



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:22 PM UTC

PDB ID : 5OOB / pdb_00005oob
Title : COMPLEX OF HUMAN NUCLEAR CAP-BINDING COMPLEX WITH
M7GTP AND NELF-E C-TERMINAL PEPTIDE
Authors : Cusack, S.; Schulze, W.M.
Deposited on : 2017-08-07
Resolution : 2.79 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

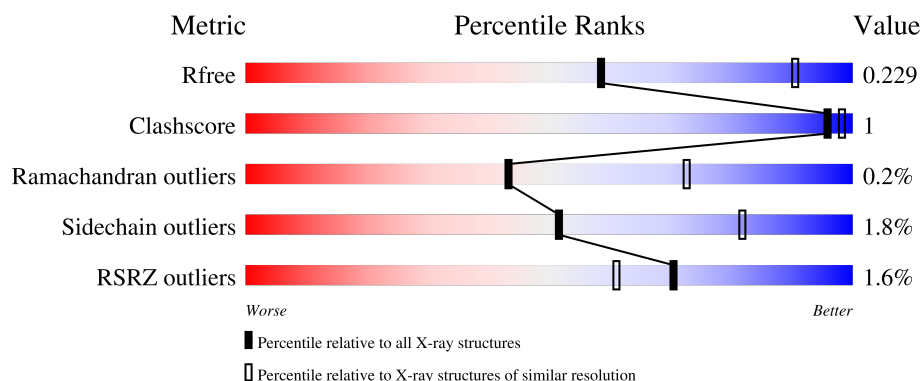
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	772	91% 5% .
1	C	772	91% 5% .
1	F	772	3% 88% 5% 7%
1	I	772	90% 6%
2	B	158	3% 91% 6% .

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Mol	Chain	Length	Quality of chain
2	D	158	2% 92%
2	G	158	3% 91% 6%
2	J	158	% 90% 6%
3	E	21	10% 86% 14%
3	K	21	19% 71% 10% 19%
3	Z	21	14% 67% 33%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 29296 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 Nuclear cap-binding protein subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	739	Total	C	N	O	S	0	0	0
			6045	3897	1018	1092	38			
1	C	731	Total	C	N	O	S	0	0	0
			5980	3853	1006	1083	38			
1	F	718	Total	C	N	O	S	0	0	0
			5879	3791	992	1058	38			
1	I	729	Total	C	N	O	S	0	0	0
			5964	3845	1005	1076	38			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	MET	-	initiating methionine	UNP Q09161
C	19	MET	-	initiating methionine	UNP Q09161
F	19	MET	-	initiating methionine	UNP Q09161
I	19	MET	-	initiating methionine	UNP Q09161

- Molecule 2 is a protein called Nuclear cap-binding protein subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	152	Total	C	N	O	S	0	0	0
			1237	769	222	240	6			
2	D	151	Total	C	N	O	S	0	0	0
			1229	765	220	238	6			
2	G	149	Total	C	N	O	S	0	0	0
			1215	757	217	235	6			
2	J	148	Total	C	N	O	S	0	0	0
			1207	751	216	234	6			

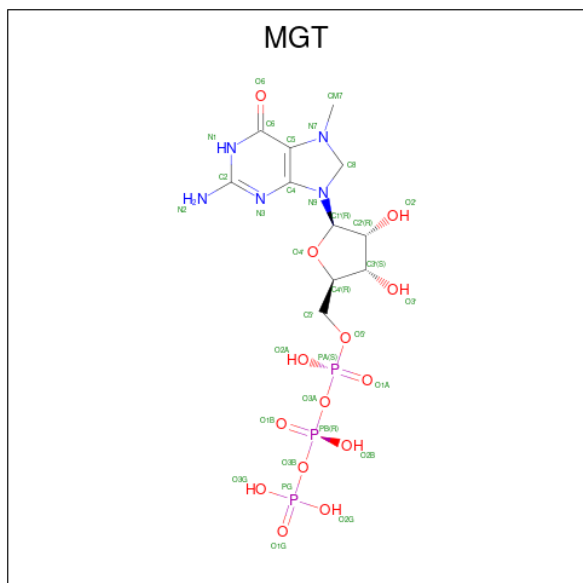
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P52298
B	0	ALA	-	expression tag	UNP P52298
D	-1	GLY	-	expression tag	UNP P52298
D	0	ALA	-	expression tag	UNP P52298
G	-1	GLY	-	expression tag	UNP P52298
G	0	ALA	-	expression tag	UNP P52298
J	-1	GLY	-	expression tag	UNP P52298
J	0	ALA	-	expression tag	UNP P52298

- Molecule 3 is a protein called Negative elongation factor E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	18	Total	C	N	O	0	0	0
			150	93	24	33			
3	K	17	Total	C	N	O	0	0	0
			142	89	22	31			
3	Z	14	Total	C	N	O	0	0	0
			116	74	18	24			

- Molecule 4 is 7N-METHYL-8-HYDROGUANOSINE-5'-TRIPHOSPHATE (CCD ID: MGT) (formula: $C_{11}H_{20}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			33	11	5	14		
4	D	1	Total	C	N	O	0	0
			33	11	5	14		

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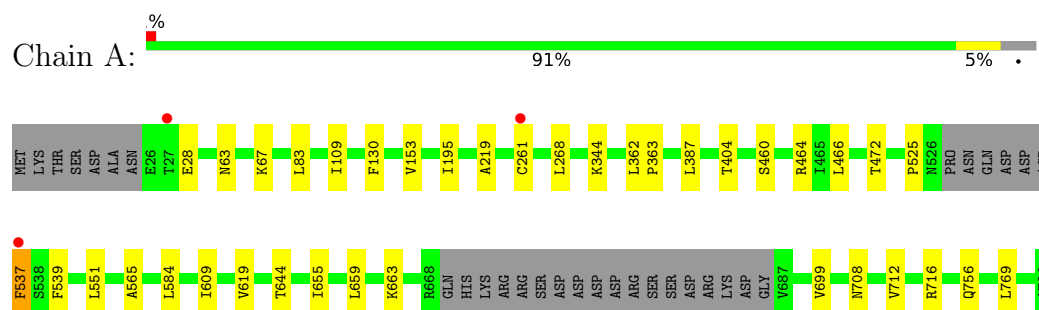
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	G	1	Total	C	N	O	P	0	0
			33	11	5	14	3		
4	J	1	Total	C	N	O	P	0	0
			33	11	5	14	3		

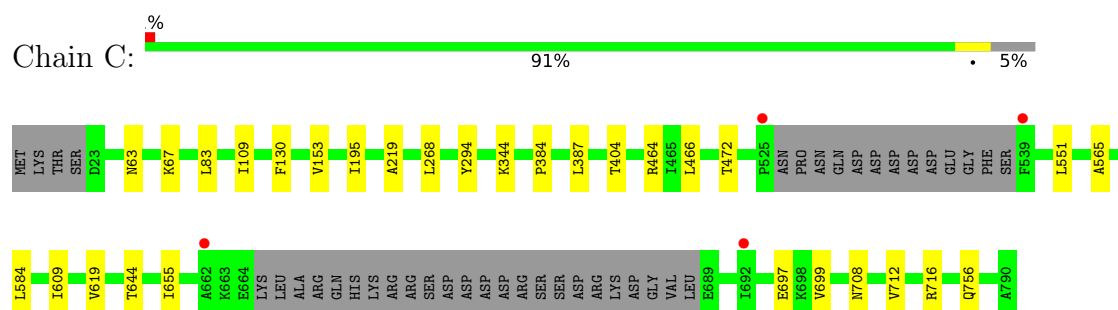
3 Residue-property plots [i](#)

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.

