wwPDB X-ray Structure Validation Summary Report (i)

Oct 9, 2023 – 01:50 PM EDT

PDB ID	:	6XL4
Title	:	EGFR(T790M/V948R) in complex with AZD9291 and DDC4002
Authors	:	Heppner, D.E.; Beyett, T.S.; Eck, M.J.
Deposited on	:	2020-06-28
Resolution	:	2.06 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 (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:

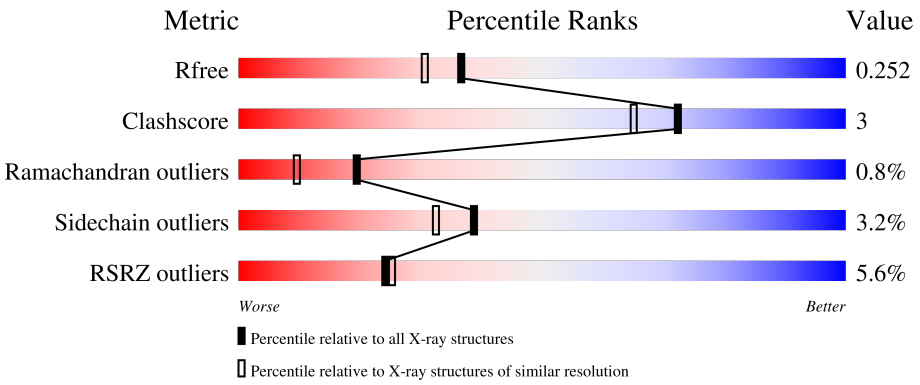
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 2.06 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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	328	3% 81% 8% 11%
1	B	328	5% 78% 9% • 11%
1	C	328	5% 81% 9% • 8%
1	D	328	7% 81% 10% 9%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9977 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.

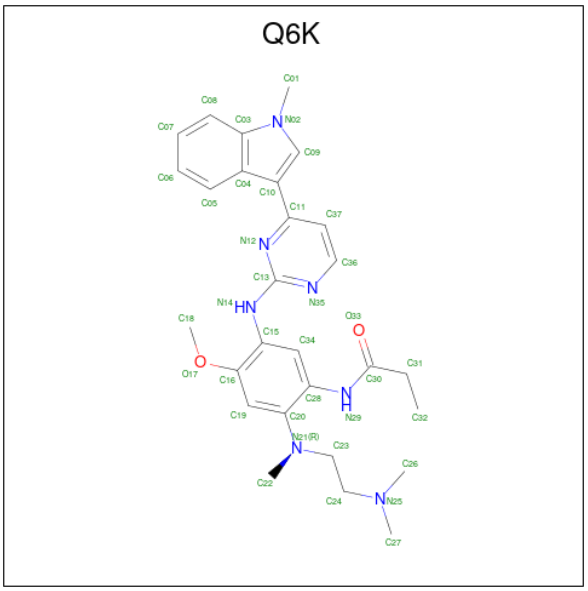
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	293	2360	1515	402	424	19	0	0	0
1	B	292	2347	1507	400	421	19	0	0	0
1	C	302	2419	1551	411	438	19	0	0	0
1	D	300	2400	1540	408	433	19	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

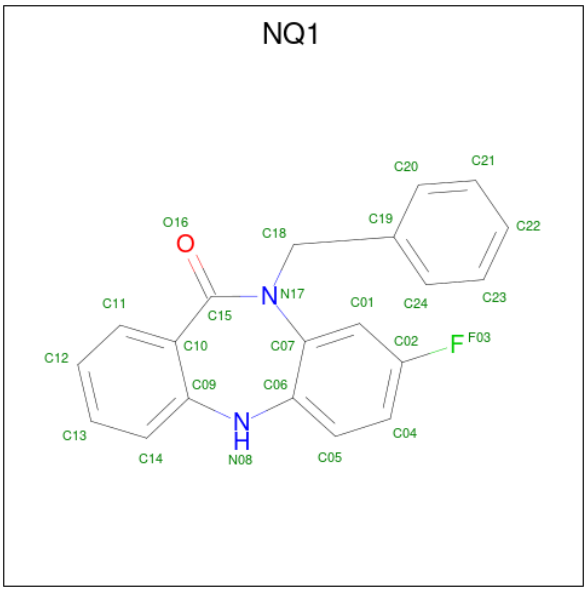
Chain	Residue	Modelled	Actual	Comment	Reference
A	790	MET	THR	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533
C	790	MET	THR	engineered mutation	UNP P00533
C	948	ARG	VAL	engineered mutation	UNP P00533
D	790	MET	THR	engineered mutation	UNP P00533
D	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is {N}-[2-[2-(dimethylamino)ethyl-methyl-amino]-4-methoxy-5-[[4-(1-methylindol-3-yl)pyrimidin-2-yl]amino]phenyl]propanamide (three-letter code: Q6K) (formula: $C_{28}H_{35}N_7O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	37	28	7	2	0	0
			Total	C	N	O		
2	B	1	37	28	7	2	0	0

- Molecule 3 is 10-benzyl-8-fluoro-5,10-dihydro-11H-dibenzo[b,e][1,4]diazepin-11-one (three-letter code: NQ1) (formula: $C_{20}H_{15}FN_2O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
3	A	1	24	20	1	2	1	0	0

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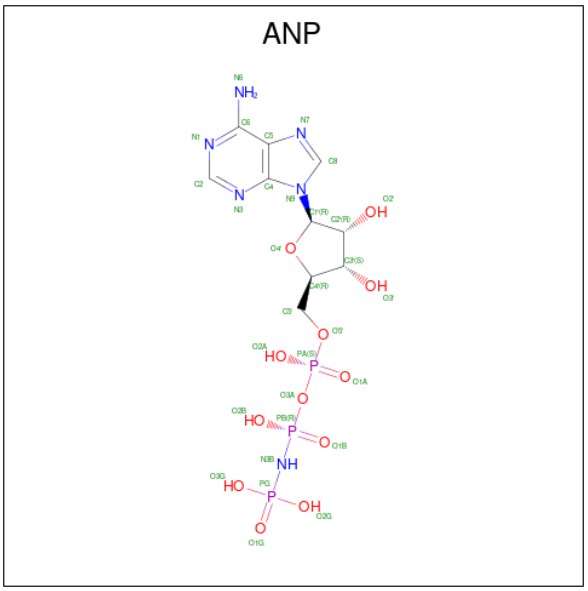
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
3	B	1	24	20	1	2	1	0	0
			Total	C	F	N	O		
3	D	1	24	20	1	2	1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	D	1	1	1	0	0

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	D	1	31	10	6	12	3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	79	79	79	0	0
			Total	O		
6	B	66	66	66	0	0

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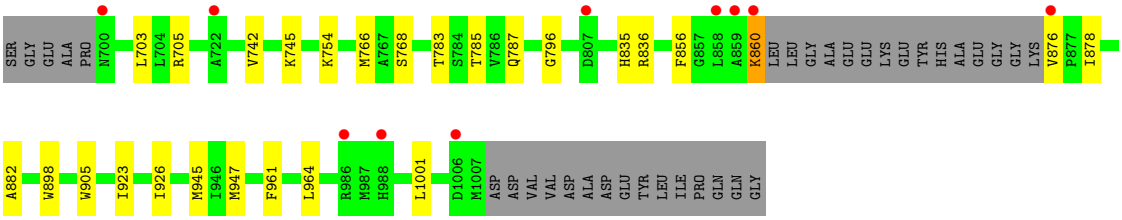
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	C	69	69	69	0	0
			Total	O		
6	D	59	59	59	0	0

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.

