39	0.95	0.21	40,61,104,121	0
3	UD1	H	402	39/39	0.96	0.15	27,47,96,116	0
4	MG	C	403	1/1	0.96	0.16	55,55,55,55	0
5	CL	B	406	1/1	0.96	0.09	49,49,49,49	0
5	CL	D	404	1/1	0.96	0.15	65,65,65,65	0
4	MG	F	403	1/1	0.96	0.20	50,50,50,50	0
3	UD1	B	402	39/39	0.96	0.17	30,54,125,148	0
2	FQ8	O	401	40/40	0.96	0.26	27,59,113,146	0
5	CL	B	405	1/1	0.97	0.08	47,47,47,47	0
4	MG	Q	403	1/1	0.97	0.32	53,53,53,53	0
5	CL	C	404	1/1	0.97	0.12	63,63,63,63	0
4	MG	E	403	1/1	0.97	0.30	44,44,44,44	0
5	CL	H	405	1/1	0.98	0.08	38,38,38,38	0
5	CL	F	404	1/1	0.98	0.15	45,45,45,45	0
5	CL	A	405	1/1	0.98	0.10	48,48,48,48	0
5	CL	H	406	1/1	0.99	0.13	56,56,56,56	0
5	CL	O	404	1/1	0.99	0.11	41,41,41,41	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

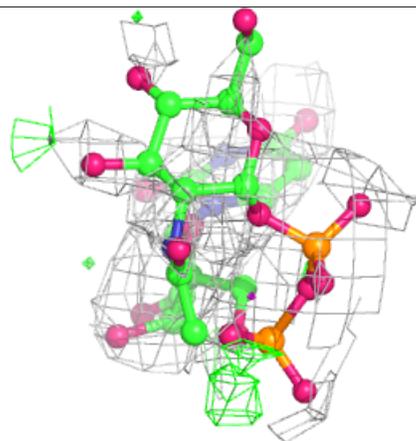
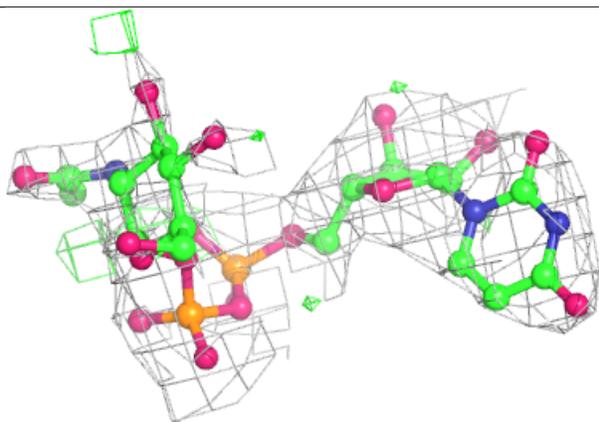
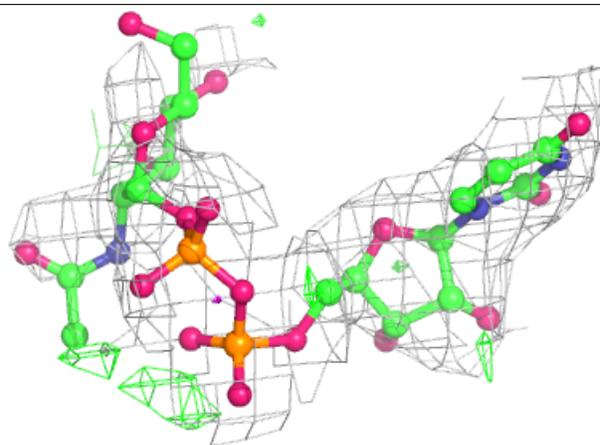
orientation to approximate a three-dimensional view.



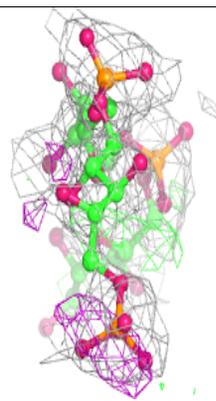
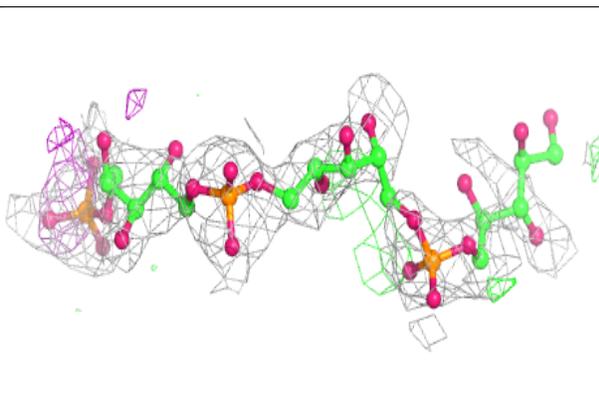
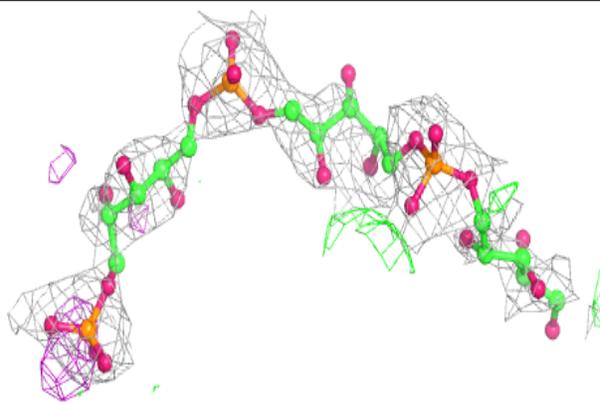


