WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Sep 24, 2023 – 12:20 PM EDT

PDB ID	:	5U7K
Title	:	PDE2 catalytic domain complexed with inhibitors
Authors	:	Pandit, J.; Parris, K.
Deposited on	:	2016-12-12
Resolution	:	2.06 Å(reported)

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

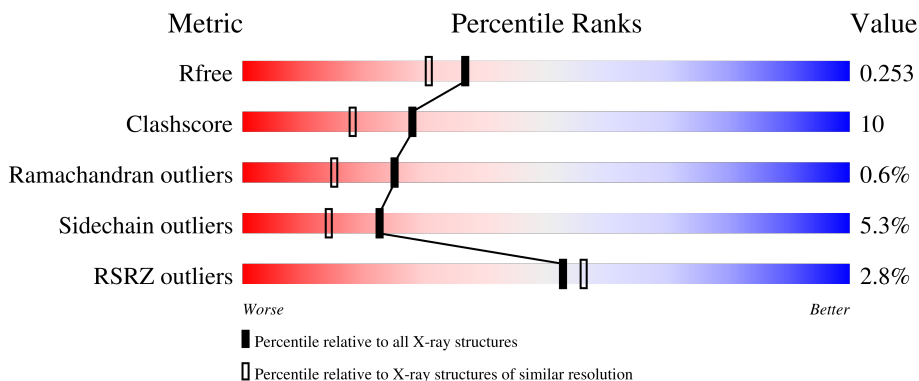|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh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

1   Overall quality at a glance ⓘ

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	Percentile Ranks	Value
Rfree		0.253
Clashscore		10
Ramachandran outliers		0.6%
Sidechain outliers		5.3%
RSRZ outliers		2.8%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	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	345	2% / 78% / 19% / ••
1	B	345	2% / 79% / 18% / ••
1	C	345	3% / 76% / 19% / • •
1	D	345	3% / 72% / 22% / • 5%

2   Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 11869 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 cGMP-dependent 3',5'-cyclic phosphodiesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total 2810	C 1793	N 480	O 510	S 27	0	5	0
1	B	343	Total 2810	C 1789	N 479	O 516	S 26	0	2	0
1	C	339	Total 2807	C 1791	N 477	O 513	S 26	0	6	0
1	D	327	Total 2693	C 1720	N 461	O 486	S 26	0	4	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	575	GLY	-	expression tag	UNP O00408
A	576	SER	-	expression tag	UNP O00408
A	577	ALA	-	expression tag	UNP O00408
A	578	MET	-	expression tag	UNP O00408
B	575	GLY	-	expression tag	UNP O00408
B	576	SER	-	expression tag	UNP O00408
B	577	ALA	-	expression tag	UNP O00408
B	578	MET	-	expression tag	UNP O00408
C	575	GLY	-	expression tag	UNP O00408
C	576	SER	-	expression tag	UNP O00408
C	577	ALA	-	expression tag	UNP O00408
C	578	MET	-	expression tag	UNP O00408
D	575	GLY	-	expression tag	UNP O00408
D	576	SER	-	expression tag	UNP O00408
D	577	ALA	-	expression tag	UNP O00408
D	578	MET	-	expression tag	UNP O00408