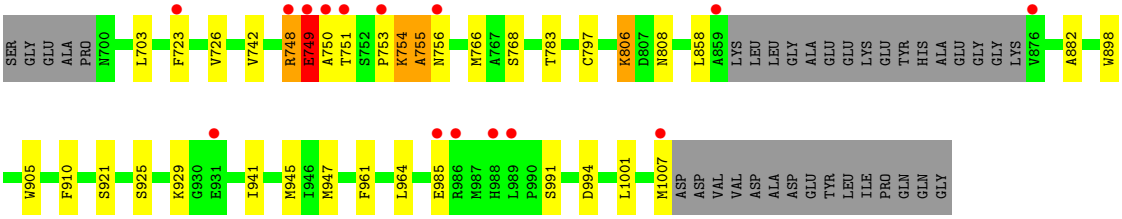
• Molecule 1: Epidermal growth factor receptor

Chain A:



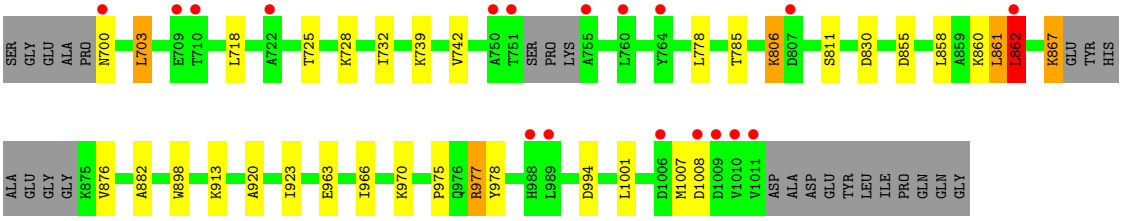
• Molecule 1: Epidermal growth factor receptor

Chain B:



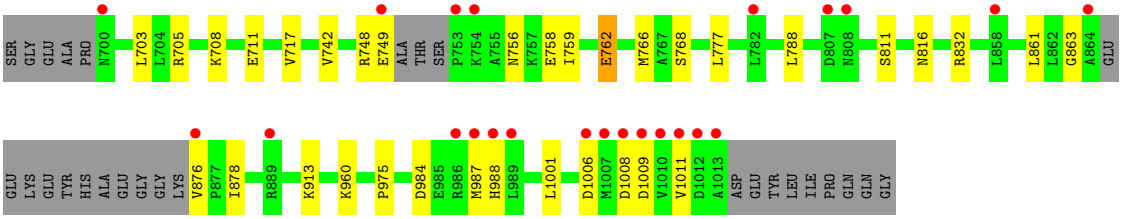
• Molecule 1: Epidermal growth factor receptor

Chain C:



• Molecule 1: Epidermal growth factor receptor

Chain D:


SER
GLY
GLU
ALA
PRO
N700
L703
L704
R705
K708
E711
V717
V742
R748
E749
ALA
THR
SER
P753
K754
A755
N756
K757
E758
I759
E762
M766
A767
S768
L777
L782
L788
D807
N808
S811
N816
R832
L858
L861
L862
G863
A864
GLU
GLU
LYS
GLU
TYR
HIS
ALA
GLU
GLY
GLY
LYS
V876
P877
I878
R889
K913
K960
P975
D984
E985
R986
M987
H988
L989
L1001
D1006
M1007
D1008
D1009
V1010
V1011
D1012
A1013
ASP
GLU
TYR
LEU
ILE
PRO
GLN
GLN
GLY

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	71.54Å 101.71Å 86.97Å 90.00° 102.72° 90.00°	Depositor
Resolution (Å)	84.84 – 2.06 84.84 – 2.06	Depositor EDS
% Data completeness (in resolution range)	98.9 (84.84-2.06) 89.2 (84.84-2.06)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.18 (at 2.07Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.214 , 0.252 0.214 , 0.252	Depositor DCC
R_{free} test set	3628 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å^2)	26.7	Xtriage
Anisotropy	0.896	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 48.9	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	0.94	EDS
Total number of atoms	9977	wwPDB-VP
Average B, all atoms (Å^2)	40.0	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 30.64 % 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 1.2650e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: ANP, MG, NQ1, Q6K

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	0.29	0/2412	0.49	0/3262
1	B	0.29	0/2399	0.52	0/3246
1	C	0.31	0/2469	0.52	0/3338
1	D	0.32	0/2451	0.50	0/3315
All	All	0.30	0/9731	0.51	0/13161

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2360	0	2398	16	0
1	B	2347	0	2382	20	0
1	C	2419	0	2445	19	0
1	D	2400	0	2425	20	0
2	A	37	0	0	1	0
2	B	37	0	0	2	0
3	A	24	0	0	1	0
3	B	24	0	0	1	0
3	D	24	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	0	0
5	D	31	0	13	0	0
6	A	79	0	0	0	0
6	B	66	0	0	1	0
6	C	69	0	0	1	0
6	D	59	0	0	2	0
All	All	9977	0	9663	66	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 3.

The worst 5 of 66 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:753:PRO:HG2	1:B:754:LYS:HE2	1.47	0.96
1:B:754:LYS:O	1:B:755:ALA:HB3	1.86	0.75
1:B:994:ASP:OD1	1:D:705:ARG:NH1	2.22	0.73
1:A:742:VAL:HG12	1:C:1001:LEU:HD11	1.75	0.68
1:D:703:LEU:HD13	1:D:768:SER:HA	1.78	0.65

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	289/328 (88%)	284 (98%)	5 (2%)	0	100 100
1	B	288/328 (88%)	275 (96%)	6 (2%)	7 (2%)	6 1
1	C	296/328 (90%)	282 (95%)	13 (4%)	1 (0%)	41 32
1	D	294/328 (90%)	279 (95%)	14 (5%)	1 (0%)	41 32
All	All	1167/1312 (89%)	1120 (96%)	38 (3%)	9 (1%)	19 9

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	754	LYS
1	B	756	ASN
1	B	806	LYS
1	C	862	LEU
1	B	755	ALA

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	261/288 (91%)	258 (99%)	3 (1%)	73	72
1	B	259/288 (90%)	250 (96%)	9 (4%)	36	29
1	C	265/288 (92%)	252 (95%)	13 (5%)	25	17
1	D	263/288 (91%)	254 (97%)	9 (3%)	37	30
All	All	1048/1152 (91%)	1014 (97%)	34 (3%)	39	32

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	832	ARG
1	D	984	ASP
1	D	1008	ASP
1	C	703	LEU
1	B	1007	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	816	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)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	$\#\|Z\| > 2$
3	NQ1	A	1302	-	27,27,27	2.49	8 (29%)	37,38,38	1.39	6 (16%)
2	Q6K	A	1301	1	38,40,40	5.26	24 (63%)	50,56,56	1.99	12 (24%)
3	NQ1	D	1103	-	27,27,27	2.49	8 (29%)	37,38,38	1.48	8 (21%)
5	ANP	D	1102	4	29,33,33	1.06	3 (10%)	31,52,52	1.04	2 (6%)
3	NQ1	B	1201	-	27,27,27	2.48	7 (25%)	37,38,38	1.46	6 (16%)
2	Q6K	B	1202	-	38,40,40	5.25	24 (63%)	50,56,56	2.18	13 (26%)