**Electron density around UD1 Q 402:**

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

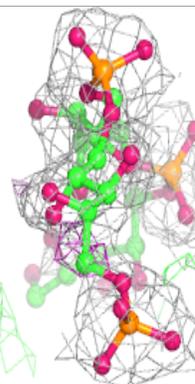
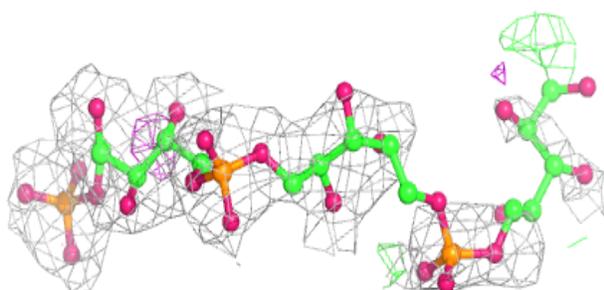
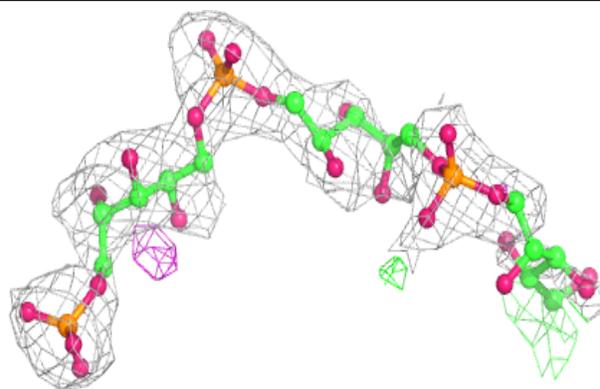
**Electron density around FQ8 H 401:**

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

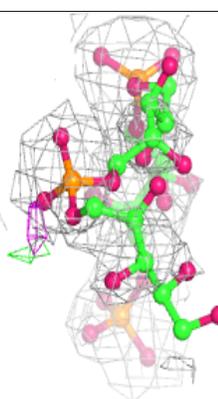
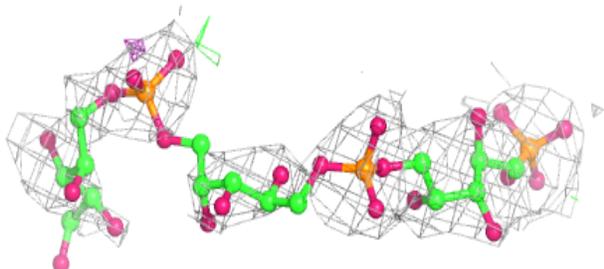
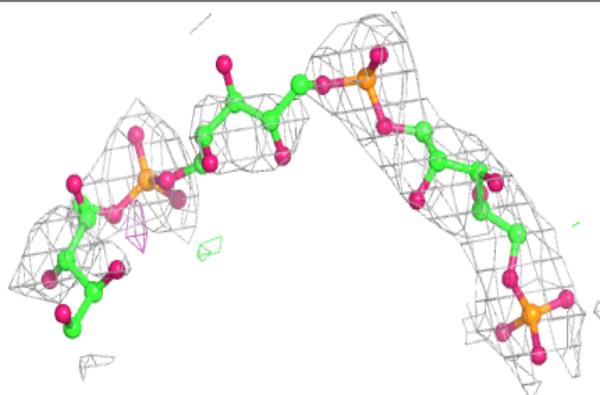


**Electron density around FQ8 D 401:**

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

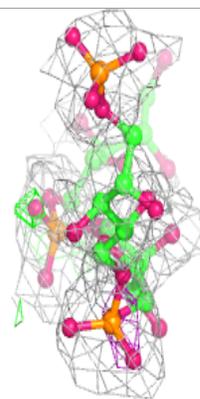
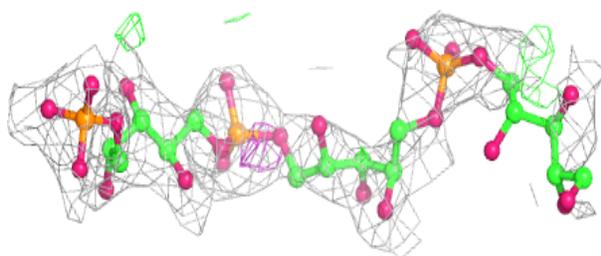
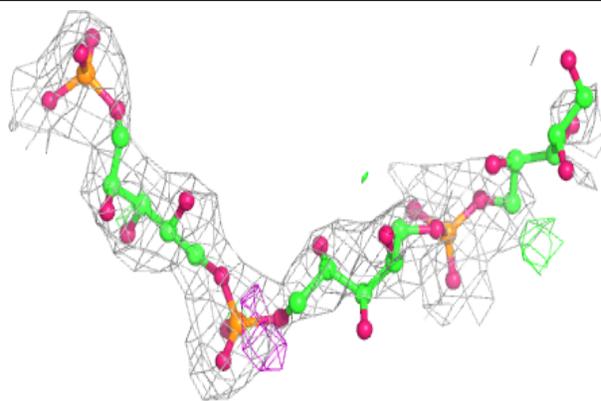
**Electron density around FQ8 Q 401:**

