



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:27 AM UTC

PDB ID : 7XD9 / pdb_00007xd9
Title : Crystal Structure of Dengue Virus serotype 2 (DENV2) Polymerase Elongation Complex (CTP Form)
Authors : Wu, J.; Wang, X.; Gong, P.
Deposited on : 2022-03-26
Resolution : 2.58 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

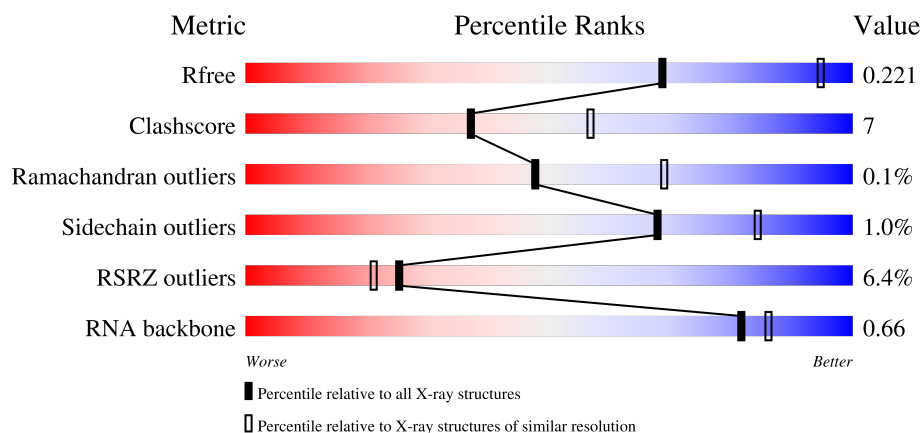
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)
RNA backbone	3983	1011 (2.82-2.34)

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	647	3% 83% 13% .
1	D	647	2% 81% 15% .
1	G	647	2% 82% 14% .
1	J	647	4% 79% 18% .

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Mol	Chain	Length	Quality of chain
1	M	647	 % 79% 17% •
1	P	647	 23% 73% 21% • 5%
2	B	30	 3% 27% 13% 60%
2	E	30	 7% 37% • • 57%
2	H	30	 30% 7% • 60%
2	K	30	 17% 37% 17% 47%
2	N	30	 17% 43% 20% 37%
2	Q	30	 7% 37% • 60%
3	C	9	 67% 33%
3	F	9	 89% 11%
3	I	9	 78% 22%
3	L	9	 11% 89% 11%
3	O	9	 78% 22%
3	R	9	 67% 33%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 32878 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 NS5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	621	Total	C	N	O	S	0	0	0
			4913	3095	878	907	33			
1	D	622	Total	C	N	O	S	0	0	0
			4973	3131	886	922	34			
1	G	623	Total	C	N	O	S	0	0	0
			4913	3095	880	904	34			
1	J	625	Total	C	N	O	S	0	0	0
			4917	3100	872	911	34			
1	M	624	Total	C	N	O	S	0	0	0
			4929	3101	879	915	34			
1	P	616	Total	C	N	O	S	0	0	0
			4537	2851	818	834	34			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	901	GLY	-	expression tag	UNP Q91H74
A	902	SER	-	expression tag	UNP Q91H74
A	903	SER	-	expression tag	UNP Q91H74
A	904	SER	-	expression tag	UNP Q91H74
A	905	HIS	-	expression tag	UNP Q91H74
A	906	HIS	-	expression tag	UNP Q91H74
A	907	HIS	-	expression tag	UNP Q91H74
A	908	HIS	-	expression tag	UNP Q91H74
A	909	HIS	-	expression tag	UNP Q91H74
A	910	HIS	-	expression tag	UNP Q91H74
D	901	GLY	-	expression tag	UNP Q91H74
D	902	SER	-	expression tag	UNP Q91H74
D	903	SER	-	expression tag	UNP Q91H74
D	904	SER	-	expression tag	UNP Q91H74
D	905	HIS	-	expression tag	UNP Q91H74
D	906	HIS	-	expression tag	UNP Q91H74
D	907	HIS	-	expression tag	UNP Q91H74

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Chain	Residue	Modelled	Actual	Comment	Reference
D	908	HIS	-	expression tag	UNP Q91H74
D	909	HIS	-	expression tag	UNP Q91H74
D	910	HIS	-	expression tag	UNP Q91H74
G	901	GLY	-	expression tag	UNP Q91H74
G	902	SER	-	expression tag	UNP Q91H74
G	903	SER	-	expression tag	UNP Q91H74
G	904	SER	-	expression tag	UNP Q91H74
G	905	HIS	-	expression tag	UNP Q91H74
G	906	HIS	-	expression tag	UNP Q91H74
G	907	HIS	-	expression tag	UNP Q91H74
G	908	HIS	-	expression tag	UNP Q91H74
G	909	HIS	-	expression tag	UNP Q91H74
G	910	HIS	-	expression tag	UNP Q91H74
J	901	GLY	-	expression tag	UNP Q91H74
J	902	SER	-	expression tag	UNP Q91H74
J	903	SER	-	expression tag	UNP Q91H74
J	904	SER	-	expression tag	UNP Q91H74
J	905	HIS	-	expression tag	UNP Q91H74
J	906	HIS	-	expression tag	UNP Q91H74
J	907	HIS	-	expression tag	UNP Q91H74
J	908	HIS	-	expression tag	UNP Q91H74
J	909	HIS	-	expression tag	UNP Q91H74
J	910	HIS	-	expression tag	UNP Q91H74
M	901	GLY	-	expression tag	UNP Q91H74
M	902	SER	-	expression tag	UNP Q91H74
M	903	SER	-	expression tag	UNP Q91H74
M	904	SER	-	expression tag	UNP Q91H74
M	905	HIS	-	expression tag	UNP Q91H74
M	906	HIS	-	expression tag	UNP Q91H74
M	907	HIS	-	expression tag	UNP Q91H74
M	908	HIS	-	expression tag	UNP Q91H74
M	909	HIS	-	expression tag	UNP Q91H74
M	910	HIS	-	expression tag	UNP Q91H74
P	901	GLY	-	expression tag	UNP Q91H74
P	902	SER	-	expression tag	UNP Q91H74
P	903	SER	-	expression tag	UNP Q91H74
P	904	SER	-	expression tag	UNP Q91H74
P	905	HIS	-	expression tag	UNP Q91H74
P	906	HIS	-	expression tag	UNP Q91H74
P	907	HIS	-	expression tag	UNP Q91H74
P	908	HIS	-	expression tag	UNP Q91H74
P	909	HIS	-	expression tag	UNP Q91H74

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Chain	Residue	Modelled	Actual	Comment	Reference
P	910	HIS	-	expression tag	UNP Q91H74

- Molecule 2 is a RNA chain called RNA (30-mer).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	12	Total	C	N	O	P	0	0	0
			251	113	42	84	12			
2	E	13	Total	C	N	O	P	0	0	0
			273	123	47	90	13			
2	H	12	Total	C	N	O	P	0	0	0
			251	113	42	84	12			
2	K	16	Total	C	N	O	P	0	0	0
			336	152	60	109	15			
2	N	19	Total	C	N	O	P	0	0	0
			401	181	73	129	18			
2	Q	12	Total	C	N	O	P	0	0	0
			251	113	42	84	12			

- Molecule 3 is a RNA chain called RNA (9-mer).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	P	0	0	0
			195	87	36	63	9			
3	F	9	Total	C	N	O	P	0	0	0
			195	87	36	63	9			
3	I	9	Total	C	N	O	P	0	0	0
			195	87	36	63	9			
3	L	9	Total	C	N	O	P	0	0	0
			194	87	36	62	9			
3	O	9	Total	C	N	O	P	0	0	0
			195	87	36	63	9			
3	R	9	Total	C	N	O	P	0	0	0
			195	87	36	63	9			

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

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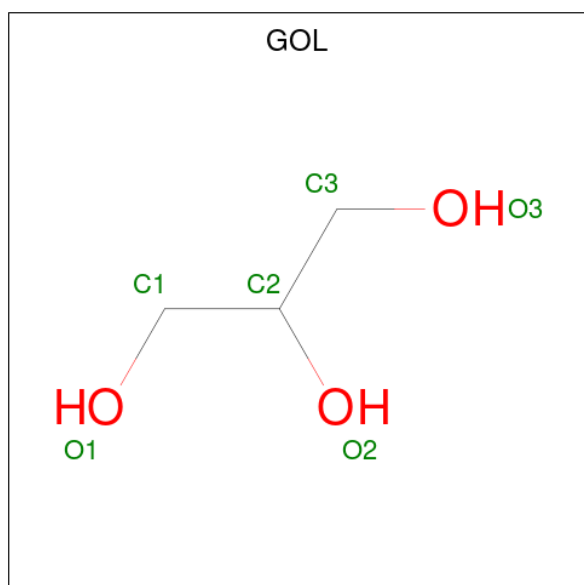
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	2	Total 2	Mg 2	0	0
4	J	2	Total 2	Mg 2	0	0
4	M	2	Total 2	Mg 2	0	0
4	P	2	Total 2	Mg 2	0	0

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

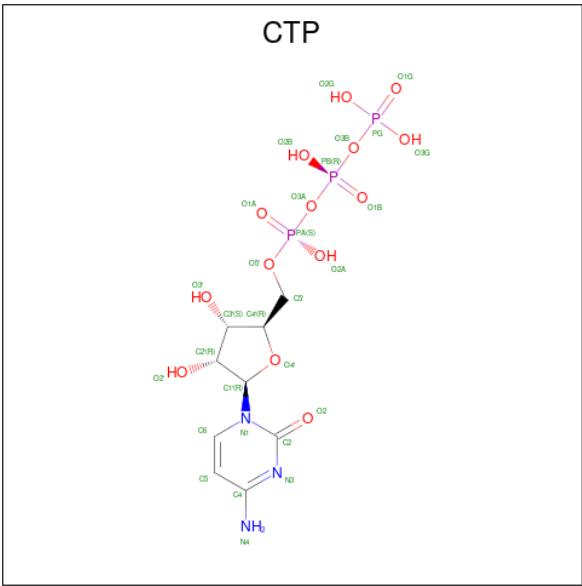
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total 2	Zn 2	0	0
5	D	2	Total 2	Zn 2	0	0
5	G	2	Total 2	Zn 2	0	0
5	J	2	Total 2	Zn 2	0	0
5	M	2	Total 2	Zn 2	0	0
5	P	2	Total 2	Zn 2	0	0

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		
6	E	1	Total	C	O	0	0
			6	3	3		
6	E	1	Total	C	O	0	0
			6	3	3		
6	H	1	Total	C	O	0	0
			6	3	3		
6	J	1	Total	C	O	0	0
			6	3	3		
6	K	1	Total	C	O	0	0
			6	3	3		
6	M	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is CYTIDINE-5'-TRIPHOSPHATE (CCD ID: CTP) (formula: C₉H₁₆N₃O₁₄P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			29	9	3	14	3		
7	D	1	Total	C	N	O	P	0	0
			29	9	3	14	3		
7	G	1	Total	C	N	O	P	0	0
			29	9	3	14	3		
7	J	1	Total	C	N	O	P	0	0
			29	9	3	14	3		
7	M	1	Total	C	N	O	P	0	0
			29	9	3	14	3		
7	P	1	Total	C	N	O	P	0	0
			29	9	3	14	3		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	98	Total	O	0	0
			98	98		
8	B	6	Total	O	0	0
			6	6		
8	C	3	Total	O	0	0
			3	3		
8	D	111	Total	O	0	0
			111	111		
8	E	8	Total	O	0	0
			8	8		
8	F	5	Total	O	0	0
			5	5		
8	G	74	Total	O	0	0
			74	74		
8	H	2	Total	O	0	0
			2	2		
8	I	2	Total	O	0	0
			2	2		
8	J	68	Total	O	0	0
			68	68		
8	K	2	Total	O	0	0
			2	2		
8	L	1	Total	O	0	0
			1	1		
8	M	84	Total	O	0	0
			84	84		
8	N	7	Total	O	0	0
			7	7		

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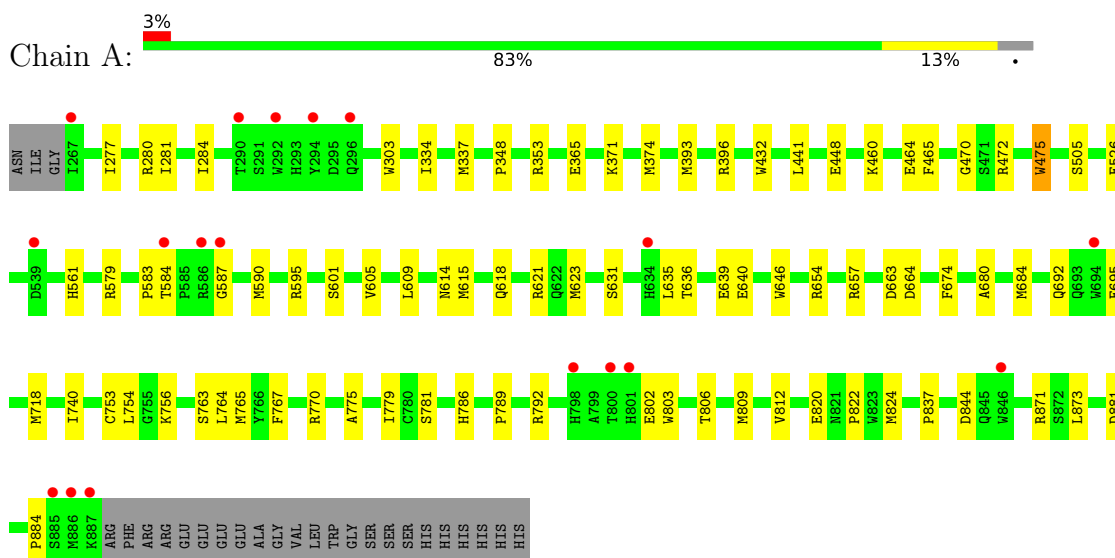
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	O	4	Total 4	O 4	0	0
8	P	18	Total 18	O 18	0	0
8	R	1	Total 1	O 1	0	0

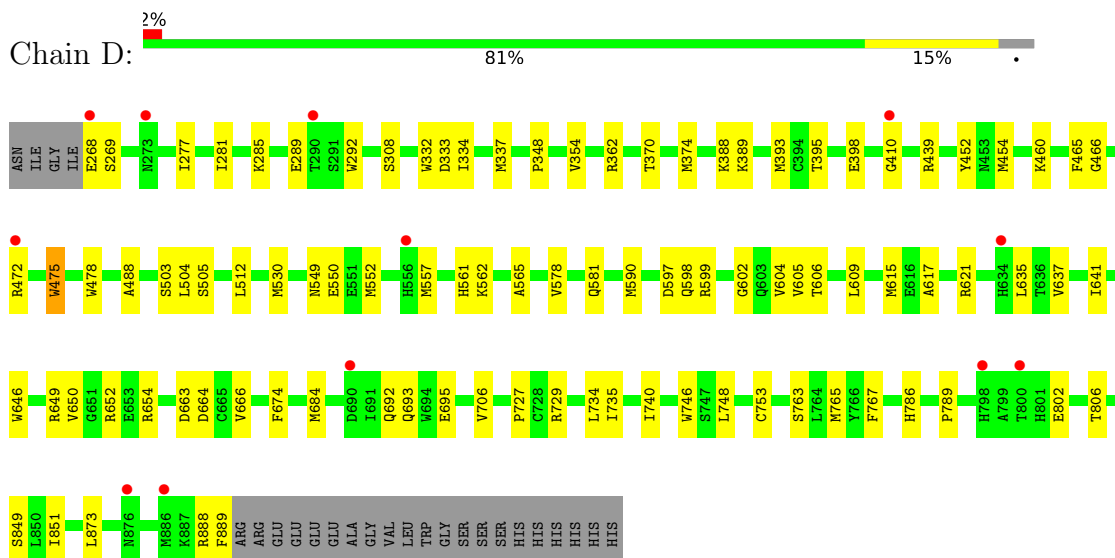
3 Residue-property plots [i](#)

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.

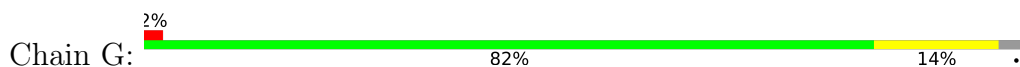
• Molecule 1: NS5

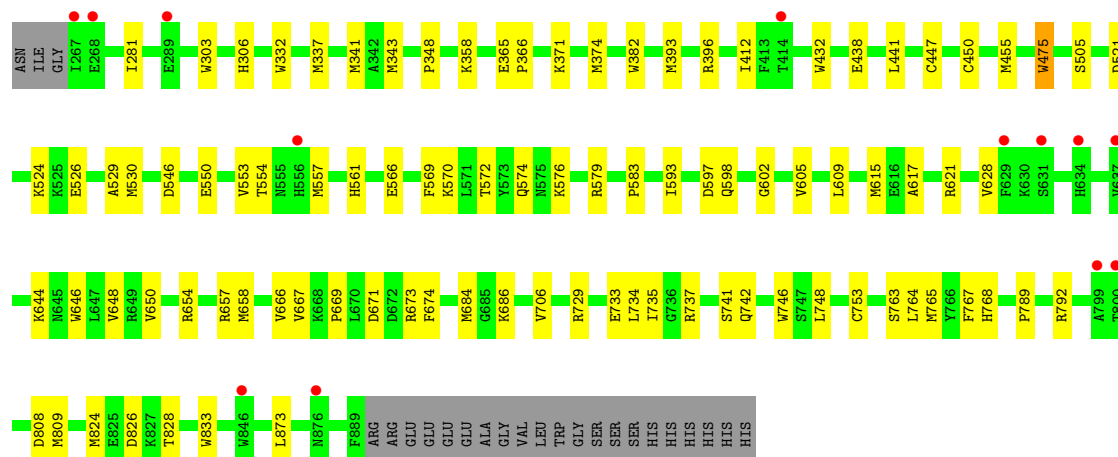


• Molecule 1: NS5

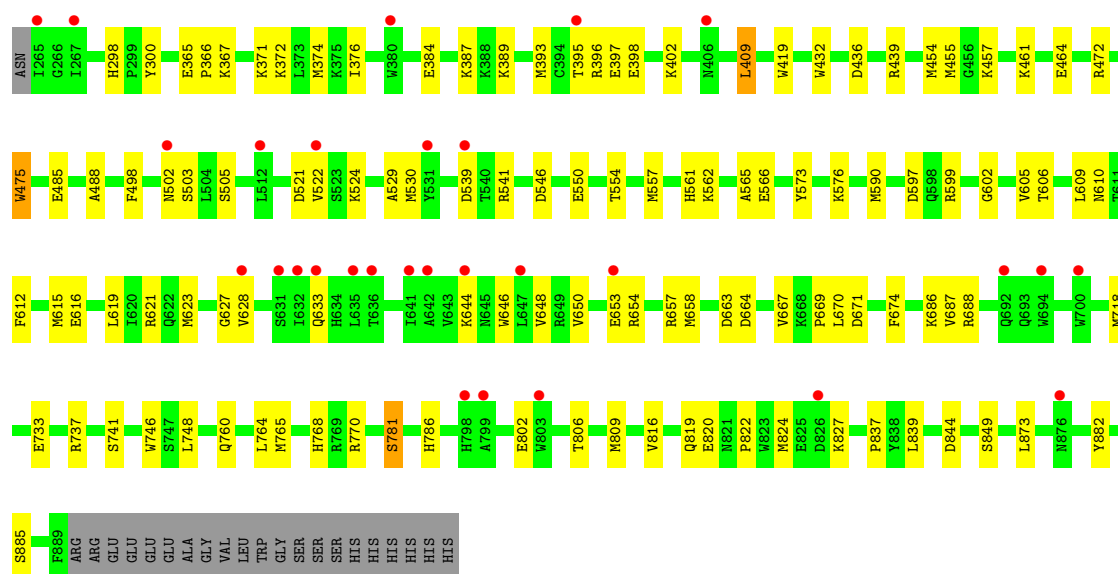
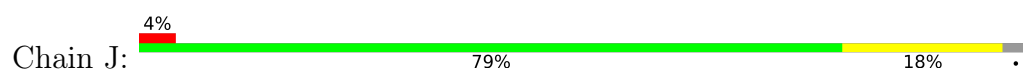


