



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 25, 2025 – 10:10 AM JST

PDB ID : 9L6F / pdb_00009L6f
Title : Crystal structure of KRas G12D (GDP) in complex with ASP3082
Authors : Amano, Y.; Tateishi, Y.
Deposited on : 2024-12-24
Resolution : 3.18 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

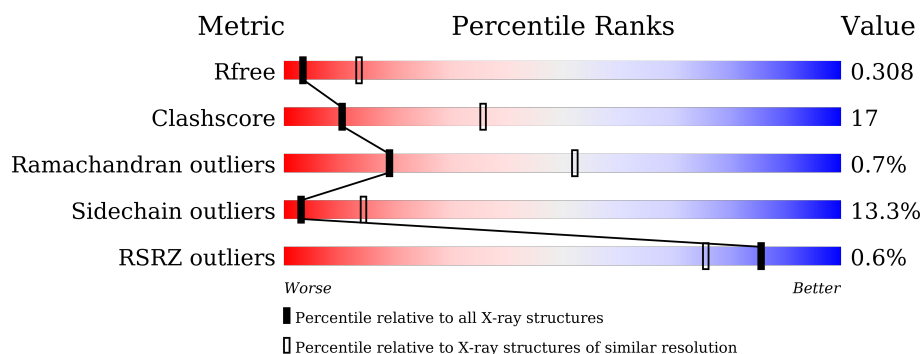
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.18 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}	164625	1851 (3.20-3.16)
Clashscore	180529	1999 (3.20-3.16)
Ramachandran outliers	177936	1961 (3.20-3.16)
Sidechain outliers	177891	1960 (3.20-3.16)
RSRZ outliers	164620	1852 (3.20-3.16)

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	163	<div> <div></div> <div>42%</div> <div>44%</div> <div>6%</div> <div>9%</div> </div>
1	E	163	<div> <div></div> <div>45%</div> <div>39%</div> <div>7%</div> <div>9%</div> </div>
1	I	163	<div> <div></div> <div>52%</div> <div>30%</div> <div>9%</div> <div>9%</div> </div>
1	M	163	<div> <div></div> <div>52%</div> <div>32%</div> <div>8%</div> <div>9%</div> </div>
2	B	96	<div> <div></div> <div>58%</div> <div>28%</div> <div>5%</div> <div>8%</div> </div>
2	F	96	<div> <div></div> <div>49%</div> <div>33%</div> <div>7%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
2	J	96	
2	N	96	
3	C	118	
3	G	118	
3	K	118	
3	O	118	
4	D	170	
4	H	170	
4	L	170	
4	P	170	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16509 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 von Hippel-Lindau disease tumor suppressor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	149	Total	C	N	O	S	0	0	0
			1207	766	227	212	2			
1	E	149	Total	C	N	O	S	0	0	0
			1203	764	226	211	2			
1	I	149	Total	C	N	O	S	0	0	0
			1203	764	226	211	2			
1	M	149	Total	C	N	O	S	0	0	0
			1203	764	226	211	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	GLY	-	expression tag	UNP P40337
A	52	SER	-	expression tag	UNP P40337
A	53	HIS	-	expression tag	UNP P40337
E	51	GLY	-	expression tag	UNP P40337
E	52	SER	-	expression tag	UNP P40337
E	53	HIS	-	expression tag	UNP P40337
I	51	GLY	-	expression tag	UNP P40337
I	52	SER	-	expression tag	UNP P40337
I	53	HIS	-	expression tag	UNP P40337
M	51	GLY	-	expression tag	UNP P40337
M	52	SER	-	expression tag	UNP P40337
M	53	HIS	-	expression tag	UNP P40337

- Molecule 2 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	88	Total	C	N	O	S	0	0	0
			689	445	109	130	5			
2	F	86	Total	C	N	O	S	0	0	0
			678	438	107	128	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	88	Total	C	N	O	S	0	0	0
			689	445	109	130	5			
2	N	86	Total	C	N	O	S	0	0	0
			678	438	107	128	5			

- Molecule 3 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	99	Total	C	N	O	S	0	0	0
			779	493	129	152	5			
3	G	105	Total	C	N	O	S	0	0	0
			826	524	139	158	5			
3	K	101	Total	C	N	O	S	0	0	0
			792	504	129	154	5			
3	O	105	Total	C	N	O	S	0	0	0
			826	524	139	158	5			

- Molecule 4 is a protein called Isoform 2B of GTPase KRas.

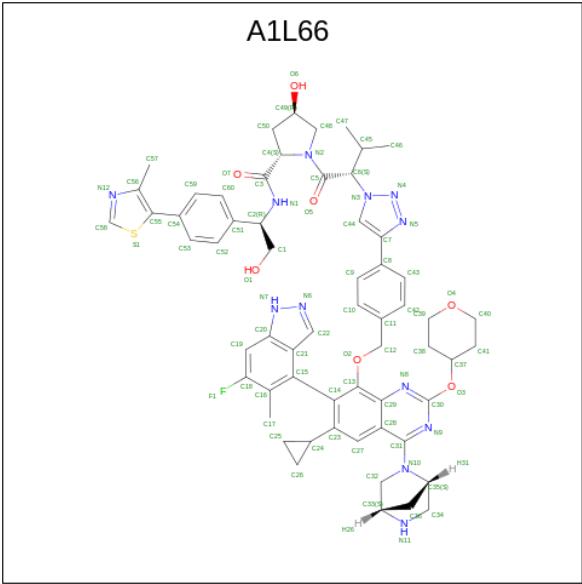
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	166	Total	C	N	O	S	0	0	0
			1328	831	228	263	6			
4	H	164	Total	C	N	O	S	0	0	0
			1312	819	226	261	6			
4	L	166	Total	C	N	O	S	0	0	0
			1328	831	228	263	6			
4	P	166	Total	C	N	O	S	0	0	0
			1328	831	228	263	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	GLY	-	expression tag	UNP P01116
D	12	ASP	GLY	engineered mutation	UNP P01116
H	0	GLY	-	expression tag	UNP P01116
H	12	ASP	GLY	engineered mutation	UNP P01116
L	0	GLY	-	expression tag	UNP P01116
L	12	ASP	GLY	engineered mutation	UNP P01116
P	0	GLY	-	expression tag	UNP P01116
P	12	ASP	GLY	engineered mutation	UNP P01116

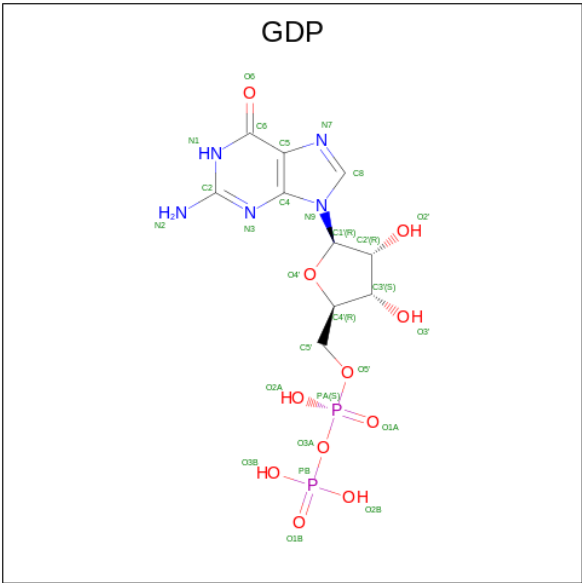
- Molecule 5 is ASP3082 (CCD ID: A1L66) (formula: C₆₀H₆₅FN₁₂O₇S) (labeled as "Ligand of

Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	F	N	O	S	0	0
			81	60	1	12	7	1		
5	H	1	Total	C	F	N	O	S	0	0
			81	60	1	12	7	1		
5	L	1	Total	C	F	N	O	S	0	0
			81	60	1	12	7	1		
5	P	1	Total	C	F	N	O	S	0	0
			81	60	1	12	7	1		

- Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
6	H	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
6	L	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
6	P	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

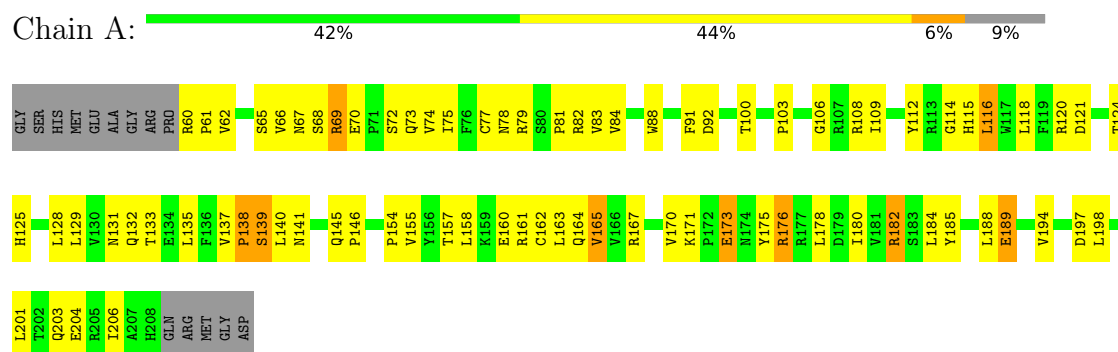
- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	1	Total	Mg	0	0
			1	1		
7	H	1	Total	Mg	0	0
			1	1		
7	L	1	Total	Mg	0	0
			1	1		
7	P	1	Total	Mg	0	0
			1	1		

