wwPDB X-ray Structure Validation Summary Report (i)

Jul 12, 2022 – 10:18 AM EDT

PDB ID	:	7SR6
Title	:	Human Endogenous Retrovirus (HERV-K) reverse transcriptase ternary complex with dsDNA template Primer and dNTP
Authors	:	Baldwin, E.T.; Nichols, C.
Deposited on	:	2021-11-08
Resolution	:	2.62 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

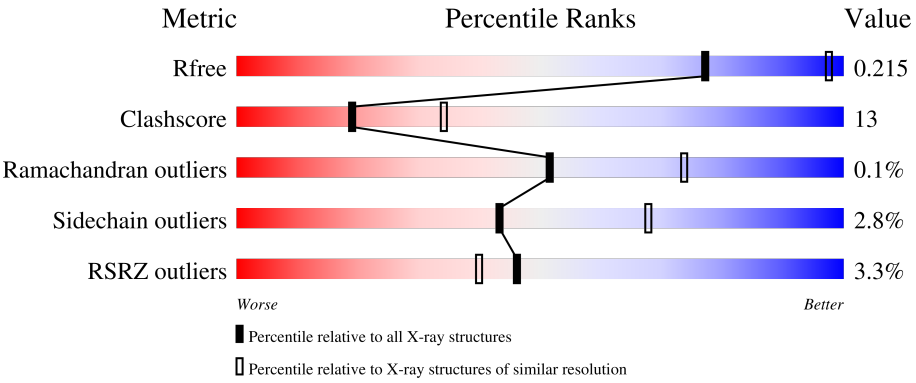
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

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 2.62 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	618	68% 23% 8%
1	B	618	5% 50% 19% · 30%
1	F	618	66% 25% 8%
1	G	618	5% 52% 17% 30%
2	D	24	4% 38% 50% 8% ·

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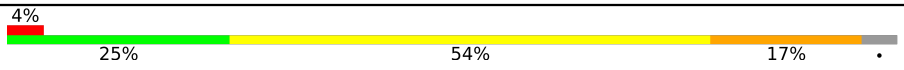
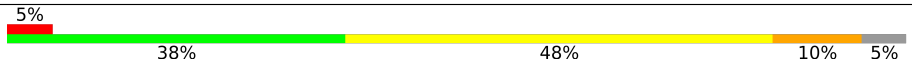
Mol	Chain	Length	Quality of chain
2	H	24	
3	E	21	
3	I	21	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	DIO	G	601	-	-	X	-

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 18265 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 Polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	566	Total	C	N	O	S	17	3	0
			4507	2912	760	820	15			
1	B	432	Total	C	N	O	S	11	2	0
			3423	2225	579	606	13			
1	F	566	Total	C	N	O	S	3	4	0
			4510	2913	762	819	16			
1	G	432	Total	C	N	O	S	13	4	0
			3428	2230	572	613	13			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP V9H0F6
A	-20	ALA	-	expression tag	UNP V9H0F6
A	-19	HIS	-	expression tag	UNP V9H0F6
A	-18	HIS	-	expression tag	UNP V9H0F6
A	-17	HIS	-	expression tag	UNP V9H0F6
A	-16	HIS	-	expression tag	UNP V9H0F6
A	-15	HIS	-	expression tag	UNP V9H0F6
A	-14	HIS	-	expression tag	UNP V9H0F6
A	-13	ASP	-	expression tag	UNP V9H0F6
A	-12	TYR	-	expression tag	UNP V9H0F6
A	-11	ASP	-	expression tag	UNP V9H0F6
A	-10	ILE	-	expression tag	UNP V9H0F6
A	-9	PRO	-	expression tag	UNP V9H0F6
A	-8	THR	-	expression tag	UNP V9H0F6
A	-7	THR	-	expression tag	UNP V9H0F6
A	-6	GLU	-	expression tag	UNP V9H0F6
A	-5	ASN	-	expression tag	UNP V9H0F6
A	-4	LEU	-	expression tag	UNP V9H0F6
A	-3	TYR	-	expression tag	UNP V9H0F6
A	-2	PHE	-	expression tag	UNP V9H0F6
A	-1	GLN	-	expression tag	UNP V9H0F6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP V9H0F6
B	-21	MET	-	initiating methionine	UNP V9H0F6
B	-20	ALA	-	expression tag	UNP V9H0F6
B	-19	HIS	-	expression tag	UNP V9H0F6
B	-18	HIS	-	expression tag	UNP V9H0F6
B	-17	HIS	-	expression tag	UNP V9H0F6
B	-16	HIS	-	expression tag	UNP V9H0F6
B	-15	HIS	-	expression tag	UNP V9H0F6
B	-14	HIS	-	expression tag	UNP V9H0F6
B	-13	ASP	-	expression tag	UNP V9H0F6
B	-12	TYR	-	expression tag	UNP V9H0F6
B	-11	ASP	-	expression tag	UNP V9H0F6
B	-10	ILE	-	expression tag	UNP V9H0F6
B	-9	PRO	-	expression tag	UNP V9H0F6
B	-8	THR	-	expression tag	UNP V9H0F6
B	-7	THR	-	expression tag	UNP V9H0F6
B	-6	GLU	-	expression tag	UNP V9H0F6
B	-5	ASN	-	expression tag	UNP V9H0F6
B	-4	LEU	-	expression tag	UNP V9H0F6
B	-3	TYR	-	expression tag	UNP V9H0F6
B	-2	PHE	-	expression tag	UNP V9H0F6
B	-1	GLN	-	expression tag	UNP V9H0F6
B	0	GLY	-	expression tag	UNP V9H0F6
F	-21	MET	-	initiating methionine	UNP V9H0F6
F	-20	ALA	-	expression tag	UNP V9H0F6
F	-19	HIS	-	expression tag	UNP V9H0F6
F	-18	HIS	-	expression tag	UNP V9H0F6
F	-17	HIS	-	expression tag	UNP V9H0F6
F	-16	HIS	-	expression tag	UNP V9H0F6
F	-15	HIS	-	expression tag	UNP V9H0F6
F	-14	HIS	-	expression tag	UNP V9H0F6
F	-13	ASP	-	expression tag	UNP V9H0F6
F	-12	TYR	-	expression tag	UNP V9H0F6
F	-11	ASP	-	expression tag	UNP V9H0F6
F	-10	ILE	-	expression tag	UNP V9H0F6
F	-9	PRO	-	expression tag	UNP V9H0F6
F	-8	THR	-	expression tag	UNP V9H0F6
F	-7	THR	-	expression tag	UNP V9H0F6
F	-6	GLU	-	expression tag	UNP V9H0F6
F	-5	ASN	-	expression tag	UNP V9H0F6
F	-4	LEU	-	expression tag	UNP V9H0F6
F	-3	TYR	-	expression tag	UNP V9H0F6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-2	PHE	-	expression tag	UNP V9H0F6
F	-1	GLN	-	expression tag	UNP V9H0F6
F	0	GLY	-	expression tag	UNP V9H0F6
G	-21	MET	-	initiating methionine	UNP V9H0F6
G	-20	ALA	-	expression tag	UNP V9H0F6
G	-19	HIS	-	expression tag	UNP V9H0F6
G	-18	HIS	-	expression tag	UNP V9H0F6
G	-17	HIS	-	expression tag	UNP V9H0F6
G	-16	HIS	-	expression tag	UNP V9H0F6
G	-15	HIS	-	expression tag	UNP V9H0F6
G	-14	HIS	-	expression tag	UNP V9H0F6
G	-13	ASP	-	expression tag	UNP V9H0F6
G	-12	TYR	-	expression tag	UNP V9H0F6
G	-11	ASP	-	expression tag	UNP V9H0F6
G	-10	ILE	-	expression tag	UNP V9H0F6
G	-9	PRO	-	expression tag	UNP V9H0F6
G	-8	THR	-	expression tag	UNP V9H0F6
G	-7	THR	-	expression tag	UNP V9H0F6
G	-6	GLU	-	expression tag	UNP V9H0F6
G	-5	ASN	-	expression tag	UNP V9H0F6
G	-4	LEU	-	expression tag	UNP V9H0F6
G	-3	TYR	-	expression tag	UNP V9H0F6
G	-2	PHE	-	expression tag	UNP V9H0F6
G	-1	GLN	-	expression tag	UNP V9H0F6
G	0	GLY	-	expression tag	UNP V9H0F6