• Molecule 1: NS5

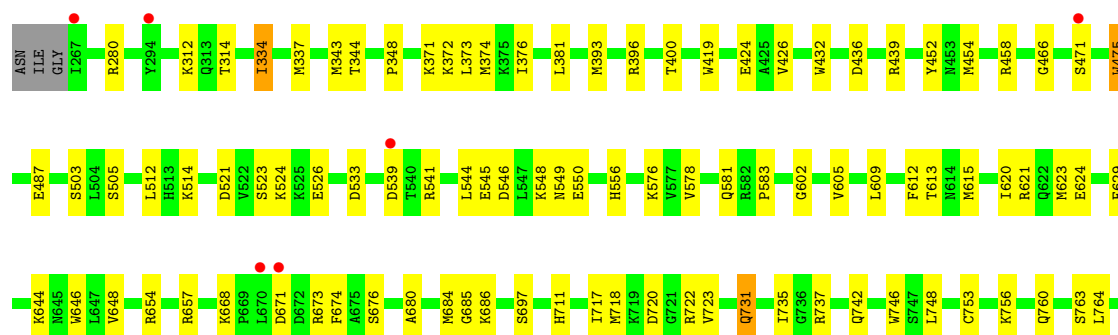
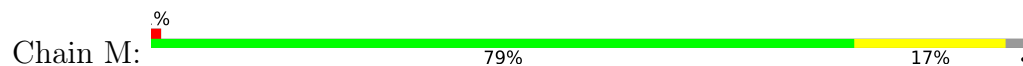




• Molecule 1: NS5

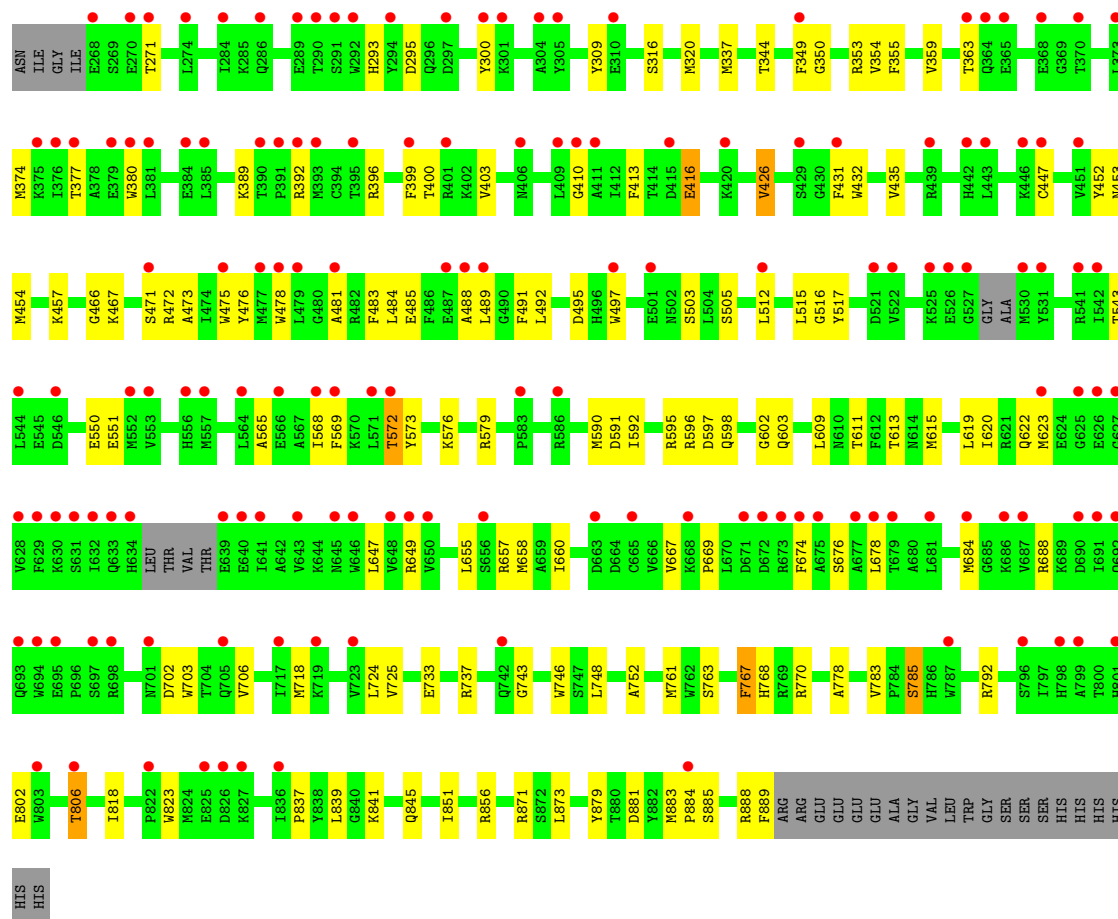


• Molecule 1: NS5





• Molecule 1: NS5



• Molecule 2: RNA (30-mer)



• Molecule 2: RNA (30-mer)



- Molecule 2: RNA (30-mer)

Chain H:  30% 7% 60%



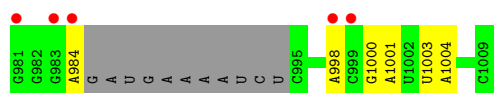
- Molecule 2: RNA (30-mer)

Chain K:  17% 37% 17% 47%



- Molecule 2: RNA (30-mer)

Chain N:  17% 43% 20% 37%



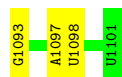
- Molecule 2: RNA (30-mer)

Chain Q:  7% 37% 60%



- Molecule 3: RNA (9-mer)

Chain C:  67% 33%



- Molecule 3: RNA (9-mer)

Chain F:  89% 11%

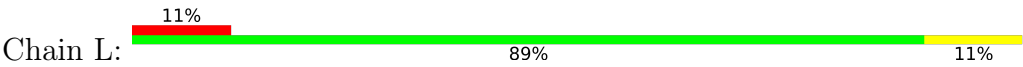


- Molecule 3: RNA (9-mer)

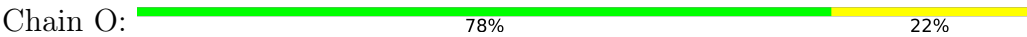
Chain I:  78% 22%



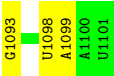
● Molecule 3: RNA (9-mer)



● Molecule 3: RNA (9-mer)



● Molecule 3: RNA (9-mer)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	139.43Å 154.58Å 172.35Å 90.00° 94.68° 90.00°	Depositor
Resolution (Å)	48.84 – 2.58 48.84 – 2.58	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.84-2.58) 99.8 (48.84-2.58)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.19	Depositor
R, R_{free}	0.191 , 0.221 0.191 , 0.221	Depositor DCC
R_{free} test set	11578 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	58.3	Xtriage
Anisotropy	0.116	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32878	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CTP, MG, GOL, ZN

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	0.38	0/5031	0.59	0/6822
1	D	0.39	0/5093	0.60	0/6898
1	G	0.34	0/5033	0.55	0/6832
1	J	0.36	0/5037	0.56	0/6836
1	M	0.38	0/5047	0.56	0/6846
1	P	0.30	1/4649 (0.0%)	0.48	0/6345
2	B	0.47	0/279	0.65	0/431
2	E	0.42	0/304	0.58	0/470
2	H	0.56	1/279 (0.4%)	0.65	0/431
2	K	0.69	2/374 (0.5%)	0.65	0/578
2	N	0.34	0/447	0.48	0/692
2	Q	0.33	0/279	0.54	0/431
3	C	0.62	1/218 (0.5%)	0.57	0/336
3	F	0.63	1/218 (0.5%)	0.57	0/336
3	I	0.68	1/218 (0.5%)	0.61	0/336
3	L	0.63	1/217 (0.5%)	0.78	0/334
3	O	0.61	1/218 (0.5%)	0.61	0/336
3	R	0.67	1/218 (0.5%)	0.77	0/336
All	All	0.39	10/33159 (0.0%)	0.57	0/45626

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	996	C	C2-O2	6.64	1.37	1.24
3	R	1093	G	OP3-P	6.58	1.61	1.48
3	I	1093	G	OP3-P	6.37	1.61	1.48
3	F	1093	G	OP3-P	6.25	1.60	1.48
3	C	1093	G	OP3-P	6.07	1.60	1.48
2	K	996	C	C4-N4	6.01	1.46	1.33
3	O	1093	G	OP3-P	5.66	1.59	1.48
3	L	1093	G	OP3-P	5.63	1.59	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	999	C	O3'-P	-5.27	1.53	1.61
1	P	649	ARG	CA-C	-5.26	1.49	1.52

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4913	0	4699	50	0
1	D	4973	0	4775	68	0
1	G	4913	0	4657	60	0
1	J	4917	0	4659	80	0
1	M	4929	0	4688	73	0
1	P	4537	0	3973	105	0
2	B	251	0	129	2	0
2	E	273	0	140	2	0
2	H	251	0	129	2	0
2	K	336	0	175	4	0
2	N	401	0	208	2	0
2	Q	251	0	129	1	0
3	C	195	0	97	1	0
3	F	195	0	97	0	0
3	I	195	0	97	0	0
3	L	194	0	97	0	0
3	O	195	0	97	1	0
3	R	195	0	97	3	0
4	A	2	0	0	0	0
4	D	2	0	0	0	0
4	G	2	0	0	0	0
4	J	2	0	0	0	0
4	M	2	0	0	0	0
4	P	2	0	0	0	0
5	A	2	0	0	0	0
5	D	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	2	0	0	0	0
5	J	2	0	0	0	0
5	M	2	0	0	0	0
5	P	2	0	0	0	0
6	A	12	0	16	0	0
6	D	24	0	32	0	0
6	E	12	0	16	1	0
6	H	6	0	8	1	0
6	J	6	0	8	0	0
6	K	6	0	8	0	0
6	M	6	0	8	2	0
7	A	29	0	12	2	0
7	D	29	0	12	1	0
7	G	29	0	12	0	0
7	J	29	0	12	1	0
7	M	29	0	12	0	0
7	P	29	0	12	0	0
8	A	98	0	0	1	0
8	B	6	0	0	0	0
8	C	3	0	0	0	0
8	D	111	0	0	2	0
8	E	8	0	0	0	0
8	F	5	0	0	0	0
8	G	74	0	0	1	0
8	H	2	0	0	0	0
8	I	2	0	0	0	0
8	J	68	0	0	0	0
8	K	2	0	0	0	0
8	L	1	0	0	0	0
8	M	84	0	0	1	0
8	N	7	0	0	0	0
8	O	4	0	0	0	0
8	P	18	0	0	1	0
8	R	1	0	0	0	0
All	All	32878	0	29111	436	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 7.