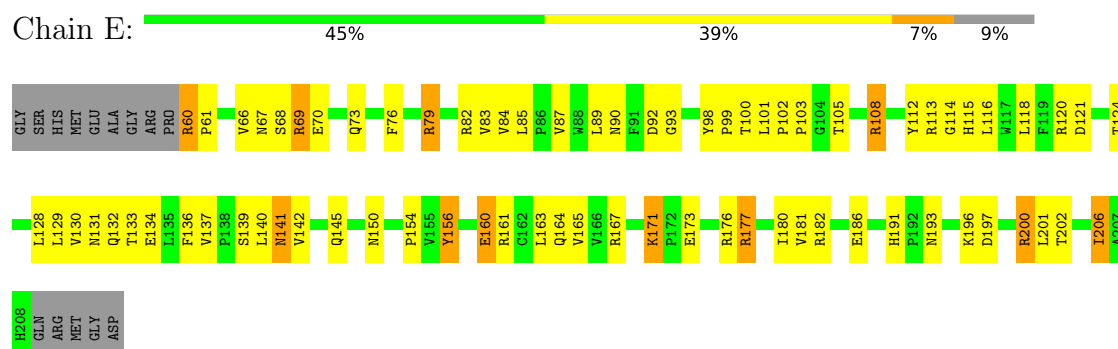
3 Residue-property plots [i](#)

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.

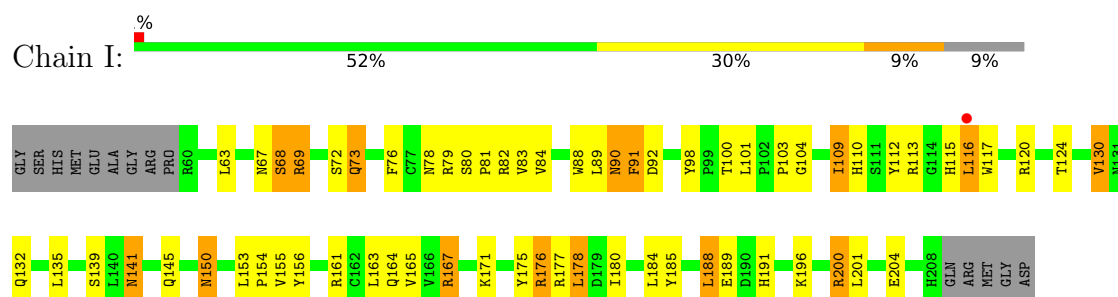
- Molecule 1: von Hippel-Lindau disease tumor suppressor



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- Molecule 2: Elongin-C

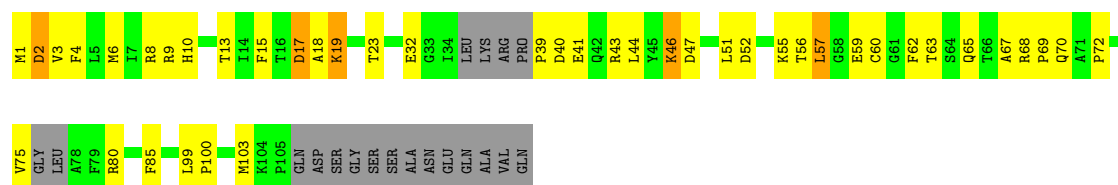
- Molecule 2: Elongin-C

- Molecule 2: Elongin-C

- Molecule 2: Elongin-C

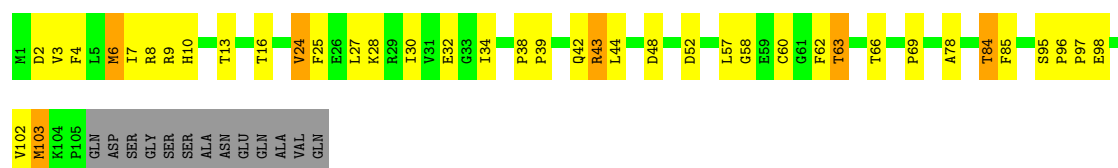
- Molecule 3: Elongin-B

Chain C:  47% 32% 16%



• Molecule 3: Elongin-B

Chain G:  55% 29% 11% 5%



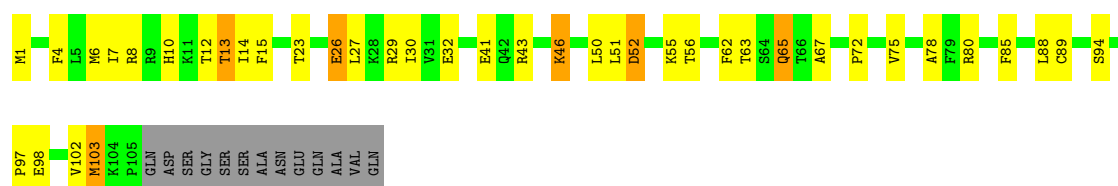
• Molecule 3: Elongin-B

Chain K:  62% 23% 14%



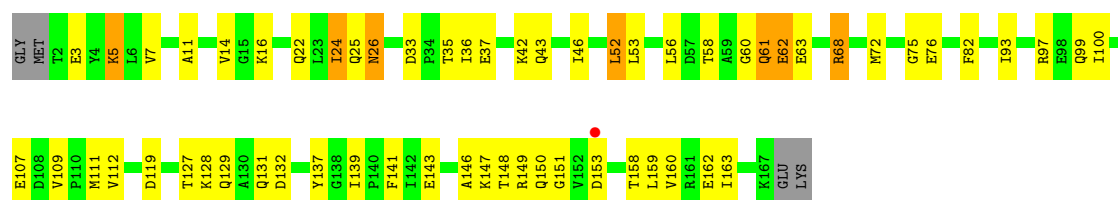
• Molecule 3: Elongin-B

Chain O:  55% 29% 11% 5%

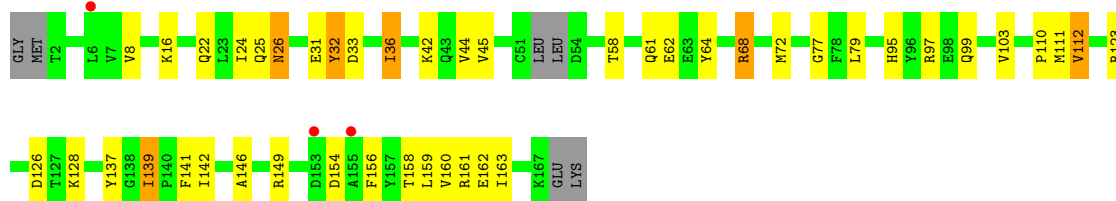


• Molecule 4: Isoform 2B of GTPase KRas

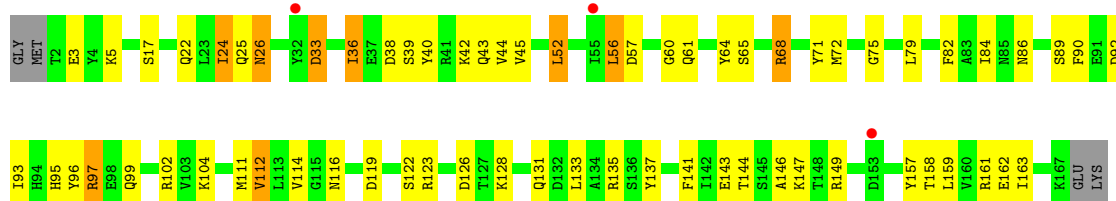
Chain D:  62% 31% 7%



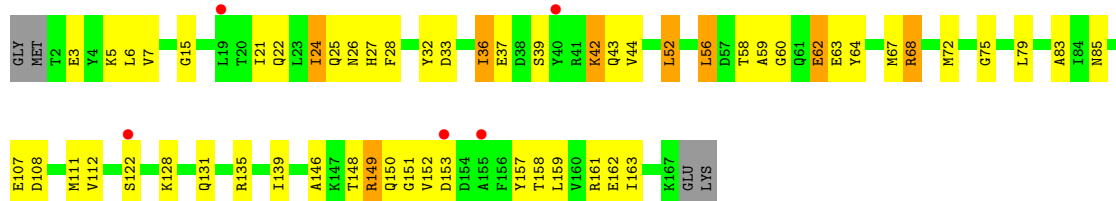
• Molecule 4: Isoform 2B of GTPase KRas



• Molecule 4: Isoform 2B of GTPase KRas



• Molecule 4: Isoform 2B of GTPase KRas



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.35Å 58.91Å 165.98Å 90.00° 104.30° 90.00°	Depositor
Resolution (Å)	48.76 – 3.18 48.76 – 3.18	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.76-3.18) 99.9 (48.76-3.18)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.241 , 0.305 0.248 , 0.308	Depositor DCC
R_{free} test set	2333 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	82.6	Xtriage
Anisotropy	0.538	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 104.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16509	wwPDB-VP
Average B, all atoms (Å ²)	142.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.42 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0448e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: A1L66, GDP, MG

