Full wwPDB X-ray Structure Validation Report (i)

Sep 20, 2023 – 07:52 AM EDT

PDB ID	:	5F5W
Title	:	Crystal structure of the alpha subunit of glycyl tRNA synthetase (GlyRS) from Aquifex aeolicus in complex with an analog of glycyl adenylate (Gly-SA)
Authors	:	Valencia-Sanchez, M.I.; Torres-Larios, A.
Deposited on	:	2015-12-04
Resolution	:	2.81 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 (i) symbol.

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

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

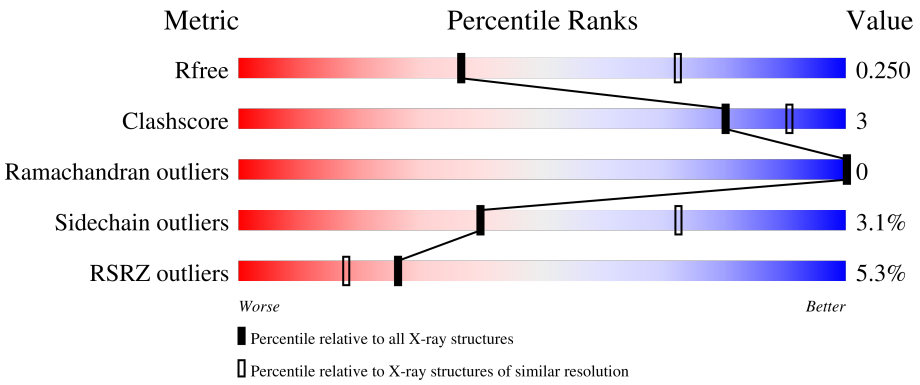
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.81 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	299	87% 7% 5%
1	B	299	87% 7% 6%
1	C	299	4% 88% 5% • 6%
1	D	299	8% 79% 11% • 7%
1	E	299	13% 85% 7% • 7%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 11877 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 Glycine–tRNA ligase alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	283	2368	1535	388	434	11	0	0	0
1	B	281	2357	1528	386	432	11	0	0	0
1	C	281	2357	1528	386	432	11	0	0	0
1	D	278	2329	1510	382	427	10	0	0	0
1	E	278	2329	1510	382	427	10	0	0	0

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP O67081
A	-12	HIS	-	expression tag	UNP O67081
A	-11	HIS	-	expression tag	UNP O67081
A	-10	HIS	-	expression tag	UNP O67081
A	-9	HIS	-	expression tag	UNP O67081
A	-8	HIS	-	expression tag	UNP O67081
A	-7	HIS	-	expression tag	UNP O67081
A	-6	GLU	-	expression tag	UNP O67081
A	-5	ASN	-	expression tag	UNP O67081
A	-4	LEU	-	expression tag	UNP O67081
A	-3	TYR	-	expression tag	UNP O67081
A	-2	PHE	-	expression tag	UNP O67081
A	-1	GLN	-	expression tag	UNP O67081
A	0	SER	-	expression tag	UNP O67081
B	-13	MET	-	initiating methionine	UNP O67081
B	-12	HIS	-	expression tag	UNP O67081
B	-11	HIS	-	expression tag	UNP O67081
B	-10	HIS	-	expression tag	UNP O67081
B	-9	HIS	-	expression tag	UNP O67081

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	HIS	-	expression tag	UNP O67081
B	-7	HIS	-	expression tag	UNP O67081
B	-6	GLU	-	expression tag	UNP O67081
B	-5	ASN	-	expression tag	UNP O67081
B	-4	LEU	-	expression tag	UNP O67081
B	-3	TYR	-	expression tag	UNP O67081
B	-2	PHE	-	expression tag	UNP O67081
B	-1	GLN	-	expression tag	UNP O67081
B	0	SER	-	expression tag	UNP O67081
C	-13	MET	-	initiating methionine	UNP O67081
C	-12	HIS	-	expression tag	UNP O67081
C	-11	HIS	-	expression tag	UNP O67081
C	-10	HIS	-	expression tag	UNP O67081
C	-9	HIS	-	expression tag	UNP O67081
C	-8	HIS	-	expression tag	UNP O67081
C	-7	HIS	-	expression tag	UNP O67081
C	-6	GLU	-	expression tag	UNP O67081
C	-5	ASN	-	expression tag	UNP O67081
C	-4	LEU	-	expression tag	UNP O67081
C	-3	TYR	-	expression tag	UNP O67081
C	-2	PHE	-	expression tag	UNP O67081
C	-1	GLN	-	expression tag	UNP O67081
C	0	SER	-	expression tag	UNP O67081
D	-13	MET	-	initiating methionine	UNP O67081
D	-12	HIS	-	expression tag	UNP O67081
D	-11	HIS	-	expression tag	UNP O67081
D	-10	HIS	-	expression tag	UNP O67081
D	-9	HIS	-	expression tag	UNP O67081
D	-8	HIS	-	expression tag	UNP O67081
D	-7	HIS	-	expression tag	UNP O67081
D	-6	GLU	-	expression tag	UNP O67081
D	-5	ASN	-	expression tag	UNP O67081
D	-4	LEU	-	expression tag	UNP O67081
D	-3	TYR	-	expression tag	UNP O67081
D	-2	PHE	-	expression tag	UNP O67081
D	-1	GLN	-	expression tag	UNP O67081
D	0	SER	-	expression tag	UNP O67081
E	-13	MET	-	initiating methionine	UNP O67081
E	-12	HIS	-	expression tag	UNP O67081
E	-11	HIS	-	expression tag	UNP O67081
E	-10	HIS	-	expression tag	UNP O67081
E	-9	HIS	-	expression tag	UNP O67081

