



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 08:07 pm BST

PDB ID : 4QG1
Title : Crystal structure of the tetrameric GTP/dATP-bound SAMHD1 (RN206) mutant catalytic core
Authors : Koharudin, L.M.I.; Wu, Y.; DeLucia, M.; Mehrens, J.; Gronenborn, A.M.; Ahn, J.
Deposited on : 2014-05-22
Resolution : 2.20 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

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

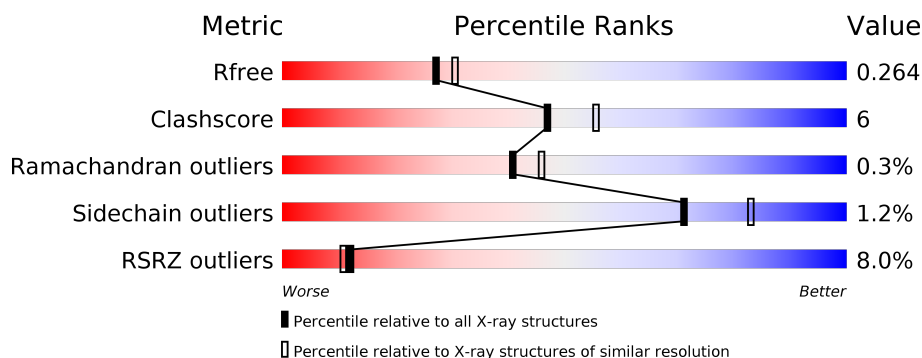
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 ≥ 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	550	<div> <div>8%</div> <div> <div></div> <div>74%</div> <div>13%</div> <div>•</div> <div>13%</div> </div> </div>
1	B	550	<div> <div>7%</div> <div> <div></div> <div>75%</div> <div>12%</div> <div>•</div> <div>13%</div> </div> </div>
1	C	550	<div> <div>9%</div> <div> <div></div> <div>76%</div> <div>11%</div> <div>•</div> <div>13%</div> </div> </div>
1	D	550	<div> <div>4%</div> <div> <div></div> <div>77%</div> <div>9%</div> <div>•</div> <div>13%</div> </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 16302 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 Deoxynucleoside triphosphate triphosphohydrolase SAMHD1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	481	Total	C	N	O	S	0	0	0
			3933	2517	685	711	20			
1	B	481	Total	C	N	O	S	0	0	0
			3933	2517	685	711	20			
1	C	481	Total	C	N	O	S	0	0	0
			3933	2517	685	711	20			
1	D	481	Total	C	N	O	S	0	1	0
			3940	2522	687	711	20			

There are 152 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
A	78	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	79	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	80	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	81	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	82	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	83	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	84	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	85	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	86	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	87	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	88	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	89	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	90	LEU	-	EXPRESSION TAG	UNP Q9Y3Z3
A	91	VAL	-	EXPRESSION TAG	UNP Q9Y3Z3
A	92	PRO	-	EXPRESSION TAG	UNP Q9Y3Z3
A	93	ARG	-	EXPRESSION TAG	UNP Q9Y3Z3
A	94	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	95	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	96	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	97	MET	-	EXPRESSION TAG	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	98	ALA	-	EXPRESSION TAG	UNP Q9Y3Z3
A	99	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	100	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
A	101	THR	-	EXPRESSION TAG	UNP Q9Y3Z3
A	102	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	103	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	104	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
A	105	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
A	106	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
A	107	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	108	ARG	-	EXPRESSION TAG	UNP Q9Y3Z3
A	109	ASP	-	EXPRESSION TAG	UNP Q9Y3Z3
A	110	PRO	-	EXPRESSION TAG	UNP Q9Y3Z3
A	111	ASN	-	EXPRESSION TAG	UNP Q9Y3Z3
A	112	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	206	ARG	HIS	ENGINEERED MUTATION	UNP Q9Y3Z3
A	207	ASN	ASP	ENGINEERED MUTATION	UNP Q9Y3Z3
B	77	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
B	78	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	79	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	80	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	81	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	82	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	83	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	84	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	85	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	86	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	87	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	88	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	89	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	90	LEU	-	EXPRESSION TAG	UNP Q9Y3Z3
B	91	VAL	-	EXPRESSION TAG	UNP Q9Y3Z3
B	92	PRO	-	EXPRESSION TAG	UNP Q9Y3Z3
B	93	ARG	-	EXPRESSION TAG	UNP Q9Y3Z3
B	94	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	95	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	96	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	97	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
B	98	ALA	-	EXPRESSION TAG	UNP Q9Y3Z3
B	99	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	100	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
B	101	THR	-	EXPRESSION TAG	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	102	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	103	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	104	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
B	105	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
B	106	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
B	107	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	108	ARG	-	EXPRESSION TAG	UNP Q9Y3Z3
B	109	ASP	-	EXPRESSION TAG	UNP Q9Y3Z3
B	110	PRO	-	EXPRESSION TAG	UNP Q9Y3Z3
B	111	ASN	-	EXPRESSION TAG	UNP Q9Y3Z3
B	112	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	206	ARG	HIS	ENGINEERED MUTATION	UNP Q9Y3Z3
B	207	ASN	ASP	ENGINEERED MUTATION	UNP Q9Y3Z3
C	77	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
C	78	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
C	79	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
C	80	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
C	81	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
C	82	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
C	83	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
C	84	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
C	85	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
C	86	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
C	87	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
C	88	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
C	89	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
C	90	LEU	-	EXPRESSION TAG	UNP Q9Y3Z3
C	91	VAL	-	EXPRESSION TAG	UNP Q9Y3Z3
C	92	PRO	-	EXPRESSION TAG	UNP Q9Y3Z3
C	93	ARG	-	EXPRESSION TAG	UNP Q9Y3Z3
C	94	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
C	95	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
C	96	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
C	97	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
C	98	ALA	-	EXPRESSION TAG	UNP Q9Y3Z3
C	99	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
C	100	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
C	101	THR	-	EXPRESSION TAG	UNP Q9Y3Z3
C	102	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
C	103	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
C	104	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
C	105	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3

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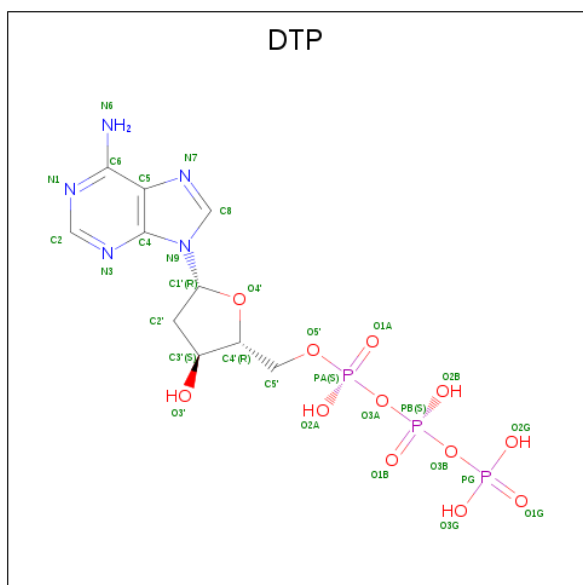
Chain	Residue	Modelled	Actual	Comment	Reference
C	106	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
C	107	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
C	108	ARG	-	EXPRESSION TAG	UNP Q9Y3Z3
C	109	ASP	-	EXPRESSION TAG	UNP Q9Y3Z3
C	110	PRO	-	EXPRESSION TAG	UNP Q9Y3Z3
C	111	ASN	-	EXPRESSION TAG	UNP Q9Y3Z3
C	112	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
C	206	ARG	HIS	ENGINEERED MUTATION	UNP Q9Y3Z3
C	207	ASN	ASP	ENGINEERED MUTATION	UNP Q9Y3Z3
D	77	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
D	78	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
D	79	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
D	80	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
D	81	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
D	82	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
D	83	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
D	84	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
D	85	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
D	86	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
D	87	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
D	88	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
D	89	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
D	90	LEU	-	EXPRESSION TAG	UNP Q9Y3Z3
D	91	VAL	-	EXPRESSION TAG	UNP Q9Y3Z3
D	92	PRO	-	EXPRESSION TAG	UNP Q9Y3Z3
D	93	ARG	-	EXPRESSION TAG	UNP Q9Y3Z3
D	94	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
D	95	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
D	96	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
D	97	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
D	98	ALA	-	EXPRESSION TAG	UNP Q9Y3Z3
D	99	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
D	100	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
D	101	THR	-	EXPRESSION TAG	UNP Q9Y3Z3
D	102	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
D	103	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
D	104	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
D	105	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
D	106	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
D	107	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
D	108	ARG	-	EXPRESSION TAG	UNP Q9Y3Z3
D	109	ASP	-	EXPRESSION TAG	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	110	PRO	-	EXPRESSION TAG	UNP Q9Y3Z3
D	111	ASN	-	EXPRESSION TAG	UNP Q9Y3Z3
D	112	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
D	206	ARG	HIS	ENGINEERED MUTATION	UNP Q9Y3Z3
D	207	ASN	ASP	ENGINEERED MUTATION	UNP Q9Y3Z3

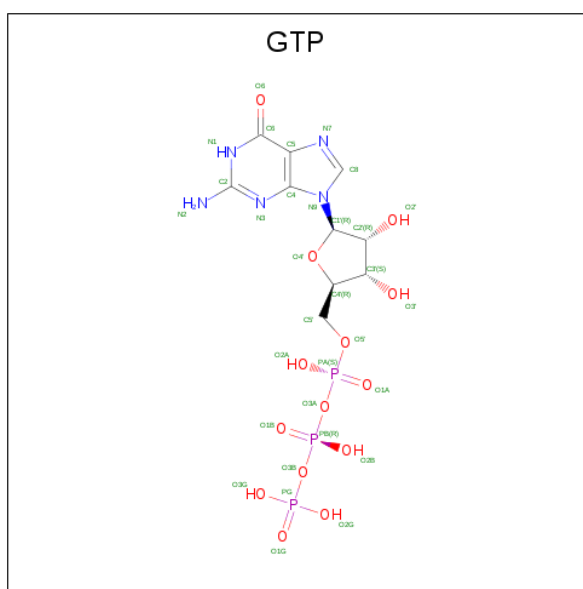
- Molecule 2 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (three-letter code: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$).



- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	D	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
4	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
4	D	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
4	D	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	37	Total	O	0	0
			37	37		

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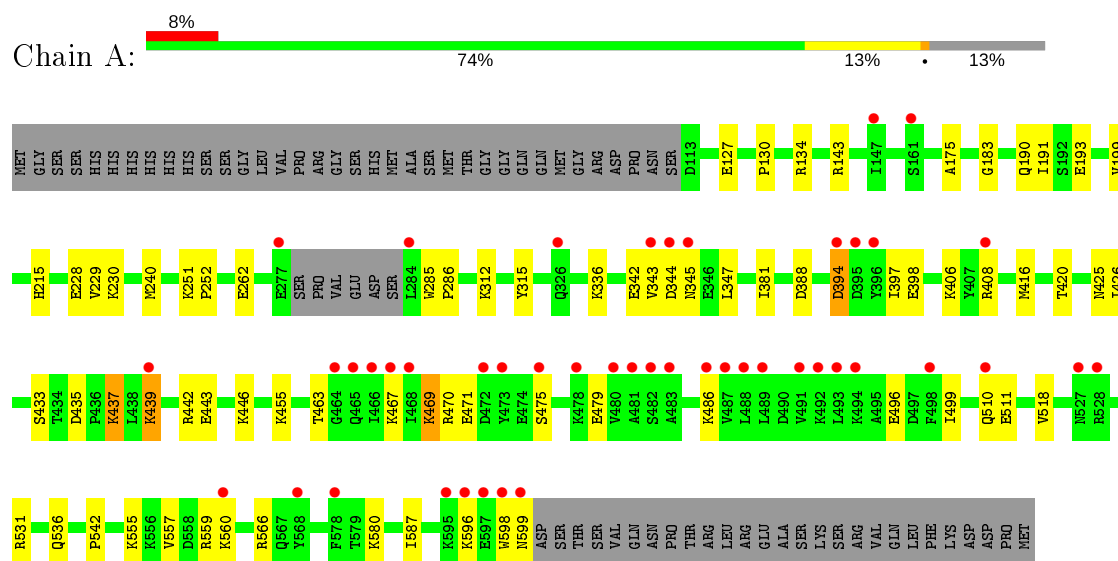
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	56	Total 56	O 56	0	0
5	C	38	Total 38	O 38	0	0
5	D	60	Total 60	O 60	0	0

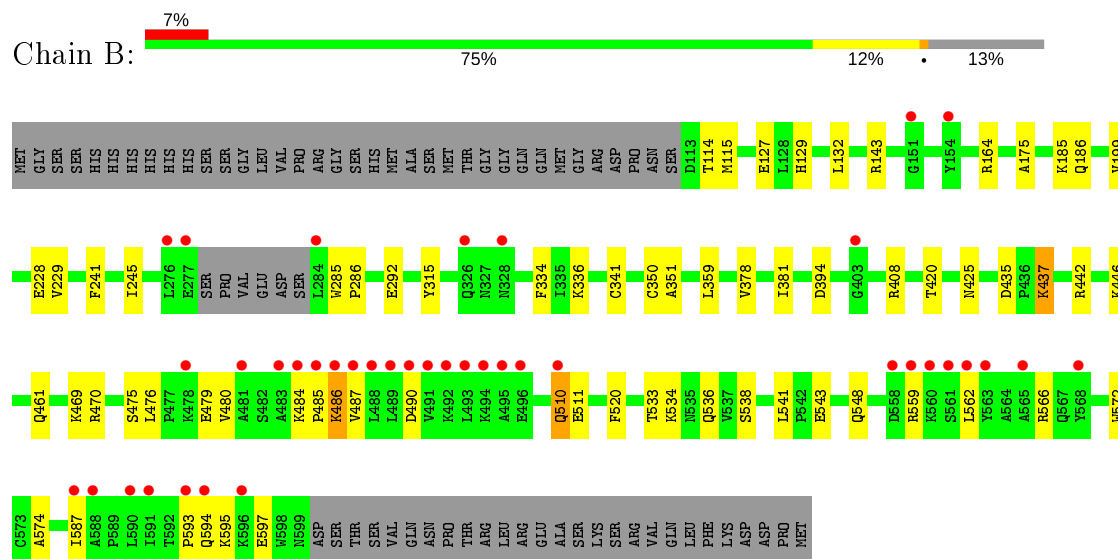
3 Residue-property plots

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.