- Molecule 2 is a DNA chain called DNA (5'-D(P*GP*GP*GP*AP*CP*CP*TP*GP*AP*AP *AP*GP*CP*GP*AP*AP*AP*GP*GP*GP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	23	Total	C	N	O	P	0	0	0
			485	227	106	129	23			
2	H	23	Total	C	N	O	P	0	0	0
			482	226	104	129	23			

- Molecule 3 is a DNA chain called DNA (5'-D(P*TP*TP*TP*CP*CP*CP*TP*TP*TP*CP *GP*CP*TP*TP*TP*CP*AP*GP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	20	Total	C	N	O	P	0	0	0
			400	194	58	128	20			

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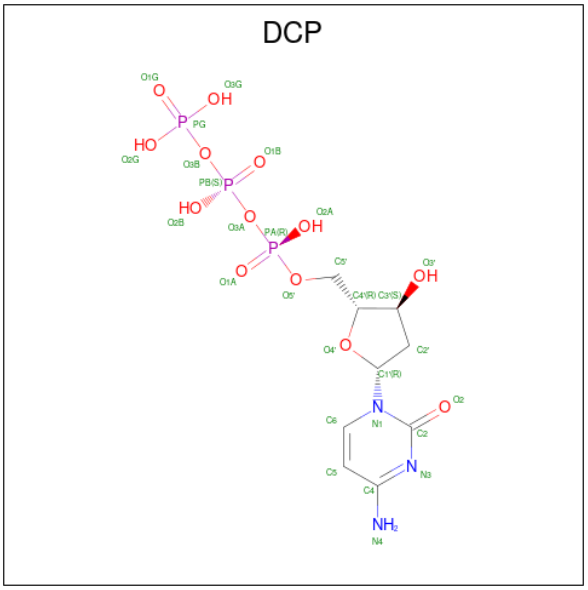
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	20	Total	C	N	O	P	0	0	0
			403	194	61	128	20			

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

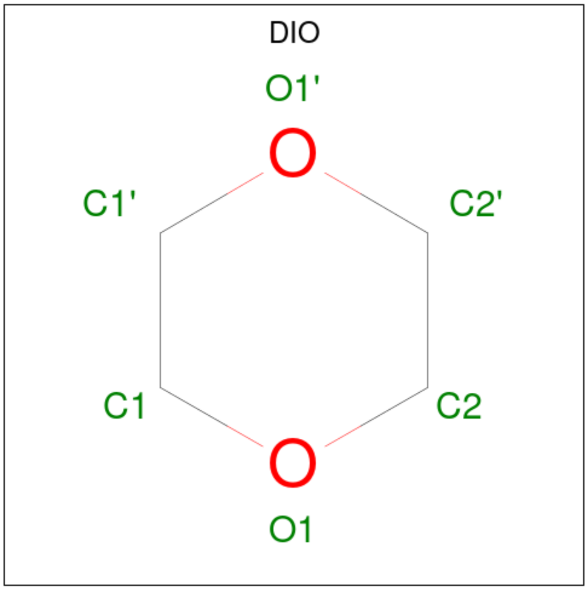
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		
4	D	1	Total	Mg	0	0
			1	1		
4	F	1	Total	Mg	0	0
			1	1		
4	G	1	Total	Mg	0	0
			1	1		

- Molecule 5 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: $C_9H_{16}N_3O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

- Molecule 6 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: $C_4H_8O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 6 4 2	0	0
6	A	1	Total C O 6 4 2	0	0
6	A	1	Total C O 6 4 2	0	0
6	A	1	Total C O 6 4 2	0	0
6	A	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0

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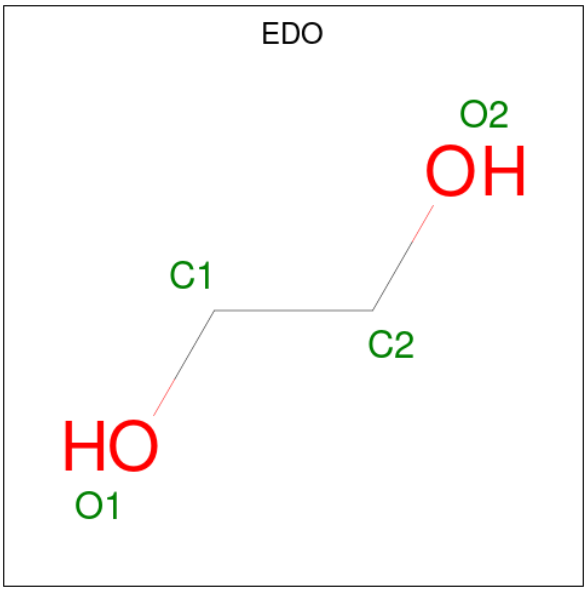
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 6 4 2	0	0
6	B	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	F	1	Total C O 6 4 2	0	0
6	G	1	Total C O 6 4 2	0	0
6	G	1	Total C O 6 4 2	0	0
6	G	1	Total C O 6 4 2	0	0
6	G	1	Total C O 6 4 2	0	0
6	G	1	Total C O 6 4 2	0	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).

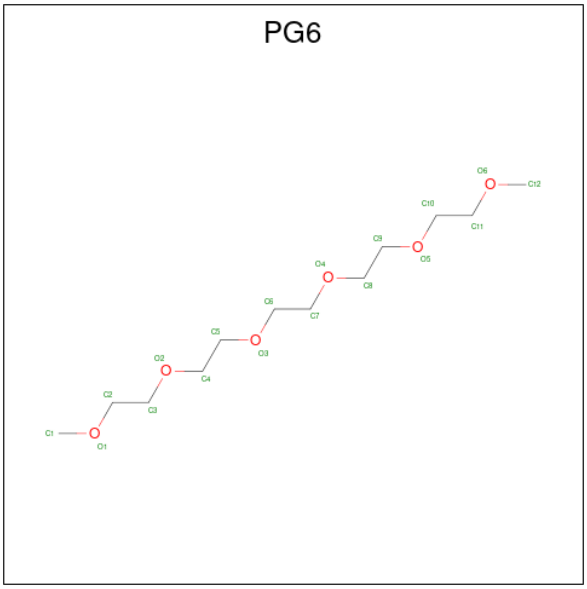


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	F	1	Total C O 4 2 2	0	0
7	F	1	Total C O 4 2 2	0	0
7	F	1	Total C O 4 2 2	0	0
7	F	1	Total C O 4 2 2	0	0
7	G	1	Total C O 4 2 2	0	0

- Molecule 8 is POTASSIUM ION (three-letter code: K) (formula: K).

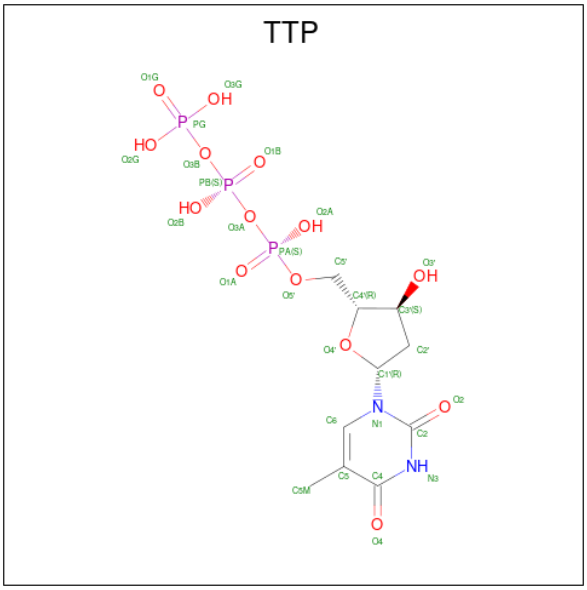
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	3	Total K 3 3	0	0
8	B	2	Total K 2 2	0	0
8	D	2	Total K 2 2	0	0
8	F	2	Total K 2 2	0	0
8	G	2	Total K 2 2	0	0

- Molecule 9 is 1-(2-METHOXY-ETHOXY)-2-{2-[2-(2-METHOXY-ETHOXY]-ETHOXY}-ETHANE (three-letter code: PG6) (formula: $C_{12}H_{26}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C O 18 12 6	0	0
9	G	1	Total C O 18 12 6	0	0

- Molecule 10 is THYMIDINE-5'-TRIPHOSPHATE (three-letter code: TTP) (formula: $C_{10}H_{17}N_2O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	F	1	Total	C	N	O	P	0	0
			29	10	2	14	3		

- Molecule 11 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	F	1	Total	Cl	0	0
			1	1		
11	G	1	Total	Cl	0	0
			1	1		

- Molecule 12 is water.