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	0.46	0/1239	0.97	0/1691
1	E	0.49	0/1235	1.00	1/1686 (0.1%)
1	I	0.47	0/1235	1.00	1/1686 (0.1%)
1	M	0.50	0/1235	1.04	0/1686
2	B	0.44	0/704	0.96	0/952
2	F	0.48	0/692	1.02	0/935
2	J	0.43	0/704	1.00	0/952
2	N	0.48	0/692	1.04	0/935
3	C	0.44	0/793	0.94	0/1069
3	G	0.46	0/843	1.05	0/1140
3	K	0.48	0/807	1.01	1/1090 (0.1%)
3	O	0.48	0/843	1.04	0/1140
4	D	0.41	0/1349	0.98	0/1821
4	H	0.43	0/1332	0.99	0/1796
4	L	0.41	0/1349	0.96	0/1821
4	P	0.41	0/1349	0.97	0/1821
All	All	0.45	0/16401	1.00	3/22221 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	38	PRO	N-CA-C	5.87	116.10	110.47
1	I	91	PHE	CB-CA-C	-5.79	101.14	110.74
1	E	156	TYR	CB-CA-C	-5.74	98.98	109.54

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	1207	0	1198	72	0
1	E	1203	0	1192	56	0
1	I	1203	0	1192	50	0
1	M	1203	0	1192	56	0
2	B	689	0	680	27	0
2	F	678	0	670	26	0
2	J	689	0	680	30	0
2	N	678	0	670	23	0
3	C	779	0	770	35	0
3	G	826	0	829	25	0
3	K	792	0	787	25	0
3	O	826	0	829	26	0
4	D	1328	0	1303	43	0
4	H	1312	0	1281	30	0
4	L	1328	0	1303	46	0
4	P	1328	0	1303	42	0
5	A	81	0	0	2	0
5	H	81	0	0	3	0
5	L	81	0	0	5	0
5	P	81	0	0	10	0
6	D	28	0	12	2	0
6	H	28	0	12	1	0
6	L	28	0	12	2	0
6	P	28	0	12	1	0
7	D	1	0	0	0	0
7	H	1	0	0	0	0
7	L	1	0	0	0	0
7	P	1	0	0	0	0
All	All	16509	0	15927	543	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 17.

The worst 5 of 543 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)
3:K:41:GLU:HB2	3:K:79:PHE:CE1	1.35	1.59
3:K:41:GLU:CB	3:K:79:PHE:HE1	1.37	1.34
2:J:101:LEU:HD22	3:K:103:MET:SD	1.90	1.12
1:E:69:ARG:HG3	4:H:62:GLU:HB2	1.39	1.02
4:D:149:ARG:HD3	4:P:148:THR:O	1.60	1.00

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	147/163 (90%)	131 (89%)	13 (9%)	3 (2%)	6	29
1	E	147/163 (90%)	137 (93%)	9 (6%)	1 (1%)	19	52
1	I	147/163 (90%)	132 (90%)	15 (10%)	0	100	100
1	M	147/163 (90%)	138 (94%)	9 (6%)	0	100	100
2	B	84/96 (88%)	78 (93%)	5 (6%)	1 (1%)	11	41
2	F	82/96 (85%)	75 (92%)	6 (7%)	1 (1%)	11	41
2	J	84/96 (88%)	77 (92%)	7 (8%)	0	100	100
2	N	82/96 (85%)	79 (96%)	2 (2%)	1 (1%)	11	41
3	C	93/118 (79%)	81 (87%)	11 (12%)	1 (1%)	12	42
3	G	103/118 (87%)	92 (89%)	11 (11%)	0	100	100
3	K	95/118 (80%)	84 (88%)	10 (10%)	1 (1%)	12	42
3	O	103/118 (87%)	95 (92%)	8 (8%)	0	100	100
4	D	164/170 (96%)	145 (88%)	18 (11%)	1 (1%)	22	55
4	H	160/170 (94%)	147 (92%)	12 (8%)	1 (1%)	22	55
4	L	164/170 (96%)	148 (90%)	15 (9%)	1 (1%)	22	55
4	P	164/170 (96%)	147 (90%)	15 (9%)	2 (1%)	11	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1966/2188 (90%)	1786 (91%)	166 (8%)	14 (1%)	19	52

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	26	ASN
4	H	26	ASN
4	L	26	ASN
1	A	139	SER
2	N	59	GLU

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	134/149 (90%)	119 (89%)	15 (11%)	5	20
1	E	133/149 (89%)	113 (85%)	20 (15%)	2	11
1	I	133/149 (89%)	102 (77%)	31 (23%)	0	3
1	M	133/149 (89%)	112 (84%)	21 (16%)	2	9
2	B	77/85 (91%)	68 (88%)	9 (12%)	4	19
2	F	76/85 (89%)	64 (84%)	12 (16%)	2	9
2	J	77/85 (91%)	66 (86%)	11 (14%)	2	12
2	N	76/85 (89%)	66 (87%)	10 (13%)	3	15
3	C	87/103 (84%)	76 (87%)	11 (13%)	3	16
3	G	92/103 (89%)	81 (88%)	11 (12%)	4	18
3	K	89/103 (86%)	80 (90%)	9 (10%)	6	23
3	O	92/103 (89%)	76 (83%)	16 (17%)	1	7
4	D	147/150 (98%)	133 (90%)	14 (10%)	7	26
4	H	145/150 (97%)	133 (92%)	12 (8%)	9	32
4	L	147/150 (98%)	129 (88%)	18 (12%)	4	17
4	P	147/150 (98%)	129 (88%)	18 (12%)	4	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1785/1948 (92%)	1547 (87%)	238 (13%)	3 14

5 of 238 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	116	LEU
4	P	21	ILE
2	J	99	ILE
3	O	103	MET
4	P	128	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
3	K	10	HIS
1	M	110	HIS
4	L	22	GLN
4	L	70	GLN
1	M	191	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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
5	A1L66	H	203	-	82,93,93	1.30	8 (9%)	96,138,138	1.42	15 (15%)
5	A1L66	L	203	-	82,93,93	1.69	12 (14%)	96,138,138	1.49	14 (14%)
6	GDP	D	201	7	24,30,30	0.95	1 (4%)	30,47,47	1.38	3 (10%)
6	GDP	P	201	7	24,30,30	1.06	3 (12%)	30,47,47	1.45	3 (10%)
5	A1L66	P	203	-	82,93,93	1.58	10 (12%)	96,138,138	1.60	17 (17%)
6	GDP	L	201	7	24,30,30	1.06	3 (12%)	30,47,47	1.59	4 (13%)
5	A1L66	A	301	-	82,93,93	1.41	9 (10%)	96,138,138	1.68	17 (17%)
6	GDP	H	201	7	24,30,30	1.01	1 (4%)	30,47,47	1.51	4 (13%)

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
5	A1L66	H	203	-	-	8/53/98/98	0/13/13/13
5	A1L66	L	203	-	-	5/53/98/98	0/13/13/13
6	GDP	D	201	7	-	0/12/32/32	0/3/3/3
6	GDP	P	201	7	-	0/12/32/32	0/3/3/3
5	A1L66	P	203	-	-	10/53/98/98	0/13/13/13
6	GDP	L	201	7	-	5/12/32/32	0/3/3/3
5	A1L66	A	301	-	-	11/53/98/98	0/13/13/13
6	GDP	H	201	7	-	0/12/32/32	0/3/3/3

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	203	A1L66	C14-C15	-9.04	1.44	1.50
5	P	203	A1L66	C14-C15	-8.38	1.44	1.50
5	A	301	A1L66	C14-C15	-6.74	1.45	1.50
5	H	203	A1L66	C14-C15	-4.95	1.47	1.50
5	P	203	A1L66	C13-C29	-3.86	1.37	1.42

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	301	A1L66	C40-C41-C37	6.88	117.93	109.78
5	L	203	A1L66	C40-C41-C37	5.87	116.74	109.78
5	A	301	A1L66	C1-C2-N1	5.77	116.78	109.17
5	P	203	A1L66	C36-C35-N10	-5.13	95.60	102.20
6	P	201	GDP	O6-C6-N1	4.79	126.30	120.65