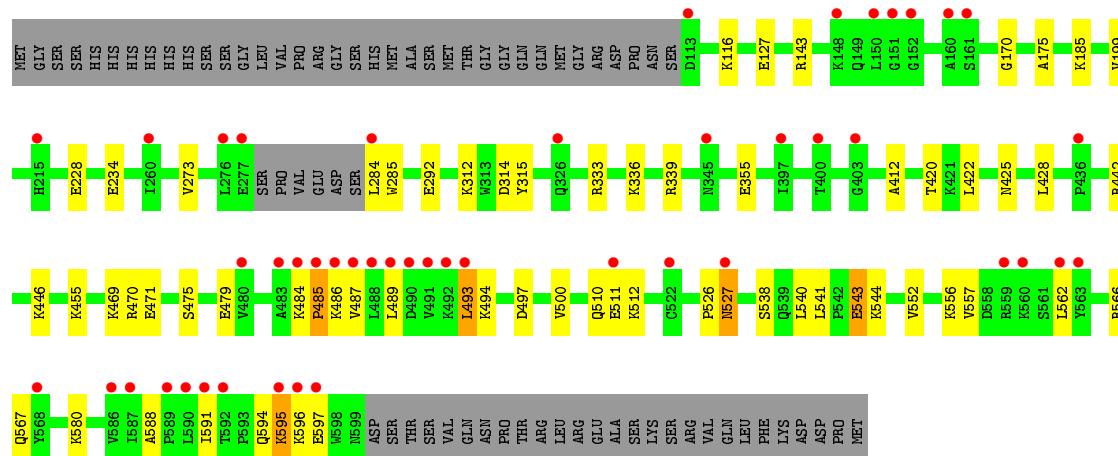
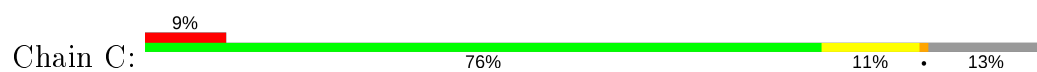
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



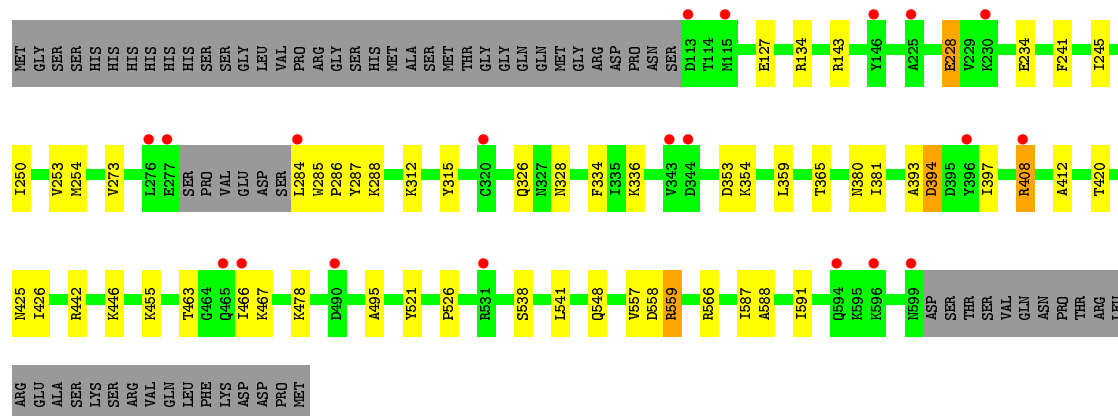
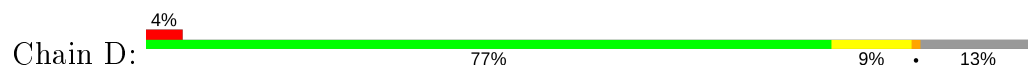
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.69Å 146.72Å 99.26Å 90.00° 114.76° 90.00°	Depositor
Resolution (Å)	42.99 – 2.20 42.99 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.2 (42.99-2.20) 93.9 (42.99-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496, REFMAC 5.5.0109	Depositor
R, R_{free}	0.214 , 0.264 0.215 , 0.264	Depositor DCC
R_{free} test set	2002 reflections (1.75%)	wwPDB-VP
Wilson B-factor (Å ²)	48.3	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.008 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16302	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, DTP

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	0.33	0/4025	0.58	0/5433
1	B	0.30	0/4025	0.53	0/5433
1	C	0.31	0/4025	0.55	1/5433 (0.0%)
1	D	0.32	0/4036	0.59	3/5448 (0.1%)
All	All	0.32	0/16111	0.56	4/21747 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	408	ARG	NE-CZ-NH1	-10.40	115.10	120.30
1	D	408	ARG	NE-CZ-NH2	7.00	123.80	120.30
1	C	596	LYS	N-CA-C	5.23	125.11	111.00
1	D	394	ASP	CB-CG-OD1	-5.07	113.73	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3933	0	3919	61	0
1	B	3933	0	3921	40	0
1	C	3933	0	3919	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3940	0	3926	51	0
2	A	60	0	24	3	0
2	B	60	0	24	2	0
2	C	60	0	24	1	0
2	D	60	0	24	1	0
3	A	2	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	32	0	11	2	0
4	C	32	0	11	1	0
4	D	64	0	22	1	0
5	A	37	0	0	0	0
5	B	56	0	0	0	0
5	C	38	0	0	0	0
5	D	60	0	0	1	0
All	All	16302	0	15825	198	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (198) 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:A:510:GLN:HG2	1:A:511:GLU:H	1.12	1.14
1:D:397:ILE:O	1:D:408:ARG:NH1	1.92	1.02
1:C:469:LYS:HD2	1:C:470:ARG:H	1.41	0.85
1:A:439:LYS:HE3	1:A:443:GLU:HG2	1.60	0.83
1:A:510:GLN:HG2	1:A:511:GLU:N	1.95	0.80
1:A:397:ILE:HG21	1:A:426:ILE:HD11	1.64	0.78
1:C:485:PRO:HB3	1:C:489:LEU:HD21	1.65	0.77
1:A:435:ASP:OD2	1:A:437:LYS:HG3	1.90	0.72
1:C:455:LYS:HG2	1:C:557:VAL:HG12	1.71	0.71
1:D:234:GLU:HB3	1:D:273:VAL:HG22	1.71	0.71
1:B:469:LYS:HD2	1:B:470:ARG:H	1.55	0.70
1:A:559:ARG:HH21	1:A:560:LYS:NZ	1.91	0.68
1:B:574:ALA:O	1:B:595:LYS:NZ	2.18	0.68
1:C:527:ASN:HD22	1:C:527:ASN:N	1.91	0.67
1:A:510:GLN:CG	1:A:511:GLU:H	1.94	0.66
1:D:328:ASN:OD1	1:D:365:THR:OG1	2.10	0.66
1:A:559:ARG:HH21	1:A:560:LYS:HZ2	1.41	0.66
1:D:393:ALA:O	1:D:408:ARG:NH2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:245:ILE:HD12	1:D:250:ILE:HD11	1.78	0.65
1:A:469:LYS:HB2	1:A:471:GLU:HG2	1.78	0.65
1:C:493:LEU:HD11	1:C:556:LYS:HD2	1.78	0.64
1:A:398:GLU:CD	1:A:406:LYS:HE3	2.18	0.64
1:A:475:SER:O	1:A:479:GLU:HG3	1.99	0.62
1:A:408:ARG:HB3	1:A:408:ARG:CZ	2.29	0.62
1:A:455:LYS:HG2	1:A:557:VAL:HG12	1.82	0.62
1:B:486:LYS:HG3	1:B:486:LYS:O	2.00	0.62
1:C:339:ARG:HH21	1:C:527:ASN:ND2	1.99	0.60
1:D:397:ILE:C	1:D:408:ARG:HH12	2.04	0.60
1:B:425:ASN:OD1	1:C:425:ASN:ND2	2.33	0.60
1:D:285:TRP:O	1:D:288:LYS:NZ	2.32	0.60
1:B:574:ALA:HA	1:B:595:LYS:HE2	1.84	0.59
1:C:336:LYS:HE3	1:D:127:GLU:HG3	1.85	0.58
1:B:484:LYS:HD2	1:B:485:PRO:HD2	1.85	0.58
1:B:484:LYS:HD2	1:B:485:PRO:CD	2.34	0.58
1:C:442:ARG:O	1:C:446:LYS:HG3	2.03	0.57
1:A:394:ASP:O	1:A:408:ARG:NH1	2.26	0.57
1:C:493:LEU:HG	1:C:497:ASP:CB	2.35	0.57
1:D:467:LYS:HE3	1:D:548:GLN:HG3	1.86	0.57
1:C:475:SER:O	1:C:479:GLU:HG3	2.05	0.56
1:C:484:LYS:HB2	1:C:486:LYS:NZ	2.19	0.56
1:D:287:TYR:O	1:D:288:LYS:HD3	2.05	0.56
1:B:461:GLN:HG3	1:B:548:GLN:O	2.06	0.56
1:C:127:GLU:HG3	1:D:336:LYS:HE3	1.88	0.56
1:A:425:ASN:ND2	1:D:425:ASN:OD1	2.39	0.56
1:D:241:PHE:O	1:D:245:ILE:HG12	2.06	0.55
1:A:394:ASP:C	1:A:408:ARG:HH12	2.08	0.55
1:A:580:LYS:HG3	1:A:598:TRP:CE3	2.41	0.55
1:D:442:ARG:O	1:D:446:LYS:HG3	2.08	0.54
1:A:439:LYS:CE	1:A:443:GLU:HG2	2.34	0.53
1:A:518:VAL:O	1:A:531:ARG:NH1	2.41	0.53
1:B:538:SER:HB3	1:B:541:LEU:HG	1.90	0.53
1:D:397:ILE:HB	1:D:408:ARG:HH22	1.73	0.53
1:C:543:GLU:HG2	1:C:544:LYS:HG3	1.91	0.53
1:A:536:GLN:HE21	1:C:580:LYS:HB3	1.74	0.53
1:C:484:LYS:HB2	1:C:486:LYS:HE2	1.90	0.53
1:C:442:ARG:HG2	1:C:446:LYS:HE2	1.90	0.52
1:A:394:ASP:C	1:A:408:ARG:HH22	2.13	0.52
1:C:484:LYS:HB2	1:C:486:LYS:CE	2.40	0.52
1:C:588:ALA:HB1	1:C:591:ILE:HD13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:397:ILE:CA	1:D:408:ARG:HH12	2.22	0.52
1:D:588:ALA:HB1	1:D:591:ILE:HD13	1.91	0.52
1:B:534:LYS:NZ	1:B:543:GLU:OE2	2.43	0.51
1:C:469:LYS:HD2	1:C:470:ARG:N	2.19	0.51
1:B:442:ARG:O	1:B:446:LYS:HG3	2.11	0.51
1:C:526:PRO:C	1:C:527:ASN:HD22	2.15	0.50
1:B:484:LYS:NZ	1:B:487:VAL:O	2.44	0.50
1:D:394:ASP:HA	1:D:408:ARG:HE	1.76	0.50
1:C:486:LYS:HD3	1:C:486:LYS:N	2.27	0.50
1:A:433:SER:OG	1:A:442:ARG:NH1	2.43	0.50
1:A:580:LYS:HD2	1:A:598:TRP:HB3	1.94	0.50
1:C:284:LEU:HD23	1:C:284:LEU:O	2.12	0.50
1:C:469:LYS:HZ2	1:C:471:GLU:HG3	1.76	0.50
1:D:250:ILE:HD12	1:D:254:MET:HG3	1.94	0.50
1:A:342:GLU:HG2	1:A:347:LEU:CD2	2.42	0.49
1:C:339:ARG:NH2	1:C:527:ASN:ND2	2.60	0.49
1:A:397:ILE:H	1:A:408:ARG:HH21	1.60	0.49
1:B:435:ASP:OD2	1:B:437:LYS:HE2	2.12	0.49
1:A:439:LYS:HD3	1:A:442:ARG:NH2	2.28	0.49
1:C:185:LYS:HB3	1:C:185:LYS:HE2	1.66	0.48
1:D:538:SER:HB3	1:D:541:LEU:HG	1.96	0.48
1:C:285:TRP:CD2	1:C:292:GLU:HG2	2.49	0.48
1:C:487:VAL:HG21	1:C:567:GLN:HG3	1.94	0.48
1:A:439:LYS:HD3	1:A:442:ARG:CZ	2.43	0.48
1:A:439:LYS:HD2	1:A:442:ARG:HB3	1.96	0.48
1:C:510:GLN:HG3	1:C:511:GLU:H	1.77	0.48
1:D:284:LEU:HG	1:D:285:TRP:H	1.78	0.48
1:B:378:VAL:O	1:B:381:ILE:HG22	2.14	0.48
1:A:486:LYS:HB3	1:A:486:LYS:HE2	1.46	0.48
1:B:479:GLU:HG2	1:B:572:TRP:HE1	1.79	0.48
1:A:343:VAL:O	1:A:345:ASN:N	2.47	0.47
1:A:336:LYS:HE3	1:B:127:GLU:HG3	1.96	0.47
1:C:594:GLN:O	1:C:595:LYS:O	2.30	0.47
1:A:215:HIS:NE2	2:A:701:DTP:O2A	2.43	0.47
1:C:333:ARG:NE	1:C:355:GLU:OE2	2.48	0.47
1:C:339:ARG:NH2	1:C:527:ASN:HD21	2.12	0.47
1:D:397:ILE:HG21	1:D:426:ILE:HD11	1.96	0.47
1:B:562:LEU:HD21	1:B:566:ARG:NH2	2.29	0.47
1:D:394:ASP:O	1:D:408:ARG:NE	2.48	0.47
1:D:455:LYS:HG2	1:D:557:VAL:HG12	1.97	0.47
1:C:469:LYS:NZ	1:C:471:GLU:HG3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:ALA:HB1	1:A:199:VAL:HG12	1.95	0.47
4:B:701:GTP:O1G	1:C:116:LYS:NZ	2.41	0.47
1:A:531:ARG:HH11	1:A:531:ARG:HG2	1.80	0.46
1:B:566:ARG:HD3	1:B:587:ILE:HB	1.97	0.46
1:B:597:GLU:CD	1:B:597:GLU:H	2.18	0.46
1:A:381:ILE:HA	1:A:381:ILE:HD12	1.76	0.46
1:C:175:ALA:HB1	1:C:199:VAL:HG12	1.97	0.46
1:D:381:ILE:HD12	1:D:381:ILE:HA	1.78	0.46
1:A:398:GLU:HB3	1:A:406:LYS:HD2	1.97	0.46
1:B:510:GLN:HB3	1:B:511:GLU:H	1.48	0.46
1:D:287:TYR:C	1:D:288:LYS:HD3	2.35	0.46
1:A:127:GLU:HG3	1:B:336:LYS:HE3	1.98	0.46
1:B:241:PHE:O	1:B:245:ILE:HG12	2.16	0.45
1:B:593:PRO:C	1:B:595:LYS:H	2.20	0.45
1:C:597:GLU:HG3	1:C:597:GLU:O	2.16	0.45
1:B:341:CYS:HB2	1:B:350:CYS:SG	2.56	0.45
1:A:312:LYS:HA	1:A:315:TYR:CE2	2.51	0.45
1:A:439:LYS:HD3	1:A:442:ARG:NE	2.32	0.45
1:D:463:THR:O	1:D:466:ILE:HG22	2.16	0.45
1:A:342:GLU:HG2	1:A:347:LEU:HD21	1.98	0.45
1:B:175:ALA:HB1	1:B:199:VAL:HG12	1.99	0.45
1:B:285:TRP:CG	1:B:292:GLU:HG2	2.52	0.45
1:D:241:PHE:CZ	1:D:245:ILE:HD11	2.52	0.45
1:D:285:TRP:HA	1:D:286:PRO:HD3	1.83	0.44
1:D:380:ASN:OD1	5:D:834:HOH:O	2.20	0.44
1:D:566:ARG:HD3	1:D:587:ILE:HB	1.99	0.44
1:C:234:GLU:HB3	1:C:273:VAL:HG23	1.99	0.44
1:A:566:ARG:HD3	1:A:587:ILE:HB	2.00	0.44
1:B:394:ASP:O	1:B:408:ARG:HD2	2.18	0.44
1:A:215:HIS:HE2	2:A:701:DTP:PA	2.40	0.44
1:A:397:ILE:N	1:A:408:ARG:HH21	2.15	0.44
1:B:114:THR:OG1	1:B:115:MET:N	2.51	0.44
1:C:494:LYS:HB3	1:C:494:LYS:HE3	1.70	0.44
1:B:228:GLU:HG2	1:B:229:VAL:N	2.32	0.44
1:A:442:ARG:O	1:A:446:LYS:HG3	2.18	0.43
1:D:408:ARG:O	1:D:412:ALA:N	2.51	0.43
1:D:394:ASP:HA	1:D:408:ARG:HH21	1.83	0.43
1:C:500:VAL:HG22	1:C:552:VAL:HG22	1.99	0.43
1:D:284:LEU:HG	1:D:285:TRP:N	2.34	0.43
1:D:397:ILE:HB	1:D:408:ARG:HH12	1.84	0.43
1:B:129:HIS:HB3	1:B:132:LEU:HG	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:701:DTP:O1B	4:D:701:GTP:H5"	2.19	0.43
1:D:467:LYS:HD2	1:D:467:LYS:HA	1.68	0.43
1:A:439:LYS:HD2	1:A:439:LYS:HA	1.51	0.43
1:B:285:TRP:HA	1:B:286:PRO:HD3	1.86	0.42
1:B:594:GLN:O	1:B:594:GLN:HG3	2.19	0.42
1:A:499:ILE:HD11	1:A:555:LYS:HE2	2.01	0.42
1:C:143:ARG:HD2	1:C:420:THR:HA	2.01	0.42
1:A:536:GLN:NE2	1:C:580:LYS:HD3	2.35	0.42
1:D:228:GLU:H	1:D:228:GLU:HG3	1.32	0.42
1:A:240:MET:HG2	1:A:416:MET:SD	2.59	0.42
1:C:562:LEU:O	1:C:566:ARG:HG3	2.18	0.42
1:D:353:ASP:OD1	1:D:354:LYS:N	2.47	0.42
1:A:542:PRO:HB3	1:C:540:LEU:O	2.19	0.42
1:A:580:LYS:HA	1:A:598:TRP:CZ2	2.55	0.42
1:D:143:ARG:HD2	1:D:420:THR:HA	2.02	0.42
1:A:130:PRO:O	1:A:134:ARG:HG2	2.20	0.41
1:A:183:GLY:HA2	1:A:191:ILE:HD12	2.00	0.41
1:A:143:ARG:HD2	1:A:420:THR:HA	2.01	0.41
1:C:170:GLY:HA3	1:C:314:ASP:OD2	2.19	0.41
1:C:512:LYS:HA	1:C:512:LYS:HD3	1.75	0.41
1:B:476:LEU:O	1:B:480:VAL:HG23	2.20	0.41
1:C:484:LYS:HA	1:C:485:PRO:HD3	1.76	0.41
1:D:326:GLN:HE21	1:D:326:GLN:HB2	1.68	0.41
1:A:496:GLU:O	1:A:555:LYS:HD2	2.20	0.41
1:B:185:LYS:HG3	1:B:186:GLN:HG3	2.01	0.41
1:B:143:ARG:HD2	1:B:420:THR:HA	2.02	0.41
1:B:351:ALA:O	1:B:520:PHE:HA	2.19	0.41
4:B:701:GTP:H5"	2:D:702:DTP:O1B	2.20	0.41
1:C:412:ALA:HB3	1:C:422:LEU:HD22	2.02	0.41
1:D:467:LYS:HE3	1:D:548:GLN:CG	2.48	0.41
1:A:398:GLU:HB3	1:A:406:LYS:CD	2.51	0.41
1:D:312:LYS:HA	1:D:315:TYR:CE2	2.56	0.41
1:A:471:GLU:HG2	1:A:471:GLU:H	1.61	0.41
1:B:334:PHE:CE1	1:B:359:LEU:HD21	2.56	0.41
1:A:285:TRP:HA	1:A:286:PRO:HD3	1.94	0.41
1:C:228:GLU:H	1:C:228:GLU:HG3	1.48	0.41
1:D:334:PHE:CE2	1:D:359:LEU:HD21	2.55	0.41
1:D:559:ARG:HG3	1:D:559:ARG:H	1.41	0.41
1:A:251:LYS:HB2	1:A:252:PRO:HD3	2.02	0.41
1:C:494:LYS:HG2	1:C:497:ASP:OD2	2.21	0.41
1:D:558:ASP:HB2	1:D:559:ARG:NH1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:428:LEU:HA	1:C:428:LEU:HD23	1.90	0.41
1:A:193:GLU:CD	1:A:193:GLU:H	2.16	0.41
1:B:315:TYR:CD2	2:B:702:DTP:H5'1	2.55	0.41
2:A:702:DTP:O1B	4:C:702:GTP:H5''	2.21	0.40
1:B:533:THR:OG1	1:B:536:GLN:HG3	2.20	0.40
1:C:538:SER:HB3	1:C:541:LEU:HG	2.02	0.40
1:A:228:GLU:HG2	1:A:229:VAL:N	2.36	0.40
1:B:164:ARG:HH22	2:B:702:DTP:H4'	1.85	0.40
1:C:312:LYS:HA	1:C:315:TYR:CE2	2.56	0.40
1:D:134:ARG:NH2	1:D:253:VAL:HG22	2.36	0.40
1:D:408:ARG:HA	1:D:408:ARG:HD2	1.60	0.40
1:D:478:LYS:HG3	1:D:495:ALA:CB	2.52	0.40
1:D:241:PHE:CE1	1:D:245:ILE:HD11	2.56	0.40
1:A:467:LYS:HD2	1:A:467:LYS:N	2.35	0.40
1:D:521:TYR:CD1	1:D:526:PRO:HA	2.57	0.40
1:D:397:ILE:HB	1:D:408:ARG:NH2	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	477/550 (87%)	460 (96%)	15 (3%)	2 (0%)	34	37
1	B	477/550 (87%)	461 (97%)	15 (3%)	1 (0%)	47	55
1	C	477/550 (87%)	457 (96%)	18 (4%)	2 (0%)	34	37
1	D	478/550 (87%)	461 (96%)	17 (4%)	0	100	100
All	All	1909/2200 (87%)	1839 (96%)	65 (3%)	5 (0%)	41	46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	344	ASP
1	C	485	PRO
1	C	595	LYS
1	A	394	ASP
1	B	490	ASP