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
3	NQ1	A	1302	-	-	2/4/4/4	0/4/4/4
2	Q6K	A	1301	1	-	6/21/25/25	0/4/4/4
3	NQ1	D	1103	-	-	2/4/4/4	0/4/4/4
5	ANP	D	1102	4	-	3/14/38/38	0/3/3/3
3	NQ1	B	1201	-	-	0/4/4/4	0/4/4/4
2	Q6K	B	1202	-	-	8/21/25/25	0/4/4/4

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1301	Q6K	C28-C20	11.63	1.53	1.40
2	B	1202	Q6K	C28-C20	10.99	1.53	1.40
2	B	1202	Q6K	C13-N35	10.23	1.49	1.34
2	A	1301	Q6K	C13-N35	10.21	1.49	1.34
2	A	1301	Q6K	C34-C28	9.81	1.54	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1202	Q6K	N35-C13-N12	-8.02	118.95	126.55
2	A	1301	Q6K	N35-C13-N12	-7.46	119.48	126.55
2	B	1202	Q6K	C36-N35-C13	5.75	120.55	115.45
2	A	1301	Q6K	C36-N35-C13	5.50	120.33	115.45
2	B	1202	Q6K	C11-N12-C13	5.49	121.21	116.69

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1301	Q6K	C24-C23-N21-C22
2	B	1202	Q6K	C19-C20-N21-C23
5	D	1102	ANP	PG-N3B-PB-O1B
5	D	1102	ANP	PA-O3A-PB-O1B
5	D	1102	ANP	PA-O3A-PB-O2B

There are no ring outliers.

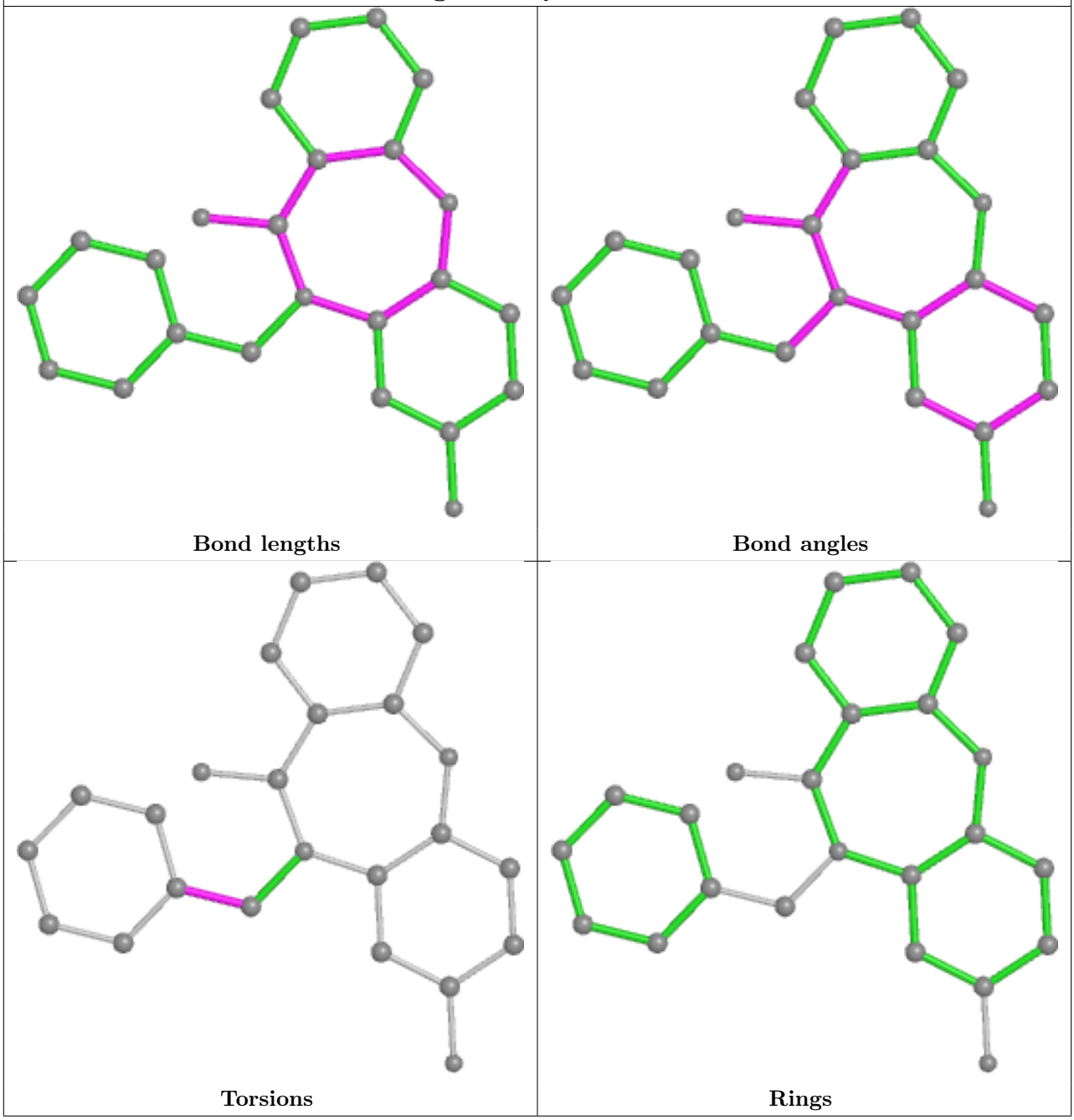
5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1302	NQ1	1	0
2	A	1301	Q6K	1	0
3	D	1103	NQ1	1	0
3	B	1201	NQ1	1	0
2	B	1202	Q6K	2	0

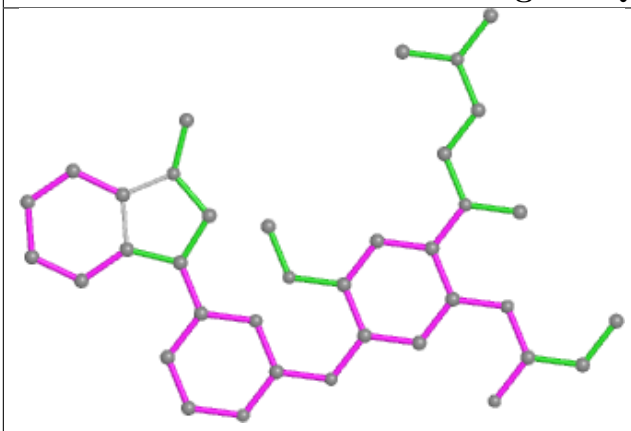
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