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0

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

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

- Molecule 4 is 3-[5-(4-ethylphenyl)-1-methyl-1H-pyrazol-4-yl]-5-propoxy[1,2,4]triazolo[4,3-a]pyrazine (three-letter code: 7Y1) (formula: $C_{20}H_{22}N_6O$).
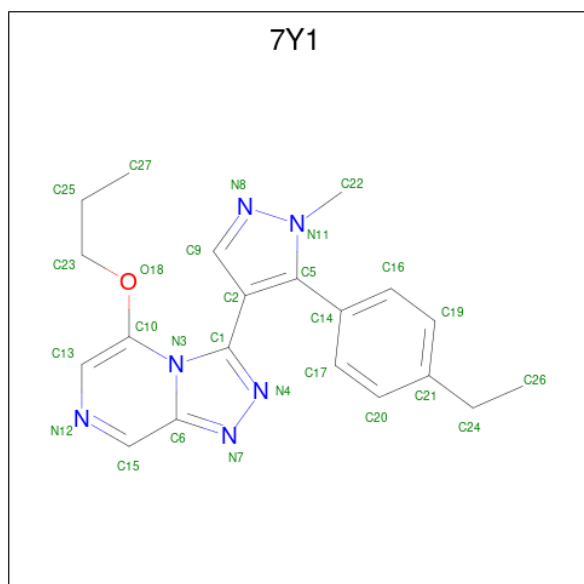
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 27	C 20	N 6	O 1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total 27	C 20	N 6	O 1	0	0
4	C	1	Total 27	C 20	N 6	O 1	0	0
4	D	1	Total 27	C 20	N 6	O 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total 1	Cl 1	0	0

- Molecule 6 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	159	Total 159	O 159	0	0
6	B	192	Total 192	O 192	0	0
6	C	150	Total 150	O 150	0	0
6	D	131	Total 131	O 131	0	0

3 Residue-property plots ⓘ

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.
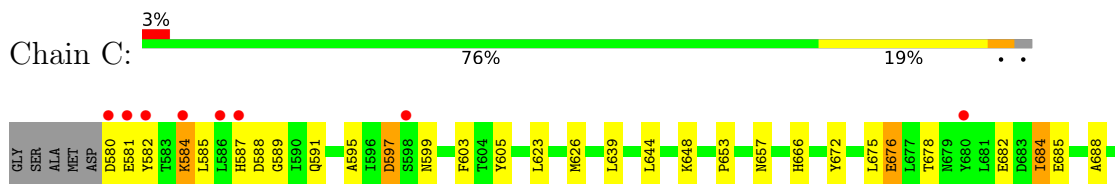
- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase
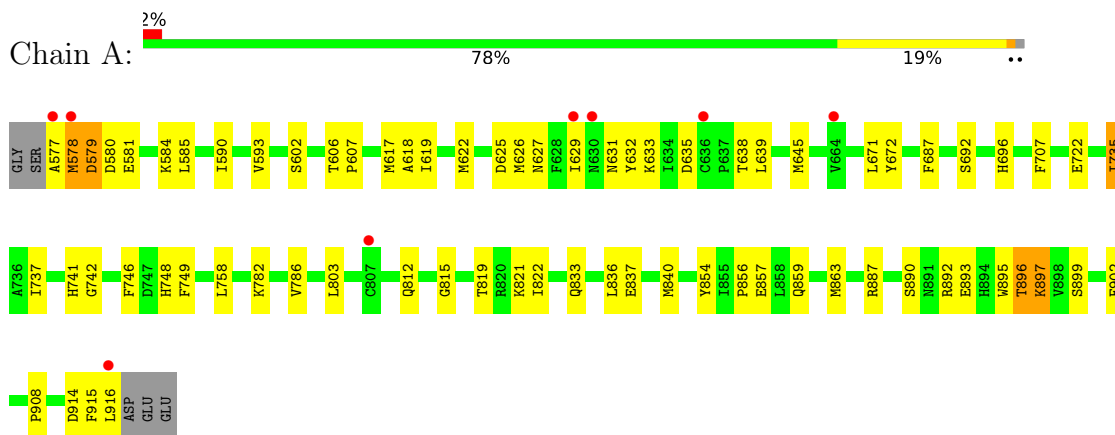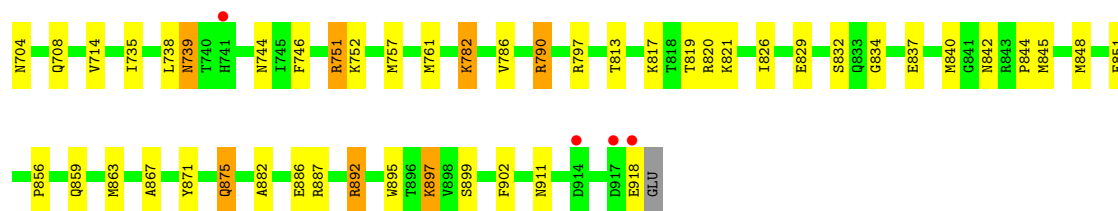
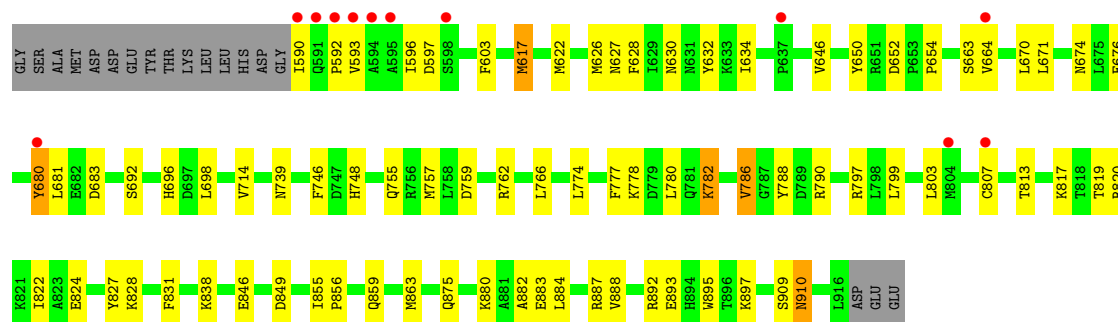Chain A:
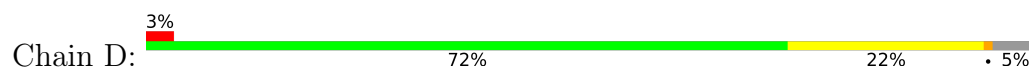
- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase