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

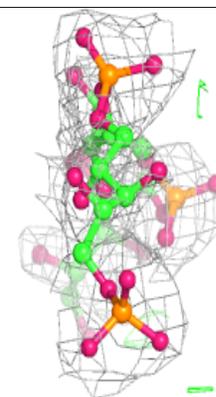
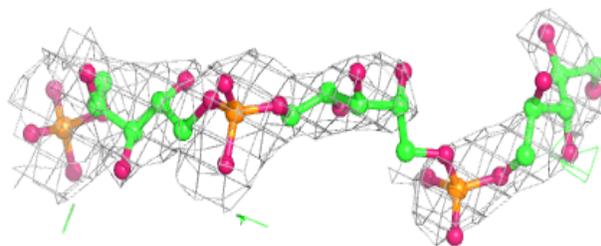
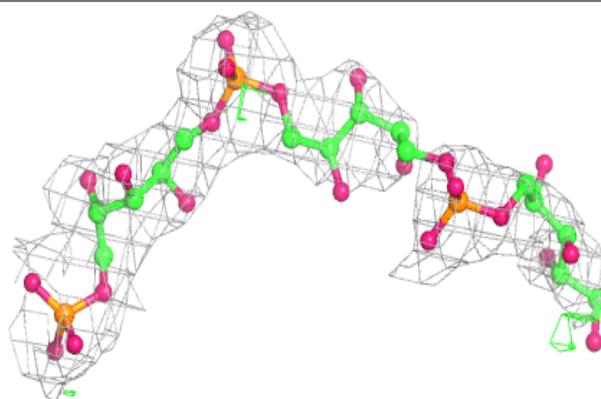


**Electron density around FQ8 B 401:**

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

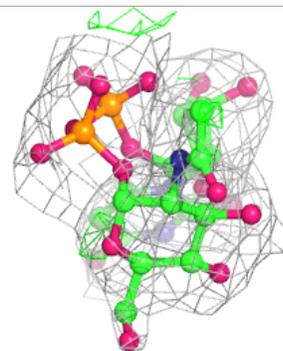
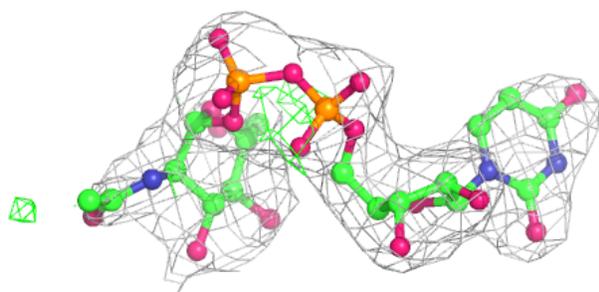
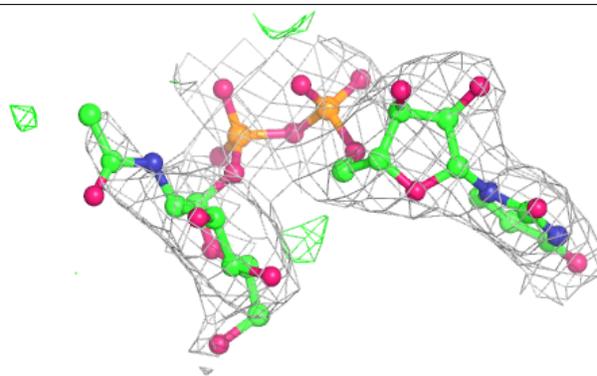
**Electron density around FQ8 P 401:**

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

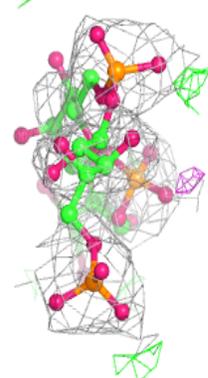
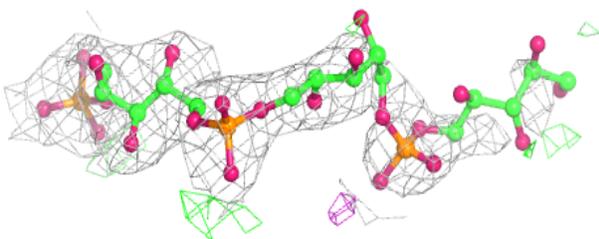
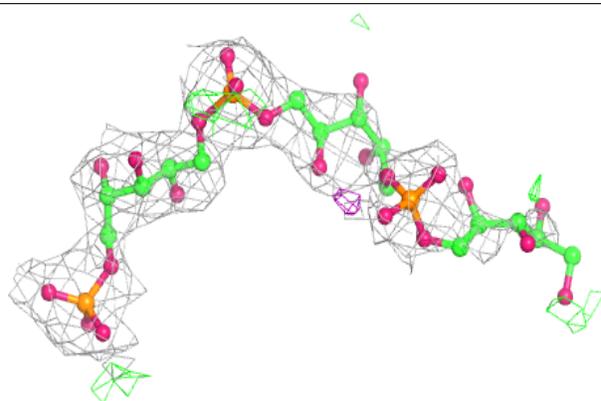