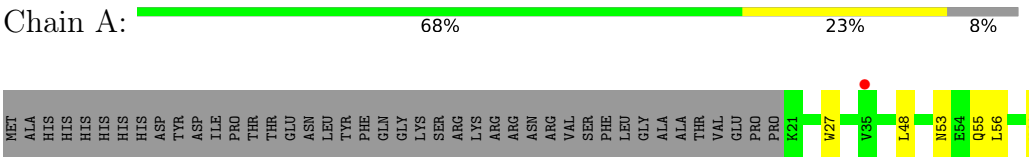
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	90	Total	O	0	0
			90	90		
12	B	54	Total	O	0	0
			54	54		
12	D	4	Total	O	0	0
			4	4		
12	E	1	Total	O	0	0
			1	1		
12	F	75	Total	O	0	0
			75	75		
12	G	58	Total	O	0	0
			58	58		
12	H	2	Total	O	0	0
			2	2		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

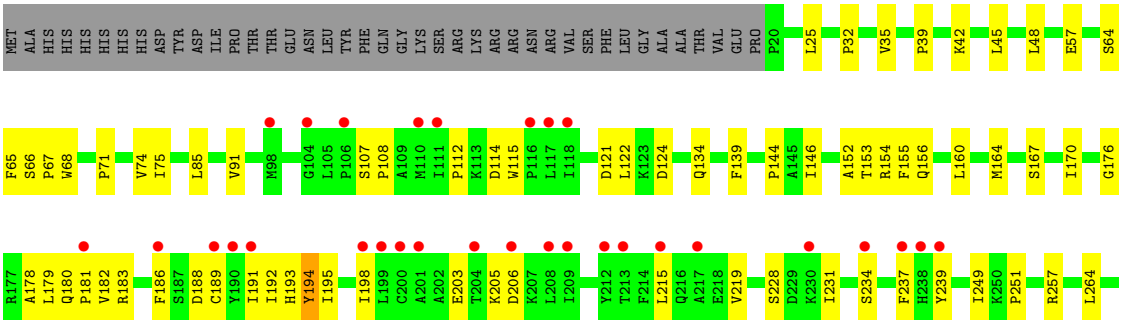
• Molecule 1: Polymerase

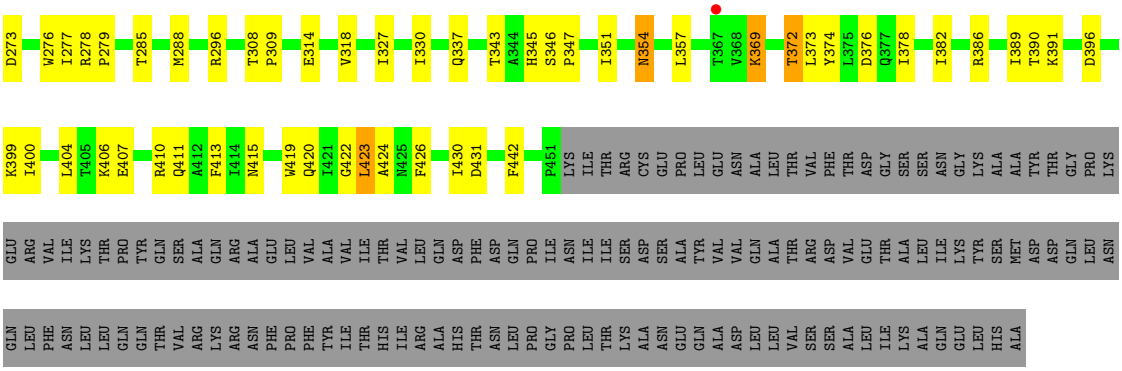
Chain A:



• Molecule 1: Polymerase

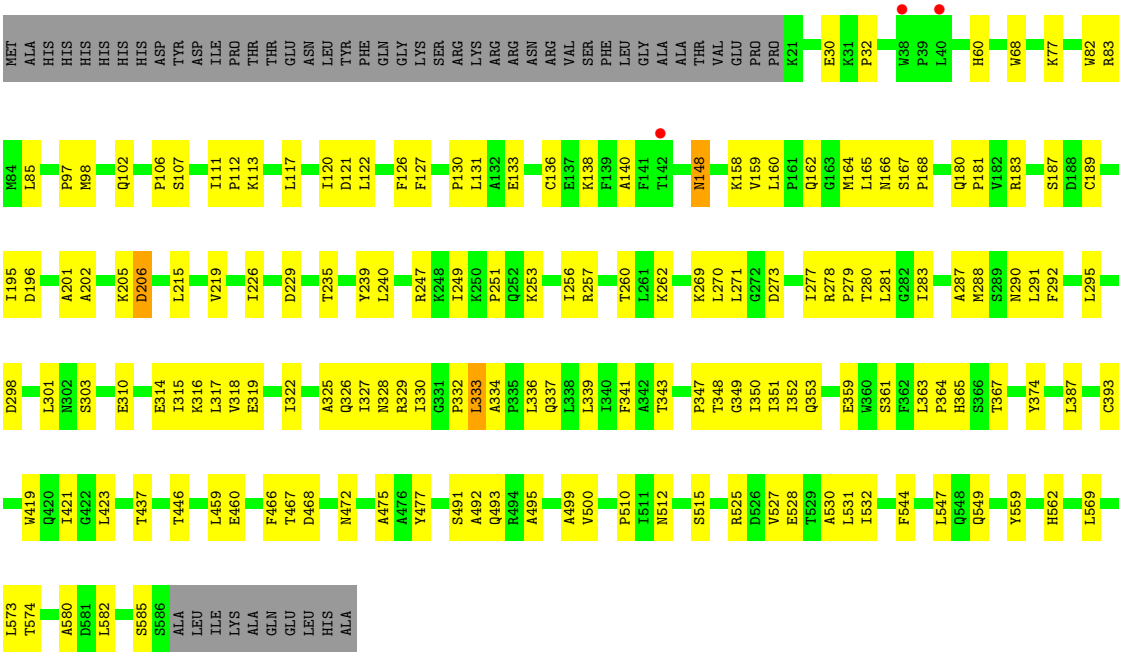
Chain B:





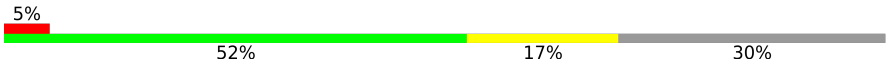
• Molecule 1: Polymerase

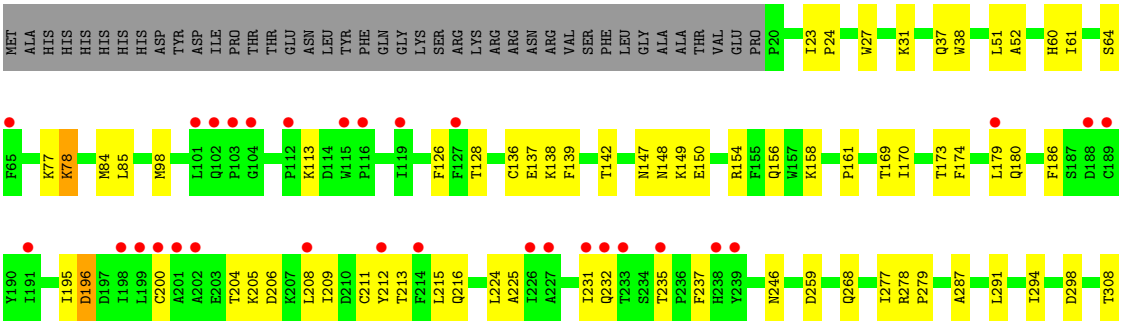
Chain F:

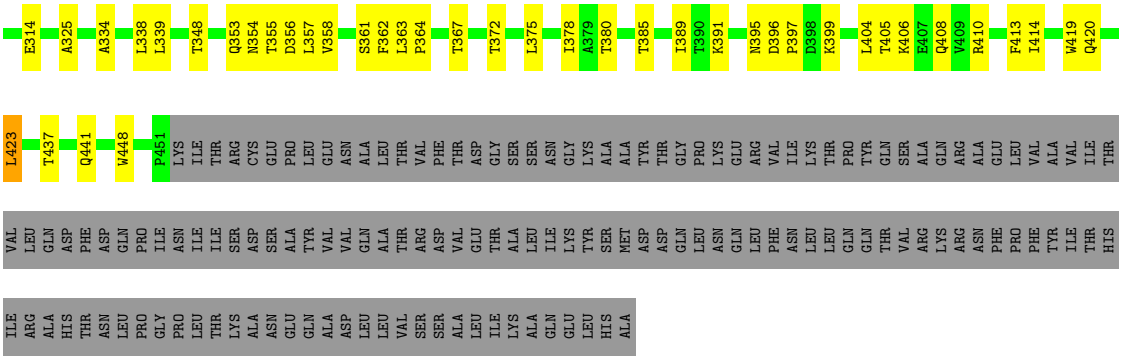


• Molecule 1: Polymerase

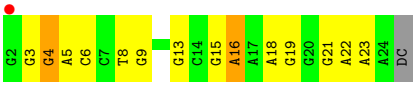
Chain G:



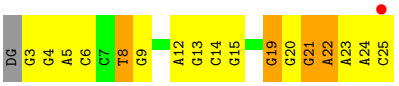




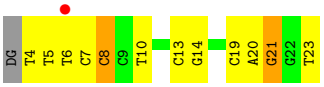
• Molecule 2: DNA (5'-D(P*GP*GP*GP*AP*CP*CP*TP*GP*AP*AP*AP*GP*CP*GP*AP*A P*AP*GP*GP*GP*AP*AP*A)-3')



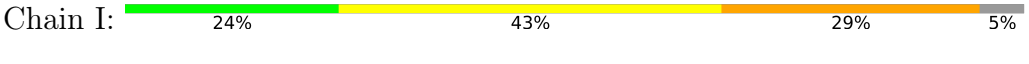
• Molecule 2: DNA (5'-D(P*GP*GP*GP*AP*CP*CP*TP*GP*AP*AP*AP*GP*CP*GP*AP*A P*AP*GP*GP*GP*AP*AP*A)-3')

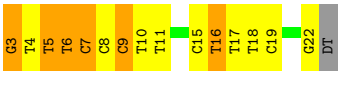


• Molecule 3: DNA (5'-D(P*TP*TP*TP*TP*CP*CP*CP*TP*TP*TP*TP*CP*GP*CP*TP*TP*TP*C P*AP*GP*GP*T)-3')



• Molecule 3: DNA (5'-D(P*TP*TP*TP*TP*CP*CP*CP*TP*TP*TP*TP*CP*GP*CP*TP*TP*TP*C P*AP*GP*GP*T)-3')





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	177.70Å 177.70Å 117.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	88.85 – 2.62 88.85 – 2.62	Depositor EDS
% Data completeness (in resolution range)	91.8 (88.85-2.62) 92.6 (88.85-2.62)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.20 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.168 , 0.218 0.174 , 0.215	Depositor DCC
R_{free} test set	5690 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	70.4	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 52.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.54$, $< L^2 > = 0.38$	Xtriage
Estimated twinning fraction	0.207 for -h,-k,l 0.000 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
Reported twinning fraction	0.499 for H, K, L 0.501 for -h,-k,l	Depositor
Outliers	0 of 115355 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	18265	wwPDB-VP
Average B, all atoms (Å^2)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, DCP, EDO, PG6, K, MG, DIO, TTP

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	0.65	0/4618	0.82	2/6297 (0.0%)
1	B	0.67	0/3517	0.81	0/4795
1	F	0.65	1/4621 (0.0%)	0.82	0/6302
1	G	0.69	1/3522 (0.0%)	0.81	1/4808 (0.0%)
2	D	0.91	0/549	1.55	6/847 (0.7%)
2	H	0.96	0/545	1.47	6/840 (0.7%)
3	E	0.97	0/443	1.61	5/680 (0.7%)
3	I	0.95	0/447	1.54	9/687 (1.3%)
All	All	0.70	2/18262 (0.0%)	0.94	29/25256 (0.1%)

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	2
1	F	0	2
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	31	LYS	CE-NZ	-10.46	1.23	1.49
1	F	205	LYS	CD-CE	-5.22	1.38	1.51

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	4	DG	P-O3'-C3'	-8.52	109.47	119.70
3	E	20	DA	P-O3'-C3'	-8.26	109.79	119.70
3	E	10	DT	P-O3'-C3'	-7.24	111.01	119.70
2	H	22	DA	C6-N1-C2	-7.20	114.28	118.60
3	I	15	DC	P-O3'-C3'	-7.10	111.18	119.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	354	ASN	Mainchain
1	B	194	TYR	Mainchain
1	B	423	LEU	Mainchain
1	F	235	THR	Peptide
1	F	530	ALA	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4507	0	4584	108	0
1	B	3423	0	3454	90	0
1	F	4510	0	4583	133	0
1	G	3428	0	3458	86	0
2	D	485	0	255	10	0
2	H	482	0	255	21	0
3	E	400	0	229	12	0
3	I	403	0	230	20	0
4	A	2	0	0	0	0
4	D	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
5	A	28	0	12	1	0
6	A	30	0	40	1	0
6	B	66	0	88	10	0
6	F	78	0	104	10	0
6	G	30	0	40	12	0
7	A	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	4	0	6	0	0
7	F	16	0	24	0	0
7	G	4	0	6	0	0
8	A	3	0	0	0	0
8	B	2	0	0	0	0
8	D	2	0	0	0	0
8	F	2	0	0	0	0
8	G	2	0	0	0	0
9	B	18	0	26	2	0
9	G	18	0	26	2	0
10	F	29	0	13	4	0
11	F	1	0	0	0	0
11	G	1	0	0	0	0
12	A	90	0	0	11	0
12	B	54	0	0	5	0
12	D	4	0	0	0	0
12	E	1	0	0	0	0
12	F	75	0	0	7	0
12	G	58	0	0	5	0
12	H	2	0	0	0	0
All	All	18265	0	17439	457	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 13.

The worst 5 of 457 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:F:247:ARG:HB3	12:F:753:HOH:O	1.44	1.15
1:F:206:ASP:HB3	12:F:769:HOH:O	1.65	0.96
1:G:98:MET:H	1:G:169[A]:THR:HG21	1.39	0.88
2:H:23:DA:H2"	2:H:24:DA:OP2	1.77	0.84
1:B:372:THR:HG23	12:B:735:HOH:O	1.82	0.80

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	567/618 (92%)	548 (97%)	19 (3%)	0	100 100
1	B	432/618 (70%)	418 (97%)	14 (3%)	0	100 100
1	F	568/618 (92%)	543 (96%)	24 (4%)	1 (0%)	47 69
1	G	434/618 (70%)	417 (96%)	17 (4%)	0	100 100
All	All	2001/2472 (81%)	1926 (96%)	74 (4%)	1 (0%)	51 100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	195	ILE

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	500/549 (91%)	488 (98%)	12 (2%)	49 72
1	B	370/549 (67%)	357 (96%)	13 (4%)	36 60
1	F	500/549 (91%)	487 (97%)	13 (3%)	46 70
1	G	374/549 (68%)	363 (97%)	11 (3%)	42 67
All	All	1744/2196 (79%)	1695 (97%)	49 (3%)	43 68