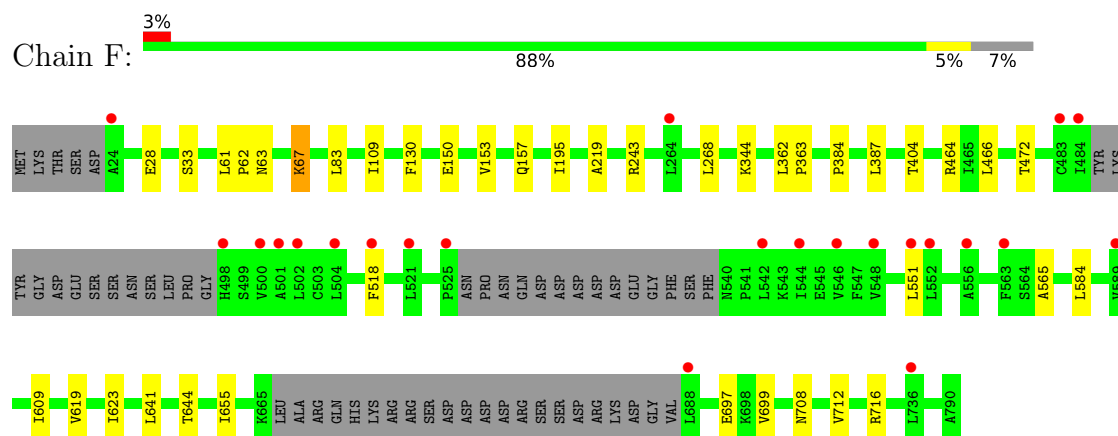
- Molecule 1: Nuclear cap-binding protein subunit 1



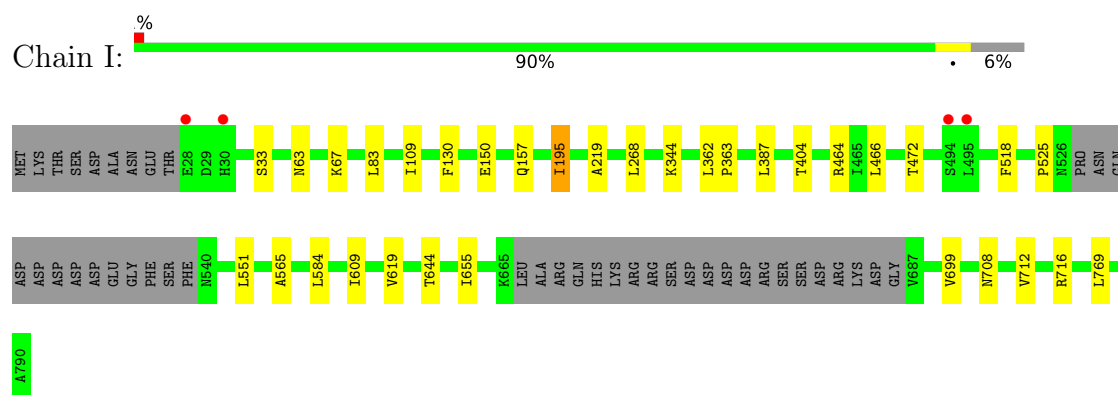
- Molecule 1: Nuclear cap-binding protein subunit 1



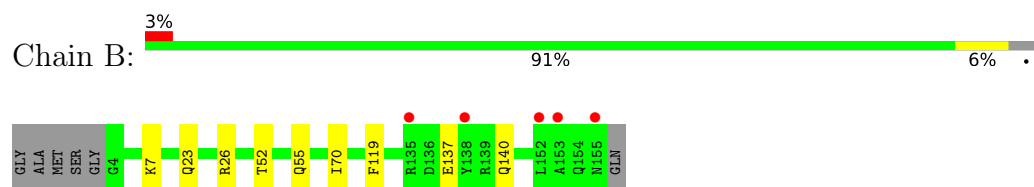
- Molecule 1: Nuclear cap-binding protein subunit 1



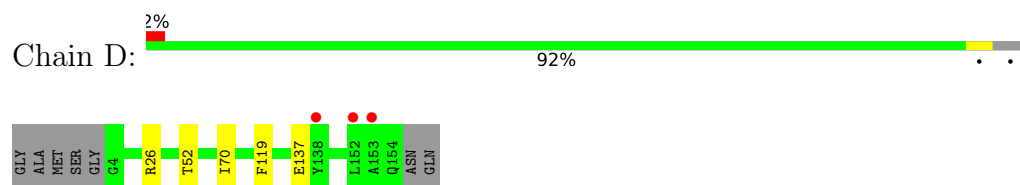
- Molecule 1: Nuclear cap-binding protein subunit 1



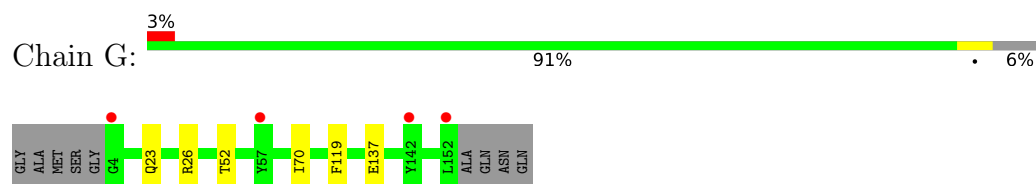
- Molecule 2: Nuclear cap-binding protein subunit 2



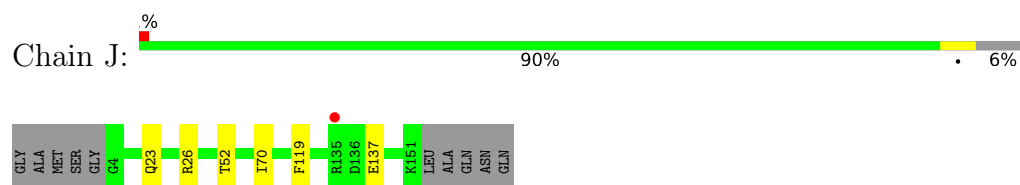
- Molecule 2: Nuclear cap-binding protein subunit 2



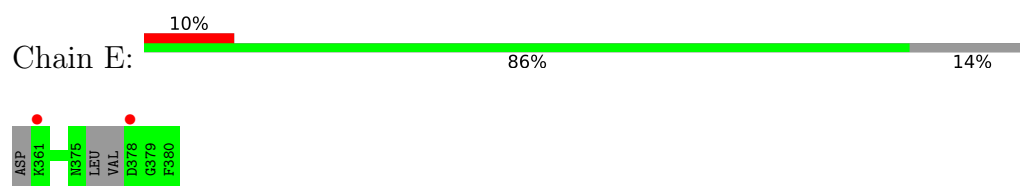
- Molecule 2: Nuclear cap-binding protein subunit 2