**Electron density around UD1 G 402:**

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

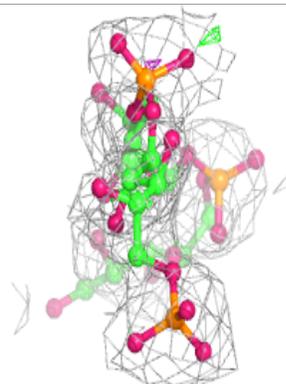
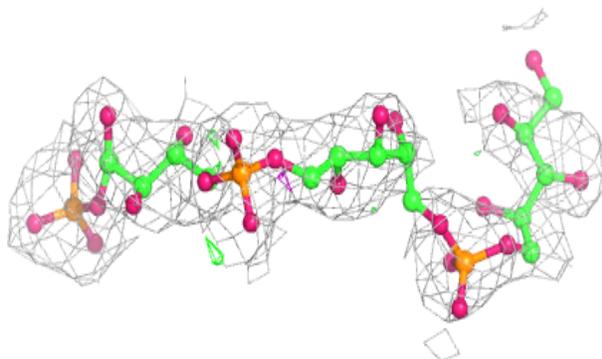
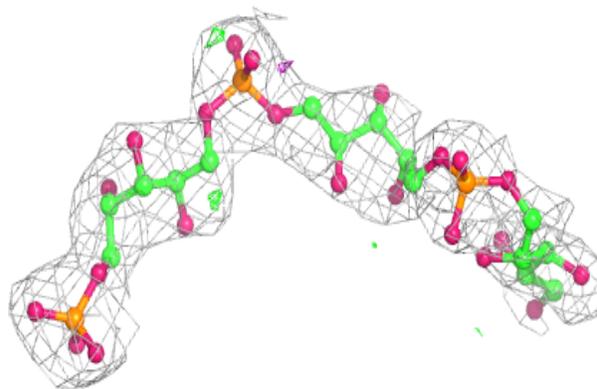
**Electron density around FQ8 G 401:**

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

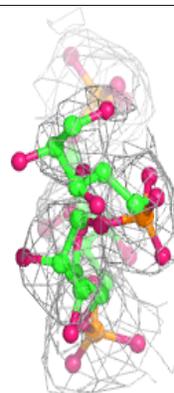
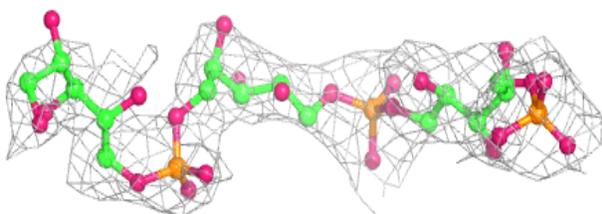
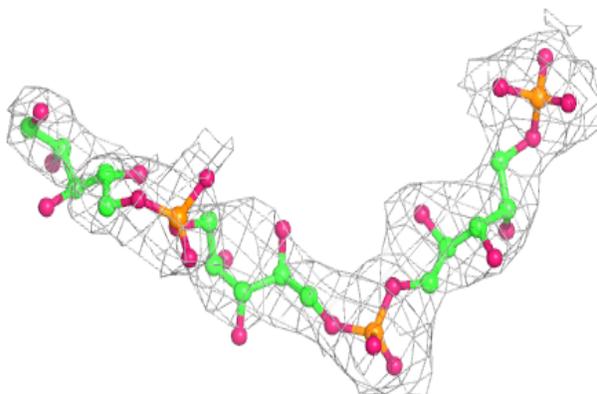