All (436) 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:J:389:LYS:HE2	1:J:502:ASN:HD22	1.17	1.08
1:J:521:ASP:HA	1:J:524:LYS:HE2	1.59	0.84
1:M:344:THR:HG21	1:M:471:SER:HB2	1.59	0.83
1:P:309:TYR:HE1	1:P:592:ILE:HD11	1.46	0.81
1:P:475:TRP:HZ3	1:P:576:LYS:HD2	1.45	0.79
1:M:753:CYS:HB3	1:M:789:PRO:HG3	1.66	0.76
1:M:620:ILE:HA	1:M:623:MET:HE2	1.68	0.75
1:G:554:THR:HG21	1:G:566:GLU:HG3	1.67	0.75
1:J:557:MET:HE2	1:J:562:LYS:HA	1.69	0.74
1:J:658:MET:HG2	1:J:667:VAL:HG13	1.69	0.74
1:P:761:MET:HE1	3:R:1099:A:H5'	1.69	0.72
1:D:410:GLY:HA3	1:D:478:TRP:HA	1.72	0.72
1:G:365:GLU:OE2	1:G:371:LYS:NZ	2.20	0.72
1:P:505:SER:HB2	1:P:615:MET:HE3	1.70	0.72
1:J:819:GLN:O	1:J:827:LYS:NZ	2.24	0.71
1:P:718:MET:HE1	1:P:818:ILE:HD11	1.73	0.71
1:A:348:PRO:HB2	1:A:583:PRO:HD3	1.73	0.71
1:M:612:PHE:HA	1:M:615:MET:HE2	1.73	0.71
1:P:392:ARG:NH2	1:P:495:ASP:OD1	2.25	0.70
1:G:554:THR:HA	1:G:557:MET:HE3	1.74	0.70
1:J:402:LYS:NZ	2:K:1003:U:OP2	2.25	0.68
1:D:557:MET:HE2	1:D:562:LYS:HA	1.73	0.68
1:M:720:ASP:OD2	1:M:722:ARG:NH2	2.26	0.68
1:P:620:ILE:HG12	1:P:684:MET:HE1	1.76	0.68
1:J:389:LYS:HE2	1:J:502:ASN:ND2	2.01	0.67
1:D:530:MET:HE2	1:D:706:VAL:HG21	1.75	0.67
1:M:717:ILE:HD13	1:M:723:VAL:HG22	1.75	0.67
1:P:778:ALA:HA	1:P:883:MET:HE1	1.76	0.67
1:P:761:MET:HE3	3:R:1098:U:O2'	1.96	0.66
1:G:455:MET:HE1	2:H:999:C:H4'	1.77	0.66
1:G:824:MET:HE3	1:G:824:MET:HA	1.77	0.66
1:P:349:PHE:O	1:P:353:ARG:HG3	1.96	0.66
1:J:653:GLU:OE2	1:J:657:ARG:NH1	2.28	0.65
1:P:573:TYR:O	1:P:576:LYS:NZ	2.21	0.65
1:G:396:ARG:HG2	1:G:432:TRP:CZ3	2.32	0.65
1:G:382:TRP:CZ2	1:G:553:VAL:HG22	2.32	0.64
1:A:663:ASP:HB3	7:A:1007:CTP:H5'2	1.79	0.64
1:P:337:MET:HG2	8:P:1110:HOH:O	1.97	0.64
1:G:374:MET:HG2	1:G:684:MET:HE3	1.78	0.64
1:A:753:CYS:HB3	1:A:789:PRO:HG3	1.78	0.64
1:M:393:MET:HE1	1:M:439:ARG:HH21	1.63	0.64
1:A:526:GLU:O	1:A:657:ARG:NH2	2.21	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:824:MET:O	1:J:827:LYS:HE2	1.97	0.64
1:J:396:ARG:HG2	1:J:432:TRP:CZ3	2.32	0.64
1:P:377:THR:HG22	1:P:647:LEU:HD11	1.80	0.64
1:D:333:ASP:HB3	6:M:1005:GOL:H11	1.80	0.63
1:D:617:ALA:HA	1:D:684:MET:HE1	1.80	0.63
1:D:649:ARG:HG3	1:D:650:VAL:HG13	1.80	0.63
1:J:824:MET:HE3	1:J:824:MET:HA	1.80	0.63
1:P:551:GLU:HA	1:P:569:PHE:CD2	2.33	0.63
1:A:763:SER:O	1:A:767:PHE:HB3	1.99	0.62
1:J:644:LYS:O	1:J:648:VAL:HG23	2.00	0.62
1:J:557:MET:HE1	1:J:565:ALA:HB3	1.82	0.62
1:M:454:MET:HE3	1:M:578:VAL:HG11	1.81	0.62
1:M:526:GLU:O	1:M:657:ARG:NH2	2.29	0.62
1:J:806:THR:HG21	1:J:885:SER:HB3	1.82	0.62
1:A:824:MET:HE3	1:A:824:MET:HA	1.82	0.61
1:P:550:GLU:OE2	1:P:613:THR:OG1	2.18	0.61
1:P:785:SER:HB2	1:P:802:GLU:HG2	1.82	0.61
1:D:268:GLU:HA	1:D:362:ARG:HG2	1.82	0.61
1:P:400:THR:HG22	1:P:426:VAL:HG13	1.83	0.61
1:P:718:MET:HE2	1:P:724:LEU:HD11	1.82	0.60
1:M:373:LEU:HD22	1:M:623:MET:HE1	1.82	0.60
1:P:806:THR:HG21	1:P:885:SER:OG	2.02	0.60
1:J:367:LYS:HD3	1:J:633:GLN:HG3	1.83	0.60
1:J:550:GLU:OE1	1:J:599:ARG:NH2	2.35	0.60
1:P:669:PRO:HG3	1:P:674:PHE:HB2	1.82	0.60
1:J:372:LYS:O	1:J:376:ILE:HD12	2.02	0.59
1:D:873:LEU:HD22	1:M:873:LEU:HD22	1.83	0.59
1:P:770:ARG:HB2	1:P:851:ILE:HD11	1.84	0.59
1:J:550:GLU:CD	1:J:599:ARG:HH22	2.09	0.59
1:D:454:MET:HE3	1:D:578:VAL:HG11	1.84	0.59
1:G:447:CYS:SG	1:G:450:CYS:HB2	2.43	0.59
1:M:722:ARG:HB3	1:M:824:MET:HE1	1.85	0.59
1:P:516:GLY:C	1:P:725:VAL:HG11	2.28	0.59
1:D:605:VAL:HB	1:D:609:LEU:HG	1.85	0.59
1:P:350:GLY:O	1:P:354:VAL:HG23	2.02	0.59
1:J:365:GLU:OE2	1:J:371:LYS:NZ	2.33	0.58
1:G:768:HIS:CD2	1:G:768:HIS:H	2.20	0.58
1:D:599:ARG:HD2	1:D:606:THR:HA	1.85	0.58
1:P:344:THR:HG21	1:P:471:SER:HB3	1.86	0.58
1:P:410:GLY:HA3	1:P:478:TRP:HA	1.84	0.58
1:G:358:LYS:NZ	8:G:1102:HOH:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:554:THR:HG21	1:J:566:GLU:HG3	1.85	0.58
1:M:646:TRP:CZ2	1:M:654:ARG:HG3	2.39	0.58
1:J:396:ARG:NH2	1:J:436:ASP:OD1	2.35	0.58
1:J:541:ARG:HG3	1:J:541:ARG:HH11	1.68	0.58
1:G:521:ASP:HA	1:G:524:LYS:HD3	1.85	0.58
1:G:644:LYS:O	1:G:648:VAL:HG23	2.03	0.58
2:B:1007:U:H2'	2:B:1008:C:C6	2.39	0.57
1:D:621:ARG:HG2	1:D:674:PHE:CE2	2.39	0.57
1:G:343:MET:HE2	1:G:742:GLN:HG3	1.85	0.57
1:P:611:THR:HG23	1:P:660:ILE:HG22	1.85	0.57
1:A:365:GLU:OE2	1:A:371:LYS:NZ	2.37	0.57
1:P:551:GLU:HA	1:P:569:PHE:CE2	2.40	0.57
1:A:636:THR:OG1	1:A:639:GLU:HG3	2.05	0.57
1:A:646:TRP:CZ2	1:A:654:ARG:HG3	2.40	0.57
1:D:505:SER:HB2	1:D:615:MET:HE3	1.87	0.57
1:J:806:THR:HA	1:J:809:MET:HE2	1.87	0.57
1:A:353:ARG:HH12	1:A:470:GLY:H	1.51	0.57
1:G:764:LEU:HG	1:G:765:MET:HE3	1.86	0.57
1:P:355:PHE:HA	1:P:359:VAL:HB	1.86	0.57
1:P:658:MET:HG2	1:P:667:VAL:HG22	1.87	0.57
1:P:733:GLU:HB3	1:P:737:ARG:NH1	2.20	0.57
1:P:752:ALA:HB1	1:P:783:VAL:HG13	1.86	0.57
1:G:526:GLU:O	1:G:657:ARG:NH2	2.35	0.56
1:J:409:LEU:HD21	1:J:419:TRP:HB2	1.86	0.56
1:J:475:TRP:O	1:J:602:GLY:HA3	2.04	0.56
1:P:293:HIS:HE1	1:P:295:ASP:HB2	1.71	0.56
1:D:888:ARG:HD2	1:D:889:PHE:CZ	2.41	0.56
1:P:374:MET:HG2	1:P:684:MET:HE2	1.87	0.56
1:M:381:LEU:HD21	1:M:615:MET:HE3	1.87	0.56
1:A:334:ILE:HG23	1:P:466:GLY:HA2	1.88	0.56
1:A:680:ALA:O	1:A:684:MET:HG3	2.06	0.55
1:A:695:GLU:HG2	1:D:693:GLN:NE2	2.22	0.55
1:M:280:ARG:HG3	8:M:1103:HOH:O	2.04	0.55
1:M:400:THR:HG23	1:M:426:VAL:HG11	1.87	0.55
1:D:605:VAL:HG21	1:D:609:LEU:HD12	1.89	0.55
1:P:746:TRP:CH2	1:P:748:LEU:HB2	2.41	0.55
1:A:472:ARG:NH2	7:A:1007:CTP:O3A	2.40	0.55
1:J:599:ARG:HD3	1:J:606:THR:HA	1.88	0.55
1:P:453:ASN:ND2	1:P:579:ARG:HD2	2.21	0.55
1:P:396:ARG:HH12	1:P:432:TRP:HB3	1.72	0.55
1:A:441:LEU:HD13	1:A:448:GLU:HG3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:624:GLU:HB2	1:M:629:PHE:CZ	2.42	0.54
1:P:770:ARG:HD2	1:P:851:ILE:HD13	1.89	0.54
1:P:396:ARG:NH1	1:P:432:TRP:HB3	2.22	0.54
1:P:489:LEU:O	1:P:492:LEU:HD12	2.08	0.54
1:P:483:PHE:HD2	1:P:484:LEU:HD23	1.73	0.54
1:P:551:GLU:HG3	1:P:569:PHE:HD2	1.73	0.54
1:A:718:MET:HA	1:A:837:PRO:HG3	1.90	0.54
1:G:617:ALA:HA	1:G:684:MET:HE1	1.89	0.54
1:G:729:ARG:HD3	1:G:734:LEU:HD21	1.90	0.54
1:G:393:MET:HG2	1:G:561:HIS:CD2	2.43	0.54
1:G:530:MET:HE2	1:G:706:VAL:HG21	1.89	0.54
1:J:781:SER:HB3	1:J:882:TYR:H	1.72	0.54
1:D:549:ASN:HA	1:D:552:MET:HE2	1.89	0.53
1:A:873:LEU:HD22	1:P:873:LEU:HD22	1.89	0.53
1:M:756:LYS:O	1:M:760:GLN:HG3	2.08	0.53
1:J:395:THR:HG22	1:J:397:GLU:H	1.73	0.53
1:J:623:MET:HG3	1:J:646:TRP:CZ3	2.43	0.53
1:M:605:VAL:HB	1:M:609:LEU:HG	1.90	0.53
1:P:851:ILE:HA	1:P:856:ARG:HD2	1.91	0.53
1:M:348:PRO:HB2	1:M:583:PRO:HG3	1.91	0.52
1:M:718:MET:HA	1:M:837:PRO:HG3	1.91	0.52
1:P:623:MET:HE1	1:P:647:LEU:HD12	1.90	0.52
1:D:557:MET:HE3	1:D:561:HIS:CG	2.44	0.52
1:D:646:TRP:CZ2	1:D:654:ARG:HG2	2.44	0.52
1:J:599:ARG:HD2	1:J:610:ASN:OD1	2.09	0.52
1:M:343:MET:HE2	1:M:742:GLN:HG3	1.91	0.52
1:M:546:ASP:OD2	1:M:686:LYS:NZ	2.43	0.52
1:M:824:MET:HE3	1:M:824:MET:HA	1.90	0.52
1:D:285:LYS:O	1:D:289:GLU:HG2	2.08	0.52
1:D:763:SER:O	1:D:767:PHE:HB3	2.10	0.52
1:J:820:GLU:O	1:J:822:PRO:HD3	2.09	0.52
1:M:644:LYS:O	1:M:648:VAL:HG23	2.10	0.52
1:P:377:THR:HA	1:P:647:LEU:HD21	1.92	0.52
1:J:733:GLU:HB3	1:J:737:ARG:NH1	2.24	0.52
1:P:485:GLU:HA	1:P:568:ILE:HD13	1.92	0.52
1:J:786:HIS:CD2	1:J:802:GLU:HG2	2.45	0.52
1:A:621:ARG:HD3	1:A:674:PHE:CZ	2.45	0.52
1:G:412:ILE:HD12	1:G:579:ARG:HD3	1.92	0.52
1:P:492:LEU:HA	1:P:497:TRP:CD1	2.45	0.52
1:A:371:LYS:HA	1:A:374:MET:HE2	1.92	0.51
1:J:522:VAL:HG12	1:J:530:MET:HE3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:337:MET:HG2	8:A:1179:HOH:O	2.09	0.51
1:A:614:ASN:O	1:A:618:GLN:HG2	2.10	0.51
1:P:792:ARG:HH21	3:R:1098:U:P	2.33	0.51
1:G:621:ARG:HD3	1:G:674:PHE:CZ	2.45	0.51
1:G:746:TRP:CH2	1:G:748:LEU:HB2	2.46	0.51
1:A:881:ASP:OD2	1:A:884:PRO:HD3	2.11	0.51
1:D:786:HIS:CD2	1:D:802:GLU:HG2	2.45	0.51
1:D:746:TRP:CH2	1:D:748:LEU:HB2	2.45	0.51
1:A:635:LEU:HD23	1:A:640:GLU:HG2	1.92	0.51
1:G:546:ASP:OD2	1:G:686:LYS:NZ	2.39	0.51
1:P:454:MET:HE3	1:P:475:TRP:NE1	2.26	0.51
1:G:753:CYS:HB3	1:G:789:PRO:HG3	1.92	0.51
1:P:452:TYR:OH	1:P:603:GLN:NE2	2.33	0.51
1:G:554:THR:HG22	1:G:557:MET:HE3	1.93	0.50
1:G:733:GLU:HB3	1:G:737:ARG:NH1	2.26	0.50
1:A:393:MET:HE2	1:A:561:HIS:HB2	1.93	0.50
1:D:354:VAL:HG11	1:D:472:ARG:HA	1.94	0.50
1:J:498:PHE:HA	1:J:503:SER:HB3	1.94	0.50
1:J:670:LEU:HD23	1:J:671:ASP:OD2	2.11	0.50
1:D:557:MET:HE1	1:D:565:ALA:HB3	1.92	0.50
1:D:370:THR:O	1:D:374:MET:HG3	2.11	0.50
1:J:503:SER:C	1:J:505:SER:H	2.20	0.50
1:M:396:ARG:HH22	1:M:436:ASP:CG	2.19	0.50
1:A:277:ILE:HD12	1:A:281:ILE:HD11	1.94	0.50
1:A:692:GLN:HB2	1:A:695:GLU:HB2	1.94	0.50
1:M:541:ARG:HD2	1:M:685:GLY:O	2.11	0.50
1:P:619:LEU:HD22	1:P:655:LEU:HD13	1.93	0.50
1:D:333:ASP:HB3	6:M:1005:GOL:C1	2.41	0.49
1:M:521:ASP:HA	1:M:524:LYS:HD2	1.93	0.49
1:P:271:THR:O	1:P:271:THR:OG1	2.30	0.49
1:P:396:ARG:O	1:P:400:THR:HG23	2.12	0.49
1:P:475:TRP:CZ3	1:P:576:LYS:HD2	2.36	0.49
1:P:503:SER:HB2	1:P:615:MET:HE1	1.94	0.49
1:G:475:TRP:O	1:G:602:GLY:HA3	2.13	0.49
1:J:455:MET:HE1	2:K:999:C:H4'	1.95	0.49
1:A:460:LYS:NZ	1:A:740:ILE:O	2.45	0.49
1:P:431:PHE:O	1:P:435:VAL:HG23	2.12	0.49
1:P:718:MET:HA	1:P:837:PRO:HG3	1.94	0.49
1:G:808:ASP:OD1	6:H:1101:GOL:H32	2.13	0.49
1:G:763:SER:O	1:G:767:PHE:HB3	2.13	0.49
1:A:781:SER:O	1:A:871:ARG:NH1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:393:MET:HE1	1:M:439:ARG:NH2	2.27	0.48
1:D:557:MET:HE1	1:D:565:ALA:CB	2.43	0.48
1:J:590:MET:HE2	1:J:590:MET:HB2	1.73	0.48
1:M:374:MET:HB3	1:M:549:ASN:ND2	2.28	0.48
1:G:475:TRP:CD1	1:G:475:TRP:N	2.79	0.48
1:G:348:PRO:HB2	1:G:583:PRO:HD3	1.94	0.48
1:P:320:MET:HE3	1:P:743:GLY:HA3	1.95	0.48
1:D:452:TYR:HB2	1:D:578:VAL:HG22	1.96	0.48
1:G:826:ASP:OD1	1:G:828:THR:OG1	2.30	0.48
1:J:733:GLU:HB3	1:J:737:ARG:HH12	1.79	0.48
1:J:393:MET:HE1	1:J:439:ARG:HH21	1.79	0.48
1:D:475:TRP:N	1:D:475:TRP:CD1	2.81	0.48
1:P:488:ALA:HB1	1:P:565:ALA:HA	1.96	0.48
1:P:623:MET:HE1	1:P:647:LEU:CD1	2.44	0.48
1:G:505:SER:HB2	1:G:615:MET:HE3	1.97	0.47
1:G:628:VAL:HG21	1:G:646:TRP:CD1	2.49	0.47
1:M:888:ARG:HD3	1:M:889:PHE:CZ	2.49	0.47
1:A:764:LEU:HG	1:A:765:MET:HE3	1.96	0.47
1:D:727:PRO:HG3	1:D:765:MET:HE3	1.96	0.47
1:P:595:ARG:NE	1:P:597:ASP:OD1	2.46	0.47
1:A:303:TRP:CE3	1:A:595:ARG:HB2	2.49	0.47
1:M:514:LYS:HD3	1:M:823:TRP:HZ3	1.79	0.47
1:G:597:ASP:O	1:G:598:GLN:HB2	2.15	0.47
1:A:584:THR:HG22	1:A:587:GLY:O	2.14	0.47
1:P:457:LYS:HB3	1:P:472:ARG:HG2	1.96	0.47
1:D:530:MET:HE3	1:D:666:VAL:HG11	1.97	0.47
1:D:597:ASP:O	1:D:598:GLN:HB2	2.14	0.47
1:J:576:LYS:NZ	1:J:597:ASP:O	2.35	0.47
1:J:650:VAL:O	1:J:654:ARG:HG2	2.15	0.47
1:M:314:THR:HG22	1:M:581:GLN:OE1	2.15	0.47
1:M:512:LEU:HD21	1:M:711:HIS:CE1	2.50	0.47
1:P:770:ARG:HD2	1:P:851:ILE:CD1	2.44	0.47
1:D:285:LYS:HG3	1:D:292:TRP:CD2	2.49	0.47
1:G:341:MET:HE2	1:G:341:MET:HB2	1.74	0.47
1:A:464:GLU:HG3	1:A:465:PHE:CD2	2.49	0.47
1:D:285:LYS:HG3	1:D:292:TRP:CE2	2.50	0.47
1:D:692:GLN:HG3	1:D:695:GLU:HB2	1.96	0.47
1:A:396:ARG:HD3	1:A:432:TRP:CE3	2.49	0.47
1:A:770:ARG:HG3	1:A:770:ARG:HH11	1.80	0.47
1:G:521:ASP:O	1:G:524:LYS:HB2	2.14	0.47
1:M:372:LYS:O	1:M:376:ILE:HG13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:746:TRP:CH2	1:J:748:LEU:HB2	2.50	0.46
1:P:491:PHE:O	1:P:495:ASP:HB2	2.15	0.46
1:P:888:ARG:HD2	1:P:889:PHE:CZ	2.50	0.46
2:B:1000:G:H2'	2:B:1001:A:C8	2.50	0.46
1:D:637:VAL:O	1:D:641:ILE:HG12	2.15	0.46
1:J:653:GLU:CD	1:J:657:ARG:NH1	2.74	0.46
1:J:768:HIS:CD2	1:J:768:HIS:H	2.32	0.46
1:M:731:GLN:HG3	1:M:735:ILE:HD12	1.97	0.46
1:P:768:HIS:CD2	1:P:768:HIS:H	2.32	0.46
1:J:374:MET:HG2	1:J:616:GLU:OE2	2.15	0.46
1:J:612:PHE:HA	1:J:615:MET:HE3	1.96	0.46
1:D:504:LEU:HD11	1:D:652:ARG:NH2	2.30	0.46
1:J:457:LYS:HB3	1:J:472:ARG:HG3	1.97	0.46
1:A:579:ARG:HG2	1:A:590:MET:SD	2.56	0.46
1:A:631:SER:HB2	1:D:465:PHE:CZ	2.50	0.46
1:J:475:TRP:CD1	1:J:475:TRP:N	2.84	0.46
1:M:396:ARG:HD3	1:M:432:TRP:CE3	2.50	0.46
1:P:389:LYS:HE2	1:P:389:LYS:HB2	1.68	0.46
1:A:505:SER:HB2	1:A:615:MET:HE3	1.98	0.46
1:G:873:LEU:HD22	1:J:873:LEU:HD22	1.97	0.46
1:M:475:TRP:O	1:M:602:GLY:HA3	2.15	0.46
1:J:461:LYS:HD2	1:J:461:LYS:HA	1.90	0.46
1:J:505:SER:OG	1:J:658:MET:HB2	2.16	0.46
1:M:746:TRP:CH2	1:M:748:LEU:HB2	2.49	0.46
1:P:597:ASP:O	1:P:598:GLN:HB2	2.16	0.46
1:D:753:CYS:HB3	1:D:789:PRO:HG3	1.98	0.46
1:M:533:ASP:OD2	1:M:697:SER:OG	2.29	0.46
1:D:395:THR:OG1	1:D:398:GLU:HB2	2.15	0.45
1:P:399:PHE:O	1:P:403:VAL:HG22	2.16	0.45
1:J:539:ASP:OD1	1:J:539:ASP:N	2.49	0.45
1:A:764:LEU:HD13	1:A:812:VAL:HG12	1.99	0.45
3:C:1097:A:H2'	3:C:1098:U:O4'	2.16	0.45
1:D:765:MET:HE3	1:D:765:MET:HB3	1.79	0.45
1:M:419:TRP:HD1	1:M:424:GLU:HG2	1.81	0.45
1:M:539:ASP:OD1	1:M:539:ASP:N	2.46	0.45
1:P:733:GLU:HB3	1:P:737:ARG:HH12	1.82	0.45
1:J:764:LEU:HG	1:J:765:MET:HE2	1.97	0.45
1:M:556:HIS:N	1:M:556:HIS:CD2	2.84	0.45
1:P:881:ASP:OD2	1:P:884:PRO:HD3	2.17	0.45
2:K:1003:U:H2'	2:K:1004:A:C8	2.52	0.45
1:M:544:LEU:O	1:M:548:LYS:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:655:LEU:HD12	1:P:655:LEU:HA	1.79	0.45
1:A:765:MET:HE2	1:A:765:MET:HA	1.99	0.45
1:J:688:ARG:HE	1:J:688:ARG:HB2	1.56	0.45
1:P:413:PHE:HB2	1:P:416:GLU:HG3	1.98	0.45
1:P:703:TRP:HA	1:P:706:VAL:HG23	1.98	0.45
1:M:523:SER:O	1:M:668:LYS:NZ	2.48	0.45
1:D:410:GLY:CA	1:D:478:TRP:HA	2.45	0.45
1:D:466:GLY:HA2	1:M:334:ILE:HG23	1.98	0.45
1:J:395:THR:HB	1:J:398:GLU:H	1.82	0.45
1:M:671:ASP:CG	1:M:673:ARG:HE	2.24	0.45
1:M:646:TRP:CH2	1:M:654:ARG:HG3	2.53	0.44
1:P:380:TRP:HB2	1:P:647:LEU:HD23	1.99	0.44
1:P:454:MET:HE2	1:P:473:ALA:HB1	1.99	0.44
1:P:512:LEU:HA	1:P:515:LEU:HD22	1.99	0.44
1:G:572:THR:O	1:G:576:LYS:HG2	2.17	0.44
1:J:541:ARG:NH1	1:J:687:VAL:HG22	2.32	0.44
1:J:621:ARG:HD3	1:J:674:PHE:CZ	2.53	0.44
1:M:344:THR:O	1:M:458:ARG:NH1	2.50	0.44
1:M:763:SER:O	1:M:767:PHE:HB3	2.18	0.44
1:D:849:SER:OG	1:D:851:ILE:HG12	2.17	0.44
1:M:550:GLU:OE2	1:M:613:THR:OG1	2.35	0.44
1:J:628:VAL:HG21	1:J:646:TRP:CD1	2.52	0.44
1:P:622:GLN:HE22	1:P:657:ARG:HG3	1.82	0.44
1:P:453:ASN:HB2	1:P:476:TYR:O	2.17	0.44
1:P:478:TRP:NE1	1:P:481:ALA:H	2.16	0.44
1:A:475:TRP:CD1	1:A:475:TRP:N	2.85	0.44
1:G:303:TRP:CE3	1:G:593:ILE:HD12	2.53	0.44
2:H:1007:U:H2'	2:H:1008:C:C6	2.52	0.44
1:A:786:HIS:CD2	1:A:802:GLU:HG2	2.53	0.44
1:G:550:GLU:O	1:G:553:VAL:HG23	2.17	0.44
1:J:485:GLU:OE1	1:J:573:TYR:OH	2.32	0.44
1:D:388:LYS:C	1:D:389:LYS:HG2	2.43	0.44
1:J:718:MET:HA	1:J:837:PRO:HG3	1.99	0.44
1:D:602:GLY:HA2	2:E:1000:G:N3	2.33	0.43
1:G:646:TRP:CZ2	1:G:654:ARG:HG3	2.53	0.43
1:J:298:HIS:HD2	1:J:300:TYR:H	1.65	0.43
1:P:568:ILE:HA	1:P:572:THR:CG2	2.48	0.43
1:D:512:LEU:HD23	1:D:765:MET:HE2	1.99	0.43
1:G:281:ILE:HD13	1:G:306:HIS:CD2	2.53	0.43
1:D:663:ASP:CB	7:D:1009:CTP:H5'1	2.48	0.43
1:M:768:HIS:CD2	1:M:768:HIS:H	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:729:ARG:HD3	1:D:734:LEU:HD21	2.01	0.43
1:J:844:ASP:OD1	1:J:849:SER:HB2	2.19	0.43
1:P:300:TYR:OH	1:P:591:ASP:OD2	2.29	0.43
1:P:309:TYR:OH	1:P:579:ARG:NH2	2.51	0.43
1:J:546:ASP:OD2	1:J:686:LYS:NZ	2.45	0.43
1:J:623:MET:O	1:J:627:GLY:N	2.51	0.43
1:P:475:TRP:CD1	1:P:475:TRP:N	2.87	0.43
1:P:678:LEU:HD13	1:P:688:ARG:NH2	2.34	0.43
1:M:312:LYS:O	1:M:581:GLN:NE2	2.50	0.43
1:P:590:MET:HE2	1:P:590:MET:HB2	1.69	0.43
1:D:393:MET:HE1	1:D:439:ARG:HH21	1.84	0.43
1:P:763:SER:O	1:P:767:PHE:HB3	2.19	0.43
1:A:756:LYS:HD3	1:A:803:TRP:CE3	2.54	0.42
1:G:382:TRP:CH2	1:G:553:VAL:HG22	2.54	0.42
1:G:671:ASP:CG	1:G:673:ARG:HE	2.27	0.42
2:N:1000:G:H2'	2:N:1001:A:C8	2.54	0.42
1:P:703:TRP:HH2	1:P:725:VAL:HG22	1.84	0.42
1:D:348:PRO:HG3	1:D:581:GLN:OE1	2.19	0.42
1:D:635:LEU:HD12	1:D:635:LEU:HA	1.84	0.42
1:G:530:MET:HE3	1:G:666:VAL:HG11	2.00	0.42
1:G:570:LYS:HA	1:G:574:GLN:HG2	2.01	0.42
1:M:337:MET:SD	1:M:337:MET:N	2.90	0.42
1:M:452:TYR:HB2	1:M:578:VAL:HG22	2.01	0.42
1:P:658:MET:HG2	1:P:667:VAL:HG13	2.01	0.42
1:D:530:MET:HE3	1:D:666:VAL:CG1	2.48	0.42
1:G:337:MET:HE2	1:G:337:MET:HA	2.01	0.42
1:A:806:THR:HA	1:A:809:MET:HE2	2.02	0.42
1:A:820:GLU:O	1:A:822:PRO:HD3	2.20	0.42
1:D:308:SER:HA	1:D:590:MET:O	2.20	0.42
1:G:366:PRO:O	1:G:371:LYS:HE2	2.19	0.42
1:A:623:MET:HE2	1:A:646:TRP:CZ3	2.54	0.42
1:D:337:MET:HG2	8:D:1181:HOH:O	2.19	0.42
1:J:760:GLN:HE21	1:J:760:GLN:HB2	1.62	0.42
1:M:371:LYS:HG2	1:M:545:GLU:HG2	2.01	0.42
1:D:503:SER:C	1:D:505:SER:H	2.27	0.42
1:M:621:ARG:HG2	1:M:674:PHE:CE1	2.54	0.42
1:P:609:LEU:HA	1:P:609:LEU:HD23	1.62	0.42
1:P:702:ASP:OD1	1:P:703:TRP:N	2.53	0.42
1:A:605:VAL:HB	1:A:609:LEU:HG	2.00	0.42
1:D:332:TRP:CE2	1:D:735:ILE:HD13	2.54	0.42
1:J:557:MET:HE3	1:J:561:HIS:CG	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:374:MET:HE3	1:M:684:MET:SD	2.60	0.42
1:G:605:VAL:HB	1:G:609:LEU:HG	2.01	0.42
1:J:605:VAL:HB	1:J:609:LEU:HG	2.02	0.42
1:P:475:TRP:O	1:P:602:GLY:HA3	2.19	0.42
1:P:768:HIS:HB2	1:P:839:LEU:HG	2.02	0.42
1:D:475:TRP:O	1:D:602:GLY:HA3	2.20	0.42
1:G:809:MET:HB3	1:G:833:TRP:HZ2	1.85	0.42
1:J:454:MET:HE3	1:J:454:MET:HB2	1.83	0.42
1:G:438:GLU:HA	1:G:441:LEU:HD12	2.02	0.41
1:J:557:MET:HE1	1:J:565:ALA:CB	2.48	0.41
1:M:475:TRP:CZ3	1:M:576:LYS:HD2	2.55	0.41
1:M:851:ILE:HA	1:M:856:ARG:HD2	2.02	0.41
1:A:280:ARG:O	1:A:284:ILE:HG13	2.20	0.41
1:D:806:THR:HG22	8:D:1187:HOH:O	2.19	0.41
1:G:658:MET:HG2	1:G:667:VAL:HG22	2.01	0.41
1:M:503:SER:C	1:M:505:SER:H	2.27	0.41
1:P:363:THR:HG21	1:P:543:THR:HG22	2.01	0.41
1:D:550:GLU:CD	1:D:599:ARG:HH12	2.28	0.41
1:D:604:VAL:HA	2:E:1001:A:O2'	2.20	0.41
1:J:529:ALA:O	1:J:669:PRO:HD2	2.19	0.41
1:M:680:ALA:O	1:M:684:MET:HG3	2.20	0.41
1:P:416:GLU:HB3	1:P:478:TRP:CE3	2.55	0.41
1:P:478:TRP:CD1	1:P:481:ALA:H	2.38	0.41
1:A:770:ARG:HG3	1:A:844:ASP:OD2	2.21	0.41
1:M:784:PRO:HG2	1:M:787:TRP:CE2	2.56	0.41
1:M:792:ARG:HH21	3:O:1098:U:P	2.42	0.41
1:D:277:ILE:HD12	1:D:281:ILE:HD11	2.03	0.41
1:D:460:LYS:NZ	1:D:740:ILE:O	2.50	0.41
1:J:366:PRO:HB2	1:J:371:LYS:HG3	2.03	0.41
1:J:619:LEU:HD23	1:J:619:LEU:HA	1.89	0.41
1:J:653:GLU:OE1	1:J:657:ARG:NH1	2.53	0.41
1:P:377:THR:HG21	1:P:620:ILE:HG22	2.00	0.41
1:A:775:ALA:O	1:A:779:ILE:HG13	2.21	0.41
1:J:663:ASP:HB3	7:J:1006:CTP:C5'	2.51	0.41
1:J:764:LEU:HD11	1:J:816:VAL:CG2	2.51	0.41
2:K:1004:A:H2'	2:K:1005:U:C6	2.56	0.41
1:P:453:ASN:HD22	1:P:453:ASN:HA	1.57	0.41
1:G:382:TRP:CE2	1:G:553:VAL:HG22	2.55	0.41
1:M:609:LEU:HD23	1:M:609:LEU:HA	1.83	0.41
1:M:849:SER:OG	1:M:851:ILE:HG22	2.21	0.41
1:P:517:TYR:HB3	1:P:823:TRP:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:646:TRP:CH2	1:G:654:ARG:HG3	2.55	0.41
1:J:488:ALA:HB1	1:J:565:ALA:HB2	2.03	0.41
1:M:334:ILE:HD13	1:M:334:ILE:HG21	1.75	0.41
1:M:396:ARG:HD3	1:M:432:TRP:CZ3	2.56	0.41
1:M:439:ARG:HE	1:M:487:GLU:CD	2.28	0.41
1:D:285:LYS:HE3	1:D:292:TRP:CD1	2.56	0.41
1:D:488:ALA:HB1	1:D:565:ALA:HA	2.03	0.41
1:J:384:GLU:OE1	1:J:387:LYS:NZ	2.51	0.41
1:M:372:LYS:HE2	1:M:372:LYS:HB2	1.90	0.41
1:G:529:ALA:O	1:G:669:PRO:HD2	2.21	0.40
1:A:754:LEU:HD22	1:A:792:ARG:HG3	2.03	0.40
1:D:512:LEU:HB3	6:E:1102:GOL:H11	2.03	0.40
1:G:646:TRP:O	1:G:650:VAL:HG22	2.21	0.40
2:N:1003:U:H2'	2:N:1004:A:C8	2.56	0.40
1:P:595:ARG:HG3	1:P:596:ARG:N	2.36	0.40
1:G:332:TRP:CE2	1:G:735:ILE:HD13	2.57	0.40
1:M:475:TRP:CD1	1:M:475:TRP:N	2.88	0.40
1:P:841:LYS:O	1:P:845:GLN:HG3	2.22	0.40
1:D:334:ILE:HG23	1:M:466:GLY:HA2	2.03	0.40
1:P:871:ARG:HG2	1:P:879:TYR:CD1	2.57	0.40
1:G:569:PHE:O	1:G:574:GLN:HG2	2.21	0.40
1:J:770:ARG:NH1	1:J:839:LEU:O	2.52	0.40
1:M:764:LEU:HD13	1:M:812:VAL:HG12	2.02	0.40
1:P:483:PHE:CD2	1:P:484:LEU:HD23	2.55	0.40
1:P:602:GLY:N	2:Q:1000:G:H21	2.20	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	619/647 (96%)	595 (96%)	23 (4%)	1 (0%)	43 63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	620/647 (96%)	598 (96%)	22 (4%)	0	100	100
1	G	621/647 (96%)	603 (97%)	18 (3%)	0	100	100
1	J	623/647 (96%)	589 (94%)	34 (6%)	0	100	100
1	M	622/647 (96%)	600 (96%)	22 (4%)	0	100	100
1	P	610/647 (94%)	565 (93%)	44 (7%)	1 (0%)	43	63
All	All	3715/3882 (96%)	3550 (96%)	163 (4%)	2 (0%)	48	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	601	SER
1	P	767	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	507/564 (90%)	505 (100%)	2 (0%)	84	92
1	D	520/564 (92%)	517 (99%)	3 (1%)	78	89
1	G	502/564 (89%)	499 (99%)	3 (1%)	78	89
1	J	504/564 (89%)	498 (99%)	6 (1%)	63	82
1	M	509/564 (90%)	502 (99%)	7 (1%)	59	79
1	P	408/564 (72%)	399 (98%)	9 (2%)	45	70
All	All	2950/3384 (87%)	2920 (99%)	30 (1%)	68	84