Chain B:

- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase

Chain C:

• Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase

Chain D:
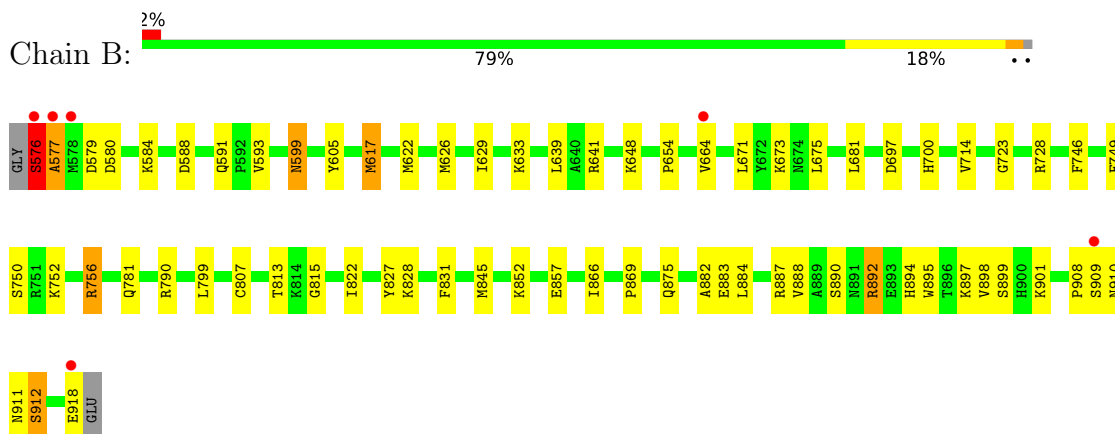
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	55.87Å 73.51Å 91.49Å 109.38° 91.23° 90.67°	Depositor
Resolution (Å)	36.00 – 2.06 35.45 – 2.06	Depositor EDS
% Data completeness (in resolution range)	96.2 (36.00-2.06) 96.2 (35.45-2.06)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.59 (at 2.06Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.192 , 0.255 0.193 , 0.253	Depositor DCC
R_{free} test set	4077 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	28.6	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 51.9	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	11869	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.53% of the height of the origin peak. No significant pseudotranslation is detected.*

