W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 12:11 am BST

PDB ID	:	1XPU
Title	:	Structural mechanism of inhibition of the Rho transcription termination factor
		by the antibiotic 5a-(3-formylphenylsulfanyl)-dihydrobicyclomycin (FPDB)
Authors	:	Skordalakes, E.; Brogan, A.P.; Park, B.S.; Kohn, H.; Berger, J.M.
Deposited on	:	2004-10-09
Resolution	:	3.05 Å(reported)

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

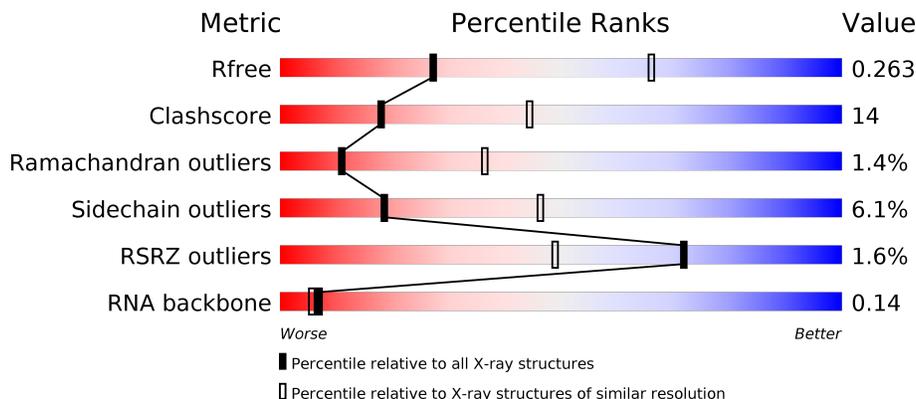|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	Percentile Ranks	Value
Rfree		0.263
Clashscore		14
Ramachandran outliers		1.4%
Sidechain outliers		6.1%
RSRZ outliers		1.6%
RNA backbone		0.14

Worse ← → *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1754 (3.10-3.02)
Clashscore	141614	1864 (3.10-3.02)
Ramachandran outliers	138981	1794 (3.10-3.02)
Sidechain outliers	138945	1793 (3.10-3.02)
RSRZ outliers	127900	1713 (3.10-3.02)
RNA backbone	3102	1036 (3.32-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	G	8	13% · 13% · 75%
1	H	8	13% · 25% · 75%
1	J	8	25% · 13% · 13% · 75%
1	K	8	25% · 13% · 13% · 75%

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Mol	Chain	Length	Quality of chain
1	L	8	25% / 13% / 13% / 75%
1	M	8	25% / 25% / 75%
2	A	419	2% / 66% / 28%
2	B	419	% / 68% / 26%
2	C	419	% / 66% / 27%
2	D	419	58% / 35% / 5%
2	E	419	% / 67% / 25% / 5%
2	F	419	% / 71% / 24%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MG	C	3601	-	-	-	X
4	AGS	E	5600	-	-	X	-
5	FPD	B	2701	-	-	-	X
5	FPD	C	3701	-	-	X	X
5	FPD	D	4701	-	-	-	X
5	FPD	E	5701	-	-	X	X
5	FPD	F	6701	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 19873 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 RNA chain called 5'-R(*CP*UP*CP*UP*CP*UP*CP*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	2	Total	C	N	O	P	0	0	0
			40	18	5	15	2			
1	M	2	Total	C	N	O	P	0	0	0
			40	18	5	15	2			
1	H	2	Total	C	N	O	P	0	0	0
			40	18	5	15	2			
1	J	2	Total	C	N	O	P	0	0	0
			40	18	5	15	2			
1	K	2	Total	C	N	O	P	0	0	0
			40	18	5	15	2			
1	L	2	Total	C	N	O	P	0	0	0
			40	18	5	15	2			

- Molecule 2 is a protein called Rho transcription termination factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	408	Total	C	N	O	S	0	0	0
			3213	2028	564	604	17			
2	B	408	Total	C	N	O	S	0	0	0
			3213	2028	564	604	17			
2	C	408	Total	C	N	O	S	0	0	0
			3213	2028	564	604	17			
2	D	408	Total	C	N	O	S	0	0	0
			3213	2028	564	604	17			
2	E	407	Total	C	N	O	S	0	0	0
			3206	2023	563	603	17			
2	F	408	Total	C	N	O	S	0	0	0
			3213	2028	564	604	17			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total 1	Mg 1	0	0
3	E	1	Total 1	Mg 1	0	0
3	B	1	Total 1	Mg 1	0	0
3	C	1	Total 1	Mg 1	0	0
3	A	1	Total 1	Mg 1	0	0
3	F	1	Total 1	Mg 1	0	0

- Molecule 4 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$).
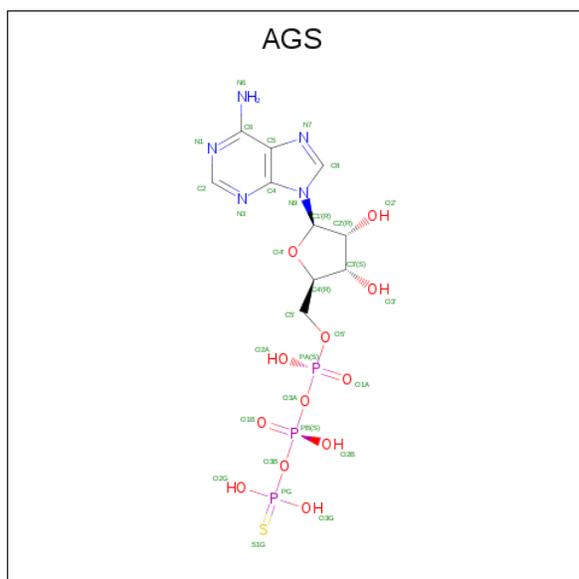
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 31	C 10	N 5	O 12	P 3	S 1	0	0
4	B	1	Total 31	C 10	N 5	O 12	P 3	S 1	0	0
4	C	1	Total 31	C 10	N 5	O 12	P 3	S 1	0	0
4	D	1	Total 31	C 10	N 5	O 12	P 3	S 1	0	0
4	E	1	Total 31	C 10	N 5	O 12	P 3	S 1	0	0

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
4	E	1	31	10	5	12	3	1	0	0

- Molecule 5 is 5A-(3-FORMYLPHENYLSULFANYL)-DIHYDROBICYCLOMYCIN (three-letter code: FPD) (formula: $C_{19}H_{24}N_2O_8S$).