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	475	TRP
1	A	664	ASP
1	D	269	SER
1	D	475	TRP

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Mol	Chain	Res	Type
1	D	664	ASP
1	G	475	TRP
1	G	741	SER
1	G	792	ARG
1	J	409	LEU
1	J	464	GLU
1	J	475	TRP
1	J	664	ASP
1	J	741	SER
1	J	781	SER
1	M	334	ILE
1	M	475	TRP
1	M	676	SER
1	M	731	GLN
1	M	737	ARG
1	M	818	ILE
1	M	869	GLN
1	P	316	SER
1	P	416	GLU
1	P	426	VAL
1	P	447	CYS
1	P	467	LYS
1	P	572	THR
1	P	676	SER
1	P	785	SER
1	P	806	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	273	ASN
1	A	286	GLN
1	A	298	HIS
1	A	340	GLN
1	A	575	ASN
1	A	633	GLN
1	A	869	GLN
1	D	273	ASN
1	D	313	GLN
1	D	496	HIS
1	D	575	ASN
1	D	645	ASN

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Mol	Chain	Res	Type
1	D	701	ASN
1	D	742	GLN
1	D	777	ASN
1	D	786	HIS
1	D	798	HIS
1	G	306	HIS
1	G	352	GLN
1	G	496	HIS
1	G	555	ASN
1	G	618	GLN
1	G	633	GLN
1	G	645	ASN
1	G	786	HIS
1	G	864	GLN
1	J	293	HIS
1	J	502	ASN
1	J	730	ASN
1	J	760	GLN
1	J	801	HIS
1	J	819	GLN
1	M	313	GLN
1	M	417	ASN
1	M	622	GLN
1	M	731	GLN
1	M	768	HIS
1	P	273	ASN
1	P	352	GLN
1	P	440	ASN
1	P	453	ASN
1	P	549	ASN
1	P	556	HIS
1	P	581	GLN
1	P	622	GLN
1	P	682	ASN
1	P	845	GLN
1	P	869	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	11/30 (36%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	12/30 (40%)	1 (8%)	0
2	H	11/30 (36%)	0	0
2	K	14/30 (46%)	0	0
2	N	17/30 (56%)	2 (11%)	0
2	Q	11/30 (36%)	0	0
3	C	8/9 (88%)	0	0
3	F	8/9 (88%)	0	0
3	I	8/9 (88%)	1 (12%)	0
3	L	8/9 (88%)	0	0
3	O	8/9 (88%)	0	0
3	R	8/9 (88%)	0	0
All	All	124/234 (52%)	4 (3%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	1000	G
3	I	1094	G
2	N	984	A
2	N	998	A

There are no RNA pucker outliers to report.

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](#)

Of 42 ligands modelled in this entry, 24 are monoatomic - leaving 18 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	$\# Z > 2$
7	CTP	J	1006	4	29,30,30	0.57	0	43,47,47	0.63	0
7	CTP	P	1005	4	29,30,30	0.58	0	43,47,47	0.54	0
6	GOL	H	1101	-	5,5,5	1.13	0	5,5,5	1.16	1 (20%)
6	GOL	D	1008	-	5,5,5	0.07	0	5,5,5	0.27	0
7	CTP	G	1005	4	29,30,30	0.60	0	43,47,47	0.56	0
6	GOL	A	1006	-	5,5,5	0.08	0	5,5,5	0.32	0
6	GOL	K	1101	-	5,5,5	0.09	0	5,5,5	0.30	0
6	GOL	D	1006	-	5,5,5	0.11	0	5,5,5	0.27	0
6	GOL	D	1005	-	5,5,5	0.07	0	5,5,5	0.32	0
6	GOL	J	1005	-	5,5,5	0.08	0	5,5,5	0.34	0
7	CTP	M	1006	4	29,30,30	0.65	0	43,47,47	0.55	0
6	GOL	E	1102	-	5,5,5	0.13	0	5,5,5	0.29	0
7	CTP	D	1009	4	29,30,30	0.61	0	43,47,47	0.56	0
6	GOL	A	1005	-	5,5,5	1.07	0	5,5,5	1.07	0
6	GOL	E	1101	-	5,5,5	0.09	0	5,5,5	0.33	0
6	GOL	M	1005	-	5,5,5	0.13	0	5,5,5	0.37	0
7	CTP	A	1007	4	29,30,30	1.08	2 (6%)	43,47,47	1.14	3 (6%)
6	GOL	D	1007	-	5,5,5	0.09	0	5,5,5	0.31	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
7	CTP	J	1006	4	-	6/22/38/38	0/2/2/2
7	CTP	P	1005	4	-	4/22/38/38	0/2/2/2
6	GOL	H	1101	-	-	0/4/4/4	-
6	GOL	D	1008	-	-	0/4/4/4	-
7	CTP	G	1005	4	-	4/22/38/38	0/2/2/2
6	GOL	A	1006	-	-	2/4/4/4	-
6	GOL	K	1101	-	-	1/4/4/4	-
6	GOL	D	1006	-	-	3/4/4/4	-
6	GOL	D	1005	-	-	2/4/4/4	-
6	GOL	J	1005	-	-	2/4/4/4	-
7	CTP	M	1006	4	-	6/22/38/38	0/2/2/2
6	GOL	E	1102	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	CTP	D	1009	4	-	5/22/38/38	0/2/2/2
6	GOL	A	1005	-	-	0/4/4/4	-
6	GOL	E	1101	-	-	4/4/4/4	-
6	GOL	M	1005	-	-	2/4/4/4	-
7	CTP	A	1007	4	-	4/22/38/38	0/2/2/2
6	GOL	D	1007	-	-	4/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1007	CTP	C5-C4	-2.46	1.37	1.42
7	A	1007	CTP	C6-N1	-2.07	1.33	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1007	CTP	C2'-C1'-N1	-3.34	103.97	113.25
7	A	1007	CTP	O2-C2-N3	-2.34	118.64	122.33
6	H	1101	GOL	C3-C2-C1	-2.09	104.12	111.80
7	A	1007	CTP	O2A-PA-O1A	2.01	121.79	112.44

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	1005	GOL	C1-C2-C3-O3
6	D	1007	GOL	O1-C1-C2-O2
6	D	1007	GOL	O1-C1-C2-C3
6	D	1007	GOL	C1-C2-C3-O3
6	E	1101	GOL	O1-C1-C2-C3
6	E	1101	GOL	C1-C2-C3-O3
6	E	1102	GOL	O1-C1-C2-C3
6	J	1005	GOL	O1-C1-C2-O2
6	J	1005	GOL	O1-C1-C2-C3
7	A	1007	CTP	PB-O3B-PG-O2G
7	D	1009	CTP	C5'-O5'-PA-O1A
7	D	1009	CTP	C5'-O5'-PA-O3A
7	G	1005	CTP	C5'-O5'-PA-O2A
7	G	1005	CTP	C5'-O5'-PA-O3A
7	J	1006	CTP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
7	J	1006	CTP	C5'-O5'-PA-O2A
7	J	1006	CTP	C5'-O5'-PA-O3A
7	J	1006	CTP	PB-O3A-PA-O5'
7	M	1006	CTP	C5'-O5'-PA-O1A
7	M	1006	CTP	PB-O3A-PA-O5'
7	P	1005	CTP	C5'-O5'-PA-O2A
7	P	1005	CTP	C5'-O5'-PA-O3A
6	D	1006	GOL	O2-C2-C3-O3
6	M	1005	GOL	O2-C2-C3-O3
6	D	1006	GOL	C1-C2-C3-O3
6	M	1005	GOL	C1-C2-C3-O3
6	D	1005	GOL	O2-C2-C3-O3
6	E	1101	GOL	O2-C2-C3-O3
6	A	1006	GOL	O1-C1-C2-O2
6	D	1007	GOL	O2-C2-C3-O3
6	E	1101	GOL	O1-C1-C2-O2
6	E	1102	GOL	O1-C1-C2-O2
6	A	1006	GOL	O1-C1-C2-C3
7	D	1009	CTP	PB-O3A-PA-O5'
7	G	1005	CTP	PB-O3A-PA-O5'
7	P	1005	CTP	PB-O3A-PA-O5'
6	K	1101	GOL	O2-C2-C3-O3
7	J	1006	CTP	PB-O3B-PG-O3G
7	M	1006	CTP	PB-O3B-PG-O2G
6	D	1006	GOL	O1-C1-C2-O2
7	D	1009	CTP	C5'-O5'-PA-O2A
7	G	1005	CTP	C5'-O5'-PA-O1A
7	M	1006	CTP	C5'-O5'-PA-O2A
7	M	1006	CTP	C5'-O5'-PA-O3A
7	P	1005	CTP	C5'-O5'-PA-O1A
7	A	1007	CTP	PA-O3A-PB-O2B
7	A	1007	CTP	PB-O3B-PG-O3G
7	J	1006	CTP	PB-O3B-PG-O2G
7	M	1006	CTP	PB-O3B-PG-O3G
7	A	1007	CTP	PB-O3B-PG-O1G
7	D	1009	CTP	C3'-C4'-C5'-O5'

There are no ring outliers.