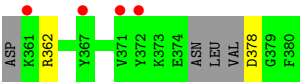
- Molecule 2: Nuclear cap-binding protein subunit 2



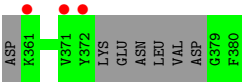
- Molecule 3: Negative elongation factor E



- Molecule 3: Negative elongation factor E



● Molecule 3: Negative elongation factor E



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	113.80Å 147.23Å 153.88Å 90.00° 91.48° 90.00°	Depositor
Resolution (Å)	153.83 – 2.79 153.83 – 2.79	Depositor EDS
% Data completeness (in resolution range)	98.3 (153.83-2.79) 98.3 (153.83-2.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.202 , 0.229 0.206 , 0.229	Depositor DCC
R_{free} test set	6345 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	63.0	Xtriage
Anisotropy	0.518	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.002 for -h,l,k 0.012 for -h,-l,-k 0.023 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	29296	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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: MGT

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	0.62	0/6198	0.88	0/8408
1	C	0.64	0/6132	0.89	0/8321
1	F	0.62	0/6026	0.88	0/8175
1	I	0.64	0/6115	0.89	0/8297
2	B	0.64	0/1257	0.88	0/1677
2	D	0.64	0/1249	0.86	0/1666
2	G	0.61	0/1235	0.85	0/1647
2	J	0.64	0/1227	0.85	0/1636
3	E	0.81	0/151	0.77	0/200
3	K	0.82	0/143	0.76	0/189
3	Z	0.80	0/117	0.72	0/155
All	All	0.63	0/29850	0.88	0/40371

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6045	0	6028	17	0
1	C	5980	0	5952	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	5879	0	5876	17	0
1	I	5964	0	5954	13	0
2	B	1237	0	1193	2	0
2	D	1229	0	1187	1	0
2	G	1215	0	1174	1	0
2	J	1207	0	1163	1	0
3	E	150	0	129	0	0
3	K	142	0	123	0	0
3	Z	116	0	100	0	0
4	B	33	0	16	0	0
4	D	33	0	16	0	0
4	G	33	0	16	0	0
4	J	33	0	16	0	0
All	All	29296	0	28943	61	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 1.

All (61) 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:C:609:ILE:HD11	1:C:619:VAL:HG21	1.63	0.81
1:F:609:ILE:HD11	1:F:619:VAL:HG21	1.61	0.80
1:I:609:ILE:HD11	1:I:619:VAL:HG21	1.62	0.79
1:A:609:ILE:HD11	1:A:619:VAL:HG21	1.63	0.77
1:A:659:LEU:HG	1:A:663:LYS:HE3	1.67	0.75
1:C:384:PRO:HG3	1:I:769:LEU:HD21	1.85	0.56
1:I:150:GLU:HG3	1:I:195:ILE:HD11	1.89	0.54
1:I:655:ILE:HG22	1:I:699:VAL:HG22	1.90	0.54
1:C:655:ILE:HG22	1:C:699:VAL:HG22	1.90	0.53
1:F:655:ILE:HG22	1:F:699:VAL:HG22	1.90	0.52
1:A:655:ILE:HG22	1:A:699:VAL:HG22	1.92	0.51
1:F:708:ASN:O	1:F:712:VAL:HG23	2.12	0.50
1:I:708:ASN:O	1:I:712:VAL:HG23	2.12	0.50
1:C:551:LEU:HD11	1:C:565:ALA:HB1	1.94	0.49
1:C:708:ASN:O	1:C:712:VAL:HG23	2.12	0.49
1:A:551:LEU:HD11	1:A:565:ALA:HB1	1.95	0.49
1:F:150:GLU:HG3	1:F:195:ILE:HD11	1.95	0.49
1:F:551:LEU:HD11	1:F:565:ALA:HB1	1.95	0.49
1:A:261:CYS:SG	1:C:294:TYR:CZ	3.06	0.49
1:A:708:ASN:O	1:A:712:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:28:GLU:HG2	1:F:67:LYS:NZ	2.29	0.48
1:F:609:ILE:HD13	1:F:644:THR:HG23	1.95	0.48
1:A:769:LEU:HD21	1:F:384:PRO:HG3	1.94	0.48
1:I:609:ILE:HD13	1:I:644:THR:HG23	1.96	0.47
1:A:609:ILE:HD13	1:A:644:THR:HG23	1.95	0.47
1:A:109:ILE:HD11	1:A:268:LEU:HD22	1.96	0.47
1:I:551:LEU:HD11	1:I:565:ALA:HB1	1.96	0.47
1:F:109:ILE:HD11	1:F:268:LEU:HD22	1.95	0.46
1:C:609:ILE:HD13	1:C:644:THR:HG23	1.96	0.46
2:D:70:ILE:HD13	2:D:119:PHE:CG	2.51	0.45
1:I:219:ALA:HB2	1:I:404:THR:HG21	1.98	0.45
1:C:109:ILE:HD11	1:C:268:LEU:HD22	1.97	0.45
1:A:219:ALA:HB2	1:A:404:THR:HG21	1.97	0.45
2:B:70:ILE:HD13	2:B:119:PHE:CG	2.52	0.45
1:C:153:VAL:HG21	1:C:195:ILE:HG23	1.98	0.45
1:I:109:ILE:HD11	1:I:268:LEU:HD22	1.98	0.45
1:C:83:LEU:HD11	1:C:130:PHE:HA	1.99	0.45
1:F:219:ALA:HB2	1:F:404:THR:HG21	1.99	0.45
1:C:219:ALA:HB2	1:C:404:THR:HG21	1.98	0.44
2:J:70:ILE:HD13	2:J:119:PHE:CG	2.53	0.44
1:A:83:LEU:HD11	1:A:130:PHE:HA	1.99	0.44
1:A:712:VAL:O	1:A:716:ARG:HG2	2.18	0.44
2:G:70:ILE:HD13	2:G:119:PHE:CG	2.53	0.43
1:C:63:ASN:N	1:C:63:ASN:OD1	2.52	0.43
1:F:63:ASN:N	1:F:63:ASN:OD1	2.52	0.42
1:F:153:VAL:HG21	1:F:195:ILE:HG23	2.01	0.42
1:A:63:ASN:OD1	1:A:63:ASN:N	2.52	0.42
1:A:153:VAL:HG21	1:A:195:ILE:HG23	2.00	0.42
1:I:712:VAL:O	1:I:716:ARG:HG2	2.18	0.42
1:F:83:LEU:HD11	1:F:130:PHE:HA	2.00	0.42
1:C:712:VAL:O	1:C:716:ARG:HG2	2.19	0.42
1:F:712:VAL:O	1:F:716:ARG:HG2	2.19	0.42
1:I:63:ASN:OD1	1:I:63:ASN:N	2.51	0.42
1:I:83:LEU:HD11	1:I:130:PHE:HA	2.02	0.41
1:A:460:SER:O	2:B:55:GLN:NE2	2.54	0.41
1:A:659:LEU:O	1:A:663:LYS:HG3	2.21	0.41
1:A:362:LEU:HA	1:A:363:PRO:C	2.46	0.41
1:I:362:LEU:HA	1:I:363:PRO:C	2.46	0.41
1:F:623:ILE:HD13	1:F:641:LEU:HB2	2.03	0.41
1:F:61:LEU:N	1:F:62:PRO:HD2	2.37	0.40
1:F:362:LEU:HA	1:F:363:PRO:C	2.46	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	733/772 (95%)	715 (98%)	15 (2%)	3 (0%)	30	60
1	C	725/772 (94%)	709 (98%)	16 (2%)	0	100	100
1	F	710/772 (92%)	697 (98%)	13 (2%)	0	100	100
1	I	723/772 (94%)	707 (98%)	15 (2%)	1 (0%)	48	77
2	B	150/158 (95%)	140 (93%)	9 (6%)	1 (1%)	18	47
2	D	149/158 (94%)	139 (93%)	9 (6%)	1 (1%)	18	47
2	G	147/158 (93%)	138 (94%)	8 (5%)	1 (1%)	18	47
2	J	146/158 (92%)	135 (92%)	10 (7%)	1 (1%)	18	47
3	E	14/21 (67%)	12 (86%)	2 (14%)	0	100	100
3	K	13/21 (62%)	11 (85%)	2 (15%)	0	100	100
3	Z	10/21 (48%)	10 (100%)	0	0	100	100
All	All	3520/3783 (93%)	3413 (97%)	99 (3%)	8 (0%)	43	72