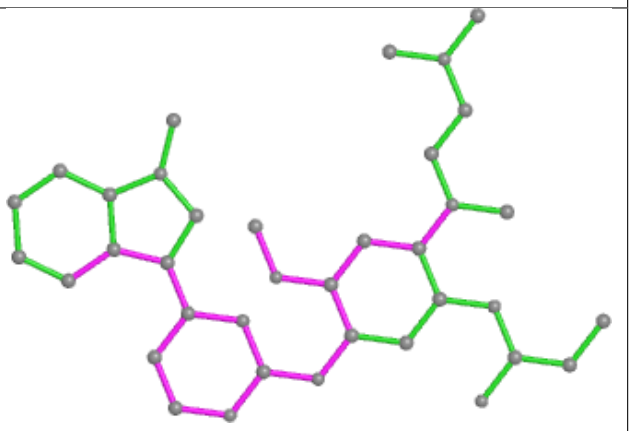
Ligand NQ1 A 1302



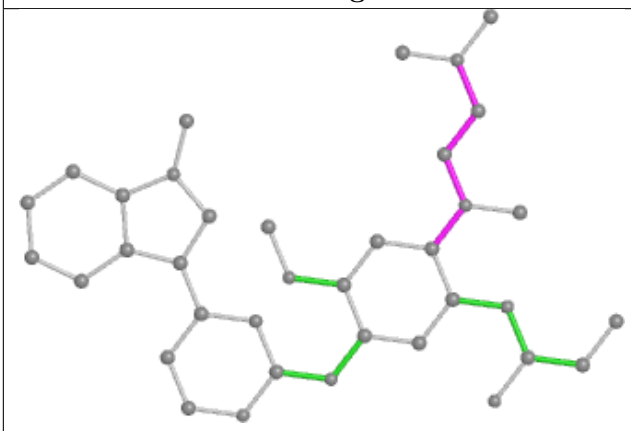
Ligand Q6K A 1301



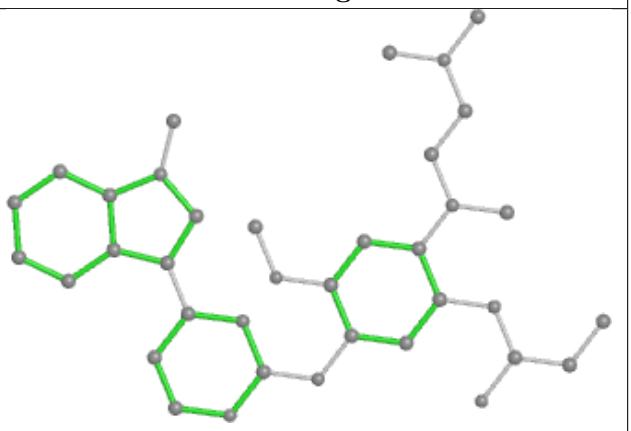
Bond lengths



Bond angles

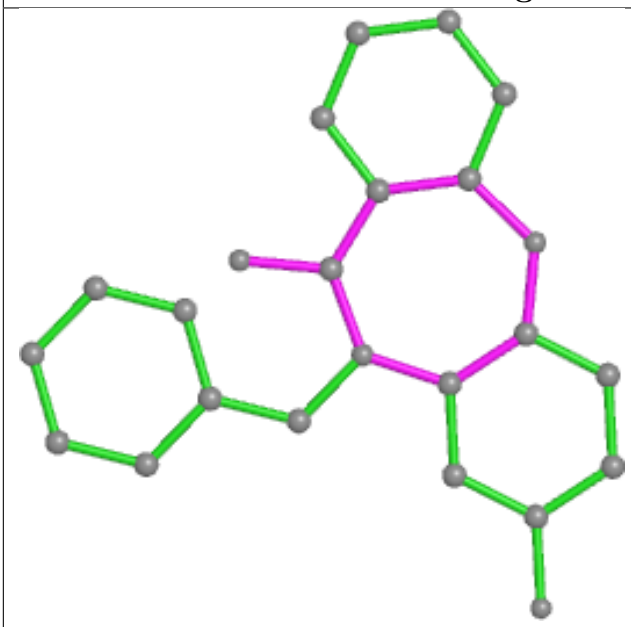


Torsions

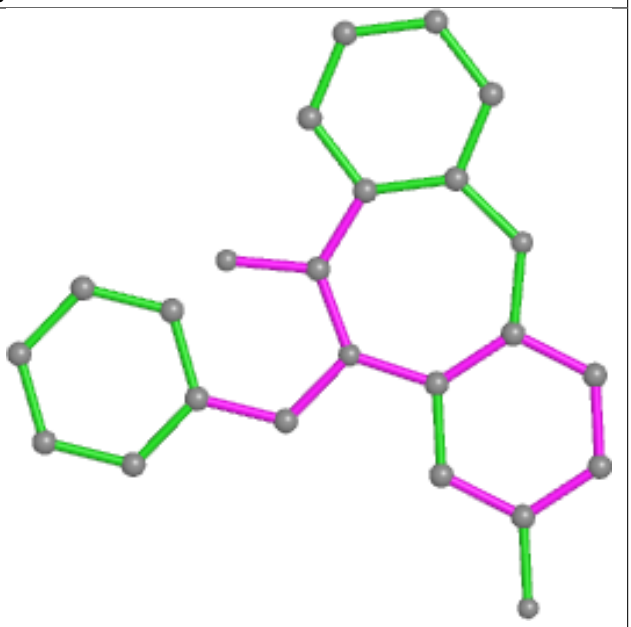


Rings

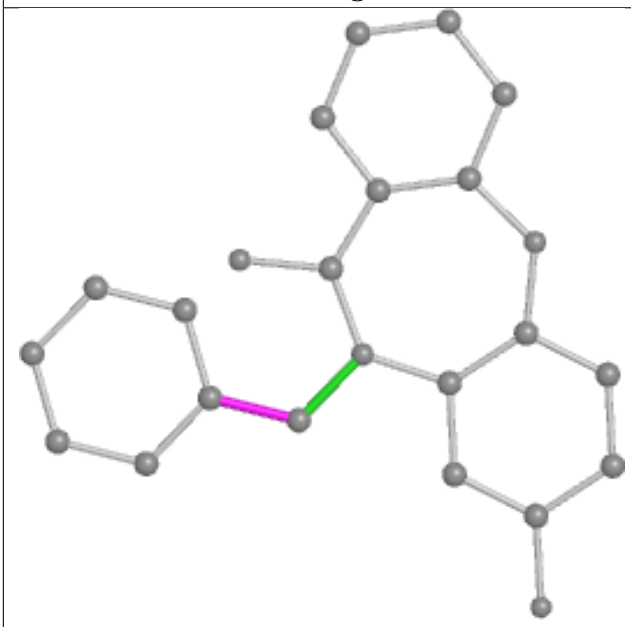
Ligand NQ1 D 1103



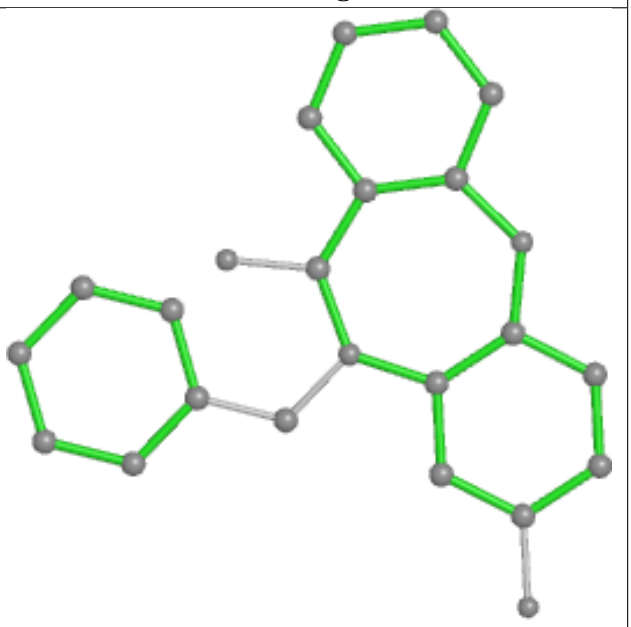
Bond lengths



Bond angles

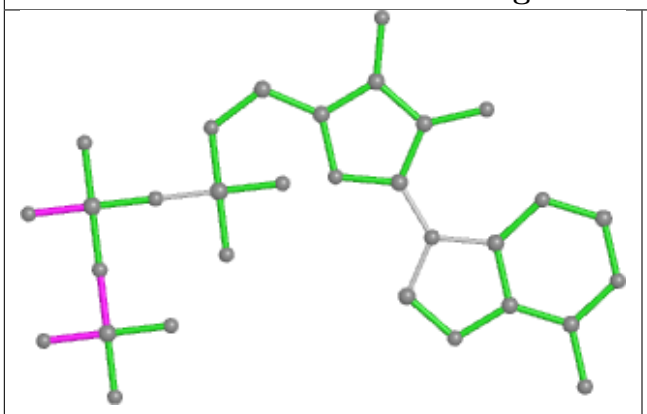


Torsions

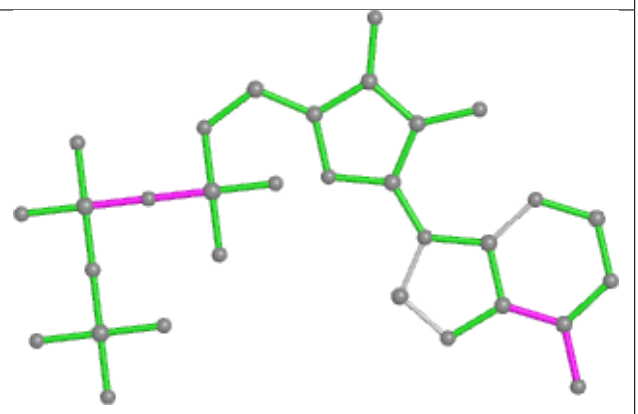


Rings