**Electron density around FQ8 C 401:**

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

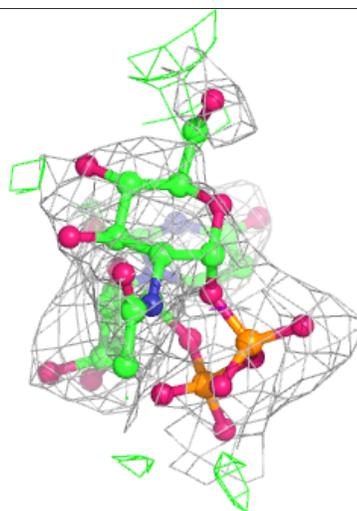
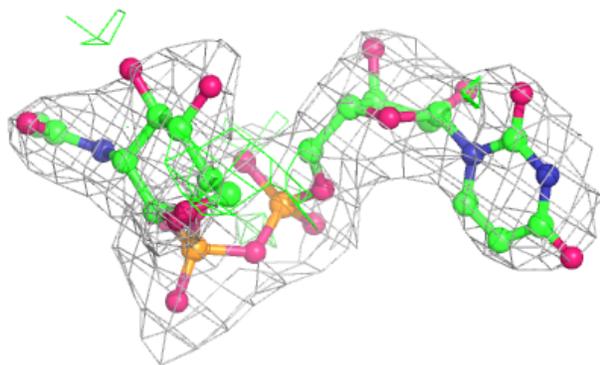
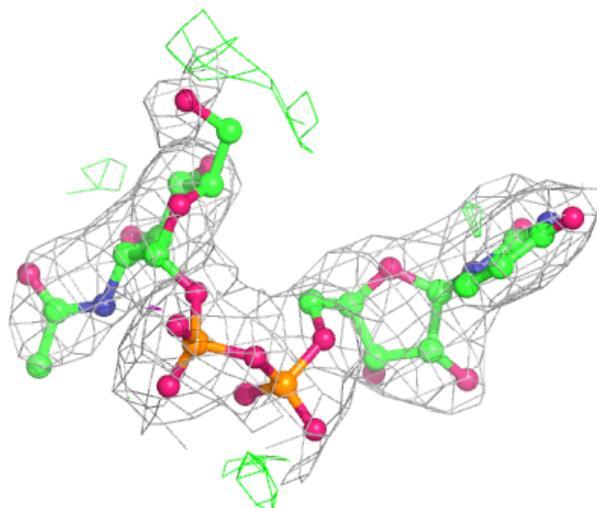
**Electron density around FQ8 I 401:**

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



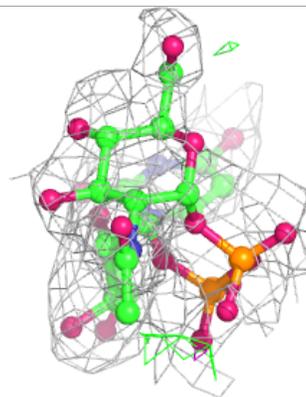
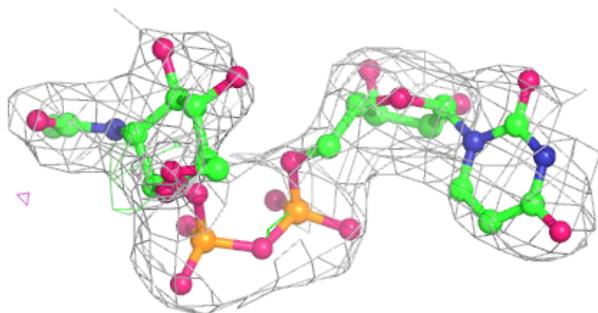
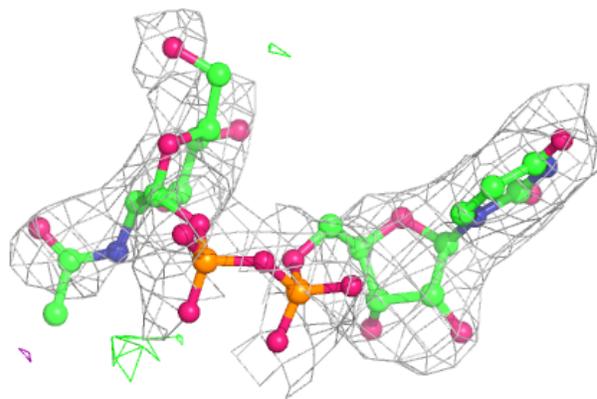
**Electron density around UD1 C 402:**

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

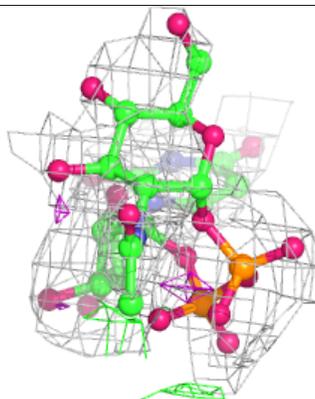
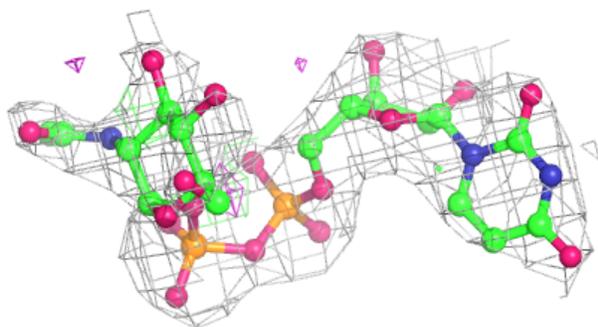
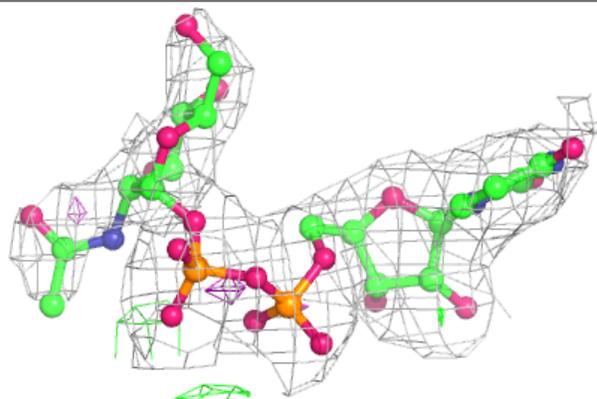