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	26	ARG
2	D	26	ARG
2	G	26	ARG
2	J	26	ARG
1	A	525	PRO
1	A	539	PHE
1	I	525	PRO
1	A	537	PHE

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	677/708 (96%)	666 (98%)	11 (2%)	55	83
1	C	670/708 (95%)	661 (99%)	9 (1%)	61	86
1	F	659/708 (93%)	647 (98%)	12 (2%)	51	82
1	I	669/708 (94%)	658 (98%)	11 (2%)	55	83
2	B	127/130 (98%)	122 (96%)	5 (4%)	28	64
2	D	126/130 (97%)	124 (98%)	2 (2%)	55	83
2	G	125/130 (96%)	122 (98%)	3 (2%)	43	77
2	J	124/130 (95%)	121 (98%)	3 (2%)	43	77
3	E	16/20 (80%)	16 (100%)	0	100	100
3	K	15/20 (75%)	13 (87%)	2 (13%)	4	14
3	Z	12/20 (60%)	12 (100%)	0	100	100
All	All	3220/3412 (94%)	3162 (98%)	58 (2%)	51	82

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	GLU
1	A	67	LYS
1	A	344	LYS
1	A	387	LEU
1	A	464	ARG
1	A	466	LEU
1	A	472	THR
1	A	535	GLU
1	A	537	PHE
1	A	584	LEU
1	A	756	GLN
2	B	7	LYS
2	B	23	GLN
2	B	52	THR
2	B	137	GLU

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Mol	Chain	Res	Type
2	B	140	GLN
1	C	67	LYS
1	C	344	LYS
1	C	387	LEU
1	C	464	ARG
1	C	466	LEU
1	C	472	THR
1	C	584	LEU
1	C	697	GLU
1	C	756	GLN
2	D	52	THR
2	D	137	GLU
1	F	33	SER
1	F	67	LYS
1	F	157	GLN
1	F	243	ARG
1	F	344	LYS
1	F	387	LEU
1	F	464	ARG
1	F	466	LEU
1	F	472	THR
1	F	518	PHE
1	F	584	LEU
1	F	697	GLU
2	G	23	GLN
2	G	52	THR
2	G	137	GLU
1	I	33	SER
1	I	67	LYS
1	I	157	GLN
1	I	195	ILE
1	I	344	LYS
1	I	387	LEU
1	I	464	ARG
1	I	466	LEU
1	I	472	THR
1	I	518	PHE
1	I	584	LEU
2	J	23	GLN
2	J	52	THR
2	J	137	GLU
3	K	362	ARG

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Mol	Chain	Res	Type
3	K	378	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	367	HIS
1	A	439	GLN
1	A	462	HIS
1	A	480	ASN
1	A	553	HIS
1	A	642	HIS
1	A	649	ASN
1	A	706	GLN
1	A	708	ASN
1	A	753	GLN
1	A	759	GLN
2	B	154	GLN
1	C	237	GLN
1	C	367	HIS
1	C	389	GLN
1	C	439	GLN
1	C	462	HIS
1	C	480	ASN
1	C	642	HIS
1	C	706	GLN
1	C	759	GLN
1	F	122	ASN
1	F	367	HIS
1	F	439	GLN
1	F	462	HIS
1	F	480	ASN
1	F	642	HIS
1	F	649	ASN
1	F	706	GLN
1	F	753	GLN
1	F	759	GLN
1	I	49	ASN
1	I	237	GLN
1	I	367	HIS
1	I	439	GLN
1	I	462	HIS
1	I	480	ASN

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Mol	Chain	Res	Type
1	I	642	HIS
1	I	649	ASN
1	I	706	GLN
1	I	715	GLN
3	K	364	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	MGT	B	201	-	34,35,35	1.52	6 (17%)	45,56,56	2.18	9 (20%)
4	MGT	J	201	-	34,35,35	1.66	7 (20%)	45,56,56	2.11	8 (17%)
4	MGT	G	201	-	34,35,35	1.74	7 (20%)	45,56,56	2.13	9 (20%)
4	MGT	D	201	-	34,35,35	1.35	6 (17%)	45,56,56	2.11	8 (17%)

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	MGT	B	201	-	-	8/22/50/50	0/3/3/3
4	MGT	J	201	-	-	5/22/50/50	0/3/3/3
4	MGT	G	201	-	-	3/22/50/50	0/3/3/3
4	MGT	D	201	-	-	8/22/50/50	0/3/3/3