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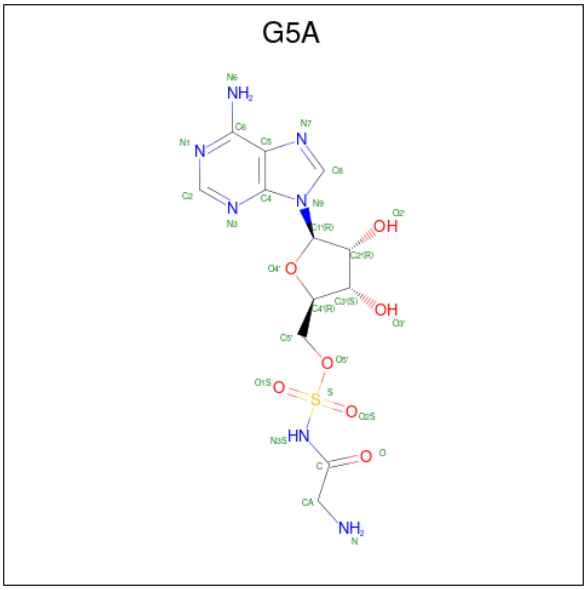
Chain	Residue	Modelled	Actual	Comment	Reference
E	-8	HIS	-	expression tag	UNP O67081
E	-7	HIS	-	expression tag	UNP O67081
E	-6	GLU	-	expression tag	UNP O67081
E	-5	ASN	-	expression tag	UNP O67081
E	-4	LEU	-	expression tag	UNP O67081
E	-3	TYR	-	expression tag	UNP O67081
E	-2	PHE	-	expression tag	UNP O67081
E	-1	GLN	-	expression tag	UNP O67081
E	0	SER	-	expression tag	UNP O67081

- Molecule 2 is 5'-O-(glycylsulfamoyl)adenosine (three-letter code: G5A) (formula: $C_{12}H_{17}N_7O_7S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	27	12	7	7	1	0	0
			Total	C	N	O	S		
2	B	1	27	12	7	7	1	0	0
			Total	C	N	O	S		
2	C	1	27	12	7	7	1	0	0
			Total	C	N	O	S		
2	D	1	27	12	7	7	1	0	0
			Total	C	N	O	S		
2	E	1	27	12	7	7	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	B	2	2	2	0	0

3 Residue-property plots (i)

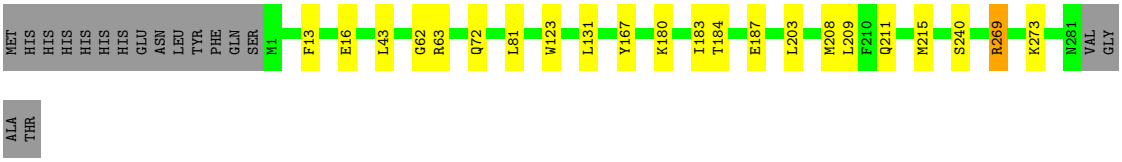
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Glycine–tRNA ligase alpha subunit

Chain A:

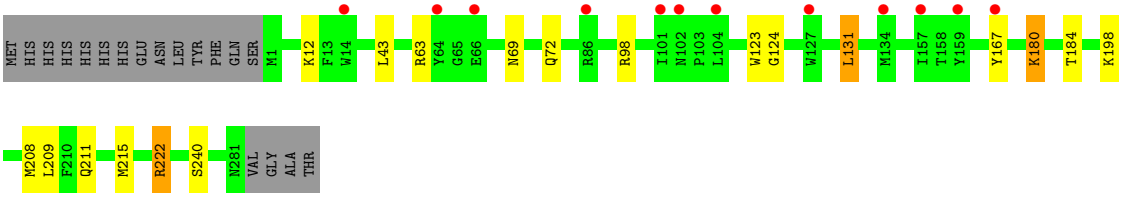
• Molecule 1: Glycine–tRNA ligase alpha subunit

Chain B:



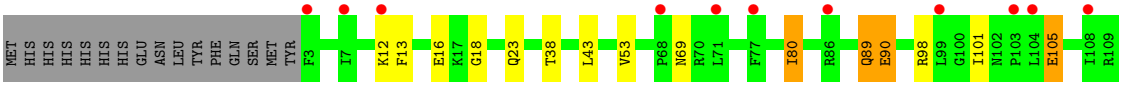
• Molecule 1: Glycine–tRNA ligase alpha subunit

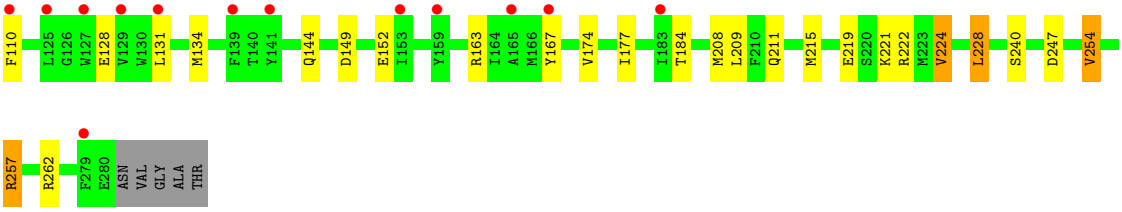
Chain C:



• Molecule 1: Glycine–tRNA ligase alpha subunit

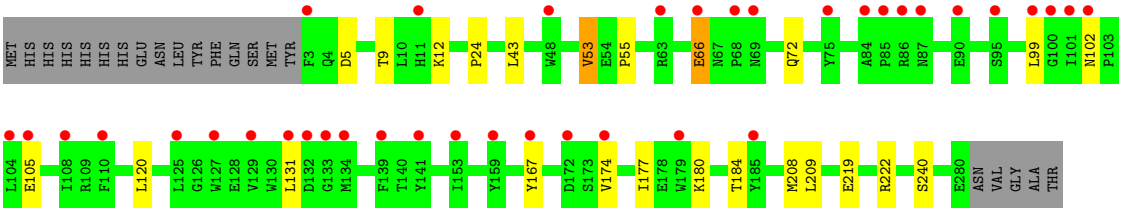
Chain D:





- Molecule 1: Glycine–tRNA ligase alpha subunit

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α, β, γ	101.83Å 130.01Å 145.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.17 – 2.81 83.43 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.9 (80.17-2.81) 95.0 (83.43-2.81)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.94 (at 2.82Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.239 , 0.252 0.240 , 0.250	Depositor DCC
R_{free} test set	2413 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	54.5	Xtriage
Anisotropy	0.551	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 28.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	11877	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