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	206	ASP
1	F	437	THR
1	F	229	ASP
1	F	280	THR
1	F	525	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	60	HIS
1	F	243	GLN
1	F	354	ASN
1	F	326	GLN
1	A	243	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 63 ligands modelled in this entry, 18 are monoatomic - leaving 45 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	$\#\|Z\|>2$
6	DIO	G	606	-	6,6,6	0.27	0	6,6,6	0.23	0
6	DIO	F	601	-	6,6,6	0.18	0	6,6,6	0.23	0
6	DIO	F	613	-	6,6,6	0.13	0	6,6,6	0.20	0
9	PG6	G	602	-	17,17,17	0.41	0	16,16,16	0.22	0
6	DIO	B	610	-	6,6,6	0.46	0	6,6,6	0.38	0
6	DIO	F	611	-	6,6,6	0.22	0	6,6,6	0.29	0
7	EDO	F	607	-	3,3,3	0.07	0	2,2,2	0.11	0
6	DIO	B	609	-	6,6,6	0.05	0	6,6,6	0.24	0
6	DIO	F	612	-	6,6,6	0.25	0	6,6,6	0.22	0
6	DIO	A	606	-	6,6,6	0.32	0	6,6,6	0.17	0
6	DIO	F	618	-	6,6,6	0.32	0	6,6,6	0.25	0
7	EDO	F	615	-	3,3,3	0.14	0	2,2,2	0.31	0
6	DIO	B	602	-	6,6,6	0.20	0	6,6,6	0.28	0
6	DIO	A	605	-	6,6,6	0.29	0	6,6,6	0.09	0
6	DIO	F	614	-	6,6,6	0.20	0	6,6,6	0.15	0
6	DIO	A	604	-	6,6,6	0.49	0	6,6,6	0.24	0
6	DIO	F	616	-	6,6,6	0.10	0	6,6,6	0.25	0
6	DIO	A	603	-	6,6,6	0.27	0	6,6,6	0.24	0
6	DIO	F	610	-	6,6,6	0.15	0	6,6,6	0.17	0
7	EDO	F	606	-	3,3,3	0.09	0	2,2,2	0.11	0
6	DIO	B	606	-	6,6,6	0.39	0	6,6,6	0.18	0
6	DIO	F	619	-	6,6,6	0.37	0	6,6,6	0.23	0
9	PG6	B	605	-	17,17,17	0.37	0	16,16,16	0.21	0
7	EDO	G	607	-	3,3,3	0.15	0	2,2,2	0.23	0
7	EDO	B	613	-	3,3,3	0.10	0	2,2,2	0.18	0
6	DIO	F	604	-	6,6,6	0.18	0	6,6,6	0.23	0
6	DIO	B	603	-	6,6,6	0.23	0	6,6,6	0.20	0
6	DIO	B	612	-	6,6,6	0.31	0	6,6,6	0.18	0
5	DCP	A	602	4	25,29,29	0.49	0	37,45,45	0.66	0
10	TTP	F	605	4	26,30,30	0.53	0	39,47,47	0.85	1 (2%)
6	DIO	F	603	-	6,6,6	0.33	0	6,6,6	0.19	0
6	DIO	A	607	-	6,6,6	0.25	0	6,6,6	0.12	0
7	EDO	A	608	-	3,3,3	0.08	0	2,2,2	0.20	0
6	DIO	F	609	-	6,6,6	0.19	0	6,6,6	0.34	0
7	EDO	F	608	-	3,3,3	0.37	0	2,2,2	0.35	0
6	DIO	G	605	-	6,6,6	0.41	0	6,6,6	0.15	0
6	DIO	B	607	-	6,6,6	0.31	0	6,6,6	0.29	0
6	DIO	F	617	-	6,6,6	0.11	0	6,6,6	0.18	0
6	DIO	G	604	-	6,6,6	0.29	0	6,6,6	0.11	0
6	DIO	B	611	-	6,6,6	0.24	0	6,6,6	0.24	0
6	DIO	G	603	-	6,6,6	0.31	0	6,6,6	0.17	0
6	DIO	B	608	-	6,6,6	0.19	0	6,6,6	0.29	0
6	DIO	G	601	-	6,6,6	0.37	0	6,6,6	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	DIO	B	601	-	6,6,6	0.43	0	6,6,6	0.22	0
6	DIO	B	604	-	6,6,6	0.20	0	6,6,6	0.19	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	DIO	G	606	-	-	-	0/1/1/1
6	DIO	F	601	-	-	-	0/1/1/1
6	DIO	F	613	-	-	-	0/1/1/1
9	PG6	G	602	-	-	8/15/15/15	-
6	DIO	B	610	-	-	-	0/1/1/1
6	DIO	F	611	-	-	-	0/1/1/1
7	EDO	F	607	-	-	0/1/1/1	-
6	DIO	B	609	-	-	-	0/1/1/1
6	DIO	F	612	-	-	-	0/1/1/1
6	DIO	A	606	-	-	-	0/1/1/1
6	DIO	F	618	-	-	-	0/1/1/1
7	EDO	F	615	-	-	1/1/1/1	-
6	DIO	B	602	-	-	-	0/1/1/1
6	DIO	A	605	-	-	-	0/1/1/1
6	DIO	F	614	-	-	-	0/1/1/1
6	DIO	A	604	-	-	-	0/1/1/1
6	DIO	F	616	-	-	-	0/1/1/1
7	EDO	F	606	-	-	0/1/1/1	-
6	DIO	A	603	-	-	-	0/1/1/1
6	DIO	F	610	-	-	-	0/1/1/1
6	DIO	B	606	-	-	-	0/1/1/1
9	PG6	B	605	-	-	11/15/15/15	-
6	DIO	F	619	-	-	-	0/1/1/1
7	EDO	G	607	-	-	1/1/1/1	-
7	EDO	B	613	-	-	1/1/1/1	-
6	DIO	F	604	-	-	-	0/1/1/1
6	DIO	B	603	-	-	-	0/1/1/1
6	DIO	B	612	-	-	-	0/1/1/1
5	DCP	A	602	4	-	2/22/34/34	0/2/2/2
10	TTP	F	605	4	-	4/22/34/34	0/2/2/2
6	DIO	F	603	-	-	-	0/1/1/1
6	DIO	A	607	-	-	-	0/1/1/1
7	EDO	A	608	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	DIO	F	609	-	-	-	0/1/1/1
7	EDO	F	608	-	-	1/1/1/1	-
6	DIO	G	605	-	-	-	0/1/1/1
6	DIO	B	607	-	-	-	0/1/1/1
6	DIO	F	617	-	-	-	0/1/1/1
6	DIO	G	604	-	-	-	0/1/1/1
6	DIO	B	611	-	-	-	0/1/1/1
6	DIO	G	603	-	-	-	0/1/1/1
6	DIO	B	608	-	-	-	0/1/1/1
6	DIO	G	601	-	-	-	0/1/1/1
6	DIO	B	601	-	-	-	0/1/1/1
6	DIO	B	604	-	-	-	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	F	605	TTP	PB-O3B-PG	-2.97	122.62	132.83

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	G	602	PG6	O2-C4-C5-O3
9	B	605	PG6	O5-C10-C11-O6
9	G	602	PG6	O4-C8-C9-O5
9	B	605	PG6	O2-C4-C5-O3
9	G	602	PG6	O3-C6-C7-O4

There are no ring outliers.

21 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	G	606	DIO	3	0
6	F	613	DIO	2	0
9	G	602	PG6	2	0
6	F	611	DIO	1	0
6	B	602	DIO	1	0
6	F	616	DIO	3	0
6	A	603	DIO	1	0
6	B	606	DIO	1	0