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	301	A1L66	O1-C1-C2-N1
5	A	301	A1L66	O1-C1-C2-C51
5	A	301	A1L66	C14-C23-C24-C26
5	H	203	A1L66	N8-C30-O3-C37
5	H	203	A1L66	N9-C30-O3-C37

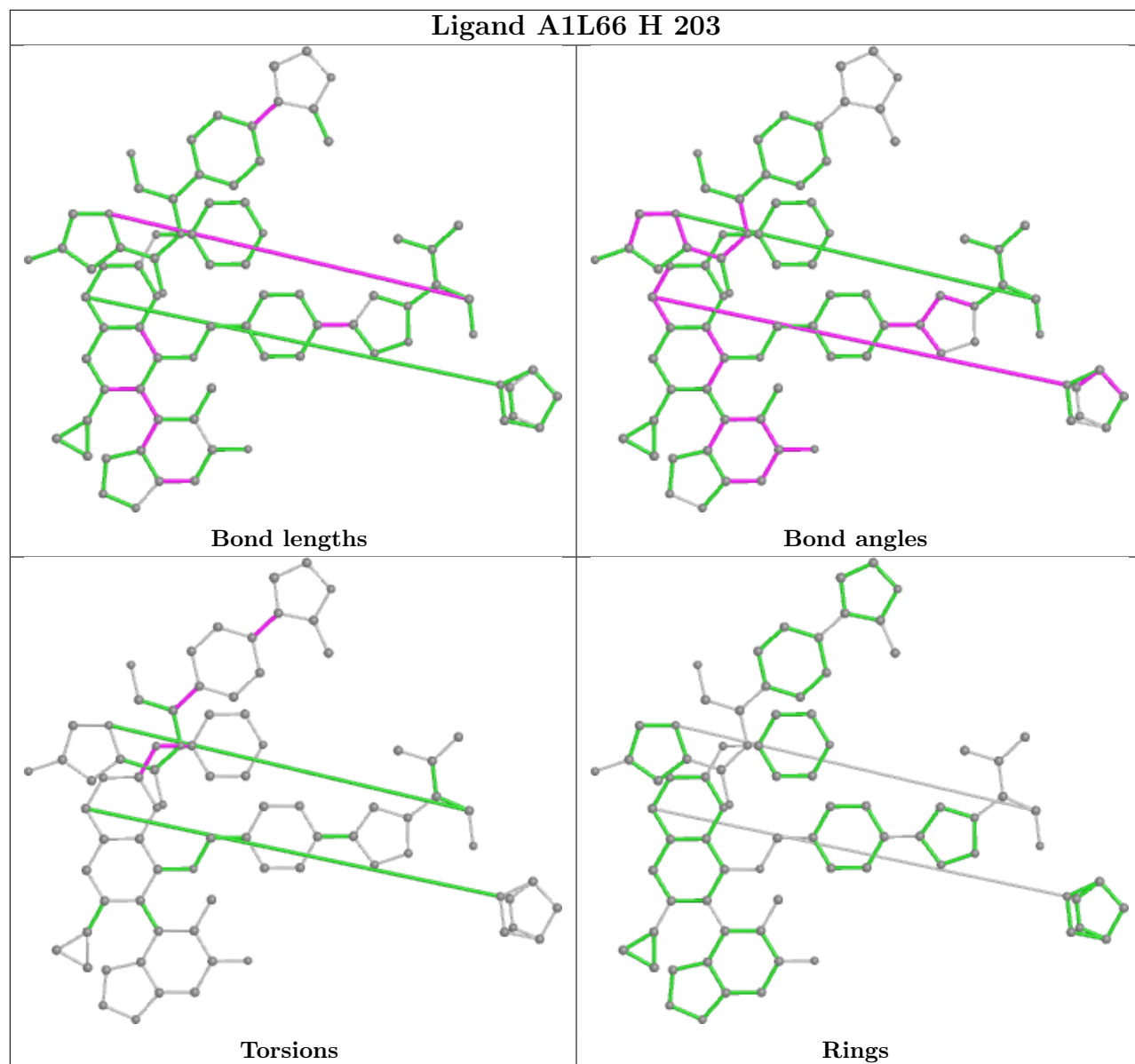
There are no ring outliers.

8 monomers are involved in 26 short contacts:

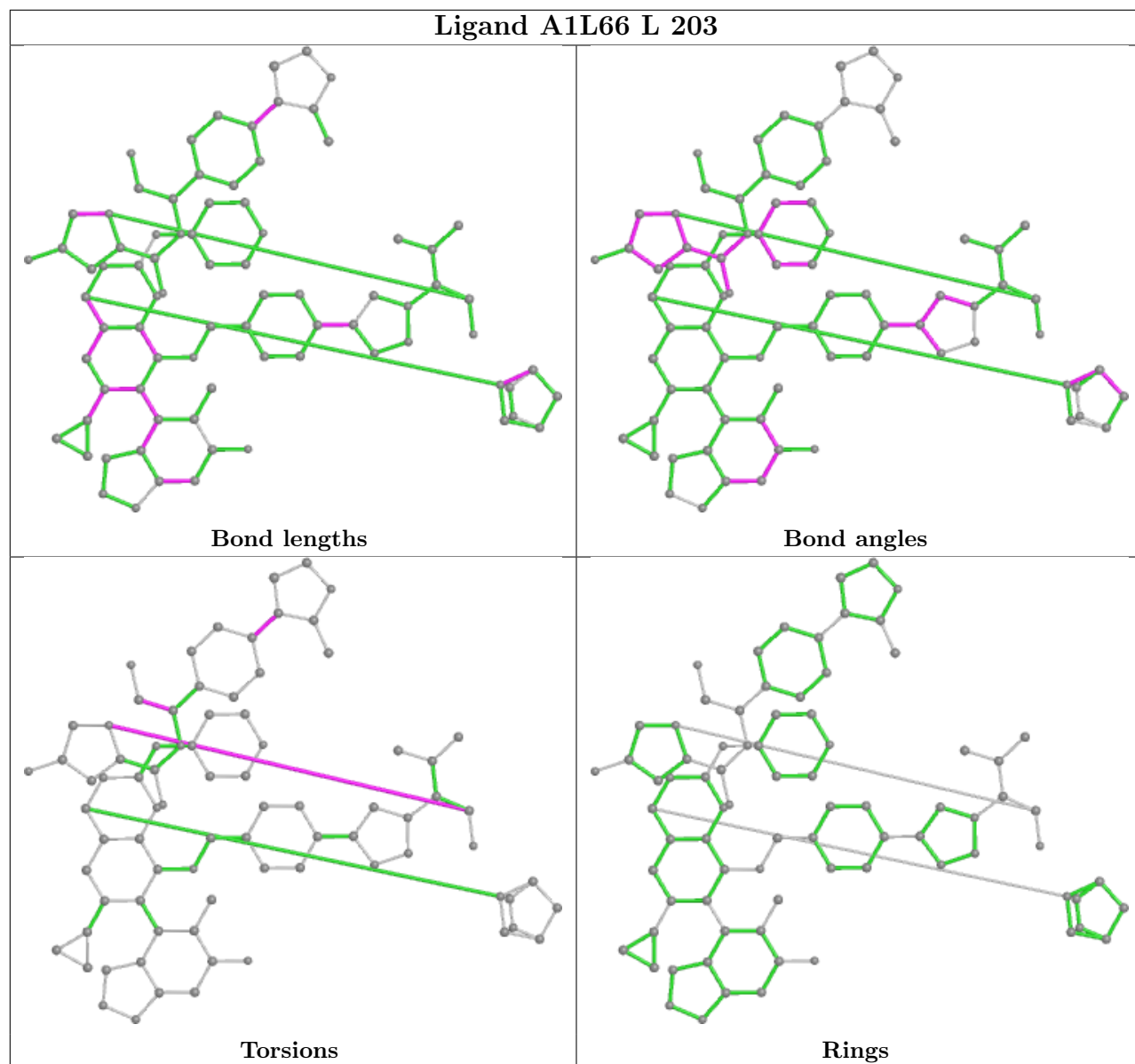
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	203	A1L66	3	0
5	L	203	A1L66	5	0
6	D	201	GDP	2	0
6	P	201	GDP	1	0
5	P	203	A1L66	10	0
6	L	201	GDP	2	0
5	A	301	A1L66	2	0
6	H	201	GDP	1	0