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	201	MGT	PA-O3A	4.72	1.64	1.59
4	B	201	MGT	PB-O3B	4.50	1.64	1.59
4	G	201	MGT	PB-O3A	4.04	1.63	1.59
4	B	201	MGT	C4-N9	-3.96	1.33	1.37
4	J	201	MGT	PA-O3A	3.84	1.63	1.59
4	J	201	MGT	PB-O3A	3.83	1.63	1.59
4	D	201	MGT	C4-N9	-3.63	1.33	1.37
4	G	201	MGT	C5-C4	3.53	1.48	1.37
4	J	201	MGT	C5-C4	3.46	1.48	1.37
4	G	201	MGT	C4-N9	-3.36	1.33	1.37
4	J	201	MGT	PB-O3B	3.34	1.63	1.59
4	G	201	MGT	PB-O3B	3.33	1.63	1.59
4	D	201	MGT	C5-C4	3.16	1.47	1.37
4	B	201	MGT	C5-C4	3.14	1.47	1.37
4	J	201	MGT	C4-N9	-2.90	1.34	1.37
4	D	201	MGT	C5-N7	-2.55	1.32	1.35
4	B	201	MGT	C6-N1	-2.46	1.34	1.38
4	D	201	MGT	C6-N1	-2.41	1.34	1.38
4	D	201	MGT	PA-O3A	2.39	1.62	1.59
4	B	201	MGT	C5-N7	-2.38	1.32	1.35
4	J	201	MGT	C1'-N9	2.22	1.50	1.46
4	J	201	MGT	C5-C6	2.18	1.48	1.43
4	D	201	MGT	PB-O3A	2.17	1.61	1.59
4	G	201	MGT	C5-C6	2.16	1.48	1.43
4	B	201	MGT	C1'-N9	2.10	1.50	1.46
4	G	201	MGT	C6-N1	-2.08	1.35	1.38

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	201	MGT	N9-C4-N3	8.24	137.53	125.46
4	J	201	MGT	N9-C4-N3	8.05	137.25	125.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	201	MGT	N9-C4-N3	7.84	136.95	125.46
4	B	201	MGT	N9-C4-N3	7.68	136.72	125.46
4	B	201	MGT	O4'-C1'-N9	6.17	117.71	109.30
4	J	201	MGT	C5-C4-N3	-5.47	117.85	128.13
4	B	201	MGT	C5-C4-N3	-5.18	118.41	128.13
4	G	201	MGT	C5-C4-N3	-5.11	118.53	128.13
4	D	201	MGT	C5-C4-N3	-5.11	118.54	128.13
4	D	201	MGT	N9-C8-N7	-5.11	96.14	103.37
4	G	201	MGT	O4'-C1'-N9	4.83	115.87	109.30
4	J	201	MGT	C2-N3-C4	4.64	120.29	112.30
4	G	201	MGT	C2-N3-C4	4.56	120.15	112.30
4	B	201	MGT	C2-N3-C4	4.43	119.92	112.30
4	G	201	MGT	N9-C8-N7	-4.39	97.16	103.37
4	B	201	MGT	N9-C8-N7	-4.38	97.17	103.37
4	J	201	MGT	N9-C8-N7	-4.24	97.37	103.37
4	D	201	MGT	C2-N3-C4	3.81	118.86	112.30
4	J	201	MGT	O4'-C1'-N9	3.72	114.37	109.30
4	D	201	MGT	O4'-C1'-N9	3.49	114.05	109.30
4	D	201	MGT	O3G-PG-O2G	2.82	118.37	107.80
4	G	201	MGT	C5-C6-N1	2.80	115.87	110.94
4	J	201	MGT	O2A-PA-O3A	2.67	114.49	107.27
4	G	201	MGT	O3G-PG-O2G	2.62	117.62	107.80
4	D	201	MGT	O2B-PB-O3B	2.60	114.29	107.27
4	J	201	MGT	C5-C6-N1	2.57	115.46	110.94
4	J	201	MGT	O3G-PG-O2G	2.45	117.00	107.80
4	B	201	MGT	O3G-PG-O2G	2.39	116.76	107.80
4	B	201	MGT	C5-C6-N1	2.38	115.12	110.94
4	B	201	MGT	O3A-PB-O1B	-2.32	103.71	110.70
4	B	201	MGT	O2A-PA-O3A	2.30	113.48	107.27
4	D	201	MGT	C5-C6-N1	2.24	114.88	110.94
4	G	201	MGT	C6-C5-C4	-2.06	118.77	122.40
4	G	201	MGT	O2A-PA-O3A	2.06	112.85	107.27

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	201	MGT	PB-O3B-PG-O2G
4	B	201	MGT	C5'-O5'-PA-O3A
4	B	201	MGT	C5'-O5'-PA-O1A
4	D	201	MGT	PB-O3B-PG-O2G
4	D	201	MGT	PB-O3B-PG-O3G