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	427/488 (88%)	416 (97%)	11 (3%)	46	58
1	B	427/488 (88%)	422 (99%)	5 (1%)	71	83
1	C	427/488 (88%)	424 (99%)	3 (1%)	84	91
1	D	428/488 (88%)	426 (100%)	2 (0%)	88	94
All	All	1709/1952 (88%)	1688 (99%)	21 (1%)	71	83

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	190	GLN
1	A	230	LYS
1	A	262	GLU
1	A	388	ASP
1	A	437	LYS
1	A	439	LYS
1	A	463	THR
1	A	469	LYS
1	A	470	ARG
1	A	596	LYS
1	A	599	ASN
1	B	437	LYS
1	B	475	SER
1	B	486	LYS
1	B	510	GLN
1	B	559	ARG
1	C	493	LEU

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Mol	Chain	Res	Type
1	C	527	ASN
1	C	543	GLU
1	D	228	GLU
1	D	559	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	326	GLN
1	A	425	ASN
1	B	461	GLN
1	C	425	ASN
1	C	527	ASN
1	C	571	GLN
1	C	594	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 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 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
4	GTP	D	703	3	26,34,34	2.33	8 (30%)	33,54,54	1.84	9 (27%)
2	DTP	A	701	-	26,32,32	1.28	4 (15%)	30,50,50	1.58	5 (16%)
2	DTP	B	703	3	26,32,32	1.28	4 (15%)	30,50,50	1.50	4 (13%)
2	DTP	A	702	3	26,32,32	1.26	4 (15%)	30,50,50	1.46	5 (16%)
2	DTP	B	702	-	26,32,32	1.26	3 (11%)	30,50,50	1.66	6 (20%)
4	GTP	C	702	3	26,34,34	2.39	8 (30%)	33,54,54	1.71	9 (27%)
2	DTP	D	702	3	26,32,32	1.31	4 (15%)	30,50,50	1.49	5 (16%)
4	GTP	D	701	3	26,34,34	2.37	7 (26%)	33,54,54	1.70	8 (24%)
2	DTP	C	703	-	26,32,32	1.27	4 (15%)	30,50,50	1.57	5 (16%)
4	GTP	B	701	3	26,34,34	2.37	8 (30%)	33,54,54	1.74	9 (27%)
2	DTP	C	701	3	26,32,32	1.29	4 (15%)	30,50,50	1.46	5 (16%)
2	DTP	D	704	-	26,32,32	1.28	4 (15%)	30,50,50	1.59	5 (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
4	GTP	D	703	3	-	8/18/38/38	0/3/3/3
2	DTP	A	701	-	-	7/18/34/34	0/3/3/3
2	DTP	B	703	3	-	1/18/34/34	0/3/3/3
2	DTP	A	702	3	-	8/18/34/34	0/3/3/3
2	DTP	B	702	-	-	5/18/34/34	0/3/3/3
4	GTP	C	702	3	-	7/18/38/38	0/3/3/3
2	DTP	D	702	3	-	2/18/34/34	0/3/3/3
4	GTP	D	701	3	-	8/18/38/38	0/3/3/3
2	DTP	C	703	-	-	7/18/34/34	0/3/3/3
4	GTP	B	701	3	-	6/18/38/38	0/3/3/3
2	DTP	C	701	3	-	3/18/34/34	0/3/3/3
2	DTP	D	704	-	-	6/18/34/34	0/3/3/3

All (62) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	701	GTP	C2-N2	7.31	1.48	1.33
4	D	701	GTP	C2-N2	7.17	1.48	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	702	GTP	C2-N2	7.10	1.48	1.33
4	D	703	GTP	C2-N2	6.96	1.47	1.33
4	C	702	GTP	O6-C6	6.79	1.41	1.24
4	D	703	GTP	O6-C6	6.77	1.41	1.24
4	D	701	GTP	O6-C6	6.71	1.41	1.24
4	B	701	GTP	O6-C6	6.63	1.41	1.24
4	D	701	GTP	O2'-C2'	-3.30	1.35	1.43
4	B	701	GTP	O2'-C2'	-3.17	1.35	1.43
4	C	702	GTP	O2'-C2'	-3.15	1.35	1.43
4	C	702	GTP	C2'-C1'	-3.11	1.49	1.53
4	D	703	GTP	O2'-C2'	-3.07	1.35	1.43
2	D	702	DTP	O3'-C3'	-2.89	1.37	1.43
4	D	701	GTP	C2'-C1'	-2.83	1.49	1.53
2	C	701	DTP	O3'-C3'	-2.80	1.37	1.43
2	B	702	DTP	C6-N6	2.78	1.44	1.34
2	D	704	DTP	O3'-C3'	-2.77	1.37	1.43
2	B	703	DTP	C6-N6	2.77	1.44	1.34
2	A	702	DTP	C6-N6	2.73	1.44	1.34
4	B	701	GTP	C2'-C1'	-2.73	1.49	1.53
2	D	702	DTP	C6-N6	2.71	1.43	1.34
2	A	701	DTP	C6-N6	2.71	1.43	1.34
2	C	701	DTP	C6-N6	2.70	1.43	1.34
2	B	702	DTP	O3'-C3'	-2.69	1.37	1.43
2	D	704	DTP	C6-N6	2.69	1.43	1.34
2	B	703	DTP	O3'-C3'	-2.68	1.37	1.43
2	A	701	DTP	O3'-C3'	-2.67	1.37	1.43
2	C	701	DTP	C5'-C4'	-2.66	1.43	1.51
4	D	703	GTP	C2'-C1'	-2.65	1.49	1.53
2	C	703	DTP	O3'-C3'	-2.65	1.37	1.43
2	C	703	DTP	C6-N6	2.64	1.43	1.34
2	A	702	DTP	O3'-C3'	-2.61	1.37	1.43
2	B	703	DTP	C5'-C4'	-2.61	1.43	1.51
2	B	702	DTP	C5'-C4'	-2.58	1.43	1.51
2	D	702	DTP	C5'-C4'	-2.56	1.43	1.51
2	A	701	DTP	C5'-C4'	-2.56	1.43	1.51
2	A	702	DTP	C5'-C4'	-2.56	1.43	1.51
2	C	703	DTP	C5'-C4'	-2.51	1.43	1.51
2	D	704	DTP	C5'-C4'	-2.46	1.43	1.51
4	B	701	GTP	C5'-C4'	-2.44	1.44	1.51
4	D	701	GTP	C5'-C4'	-2.40	1.44	1.51
4	C	702	GTP	C2'-C3'	-2.31	1.47	1.53
2	D	704	DTP	C2'-C3'	-2.28	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	701	GTP	C2'-C3'	-2.28	1.47	1.53
4	B	701	GTP	C3'-C4'	-2.27	1.47	1.53
2	D	702	DTP	C2'-C3'	-2.25	1.46	1.52
4	D	701	GTP	C3'-C4'	-2.25	1.47	1.53
2	C	703	DTP	C2'-C3'	-2.24	1.46	1.52
4	C	702	GTP	C3'-C4'	-2.24	1.47	1.53
4	B	701	GTP	C2'-C3'	-2.23	1.47	1.53
4	D	703	GTP	C3'-C4'	-2.23	1.47	1.53
4	C	702	GTP	C5'-C4'	-2.22	1.44	1.51
2	C	701	DTP	C2'-C3'	-2.19	1.47	1.52
4	D	703	GTP	C2'-C3'	-2.17	1.47	1.53
2	A	701	DTP	C2'-C3'	-2.17	1.47	1.52
2	B	703	DTP	C2'-C3'	-2.11	1.47	1.52
2	A	702	DTP	C2'-C3'	-2.10	1.47	1.52
4	D	703	GTP	PG-O2G	-2.05	1.47	1.54
4	D	703	GTP	C5'-C4'	-2.04	1.45	1.51
4	B	701	GTP	PG-O2G	-2.01	1.47	1.54
4	C	702	GTP	PG-O2G	-2.00	1.47	1.54

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	703	DTP	N3-C2-N1	-5.00	120.87	128.68
2	D	702	DTP	N3-C2-N1	-4.94	120.96	128.68
2	B	702	DTP	N3-C2-N1	-4.89	121.04	128.68
2	D	704	DTP	N3-C2-N1	-4.80	121.17	128.68
2	C	703	DTP	N3-C2-N1	-4.73	121.29	128.68
2	A	701	DTP	N3-C2-N1	-4.68	121.37	128.68
2	A	702	DTP	N3-C2-N1	-4.63	121.44	128.68
2	C	701	DTP	N3-C2-N1	-4.58	121.51	128.68
2	B	702	DTP	PA-O3A-PB	-4.42	117.66	132.83
2	A	701	DTP	PA-O3A-PB	-4.06	118.88	132.83
4	D	703	GTP	C5-C6-N1	-4.04	117.90	123.43
4	C	702	GTP	C5-C6-N1	-3.88	118.12	123.43
4	D	701	GTP	C2-N3-C4	3.82	119.72	115.36
4	D	701	GTP	C5-C6-N1	-3.81	118.22	123.43
4	B	701	GTP	C5-C6-N1	-3.75	118.30	123.43
4	D	703	GTP	C2-N3-C4	3.70	119.58	115.36
4	D	701	GTP	N3-C2-N1	-3.67	122.33	127.22
4	D	703	GTP	N3-C2-N1	-3.63	122.38	127.22
4	B	701	GTP	N3-C2-N1	-3.56	122.47	127.22
4	C	702	GTP	N3-C2-N1	-3.56	122.47	127.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	701	GTP	C2-N3-C4	3.53	119.39	115.36
4	C	702	GTP	C2-N3-C4	3.50	119.36	115.36
2	C	703	DTP	PA-O3A-PB	-3.47	120.92	132.83
2	D	704	DTP	PB-O3B-PG	-3.40	121.15	132.83
4	D	703	GTP	PA-O3A-PB	-3.36	121.28	132.83
4	D	703	GTP	C6-N1-C2	3.27	121.13	115.93
2	A	702	DTP	PA-O3A-PB	-3.23	121.73	132.83
2	D	704	DTP	O5'-C5'-C4'	3.23	120.12	108.99
4	D	703	GTP	O5'-C5'-C4'	3.17	119.90	108.99
4	D	701	GTP	PA-O3A-PB	-3.13	122.08	132.83
4	C	702	GTP	C6-N1-C2	3.11	120.87	115.93
4	B	701	GTP	C6-N1-C2	3.08	120.82	115.93
2	C	703	DTP	O5'-C5'-C4'	3.06	119.53	108.99
2	B	702	DTP	O5'-C5'-C4'	3.03	119.42	108.99
4	D	701	GTP	C6-N1-C2	3.02	120.73	115.93
4	C	702	GTP	PA-O3A-PB	-2.96	122.67	132.83
2	A	702	DTP	C4-C5-N7	-2.93	106.35	109.40
4	C	702	GTP	O3G-PG-O3B	2.91	114.39	104.64
2	B	703	DTP	C4-C5-N7	-2.90	106.38	109.40
4	D	703	GTP	O3G-PG-O3B	2.88	114.30	104.64
4	B	701	GTP	PA-O3A-PB	-2.86	123.01	132.83
2	A	701	DTP	PB-O3B-PG	-2.83	123.11	132.83
2	C	701	DTP	PA-O3A-PB	-2.82	123.14	132.83
2	C	701	DTP	C4-C5-N7	-2.80	106.48	109.40
4	C	702	GTP	O5'-C5'-C4'	2.72	118.34	108.99
2	D	702	DTP	C4-C5-N7	-2.70	106.59	109.40
4	B	701	GTP	O3G-PG-O3B	2.69	113.67	104.64
2	D	702	DTP	PA-O3A-PB	-2.69	123.59	132.83
2	D	704	DTP	PA-O3A-PB	-2.64	123.77	132.83
2	A	701	DTP	O5'-C5'-C4'	2.58	117.88	108.99
2	D	702	DTP	O2G-PG-O3B	2.55	113.18	104.64
2	C	703	DTP	PB-O3B-PG	-2.55	124.08	132.83
2	B	703	DTP	PB-O3B-PG	-2.49	124.28	132.83
2	A	702	DTP	PB-O3B-PG	-2.45	124.40	132.83
2	C	701	DTP	O2G-PG-O3B	2.45	112.85	104.64
2	A	701	DTP	C4-C5-N7	-2.40	106.89	109.40
4	B	701	GTP	O5'-C5'-C4'	2.40	117.26	108.99
4	D	701	GTP	O3G-PG-O3B	2.40	112.69	104.64
4	D	701	GTP	O5'-C5'-C4'	2.38	117.20	108.99
2	C	703	DTP	C4-C5-N7	-2.37	106.92	109.40
4	D	703	GTP	C3'-C2'-C1'	2.37	104.55	100.98
4	B	701	GTP	C3'-C2'-C1'	2.33	104.49	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	701	GTP	PB-O3B-PG	-2.32	124.85	132.83
2	D	702	DTP	PB-O3B-PG	-2.29	124.98	132.83
2	C	701	DTP	PB-O3B-PG	-2.23	125.17	132.83
2	B	702	DTP	PB-O3B-PG	-2.23	125.17	132.83
4	C	702	GTP	PB-O3B-PG	-2.19	125.31	132.83
2	B	702	DTP	C4-C5-N7	-2.15	107.16	109.40
2	B	703	DTP	O5'-C5'-C4'	2.14	116.37	108.99
4	C	702	GTP	C3'-C2'-C1'	2.08	104.11	100.98
2	D	704	DTP	C4-C5-N7	-2.08	107.23	109.40
4	D	703	GTP	PB-O3B-PG	-2.04	125.83	132.83
4	D	701	GTP	PB-O3B-PG	-2.03	125.87	132.83
2	B	702	DTP	O3G-PG-O3B	2.03	111.44	104.64
2	A	702	DTP	O2G-PG-O3B	2.00	111.36	104.64

There are no chirality outliers.