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

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: G5A

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.62	3/2435 (0.1%)	0.78	2/3299 (0.1%)
1	B	0.55	0/2424	0.74	1/3284 (0.0%)
1	C	0.58	0/2424	0.81	7/3284 (0.2%)
1	D	0.59	0/2395	0.80	5/3245 (0.2%)
1	E	0.57	0/2395	0.75	2/3245 (0.1%)
All	All	0.58	3/12073 (0.0%)	0.78	17/16357 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	256	GLU	CG-CD	6.22	1.61	1.51
1	A	256	GLU	CD-OE1	5.17	1.31	1.25
1	A	66	GLU	CD-OE1	5.07	1.31	1.25

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	222	ARG	NE-CZ-NH1	10.19	125.40	120.30
1	C	222	ARG	NE-CZ-NH2	-9.53	115.53	120.30
1	A	69	ASN	CB-CA-C	-8.34	93.72	110.40
1	A	257	ARG	NE-CZ-NH2	-7.85	116.37	120.30
1	D	228	LEU	CB-CG-CD2	7.36	123.50	111.00
1	C	222	ARG	CD-NE-CZ	6.89	133.25	123.60
1	C	131	LEU	CB-CG-CD2	-6.24	100.40	111.00
1	E	66	GLU	CA-CB-CG	5.91	126.40	113.40
1	B	269	ARG	NE-CZ-NH2	-5.63	117.48	120.30
1	D	90	GLU	CB-CA-C	5.63	121.67	110.40
1	D	254	VAL	CA-CB-CG1	5.63	119.34	110.90
1	C	180	LYS	N-CA-CB	-5.55	100.61	110.60
1	C	180	LYS	CA-CB-CG	5.50	125.51	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	63	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	D	105	GLU	OE1-CD-OE2	-5.22	117.03	123.30
1	D	257	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	E	120	LEU	CB-CG-CD1	-5.03	102.44	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2368	0	2283	8	1
1	B	2357	0	2271	14	0
1	C	2357	0	2271	8	1
1	D	2329	0	2244	26	0
1	E	2329	0	2244	16	0
2	A	27	0	17	0	0
2	B	27	0	17	0	0
2	C	27	0	17	0	0
2	D	27	0	17	0	0
2	E	27	0	17	0	0
3	B	2	0	0	0	0
All	All	11877	0	11398	62	1

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 3.

All (62) 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:B:203:LEU:O	1:C:222:ARG:NH2	2.35	0.59
1:B:208:MET:HE2	1:B:209:LEU:HD23	1.85	0.59
1:B:183:ILE:HD12	1:B:187:GLU:OE1	2.04	0.58
1:D:16:GLU:OE1	1:D:98:ARG:NH2	2.36	0.58
1:A:208:MET:HE2	1:A:209:LEU:HD23	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:38:THR:HG23	1:D:80:ILE:HD12	1.88	0.55
1:C:208:MET:HE2	1:C:209:LEU:HD23	1.90	0.54
1:A:247:ASP:OD1	1:A:257:ARG:NH2	2.41	0.53
1:D:69:ASN:O	1:D:163:ARG:NH2	2.41	0.53
1:E:9:THR:HG23	1:E:99:LEU:HD23	1.91	0.52
1:E:208:MET:HE2	1:E:209:LEU:HD23	1.92	0.52
1:D:208:MET:HE2	1:D:209:LEU:HD23	1.92	0.52
1:D:247:ASP:OD1	1:D:257:ARG:NH2	2.39	0.51
1:D:134:MET:SD	1:D:163:ARG:NH1	2.84	0.50
1:B:269:ARG:CZ	1:D:144:GLN:HE22	2.24	0.50
1:B:273:LYS:NZ	1:D:149:ASP:OD2	2.41	0.50
1:D:38:THR:HG23	1:D:80:ILE:CD1	2.42	0.49
1:E:174:VAL:HG23	1:E:177:ILE:CD1	2.42	0.49
1:D:23:GLN:NE2	1:E:53:VAL:CG1	2.75	0.49
1:B:131:LEU:HD21	1:B:167:TYR:CD2	2.48	0.49
1:D:131:LEU:HD21	1:D:167:TYR:CD2	2.48	0.49
1:E:131:LEU:HD21	1:E:167:TYR:CD2	2.48	0.49
1:B:211:GLN:O	1:B:215:MET:HG3	2.12	0.49
1:A:131:LEU:HD21	1:A:167:TYR:CD2	2.48	0.48
1:D:174:VAL:HG23	1:D:177:ILE:CD1	2.43	0.48
1:C:211:GLN:O	1:C:215:MET:HG3	2.13	0.48
1:C:131:LEU:HD21	1:C:167:TYR:CE2	2.49	0.48
1:D:18:GLY:O	1:E:180:LYS:NZ	2.47	0.48
1:C:208:MET:CE	1:C:209:LEU:HD23	2.43	0.48
1:D:208:MET:CE	1:D:209:LEU:HD23	2.44	0.48
1:A:45:LYS:HB3	1:B:63:ARG:CZ	2.44	0.47
1:A:211:GLN:O	1:A:215:MET:HG3	2.14	0.47
1:C:123:TRP:CG	1:C:124:GLY:N	2.82	0.47
1:D:211:GLN:O	1:D:215:MET:HG3	2.14	0.47
1:E:208:MET:CE	1:E:209:LEU:HD23	2.44	0.47
1:A:208:MET:CE	1:A:209:LEU:HD23	2.45	0.47
1:E:102:ASN:O	1:E:105:GLU:OE1	2.33	0.46
1:C:131:LEU:HD21	1:C:167:TYR:CD2	2.51	0.46
1:B:208:MET:CE	1:B:209:LEU:HD23	2.44	0.45
1:E:9:THR:HG23	1:E:99:LEU:CD2	2.47	0.45
1:D:23:GLN:NE2	1:E:53:VAL:HG13	2.33	0.43
1:D:69:ASN:HB2	1:D:163:ARG:CZ	2.48	0.43
1:D:23:GLN:NE2	1:E:53:VAL:HG11	2.34	0.43
1:E:174:VAL:HG23	1:E:177:ILE:HD12	2.01	0.43
1:D:89:GLN:HB2	1:D:110:PHE:CE2	2.54	0.43
1:E:219:GLU:OE1	1:E:222:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:221:LYS:O	1:D:224:VAL:HG12	2.19	0.42
1:B:208:MET:HE2	1:B:209:LEU:CD2	2.49	0.42
1:D:219:GLU:OE1	1:D:222:ARG:NH1	2.53	0.42
1:B:62:GLY:CA	1:B:72:GLN:HB3	2.51	0.41
1:D:23:GLN:HE22	1:E:53:VAL:CG1	2.34	0.41
1:E:24:PRO:HB3	1:E:55:PRO:HD2	2.03	0.41
1:D:13:PHE:O	1:D:16:GLU:HB3	2.21	0.41
1:C:98:ARG:O	1:C:98:ARG:HG3	2.21	0.41
1:E:5:ASP:O	1:E:9:THR:HG22	2.21	0.41
1:A:219:GLU:OE1	1:A:222:ARG:NH1	2.53	0.41
1:B:123:TRP:CE2	1:D:262:ARG:HD2	2.56	0.40
1:B:131:LEU:HD21	1:B:167:TYR:CE2	2.56	0.40
1:B:13:PHE:O	1:B:16:GLU:HB3	2.21	0.40
1:D:174:VAL:HG23	1:D:177:ILE:HD12	2.02	0.40
1:A:62:GLY:CA	1:A:72:GLN:HB3	2.51	0.40
1:D:228:LEU:N	1:D:228:LEU:HD12	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:GLN:O	1:C:198:LYS:NZ[4_454]	2.00	0.20