**Electron density around UD1 I 402:**

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

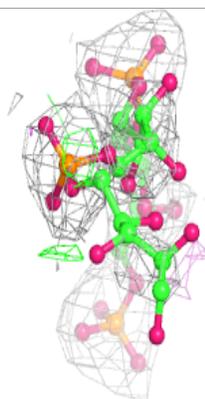
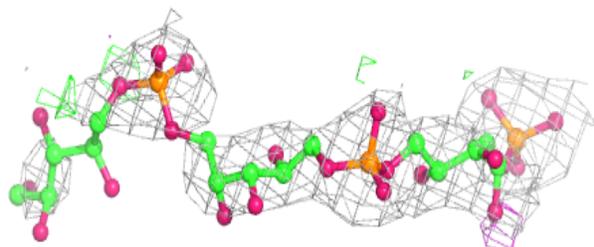
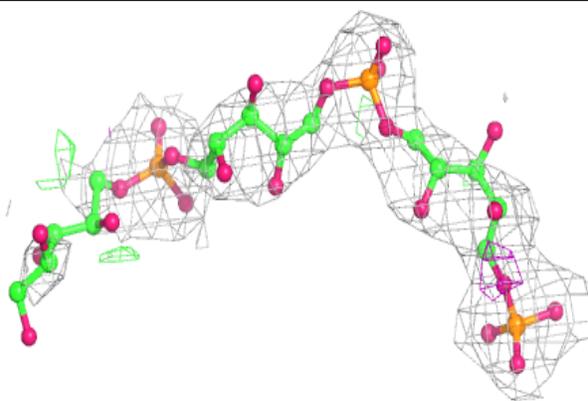
**Electron density around UD1 O 402:**

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

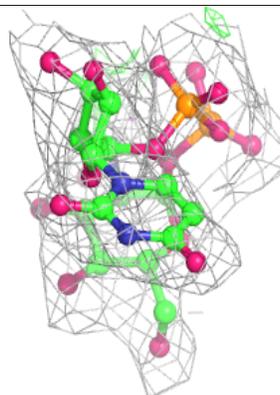
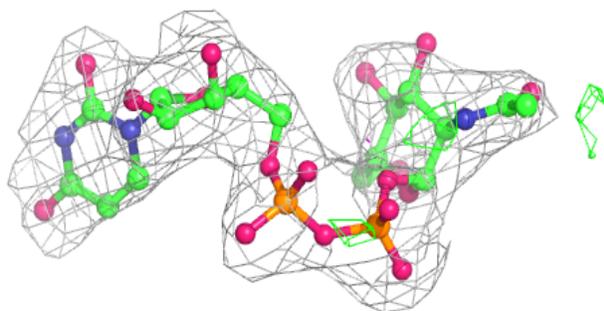
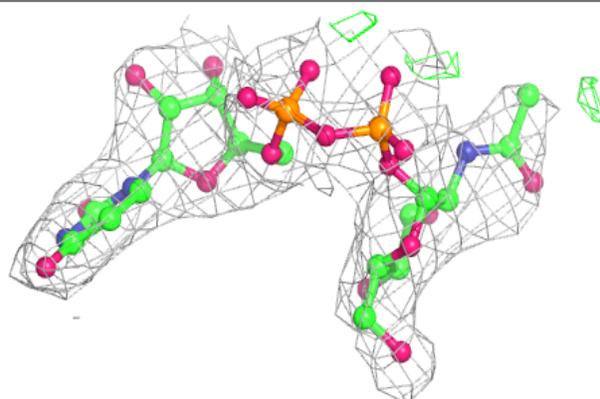


**Electron density around FQ8 F 401:**

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

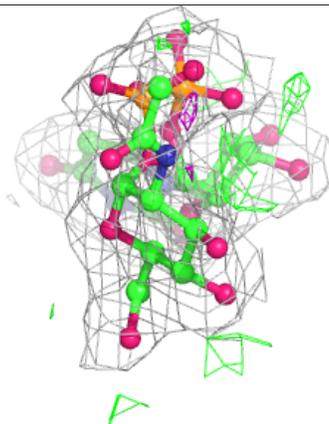
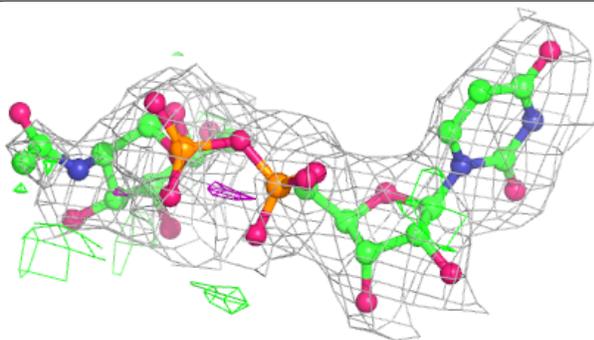
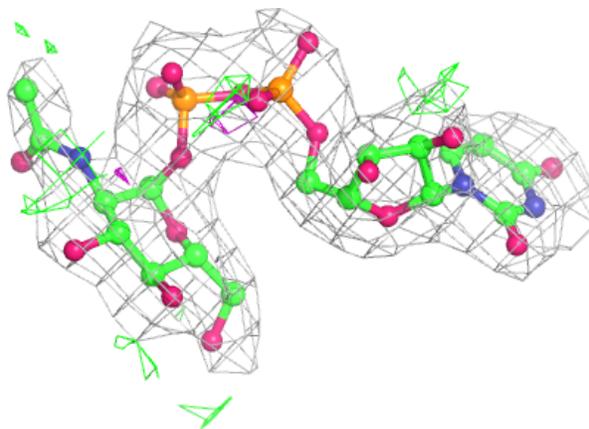
**Electron density around UD1 D 402:**