All (68) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	703	GTP	PB-O3B-PG-O3G
2	A	701	DTP	C5'-O5'-PA-O1A
2	A	702	DTP	PB-O3B-PG-O2G
2	A	702	DTP	PB-O3B-PG-O3G
2	A	702	DTP	C5'-O5'-PA-O1A
2	A	702	DTP	C5'-O5'-PA-O2A
2	A	702	DTP	C5'-O5'-PA-O3A
4	C	702	GTP	PB-O3B-PG-O3G
4	C	702	GTP	C5'-O5'-PA-O2A
4	D	701	GTP	PB-O3B-PG-O3G
2	C	703	DTP	PB-O3A-PA-O5'
2	C	703	DTP	C5'-O5'-PA-O2A
2	C	701	DTP	PB-O3B-PG-O2G
2	D	704	DTP	C5'-O5'-PA-O1A
2	D	704	DTP	C5'-O5'-PA-O2A
2	D	704	DTP	C4'-C5'-O5'-PA
4	B	701	GTP	PB-O3B-PG-O3G
2	A	702	DTP	O4'-C4'-C5'-O5'
2	C	703	DTP	C3'-C4'-C5'-O5'
2	A	702	DTP	C3'-C4'-C5'-O5'
2	C	703	DTP	O4'-C4'-C5'-O5'
2	A	701	DTP	C3'-C4'-C5'-O5'
2	A	701	DTP	C4'-C5'-O5'-PA
2	A	701	DTP	PB-O3A-PA-O5'

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Mol	Chain	Res	Type	Atoms
2	D	704	DTP	PB-O3A-PA-O5'
4	D	703	GTP	PB-O3B-PG-O2G
4	D	703	GTP	C5'-O5'-PA-O3A
2	A	701	DTP	C5'-O5'-PA-O3A
2	B	702	DTP	C5'-O5'-PA-O3A
4	C	702	GTP	C5'-O5'-PA-O3A
4	D	701	GTP	C5'-O5'-PA-O3A
2	C	703	DTP	C5'-O5'-PA-O3A
4	B	701	GTP	C5'-O5'-PA-O3A
4	C	702	GTP	PB-O3A-PA-O2A
4	D	701	GTP	PB-O3A-PA-O2A
4	B	701	GTP	PB-O3A-PA-O2A
2	B	702	DTP	C4'-C5'-O5'-PA
2	C	703	DTP	C4'-C5'-O5'-PA
4	D	703	GTP	C5'-O5'-PA-O1A
2	A	701	DTP	C5'-O5'-PA-O2A
2	B	702	DTP	C5'-O5'-PA-O2A
4	C	702	GTP	C5'-O5'-PA-O1A
4	D	701	GTP	C5'-O5'-PA-O1A
2	C	703	DTP	C5'-O5'-PA-O1A
4	B	701	GTP	C5'-O5'-PA-O1A
2	A	701	DTP	O4'-C4'-C5'-O5'
4	D	703	GTP	PB-O3A-PA-O2A
2	A	702	DTP	PG-O3B-PB-O1B
2	B	702	DTP	PG-O3B-PB-O2B
2	B	703	DTP	PG-O3B-PB-O1B
4	D	703	GTP	PB-O3B-PG-O1G
2	C	701	DTP	PB-O3B-PG-O1G
4	B	701	GTP	PB-O3B-PG-O1G
4	D	701	GTP	PB-O3B-PG-O2G
2	C	701	DTP	PB-O3B-PG-O3G
4	B	701	GTP	PB-O3B-PG-O2G
2	D	702	DTP	C5'-O5'-PA-O3A
2	D	704	DTP	C5'-O5'-PA-O3A
4	C	702	GTP	C4'-C5'-O5'-PA
4	D	703	GTP	PB-O3A-PA-O1A
2	B	702	DTP	PG-O3B-PB-O1B
2	D	702	DTP	PG-O3B-PB-O1B
4	D	701	GTP	PG-O3B-PB-O2B
2	D	704	DTP	PB-O3A-PA-O1A
4	D	703	GTP	C4'-C5'-O5'-PA
4	C	702	GTP	PB-O3B-PG-O1G

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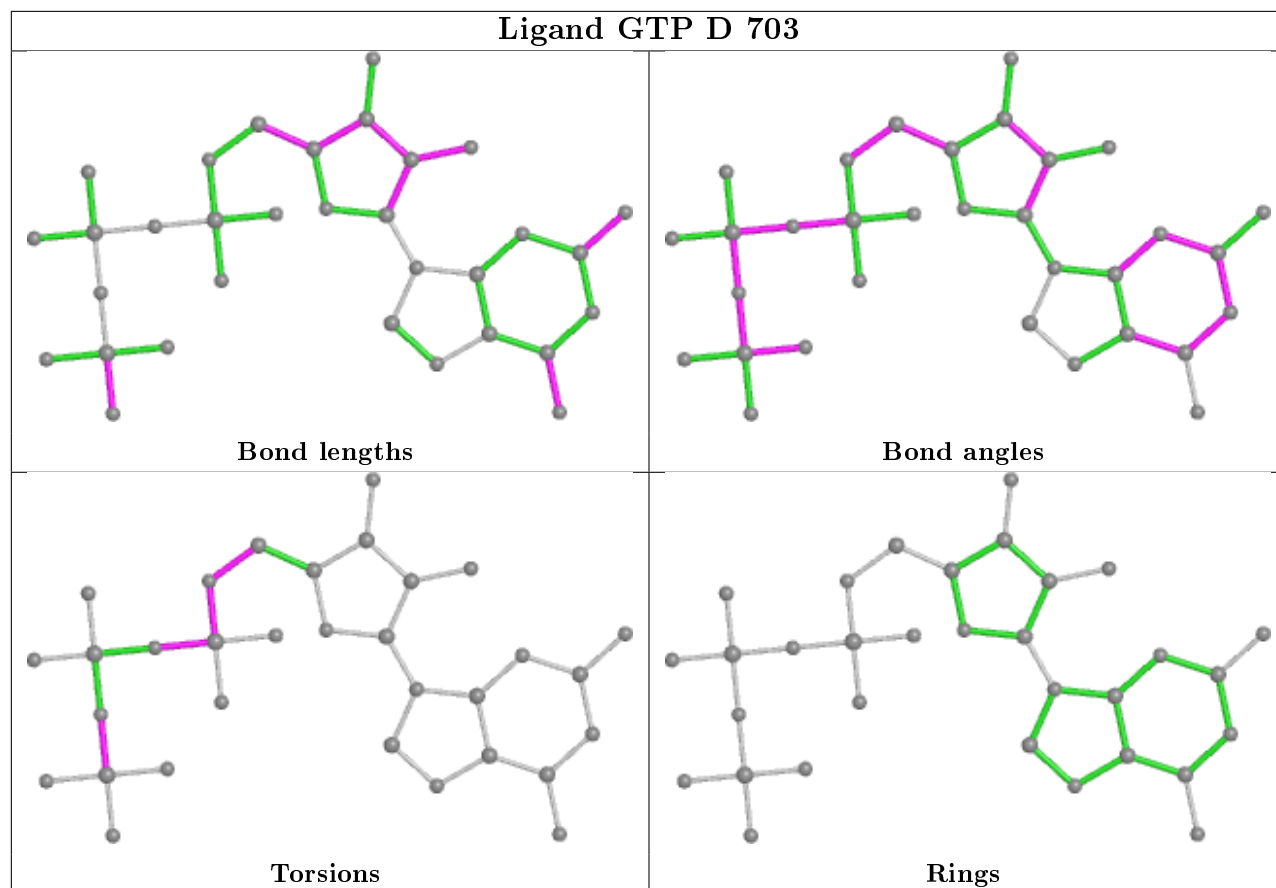
Mol	Chain	Res	Type	Atoms
4	D	701	GTP	PB-O3B-PG-O1G
4	D	701	GTP	C4'-C5'-O5'-PA

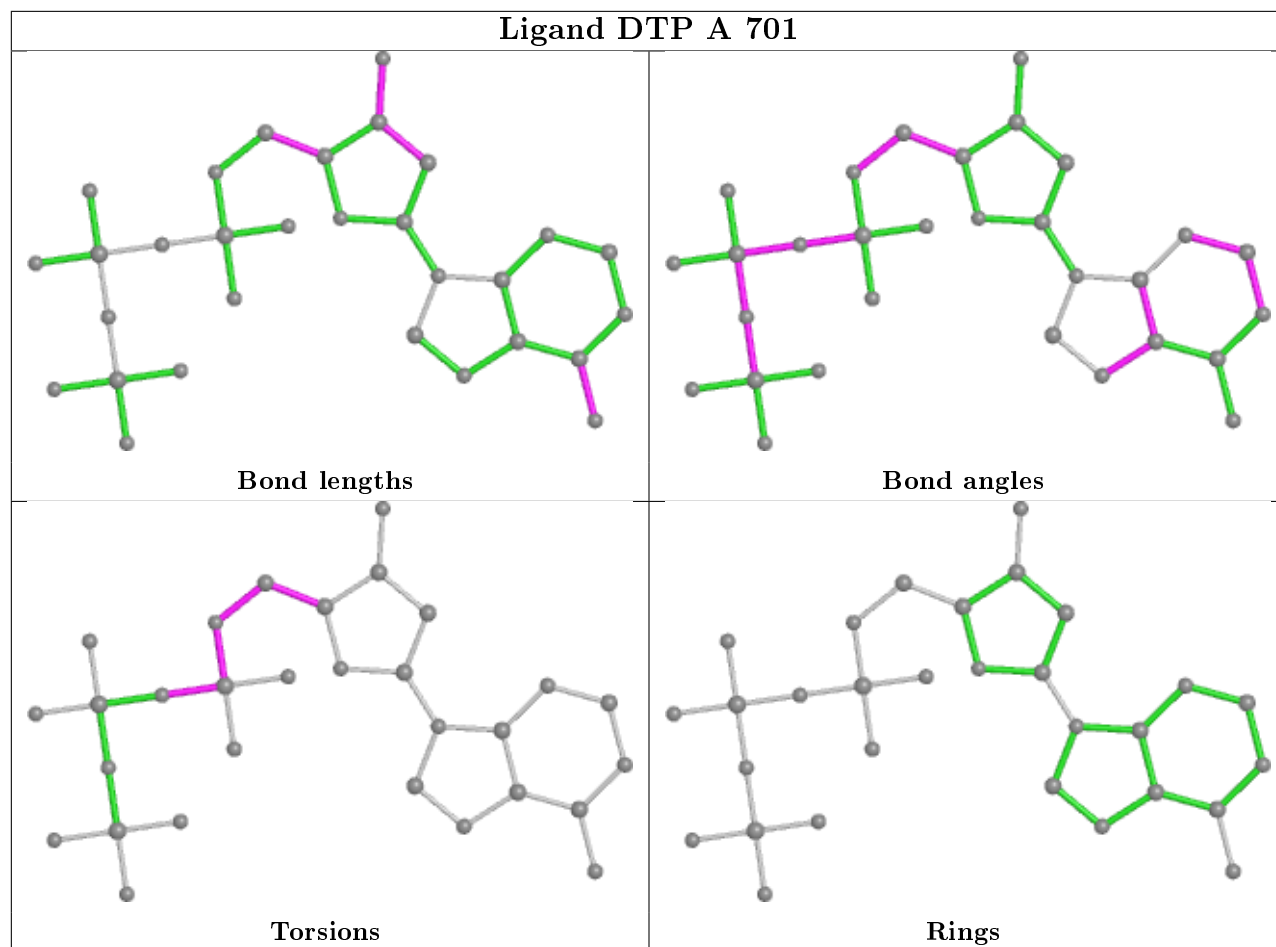
There are no ring outliers.

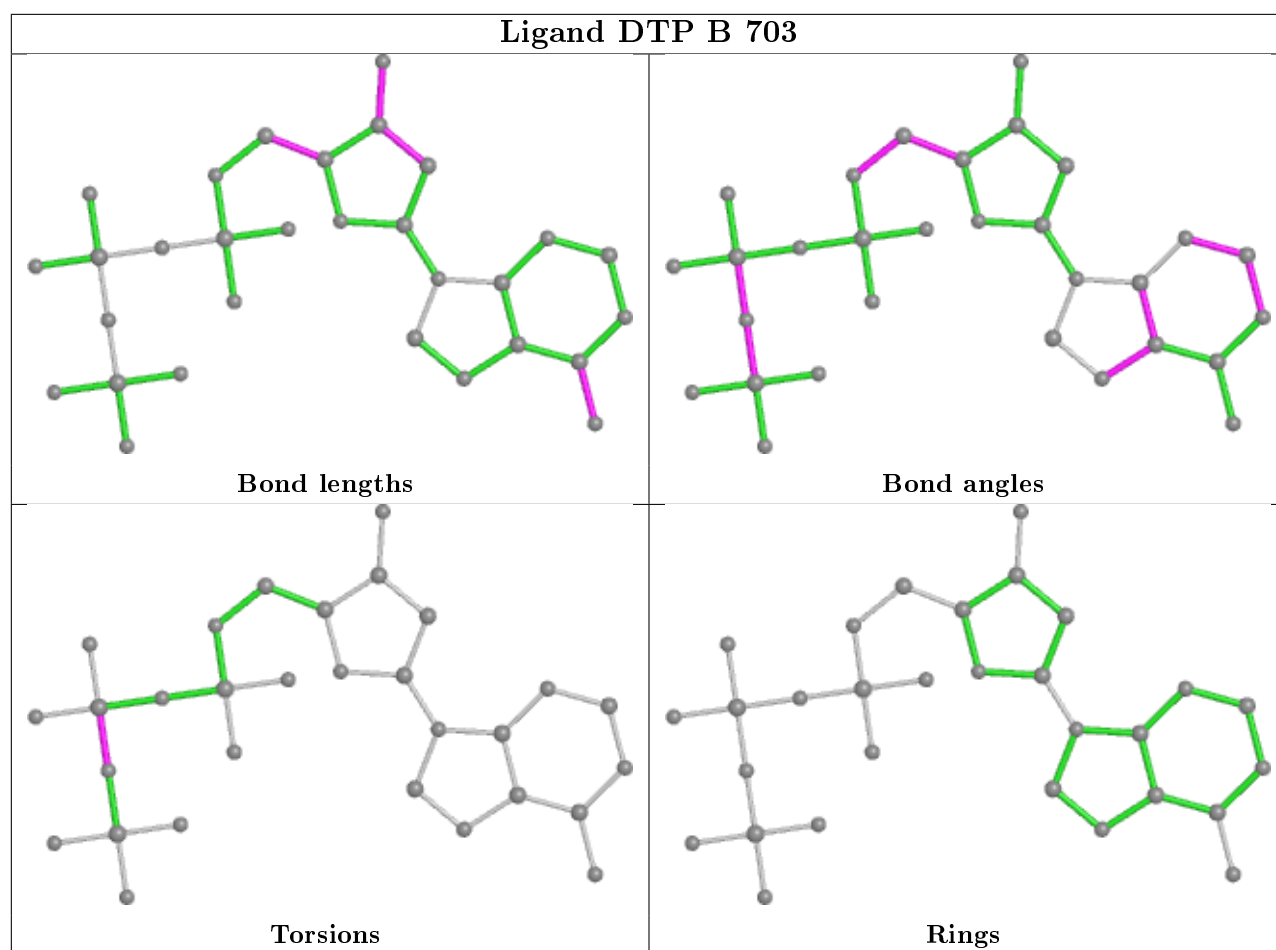
8 monomers are involved in 8 short contacts:

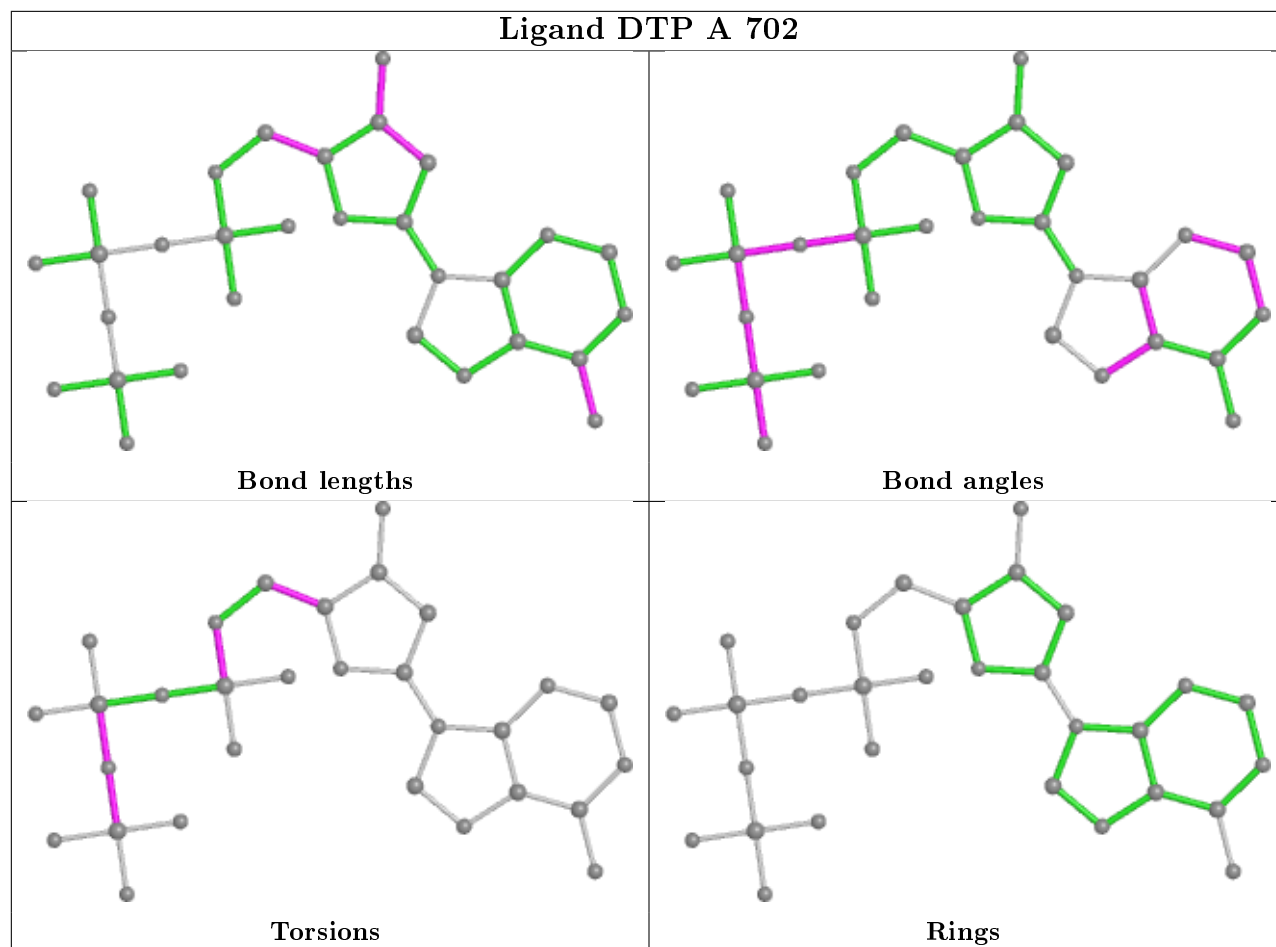
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	DTP	2	0
2	A	702	DTP	1	0
2	B	702	DTP	2	0
4	C	702	GTP	1	0
2	D	702	DTP	1	0
4	D	701	GTP	1	0
4	B	701	GTP	2	0
2	C	701	DTP	1	0

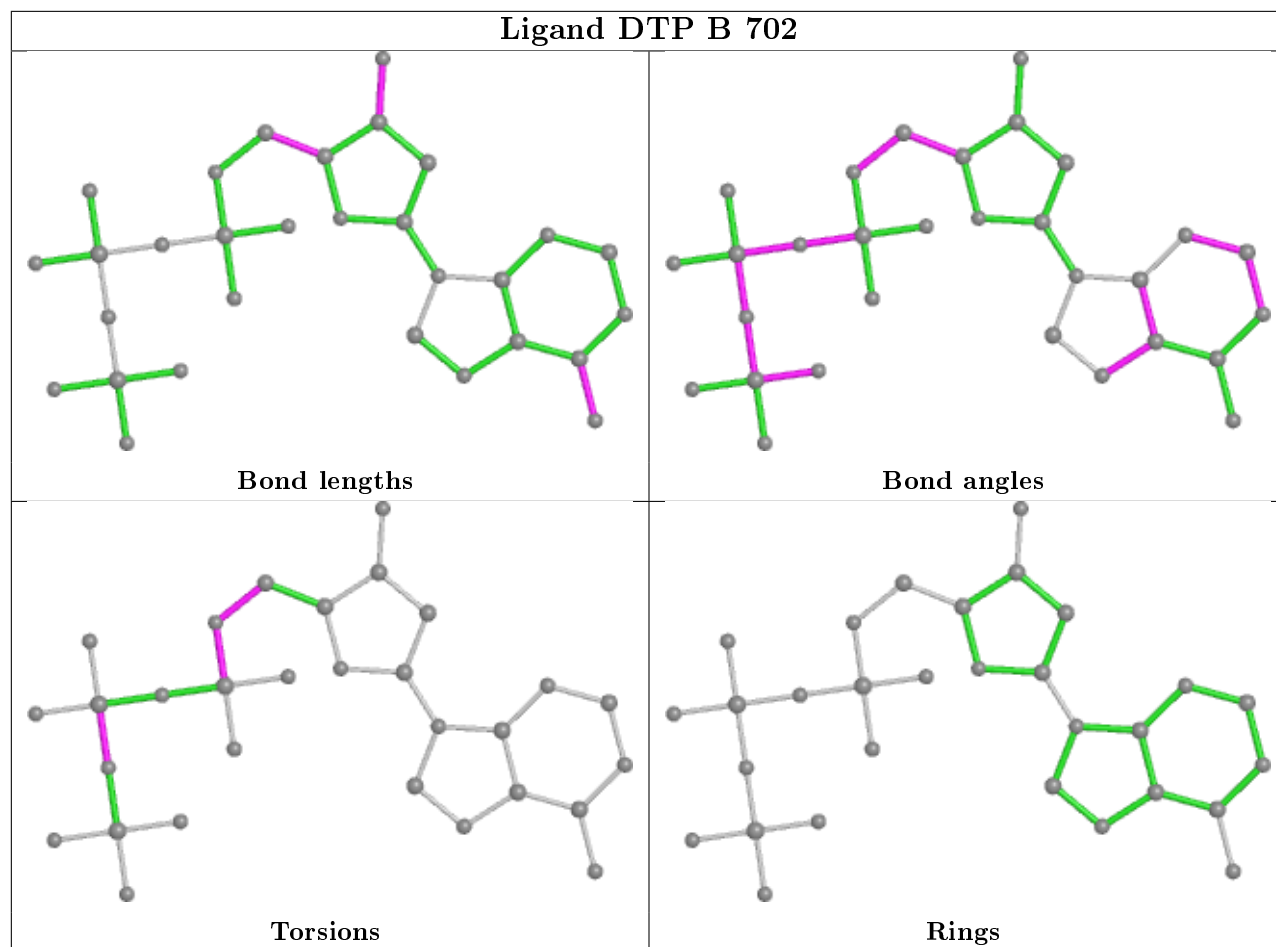
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