FPD
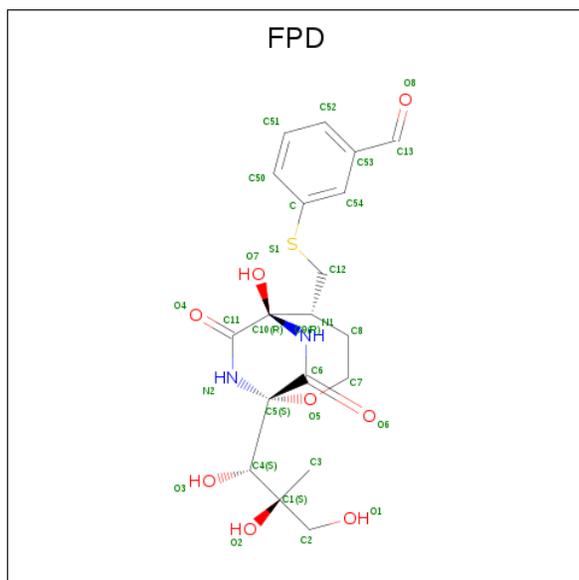
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	B	1	30	19	2	8	1	0	0
5	C	1	30	19	2	8	1	0	0
5	D	1	30	19	2	8	1	0	0
5	E	1	30	19	2	8	1	0	0
5	F	1	30	19	2	8	1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	G	1	1	1	0	0
6	H	1	1	1	0	0
6	A	2	2	2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	5	Total 5	O 5	0	0
6	C	3	Total 3	O 3	0	0
6	D	4	Total 4	O 4	0	0
6	E	3	Total 3	O 3	0	0
6	F	1	Total 1	O 1	0	0

3 Residue-property plots (i)

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

- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*UP*CP*U)-3'

Chain G:

- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*UP*CP*U)-3'

Chain M:

- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*UP*CP*U)-3'

Chain H:

- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*UP*CP*U)-3'

Chain J:

- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*UP*CP*U)-3'

Chain K:

- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*UP*CP*U)-3'

Chain L:

● Molecule 2: Rho transcription termination factor

Chain A:

● Molecule 2: Rho transcription termination factor

Chain B:

● Molecule 2: Rho transcription termination factor

Chain C:

• Molecule 2: Rho transcription termination factor

Chain D:

• Molecule 2: Rho transcription termination factor

Chain E:

• Molecule 2: Rho transcription termination factor

Chain F:
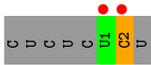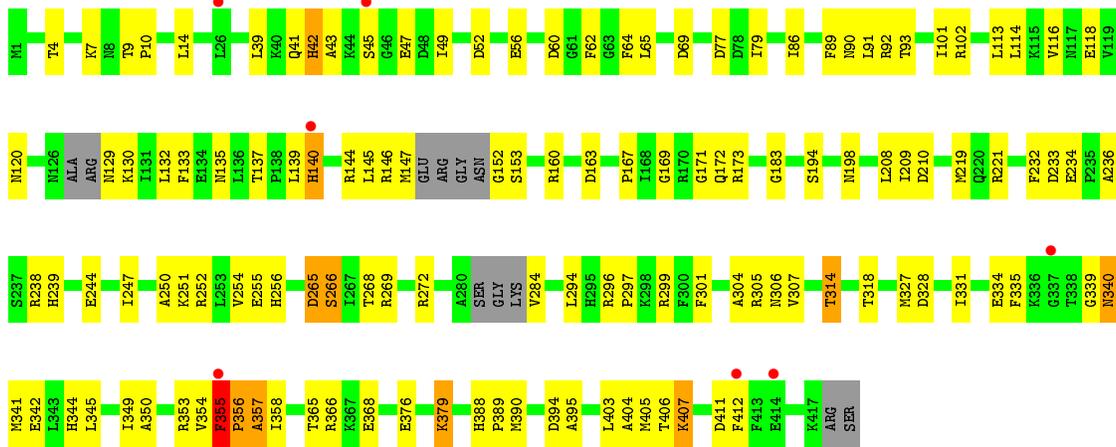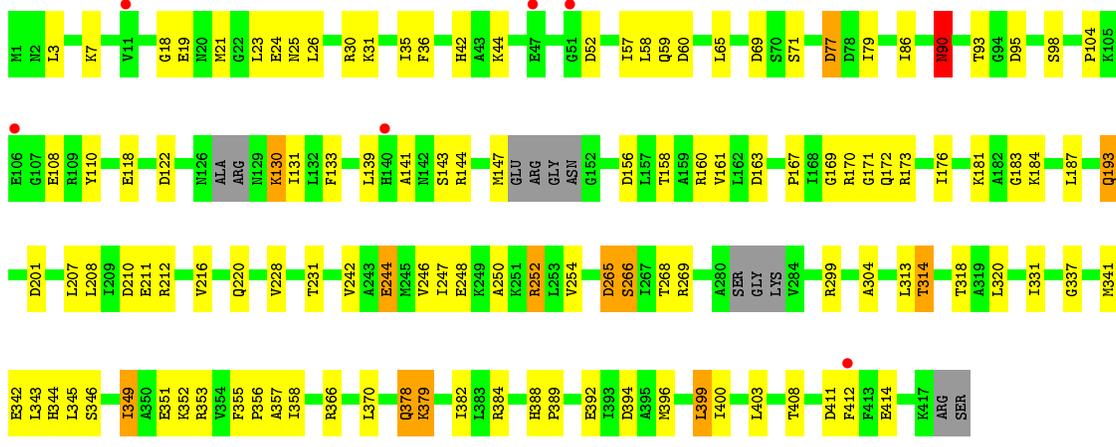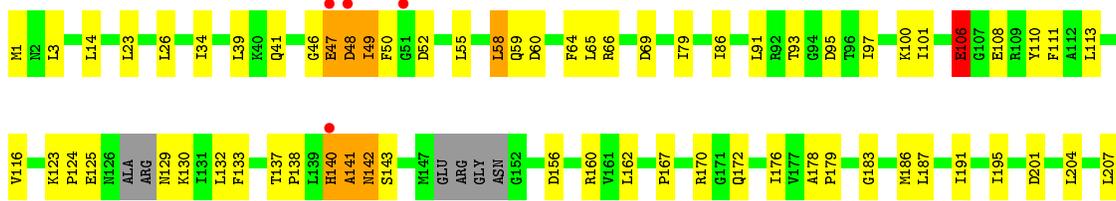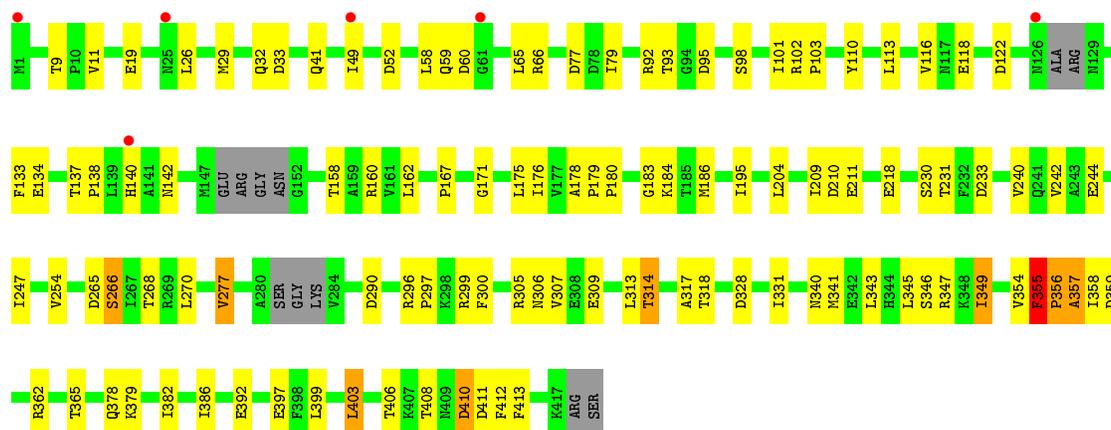
4   Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	119.48Å 206.94Å 148.61Å 90.00° 96.95° 90.00°	Depositor
Resolution (Å)	20.00 – 3.05 45.05 – 2.74	Depositor EDS
% Data completeness (in resolution range)	86.5 (20.00-3.05) 65.0 (45.05-2.74)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.92 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.276 , 0.295 0.268 , 0.263	Depositor DCC
R_{free} test set	3105 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	92.4	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 42.1	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	19873	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