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	281/299 (94%)	274 (98%)	7 (2%)	0	100	100
1	B	279/299 (93%)	272 (98%)	7 (2%)	0	100	100
1	C	279/299 (93%)	271 (97%)	8 (3%)	0	100	100
1	D	276/299 (92%)	268 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	276/299 (92%)	270 (98%)	6 (2%)	0	100	100
All	All	1391/1495 (93%)	1355 (97%)	36 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	249/264 (94%)	244 (98%)	5 (2%)	55	83
1	B	248/264 (94%)	243 (98%)	5 (2%)	55	83
1	C	248/264 (94%)	241 (97%)	7 (3%)	43	76
1	D	245/264 (93%)	231 (94%)	14 (6%)	20	49
1	E	245/264 (93%)	238 (97%)	7 (3%)	42	74
All	All	1235/1320 (94%)	1197 (97%)	38 (3%)	40	72

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LEU
1	A	134	MET
1	A	184	THR
1	A	240	SER
1	A	259	ARG
1	B	43	LEU
1	B	81	LEU
1	B	180	LYS
1	B	184	THR
1	B	240	SER
1	C	12	LYS
1	C	43	LEU
1	C	69	ASN
1	C	72	GLN

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Mol	Chain	Res	Type
1	C	180	LYS
1	C	184	THR
1	C	240	SER
1	D	12	LYS
1	D	43	LEU
1	D	53	VAL
1	D	80	ILE
1	D	89	GLN
1	D	90	GLU
1	D	101	ILE
1	D	105	GLU
1	D	128	GLU
1	D	152	GLU
1	D	184	THR
1	D	224	VAL
1	D	240	SER
1	D	254	VAL
1	E	12	LYS
1	E	43	LEU
1	E	53	VAL
1	E	66	GLU
1	E	72	GLN
1	E	184	THR
1	E	240	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	281	ASN
1	C	69	ASN
1	C	106	HIS
1	C	200	ASN
1	D	23	GLN
1	D	144	GLN
1	E	106	HIS
1	E	200	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	G5A	B	300	-	25,29,29	1.02	1 (4%)	26,43,43	1.93	3 (11%)
2	G5A	A	300	-	25,29,29	1.02	1 (4%)	26,43,43	1.93	3 (11%)
2	G5A	C	300	-	25,29,29	1.03	1 (4%)	26,43,43	1.93	3 (11%)
2	G5A	D	300	-	25,29,29	1.03	1 (4%)	26,43,43	1.93	3 (11%)
2	G5A	E	300	-	25,29,29	1.01	1 (4%)	26,43,43	1.93	3 (11%)

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
2	G5A	B	300	-	-	0/12/33/33	0/3/3/3
2	G5A	A	300	-	-	0/12/33/33	0/3/3/3
2	G5A	C	300	-	-	0/12/33/33	0/3/3/3
2	G5A	D	300	-	-	0/12/33/33	0/3/3/3
2	G5A	E	300	-	-	0/12/33/33	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	300	G5A	C-N3S	-2.88	1.33	1.38
2	C	300	G5A	C-N3S	-2.86	1.33	1.38
2	A	300	G5A	C-N3S	-2.83	1.33	1.38
2	E	300	G5A	C-N3S	-2.81	1.33	1.38
2	B	300	G5A	C-N3S	-2.80	1.33	1.38

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	300	G5A	O2S-S-O1S	-6.89	110.02	120.76
2	B	300	G5A	O2S-S-O1S	-6.89	110.03	120.76
2	C	300	G5A	O2S-S-O1S	-6.88	110.05	120.76
2	A	300	G5A	O2S-S-O1S	-6.87	110.06	120.76
2	E	300	G5A	O2S-S-O1S	-6.86	110.07	120.76
2	E	300	G5A	N3-C2-N1	-4.82	121.14	128.68
2	A	300	G5A	N3-C2-N1	-4.80	121.17	128.68
2	B	300	G5A	N3-C2-N1	-4.80	121.18	128.68
2	D	300	G5A	N3-C2-N1	-4.79	121.19	128.68
2	C	300	G5A	N3-C2-N1	-4.77	121.23	128.68
2	C	300	G5A	C4-C5-N7	-2.37	106.93	109.40
2	E	300	G5A	C4-C5-N7	-2.35	106.95	109.40
2	A	300	G5A	C4-C5-N7	-2.34	106.96	109.40
2	B	300	G5A	C4-C5-N7	-2.33	106.97	109.40
2	D	300	G5A	C4-C5-N7	-2.31	106.99	109.40

