



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2023 – 11:27 PM EDT

PDB ID : 7LTX
Title : EGFR (T790M/V948R) in complex with quinazolinone allosteric inhibitor
Authors : Beyett, T.S.; Eck, M.J.
Deposited on : 2021-02-20
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-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

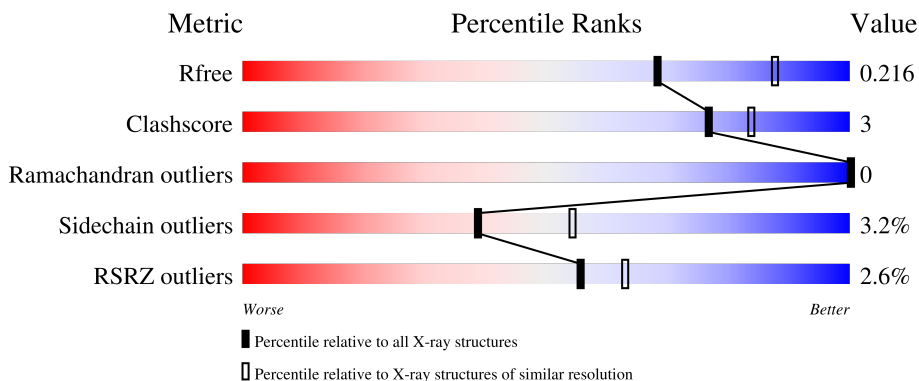
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	331	 3% 77% 11% 12%
1	B	331	 2% 82% 6% 11%
1	C	331	 2% 82% 6% 12%
1	D	331	 2% 76% 12% 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9883 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.

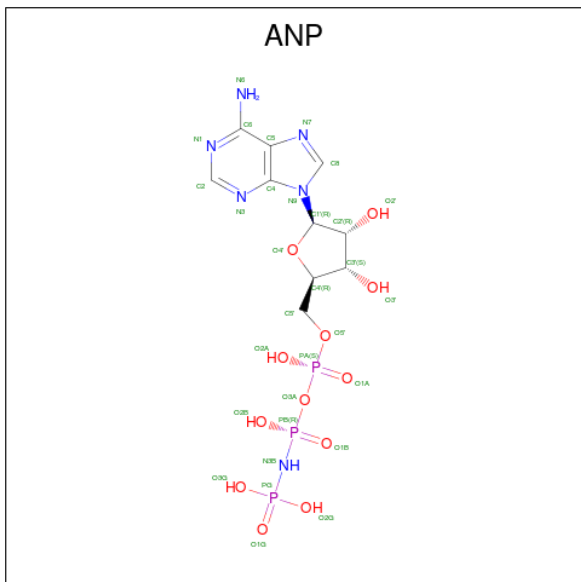
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	292	2355	1512	401	423	19	0	0	0
1	B	293	2364	1518	403	424	19	0	0	0
1	C	292	2355	1512	401	423	19	0	0	0
1	D	293	2364	1518	403	424	19	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	692	GLY	-	expression tag	UNP P00533
A	693	SER	-	expression tag	UNP P00533
A	694	THR	-	expression tag	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
B	692	GLY	-	expression tag	UNP P00533
B	693	SER	-	expression tag	UNP P00533
B	694	THR	-	expression tag	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533
C	692	GLY	-	expression tag	UNP P00533
C	693	SER	-	expression tag	UNP P00533
C	694	THR	-	expression tag	UNP P00533
C	790	MET	THR	engineered mutation	UNP P00533
C	948	ARG	VAL	engineered mutation	UNP P00533
D	692	GLY	-	expression tag	UNP P00533
D	693	SER	-	expression tag	UNP P00533
D	694	THR	-	expression tag	UNP P00533
D	790	MET	THR	engineered mutation	UNP P00533
D	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).

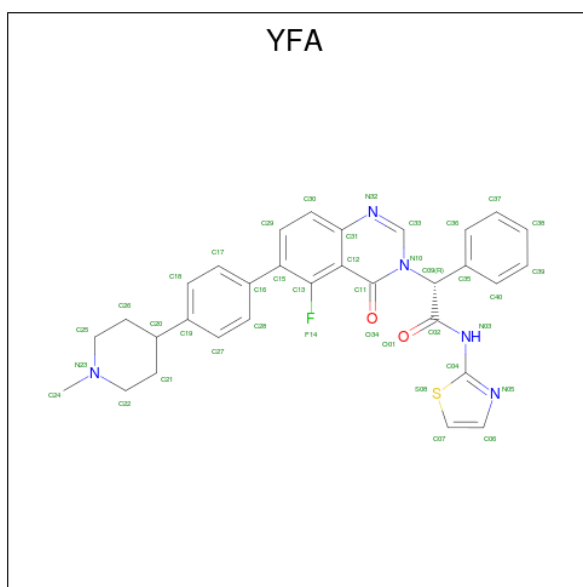


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

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

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

- Molecule 4 is (2R)-2-{5-fluoro-6-[4-(1-methylpiperidin-4-yl)phenyl]-4-oxoquinazolin-3(4H)-yl}-2-phenyl-N-(1,3-thiazol-2-yl)acetamide (three-letter code: YFA) (formula: C₃₁H₂₈FN₅O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
4	A	1	Total	C	F	N	O	S	0	0
			40	31	1	5	2	1		
4	B	1	Total	C	F	N	O	S	0	0
			40	31	1	5	2	1		
4	C	1	Total	C	F	N	O	S	0	0
			40	31	1	5	2	1		
4	D	1	Total	C	F	N	O	S	0	0
			40	31	1	5	2	1		

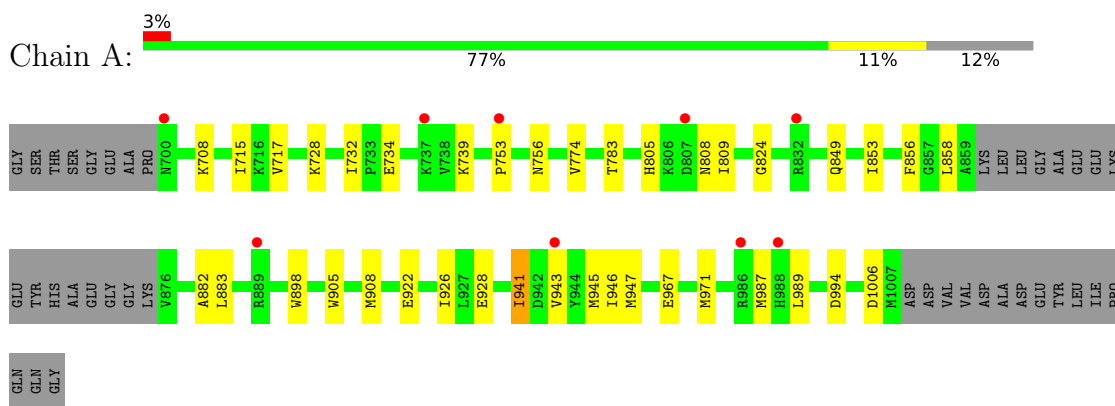
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	29	Total	O	0	0
			29	29		
5	B	42	Total	O	0	0
			42	42		
5	C	43	Total	O	0	0
			43	43		
5	D	43	Total	O	0	0
			43	43		

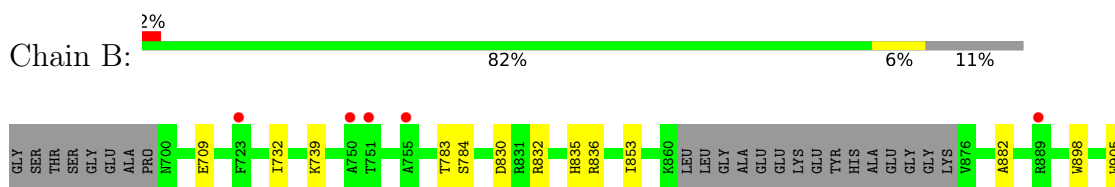
3 Residue-property plots [i](#)

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.

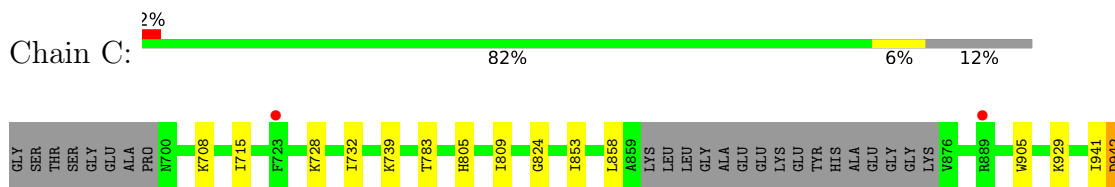
- Molecule 1: Epidermal growth factor receptor



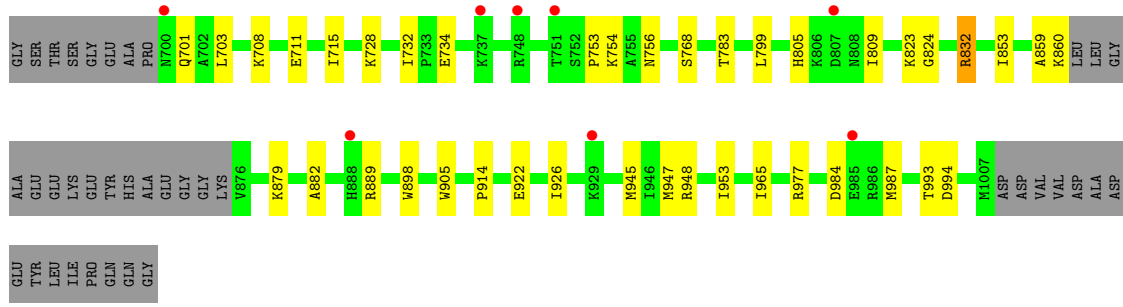
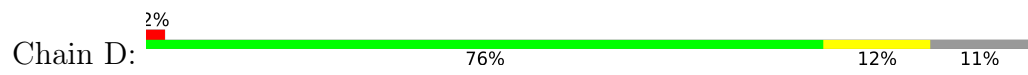
- Molecule 1: Epidermal growth factor receptor



- Molecule 1: Epidermal growth factor receptor



- Molecule 1: Epidermal growth factor receptor



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.89Å 73.49Å 150.22Å 90.00° 99.63° 90.00°	Depositor
Resolution (Å)	148.10 – 2.30 148.10 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.7 (148.10-2.30) 98.7 (148.10-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.186 , 0.216 0.189 , 0.216	Depositor DCC
R_{free} test set	2600 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	44.5	Xtrriage
Anisotropy	0.206	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.008 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9883	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.41	0/2407	0.65	2/3255 (0.1%)
1	B	0.42	0/2416	0.64	0/3266
1	C	0.45	0/2407	0.62	0/3255
1	D	0.44	0/2416	0.61	0/3266
All	All	0.43	0/9646	0.63	2/13042 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1006	ASP	CB-CG-OD1	-6.36	112.57	118.30
1	A	945	MET	CB-CG-SD	-5.98	94.45	112.40

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	2355	0	2397	16	0
1	B	2364	0	2410	11	0
1	C	2355	0	2397	9	0
1	D	2364	0	2410	21	0
2	A	31	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	31	0	13	0	0
2	C	31	0	13	0	0
2	D	31	0	13	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	40	0	0	1	0
4	B	40	0	0	0	0
4	C	40	0	0	1	0
4	D	40	0	0	1	0
5	A	29	0	0	0	0
5	B	42	0	0	0	0
5	C	43	0	0	0	0
5	D	43	0	0	1	0
All	All	9883	0	9666	59	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.