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

5 Model quality (i)

5.1 Standard geometry (i)

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

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	G	0.72	0/43	1.27	1/64 (1.6%)
1	H	0.88	0/43	1.42	1/64 (1.6%)
1	J	0.70	0/43	1.22	0/64
1	K	0.90	0/43	1.60	2/64 (3.1%)
1	L	0.67	0/43	1.08	0/64
1	M	0.81	0/43	1.21	0/64
2	A	0.30	0/3259	0.65	7/4387 (0.2%)
2	B	0.30	0/3259	0.67	12/4387 (0.3%)
2	C	0.30	0/3259	0.65	9/4387 (0.2%)
2	D	0.30	0/3259	0.65	9/4387 (0.2%)
2	E	0.30	0/3252	0.67	11/4377 (0.3%)
2	F	0.30	0/3259	0.64	11/4387 (0.3%)
All	All	0.31	0/19805	0.67	63/26696 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	1
2	E	0	1
2	F	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	1	U	P-O3'-C3'	6.60	127.61	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	77	ASP	CB-CG-OD2	6.21	123.89	118.30
2	D	77	ASP	CB-CG-OD2	6.21	123.89	118.30
2	F	233	ASP	CB-CG-OD2	6.08	123.77	118.30
2	F	290	ASP	CB-CG-OD2	6.04	123.73	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	355	PHE	Peptide
2	E	355	PHE	Peptide
2	F	355	PHE	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	40	0	22	0	0
1	H	40	0	22	2	0
1	J	40	0	22	3	0
1	K	40	0	22	2	0
1	L	40	0	22	2	0
1	M	40	0	22	0	0
2	A	3213	0	3289	106	0
2	B	3213	0	3288	76	0
2	C	3213	0	3289	81	0
2	D	3213	0	3289	118	0
2	E	3206	0	3279	87	0
2	F	3213	0	3288	62	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	31	0	12	4	0
4	B	31	0	12	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	31	0	12	7	0
4	D	31	0	12	5	0
4	E	62	0	24	16	0
5	B	30	0	24	6	0
5	C	30	0	24	9	0
5	D	30	0	24	8	0
5	E	30	0	24	11	0
5	F	30	0	24	3	0
6	A	2	0	0	0	0
6	B	5	0	0	1	0
6	C	3	0	0	0	0
6	D	4	0	0	1	0
6	E	3	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
All	All	19873	0	20046	539	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 14.

The worst 5 of 539 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)
2:C:366:ARG:NE	4:D:4600:AGS:S1G	2.12	1.22
2:A:366:ARG:NE	4:B:2600:AGS:S1G	2.13	1.20
2:D:356:PRO:HG3	2:D:400:ILE:HD11	1.26	1.15
2:B:366:ARG:NE	4:C:3600:AGS:S1G	2.23	1.11
2:D:366:ARG:NE	4:E:5600:AGS:S1G	2.24	1.11

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	400/419 (96%)	368 (92%)	25 (6%)	7 (2%)	8	30
2	B	400/419 (96%)	366 (92%)	32 (8%)	2 (0%)	29	60
2	C	400/419 (96%)	364 (91%)	29 (7%)	7 (2%)	8	30
2	D	400/419 (96%)	358 (90%)	37 (9%)	5 (1%)	12	38
2	E	399/419 (95%)	368 (92%)	25 (6%)	6 (2%)	10	35
2	F	400/419 (96%)	366 (92%)	28 (7%)	6 (2%)	10	35
All	All	2399/2514 (95%)	2190 (91%)	176 (7%)	33 (1%)	11	36

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	47	GLU
2	C	140	HIS
2	E	356	PRO
2	E	358	ILE
2	F	355	PHE

5.3.2　Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	351/359 (98%)	331 (94%)	20 (6%)	20	49
2	B	351/359 (98%)	331 (94%)	20 (6%)	20	49
2	C	351/359 (98%)	327 (93%)	24 (7%)	16	42
2	D	351/359 (98%)	329 (94%)	22 (6%)	18	45
2	E	350/359 (98%)	325 (93%)	25 (7%)	14	41
2	F	351/359 (98%)	333 (95%)	18 (5%)	24	53
All	All	2105/2154 (98%)	1976 (94%)	129 (6%)	18	46