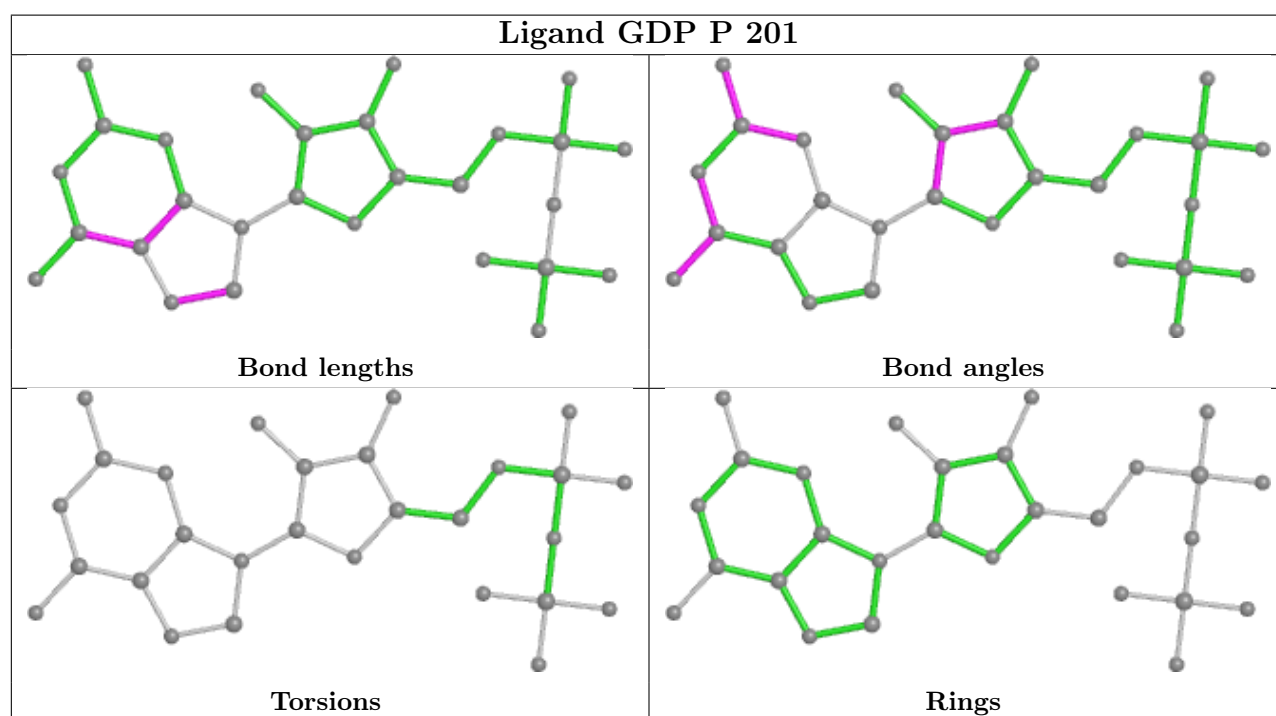
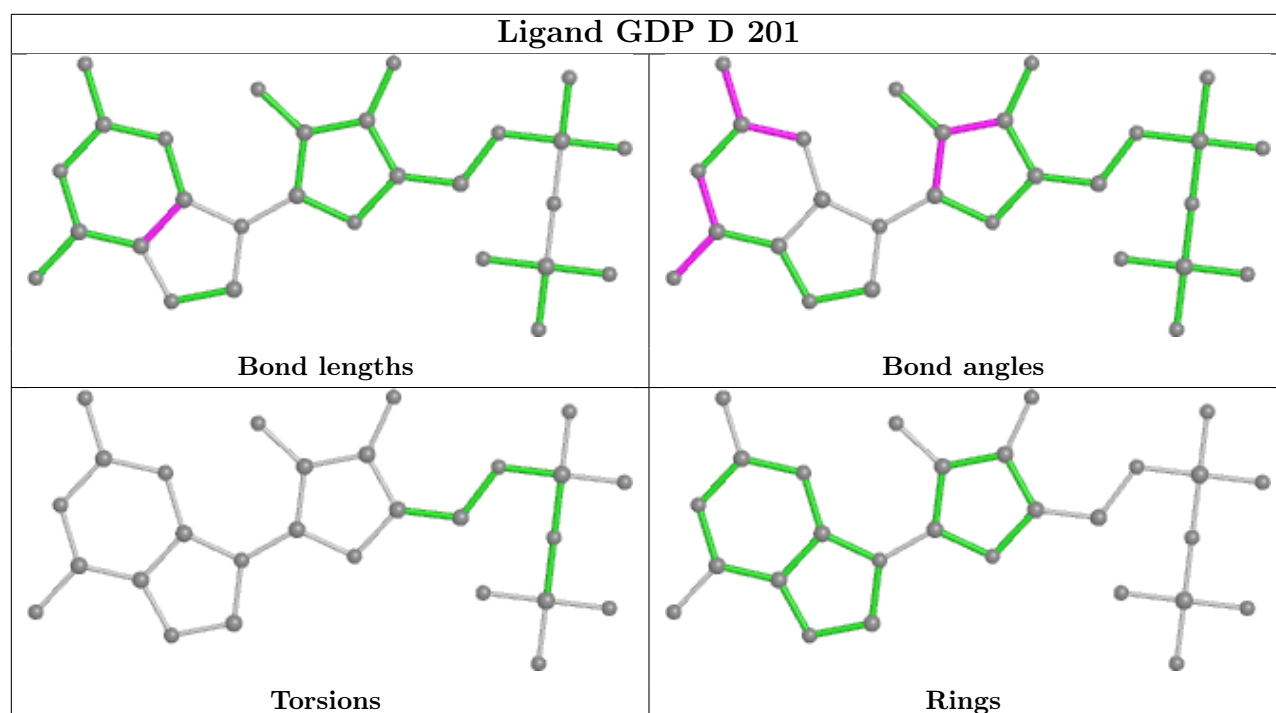
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand A1L66 H 203