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 7Y1, MG, CL

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$ >5	RMSZ	#$|Z|$ >5
1	A	0.62	0/2893	0.68	0/3901
1	B	0.64	0/2883	0.69	0/3890
1	C	0.76	2/2893 (0.1%)	0.75	2/3903 (0.1%)
1	D	0.58	0/2770	0.66	0/3735
All	All	0.65	2/11439 (0.0%)	0.69	2/15429 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2
1	C	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	832[A]	SER	CB-OG	-16.66	1.20	1.42
1	C	832[B]	SER	CB-OG	-16.66	1.20	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	832[A]	SER	CA-CB-OG	-7.63	90.60	111.20
1	C	832[B]	SER	CA-CB-OG	-7.63	90.60	111.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	576	SER	Peptide
1	B	577	ALA	Peptide
1	C	589	GLY	Peptide

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	2810	0	2766	52	0
1	B	2810	0	2752	51	0
1	C	2807	0	2757	64	0
1	D	2693	0	2662	61	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	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	27	0	0	0	0
4	B	27	0	0	0	0
4	C	27	0	0	1	0
4	D	27	0	0	0	0
5	C	1	0	0	0	0
6	A	159	0	0	6	0
6	B	192	0	0	6	0
6	C	150	0	0	5	0
6	D	131	0	0	6	0
All	All	11869	0	10937	220	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 10.

The worst 5 of 220 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:D:887:ARG:HG2	6:D:1214:HOH:O	1.43	1.18
1:B:813:THR:O	1:B:887:ARG:HD2	1.44	1.14
1:C:751:ARG:HG2	1:C:751:ARG:HH11	1.20	1.06
1:C:892:ARG:HG2	1:C:892:ARG:HH11	1.24	1.03
1:B:591:GLN:H	1:B:617:MET:CE	1.78	0.96

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	343/345 (99%)	324 (94%)	16 (5%)	3 (1%)	17	8
1	B	343/345 (99%)	326 (95%)	17 (5%)	0	100	100
1	C	343/345 (99%)	328 (96%)	12 (4%)	3 (1%)	17	8
1	D	329/345 (95%)	313 (95%)	14 (4%)	2 (1%)	25	15
All	All	1358/1380 (98%)	1291 (95%)	59 (4%)	8 (1%)	25	15

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	676	GLU
1	D	786	VAL
1	A	915	PHE
1	A	580	ASP
1	C	584	LYS

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	311/310 (100%)	299 (96%)	12 (4%)	32	25
1	B	311/310 (100%)	290 (93%)	21 (7%)	16	8
1	C	312/310 (101%)	294 (94%)	18 (6%)	20	11
1	D	299/310 (96%)	286 (96%)	13 (4%)	29	22
All	All	1233/1240 (99%)	1169 (95%)	64 (5%)	22	14

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	817	LYS
1	D	822	ILE
1	B	852	LYS
1	B	822	ILE
1	D	846	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	842	ASN
1	C	859	GLN
1	D	910	ASN
1	D	748	HIS
1	D	875	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5   Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 9 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
4	7Y1	B	1003	-	23,30,30	1.12	4 (17%)	24,42,42	2.36	5 (20%)
4	7Y1	D	1003	-	23,30,30	0.91	0	24,42,42	2.12	5 (20%)
4	7Y1	A	1003	-	23,30,30	1.07	4 (17%)	24,42,42	2.36	7 (29%)
4	7Y1	C	1004	-	23,30,30	1.11	2 (8%)	24,42,42	2.03	5 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	7Y1	B	1003	-	-	5/10/14/14	0/4/4/4
4	7Y1	D	1003	-	-	1/10/14/14	0/4/4/4
4	7Y1	A	1003	-	-	3/10/14/14	0/4/4/4
4	7Y1	C	1004	-	-	3/10/14/14	0/4/4/4