5 of 129 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	352	LYS
2	D	140	HIS
2	F	210	ASP
2	C	383	LEU
2	D	5	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	142	ASN
2	C	275	ASN
2	E	374	GLN
2	C	172	GLN
2	C	193	GLN

5.3.3   RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	G	2/8 (25%)	1 (50%)	1 (50%)
1	H	2/8 (25%)	1 (50%)	1 (50%)
1	J	1/8 (12%)	1 (100%)	0
1	K	2/8 (25%)	1 (50%)	1 (50%)
1	L	1/8 (12%)	1 (100%)	0
1	M	1/8 (12%)	0	0
All	All	9/48 (18%)	5 (55%)	3 (33%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	G	2	C
1	H	2	C
1	J	2	C
1	K	2	C
1	L	2	C

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	G	1	U
1	H	1	U
1	K	1	U

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 17 ligands modelled in this entry, 6 are monoatomic - leaving 11 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
4	AGS	E	6600	3,2	26,33,33	2.09	5 (19%)	26,52,52	1.57	5 (19%)
4	AGS	D	4600	3	26,33,33	1.99	5 (19%)	26,52,52	1.57	6 (23%)
5	FPD	C	3701	-	27,32,32	1.16	3 (11%)	24,49,49	1.09	1 (4%)
5	FPD	B	2701	3	27,32,32	1.21	3 (11%)	24,49,49	1.04	2 (8%)
5	FPD	E	5701	-	27,32,32	1.13	3 (11%)	24,49,49	1.01	2 (8%)
5	FPD	F	6701	3	27,32,32	1.17	4 (14%)	24,49,49	0.99	1 (4%)
4	AGS	C	3600	-	26,33,33	2.04	5 (19%)	26,52,52	1.57	5 (19%)
5	FPD	D	4701	-	27,32,32	1.11	3 (11%)	24,49,49	1.04	2 (8%)
4	AGS	B	2600	3	26,33,33	1.99	5 (19%)	26,52,52	1.58	5 (19%)
4	AGS	A	1600	3	26,33,33	2.08	5 (19%)	26,52,52	1.55	5 (19%)
4	AGS	E	5600	-	26,33,33	1.97	5 (19%)	26,52,52	1.58	6 (23%)

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	AGS	E	6600	3,2	-	2/17/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	AGS	D	4600	3	-	2/17/38/38	0/3/3/3
5	FPD	C	3701	-	-	14/14/57/57	0/2/3/3
5	FPD	B	2701	3	-	12/14/57/57	0/2/3/3
5	FPD	E	5701	-	-	14/14/57/57	0/2/3/3
5	FPD	F	6701	3	-	11/14/57/57	0/2/3/3
4	AGS	C	3600	-	-	2/17/38/38	0/3/3/3
5	FPD	D	4701	-	-	14/14/57/57	0/2/3/3
4	AGS	B	2600	3	-	2/17/38/38	0/3/3/3
4	AGS	A	1600	3	-	2/17/38/38	0/3/3/3
4	AGS	E	5600	-	-	3/17/38/38	0/3/3/3

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1600	AGS	PG-S1G	6.50	2.04	1.90
4	E	6600	AGS	PG-S1G	6.46	2.04	1.90
4	E	6600	AGS	C4-N3	6.35	1.44	1.35
4	C	3600	AGS	C4-N3	6.35	1.44	1.35
4	B	2600	AGS	C4-N3	6.30	1.44	1.35

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	4600	AGS	C3'-C2'-C1'	3.53	106.29	100.98
4	C	3600	AGS	N3-C2-N1	-3.51	123.19	128.68
4	B	2600	AGS	N3-C2-N1	-3.48	123.25	128.68
4	E	6600	AGS	N3-C2-N1	-3.47	123.25	128.68
4	A	1600	AGS	N3-C2-N1	-3.41	123.35	128.68

There are no chirality outliers.

5 of 78 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	6600	AGS	O4'-C4'-C5'-O5'
5	C	3701	FPD	C3-C1-C4-C5
5	C	3701	FPD	O2-C1-C4-C5
5	C	3701	FPD	C2-C1-C4-C5
5	C	3701	FPD	C3-C1-C4-O3

There are no ring outliers.

11 monomers are involved in 75 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	6600	AGS	6	0
4	D	4600	AGS	5	0
5	C	3701	FPD	9	0
5	B	2701	FPD	6	0
5	E	5701	FPD	11	0
5	F	6701	FPD	3	0
4	C	3600	AGS	7	0
5	D	4701	FPD	8	0
4	B	2600	AGS	6	0
4	A	1600	AGS	4	0
4	E	5600	AGS	10	0

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

Ligand AGS E 6600

Bond lengths

Bond angles

Torsions

Rings

Ligand AGS D 4600

Bond lengths

Bond angles

Torsions

Rings

Ligand FPD C 3701

Bond lengths

Bond angles

Torsions

Rings

Ligand FPD B 2701

Bond lengths

Bond angles

Torsions

Rings

Ligand FPD E 5701

Bond lengths

Bond angles

Torsions

Rings

Ligand FPD F 6701

Bond lengths

Bond angles

Torsions

Rings

Ligand AGS C 3600

Bond lengths

Bond angles

Torsions

Rings

Ligand FPD D 4701

Bond lengths

Bond angles

Torsions

Rings

Ligand AGS B 2600

Bond lengths

Bond angles

Torsions

Rings

Ligand AGS A 1600

Bond lengths

Bond angles

Torsions

Rings

Ligand AGS E 5600

Bond lengths

Bond angles

Torsions

Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	G	2/8 (25%)	0.03	0	100	100	53, 53, 53, 53	0
1	H	2/8 (25%)	1.91	1 (50%)	0	0	53, 53, 53, 53	0
1	J	2/8 (25%)	3.39	2 (100%)	0	0	53, 53, 53, 53	0
1	K	2/8 (25%)	4.03	2 (100%)	0	0	55, 55, 55, 56	0
1	L	2/8 (25%)	3.17	2 (100%)	0	0	53, 53, 53, 53	0
1	M	2/8 (25%)	4.24	2 (100%)	0	0	53, 53, 53, 53	0
2	A	408/419 (97%)	-0.17	7 (1%)	70	46	53, 53, 53, 53	0
2	B	408/419 (97%)	0.02	6 (1%)	73	51	53, 53, 53, 53	0
2	C	408/419 (97%)	-0.21	6 (1%)	73	51	53, 53, 53, 53	0
2	D	408/419 (97%)	-0.05	1 (0%)	95	89	53, 53, 53, 53	0
2	E	407/419 (97%)	-0.02	5 (1%)	79	58	53, 53, 53, 53	0
2	F	408/419 (97%)	-0.02	6 (1%)	73	51	53, 53, 53, 53	0
All	All	2459/2562 (95%)	-0.06	40 (1%)	72	49	53, 53, 53, 56	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	140	HIS	5.7
1	K	2	C	5.1
1	M	2	C	4.9
1	J	2	C	4.6
2	B	51	GLY	4.4