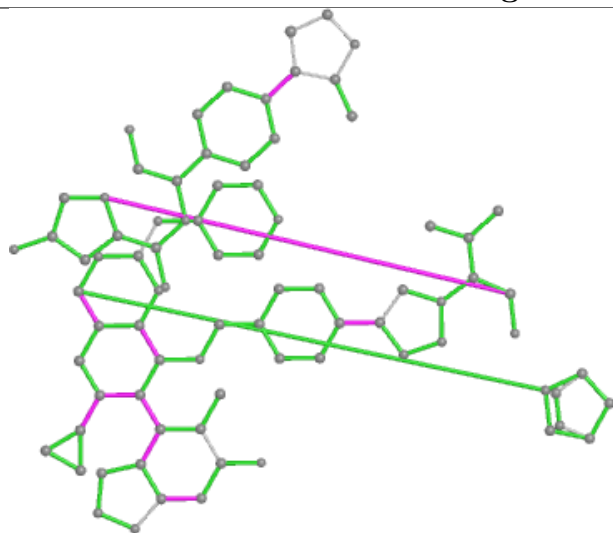


Ligand A1L66 L 203

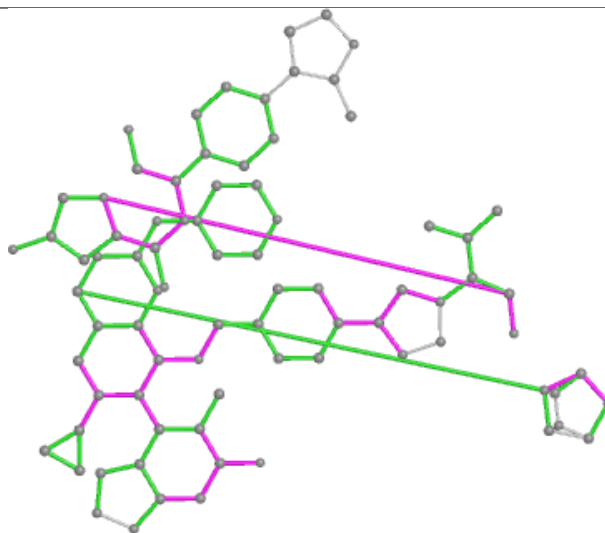




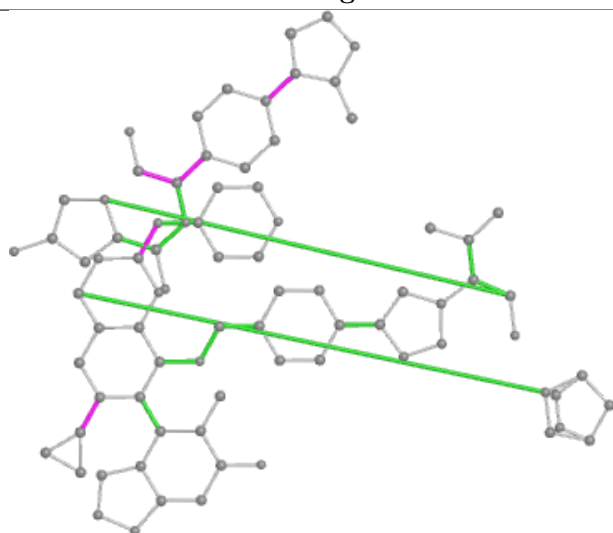
Ligand A1L66 P 203



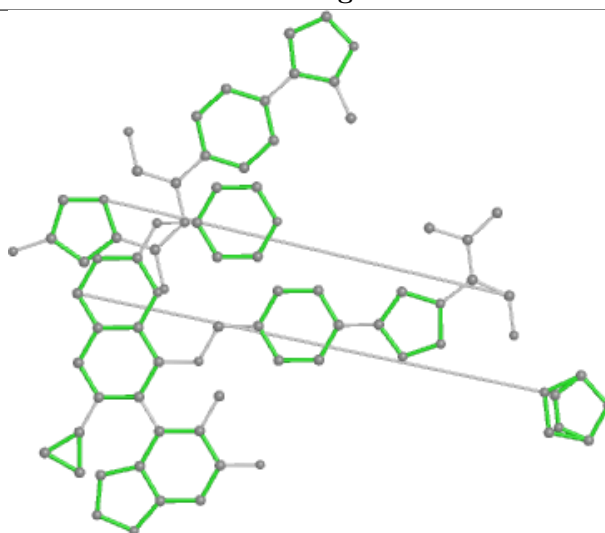
Bond lengths



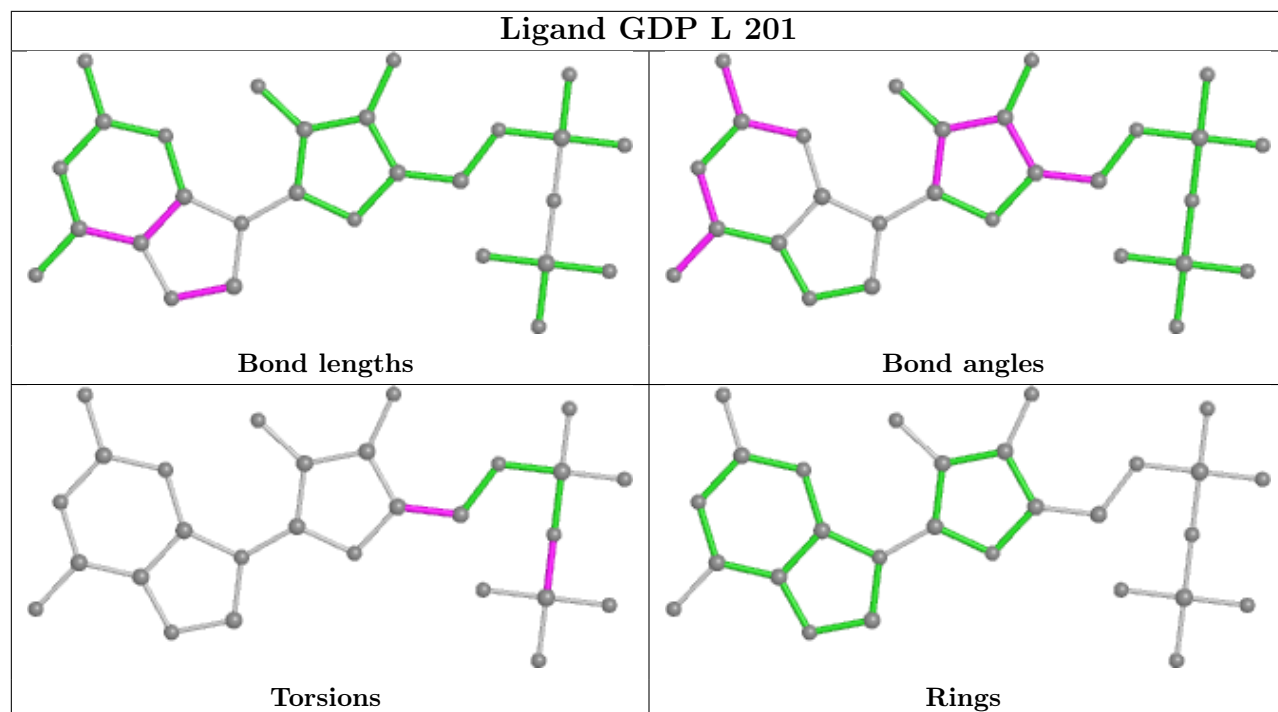
Bond angles



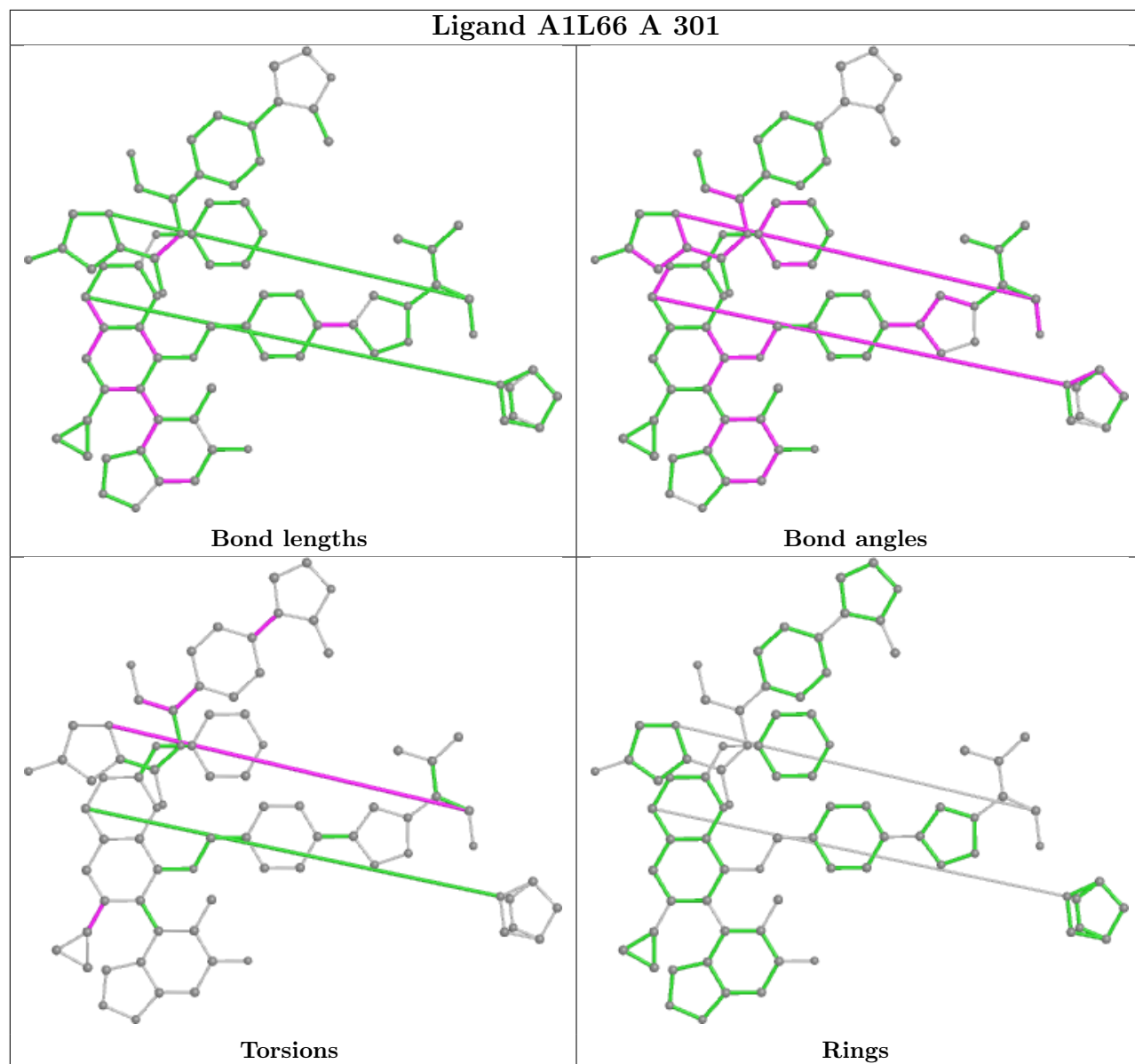
Torsions

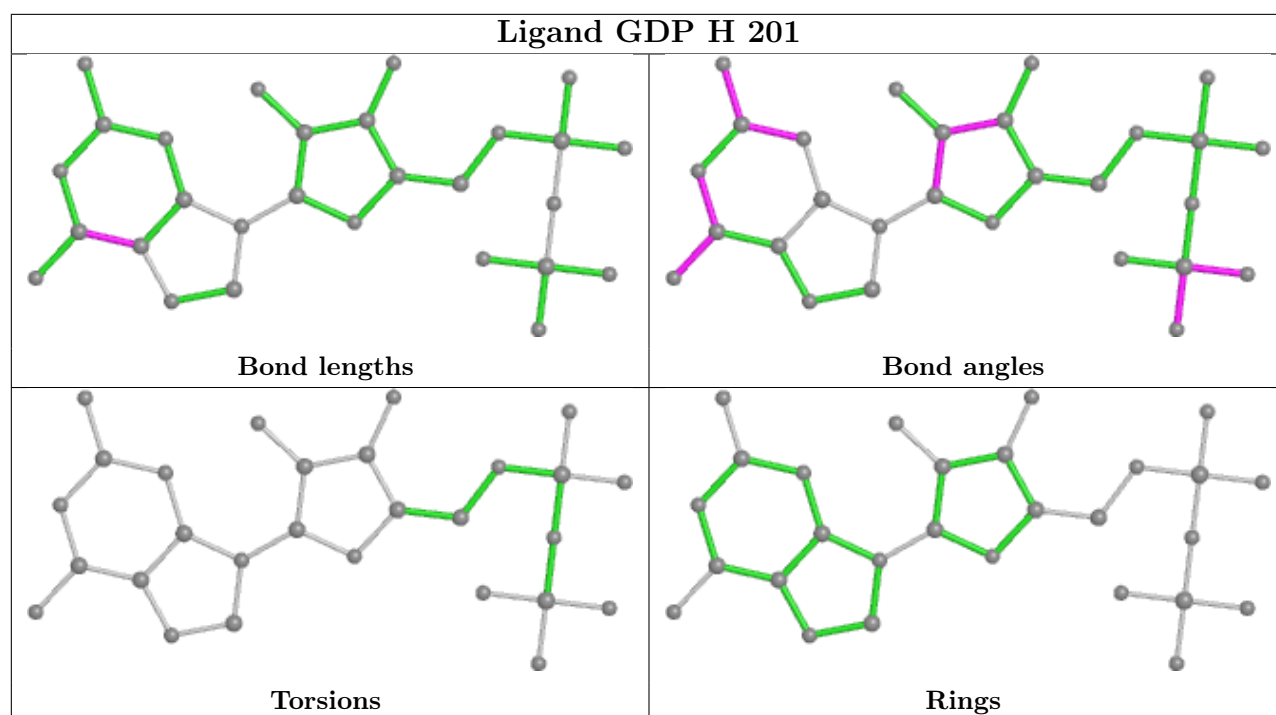


Rings



Ligand A1L66 A 301





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	149/163 (91%)	-0.59	0 100 100	85, 130, 201, 250	0
1	E	149/163 (91%)	-0.78	0 100 100	72, 105, 150, 195	0
1	I	149/163 (91%)	-0.55	1 (0%) 84 73	78, 123, 204, 284	0
1	M	149/163 (91%)	-0.82	0 100 100	66, 100, 151, 219	0
2	B	88/96 (91%)	-0.47	0 100 100	126, 182, 217, 264	0
2	F	86/96 (89%)	-0.79	0 100 100	67, 93, 132, 158	0
2	J	88/96 (91%)	-0.56	0 100 100	136, 186, 227, 262	0
2	N	86/96 (89%)	-0.83	0 100 100	68, 90, 125, 142	0
3	C	99/118 (83%)	-0.62	0 100 100	150, 194, 241, 262	0
3	G	105/118 (88%)	-0.79	0 100 100	67, 90, 124, 144	0
3	K	101/118 (85%)	-0.62	0 100 100	146, 204, 244, 267	0
3	O	105/118 (88%)	-0.93	0 100 100	67, 87, 123, 141	0
4	D	166/170 (97%)	-0.59	1 (0%) 85 76	82, 139, 177, 214	0
4	H	164/170 (96%)	-0.37	3 (1%) 67 52	105, 163, 216, 244	0
4	L	166/170 (97%)	-0.53	3 (1%) 67 52	87, 142, 183, 211	0
4	P	166/170 (97%)	-0.28	5 (3%) 52 36	113, 179, 237, 291	0