6 monomers are involved in 8 short contacts:

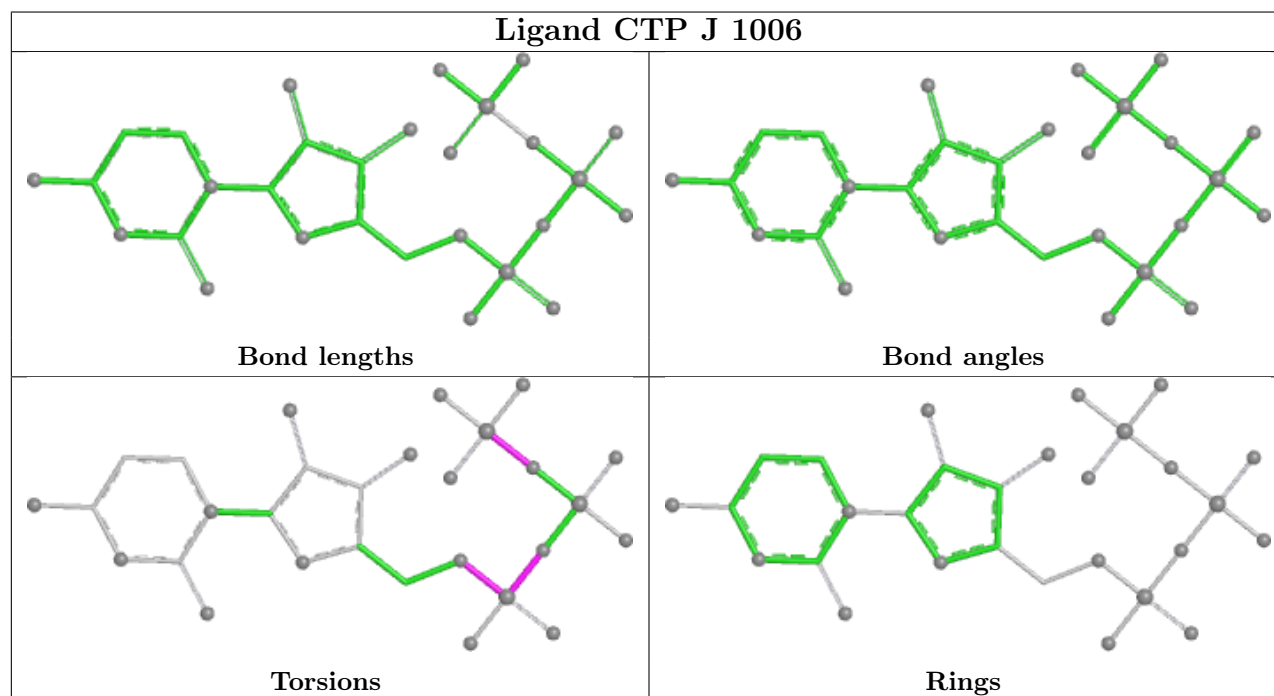
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	J	1006	CTP	1	0

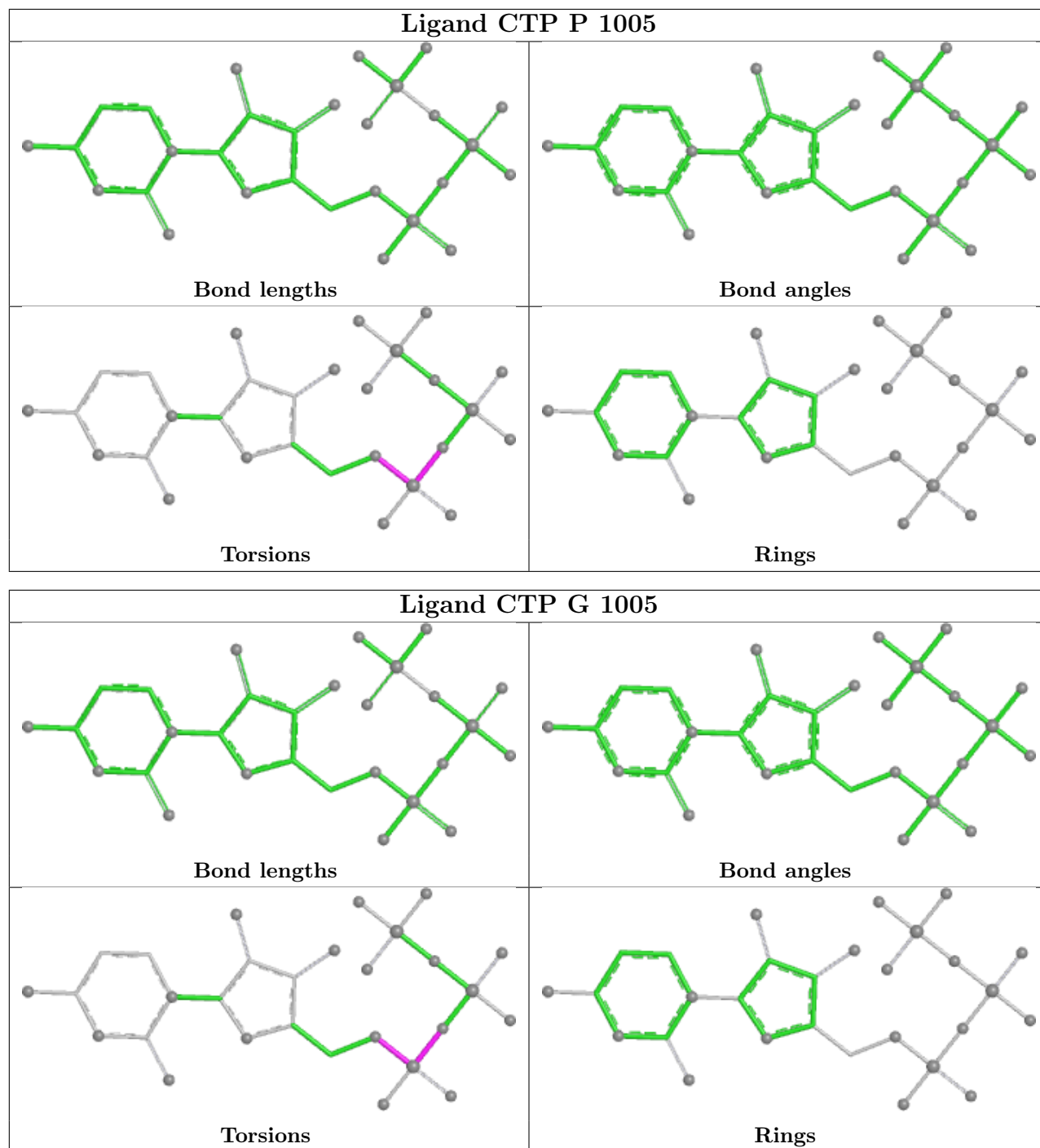
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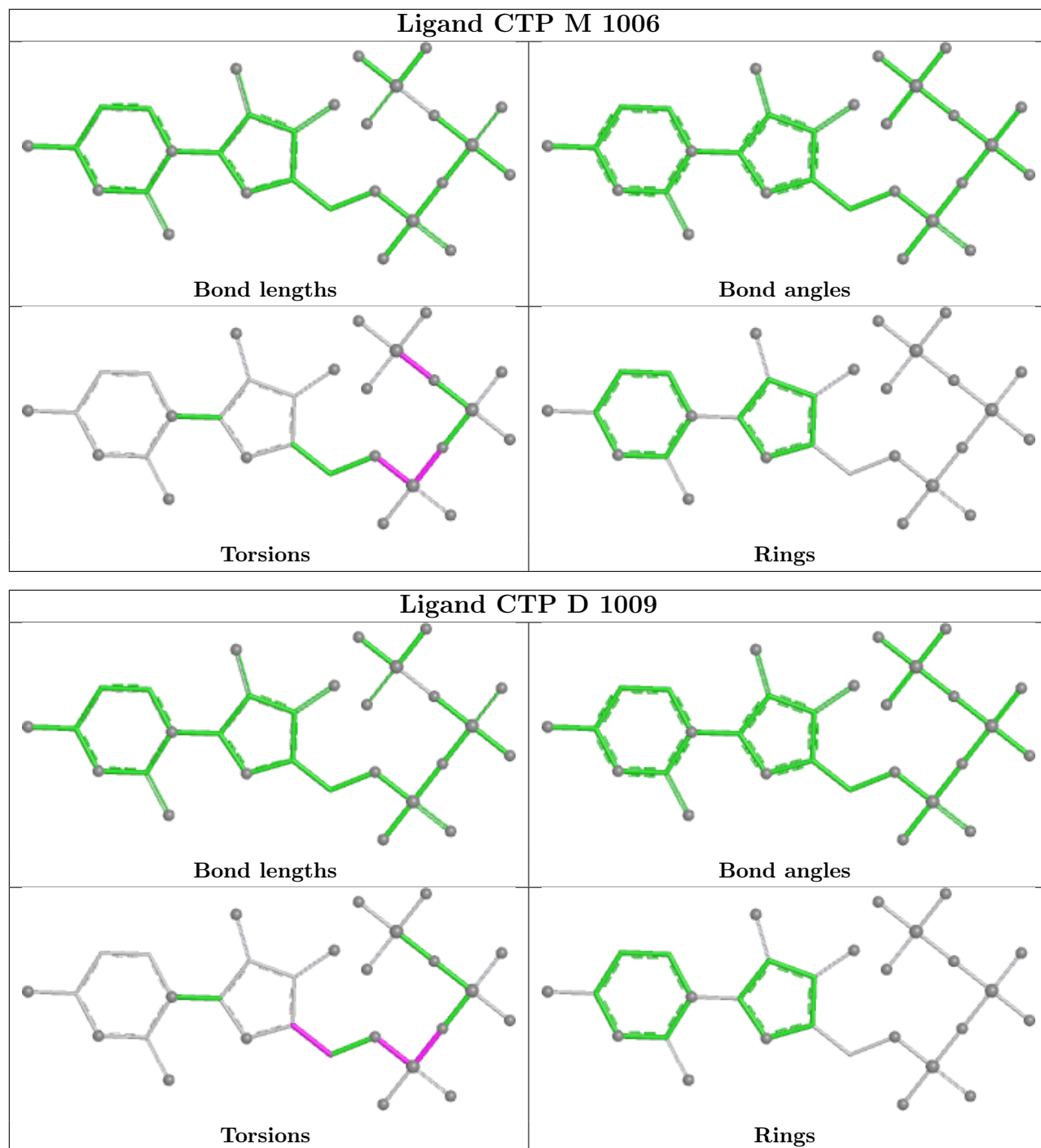
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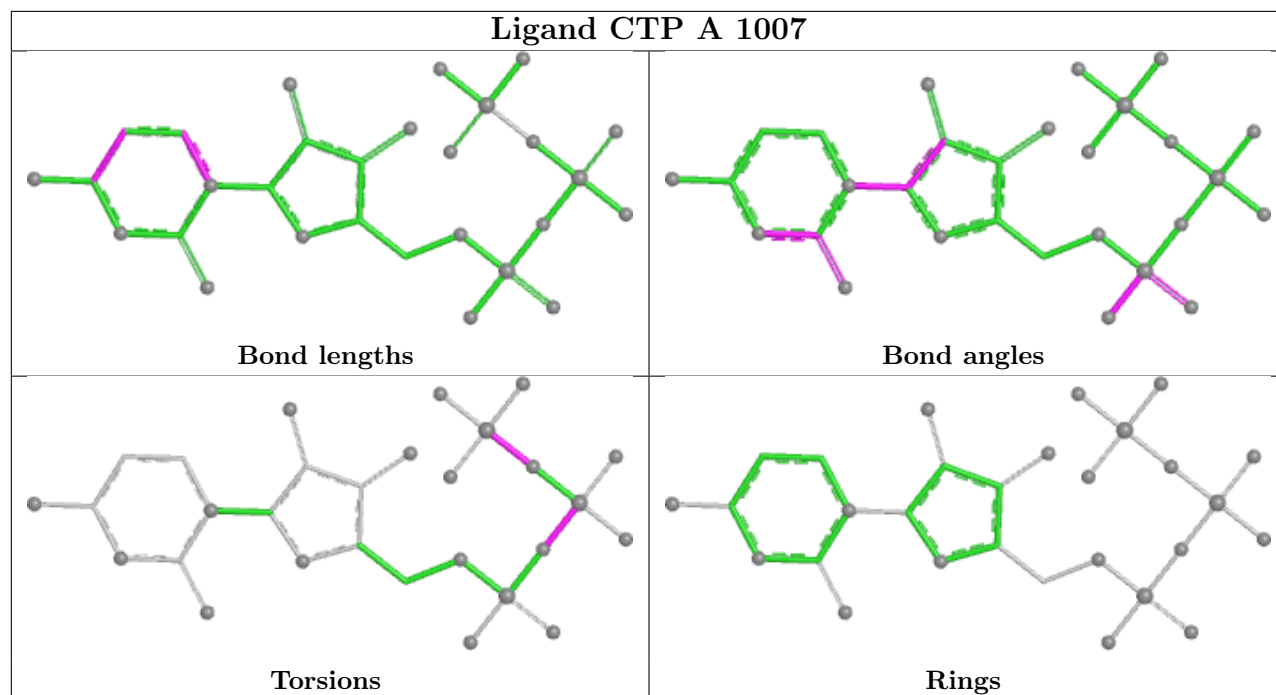
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	1101	GOL	1	0
6	E	1102	GOL	1	0
7	D	1009	CTP	1	0
6	M	1005	GOL	2	0
7	A	1007	CTP	2	0

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	621/647 (95%)	0.13	18 (2%) 53 49	40, 57, 75, 97	0
1	D	622/647 (96%)	0.02	12 (1%) 66 62	38, 54, 75, 92	0
1	G	623/647 (96%)	0.19	13 (2%) 63 59	44, 62, 81, 105	0
1	J	625/647 (96%)	0.48	29 (4%) 37 33	45, 63, 91, 108	0
1	M	624/647 (96%)	0.08	8 (1%) 75 72	42, 56, 73, 87	0
1	P	616/647 (95%)	1.41	151 (24%) 2 1	51, 93, 121, 141	0
2	B	12/30 (40%)	-0.17	1 (8%) 17 14	43, 48, 83, 99	0
2	E	13/30 (43%)	0.14	2 (15%) 5 4	47, 50, 101, 106	0
2	H	12/30 (40%)	0.03	0 100 100	53, 56, 73, 86	2 (16%)
2	K	16/30 (53%)	1.08	5 (31%) 1 1	49, 61, 87, 88	6 (37%)
2	N	19/30 (63%)	0.78	5 (26%) 1 1	46, 53, 87, 88	9 (47%)
2	Q	12/30 (40%)	0.92	2 (16%) 4 3	67, 72, 89, 94	2 (16%)
3	C	9/9 (100%)	-0.53	0 100 100	46, 48, 50, 53	0
3	F	9/9 (100%)	-0.15	0 100 100	47, 49, 58, 66	0
3	I	9/9 (100%)	-0.12	0 100 100	52, 55, 58, 64	0
3	L	9/9 (100%)	0.39	1 (11%) 10 8	51, 55, 63, 71	0
3	O	9/9 (100%)	-0.07	0 100 100	46, 49, 56, 64	0
3	R	9/9 (100%)	0.76	0 100 100	64, 71, 78, 78	0
All	All	3869/4116 (93%)	0.38	247 (6%) 25 21	38, 60, 103, 141	19 (0%)

All (247) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	P	639	GLU	6.2
1	P	634	HIS	5.7
1	P	672	ASP	5.2

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Mol	Chain	Res	Type	RSRZ
1	P	628	VAL	5.0
1	P	415	ASP	4.7
1	P	429	SER	4.5
1	P	391	PRO	4.4
1	J	265	ILE	4.3
1	P	694	TRP	4.1
1	P	693	GLN	4.0
1	P	270	GLU	4.0
1	P	541	ARG	4.0
1	P	623	MET	4.0
1	A	801	HIS	3.9
1	G	799	ALA	3.9
1	P	640	GLU	3.8
1	P	691	ILE	3.8
1	P	650	VAL	3.8
1	P	671	ASP	3.8
1	P	393	MET	3.8
1	M	671	ASP	3.7
1	G	267	ILE	3.7
1	P	364	GLN	3.7
1	P	310	GLU	3.7
1	P	409	LEU	3.6
1	P	304	ALA	3.6
1	P	268	GLU	3.5
1	P	471	SER	3.5
1	P	390	THR	3.5
2	Q	999	C	3.5
1	P	632	ILE	3.5
1	J	799	ALA	3.4
1	P	406	ASN	3.4
1	P	446	LYS	3.4
1	D	634	HIS	3.4
2	K	999	C	3.4
1	P	803	TRP	3.4
1	J	692	GLN	3.4
1	J	631	SER	3.4
1	P	825	GLU	3.4
1	P	411	ALA	3.4
1	D	268	GLU	3.3
1	P	663	ASP	3.3
1	P	687	VAL	3.3
1	J	267	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
2	N	984	A	3.3
1	P	674	PHE	3.3
1	P	475	TRP	3.3
1	A	887	LYS	3.3
1	P	645	ASN	3.2
2	E	997	A	3.2
1	P	527	GLY	3.2
1	G	637	VAL	3.1
1	P	521	ASP	3.1
1	G	800	THR	3.1
1	M	670	LEU	3.1
1	P	381	LEU	3.1
1	P	629	PHE	3.1
1	P	542	ILE	3.1
1	G	631	SER	3.0
1	P	586	ARG	3.0
1	J	644	LYS	3.0
1	P	719	LYS	3.0
1	P	392	ARG	3.0
1	J	628	VAL	3.0
1	P	370	THR	3.0
1	P	801	HIS	3.0
2	N	999	C	3.0
1	J	632	ILE	3.0
1	P	826	ASP	3.0
1	G	268	GLU	2.9
1	P	698	ARG	2.9
1	P	385	LEU	2.9
1	J	642	ALA	2.9
1	P	564	LEU	2.9
1	P	692	GLN	2.9
2	K	982	G	2.9
1	A	798	HIS	2.9
1	P	377	THR	2.9
1	P	684	MET	2.9
1	P	723	VAL	2.8
1	M	539	ASP	2.8
1	P	798	HIS	2.8
1	P	489	LEU	2.8
1	P	705	GLN	2.8
1	J	380	TRP	2.8
1	P	292	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
1	P	289	GLU	2.8
1	A	267	ILE	2.7
1	P	583	PRO	2.7
1	P	363	THR	2.7
1	P	566	GLU	2.7
1	G	556	HIS	2.7
1	P	376	ILE	2.7
1	P	553	VAL	2.7
1	D	290	THR	2.7
1	P	487	GLU	2.7
2	K	981	G	2.7
2	K	998	A	2.7
1	P	641	ILE	2.7
1	P	271	THR	2.7
2	Q	998	A	2.7
1	P	401	ARG	2.7
1	P	379	GLU	2.6
1	D	556	HIS	2.6
1	D	410	GLY	2.6
1	P	439	ARG	2.6
1	P	443	LEU	2.6
1	P	677	ALA	2.6
1	P	531	TYR	2.6
1	J	539	ASP	2.6
1	G	629	PHE	2.6
1	P	648	VAL	2.6
1	P	301	LYS	2.6
1	J	635	LEU	2.6
1	P	368	GLU	2.6
1	P	525	LYS	2.6
1	P	294	TYR	2.6
1	J	803	TRP	2.5
1	P	349	PHE	2.5
1	P	526	GLU	2.5
1	J	633	GLN	2.5
1	P	701	ASN	2.5
1	P	686	LYS	2.5
3	L	1093	G	2.5
1	P	497	TRP	2.5
1	P	546	ASP	2.5
1	P	399	PHE	2.5
1	J	798	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
1	M	890	ARG	2.5
1	P	365	GLU	2.4
1	P	552	MET	2.4
1	J	636	THR	2.4
1	P	290	THR	2.4
1	A	294	TYR	2.4
1	J	647	LEU	2.4
1	J	694	TRP	2.4
1	P	646	TRP	2.4
1	P	557	MET	2.4
1	A	800	THR	2.4
1	P	695	GLU	2.4
1	A	296	GLN	2.4
1	P	571	LEU	2.4
1	P	681	LEU	2.4
1	A	292	TRP	2.4
1	A	846	TRP	2.4
1	J	653	GLU	2.4
1	A	586	ARG	2.4
1	P	373	LEU	2.4
1	P	479	LEU	2.4
1	P	742	GLN	2.4
1	P	300	TYR	2.4
1	P	643	VAL	2.4
1	D	273	ASN	2.4
1	A	584	THR	2.3
1	D	800	THR	2.3
1	M	471	SER	2.3
1	P	796	SER	2.3
1	A	587	GLY	2.3
1	D	798	HIS	2.3
1	A	886	MET	2.3
1	P	569	PHE	2.3
1	P	451	VAL	2.3
2	N	998	A	2.3
1	P	673	ARG	2.3
1	P	697	SER	2.3
1	P	717	ILE	2.3
2	K	996	C	2.3
1	D	886	MET	2.3
1	P	679	THR	2.3
1	P	649	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	P	656	SER	2.3
1	P	568	ILE	2.3
1	A	539	ASP	2.3
1	P	630	LYS	2.3
2	B	999	C	2.3
1	G	876	ASN	2.3
1	P	625	GLY	2.3
1	P	478	TRP	2.3
1	M	876	ASN	2.2
1	P	305	TYR	2.3
1	J	395	THR	2.2
1	M	267	ILE	2.2
1	P	284	ILE	2.2
1	P	375	LYS	2.2
1	P	420	LYS	2.2
1	D	690	ASP	2.2
1	J	826	ASP	2.2
1	J	502	ASN	2.2
1	G	414	THR	2.2
1	G	634	HIS	2.2
1	P	274	LEU	2.2
1	P	512	LEU	2.2
1	P	291	SER	2.2
1	P	690	ASP	2.2
1	P	522	VAL	2.2
1	P	799	ALA	2.2
1	M	294	TYR	2.2
1	P	556	HIS	2.2
1	P	633	GLN	2.2
1	P	836	ILE	2.2
1	P	501	GLU	2.2
1	A	694	TRP	2.2
1	P	380	TRP	2.2
1	J	522	VAL	2.2
1	P	675	ALA	2.2
1	J	512	LEU	2.2
1	J	531	TYR	2.2
1	P	572	THR	2.2
1	P	631	SER	2.2
1	P	384	GLU	2.2
1	J	700	TRP	2.2
1	A	290	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	P	678	LEU	2.1
1	J	641	ILE	2.1
1	D	472	ARG	2.1
1	G	289	GLU	2.1
1	P	626	GLU	2.1
1	P	286	GLN	2.1
1	P	481	ALA	2.1
1	J	406	ASN	2.1
1	J	876	ASN	2.1
1	P	627	GLY	2.1
1	P	806	THR	2.1
2	N	981	G	2.1
1	P	827	LYS	2.1
1	P	431	PHE	2.1
1	P	442	HIS	2.1
1	G	846	TRP	2.1
1	P	544	LEU	2.1
2	E	998	A	2.1
1	P	395	THR	2.1
1	P	488	ALA	2.1
1	P	410	GLY	2.1
1	P	668	LYS	2.1
1	P	447	CYS	2.1
1	P	530	MET	2.1
2	N	983	G	2.0
1	D	876	ASN	2.0
1	P	297	ASP	2.0
1	A	885	SER	2.0
1	A	634	HIS	2.0
1	P	665	CYS	2.0
1	P	787	TRP	2.0
1	P	477	MET	2.0
1	P	822	PRO	2.0
1	P	884	PRO	2.0