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	FPD	C	3701	30/30	0.33	0.76	53,53,53,53	0
5	FPD	E	5701	30/30	0.58	0.52	53,53,53,53	0
5	FPD	D	4701	30/30	0.61	0.52	53,53,53,53	0
5	FPD	F	6701	30/30	0.67	0.59	53,53,53,53	0
5	FPD	B	2701	30/30	0.67	0.47	53,53,53,53	0
3	MG	C	3601	1/1	0.71	0.44	53,53,53,53	0
3	MG	F	6601	1/1	0.76	0.33	53,53,53,53	0
3	MG	B	2601	1/1	0.76	0.33	54,54,54,54	0
4	AGS	E	6600	31/31	0.78	0.27	53,53,53,53	0
4	AGS	C	3600	31/31	0.81	0.26	53,53,53,53	0
4	AGS	A	1600	31/31	0.83	0.33	53,53,53,53	0
3	MG	E	5601	1/1	0.84	0.72	53,53,53,53	0
3	MG	D	4601	1/1	0.86	0.38	53,53,53,53	0
4	AGS	E	5600	31/31	0.87	0.25	53,53,53,53	0
4	AGS	D	4600	31/31	0.89	0.25	53,53,53,53	0
4	AGS	B	2600	31/31	0.89	0.33	53,53,53,53	0
3	MG	A	1601	1/1	0.96	0.22	54,54,54,54	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.