All	All	2016/2188 (92%)	-0.61	13 (0%) 85 76	66, 137, 217, 291	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	P	153	ASP	4.3
4	H	155	ALA	3.3
4	D	153	ASP	3.0
4	L	153	ASP	3.0
4	H	153	ASP	2.9

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

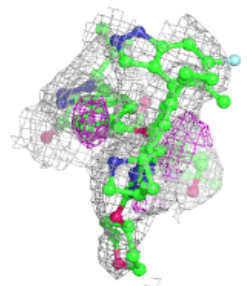
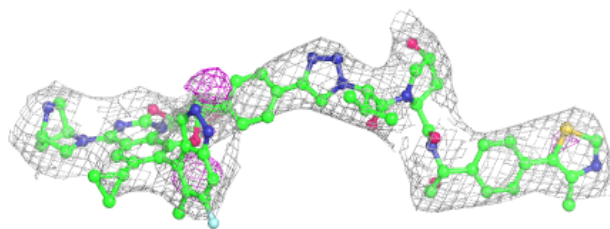
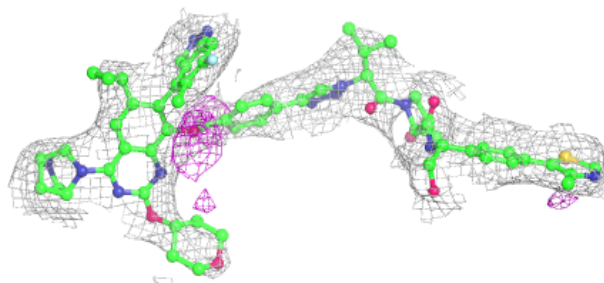
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	A1L66	H	203	81/81	0.90	0.08	94,122,144,151	0
5	A1L66	P	203	81/81	0.90	0.09	104,124,171,185	0
6	GDP	H	201	28/28	0.92	0.06	154,173,197,203	0
6	GDP	P	201	28/28	0.92	0.06	148,168,182,188	0
7	MG	L	202	1/1	0.92	0.14	96,96,96,96	0
5	A1L66	A	301	81/81	0.94	0.07	94,114,137,139	0
5	A1L66	L	203	81/81	0.94	0.07	85,102,120,140	0
7	MG	H	202	1/1	0.95	0.08	117,117,117,117	0
6	GDP	L	201	28/28	0.96	0.05	99,125,145,149	0
6	GDP	D	201	28/28	0.96	0.06	113,135,172,180	0
7	MG	D	202	1/1	0.97	0.09	103,103,103,103	0
7	MG	P	202	1/1	0.98	0.09	99,99,99,99	0

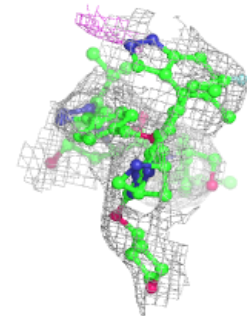
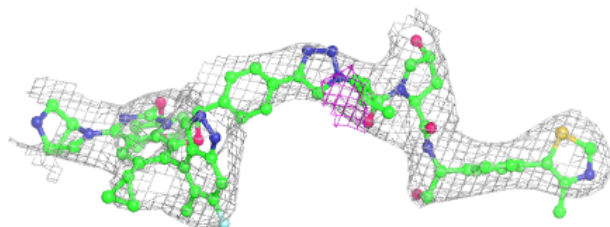
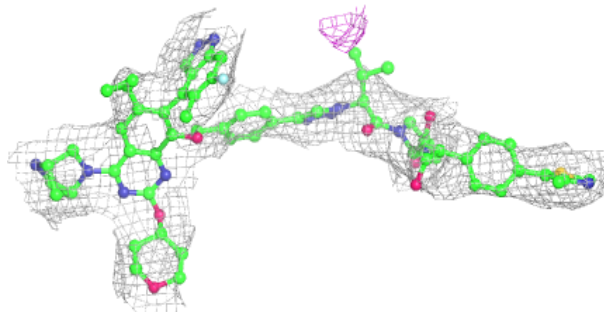
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1L66 H 203:

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

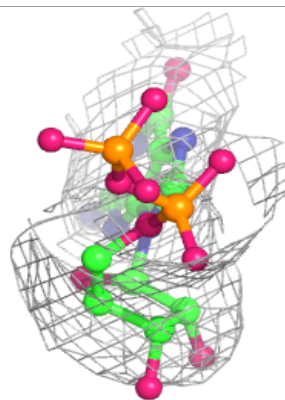
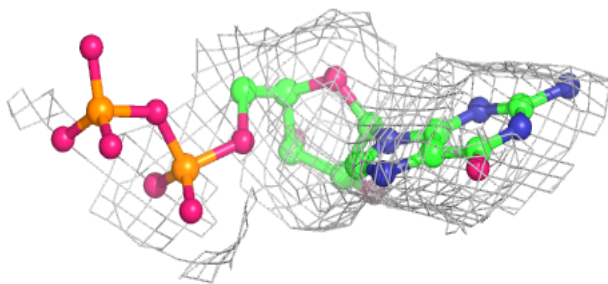
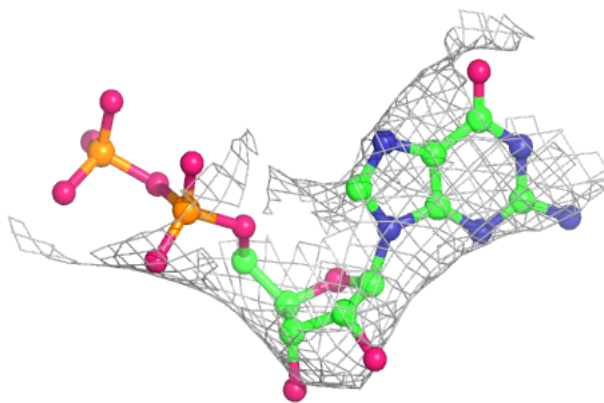
**Electron density around A1L66 P 203:**