All (59) 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:A:905:TRP:HD1	1:A:947:MET:HE1	1.49	0.78
1:B:783:THR:HG22	1:B:784:SER:H	1.47	0.77
1:A:717:VAL:HG11	1:B:830:ASP:HB3	1.68	0.74
1:D:905:TRP:HD1	1:D:947:MET:HE1	1.54	0.71
1:B:732:ILE:HD12	1:B:739:LYS:HG2	1.78	0.64
1:A:905:TRP:CD1	1:A:947:MET:HE1	2.33	0.62
1:D:859:ALA:O	1:D:860:LYS:HB2	2.03	0.57
1:D:905:TRP:CD1	1:D:947:MET:HE1	2.37	0.56
1:A:732:ILE:HD12	1:A:739:LYS:HG2	1.88	0.55
1:B:905:TRP:HD1	1:B:947:MET:HE1	1.71	0.55
1:C:905:TRP:HD1	1:C:947:MET:HE1	1.73	0.53
1:D:805:HIS:HB2	1:D:809:ILE:HD11	1.93	0.51
1:B:981:ILE:O	1:B:984:ASP:HB2	2.10	0.51
1:B:905:TRP:CD1	1:B:947:MET:HE1	2.46	0.50
1:A:882:ALA:HA	1:A:898:TRP:CD2	2.47	0.50
1:D:703:LEU:HD13	1:D:768:SER:HA	1.95	0.49
1:A:967:GLU:HG3	1:A:971:MET:HE2	1.95	0.49
1:D:945:MET:HE1	1:D:948:ARG:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:824:GLY:HA3	1:C:853:ILE:HD12	1.96	0.47
1:B:961:PHE:HA	1:B:964:LEU:HD12	1.96	0.47
1:D:882:ALA:HA	1:D:898:TRP:CD2	2.49	0.47
1:D:984:ASP:HA	1:D:987:MET:HG2	1.96	0.47
1:C:905:TRP:CD1	1:C:947:MET:HE1	2.49	0.47
1:A:824:GLY:HA3	1:A:853:ILE:HD12	1.97	0.47
4:D:1103:YFA:O01	4:D:1103:YFA:S08	2.73	0.47
1:D:753:PRO:HA	1:D:756:ASN:HB2	1.97	0.46
1:A:715:ILE:HD11	1:A:728:LYS:HE2	1.97	0.46
1:B:882:ALA:HA	1:B:898:TRP:CD2	2.50	0.46
1:D:805:HIS:O	1:D:809:ILE:HG13	2.15	0.46
1:D:823:LYS:HA	1:D:965:ILE:HD11	1.97	0.46
1:C:942:ASP:N	1:C:942:ASP:OD1	2.49	0.45
1:D:715:ILE:HD11	1:D:728:LYS:HE2	1.98	0.45
1:D:945:MET:CE	1:D:945:MET:HA	2.45	0.45
1:C:732:ILE:HD12	1:C:739:LYS:HG2	1.99	0.45
1:D:824:GLY:HA3	1:D:853:ILE:HD12	1.99	0.45
1:D:832:ARG:HA	1:D:832:ARG:HD3	1.42	0.44
1:D:922:GLU:O	1:D:926:ILE:HG23	2.16	0.44
1:C:715:ILE:HD11	1:C:728:LYS:HE2	1.99	0.44
1:A:941:ILE:HD13	1:A:941:ILE:HA	1.83	0.44
1:B:709:GLU:OE2	1:B:783:THR:HG23	2.17	0.44
4:A:1103:YFA:O01	4:A:1103:YFA:S08	2.75	0.43
1:D:879:LYS:HD3	1:D:914:PRO:O	2.18	0.43
1:D:708:LYS:O	1:D:711:GLU:HG2	2.19	0.43
1:A:753:PRO:HA	1:A:756:ASN:HB2	2.00	0.43
1:A:922:GLU:O	1:A:926:ILE:HG23	2.17	0.42
1:B:783:THR:HG22	1:B:784:SER:N	2.24	0.42
1:D:889:ARG:HD2	1:D:889:ARG:HA	1.76	0.42
1:A:708:LYS:HE3	1:A:708:LYS:HB3	1.88	0.42
1:A:805:HIS:O	1:A:809:ILE:HG13	2.19	0.42
4:C:1103:YFA:S08	4:C:1103:YFA:O01	2.78	0.42
1:D:799:LEU:HD22	5:D:1205:HOH:O	2.19	0.41
1:C:949:LYS:O	1:C:952:MET:HE2	2.20	0.41
1:C:708:LYS:HE3	1:C:708:LYS:HB3	1.95	0.41
1:D:905:TRP:HB2	1:D:947:MET:HE3	2.03	0.41
1:A:774:VAL:HG13	1:A:856:PHE:CE2	2.55	0.40
1:C:805:HIS:O	1:C:809:ILE:HG13	2.20	0.40
1:A:883:LEU:HD21	1:A:928:GLU:HG2	2.04	0.40
1:A:943:VAL:HA	1:A:946:ILE:HD12	2.03	0.40
1:B:835:HIS:O	1:B:836:ARG:HB2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	288/331 (87%)	281 (98%)	7 (2%)	0	100	100
1	B	289/331 (87%)	281 (97%)	8 (3%)	0	100	100
1	C	288/331 (87%)	283 (98%)	5 (2%)	0	100	100
1	D	289/331 (87%)	280 (97%)	9 (3%)	0	100	100
All	All	1154/1324 (87%)	1125 (98%)	29 (2%)	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	261/290 (90%)	251 (96%)	10 (4%)	33	47
1	B	262/290 (90%)	258 (98%)	4 (2%)	65	79
1	C	261/290 (90%)	252 (97%)	9 (3%)	37	51
1	D	262/290 (90%)	252 (96%)	10 (4%)	33	47
All	All	1046/1160 (90%)	1013 (97%)	33 (3%)	39	54

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	734	GLU
1	A	783	THR
1	A	808	ASN
1	A	849	GLN
1	A	858	LEU
1	A	908	MET
1	A	941	ILE
1	A	987	MET
1	A	989	LEU
1	A	994	ASP
1	B	832	ARG
1	B	853	ILE
1	B	942	ASP
1	B	994	ASP
1	C	783	THR
1	C	858	LEU
1	C	929	LYS
1	C	941	ILE
1	C	942	ASP
1	C	987	MET
1	C	989	LEU
1	C	994	ASP
1	C	1007	MET
1	D	701	GLN
1	D	732	ILE
1	D	734	GLU
1	D	754	LYS
1	D	783	THR
1	D	832	ARG
1	D	953	ILE
1	D	977	ARG
1	D	993	THR
1	D	994	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA

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 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
2	ANP	A	1101	3	29,33,33	1.23	5 (17%)	31,52,52	1.22	4 (12%)
4	YFA	A	1103	-	42,45,45	1.85	11 (26%)	48,64,64	3.15	26 (54%)
4	YFA	D	1103	-	42,45,45	1.91	11 (26%)	48,64,64	3.58	26 (54%)
2	ANP	C	1101	3	29,33,33	1.20	4 (13%)	31,52,52	1.21	4 (12%)
2	ANP	D	1101	3	29,33,33	1.19	4 (13%)	31,52,52	1.19	4 (12%)
2	ANP	B	1101	3	29,33,33	1.20	4 (13%)	31,52,52	1.22	5 (16%)
4	YFA	C	1103	-	42,45,45	2.00	11 (26%)	48,64,64	3.13	32 (66%)
4	YFA	B	1103	-	42,45,45	1.85	8 (19%)	48,64,64	3.18	24 (50%)

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	ANP	A	1101	3	-	1/14/38/38	0/3/3/3
4	YFA	A	1103	-	-	2/22/34/34	0/6/6/6
4	YFA	D	1103	-	-	0/22/34/34	0/6/6/6
2	ANP	C	1101	3	-	4/14/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ANP	D	1101	3	-	4/14/38/38	0/3/3/3
2	ANP	B	1101	3	-	4/14/38/38	0/3/3/3
4	YFA	C	1103	-	-	0/22/34/34	0/6/6/6
4	YFA	B	1103	-	-	0/22/34/34	0/6/6/6