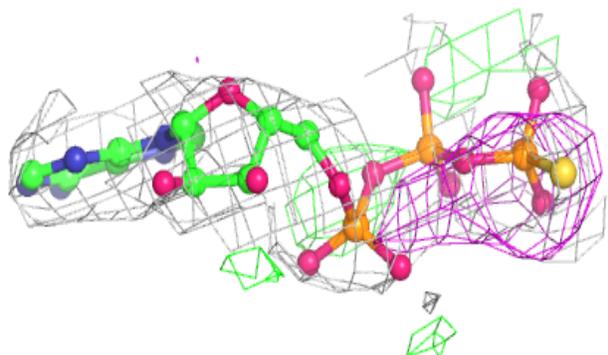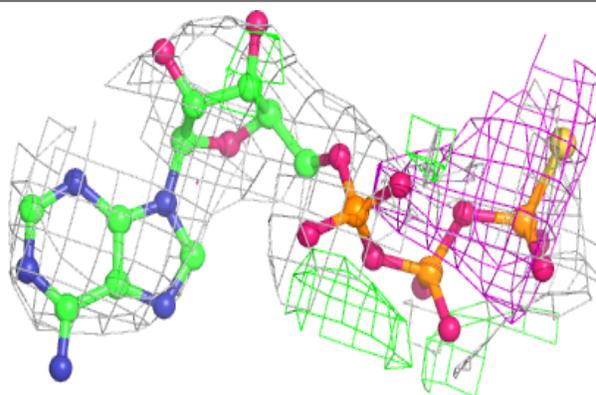
Electron density around FPD C 3701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
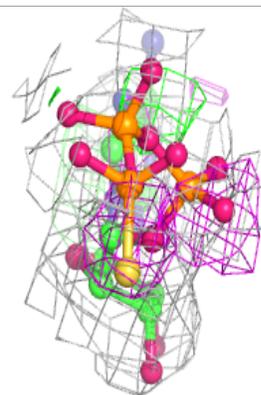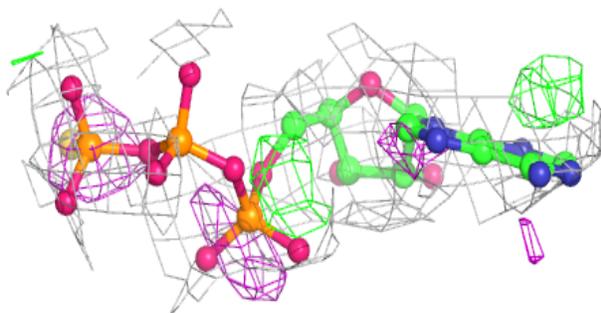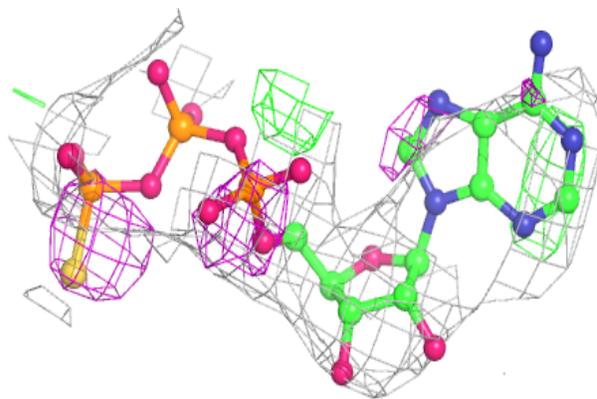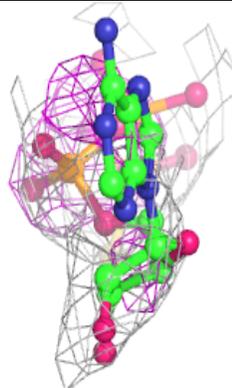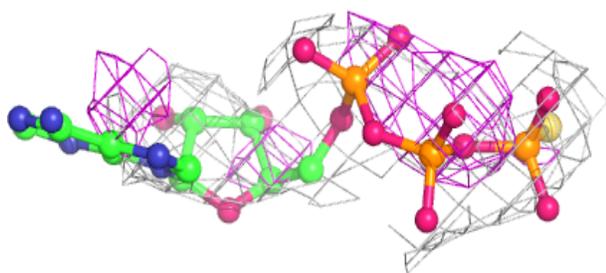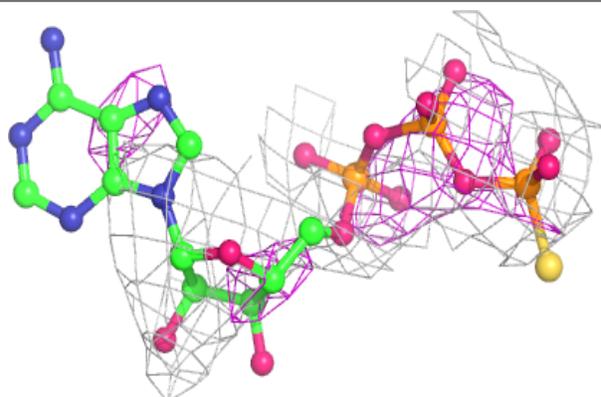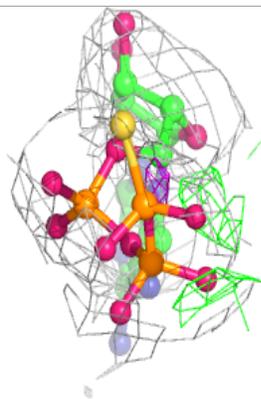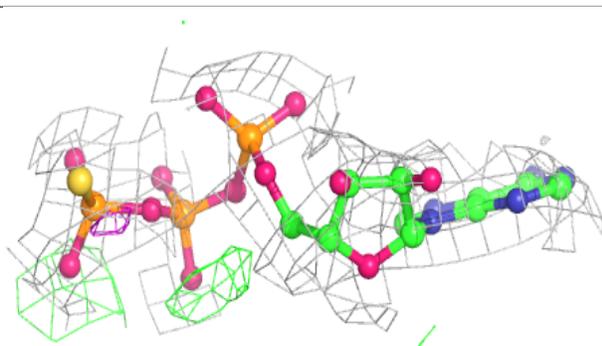mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
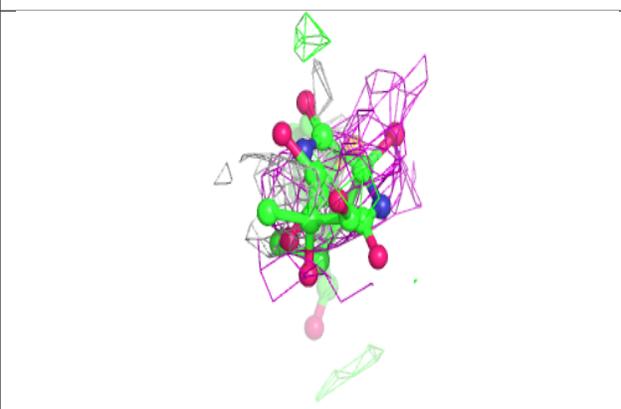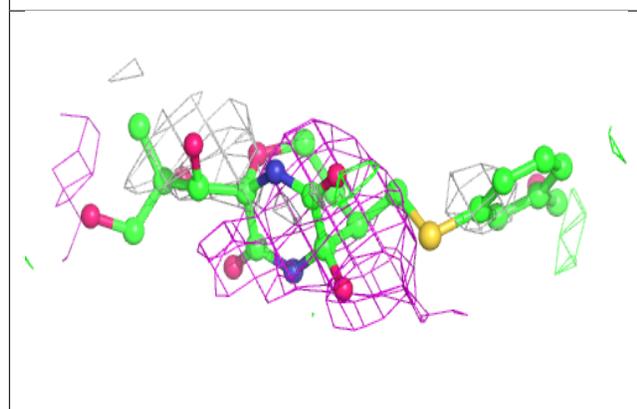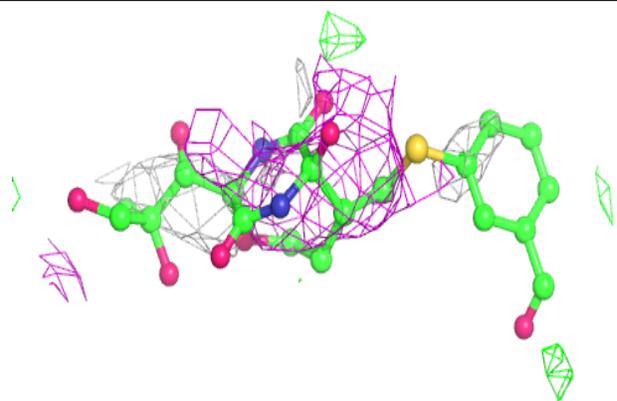
Electron density around FPD E 5701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
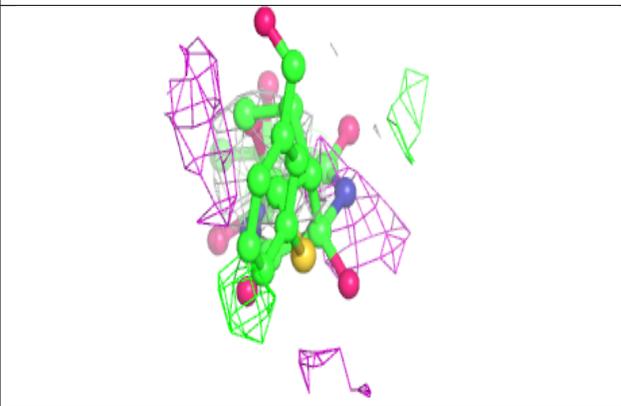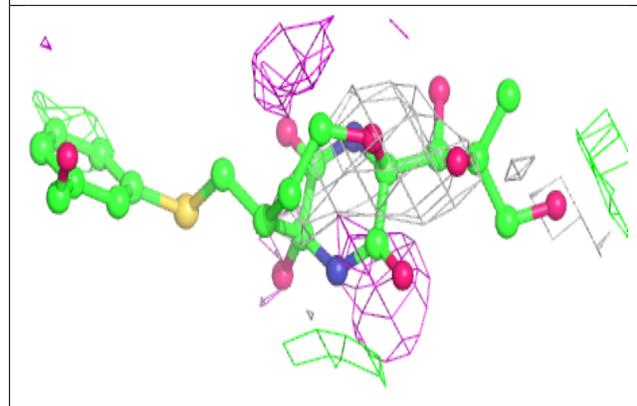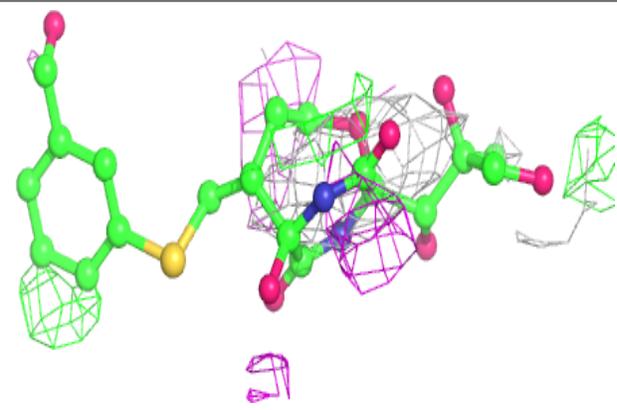