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

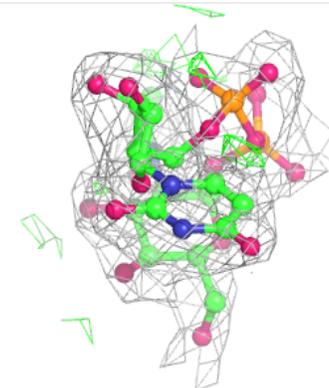
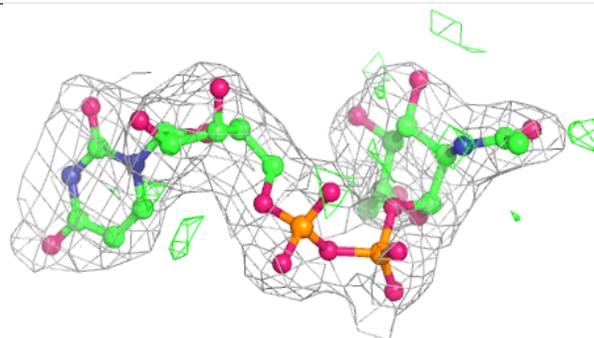
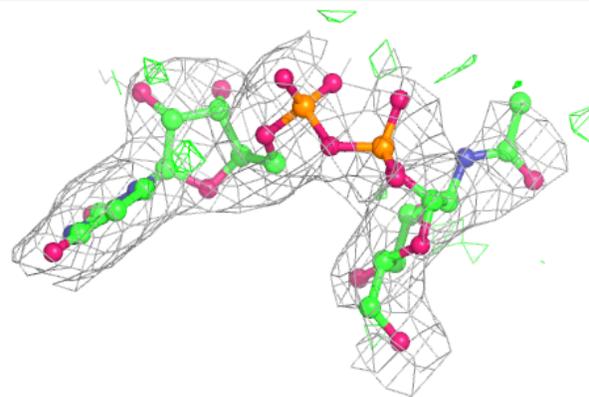


**Electron density around UD1 A 402:**

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

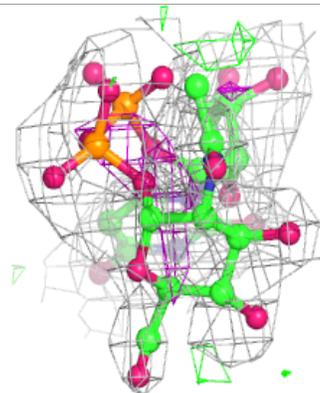
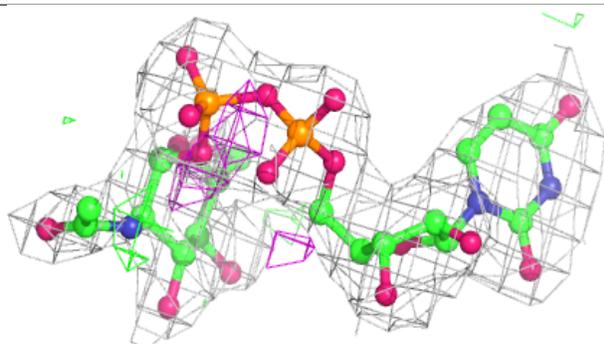
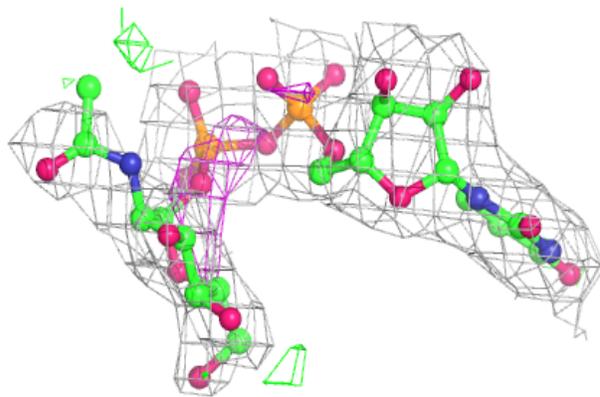
**Electron density around UD1 E 402:**