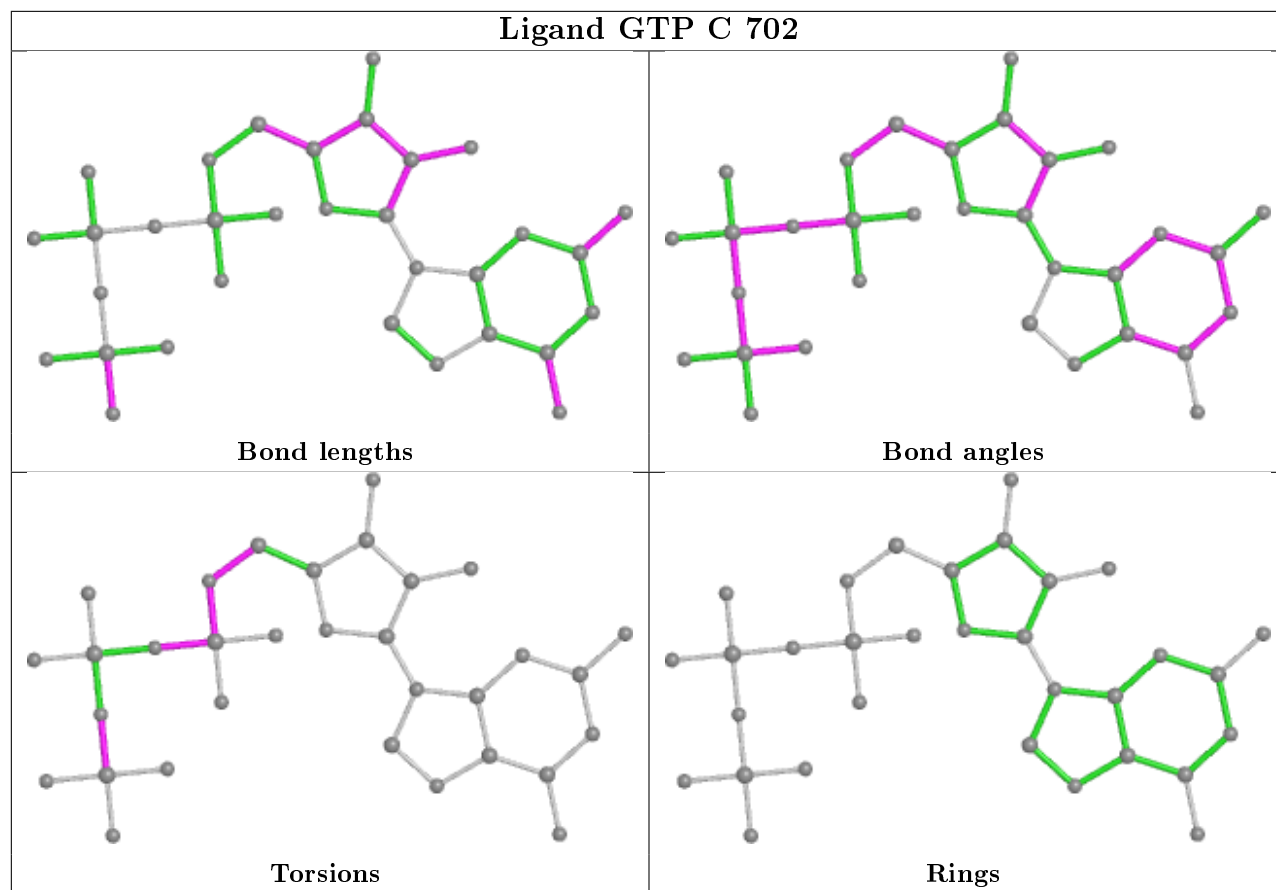


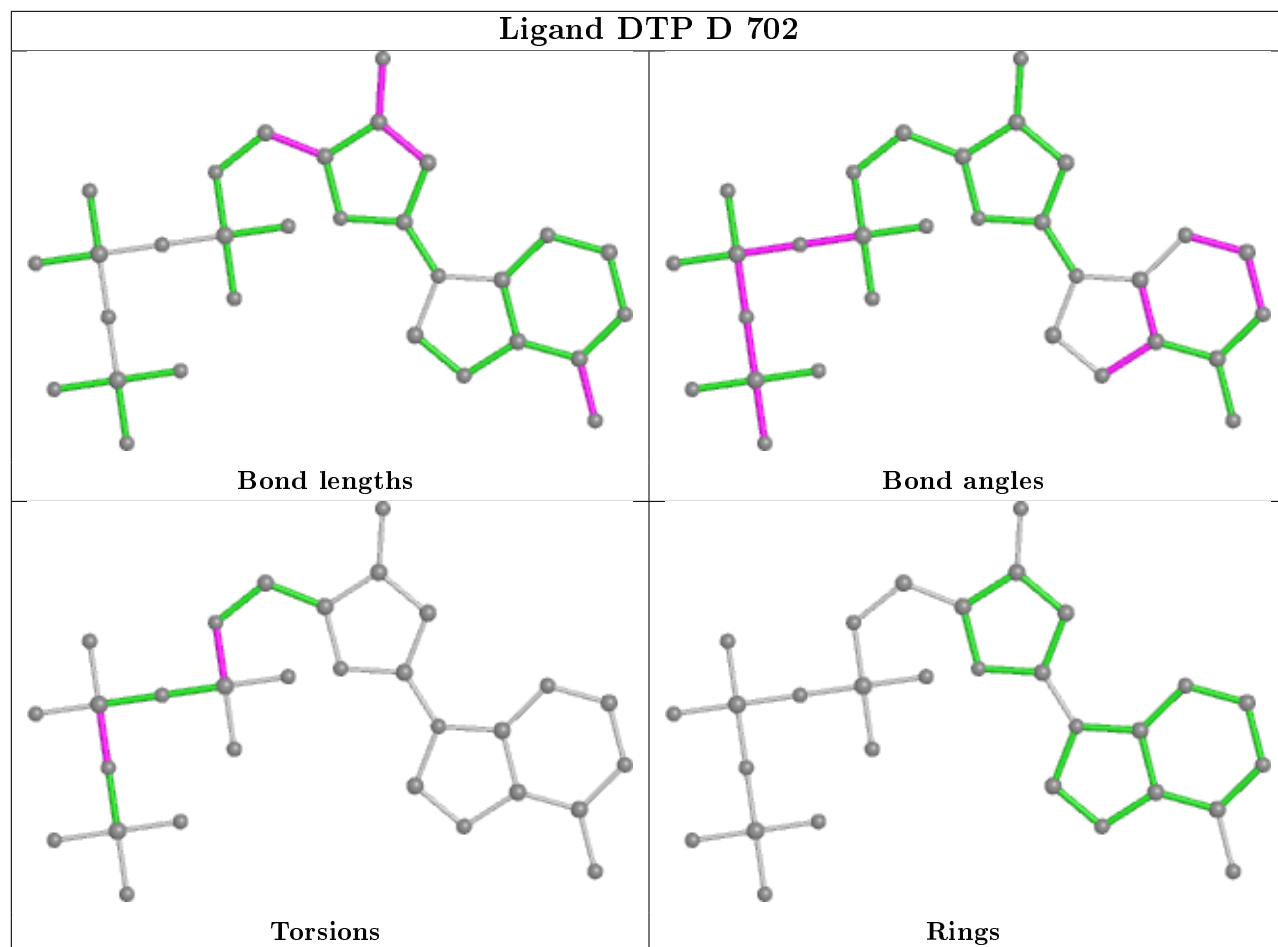


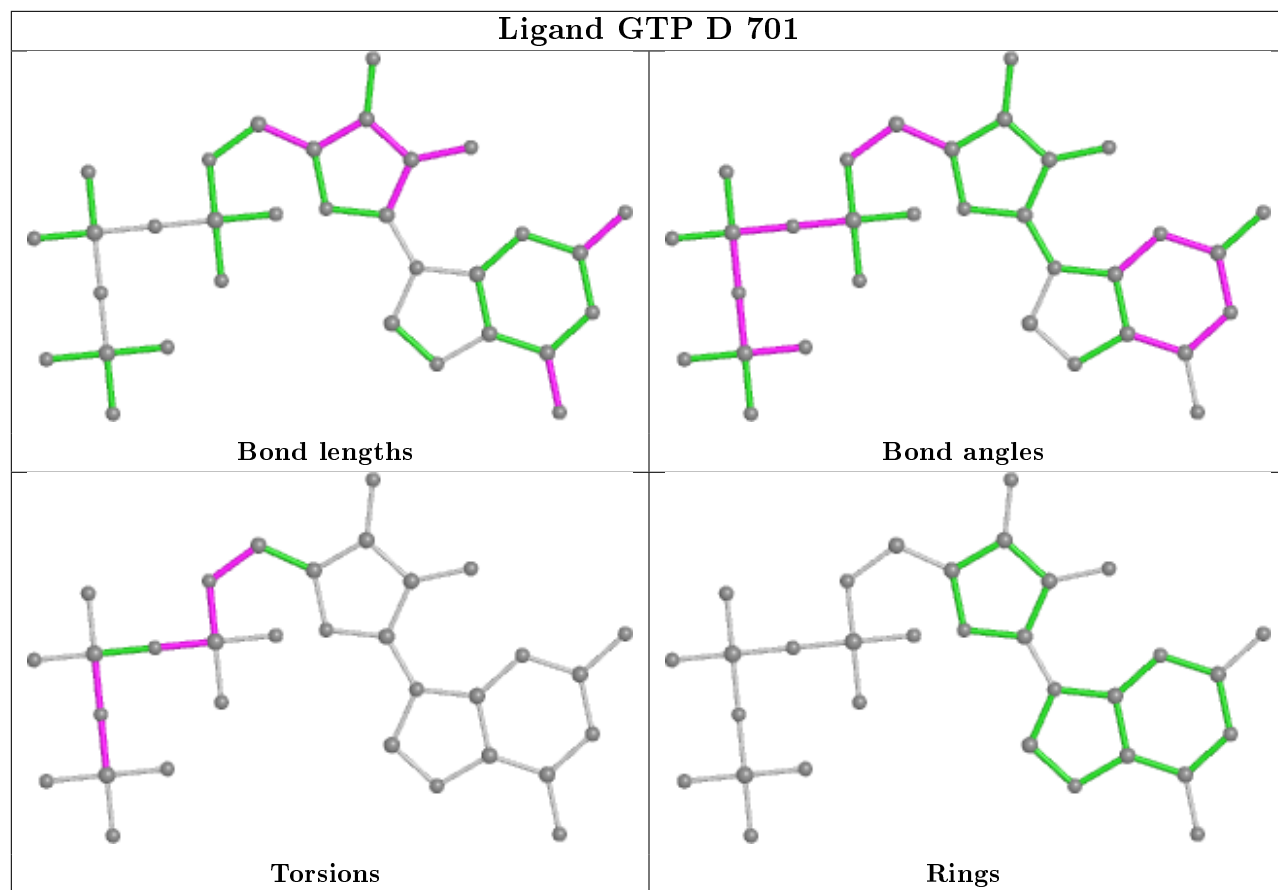


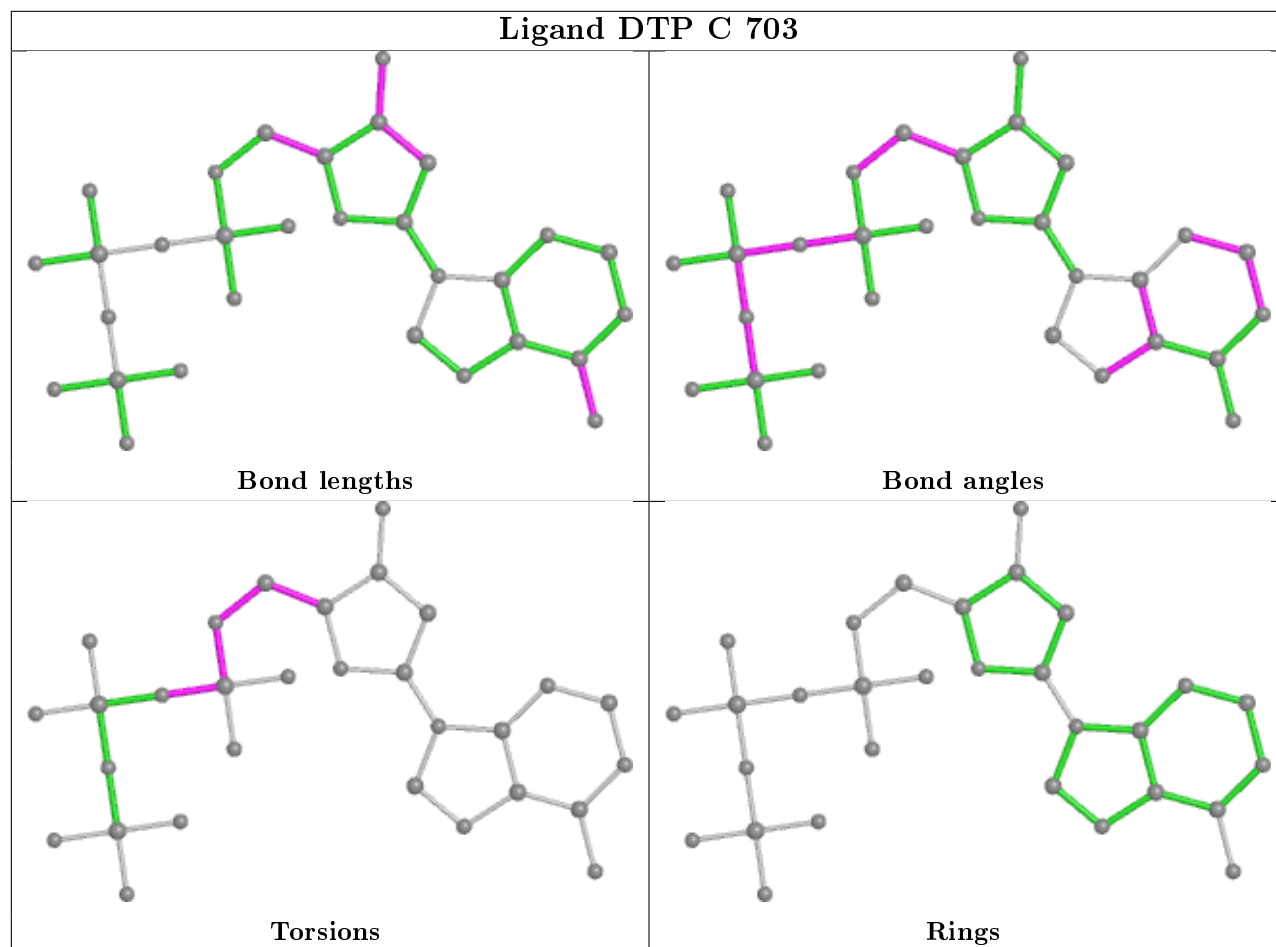


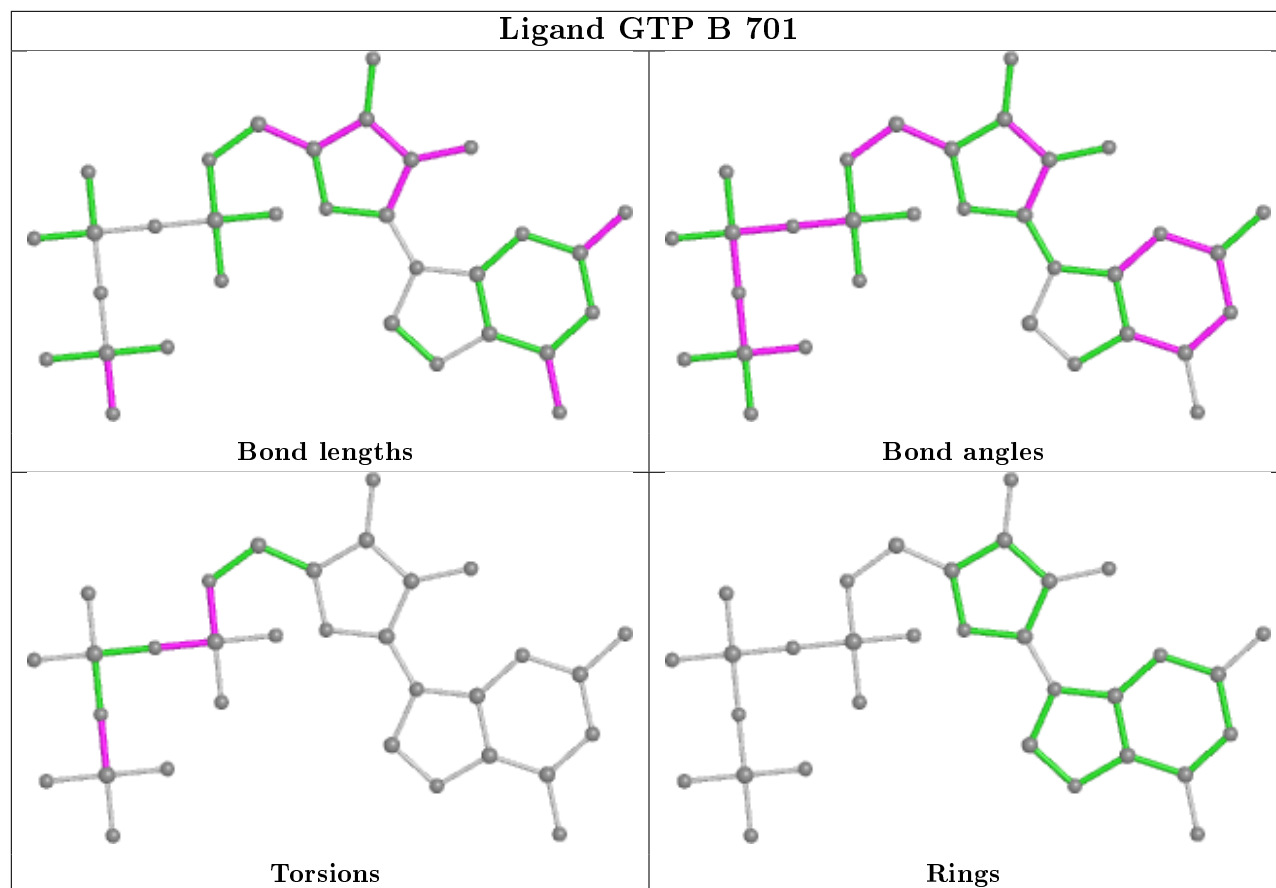


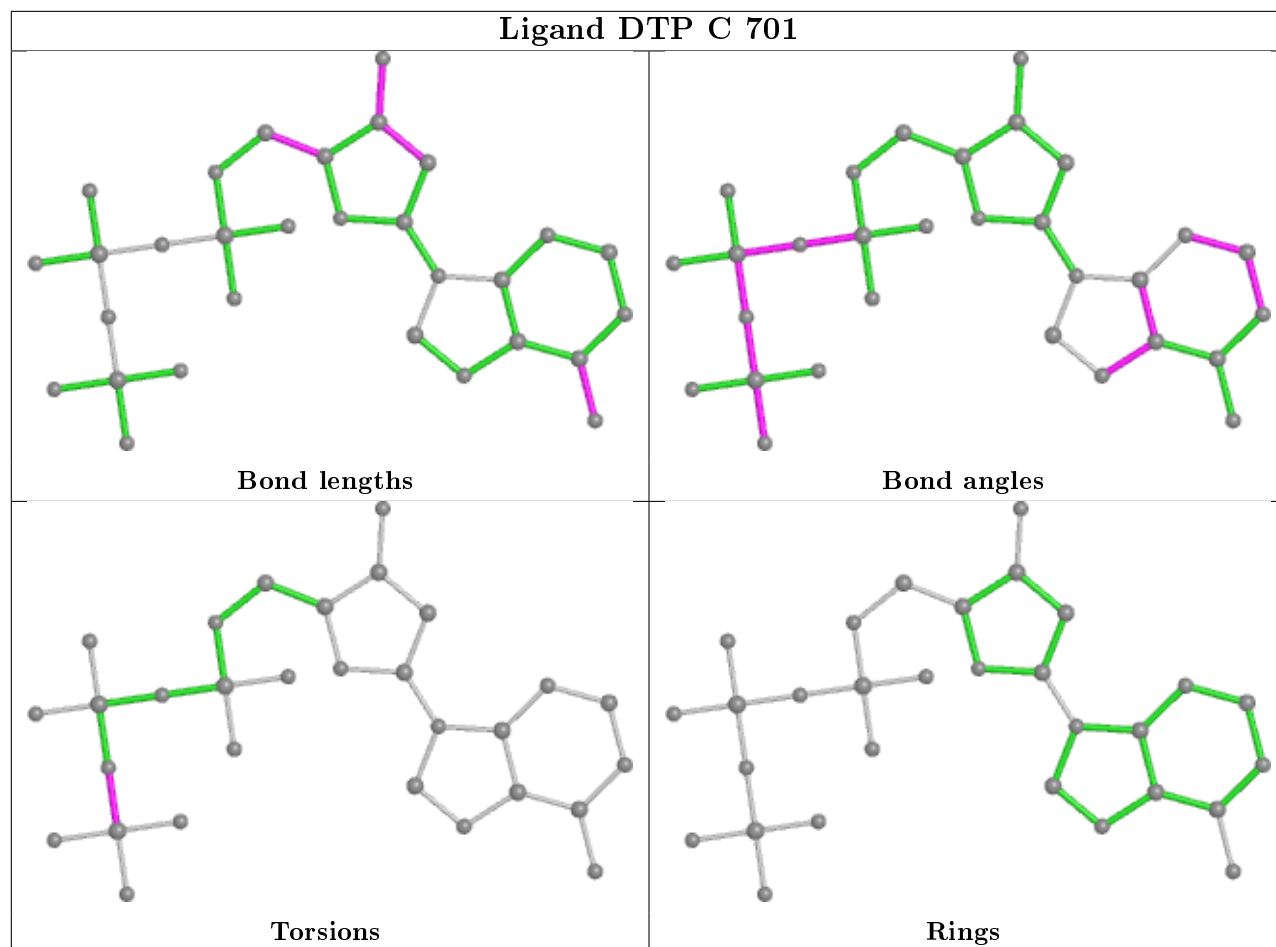


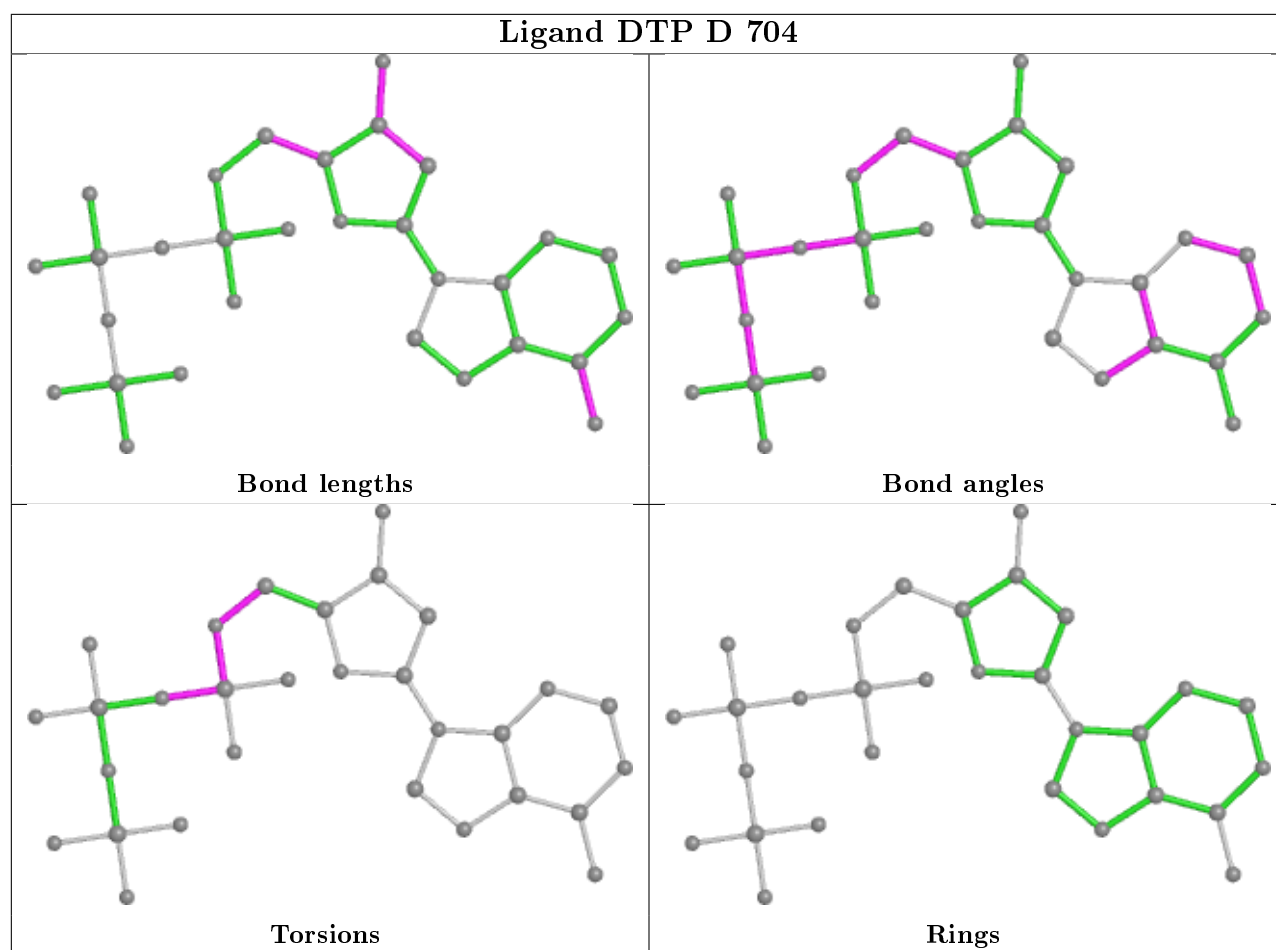












5.7 Other polymers [i](#)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	481/550 (87%)	0.56	46 (9%)	8 6	43, 68, 98, 125	460 (95%)
1	B	481/550 (87%)	0.40	40 (8%)	11 10	44, 62, 93, 120	444 (92%)
1	C	481/550 (87%)	0.59	47 (9%)	7 6	43, 65, 98, 137	457 (95%)
1	D	481/550 (87%)	0.19	20 (4%)	36 34	39, 57, 82, 96	465 (96%)
All	All	1924/2200 (87%)	0.43	153 (7%)	12 11	39, 63, 95, 137	1826 (94%)

All (153) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	489	LEU	7.5
1	D	284	LEU	6.6
1	B	483	ALA	6.5
1	A	599	ASN	6.0
1	B	559	ARG	6.0
1	A	598	TRP	5.6
1	D	490	ASP	5.2
1	C	491	VAL	5.2
1	C	276	LEU	5.1
1	A	344	ASP	5.1
1	A	488	LEU	5.1
1	B	488	LEU	4.7
1	A	597	GLU	4.5
1	B	284	LEU	4.5
1	B	562	LEU	4.4
1	A	595	LYS	4.4
1	C	590	LEU	4.3
1	C	596	LYS	4.2
1	B	495	ALA	4.1
1	C	284	LEU	4.1
1	B	590	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	568	TYR	4.0
1	C	487	VAL	4.0
1	B	489	LEU	4.0
1	C	488	LEU	3.9
1	B	491	VAL	3.9
1	A	483	ALA	3.9
1	A	487	VAL	3.8
1	D	599	ASN	3.8
1	C	591	ILE	3.8
1	C	151	GLY	3.7
1	D	113	ASP	3.7
1	A	486	LYS	3.7
1	A	480	VAL	3.7
1	C	595	LYS	3.6
1	C	560	LYS	3.6
1	B	276	LEU	3.6
1	D	276	LEU	3.6
1	B	560	LYS	3.6
1	A	466	ILE	3.6
1	A	481	ALA	3.5
1	B	485	PRO	3.5
1	A	498	PHE	3.4
1	B	484	LYS	3.4
1	B	563	TYR	3.4
1	A	284	LEU	3.4
1	B	591	ILE	3.4
1	A	473	TYR	3.4
1	D	408	ARG	3.4
1	C	400	THR	3.3
1	A	326	GLN	3.3
1	A	489	LEU	3.3
1	A	394	ASP	3.3
1	A	343	VAL	3.3
1	B	487	VAL	3.2
1	A	568	TYR	3.2
1	B	492	LYS	3.1
1	B	478	LYS	3.0
1	A	408	ARG	3.0
1	A	494	LYS	3.0
1	B	481	ALA	3.0
1	C	161	SER	3.0
1	C	568	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	343	VAL	3.0
1	D	596	LYS	2.9
1	B	277	GLU	2.9
1	C	215	HIS	2.9
1	C	484	LYS	2.9
1	A	491	VAL	2.9
1	A	396	TYR	2.9
1	C	148	LYS	2.8
1	C	490	ASP	2.8
1	B	587	ILE	2.8
1	C	493	LEU	2.8
1	B	490	ASP	2.7
1	C	597	GLU	2.7
1	C	113	ASP	2.7
1	D	277	GLU	2.7
1	B	494	LYS	2.7
1	A	493	LEU	2.7
1	B	593	PRO	2.6
1	C	562	LEU	2.6
1	A	492	LYS	2.6
1	C	485	PRO	2.5
1	C	403	GLY	2.5
1	A	478	LYS	2.5
1	B	486	LYS	2.5