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

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($\text{\AA}^2$)	Q<0.9
6	GOL	A	1006	6/6	0.68	0.25	72,74,80,80	0
6	GOL	M	1005	6/6	0.74	0.32	47,49,53,53	6
4	MG	G	1001	1/1	0.75	0.20	78,78,78,78	0
6	GOL	H	1101	6/6	0.76	0.20	77,78,80,82	0
6	GOL	J	1005	6/6	0.82	0.32	69,71,75,79	0
6	GOL	D	1005	6/6	0.82	0.20	61,64,66,71	0
6	GOL	E	1102	6/6	0.83	0.23	55,59,67,67	0
4	MG	P	1001	1/1	0.83	0.14	91,91,91,91	1
7	CTP	D	1009	29/29	0.85	0.20	55,62,70,74	29
6	GOL	E	1101	6/6	0.86	0.26	58,63,67,69	0
4	MG	D	1001	1/1	0.86	0.21	69,69,69,69	1
6	GOL	D	1008	6/6	0.86	0.18	66,67,71,74	0
6	GOL	A	1005	6/6	0.87	0.15	63,69,70,80	0
6	GOL	D	1006	6/6	0.87	0.20	57,65,69,70	0
4	MG	A	1001	1/1	0.87	0.12	72,72,72,72	0
6	GOL	K	1101	6/6	0.88	0.29	70,71,76,76	0
4	MG	D	1002	1/1	0.89	0.16	71,71,71,71	0
7	CTP	M	1006	29/29	0.89	0.16	52,61,73,77	29
6	GOL	D	1007	6/6	0.91	0.16	51,59,68,74	0
7	CTP	A	1007	29/29	0.91	0.15	43,56,69,71	29
7	CTP	G	1005	29/29	0.92	0.13	53,60,70,75	29
7	CTP	P	1005	29/29	0.92	0.14	74,84,91,93	29
7	CTP	J	1006	29/29	0.93	0.13	49,63,72,74	29
4	MG	J	1001	1/1	0.94	0.15	76,76,76,76	1
4	MG	G	1002	1/1	0.94	0.06	74,74,74,74	0
4	MG	M	1002	1/1	0.96	0.14	69,69,69,69	0
4	MG	M	1001	1/1	0.96	0.06	69,69,69,69	1
4	MG	P	1002	1/1	0.96	0.07	86,86,86,86	0
4	MG	A	1002	1/1	0.97	0.08	70,70,70,70	0
4	MG	J	1002	1/1	0.97	0.04	72,72,72,72	0
5	ZN	P	1004	1/1	0.97	0.05	113,113,113,113	0
5	ZN	P	1003	1/1	0.99	0.03	82,82,82,82	0

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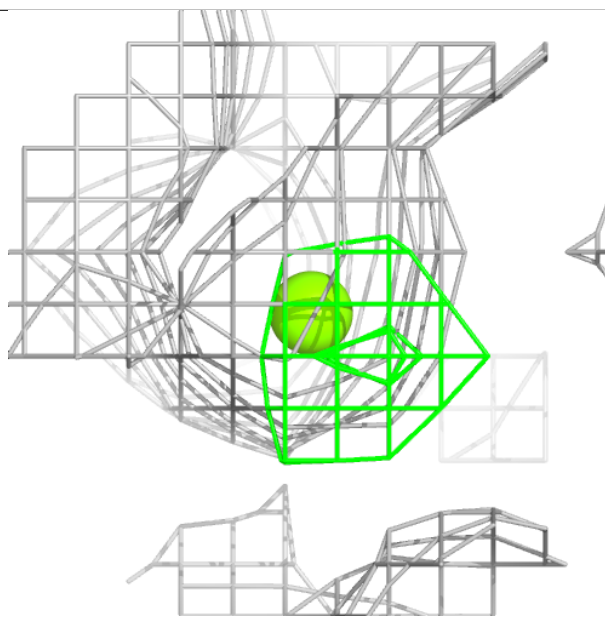
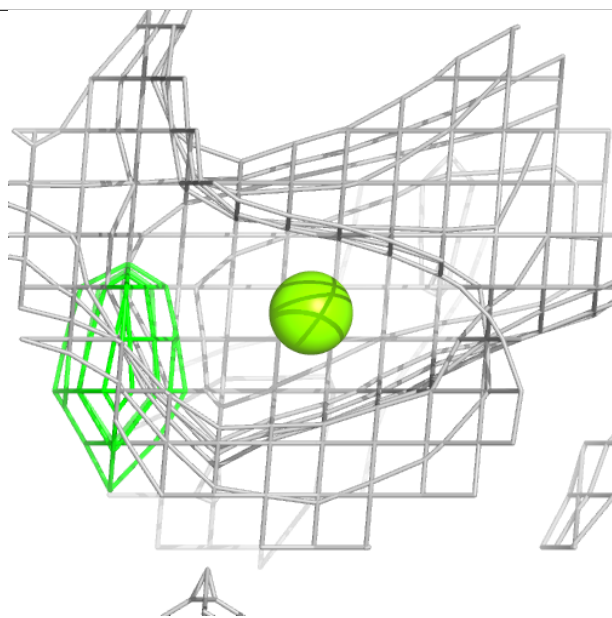
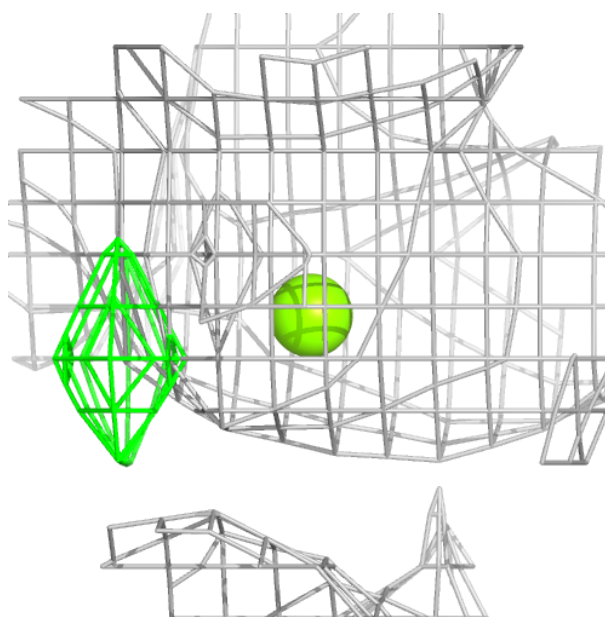
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	ZN	A	1004	1/1	0.99	0.06	63,63,63,63	0
5	ZN	D	1004	1/1	0.99	0.03	68,68,68,68	0
5	ZN	G	1004	1/1	0.99	0.04	72,72,72,72	0
5	ZN	J	1004	1/1	0.99	0.07	71,71,71,71	0
5	ZN	J	1003	1/1	1.00	0.02	58,58,58,58	0
5	ZN	A	1003	1/1	1.00	0.02	59,59,59,59	0
5	ZN	M	1003	1/1	1.00	0.03	59,59,59,59	0
5	ZN	M	1004	1/1	1.00	0.06	68,68,68,68	0
5	ZN	G	1003	1/1	1.00	0.03	52,52,52,52	0
5	ZN	D	1003	1/1	1.00	0.03	48,48,48,48	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.

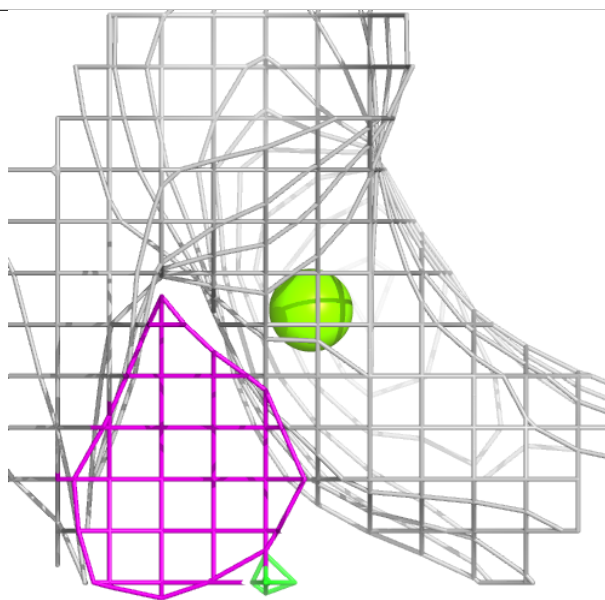
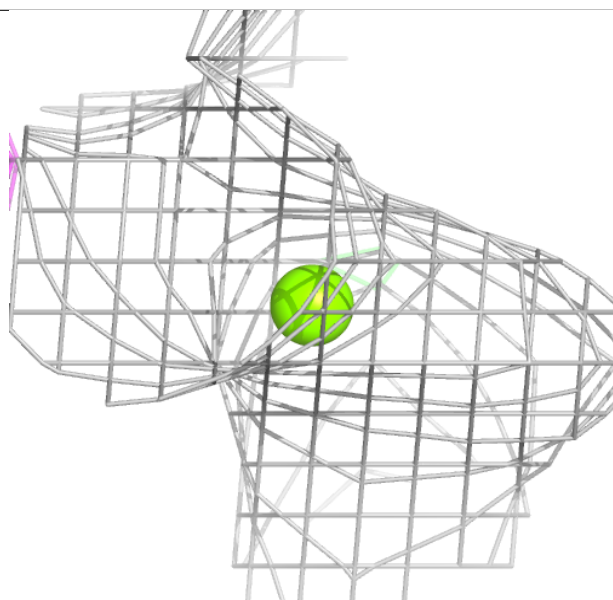
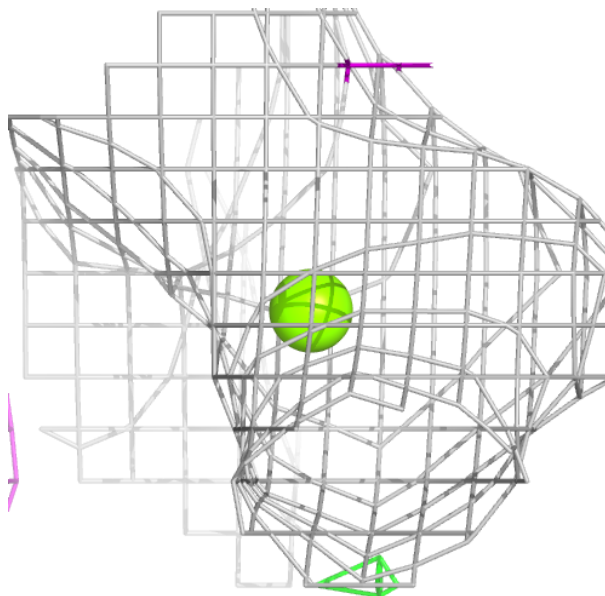
Electron density around MG G 1001:

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



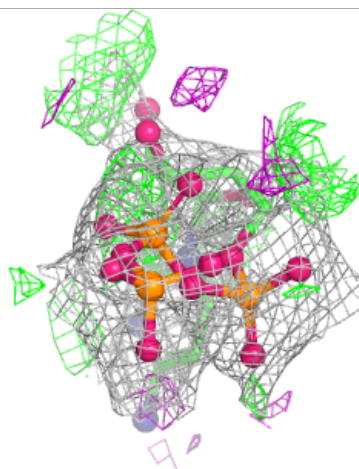
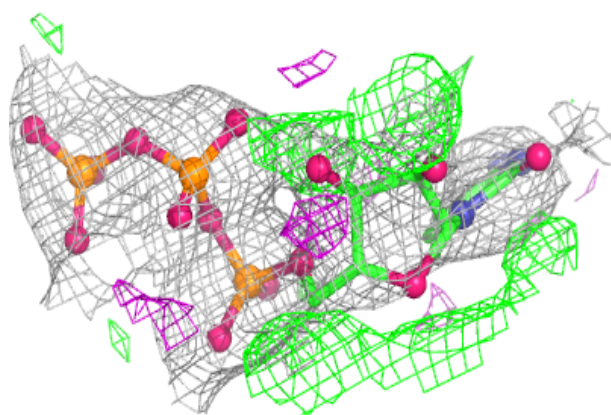
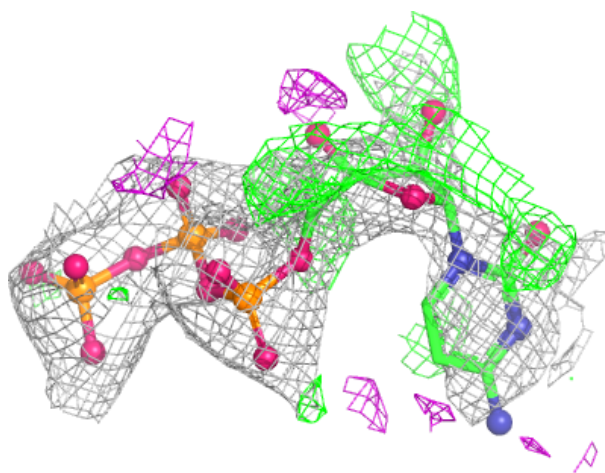
Electron density around MG P 1001:

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and green (positive)



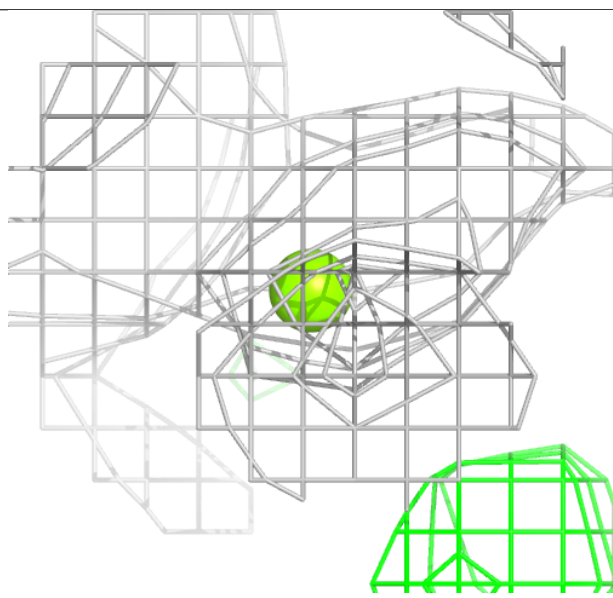
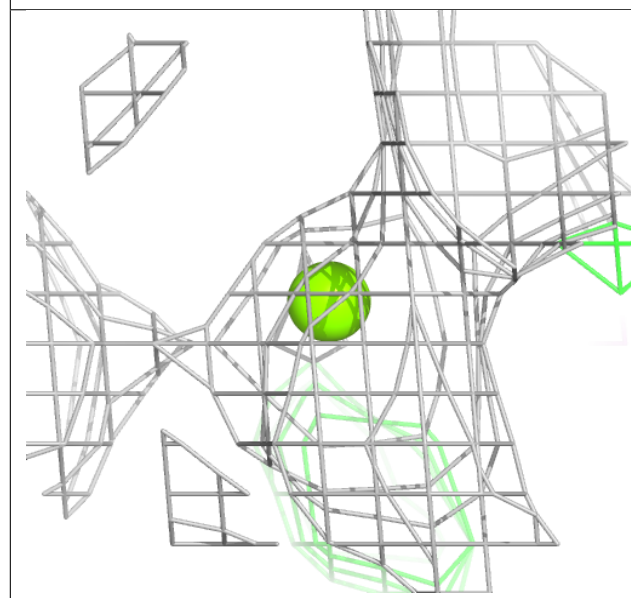
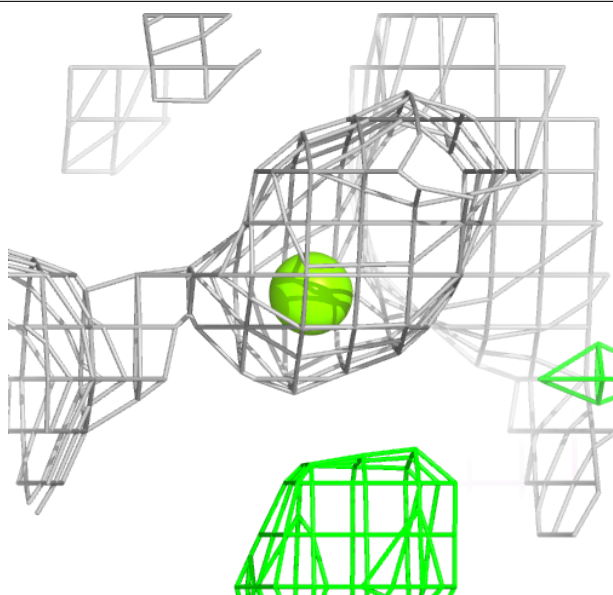
Electron density around CTP D 1009:

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



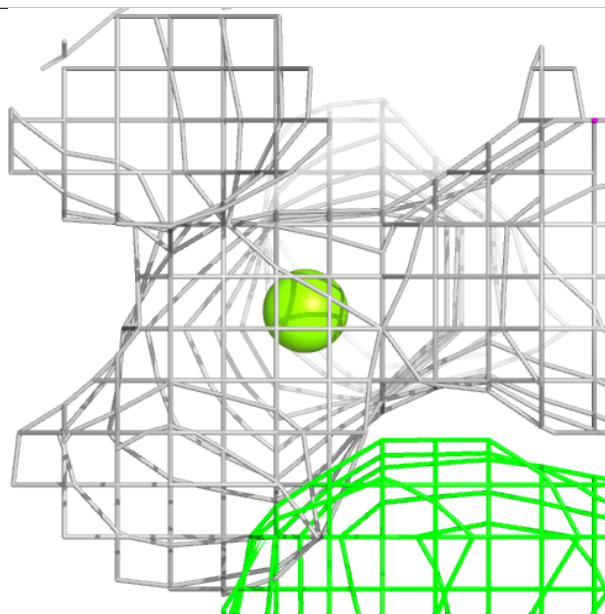
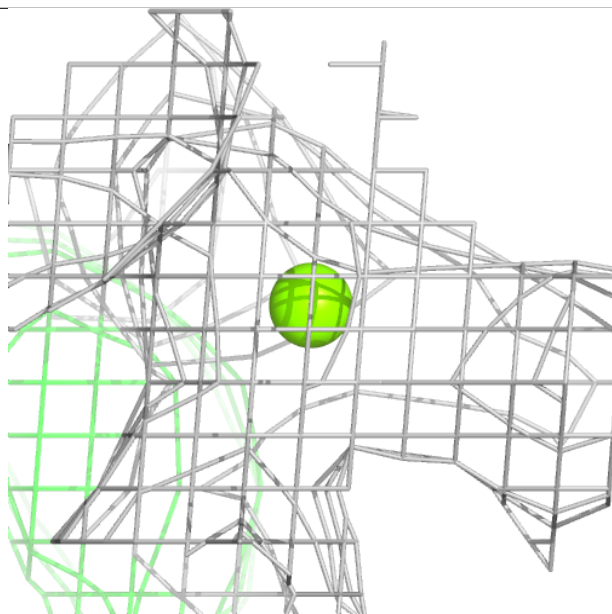
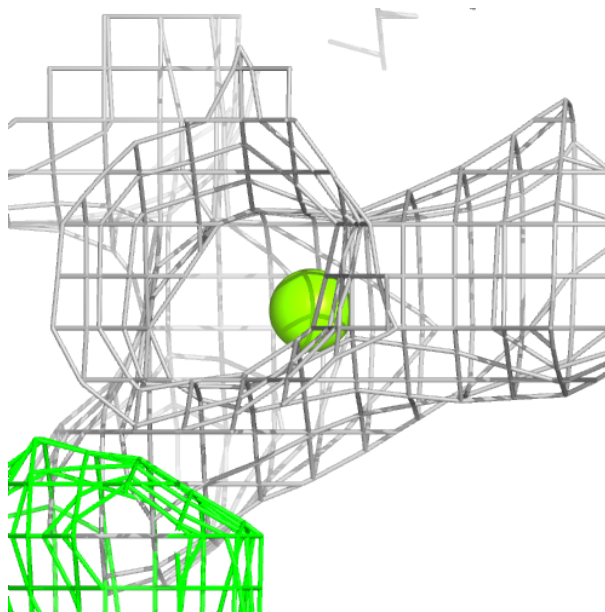
Electron density around MG D 1001:

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



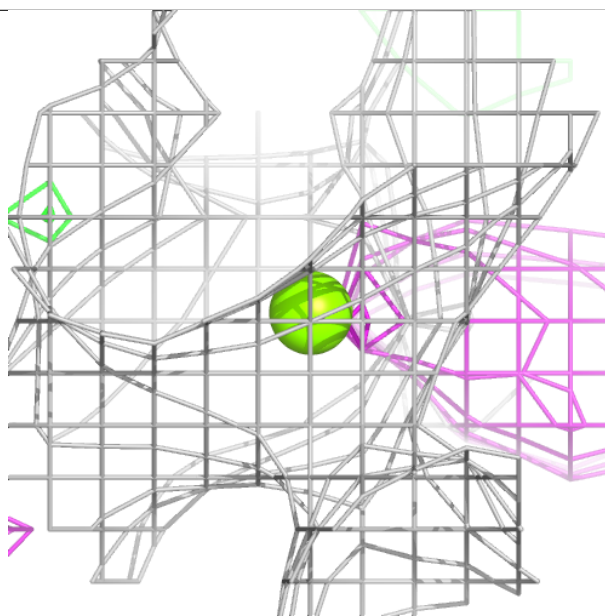
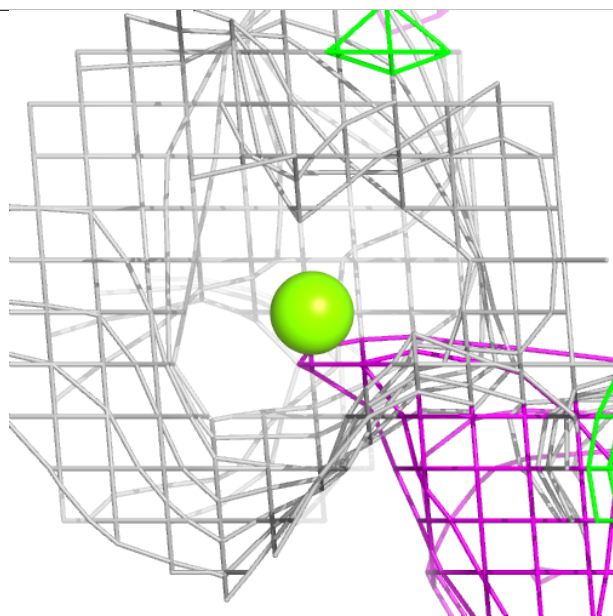
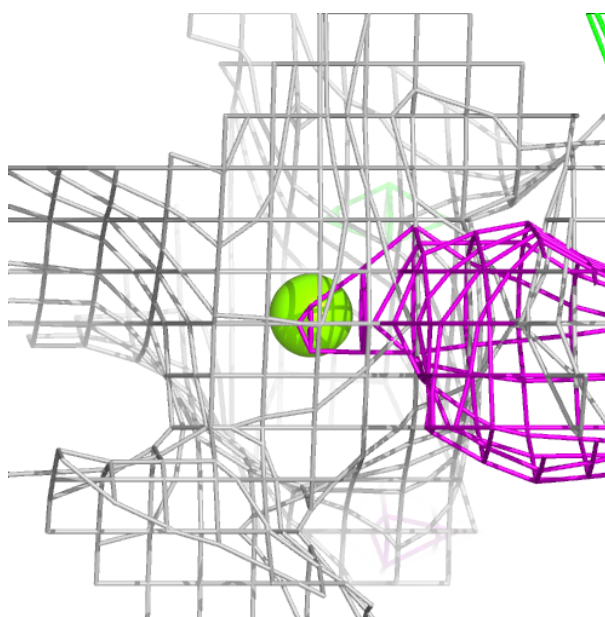
Electron density around MG A 1001:

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



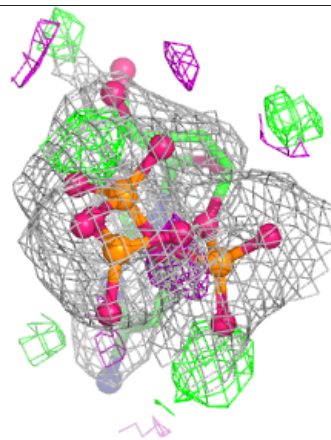
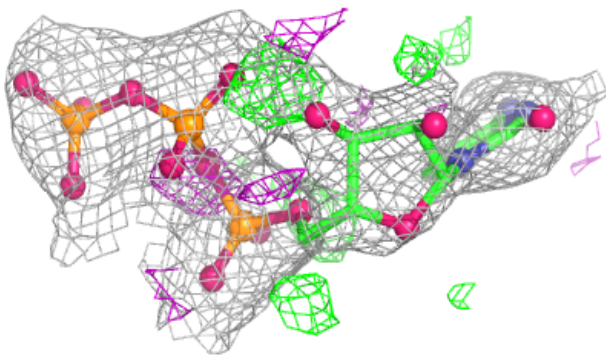
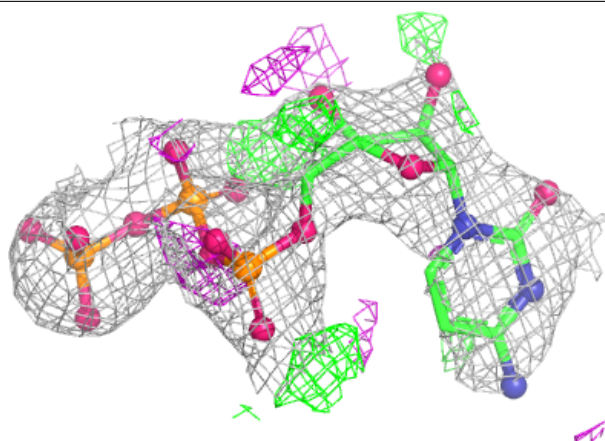
Electron density around MG D 1002:

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



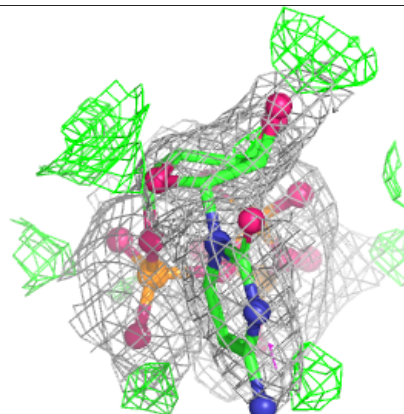
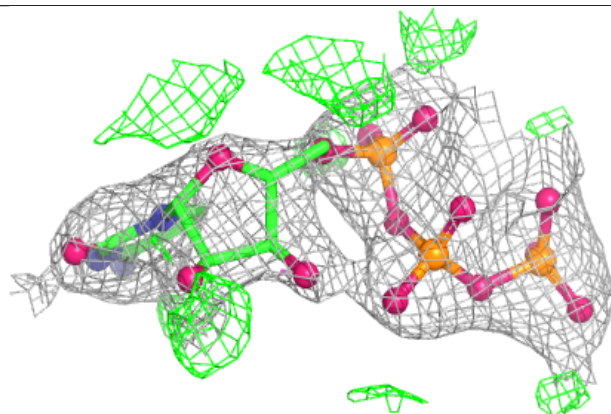
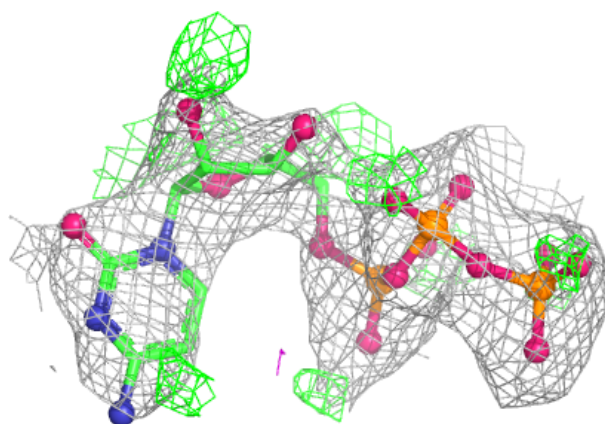
Electron density around CTP M 1006:

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

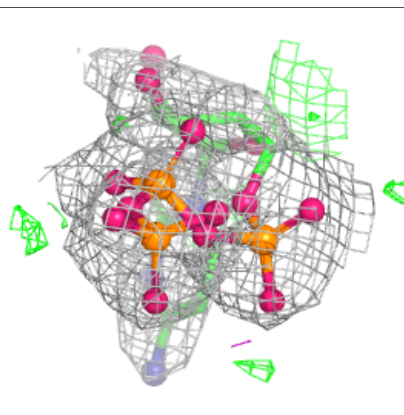
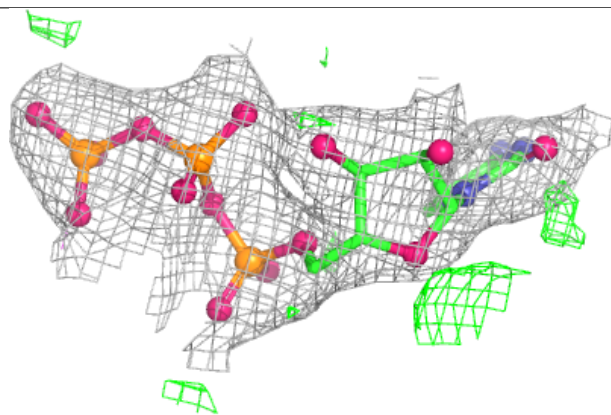
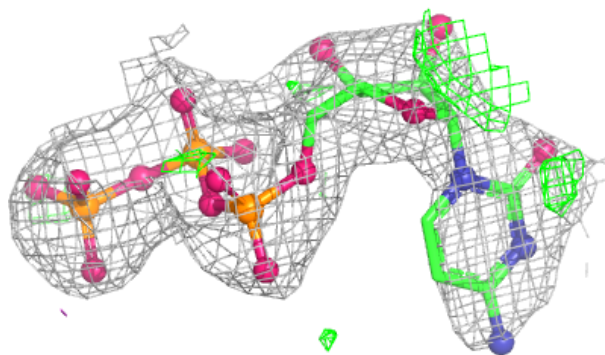


Electron density around CTP A 1007:

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

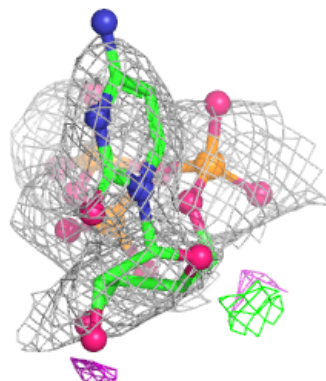
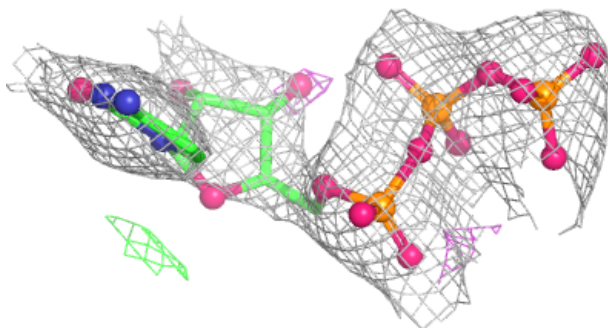
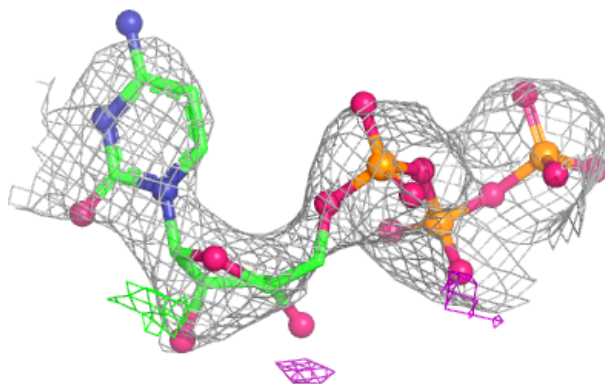
**Electron density around CTP G 1005:**

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

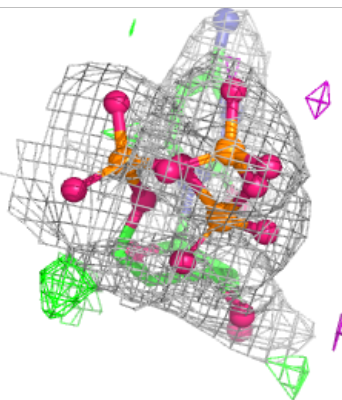
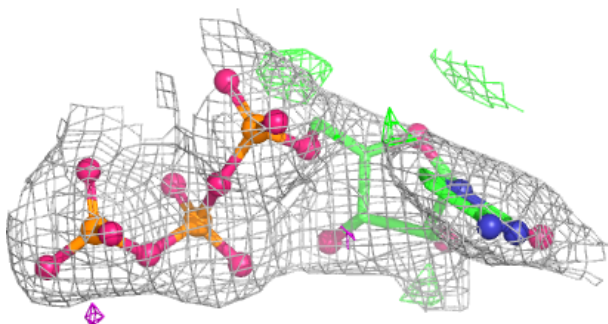
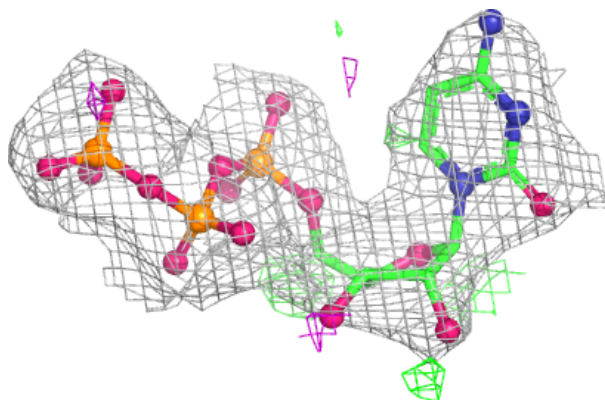


Electron density around CTP P 1005:

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and green (positive)

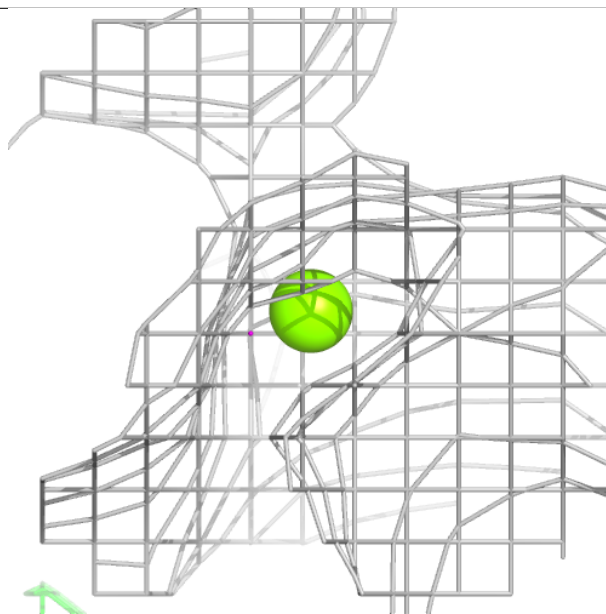
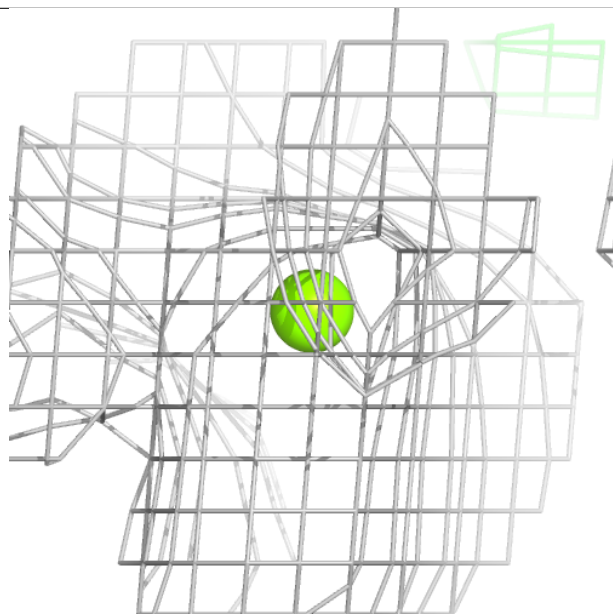
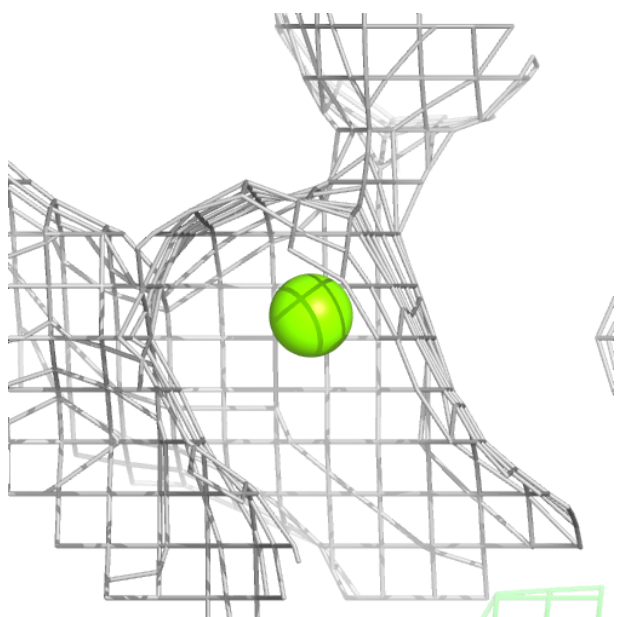
**Electron density around CTP J 1006:**