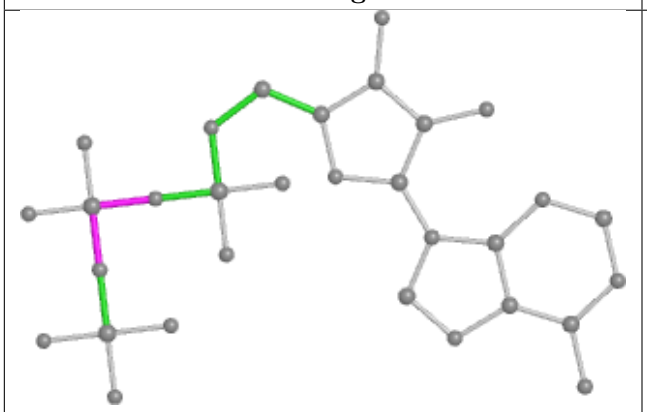
Ligand ANP D 1102



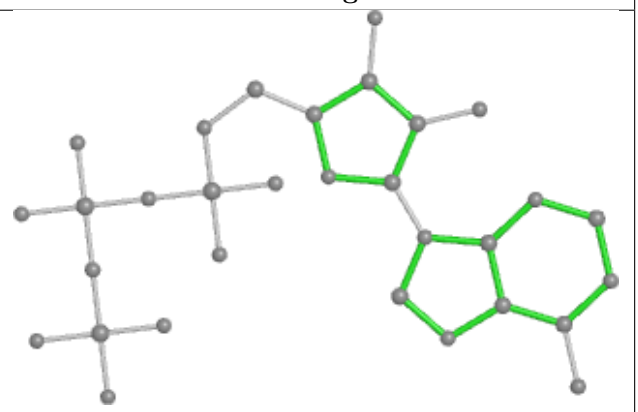
Bond lengths



Bond angles

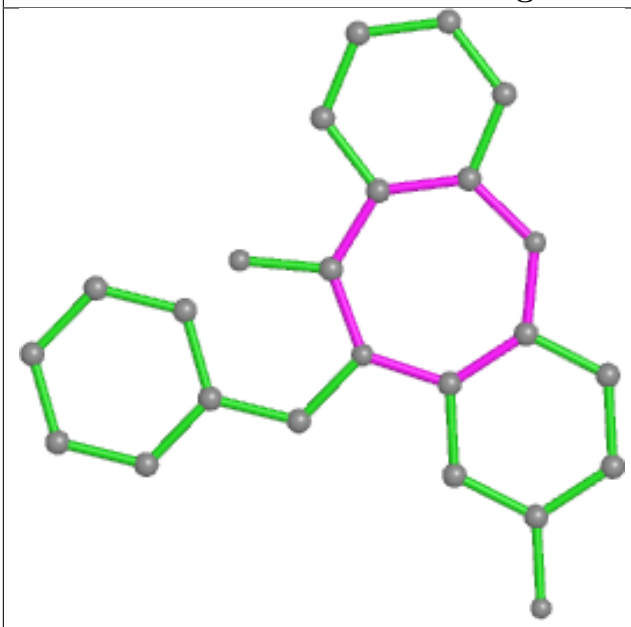


Torsions

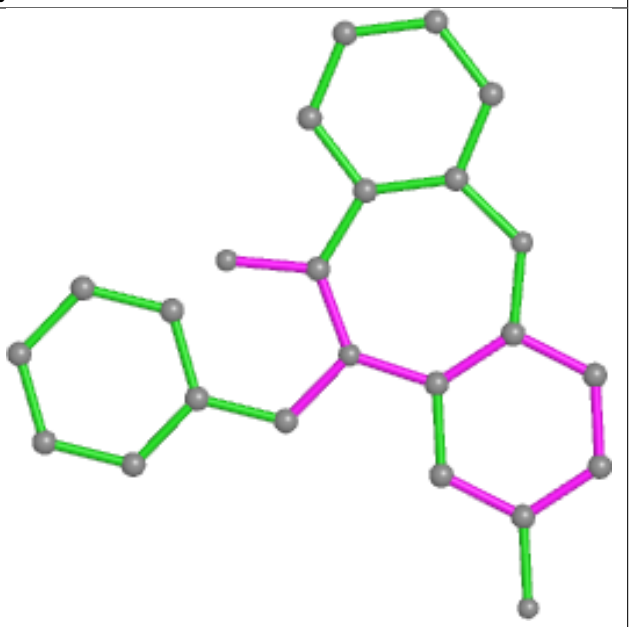


Rings

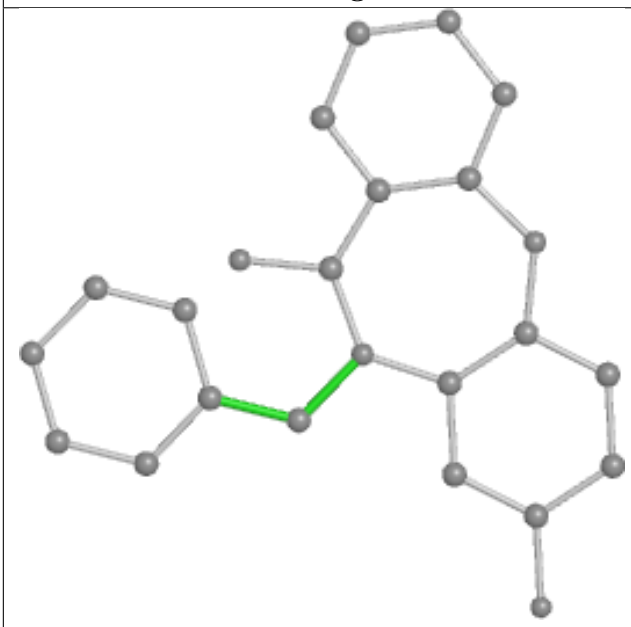
Ligand NQ1 B 1201



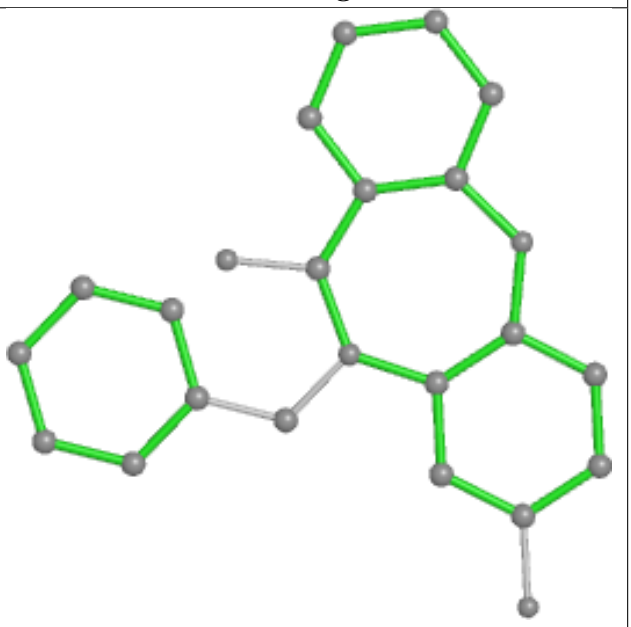
Bond lengths



Bond angles

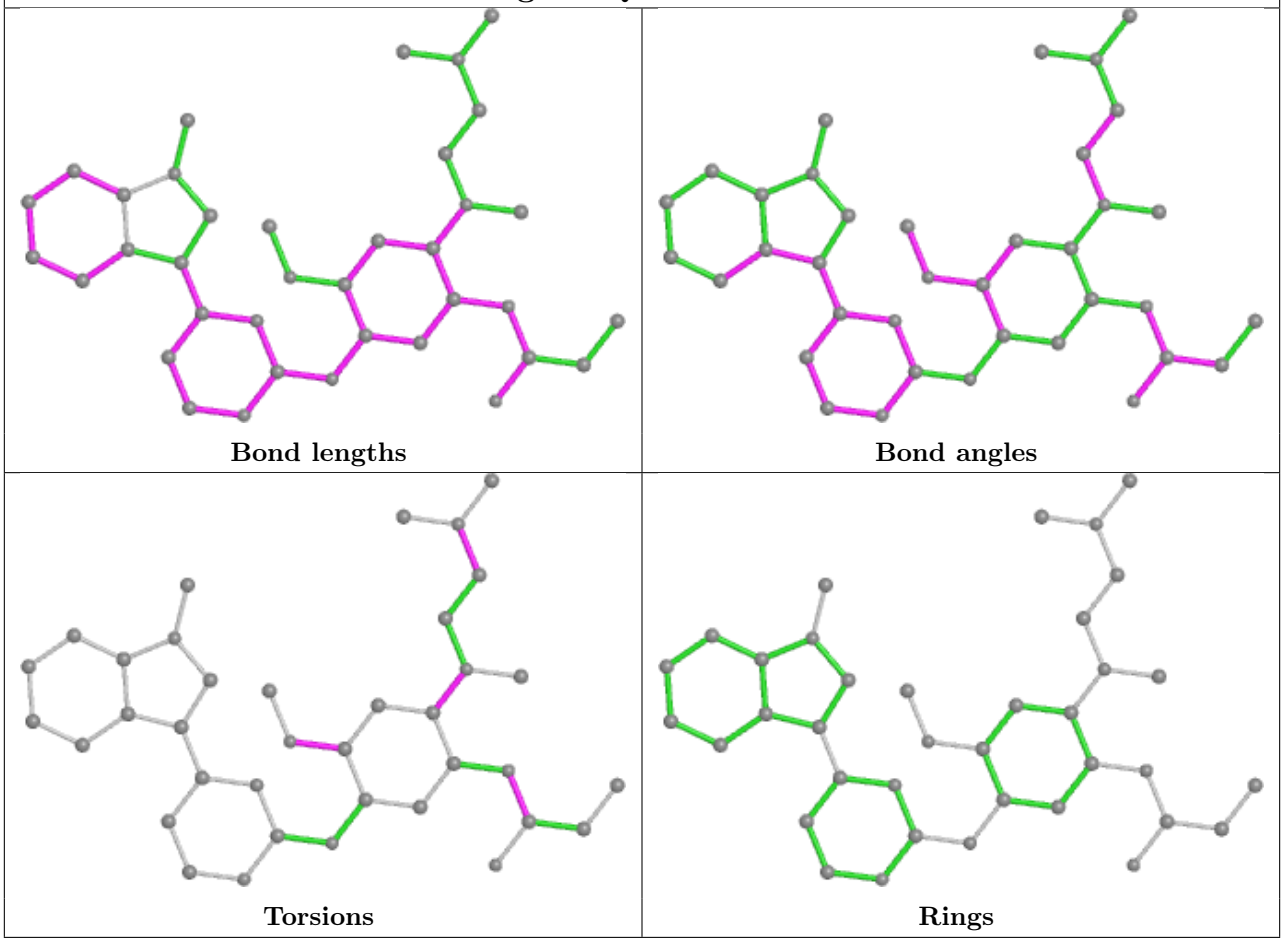


Torsions



Rings

Ligand Q6K B 1202



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	293/328 (89%)	0.16	10 (3%)	45	47	22, 35, 59, 86	0