Electron density around FPD D 4701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
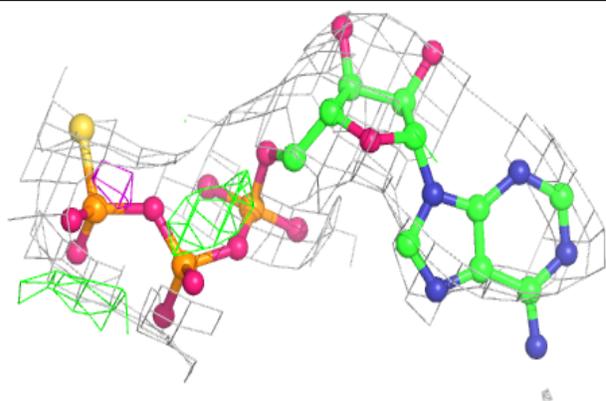and green (positive)
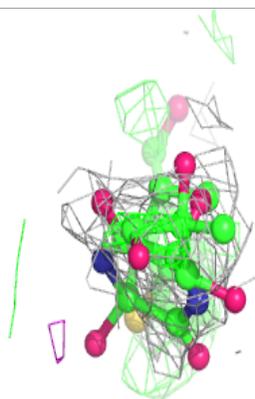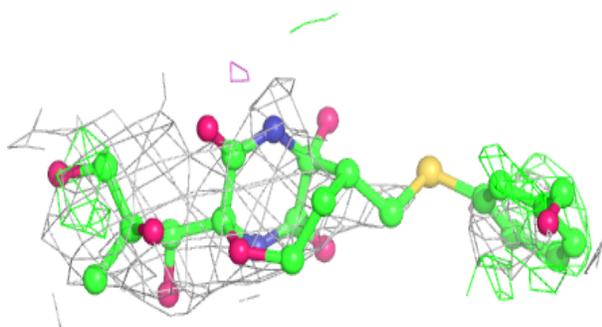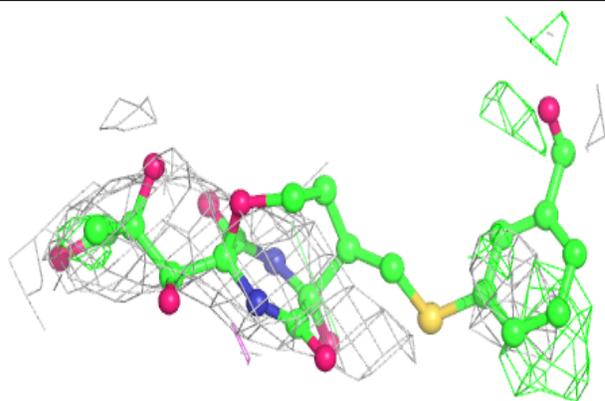
Electron density around FPD F 6701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
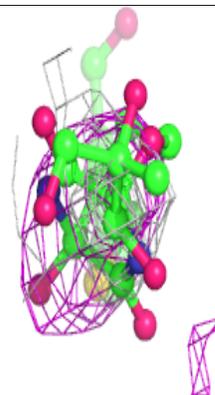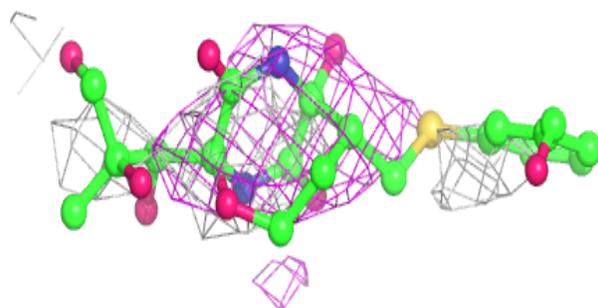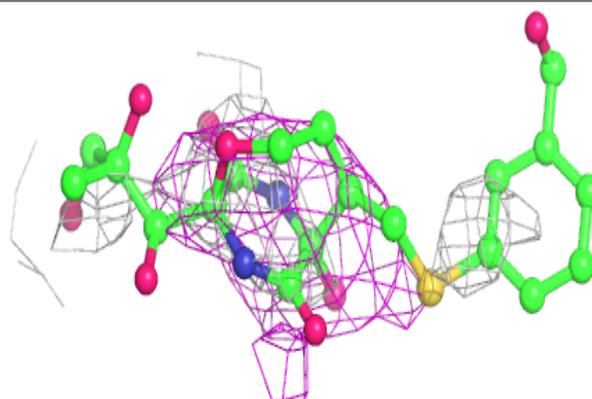
Electron density around FPD B 2701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
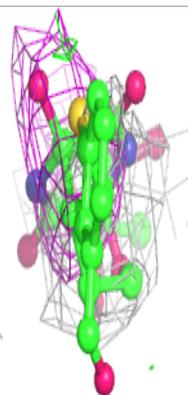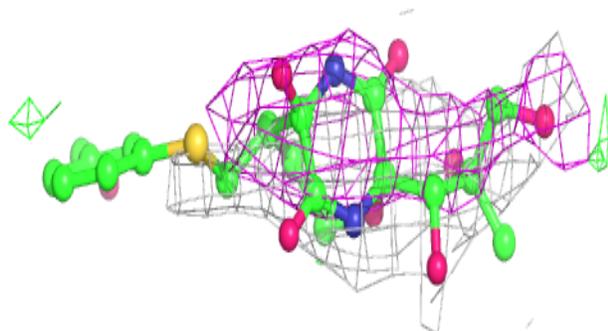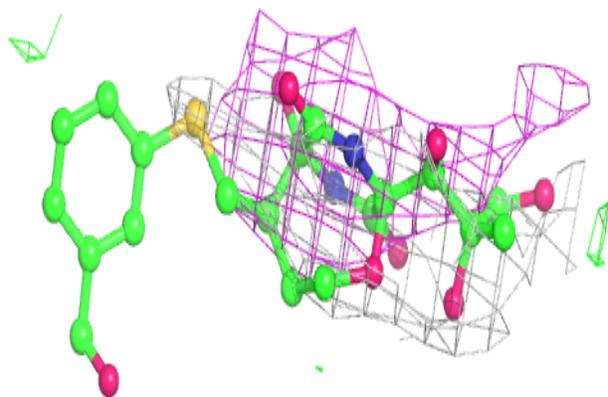
Electron density around AGS E 6600:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
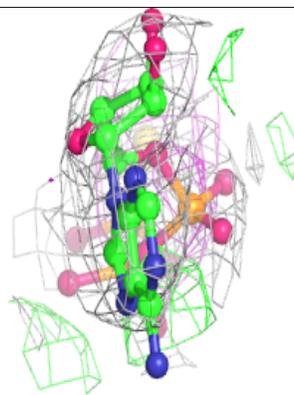
Electron density around AGS C 3600:

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

Electron density around AGS A 1600:

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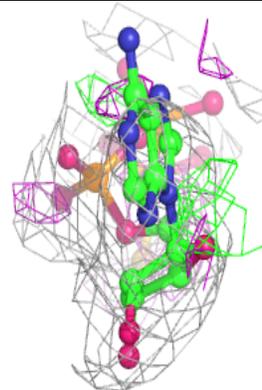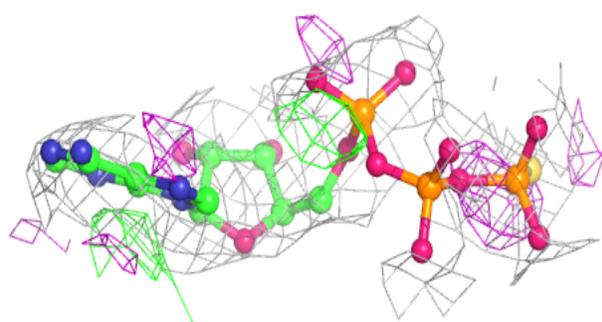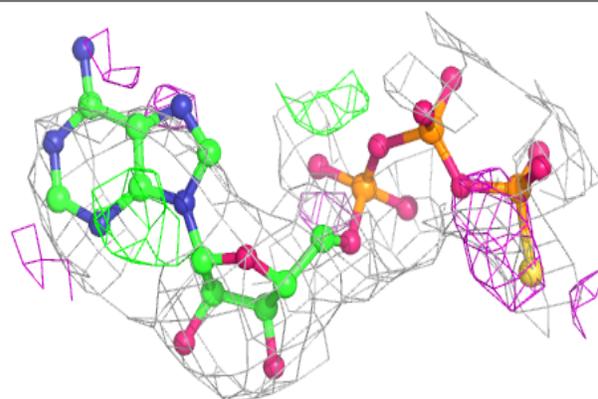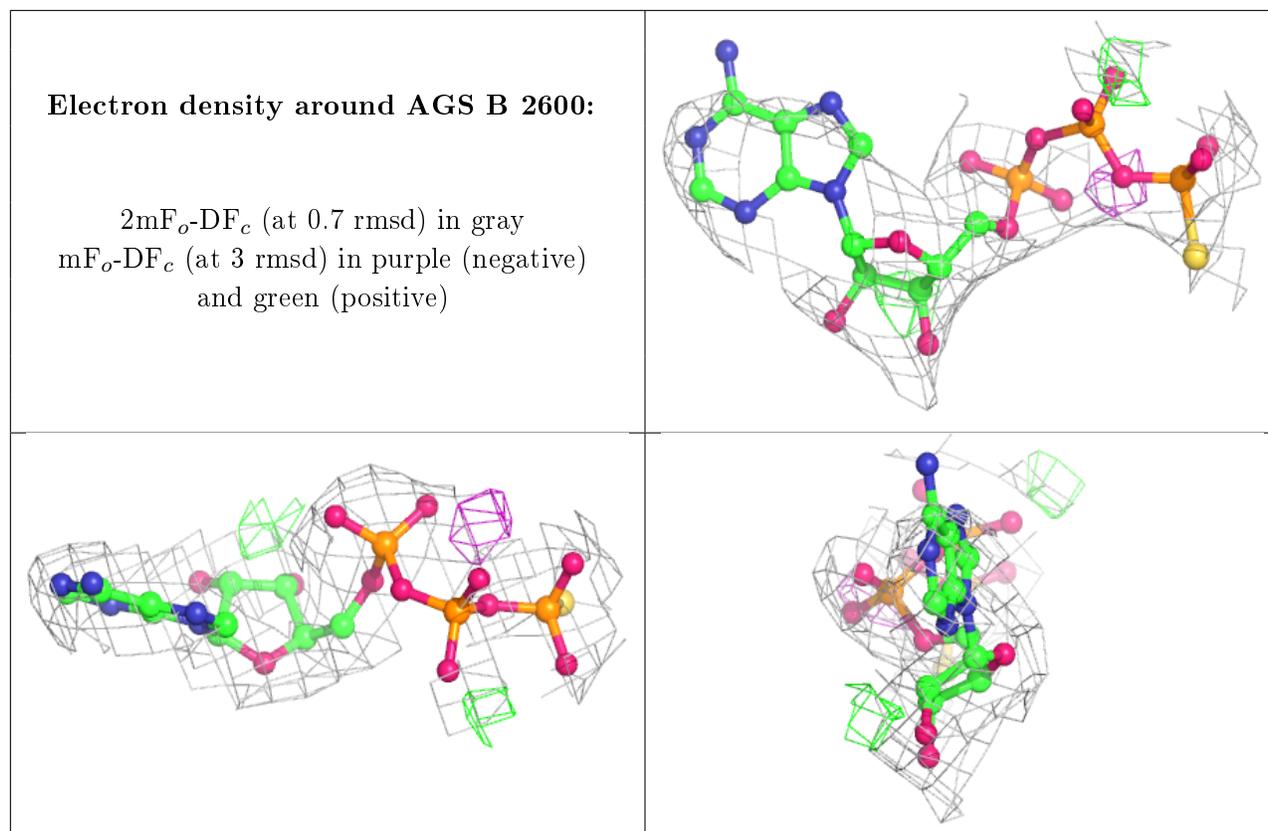$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around AGS E 5600:

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

Electron density around AGS D 4600:

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

Electron density around AGS B 2600:

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

6.5 Other polymers (i)

There are no such residues in this entry.