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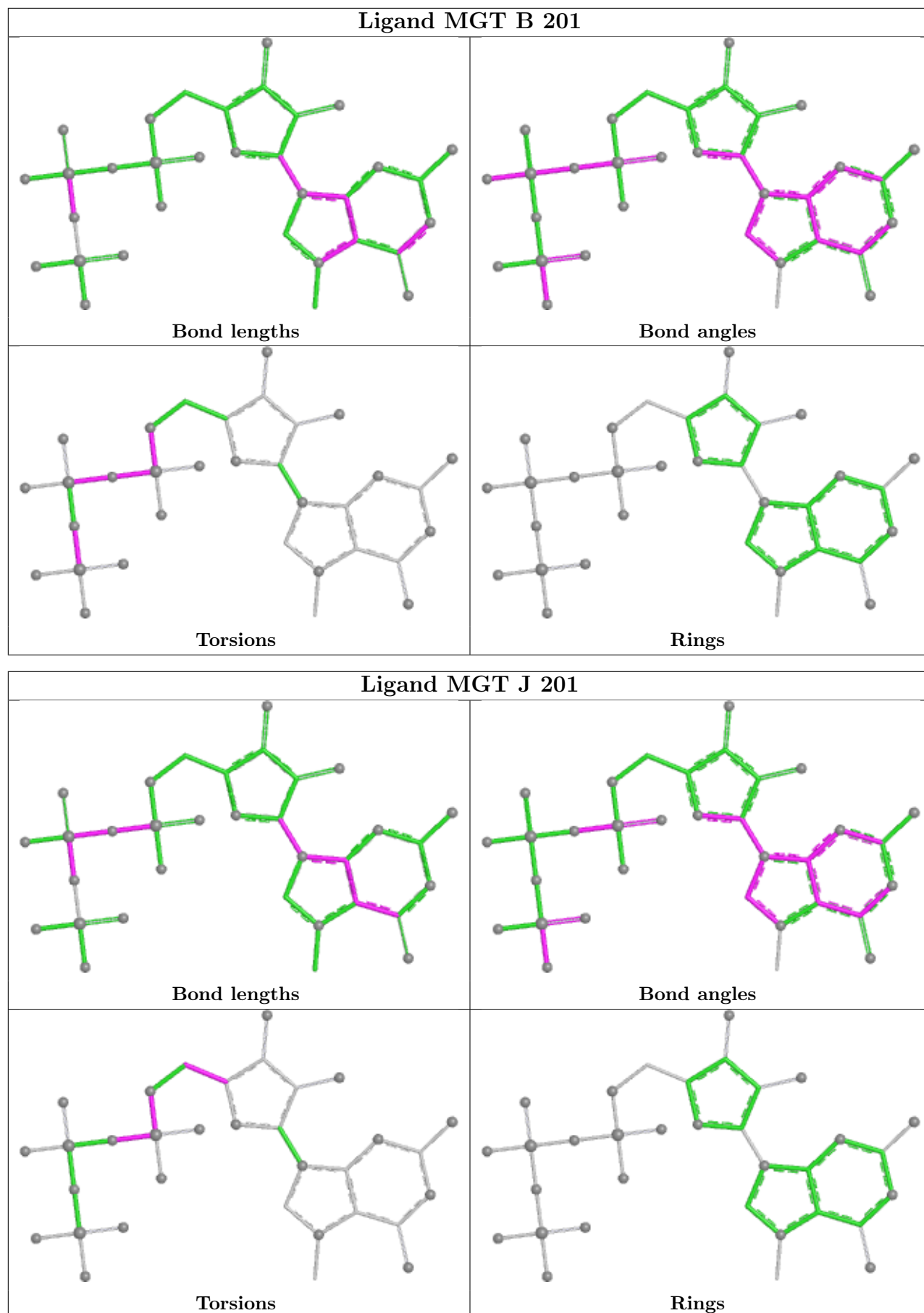
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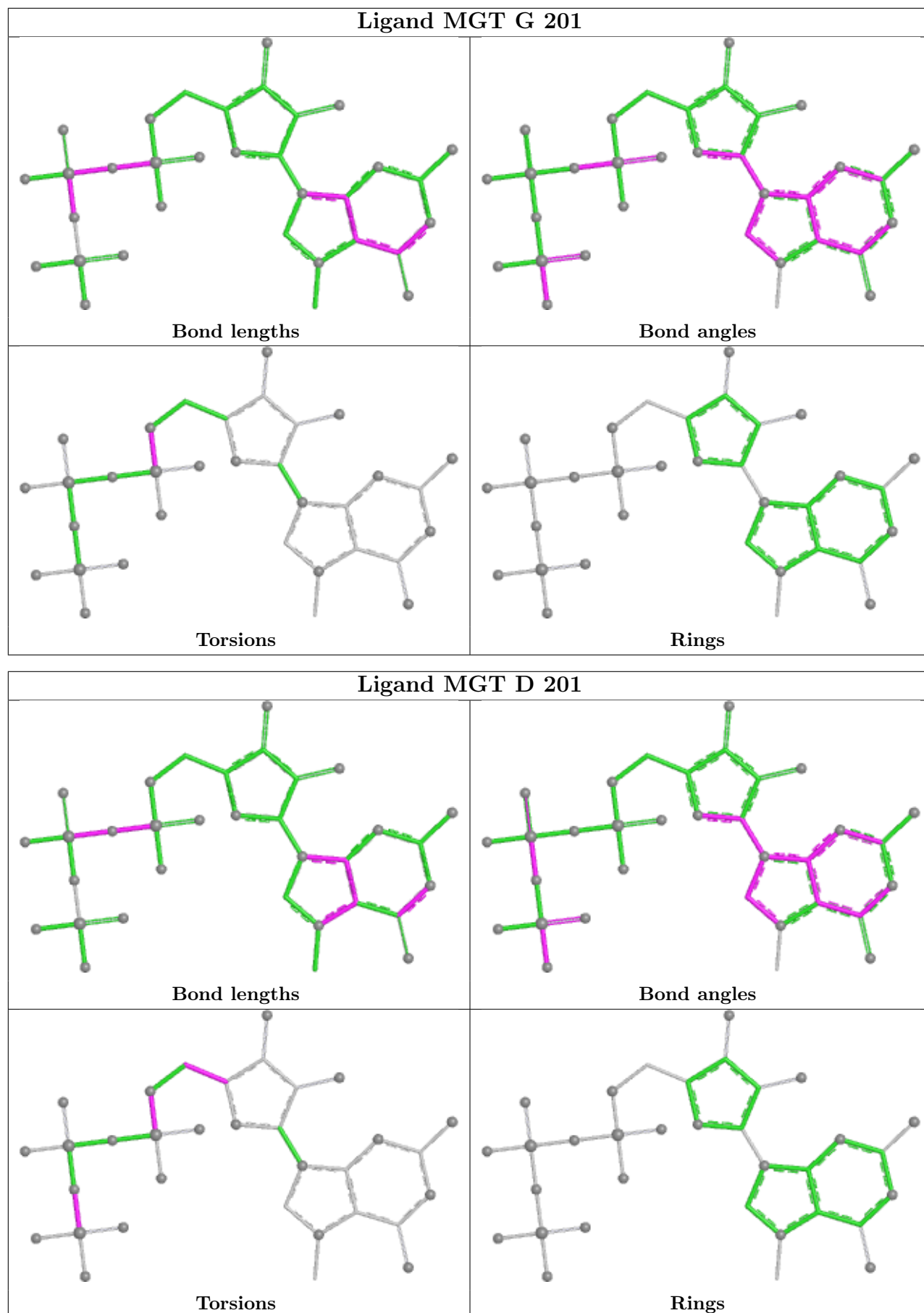
Mol	Chain	Res	Type	Atoms
4	D	201	MGT	C5'-O5'-PA-O1A
4	G	201	MGT	C5'-O5'-PA-O3A
4	G	201	MGT	C5'-O5'-PA-O1A
4	G	201	MGT	C5'-O5'-PA-O2A
4	J	201	MGT	C5'-O5'-PA-O3A
4	J	201	MGT	C5'-O5'-PA-O1A
4	D	201	MGT	O4'-C4'-C5'-O5'
4	B	201	MGT	PB-O3A-PA-O1A
4	B	201	MGT	C5'-O5'-PA-O2A
4	D	201	MGT	C5'-O5'-PA-O3A
4	D	201	MGT	C5'-O5'-PA-O2A
4	J	201	MGT	C5'-O5'-PA-O2A
4	B	201	MGT	PB-O3A-PA-O2A
4	J	201	MGT	O4'-C4'-C5'-O5'
4	D	201	MGT	PB-O3B-PG-O1G
4	B	201	MGT	PB-O3B-PG-O3G
4	B	201	MGT	PA-O3A-PB-O2B
4	D	201	MGT	C3'-C4'-C5'-O5'
4	J	201	MGT	PB-O3A-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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