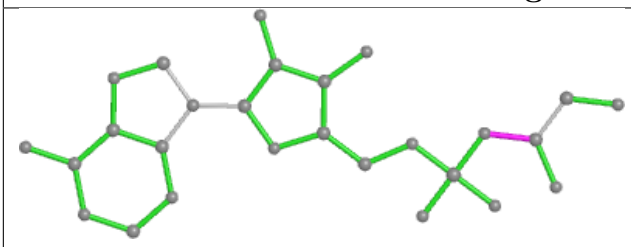
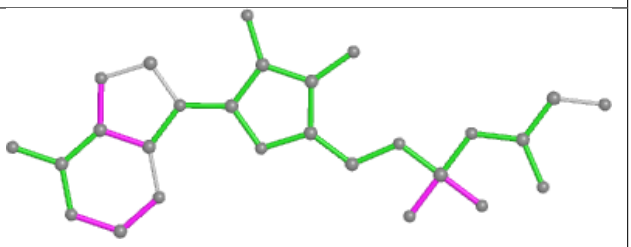
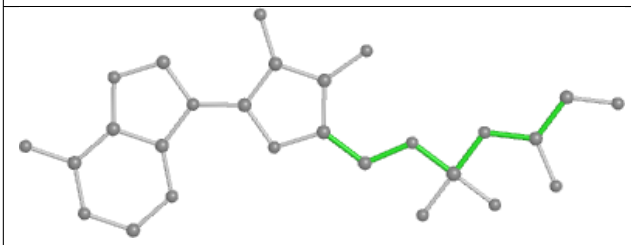
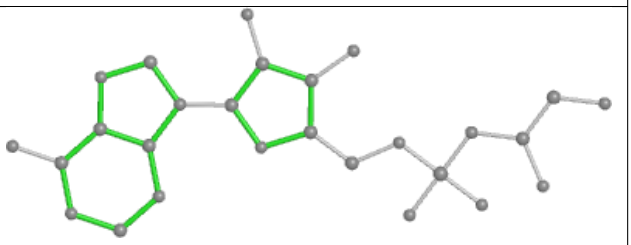
There are no chirality outliers.

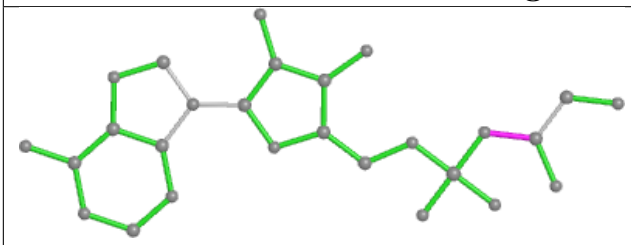
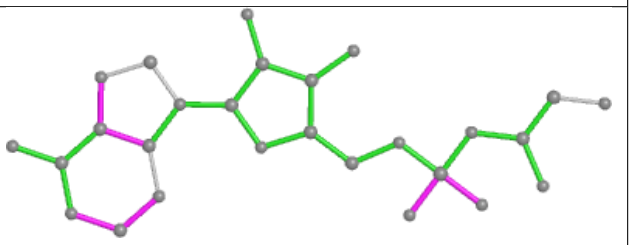
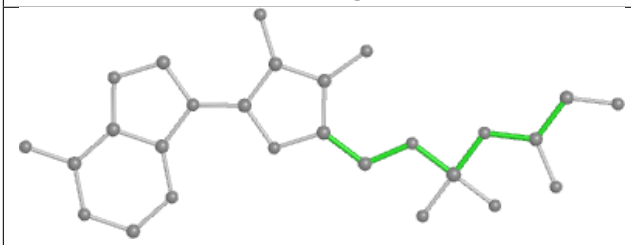
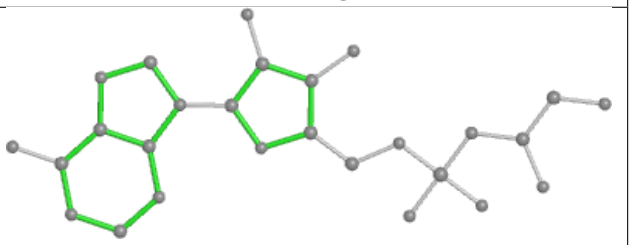
There are no torsion outliers.

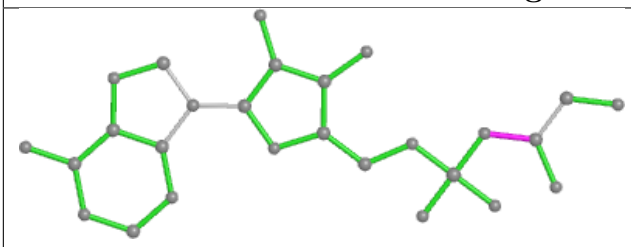
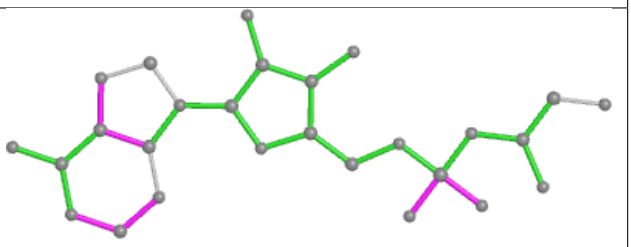
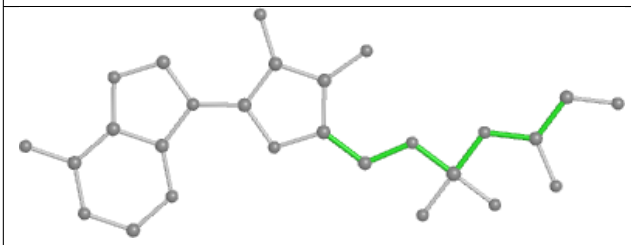
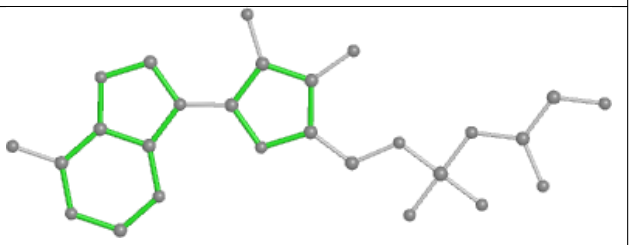
There are no ring outliers.