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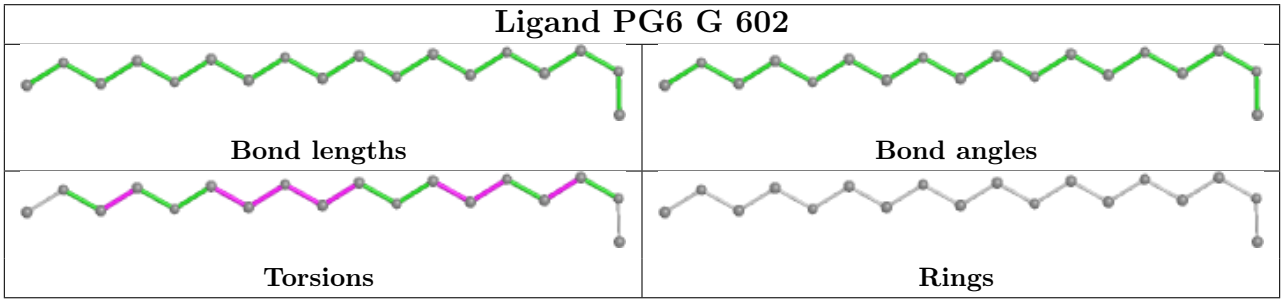
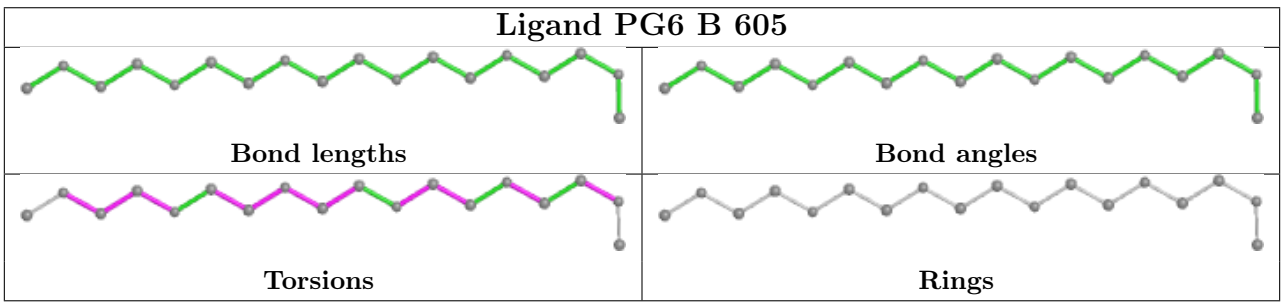
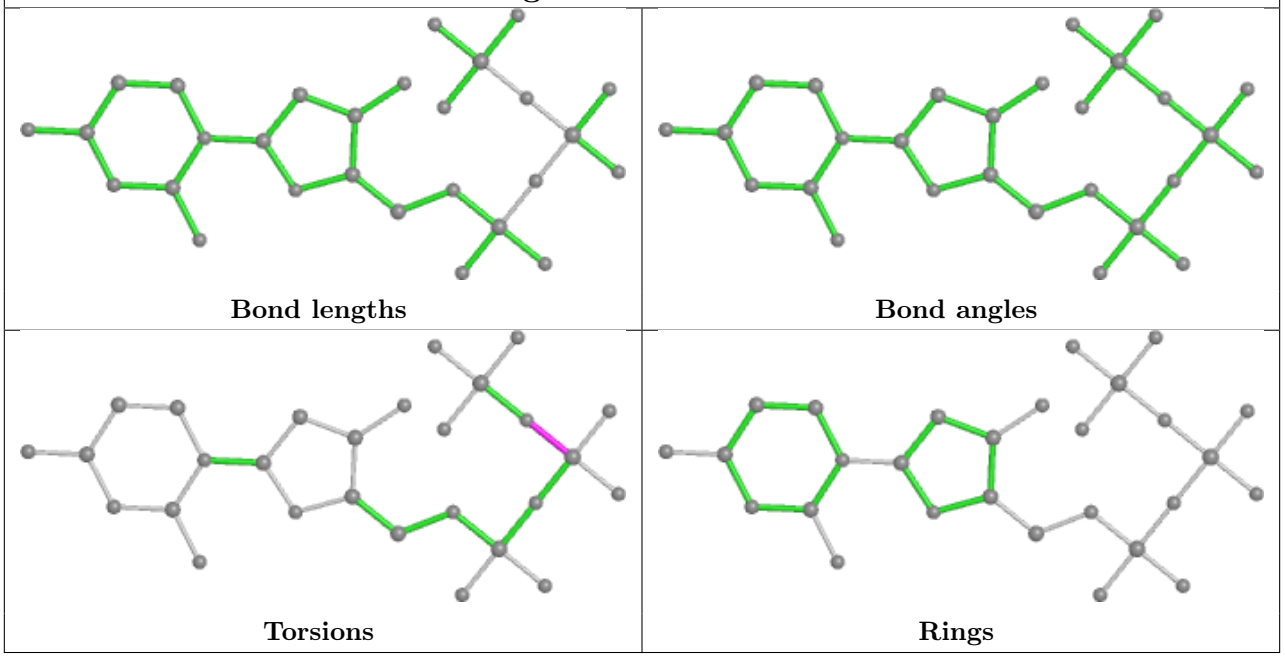
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	605	PG6	2	0
6	F	604	DIO	3	0
6	B	603	DIO	1	0
5	A	602	DCP	1	0
10	F	605	TTP	4	0
6	G	605	DIO	1	0
6	B	607	DIO	2	0
6	F	617	DIO	1	0
6	G	604	DIO	1	0
6	B	611	DIO	1	0
6	B	608	DIO	1	0
6	G	601	DIO	7	0
6	B	604	DIO	3	0

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

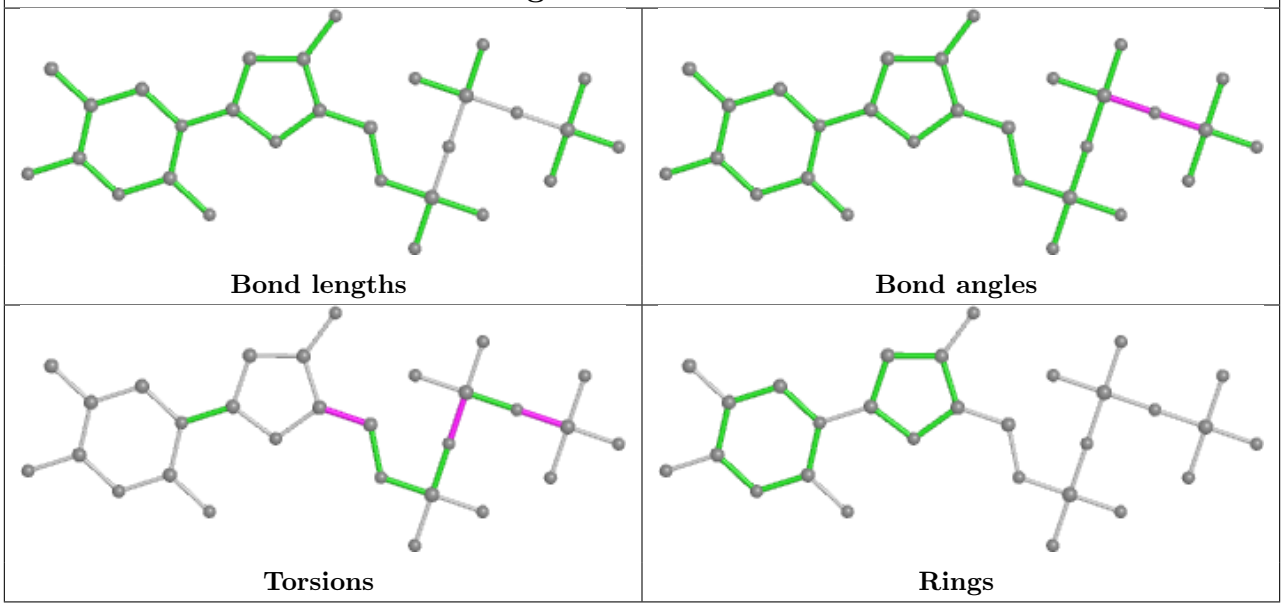




Ligand DCP A 602



Ligand TTP F 605



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	566/618 (91%)	0.06	2 (0%) 92 91	45, 73, 101, 127	15 (2%)
1	B	432/618 (69%)	0.37	31 (7%) 15 11	47, 75, 140, 173	16 (3%)
1	F	566/618 (91%)	0.02	3 (0%) 91 89	40, 72, 98, 129	8 (1%)
1	G	432/618 (69%)	0.36	30 (6%) 16 12	45, 74, 134, 165	11 (2%)
2	D	23/24 (95%)	-0.23	1 (4%) 35 29	47, 77, 137, 158	0
2	H	23/24 (95%)	-0.22	1 (4%) 35 29	57, 75, 131, 186	0
3	E	20/21 (95%)	-0.21	1 (5%) 28 23	52, 78, 183, 187	0
3	I	20/21 (95%)	-0.56	0 100 100	53, 82, 140, 163	0
All	All	2082/2562 (81%)	0.16	69 (3%) 46 40	40, 74, 125, 187	50 (2%)

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	239	TYR	8.0
1	B	201	ALA	5.3
2	H	25	DC	5.1
1	G	201	ALA	5.0
1	B	198	ILE	4.5