5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	739/772 (95%)	0.02	4 (0%) 87 82	40, 71, 117, 173	0
1	C	731/772 (94%)	-0.20	4 (0%) 87 82	33, 59, 98, 141	0
1	F	718/772 (93%)	0.25	23 (3%) 50 40	43, 77, 144, 193	0
1	I	729/772 (94%)	-0.03	4 (0%) 87 82	42, 66, 105, 144	0
2	B	152/158 (96%)	0.06	5 (3%) 49 39	43, 68, 110, 142	0
2	D	151/158 (95%)	0.05	3 (1%) 65 56	38, 68, 108, 127	0
2	G	149/158 (94%)	0.41	4 (2%) 56 46	59, 86, 118, 140	0
2	J	148/158 (93%)	0.28	1 (0%) 84 77	46, 79, 119, 144	0
3	E	18/21 (85%)	1.13	2 (11%) 10 7	84, 104, 133, 135	0
3	K	17/21 (80%)	1.42	4 (23%) 2 1	86, 114, 143, 143	0
3	Z	14/21 (66%)	1.24	3 (21%) 2 2	98, 107, 140, 157	0
All	All	3566/3783 (94%)	0.06	57 (1%) 70 61	33, 70, 121, 193	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	155	ASN	4.7
1	F	264	LEU	4.1
3	Z	361	LYS	4.1
1	F	544	ILE	4.0
2	G	152	LEU	4.0
1	F	525	PRO	3.7
3	K	361	LYS	3.7
2	D	152	LEU	3.6
1	A	537	PHE	3.6
1	F	552	LEU	3.6
1	F	518	PHE	3.6
2	B	138	TYR	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	539	PHE	3.3
2	G	142	TYR	3.2
1	F	548	VAL	3.1
3	E	378	ASP	3.1
1	F	484	ILE	3.0
1	F	483	CYS	3.0
1	F	24	ALA	2.9
1	F	498	HIS	2.9
1	F	500	VAL	2.9
2	J	135	ARG	2.8
1	F	501	ALA	2.8
3	E	361	LYS	2.8
2	B	152	LEU	2.8
3	Z	372	TYR	2.8
1	I	30	HIS	2.8
2	D	138	TYR	2.8
1	F	521	LEU	2.7
1	F	542	LEU	2.7
1	C	525	PRO	2.6
2	B	153	ALA	2.6
1	F	504	LEU	2.6
3	K	367	TYR	2.6
1	F	546	VAL	2.5
1	C	692	ILE	2.5
3	Z	371	VAL	2.5
1	C	662	ALA	2.5
1	A	536	GLY	2.4
3	K	371	VAL	2.4
1	F	556	ALA	2.4
1	I	494	SER	2.4
2	G	57	TYR	2.3
1	A	27	THR	2.3
2	B	135	ARG	2.3
1	F	589	VAL	2.3
1	I	495	LEU	2.3
1	F	551	LEU	2.2
1	F	563	PHE	2.2
1	I	28	GLU	2.2
1	F	688	LEU	2.2
1	F	736	LEU	2.1
1	F	502	LEU	2.1
2	G	4	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	153	ALA	2.0
1	A	261	CYS	2.0
3	K	372	TYR	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

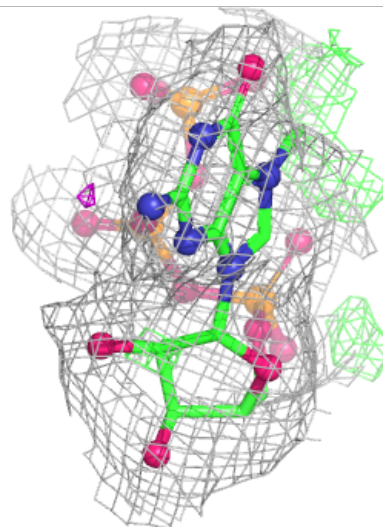
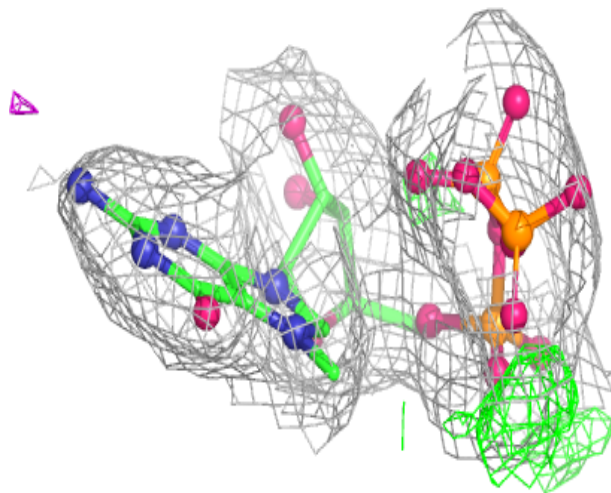
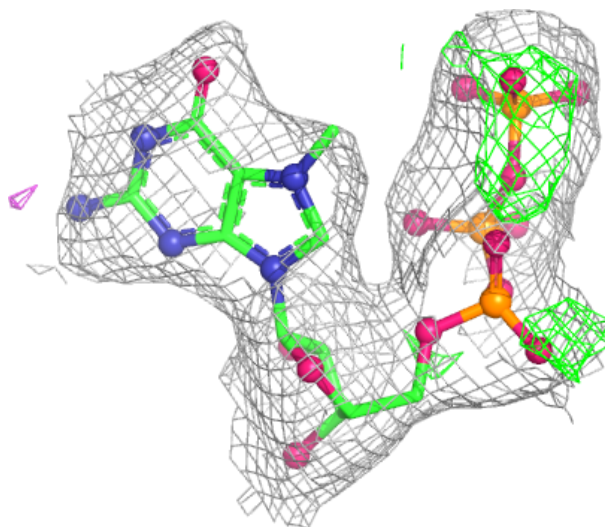
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MGT	J	201	33/33	0.92	0.08	57,74,91,105	0
4	MGT	G	201	33/33	0.94	0.07	68,76,88,102	0
4	MGT	B	201	33/33	0.96	0.06	55,64,74,79	0
4	MGT	D	201	33/33	0.96	0.07	52,60,73,82	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.

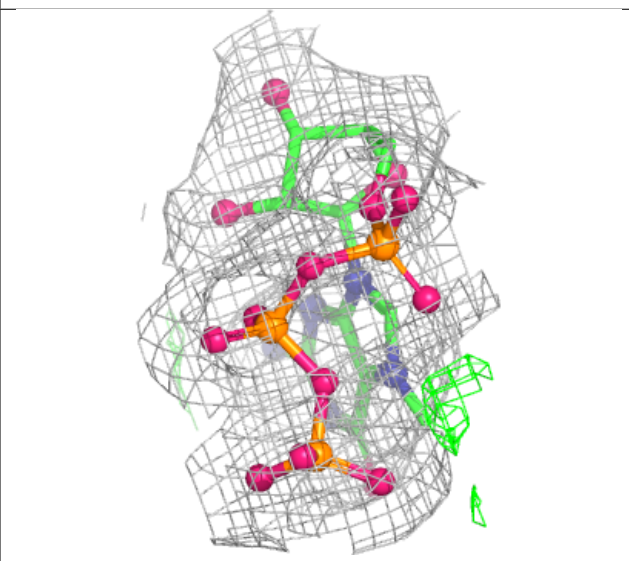
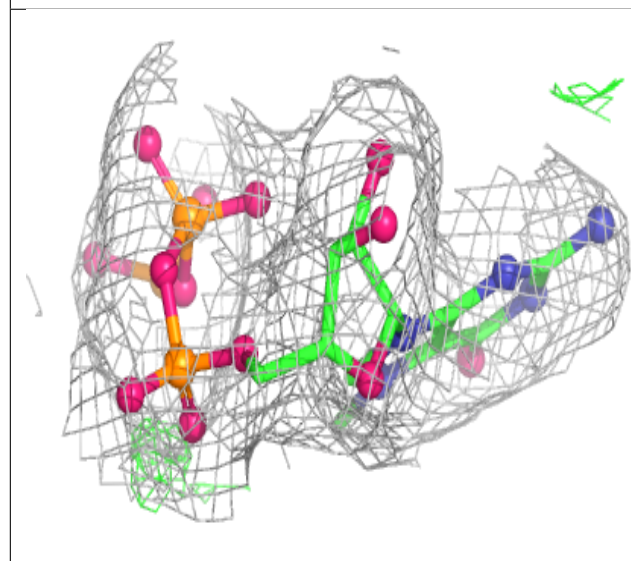
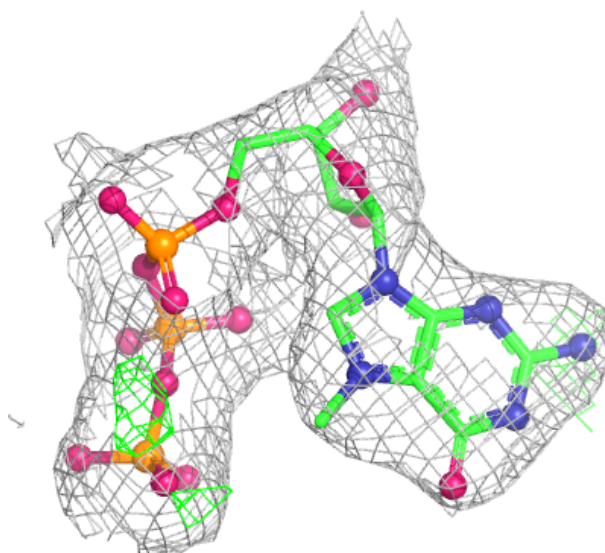
Electron density around MGT J 201:

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



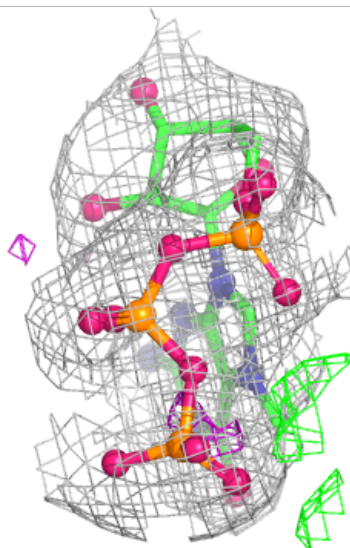
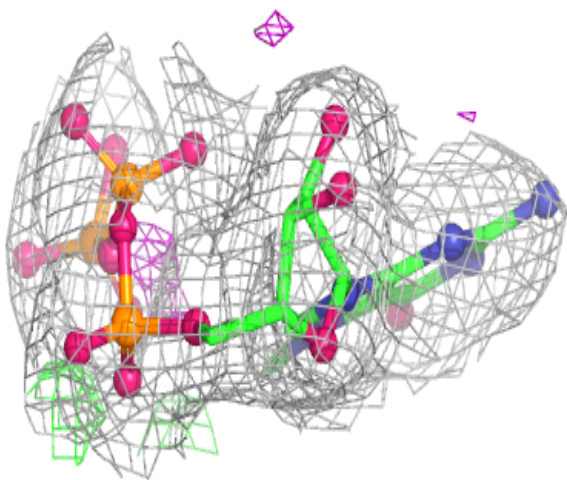
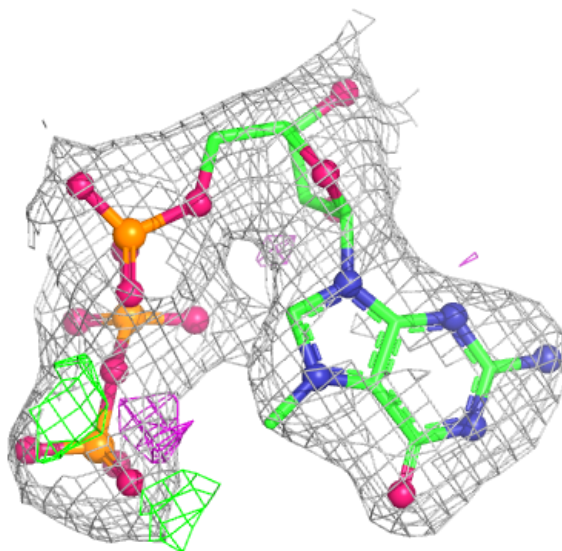
Electron density around MGT G 201:

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



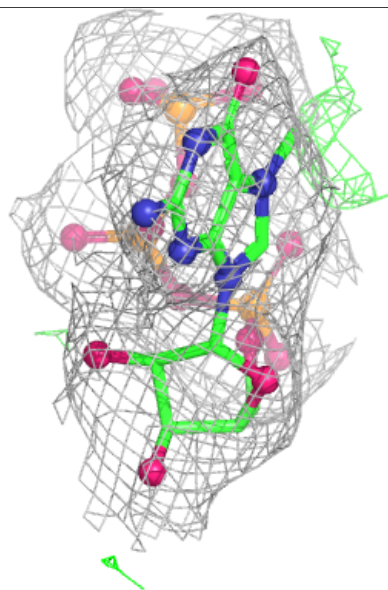
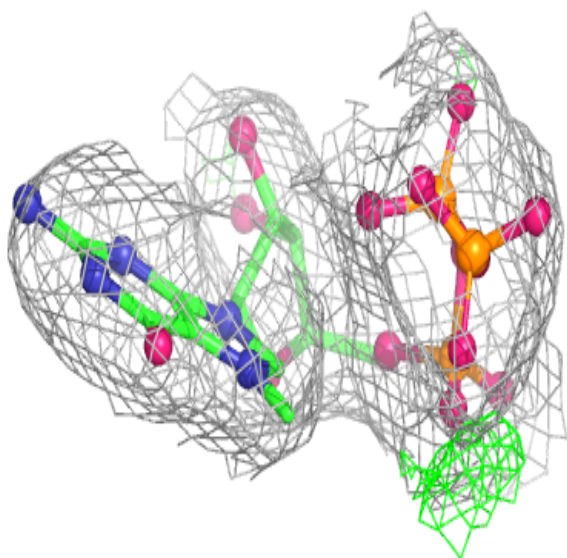
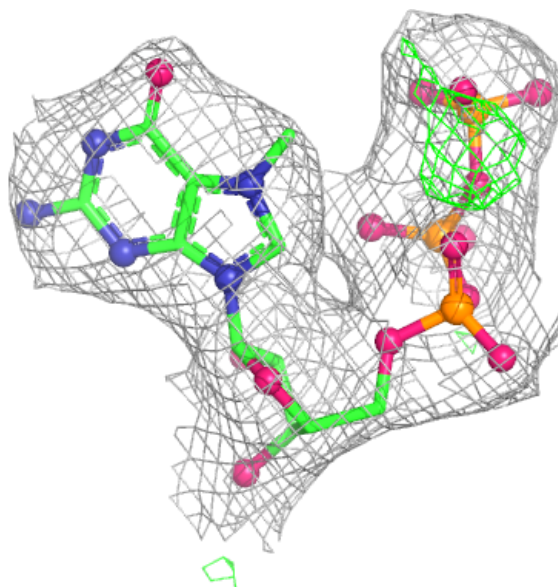
Electron density around MGT B 201:

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



Electron density around MGT D 201:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.