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

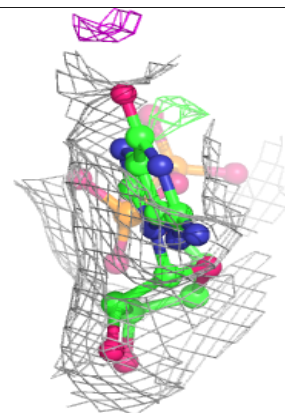
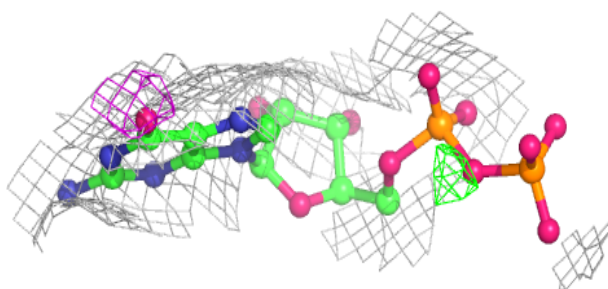
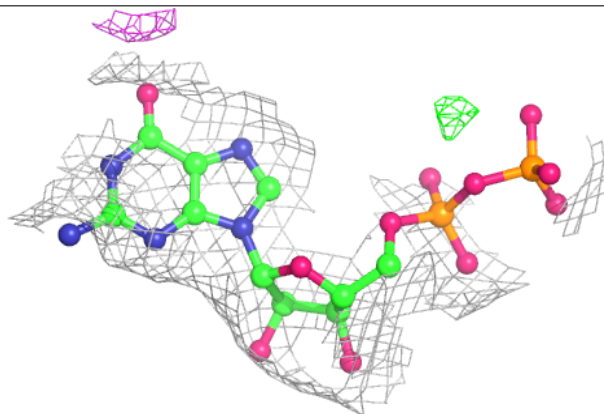


Electron density around GDP H 201:

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

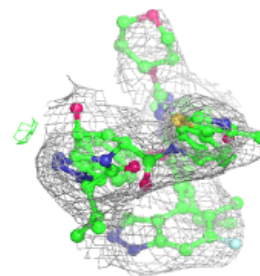
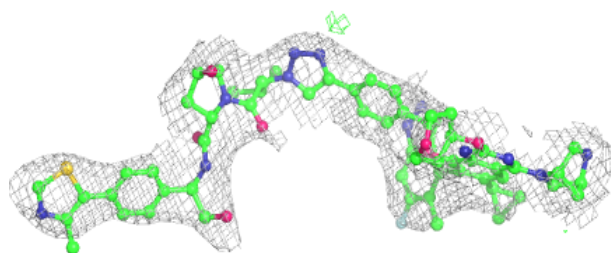
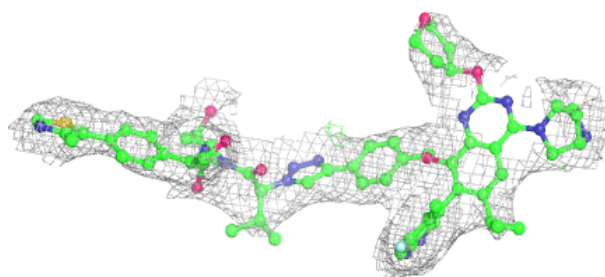
**Electron density around GDP P 201:**

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and green (positive)

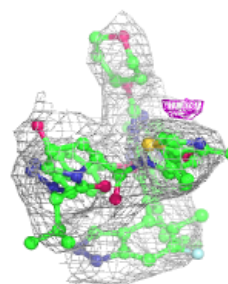
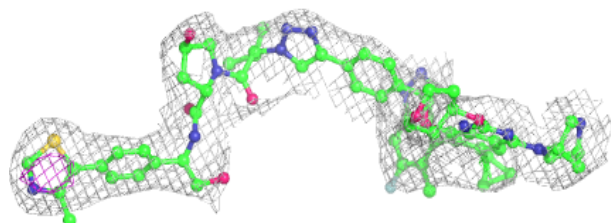
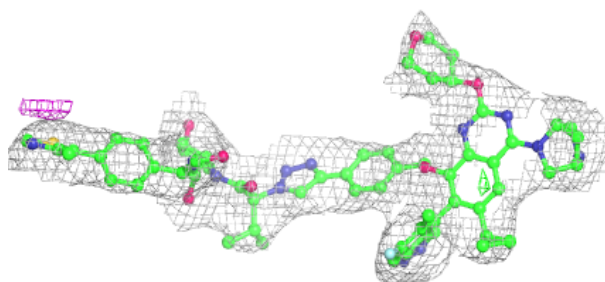


Electron density around A1L66 A 301:

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

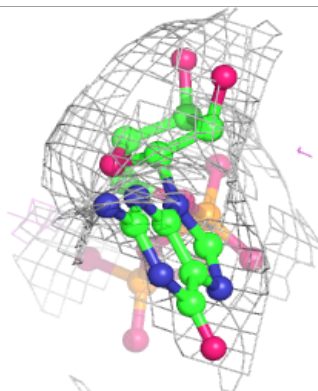
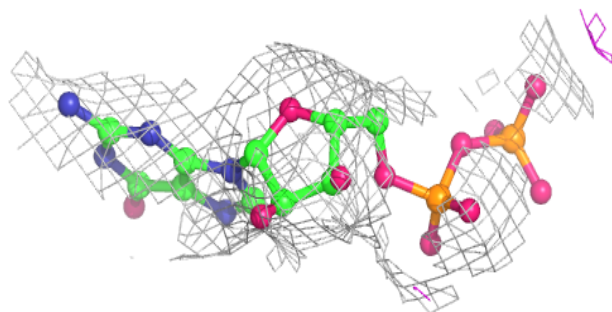
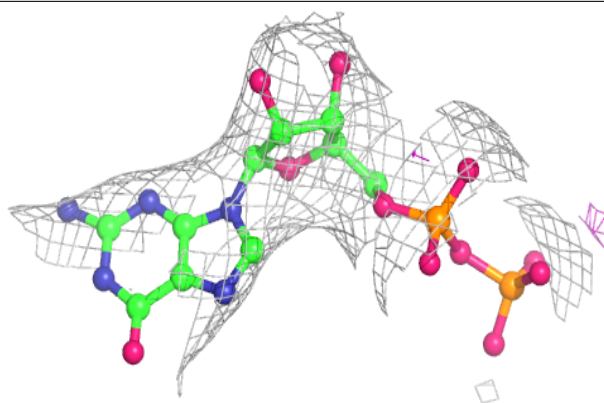
**Electron density around A1L66 L 203:**

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

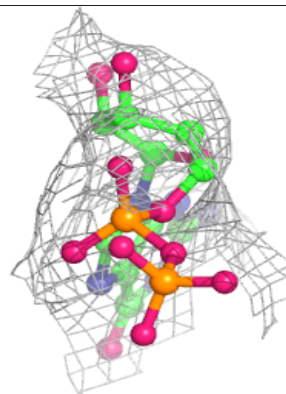
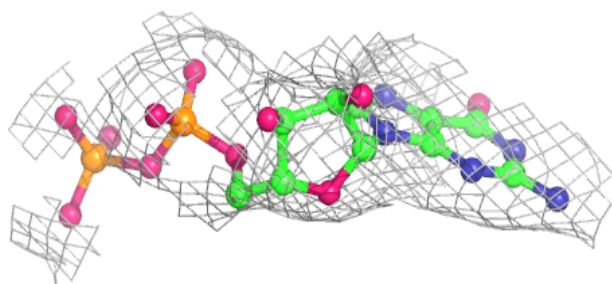
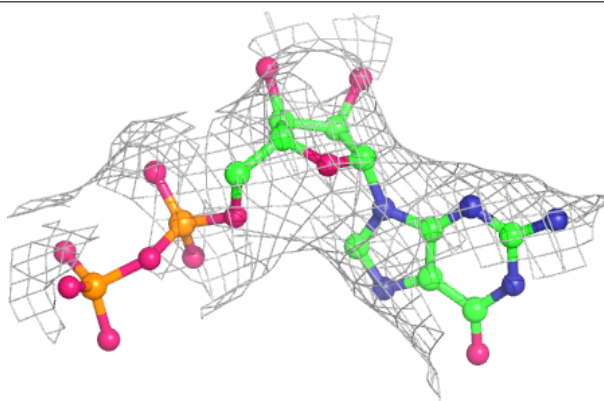


Electron density around GDP L 201:

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

**Electron density around GDP D 201:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.