All (58) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1103	YFA	C11-N10	5.69	1.47	1.39
4	C	1103	YFA	C11-N10	5.59	1.47	1.39
4	A	1103	YFA	C35-C09	5.06	1.58	1.52
4	B	1103	YFA	C12-C13	4.99	1.47	1.38
4	A	1103	YFA	C11-N10	4.68	1.45	1.39
4	C	1103	YFA	C35-C09	4.58	1.57	1.52
4	D	1103	YFA	C35-C09	4.55	1.57	1.52
4	C	1103	YFA	F14-C13	-4.42	1.28	1.35
4	D	1103	YFA	C12-C13	4.30	1.46	1.38
4	C	1103	YFA	C15-C13	4.12	1.44	1.39
4	D	1103	YFA	F14-C13	-4.05	1.28	1.35
4	A	1103	YFA	F14-C13	-4.04	1.28	1.35
4	D	1103	YFA	C09-C02	-4.02	1.50	1.54
4	B	1103	YFA	F14-C13	-3.84	1.29	1.35
4	C	1103	YFA	C09-C02	3.81	1.58	1.54
4	B	1103	YFA	C15-C13	3.55	1.44	1.39
4	A	1103	YFA	C22-N23	3.46	1.53	1.46
4	D	1103	YFA	C11-N10	3.20	1.43	1.39
4	C	1103	YFA	C12-C13	3.19	1.44	1.38
4	D	1103	YFA	C22-N23	3.07	1.53	1.46
2	C	1101	ANP	PG-O2G	-3.03	1.48	1.56
4	A	1103	YFA	C24-N23	3.03	1.53	1.46
2	A	1101	ANP	PG-O3G	-3.01	1.48	1.56
4	D	1103	YFA	C25-N23	2.96	1.52	1.46
2	D	1101	ANP	PG-O3G	-2.91	1.48	1.56
2	B	1101	ANP	PG-O3G	-2.89	1.49	1.56
4	A	1103	YFA	C12-C13	2.84	1.43	1.38
2	C	1101	ANP	PG-O3G	-2.78	1.49	1.56
4	A	1103	YFA	C21-C20	2.72	1.60	1.53
4	A	1103	YFA	C02-N03	2.70	1.41	1.35
2	A	1101	ANP	PG-O2G	-2.68	1.49	1.56
4	C	1103	YFA	C15-C16	2.60	1.54	1.49
2	D	1101	ANP	PG-O2G	-2.60	1.49	1.56
2	B	1101	ANP	PG-O2G	-2.60	1.49	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1103	YFA	C15-C13	2.58	1.42	1.39
2	C	1101	ANP	PB-O2B	-2.57	1.49	1.56
2	B	1101	ANP	PB-O2B	-2.53	1.49	1.56
2	D	1101	ANP	PB-O2B	-2.48	1.50	1.56
4	B	1103	YFA	C25-N23	2.47	1.51	1.46
2	A	1101	ANP	PB-O2B	-2.47	1.50	1.56
2	B	1101	ANP	PB-O1B	2.46	1.50	1.46
2	A	1101	ANP	PB-O1B	2.40	1.50	1.46
2	C	1101	ANP	PB-O1B	2.38	1.49	1.46
4	B	1103	YFA	C15-C16	2.38	1.53	1.49
2	D	1101	ANP	PB-O1B	2.33	1.49	1.46
4	B	1103	YFA	C31-N32	2.32	1.44	1.40
4	D	1103	YFA	C02-N03	2.31	1.40	1.35
4	A	1103	YFA	C09-C02	-2.31	1.51	1.54
2	A	1101	ANP	PG-O1G	2.24	1.49	1.46
4	B	1103	YFA	C18-C17	2.20	1.42	1.38
4	C	1103	YFA	C02-N03	2.17	1.40	1.35
4	D	1103	YFA	C31-N32	2.16	1.43	1.40
4	A	1103	YFA	C15-C13	2.15	1.42	1.39
4	C	1103	YFA	C21-C20	2.12	1.58	1.53
4	C	1103	YFA	C30-C31	2.07	1.43	1.39
4	A	1103	YFA	C36-C35	2.07	1.42	1.39
4	D	1103	YFA	C24-N23	2.03	1.51	1.46
4	C	1103	YFA	C18-C17	2.01	1.42	1.38

All (125) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1103	YFA	O34-C11-N10	-13.08	110.49	120.60
4	B	1103	YFA	O34-C11-N10	-12.44	110.98	120.60
4	A	1103	YFA	O34-C11-N10	-10.68	112.35	120.60
4	C	1103	YFA	O34-C11-N10	-9.43	113.31	120.60
4	D	1103	YFA	C25-N23-C22	9.12	122.28	109.52
4	D	1103	YFA	C25-C26-C20	-6.94	102.82	111.04
4	A	1103	YFA	C25-N23-C22	6.75	118.97	109.52
4	D	1103	YFA	C21-C20-C19	6.30	127.57	112.79
4	B	1103	YFA	C26-C20-C19	-6.19	98.29	112.79
4	D	1103	YFA	C30-C31-N32	6.10	125.84	118.35
4	C	1103	YFA	C30-C31-N32	5.95	125.66	118.35
4	A	1103	YFA	C26-C25-N23	5.82	119.02	111.22
4	A	1103	YFA	C30-C31-N32	5.49	125.10	118.35
4	B	1103	YFA	C30-C31-N32	5.28	124.83	118.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1103	YFA	C25-N23-C22	5.17	116.75	109.52
4	B	1103	YFA	C21-C20-C19	5.11	124.76	112.79
4	A	1103	YFA	C26-C20-C19	-5.06	100.93	112.79
4	A	1103	YFA	C21-C20-C19	5.02	124.56	112.79
4	C	1103	YFA	C26-C20-C19	-4.88	101.36	112.79
4	C	1103	YFA	C09-N10-C11	4.82	125.58	117.54
4	D	1103	YFA	C26-C20-C19	-4.73	101.71	112.79
4	C	1103	YFA	C22-C21-C20	4.54	116.41	111.04
4	B	1103	YFA	C17-C16-C15	4.37	127.98	120.91
4	D	1103	YFA	O01-C02-C09	-4.22	115.31	120.97
4	A	1103	YFA	C31-N32-C33	4.06	120.63	116.62
4	B	1103	YFA	C31-N32-C33	4.03	120.60	116.62
4	C	1103	YFA	C21-C20-C19	4.03	122.25	112.79
4	D	1103	YFA	C31-N32-C33	4.01	120.57	116.62
2	D	1101	ANP	O2B-PB-O1B	3.94	118.18	109.92
4	C	1103	YFA	C31-N32-C33	3.94	120.50	116.62
2	A	1101	ANP	O2B-PB-O1B	3.93	118.16	109.92
2	B	1101	ANP	O2B-PB-O1B	3.91	118.11	109.92
4	B	1103	YFA	O01-C02-C09	-3.91	115.74	120.97
4	C	1103	YFA	C17-C16-C15	3.87	127.19	120.91
4	B	1103	YFA	C27-C28-C16	3.86	126.70	121.13
4	A	1103	YFA	C09-N10-C11	3.86	123.99	117.54
2	C	1101	ANP	O2B-PB-O1B	3.86	118.01	109.92
4	B	1103	YFA	C27-C19-C18	-3.85	113.50	118.29
4	A	1103	YFA	O01-C02-C09	-3.76	115.94	120.97
4	C	1103	YFA	F14-C13-C12	-3.71	115.12	119.95
4	C	1103	YFA	C40-C35-C36	-3.64	113.75	118.29
4	D	1103	YFA	C17-C16-C15	3.60	126.74	120.91
4	A	1103	YFA	C27-C19-C18	-3.54	113.87	118.29
4	D	1103	YFA	C09-N10-C11	3.53	123.43	117.54
4	C	1103	YFA	C29-C15-C13	-3.43	111.27	115.77
4	C	1103	YFA	C25-C26-C20	-3.40	107.01	111.04
4	D	1103	YFA	C12-C31-N32	-3.33	117.81	122.54
4	C	1103	YFA	C27-C19-C18	-3.32	114.14	118.29
4	D	1103	YFA	C27-C19-C18	-3.31	114.16	118.29
4	C	1103	YFA	C12-C31-N32	-3.31	117.84	122.54
4	B	1103	YFA	C09-N10-C11	3.30	123.05	117.54
4	A	1103	YFA	C12-C31-N32	-3.26	117.90	122.54
4	B	1103	YFA	C31-C12-C11	-3.25	115.50	118.50
4	D	1103	YFA	C40-C35-C36	-3.24	114.25	118.29
4	D	1103	YFA	C02-C09-N10	3.24	114.05	110.48
4	C	1103	YFA	C28-C16-C17	-3.22	111.18	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1103	YFA	C28-C16-C17	-3.21	111.20	117.59
4	C	1103	YFA	C27-C28-C16	3.18	125.72	121.13
4	C	1103	YFA	C29-C15-C16	3.18	124.95	118.68
4	A	1103	YFA	C40-C35-C36	-3.16	114.34	118.29
4	B	1103	YFA	C29-C15-C13	-3.12	111.67	115.77
4	A	1103	YFA	C02-C09-N10	3.08	113.87	110.48
4	B	1103	YFA	C16-C15-C13	3.06	125.55	123.03
4	D	1103	YFA	C27-C28-C16	3.06	125.53	121.13
4	D	1103	YFA	C29-C15-C13	-3.02	111.80	115.77
2	D	1101	ANP	O2G-PG-O1G	-2.92	106.11	113.45
4	B	1103	YFA	C25-N23-C22	2.92	113.61	109.52
4	C	1103	YFA	C24-N23-C25	-2.86	106.38	110.66
4	A	1103	YFA	C29-C15-C16	2.85	124.30	118.68
4	C	1103	YFA	O01-C02-N03	-2.80	117.90	123.93
4	B	1103	YFA	C30-C29-C15	2.80	125.12	120.33
4	D	1103	YFA	C29-C15-C16	2.77	124.14	118.68
4	A	1103	YFA	C28-C16-C17	-2.76	112.08	117.59
4	B	1103	YFA	O01-C02-N03	-2.76	117.99	123.93
4	B	1103	YFA	C12-C31-N32	-2.75	118.63	122.54
4	D	1103	YFA	C28-C16-C17	-2.74	112.13	117.59
4	A	1103	YFA	C29-C15-C13	-2.70	112.22	115.77
4	B	1103	YFA	C40-C35-C36	-2.68	114.95	118.29
4	A	1103	YFA	F14-C13-C12	-2.67	116.46	119.95
4	D	1103	YFA	C31-C12-C11	-2.67	116.04	118.50
4	B	1103	YFA	C17-C18-C19	2.65	123.86	121.20
4	C	1103	YFA	C24-N23-C22	-2.65	106.70	110.66
4	D	1103	YFA	C30-C29-C15	2.63	124.83	120.33
2	B	1101	ANP	O2G-PG-O1G	-2.62	106.85	113.45
2	A	1101	ANP	O3A-PB-N3B	-2.61	99.36	106.59
4	A	1103	YFA	C18-C19-C20	2.59	127.85	121.11
4	C	1103	YFA	C26-C25-N23	2.59	114.70	111.22
2	A	1101	ANP	O2G-PG-O1G	-2.57	106.98	113.45
2	B	1101	ANP	O3A-PB-N3B	-2.57	99.46	106.59
4	A	1103	YFA	C30-C29-C15	2.57	124.73	120.33
4	A	1103	YFA	O01-C02-N03	-2.56	118.43	123.93
4	C	1103	YFA	C21-C22-N23	2.54	114.62	111.22
4	A	1103	YFA	C21-C22-N23	2.52	114.60	111.22
4	B	1103	YFA	C37-C36-C35	2.50	123.74	120.65
4	A	1103	YFA	C17-C16-C15	2.47	124.91	120.91
4	D	1103	YFA	O01-C02-N03	-2.43	118.69	123.93
4	C	1103	YFA	C18-C19-C20	2.37	127.26	121.11
2	D	1101	ANP	C5-C6-N6	2.36	123.94	120.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1103	YFA	C37-C36-C35	2.36	123.56	120.65
4	C	1103	YFA	O01-C02-C09	-2.34	117.83	120.97
4	A	1103	YFA	C27-C28-C16	2.34	124.50	121.13
4	C	1103	YFA	C39-C40-C35	2.34	123.54	120.65
4	D	1103	YFA	C17-C18-C19	2.33	123.54	121.20
4	C	1103	YFA	C26-C20-C21	2.30	114.36	109.56
4	C	1103	YFA	C30-C29-C15	2.30	124.27	120.33
4	D	1103	YFA	F14-C13-C12	-2.29	116.96	119.95
2	C	1101	ANP	O3A-PB-N3B	-2.28	100.27	106.59
4	A	1103	YFA	C17-C18-C19	2.27	123.49	121.20
2	A	1101	ANP	C5-C6-N6	2.27	123.80	120.35
4	B	1103	YFA	C26-C25-N23	-2.26	108.19	111.22
4	D	1103	YFA	C18-C19-C20	2.25	126.96	121.11
2	B	1101	ANP	C5-C6-N6	2.25	123.76	120.35
2	D	1101	ANP	O3A-PB-N3B	-2.24	100.37	106.59
4	D	1103	YFA	C37-C36-C35	2.24	123.41	120.65
2	C	1101	ANP	C5-C6-N6	2.23	123.74	120.35
4	C	1103	YFA	C35-C09-C02	-2.21	107.72	112.06
4	B	1103	YFA	F14-C13-C12	-2.21	117.06	119.95
2	C	1101	ANP	O2G-PG-O1G	-2.21	107.91	113.45
4	B	1103	YFA	C18-C19-C20	2.19	126.81	121.11
4	D	1103	YFA	C22-C21-C20	-2.19	108.44	111.04
4	C	1103	YFA	C17-C18-C19	2.18	123.39	121.20
2	B	1101	ANP	O3G-PG-O1G	-2.14	108.07	113.45
4	A	1103	YFA	C37-C36-C35	2.12	123.28	120.65
4	C	1103	YFA	C36-C35-C09	2.05	123.75	120.71
4	A	1103	YFA	C24-N23-C22	2.02	113.68	110.66