1	C	559	ARG	2.5
1	C	397	ILE	2.5
1	C	480	VAL	2.5
1	C	586	VAL	2.5
1	B	565	ALA	2.5
1	B	493	LEU	2.5
1	C	260	ILE	2.5
1	B	596	LYS	2.5
1	A	528	ARG	2.5
1	C	511	GLU	2.5
1	D	146	TYR	2.4
1	D	225	ALA	2.4
1	C	527	ASN	2.4
1	A	510	GLN	2.4
1	B	594	GLN	2.4
1	C	587	ILE	2.4
1	A	578	PHE	2.4
1	B	154	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	482	SER	2.4
1	A	277	GLU	2.4
1	B	403	GLY	2.4
1	A	147	ILE	2.4
1	A	560	LYS	2.4
1	C	486	LYS	2.4
1	C	152	GLY	2.4
1	A	161	SER	2.4
1	D	344	ASP	2.3
1	D	396	TYR	2.3
1	C	277	GLU	2.3
1	B	326	GLN	2.3
1	B	151	GLY	2.3
1	B	496	GLU	2.3
1	A	596	LYS	2.3
1	D	320	CYS	2.3
1	D	230	LYS	2.3
1	A	395	ASP	2.3
1	B	510	GLN	2.2
1	A	464	GLY	2.2
1	C	160	ALA	2.2
1	A	345	ASN	2.2
1	A	472	ASP	2.2
1	C	150	LEU	2.2
1	D	465	GLN	2.2
1	C	436	PRO	2.2
1	A	475	SER	2.2
1	B	588	ALA	2.2
1	A	465	GLN	2.2
1	C	589	PRO	2.1
1	B	558	ASP	2.1
1	C	592	THR	2.1
1	C	345	ASN	2.1
1	A	468	ILE	2.1
1	A	439	LYS	2.1
1	A	467	LYS	2.1
1	C	492	LYS	2.1
1	C	563	TYR	2.1
1	D	466	ILE	2.1
1	D	594	GLN	2.1
1	B	328	ASN	2.1
1	B	561	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	522	CYS	2.1
1	A	527	ASN	2.0
1	D	115	MET	2.0
1	C	483	ALA	2.0
1	D	531	ARG	2.0
1	C	326	GLN	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](#)

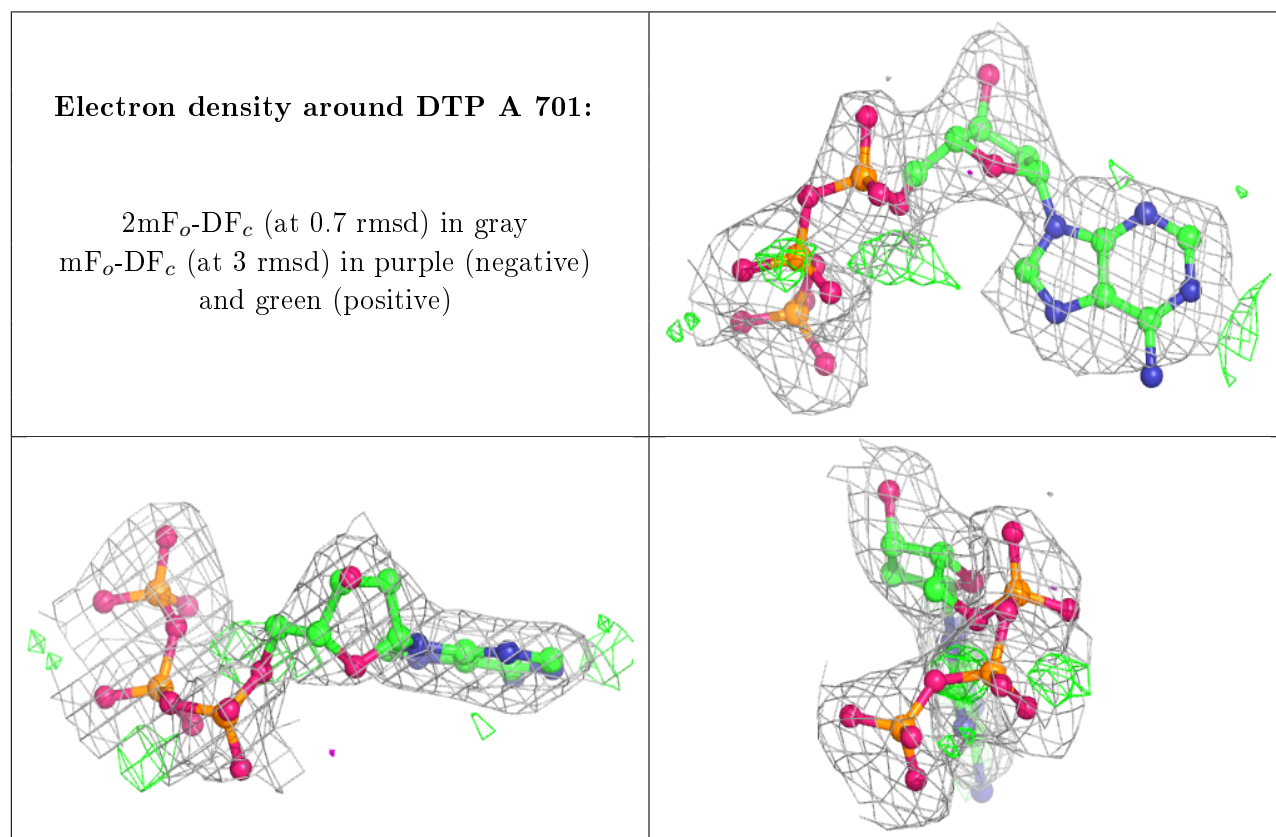
There are no carbohydrates in this entry.

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

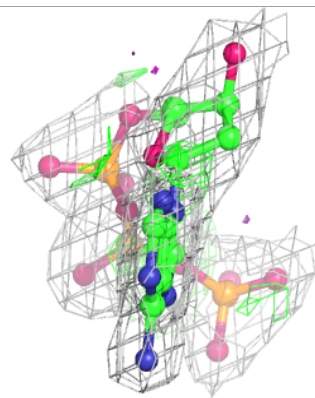
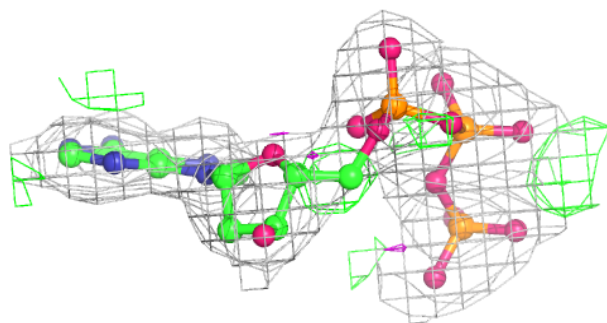
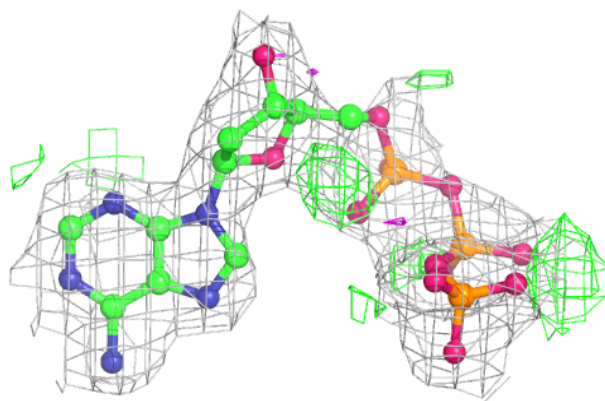
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	A	704	1/1	0.76	0.08	56,56,56,56	1
3	MG	C	704	1/1	0.83	0.07	62,62,62,62	0
3	MG	A	703	1/1	0.87	0.11	37,37,37,37	1
3	MG	D	705	1/1	0.90	0.09	60,60,60,60	0
2	DTP	A	701	30/30	0.93	0.17	55,60,71,73	28
2	DTP	B	702	30/30	0.94	0.20	48,55,61,64	28
2	DTP	D	704	30/30	0.94	0.21	36,50,56,57	30
2	DTP	C	703	30/30	0.95	0.26	44,59,66,70	28
4	GTP	C	702	32/32	0.96	0.15	42,53,62,68	32
4	GTP	D	701	32/32	0.96	0.15	48,53,61,69	32
2	DTP	C	701	30/30	0.97	0.14	48,52,58,60	18
4	GTP	D	703	32/32	0.97	0.14	37,46,52,59	32
4	GTP	B	701	32/32	0.97	0.12	43,50,58,63	32
2	DTP	A	702	30/30	0.98	0.14	47,53,57,60	21
2	DTP	D	702	30/30	0.98	0.12	43,48,56,56	19
2	DTP	B	703	30/30	0.98	0.13	32,44,57,60	20

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.