1	B	292/328 (89%)	0.24	15 (5%)	28	28	22, 37, 67, 112	0
1	C	302/328 (92%)	0.31	18 (5%)	21	22	20, 37, 70, 106	0
1	D	300/328 (91%)	0.36	23 (7%)	13	13	23, 39, 74, 97	0
All	All	1187/1312 (90%)	0.27	66 (5%)	24	25	20, 37, 67, 112	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1011	VAL	5.2
1	C	1008	ASP	5.2
1	C	1010	VAL	4.8
1	B	751	THR	4.8
1	B	753	PRO	4.8

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)

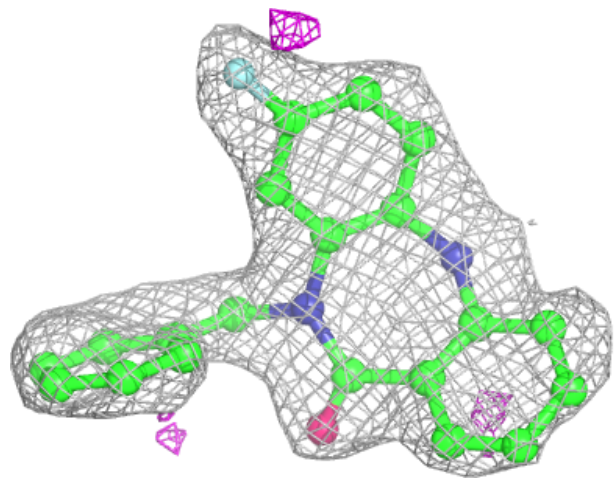
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