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	EDO	F	615	4/4	0.85	0.38	52,58,58,63	4
8	K	G	610	1/1	0.86	0.07	85,85,85,85	0
8	K	F	621	1/1	0.87	0.10	95,95,95,95	0
11	CL	F	620	1/1	0.87	0.15	85,85,85,85	0
8	K	G	609	1/1	0.90	0.09	81,81,81,81	0
6	DIO	F	611	6/6	0.91	0.39	32,38,42,42	6
8	K	A	610	1/1	0.91	0.18	71,71,71,71	0
6	DIO	F	603	6/6	0.92	0.26	39,53,62,63	6
6	DIO	A	605	6/6	0.92	0.48	52,57,65,69	6
8	K	A	611	1/1	0.92	0.08	101,101,101,101	0
6	DIO	F	618	6/6	0.92	0.25	48,54,55,62	6
6	DIO	F	619	6/6	0.92	0.35	22,25,27,27	6
7	EDO	A	608	4/4	0.92	0.25	61,68,68,71	4
7	EDO	F	607	4/4	0.92	0.18	74,77,82,83	0
6	DIO	B	603	6/6	0.93	0.23	44,51,65,69	6
7	EDO	B	613	4/4	0.93	0.09	87,89,92,92	0
9	PG6	G	602	18/18	0.93	0.18	63,80,91,94	0
7	EDO	G	607	4/4	0.93	0.24	55,56,63,71	4
6	DIO	F	609	6/6	0.94	0.30	42,45,56,59	6
6	DIO	G	604	6/6	0.94	0.23	53,58,65,68	6
8	K	B	614	1/1	0.94	0.11	92,92,92,92	0
6	DIO	F	610	6/6	0.94	0.26	41,48,50,51	6
6	DIO	B	608	6/6	0.94	0.31	30,37,39,40	6
6	DIO	F	612	6/6	0.94	0.29	38,42,43,46	6
6	DIO	F	616	6/6	0.94	0.31	48,57,60,61	6
6	DIO	A	604	6/6	0.94	0.13	60,62,70,70	0
8	K	D	101	1/1	0.95	0.14	64,64,64,64	0
6	DIO	A	607	6/6	0.95	0.20	45,53,58,65	6
6	DIO	G	606	6/6	0.95	0.28	44,51,53,61	6
6	DIO	F	617	6/6	0.95	0.25	48,56,61,61	6
6	DIO	B	604	6/6	0.95	0.35	39,44,53,56	6
6	DIO	F	614	6/6	0.95	0.20	41,51,54,60	6
8	K	B	615	1/1	0.96	0.07	84,84,84,84	0
7	EDO	F	608	4/4	0.96	0.19	48,52,53,57	0
6	DIO	A	606	6/6	0.96	0.24	43,46,54,55	6
6	DIO	F	613	6/6	0.96	0.33	40,45,52,53	6
6	DIO	F	601	6/6	0.96	0.16	54,57,63,68	0

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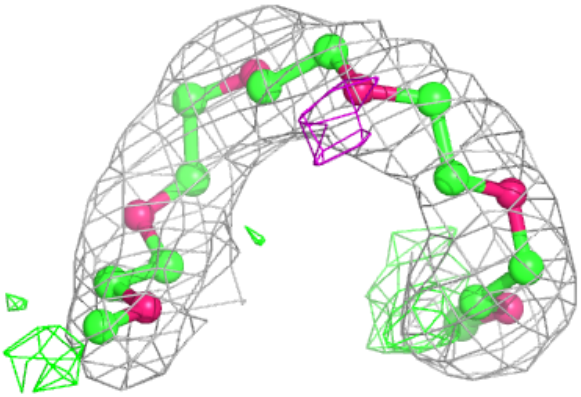
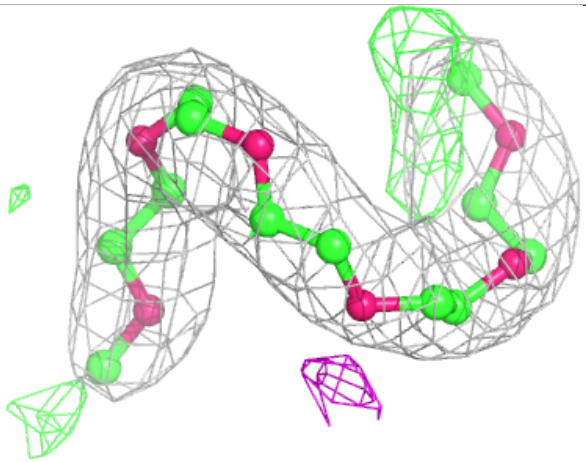
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
9	PG6	B	605	18/18	0.96	0.15	56,74,100,108	0
7	EDO	F	606	4/4	0.96	0.22	72,72,73,80	0
4	MG	A	612	1/1	0.96	0.22	45,45,45,45	1
6	DIO	B	602	6/6	0.97	0.28	32,37,39,43	6
6	DIO	B	609	6/6	0.97	0.20	39,46,51,52	6
6	DIO	B	610	6/6	0.97	0.11	57,62,74,75	0
6	DIO	B	612	6/6	0.97	0.23	57,64,77,77	0
6	DIO	G	601	6/6	0.97	0.26	23,25,27,29	6
6	DIO	G	603	6/6	0.97	0.29	57,62,69,69	0
4	MG	D	103	1/1	0.97	0.12	67,67,67,67	0
6	DIO	G	605	6/6	0.97	0.13	57,60,72,74	0
4	MG	G	611	1/1	0.97	0.25	69,69,69,69	0
4	MG	A	601	1/1	0.98	0.16	62,62,62,62	0
5	DCP	A	602	28/28	0.98	0.14	43,57,85,100	0
6	DIO	B	606	6/6	0.98	0.21	60,69,77,81	0
6	DIO	F	604	6/6	0.98	0.22	51,59,70,71	0
8	K	D	102	1/1	0.98	0.10	60,60,60,60	0
6	DIO	B	607	6/6	0.98	0.10	60,70,77,81	0
6	DIO	A	603	6/6	0.98	0.17	46,59,65,70	0
6	DIO	B	601	6/6	0.98	0.17	54,56,69,72	0
4	MG	F	602	1/1	0.98	0.15	60,60,60,60	0
8	K	A	609	1/1	0.98	0.23	92,92,92,92	0
10	TTP	F	605	29/29	0.98	0.15	48,69,82,89	0
6	DIO	B	611	6/6	0.98	0.28	60,65,70,74	0
8	K	F	622	1/1	0.99	0.21	84,84,84,84	0
11	CL	G	608	1/1	0.99	0.12	71,71,71,71	0

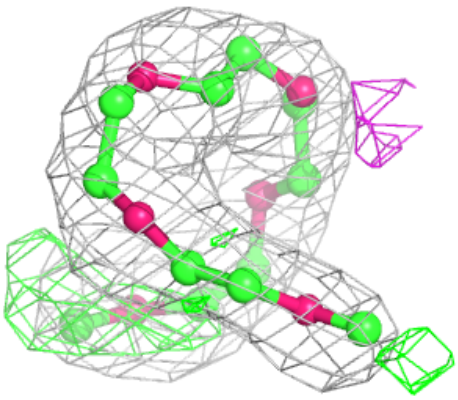
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PG6 G 602:

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

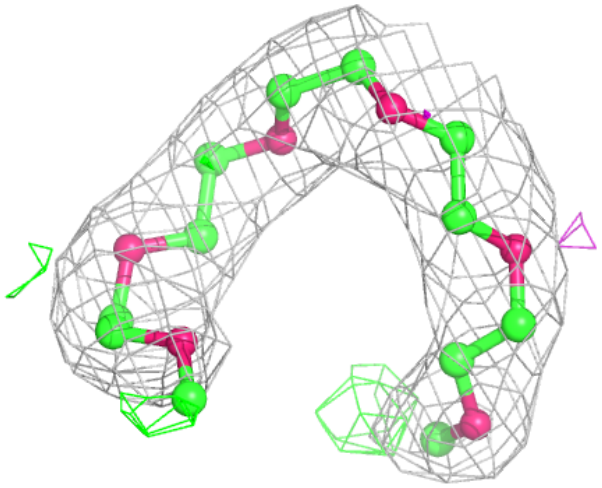


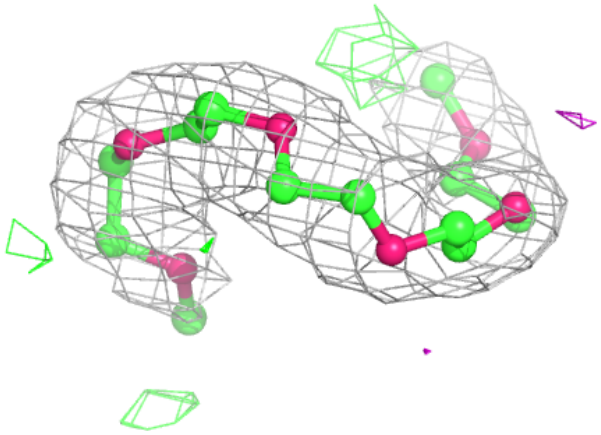


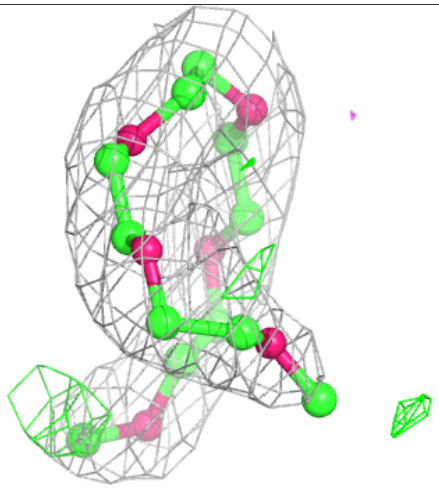


Electron density around PG6 B 605:

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

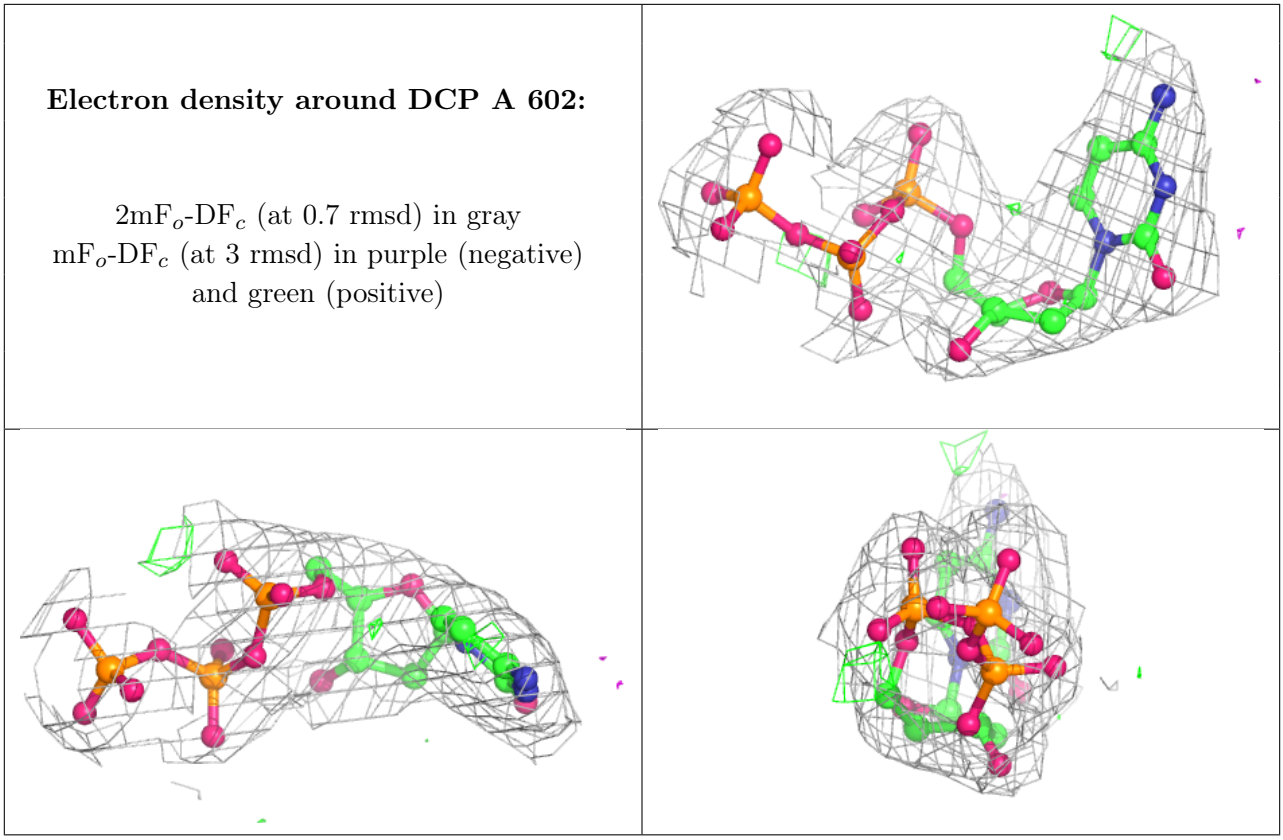






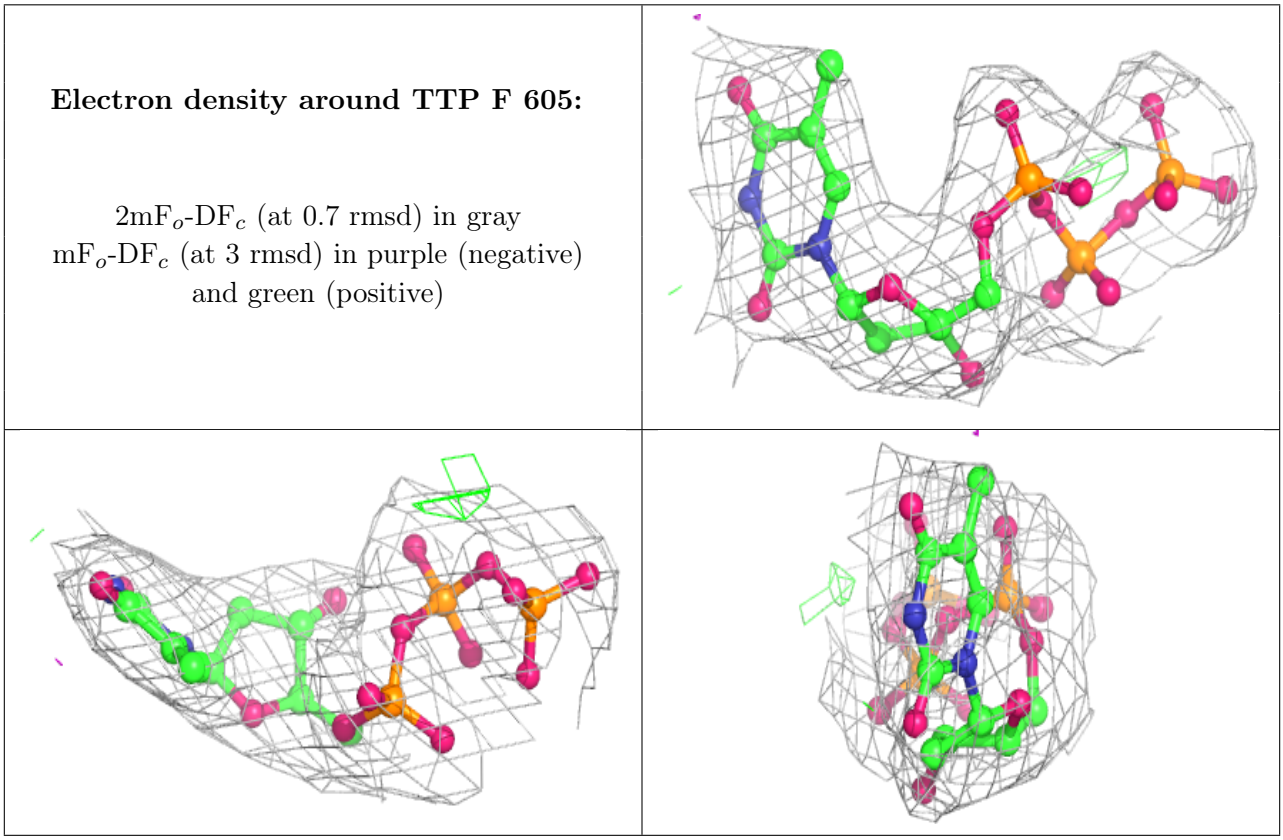
Electron density around DCP A 602:

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



Electron density around TTP F 605:

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



6.5 Other polymers (i)

There are no such residues in this entry.