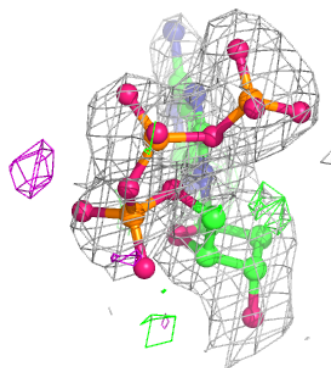
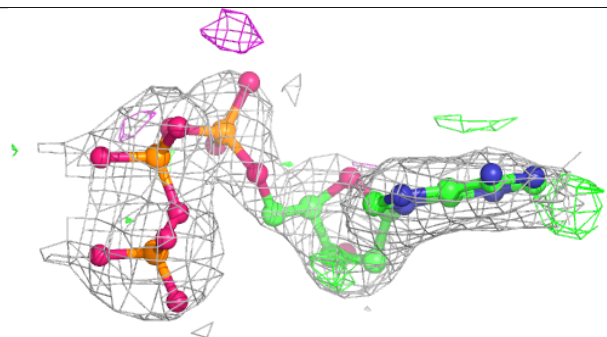
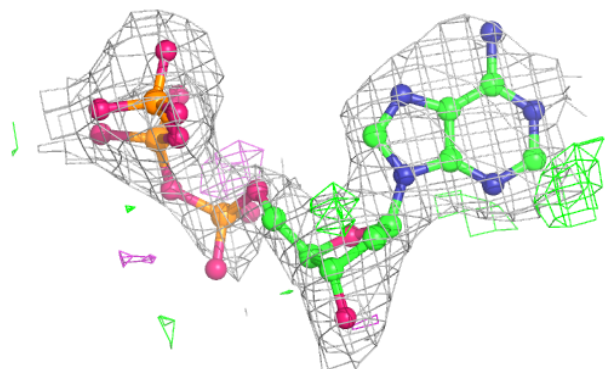


Electron density around DTP B 702:

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

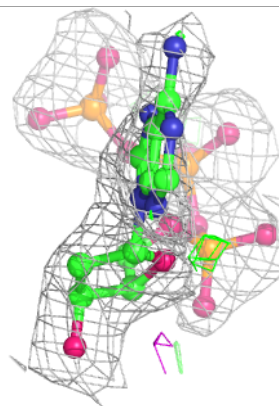
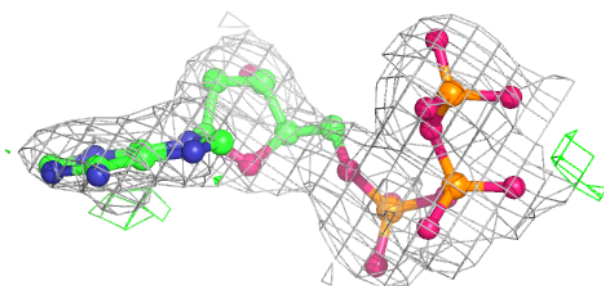
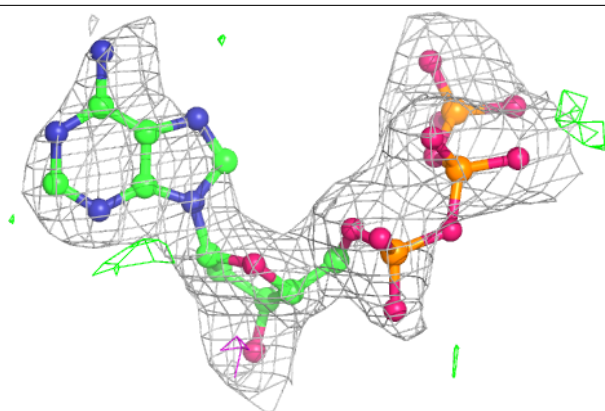
**Electron density around DTP D 704:**

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

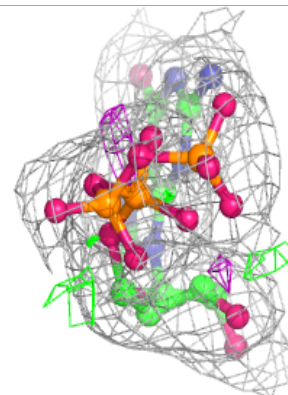
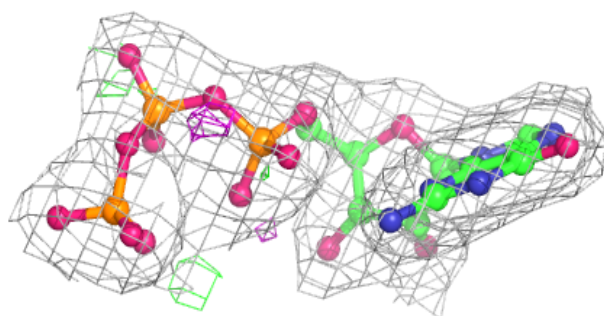
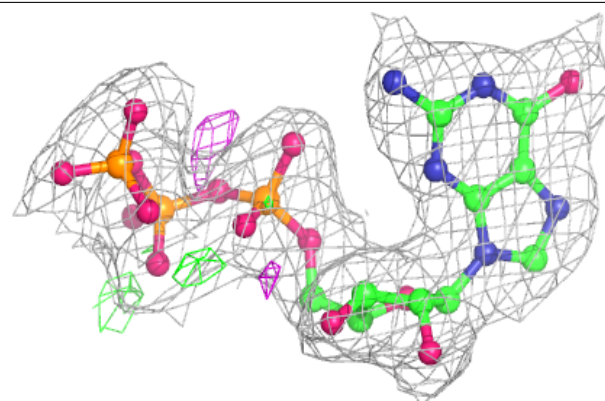


Electron density around DTP C 703:

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

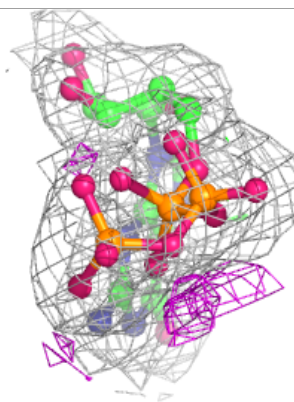
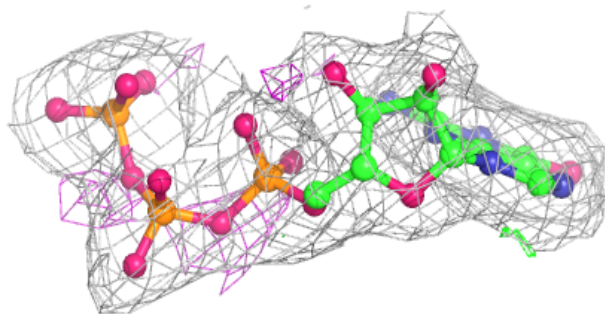
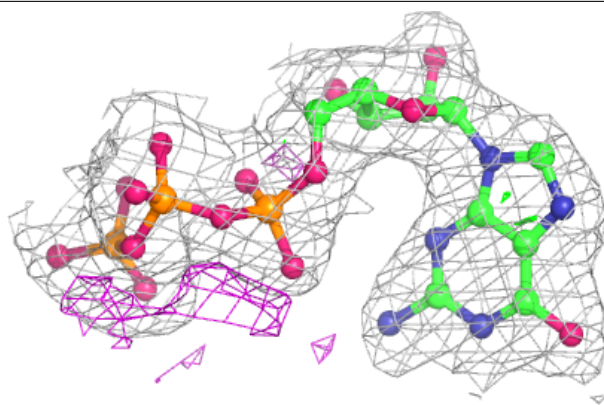
**Electron density around GTP C 702:**

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



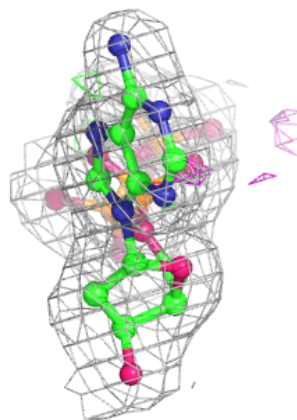
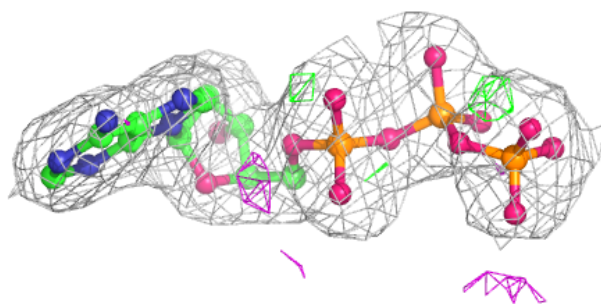
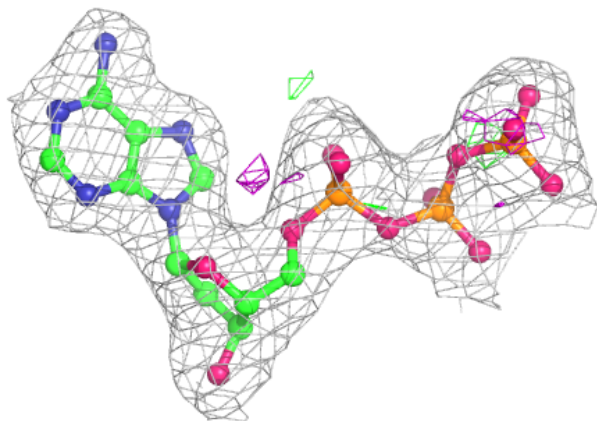
Electron density around GTP D 701:

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



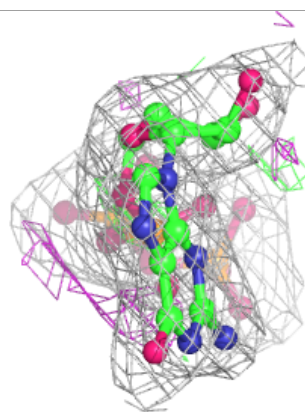
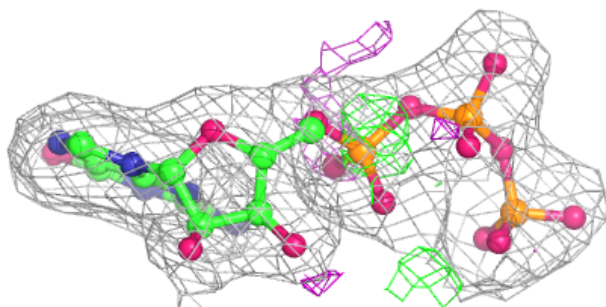
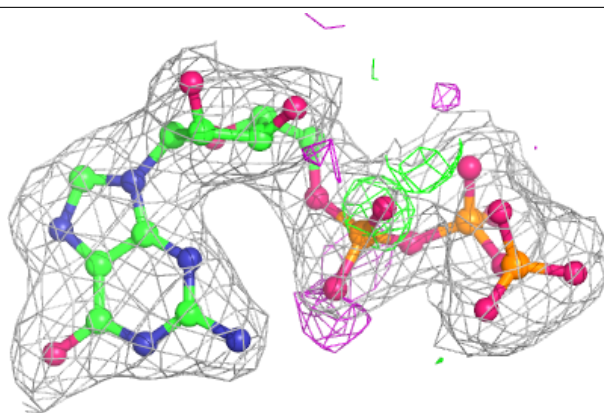
Electron density around DTP C 701:

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

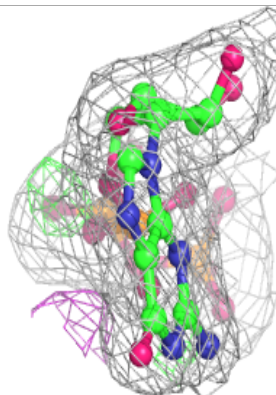
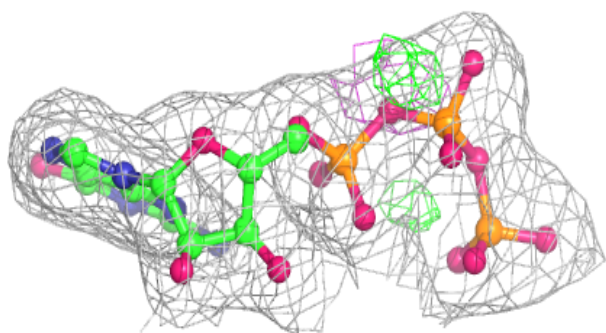
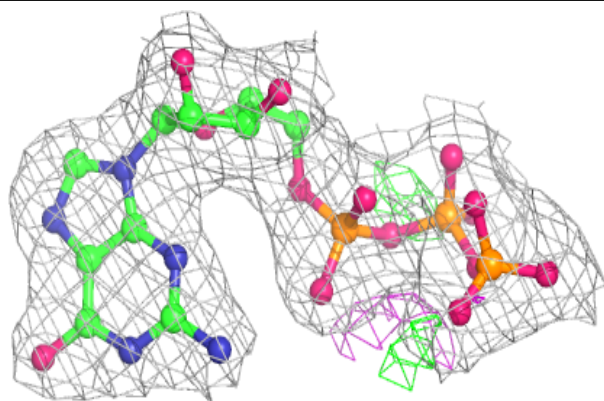


Electron density around GTP D 703:

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

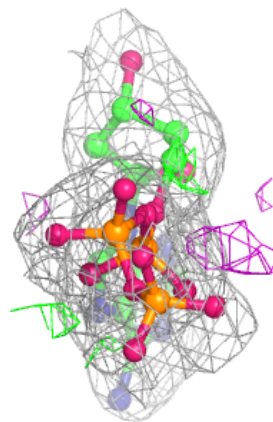
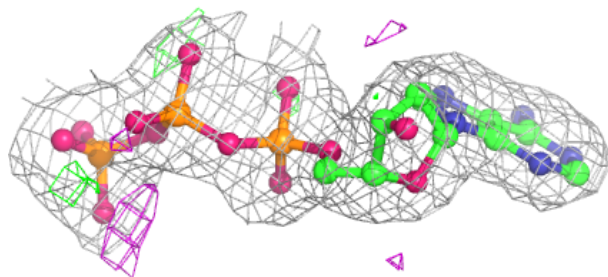
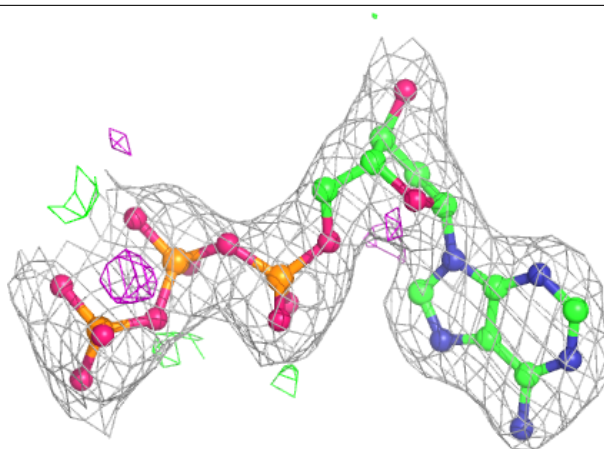
**Electron density around GTP B 701:**

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



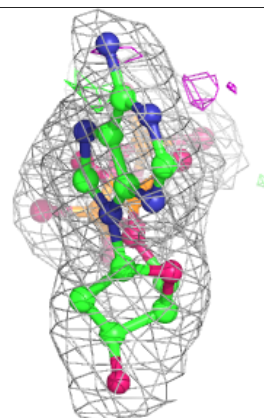
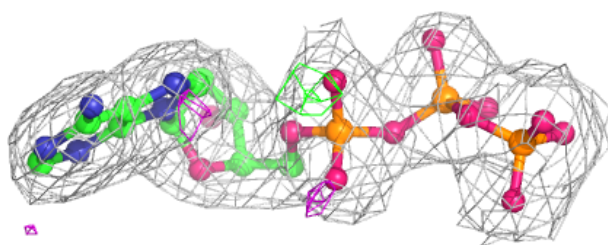
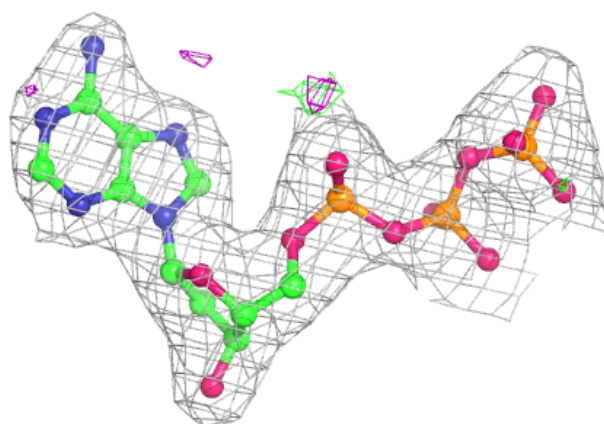
Electron density around DTP A 702:

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

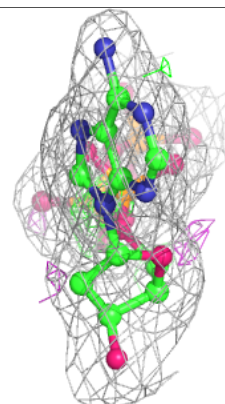
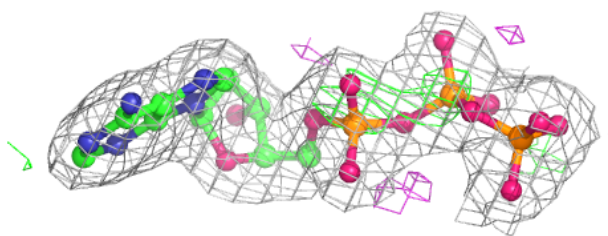
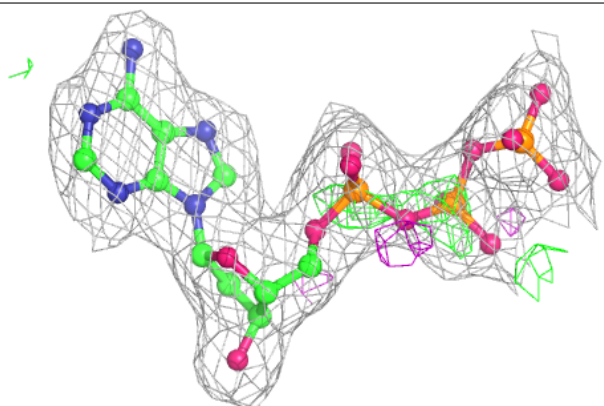


Electron density around DTP D 702:

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

**Electron density around DTP B 703:**

$2mF_o-DF_c$ (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.