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and green (positive)



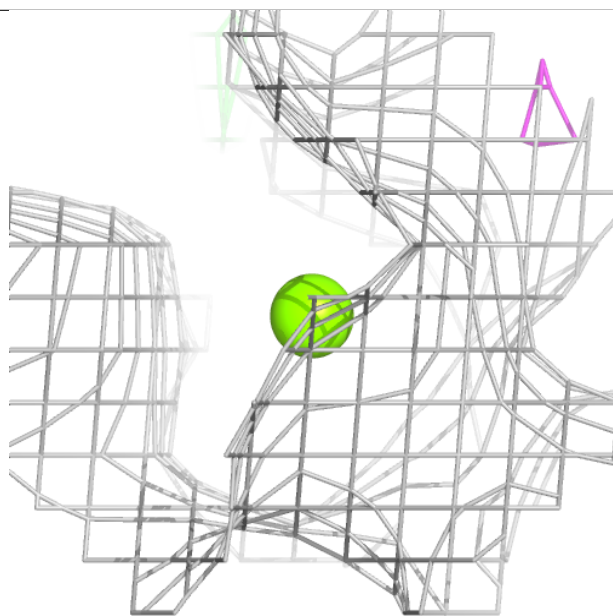
Electron density around MG J 1001:

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and green (positive)



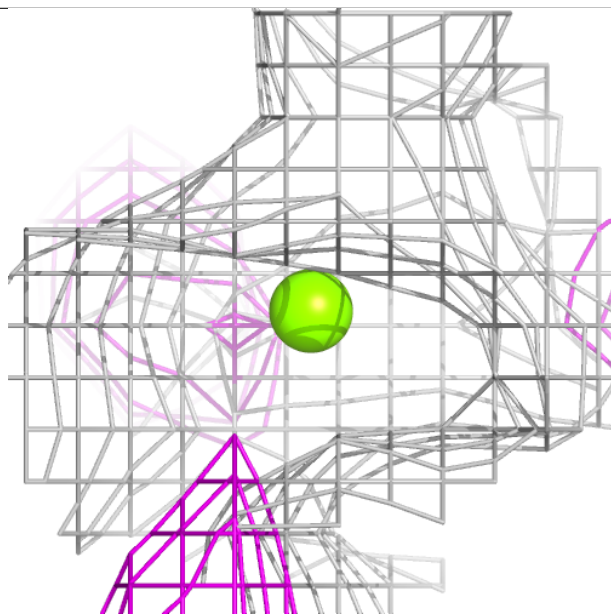
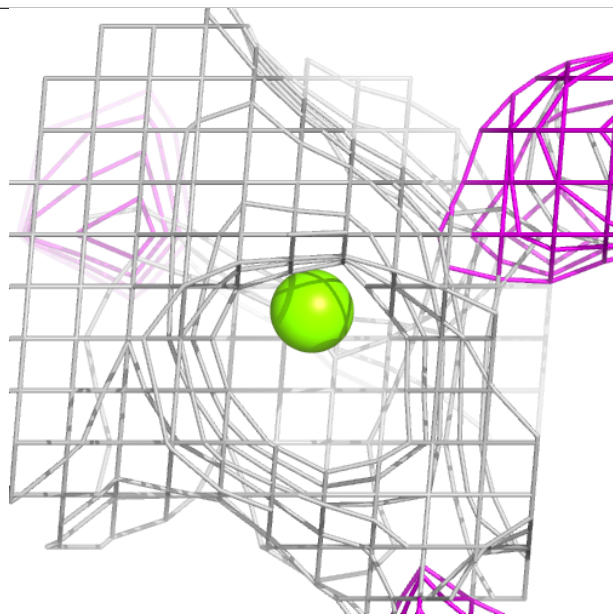
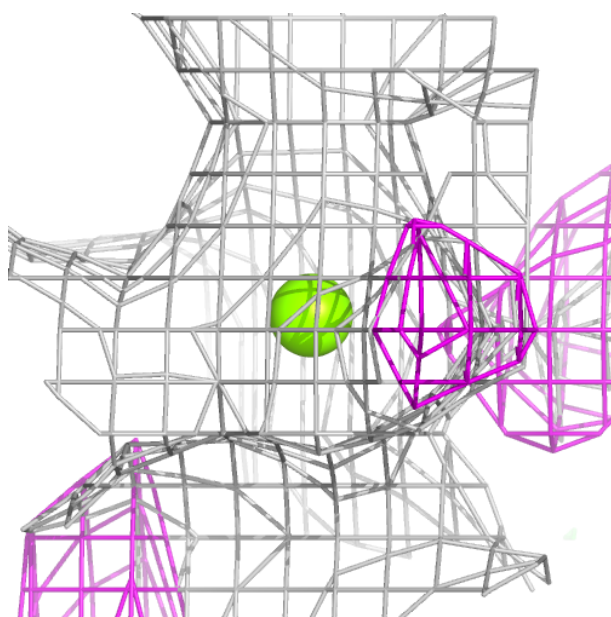
Electron density around MG G 1002:

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



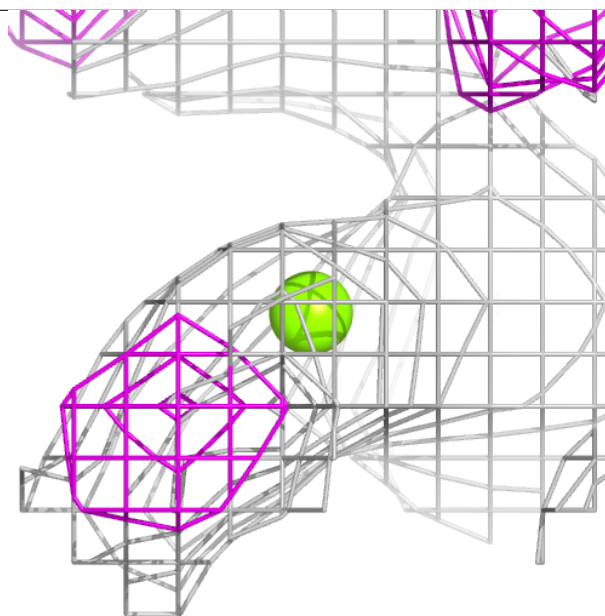
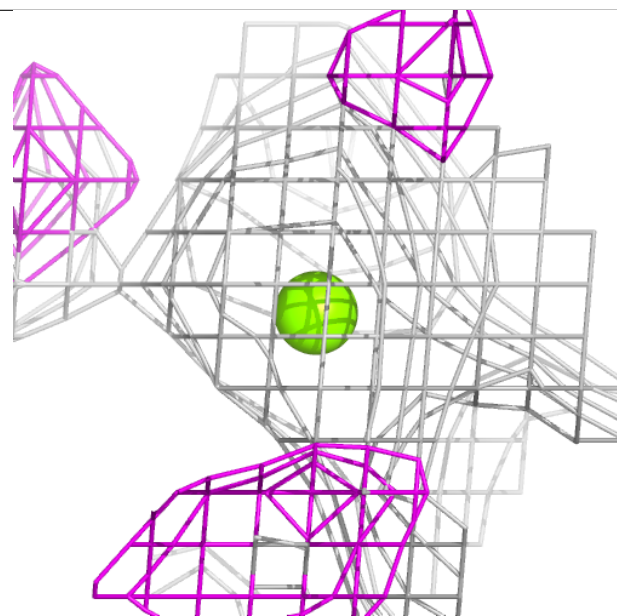
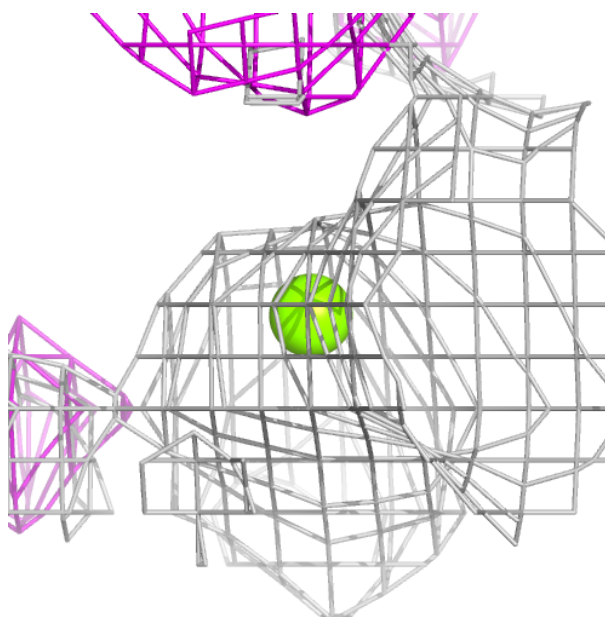
Electron density around MG M 1002:

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



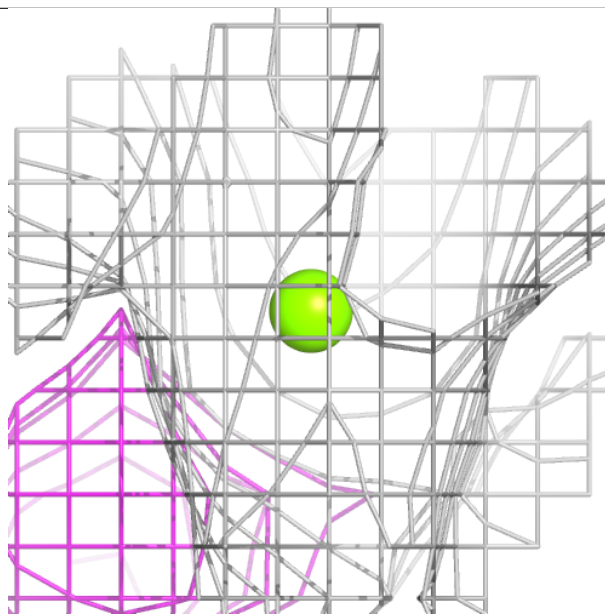
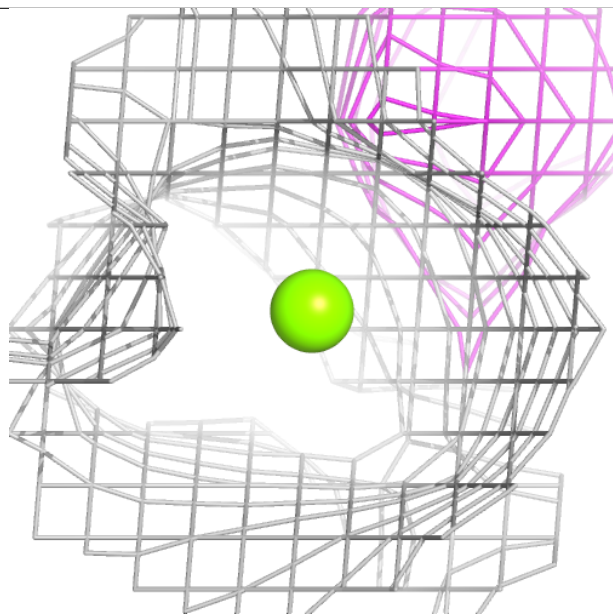
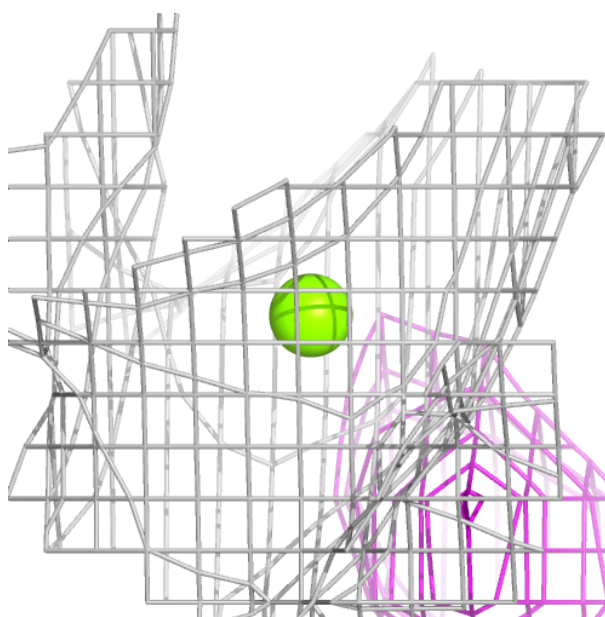
Electron density around MG M 1001:

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



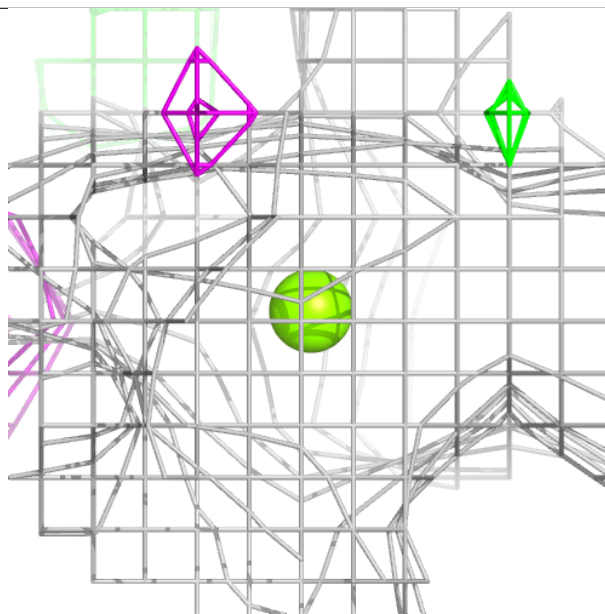
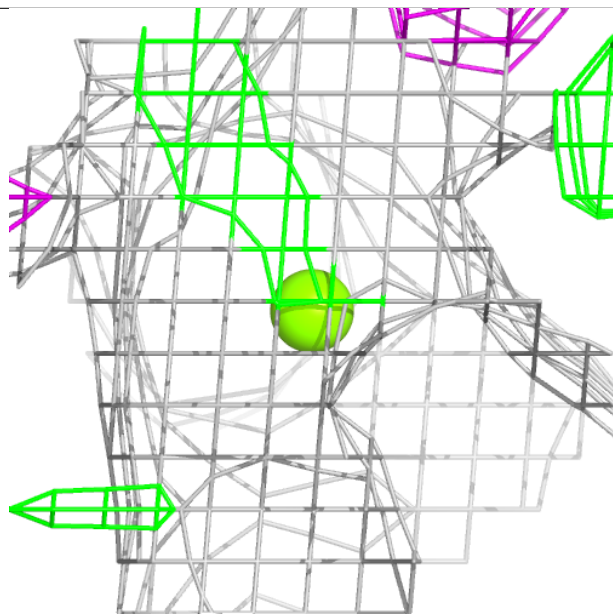
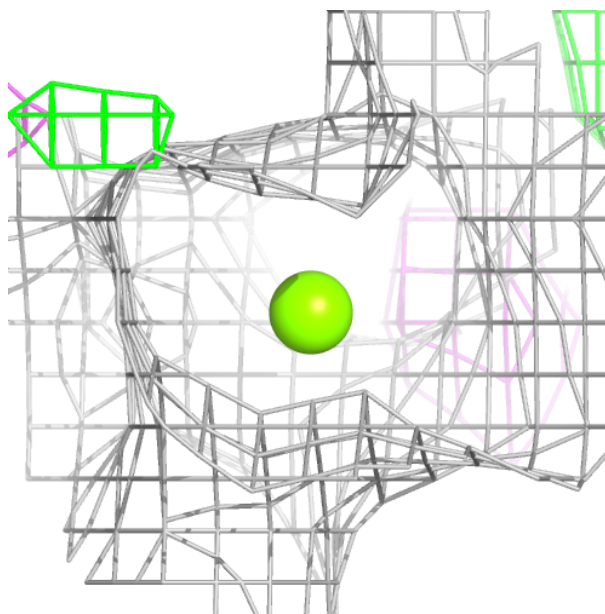
Electron density around MG P 1002:

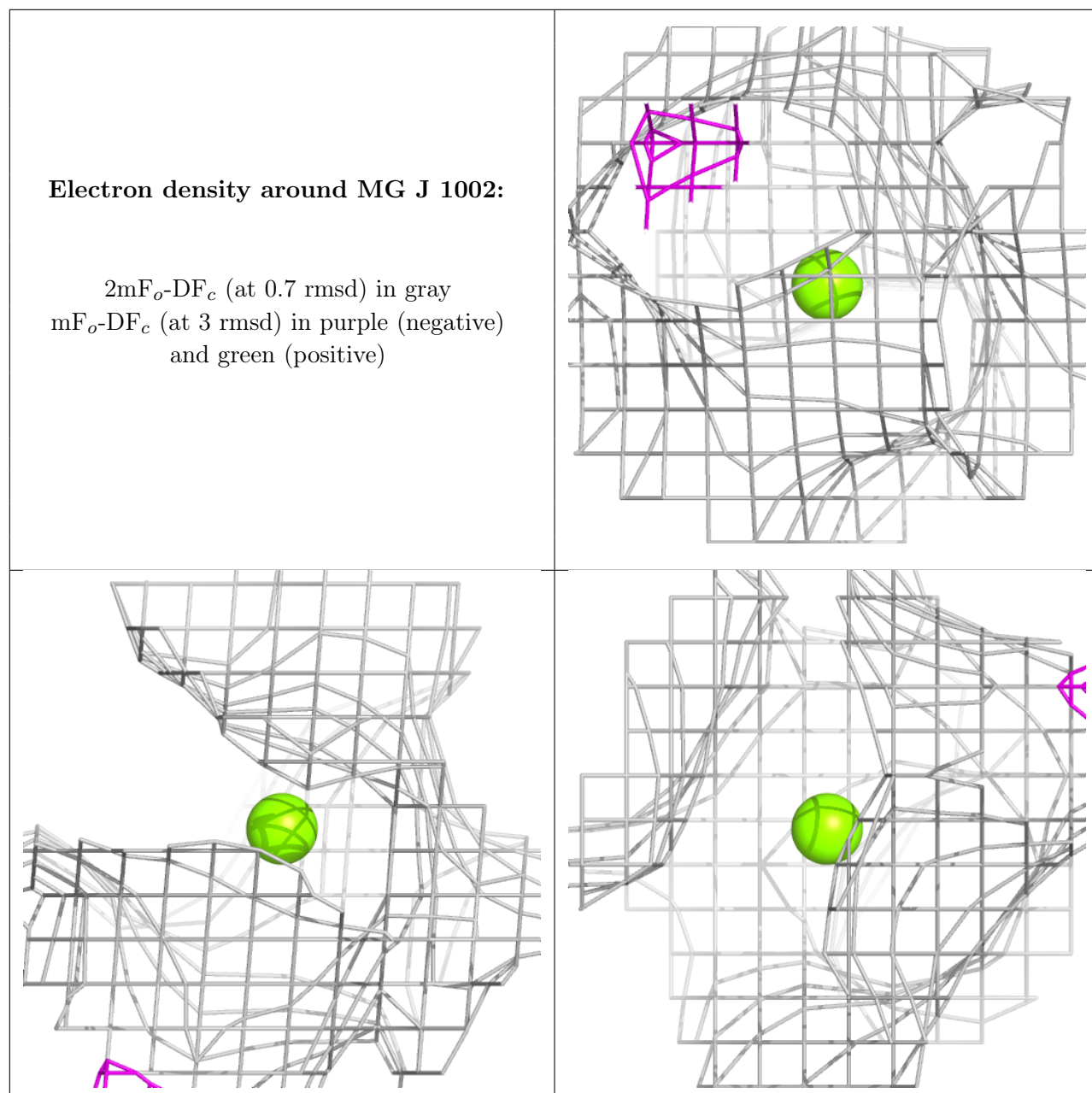
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG A 1002:

$2mF_o-DF_c$ (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.