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	ANP	PG-N3B-PB-O3A
2	B	1101	ANP	PB-N3B-PG-O1G
2	B	1101	ANP	PA-O3A-PB-O1B
2	B	1101	ANP	PA-O3A-PB-O2B
2	C	1101	ANP	PB-N3B-PG-O1G
2	C	1101	ANP	PA-O3A-PB-O1B
2	D	1101	ANP	PB-N3B-PG-O1G
2	D	1101	ANP	PG-N3B-PB-O3A
2	D	1101	ANP	PA-O3A-PB-O1B
2	D	1101	ANP	PA-O3A-PB-O2B

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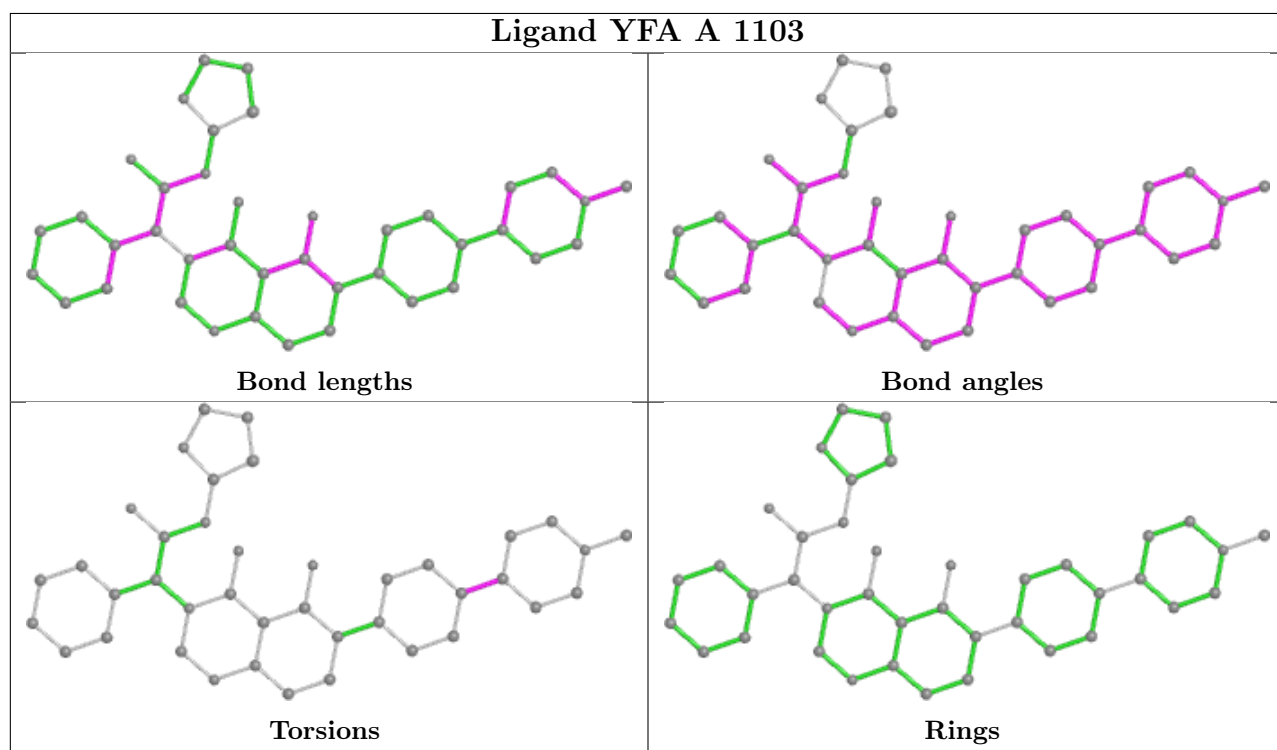
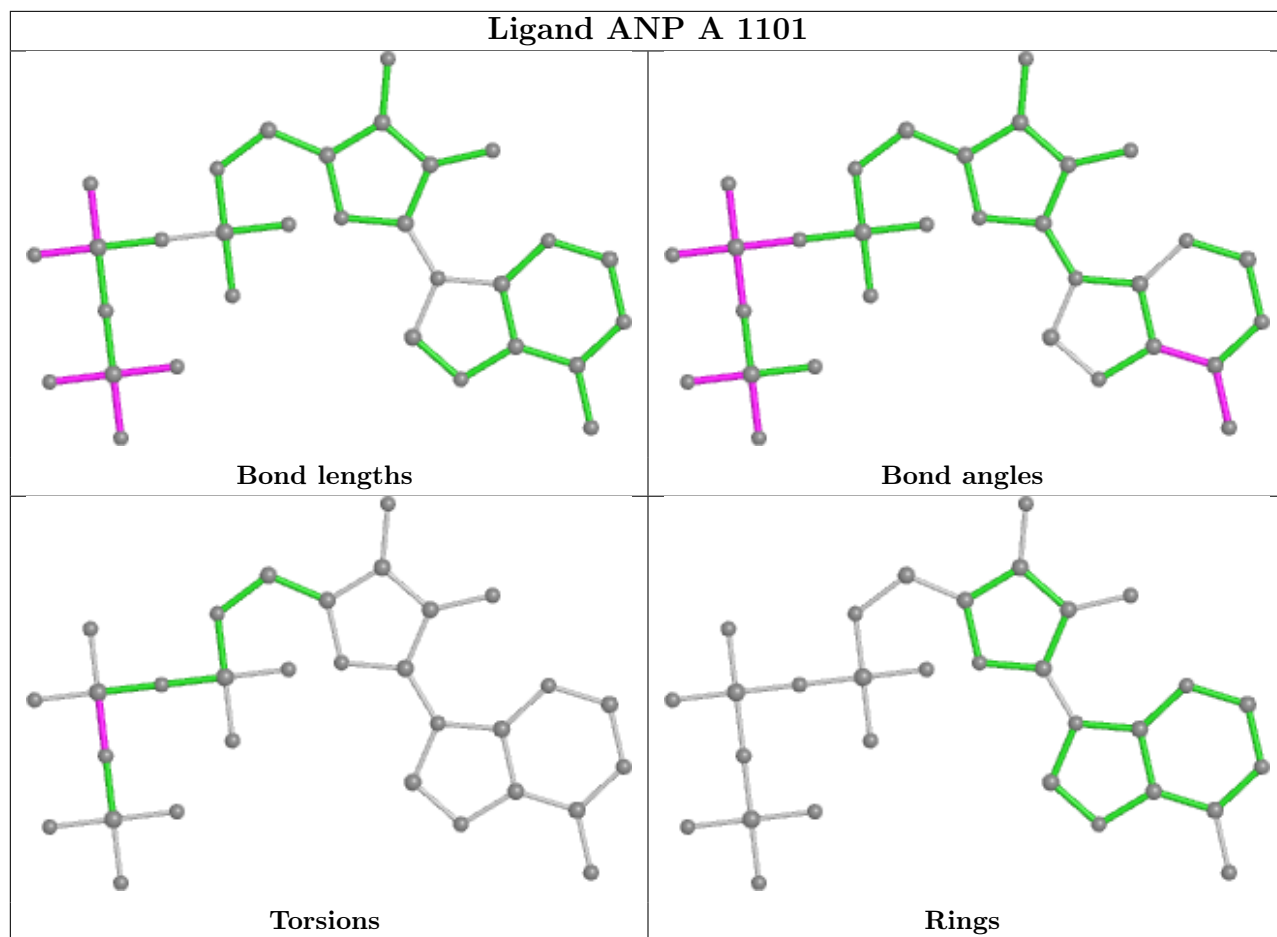
Mol	Chain	Res	Type	Atoms
2	B	1101	ANP	PG-N3B-PB-O3A
2	C	1101	ANP	PG-N3B-PB-O3A
2	C	1101	ANP	PA-O3A-PB-O2B
4	A	1103	YFA	C27-C19-C20-C21
4	A	1103	YFA	C18-C19-C20-C21