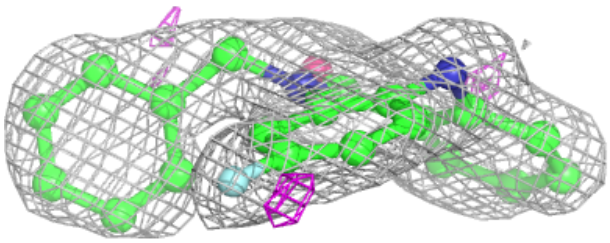
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MG	D	1101	1/1	0.84	0.05	36,36,36,36	0
3	NQ1	D	1103	24/24	0.86	0.21	33,42,50,53	0
2	Q6K	B	1202	37/37	0.88	0.19	25,39,75,79	0
3	NQ1	B	1201	24/24	0.90	0.15	34,42,50,54	0
3	NQ1	A	1302	24/24	0.93	0.13	25,31,42,47	0
2	Q6K	A	1301	37/37	0.94	0.14	18,32,45,51	0
5	ANP	D	1102	31/31	0.95	0.09	26,37,43,47	0

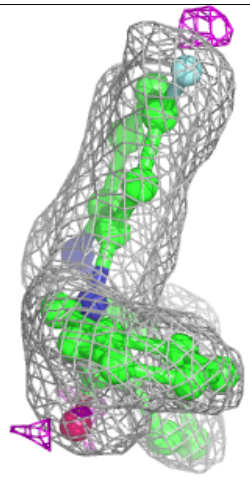
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NQ1 D 1103:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

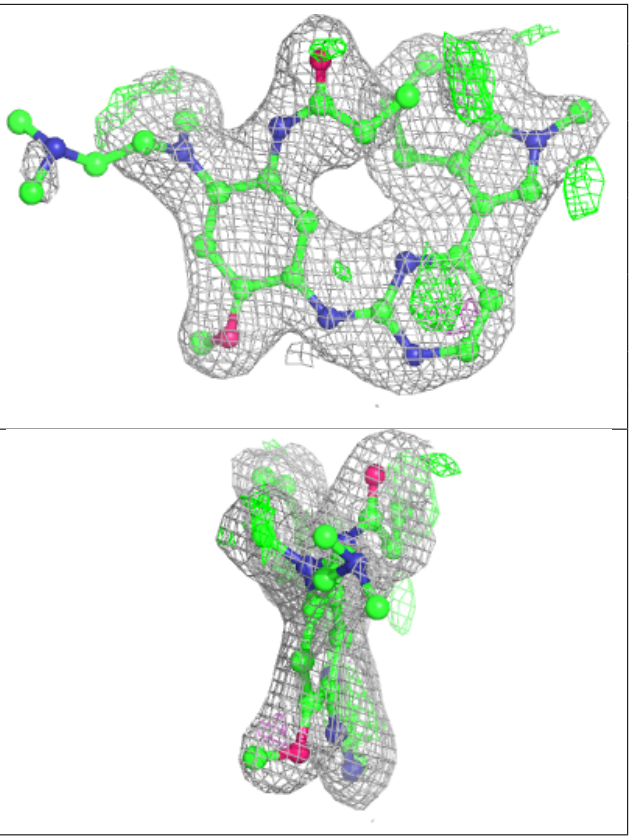






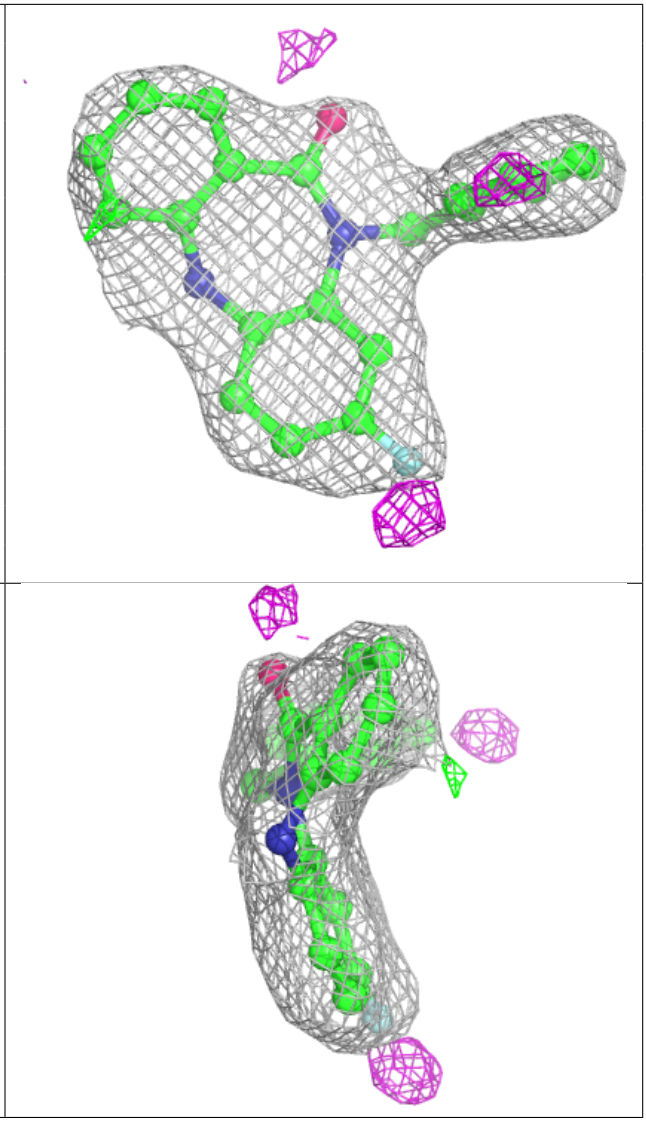
Electron density around Q6K B 1202:

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



Electron density around NQ1 B 1201:

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



Electron density around NQ1 A 1302:

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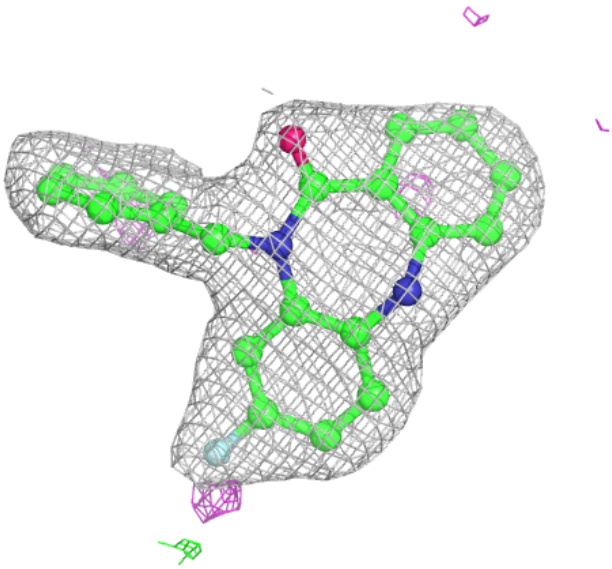
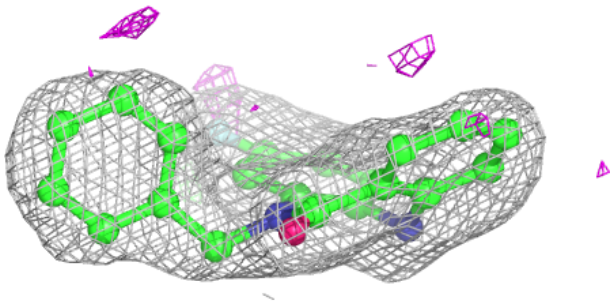
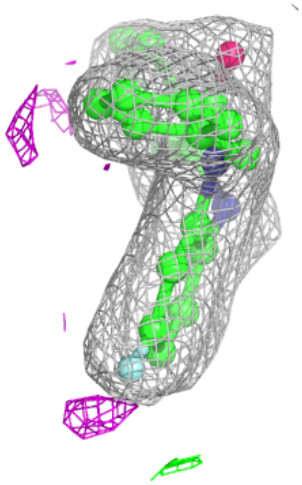
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around Q6K A 1301:

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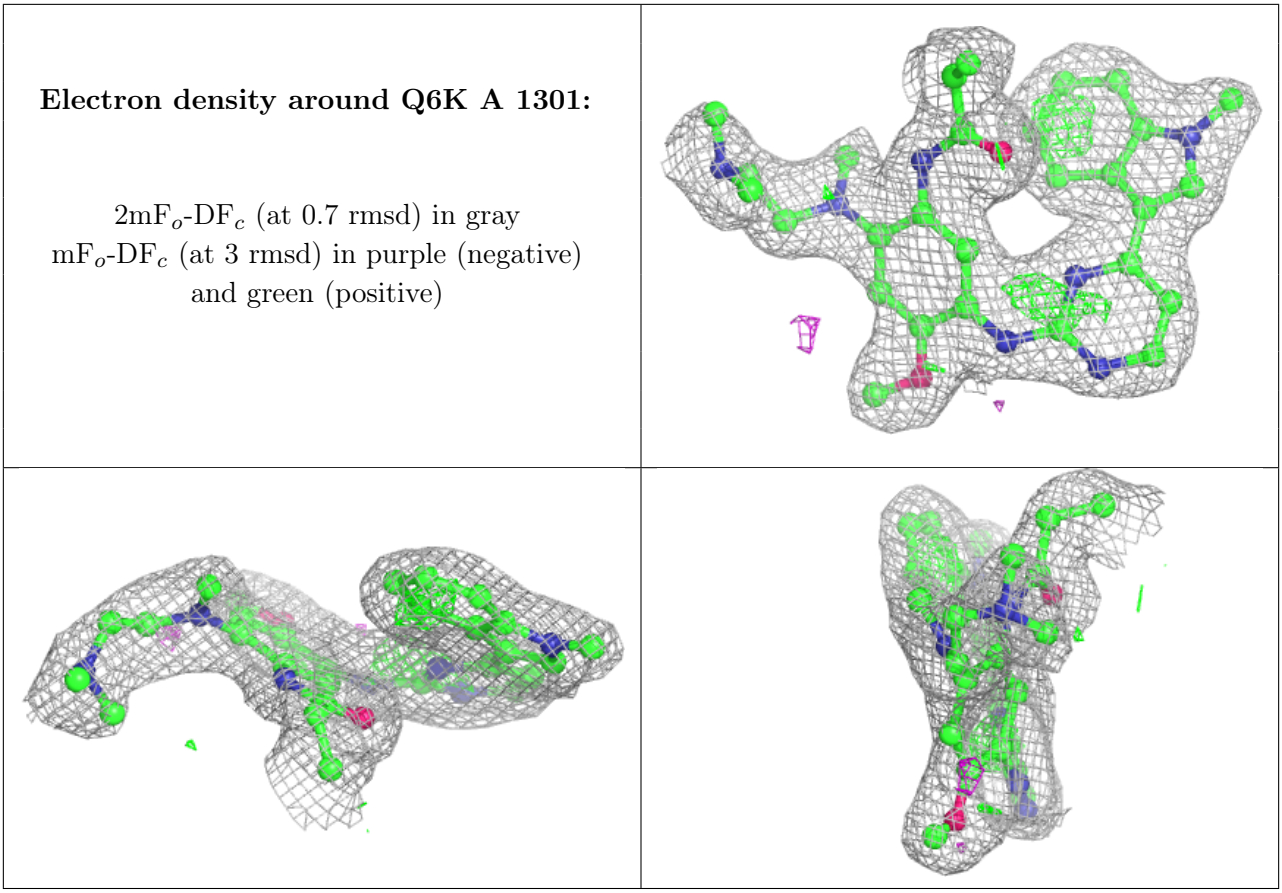
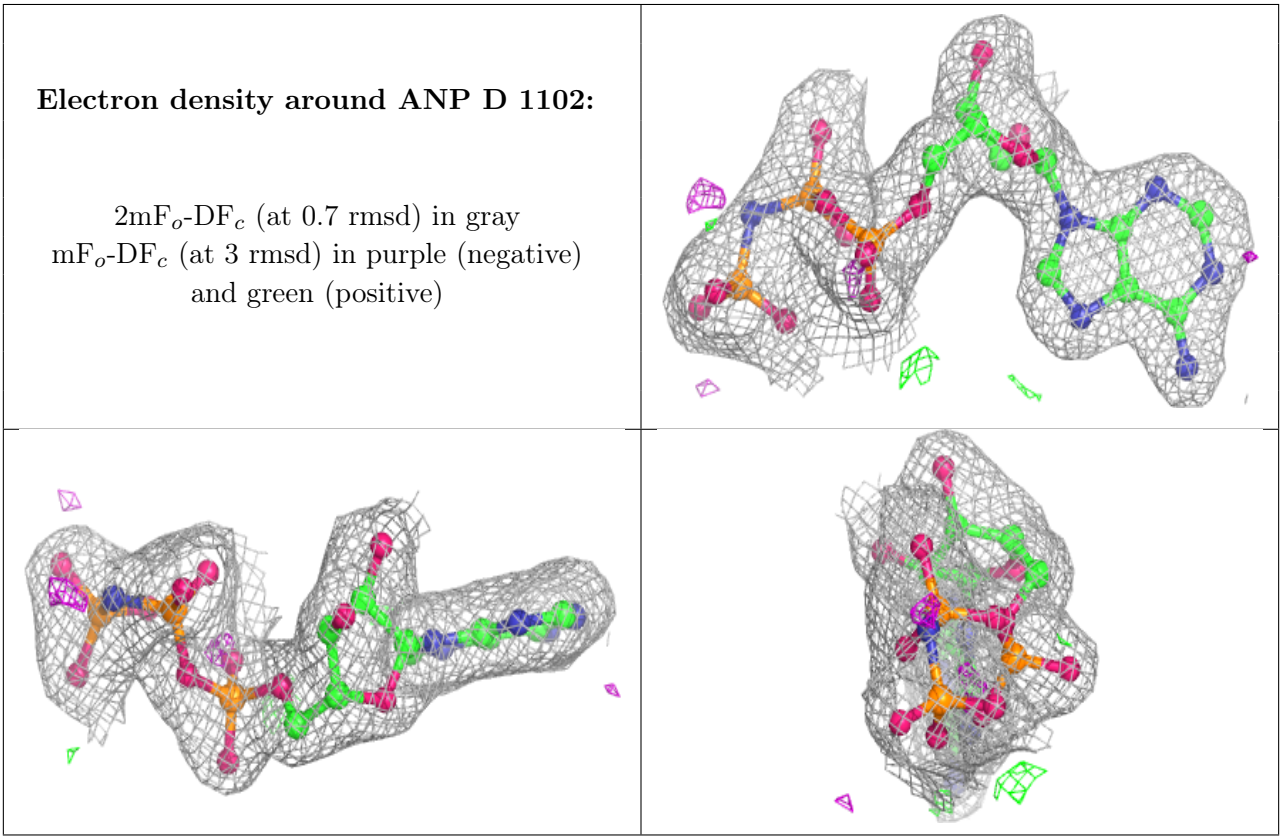
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ANP D 1102:

$2mF_o$-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.