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

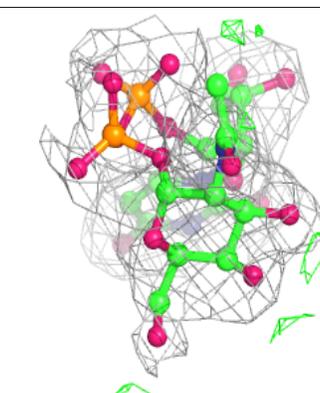
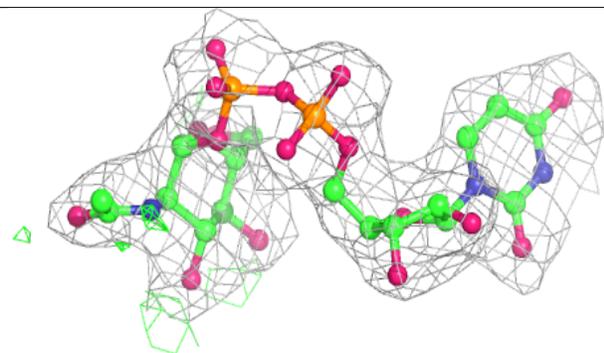
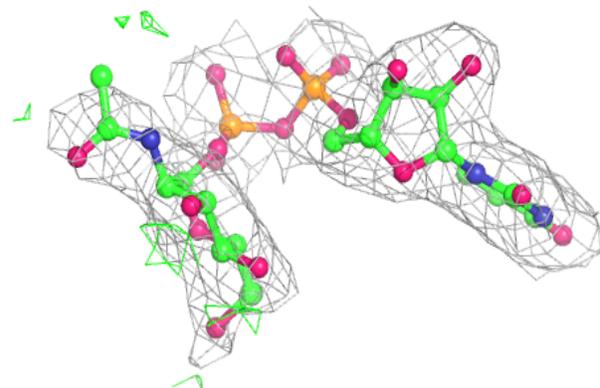


**Electron density around UD1 F 402:**

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

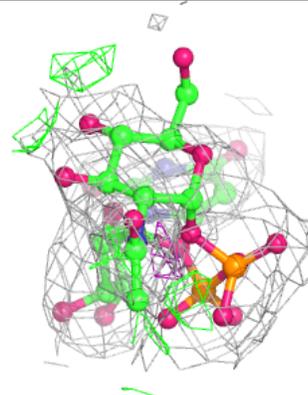
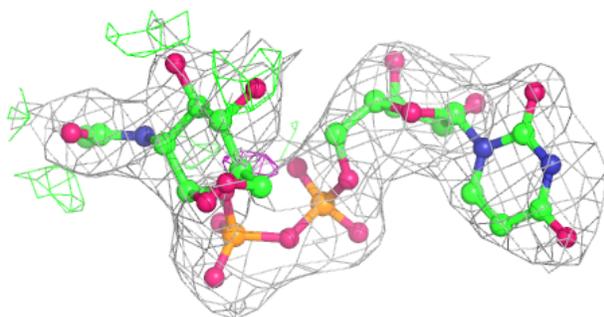
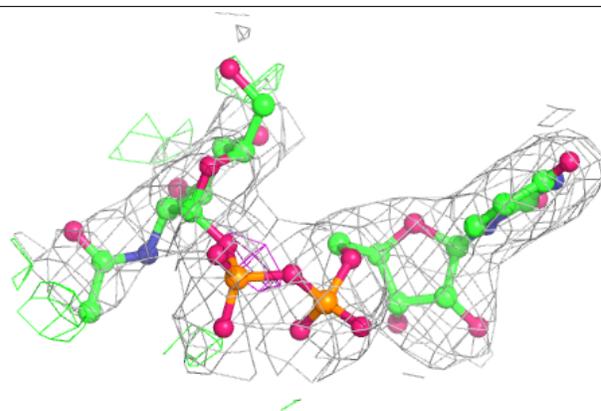
**Electron density around UD1 H 402:**

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

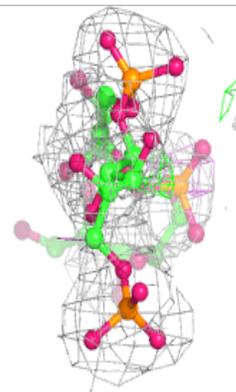
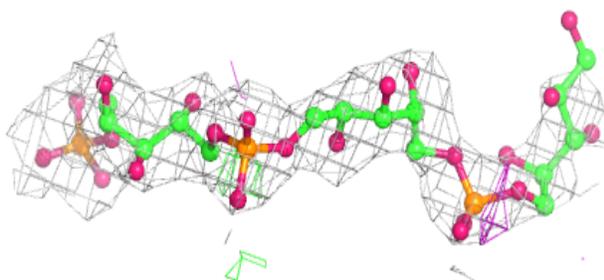
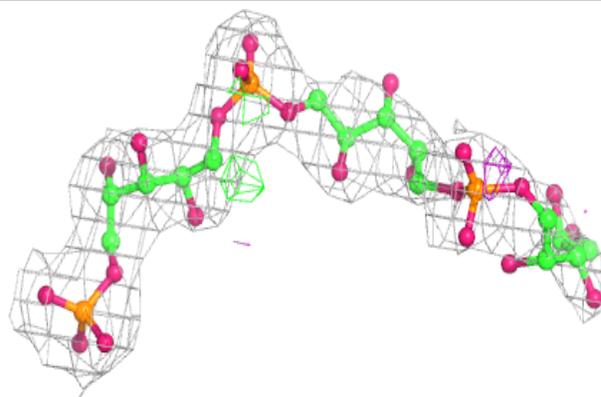


**Electron density around UD1 B 402:**

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

**Electron density around FQ8 O 401:**

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



## 6.5 Other polymers

There are no such residues in this entry.