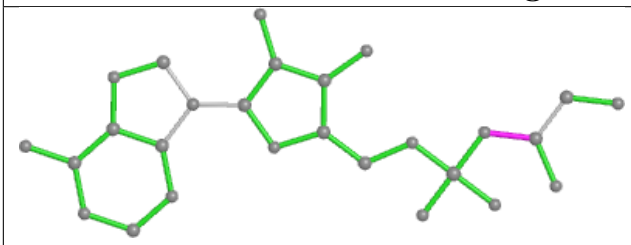
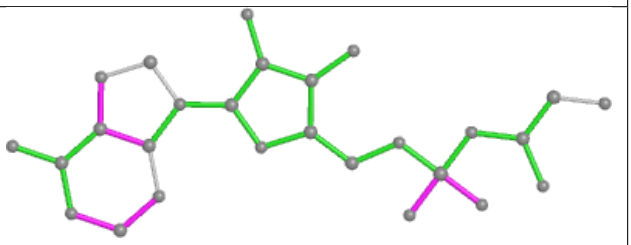
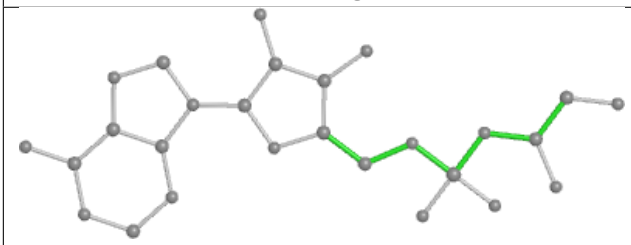
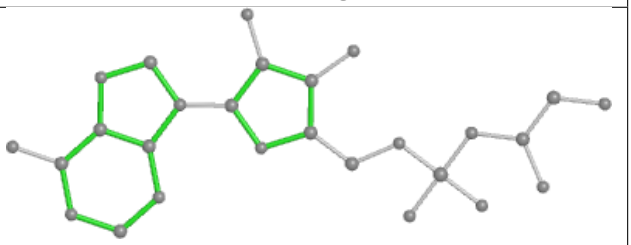
No monomer is involved in short contacts.

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

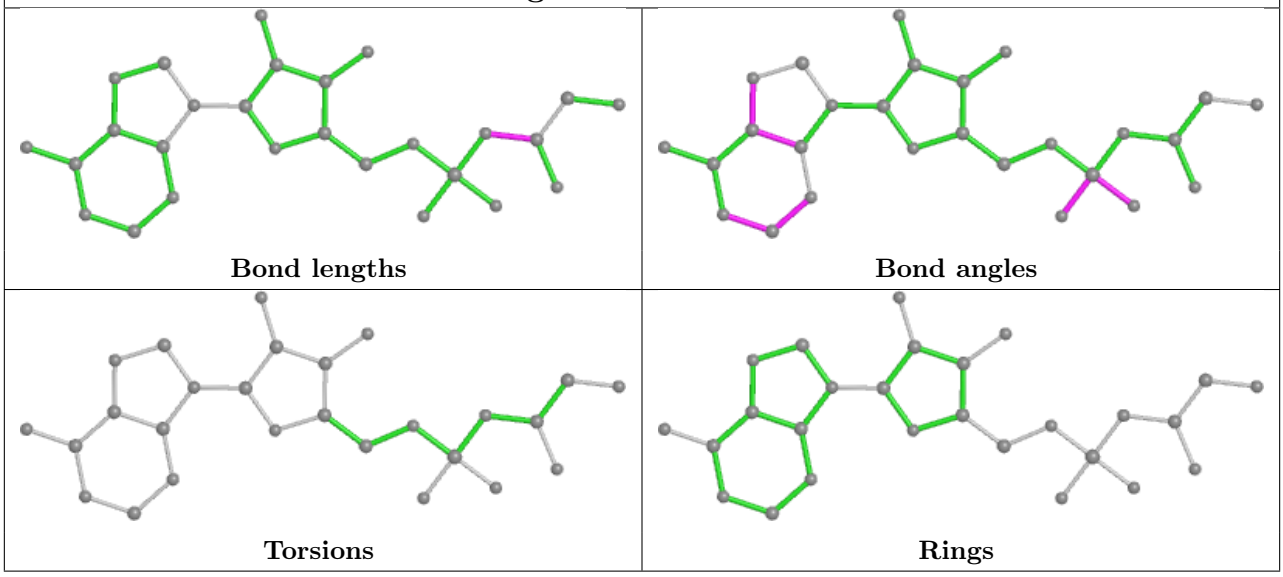
Ligand G5A B 300	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand G5A A 300	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand G5A C 300	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand G5A D 300	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand G5A E 300