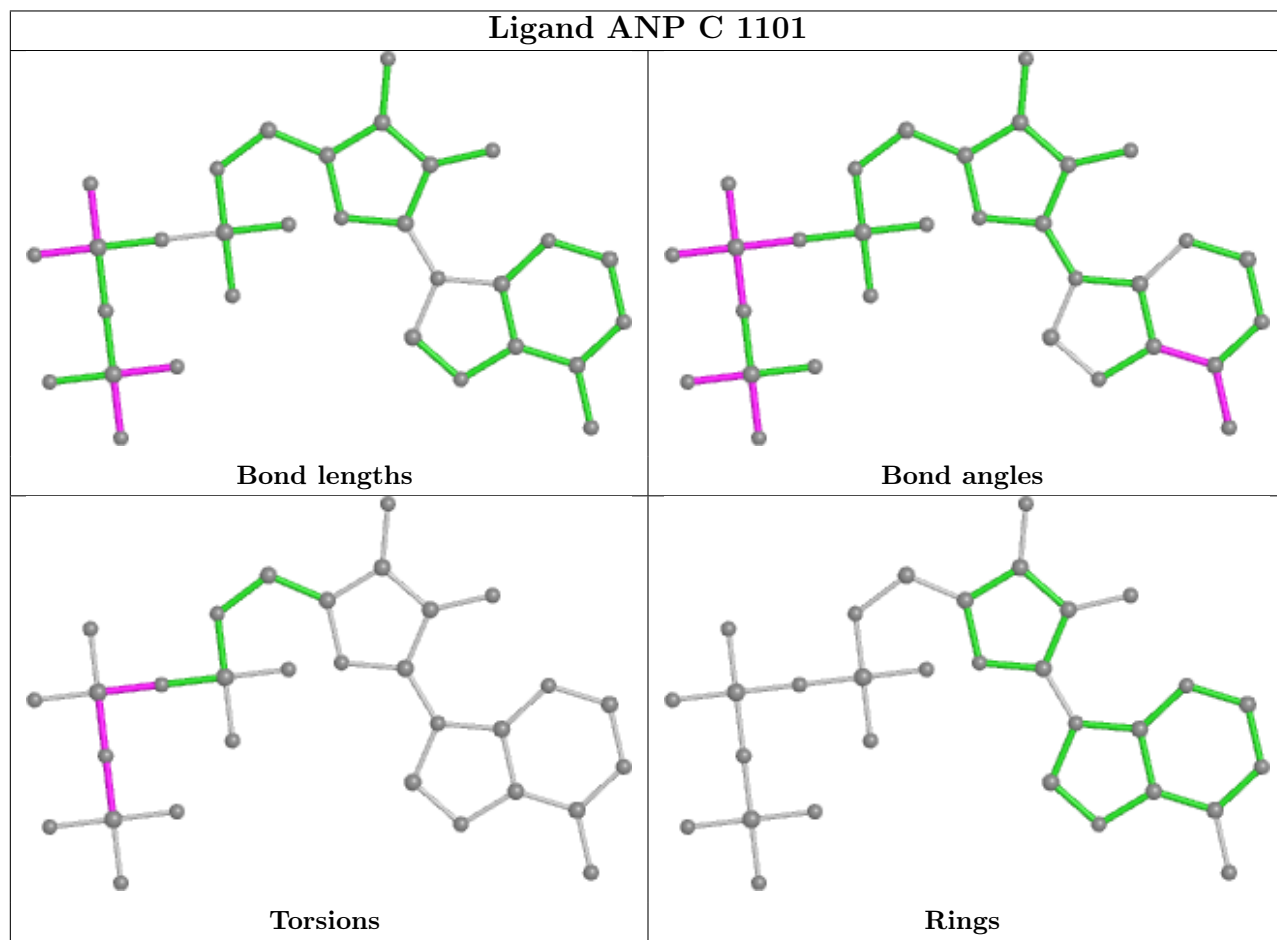
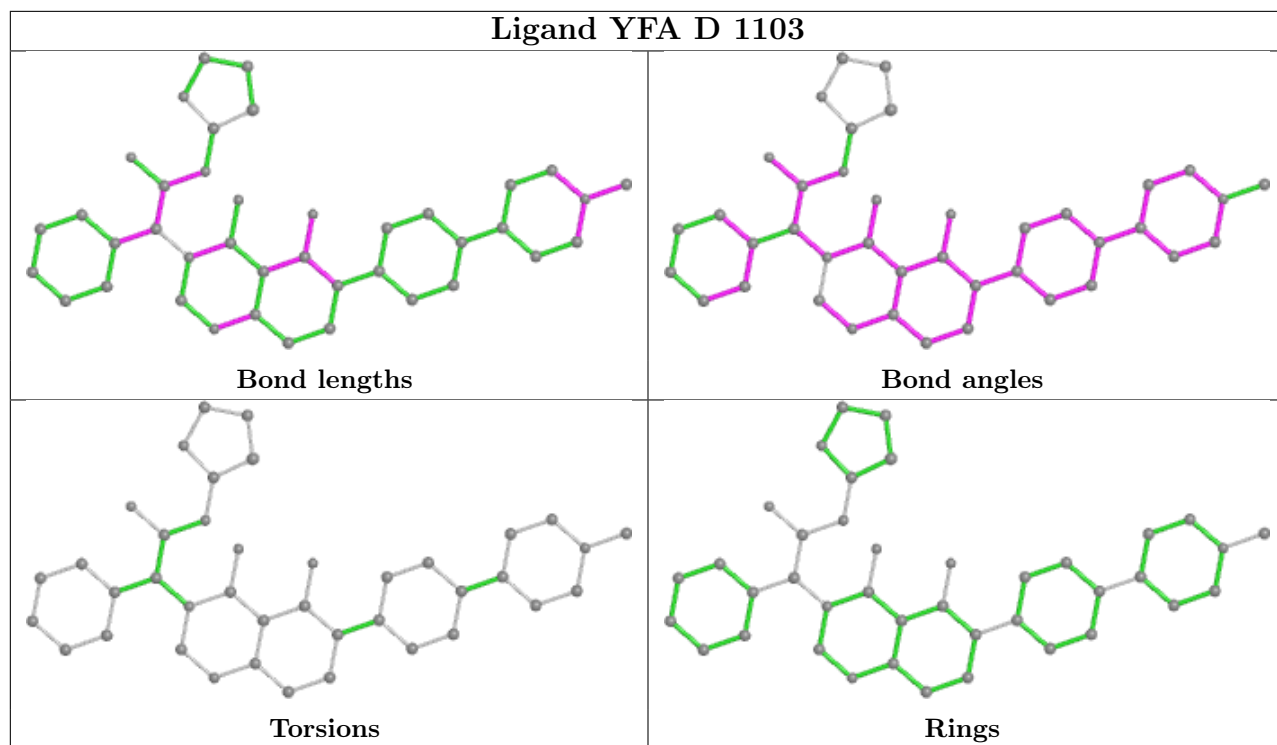
There are no ring outliers.

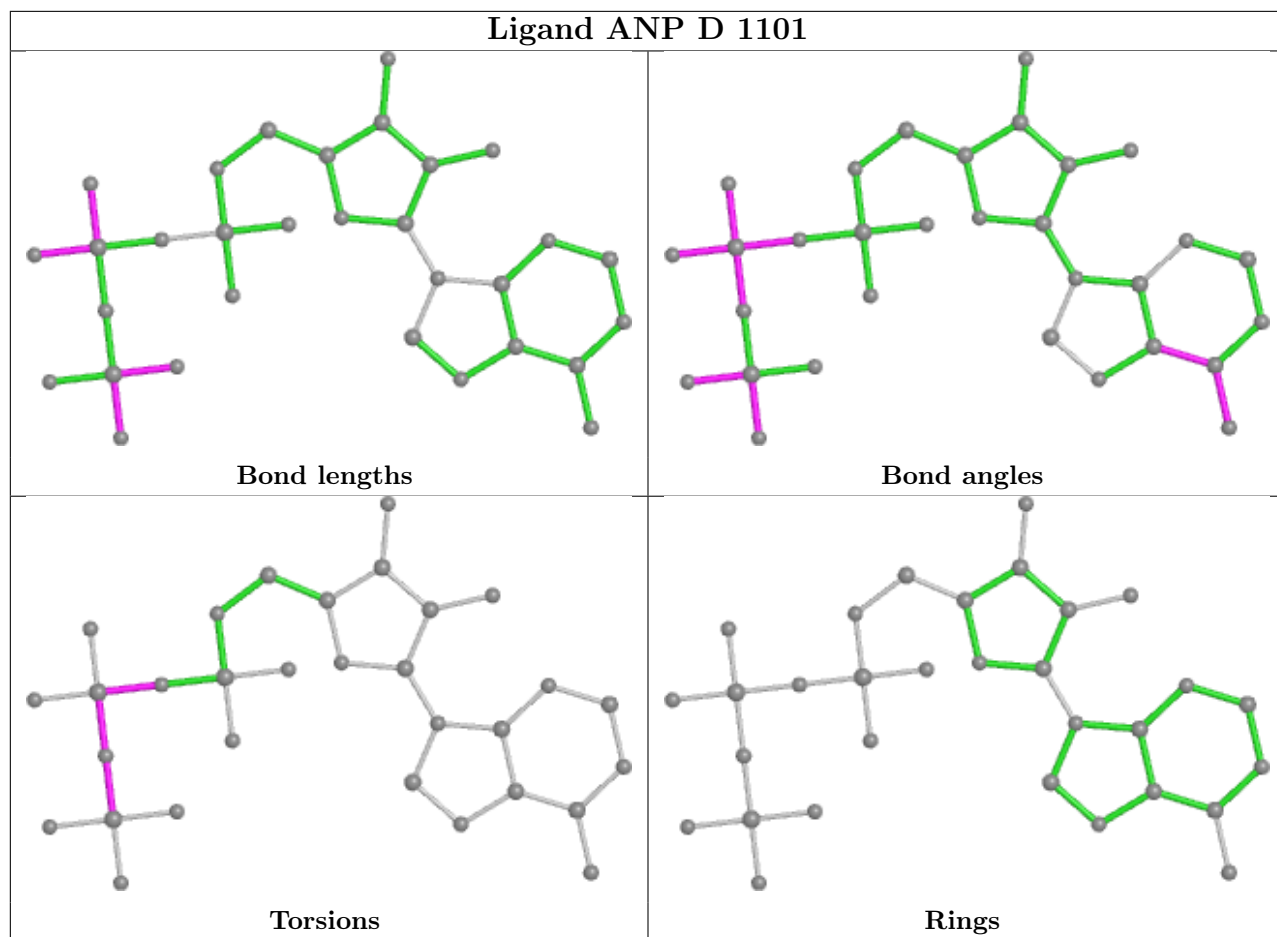
3 monomers are involved in 3 short contacts:

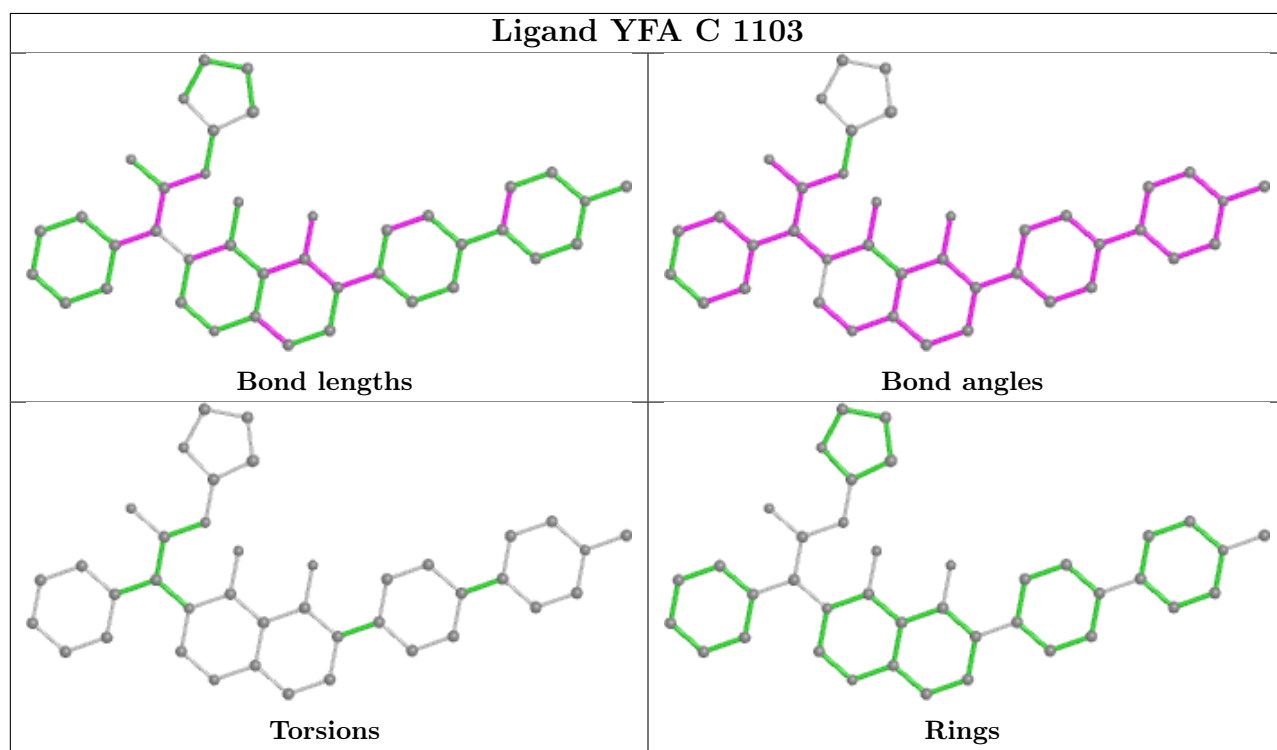
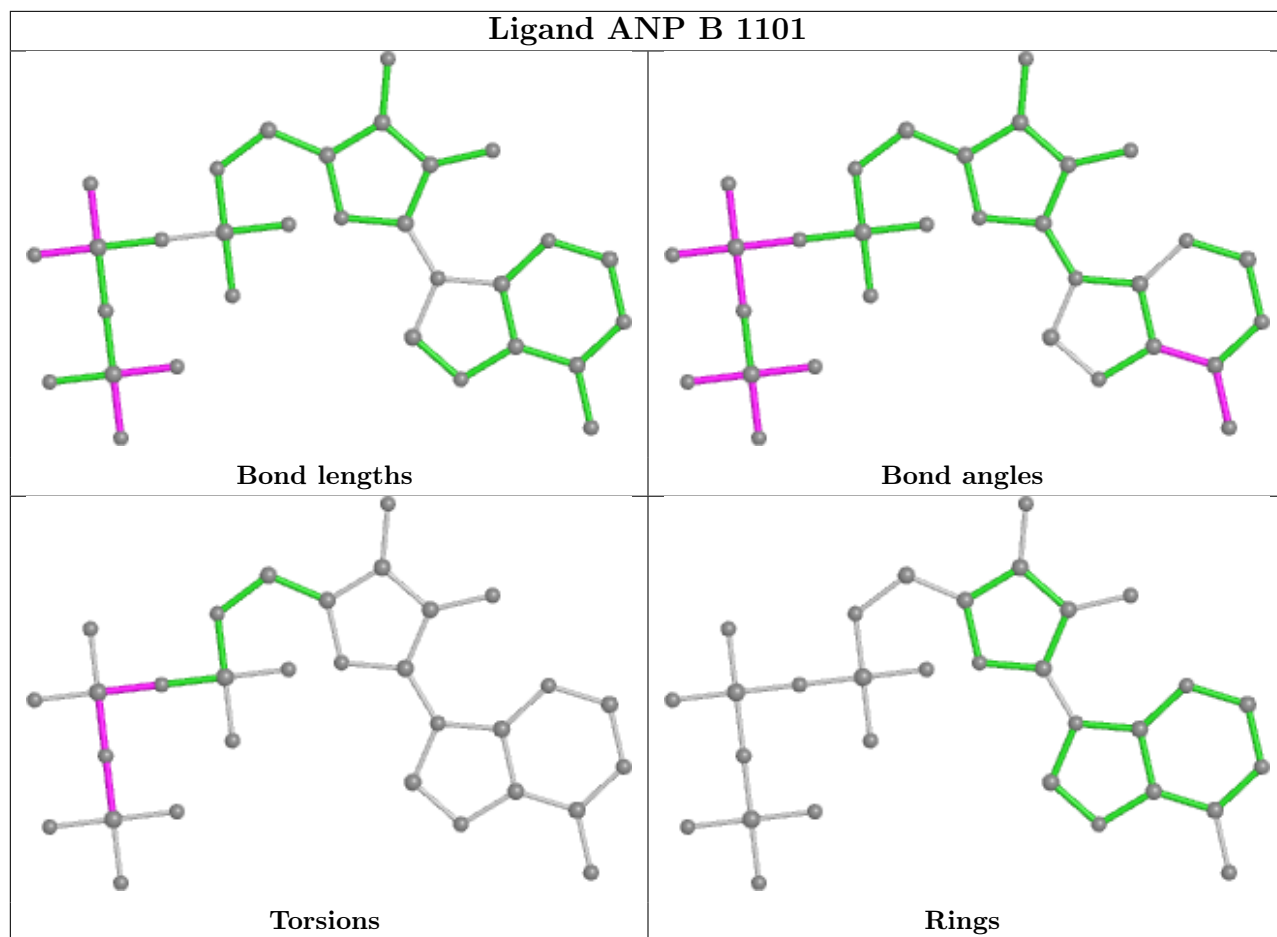
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1103	YFA	1	0
4	D	1103	YFA	1	0
4	C	1103	YFA	1	0

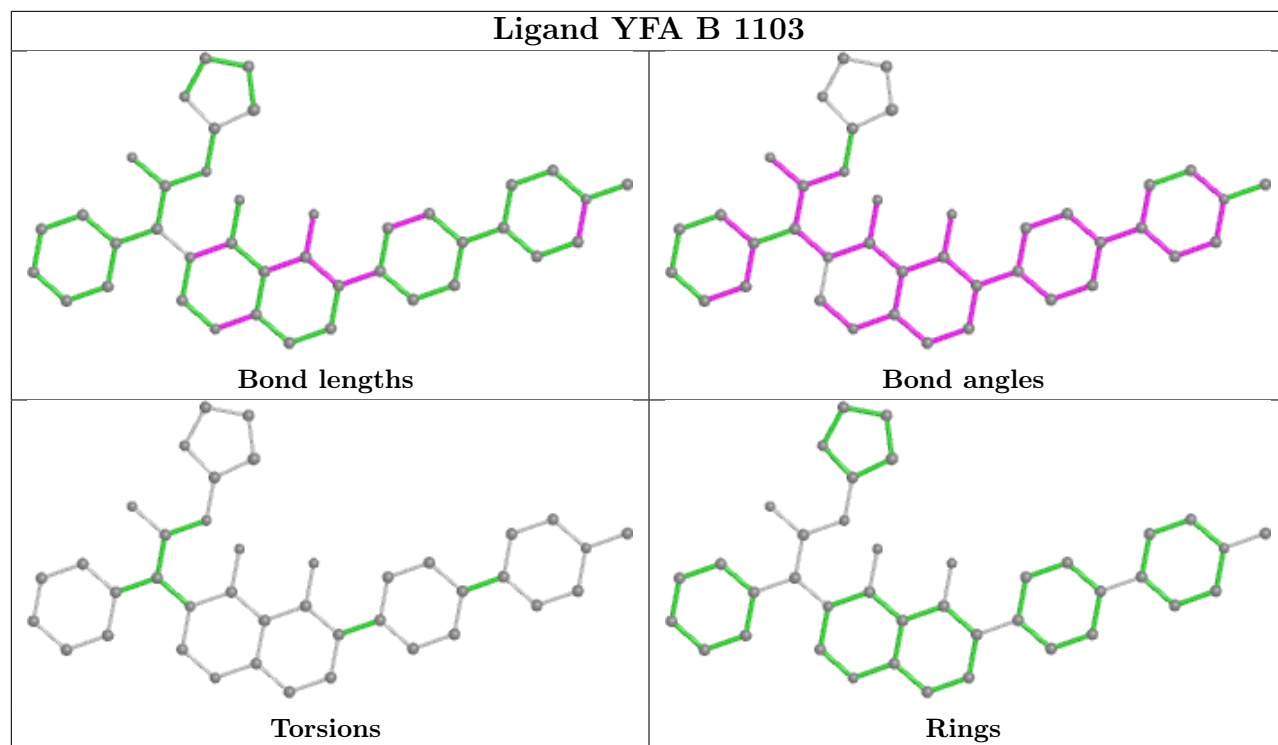
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











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	292/331 (88%)	0.29	9 (3%) 49 56	38, 57, 86, 103	0
1	B	293/331 (88%)	0.26	8 (2%) 54 62	33, 53, 83, 97	0
1	C	292/331 (88%)	0.16	5 (1%) 70 76	35, 50, 76, 110	0
1	D	293/331 (88%)	0.26	8 (2%) 54 62	34, 52, 79, 93	0
All	All	1170/1324 (88%)	0.24	30 (2%) 56 63	33, 53, 80, 110	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	751	THR	6.2
1	C	988	HIS	4.2
1	B	755	ALA	4.2
1	B	723	PHE	4.0
1	A	988	HIS	3.4
1	D	985	GLU	3.1
1	D	929	LYS	2.9
1	A	753	PRO	2.9
1	A	986	ARG	2.8
1	B	988	HIS	2.8
1	B	989	LEU	2.7
1	A	737	LYS	2.6
1	C	1006	ASP	2.5
1	D	807	ASP	2.5
1	C	723	PHE	2.4
1	B	889	ARG	2.4
1	D	888	HIS	2.4
1	B	986	ARG	2.3
1	A	943	VAL	2.3
1	D	737	LYS	2.2
1	A	832	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	889	ARG	2.2
1	D	700	ASN	2.2
1	D	751	THR	2.2
1	A	700	ASN	2.2
1	C	982	GLN	2.1
1	A	807	ASP	2.1
1	D	748	ARG	2.1
1	B	750	ALA	2.1
1	A	889	ARG	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.

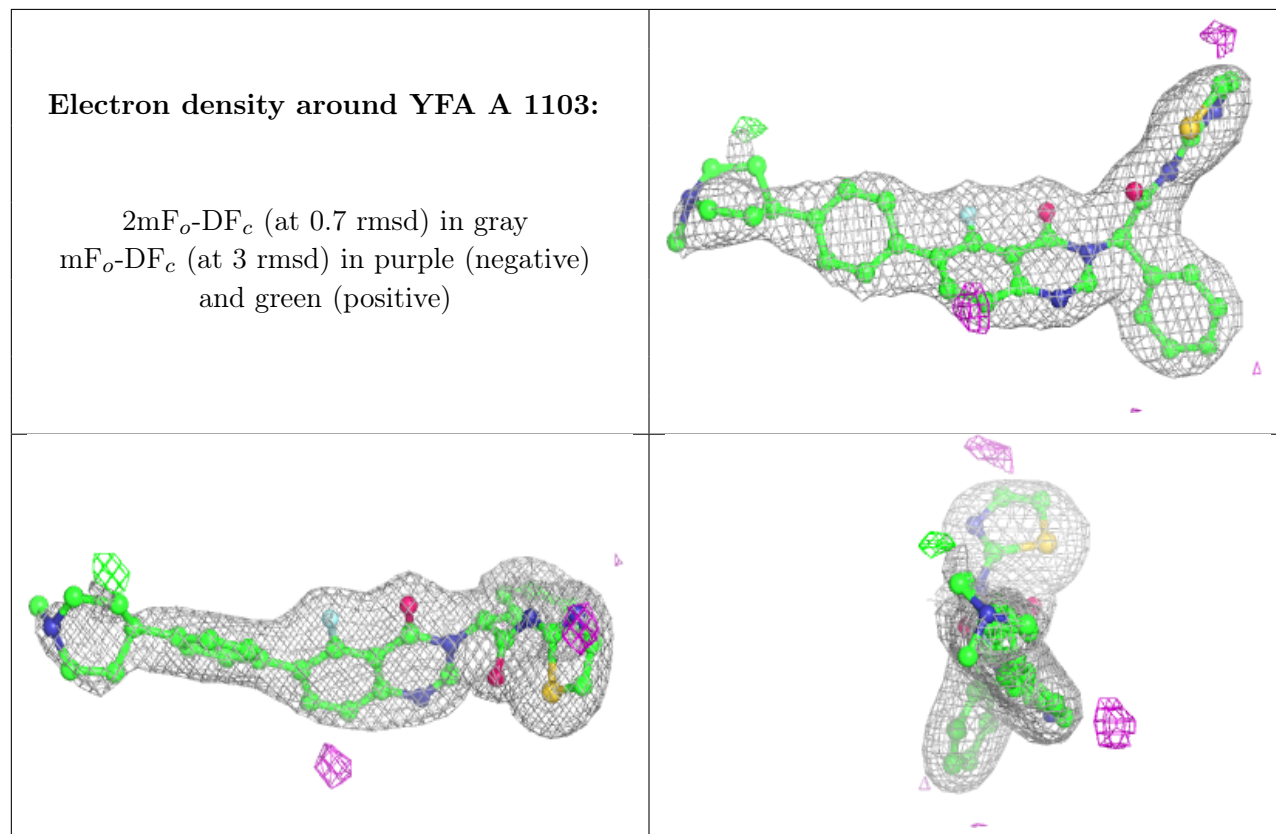
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
3	MG	D	1102	1/1	0.93	0.07	41,41,41,41	0
3	MG	B	1102	1/1	0.94	0.06	42,42,42,42	0
4	YFA	A	1103	40/40	0.96	0.17	38,45,75,77	0
4	YFA	C	1103	40/40	0.96	0.18	33,41,74,75	0
2	ANP	A	1101	31/31	0.97	0.14	39,44,50,52	0
2	ANP	B	1101	31/31	0.97	0.13	39,44,51,52	0
2	ANP	C	1101	31/31	0.97	0.14	33,40,48,55	0
4	YFA	B	1103	40/40	0.97	0.16	36,49,79,81	0
2	ANP	D	1101	31/31	0.97	0.13	35,42,47,49	0
4	YFA	D	1103	40/40	0.97	0.15	37,46,76,79	0
3	MG	C	1102	1/1	0.98	0.07	38,38,38,38	0
3	MG	A	1102	1/1	0.98	0.06	42,42,42,42	0

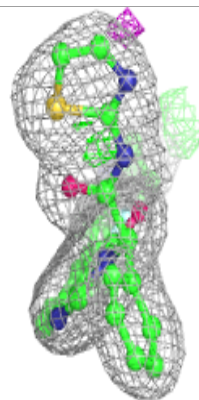
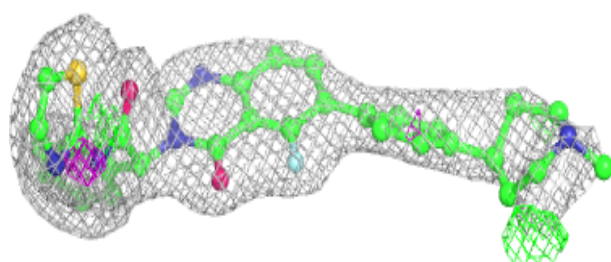
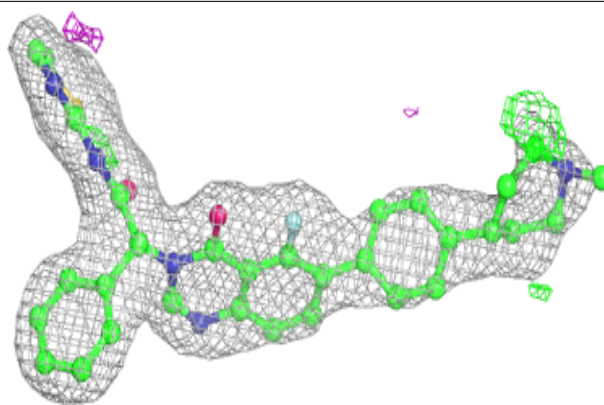
The following is a graphical depiction of the model fit to experimental electron density of all

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.

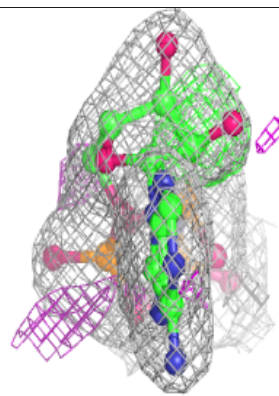
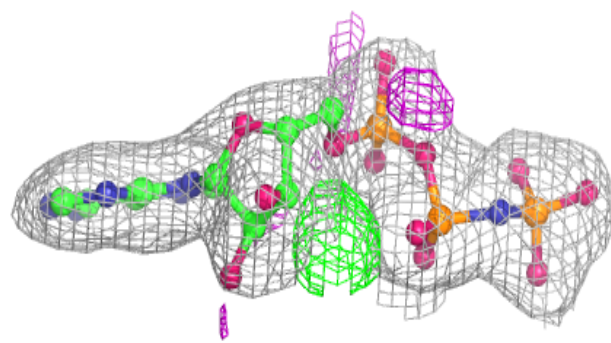
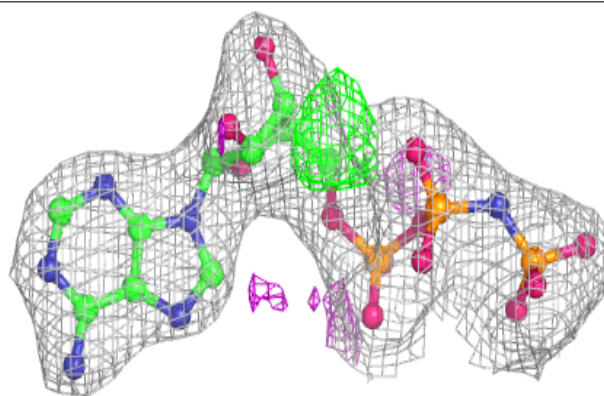


Electron density around YFA C 1103:

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

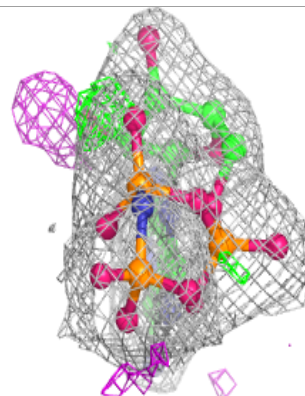
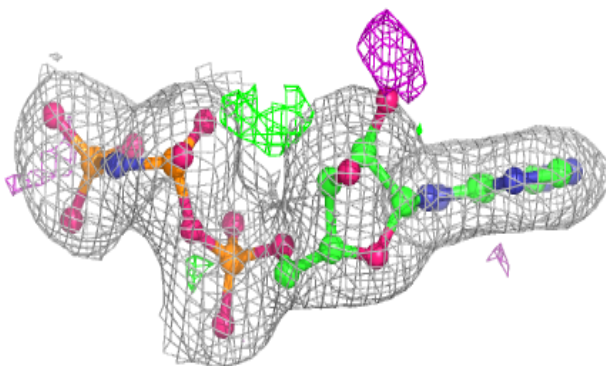
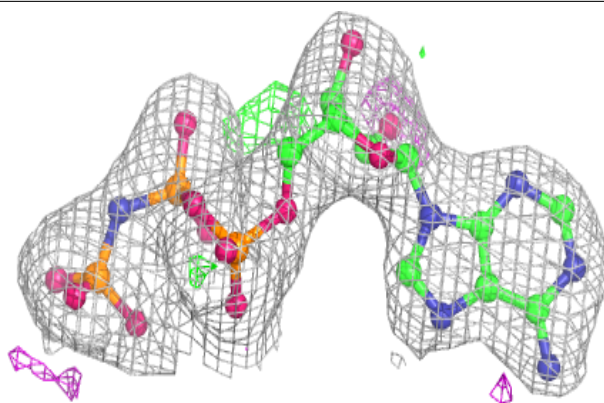
**Electron density around ANP A 1101:**

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

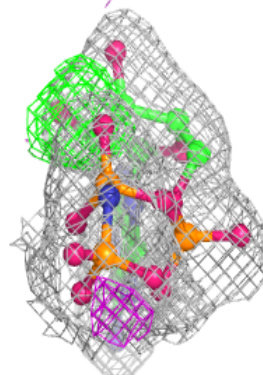
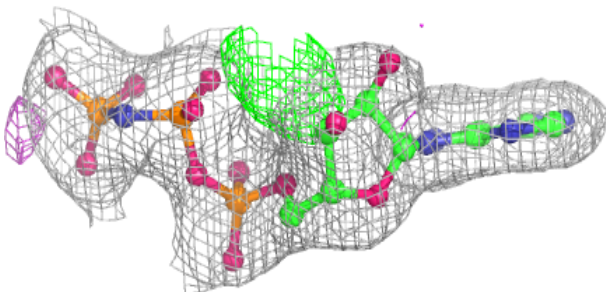
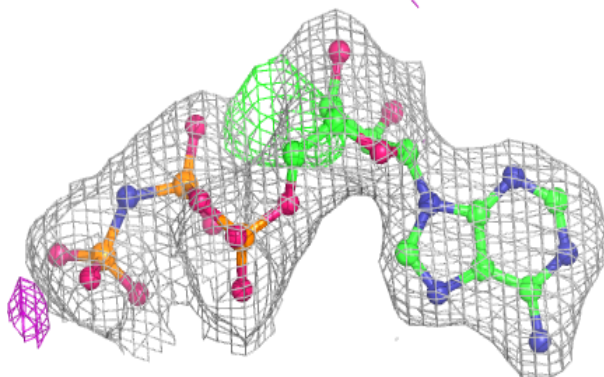


Electron density around ANP B 1101:

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

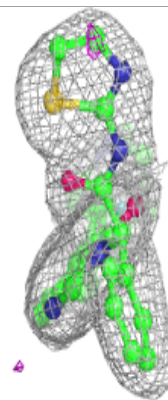
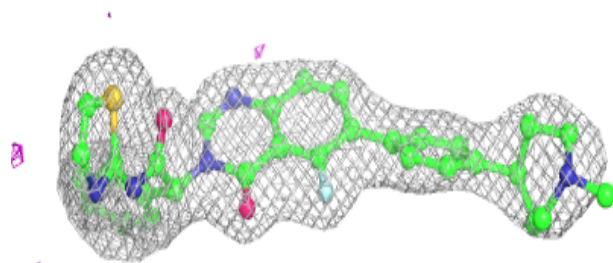
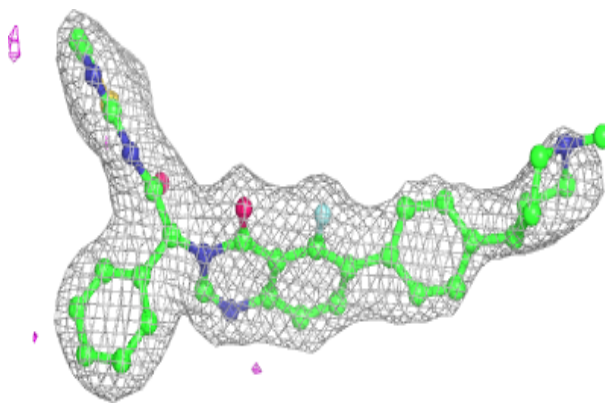
**Electron density around ANP C 1101:**

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

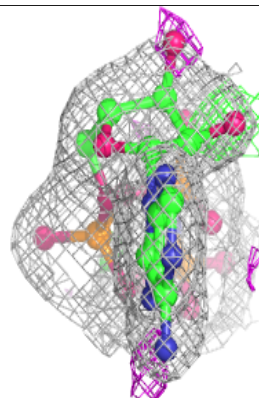
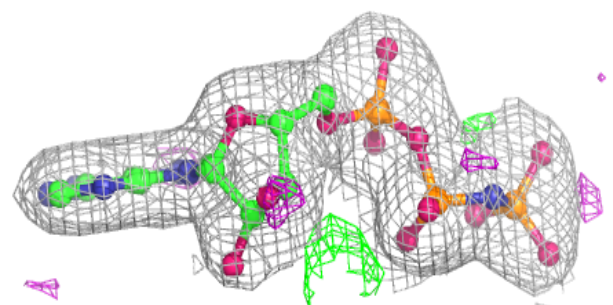
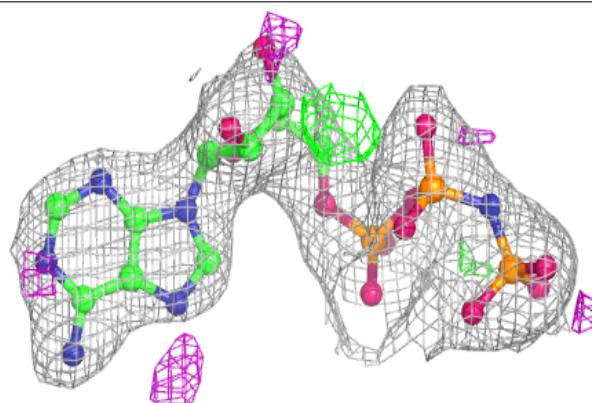


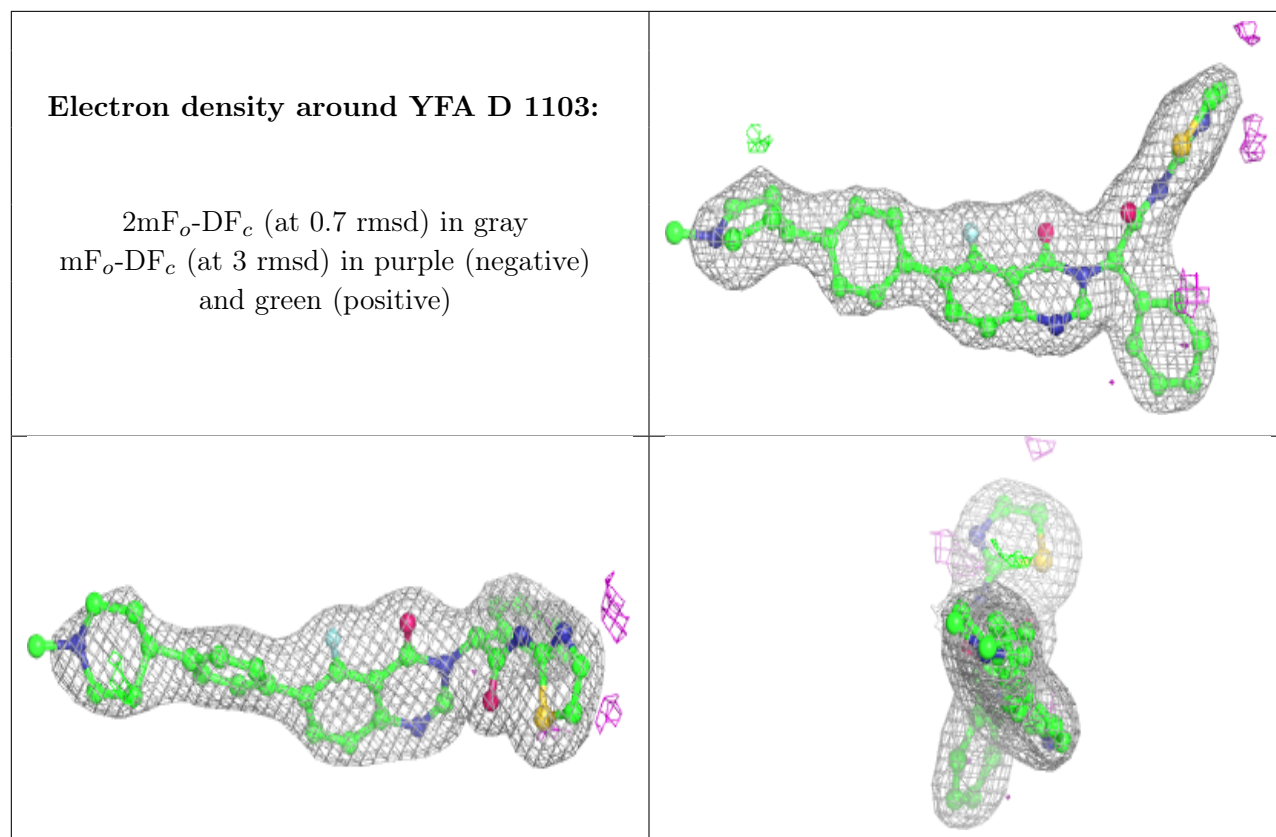
Electron density around YFA B 1103:

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

**Electron density around ANP D 1101:**

$2mF_o-DF_c$ (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.