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	A	283/299 (94%)	0.29	0 100 100	34, 44, 57, 67	0
1	B	281/299 (93%)	0.29	0 100 100	41, 53, 64, 72	0
1	C	281/299 (93%)	0.49	12 (4%) 35 25	41, 57, 70, 80	0
1	D	278/299 (92%)	0.70	24 (8%) 10 5	47, 71, 87, 95	0
1	E	278/299 (92%)	0.95	38 (13%) 3 1	51, 73, 92, 99	0
All	All	1401/1495 (93%)	0.54	74 (5%) 26 18	34, 57, 85, 99	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	85	PRO	5.7
1	E	131	LEU	5.1
1	E	104	LEU	4.9
1	E	99	LEU	4.6
1	D	3	PHE	4.1
1	E	86	ARG	4.0
1	D	104	LEU	3.9
1	C	66	GLU	3.6
1	C	104	LEU	3.5
1	D	167	TYR	3.5
1	E	3	PHE	3.5
1	D	108	ILE	3.4
1	E	69	ASN	3.4
1	E	101	ILE	3.4
1	E	133	GLY	3.4
1	E	167	TYR	3.4
1	E	102	ASN	3.2
1	E	105	GLU	3.2
1	E	134	MET	3.1
1	E	125	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	86	ARG	3.0
1	D	183	ILE	3.0
1	E	84	ALA	3.0
1	E	139	PHE	2.9
1	E	132	ASP	2.8
1	E	159	TYR	2.8
1	D	86	ARG	2.7
1	D	165	ALA	2.7
1	E	174	VAL	2.7
1	E	87	ASN	2.6
1	C	134	MET	2.6
1	D	99	LEU	2.6
1	C	102	ASN	2.6
1	E	68	PRO	2.6
1	D	129	VAL	2.5
1	E	110	PHE	2.5
1	D	127	TRP	2.4
1	D	12	LYS	2.4
1	E	100	GLY	2.4
1	E	11	HIS	2.4
1	D	125	LEU	2.4
1	E	95	SER	2.4
1	E	129	VAL	2.4
1	D	103	PRO	2.4
1	D	279	PHE	2.4
1	E	153	ILE	2.4
1	C	14	TRP	2.4
1	D	159	TYR	2.4
1	E	90	GLU	2.3
1	E	66	GLU	2.3
1	E	48	TRP	2.3
1	C	101	ILE	2.3
1	C	167	TYR	2.3
1	E	172	ASP	2.2
1	C	64	TYR	2.2
1	D	7	ILE	2.2
1	E	75	TYR	2.2
1	D	141	TYR	2.2
1	E	141	TYR	2.2
1	C	127	TRP	2.1
1	D	131	LEU	2.1
1	D	71	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	127	TRP	2.1
1	E	179	TRP	2.1
1	E	185	TYR	2.1
1	E	63	ARG	2.1
1	D	110	PHE	2.1
1	D	68	PRO	2.0
1	C	157	ILE	2.0
1	D	153	ILE	2.0
1	C	159	TYR	2.0
1	E	108	ILE	2.0
1	D	77	PHE	2.0
1	D	139	PHE	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

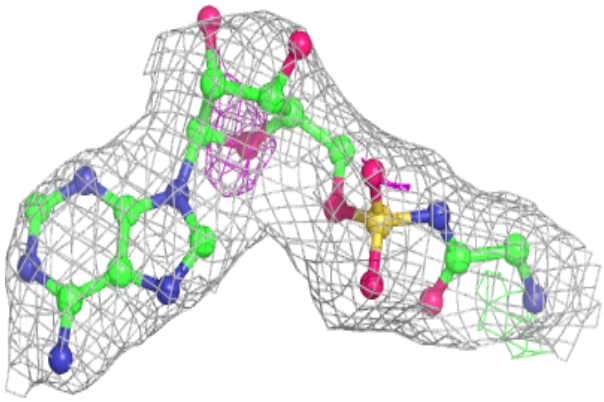
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

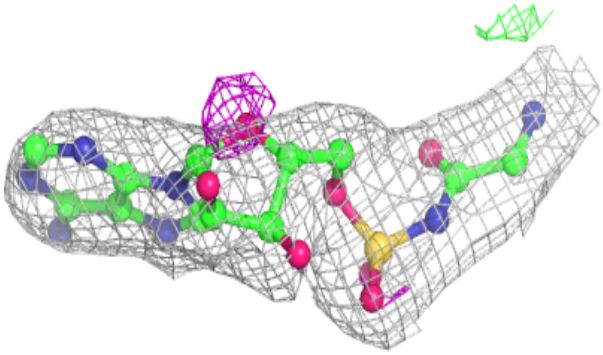
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	G5A	D	300	27/27	0.89	0.26	68,68,68,68	0
2	G5A	E	300	27/27	0.90	0.23	74,74,74,74	0
2	G5A	B	300	27/27	0.92	0.23	47,47,47,47	0
2	G5A	C	300	27/27	0.94	0.23	52,52,52,52	0
2	G5A	A	300	27/27	0.95	0.22	40,40,40,40	0

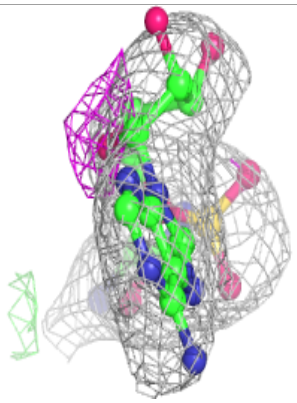
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around G5A D 300:

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

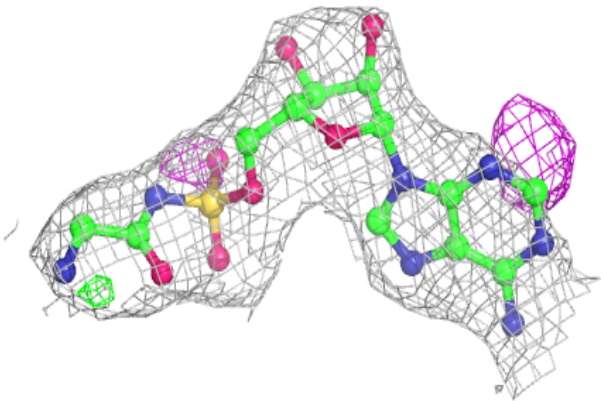


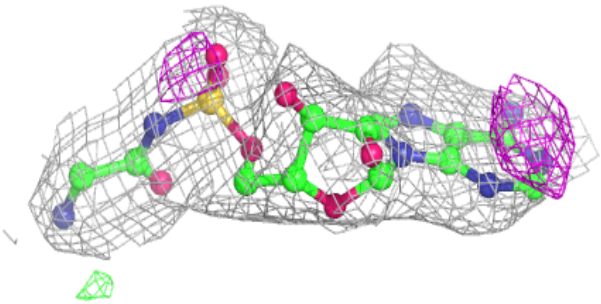


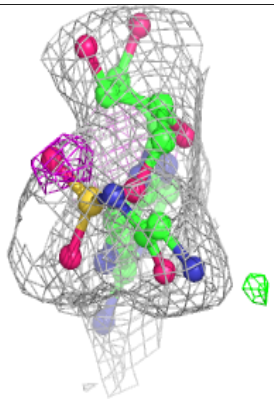


Electron density around G5A E 300:

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

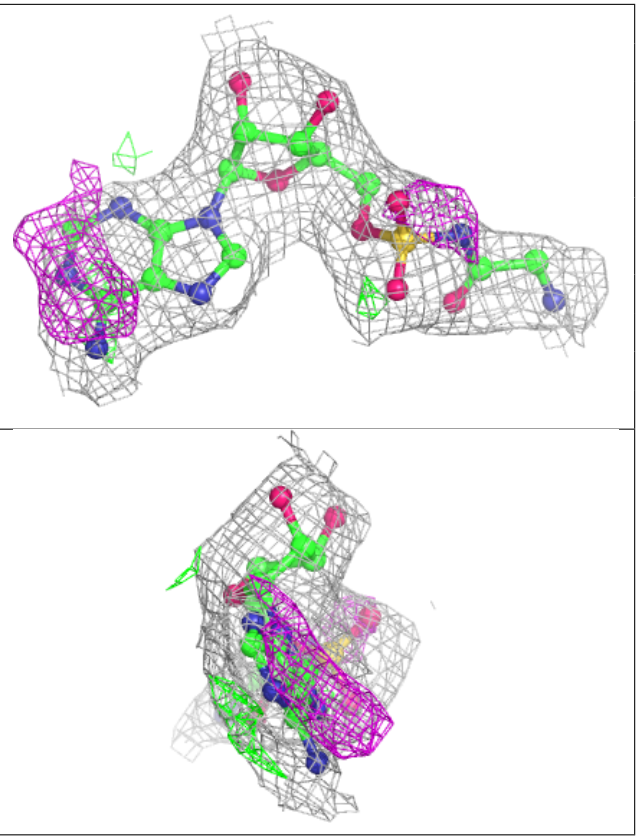


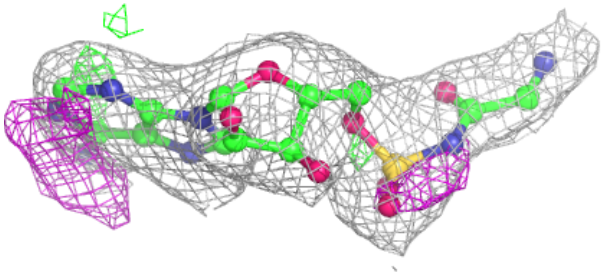




Electron density around G5A B 300:

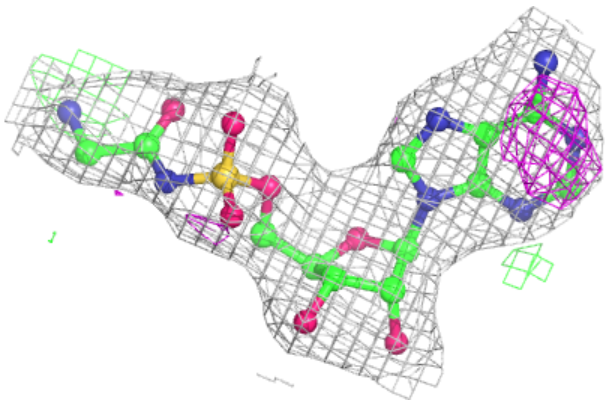
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

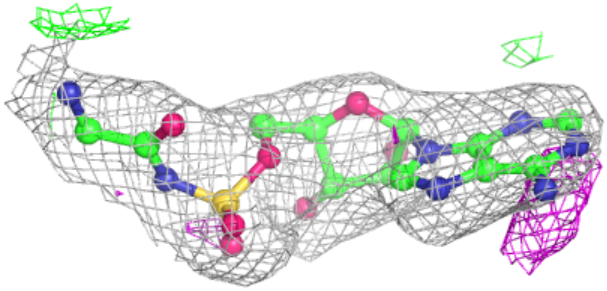


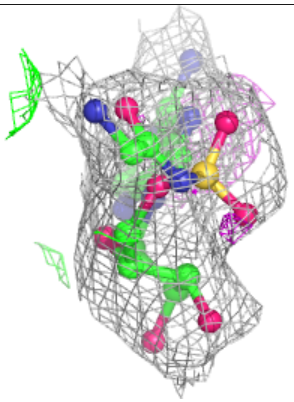


Electron density around G5A C 300:

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

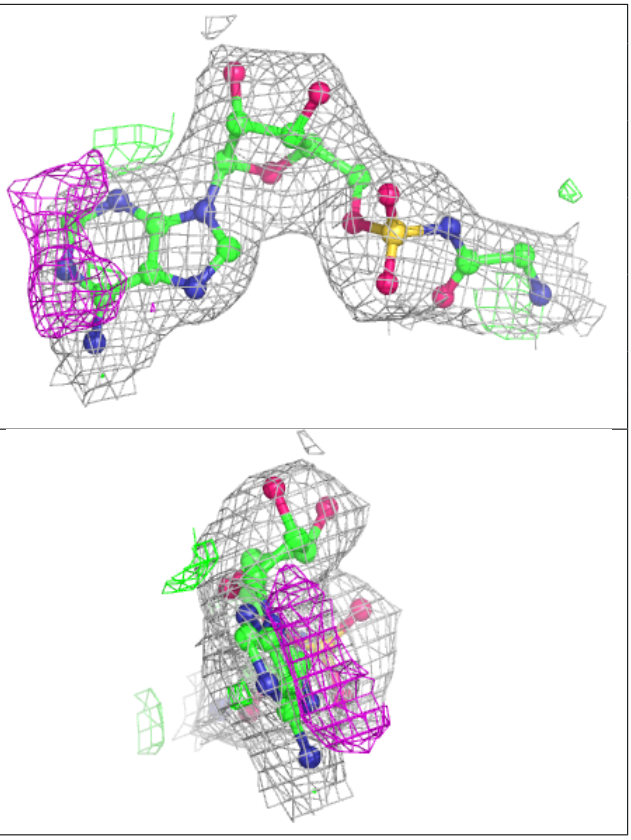






Electron density around G5A A 300:

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



6.5 Other polymers (i)

There are no such residues in this entry.