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1003	7Y1	O18-C10	2.55	1.37	1.34
4	C	1004	7Y1	C2-C5	-2.34	1.37	1.41
4	A	1003	7Y1	C5-N11	-2.33	1.33	1.36
4	B	1003	7Y1	C5-N11	-2.33	1.33	1.36
4	C	1004	7Y1	C5-N11	-2.27	1.34	1.36

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1003	7Y1	C2-C5-N11	-8.24	102.83	108.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	1003	7Y1	C2-C5-N11	-7.02	103.70	108.75
4	A	1003	7Y1	C15-N12-C13	6.59	122.47	116.87
4	C	1004	7Y1	C2-C5-N11	-6.58	104.02	108.75
4	A	1003	7Y1	C2-C5-N11	-6.47	104.09	108.75

There are no chirality outliers.
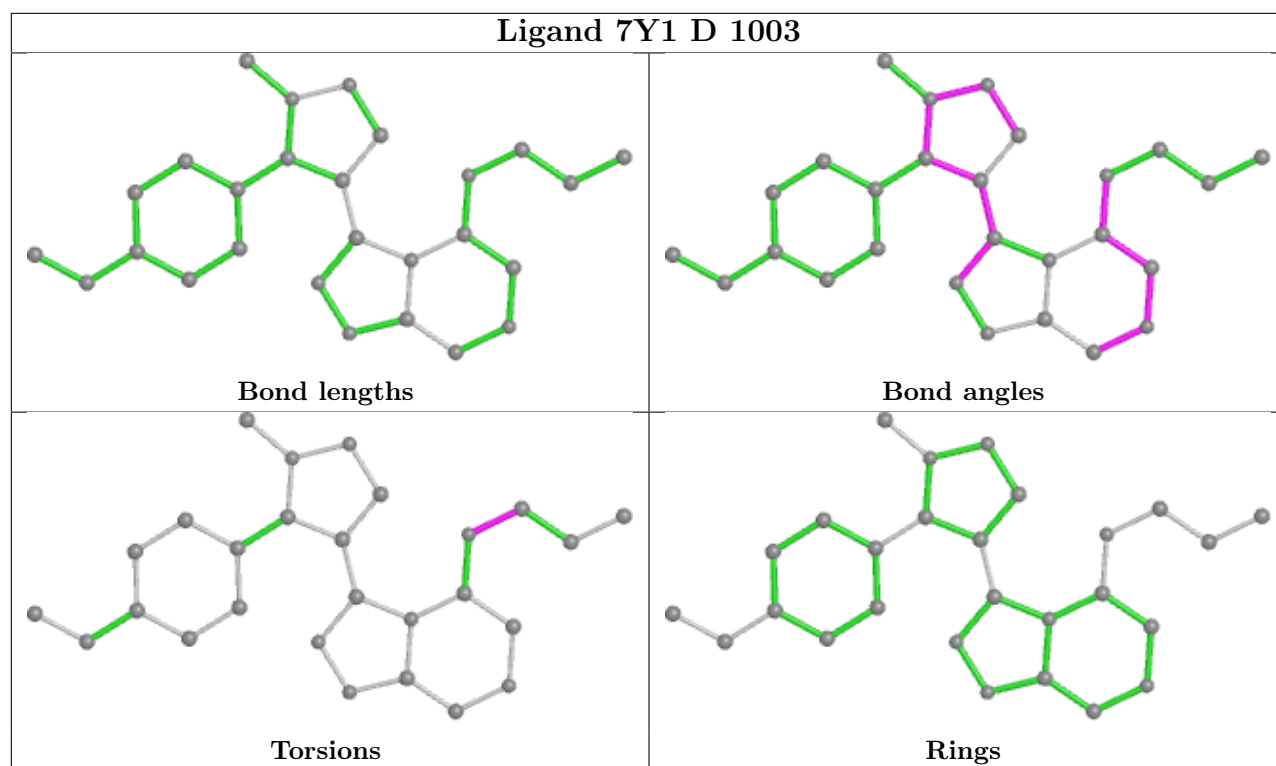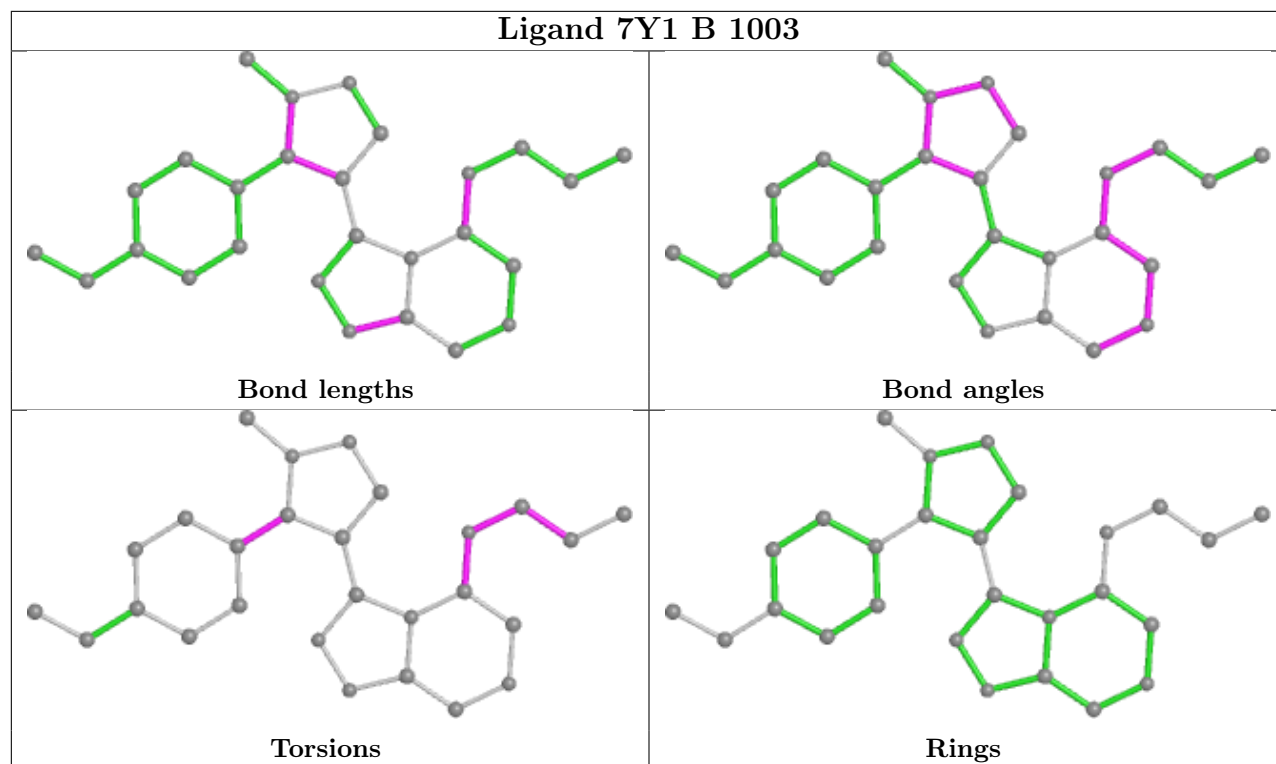
5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1003	7Y1	N3-C10-O18-C23
4	A	1003	7Y1	C13-C10-O18-C23
4	B	1003	7Y1	N3-C10-O18-C23
4	B	1003	7Y1	C13-C10-O18-C23
4	C	1004	7Y1	C25-C23-O18-C10

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1004	7Y1	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 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 7Y1 B 1003

Bond lengths

Bond angles

Torsions

Rings

Ligand 7Y1 D 1003

Bond lengths

Bond angles

Torsions

Rings

Ligand 7Y1 A 1003

Bond lengths

Bond angles

Torsions

Rings

Ligand 7Y1 C 1004

Bond lengths

Bond angles

Torsions

Rings
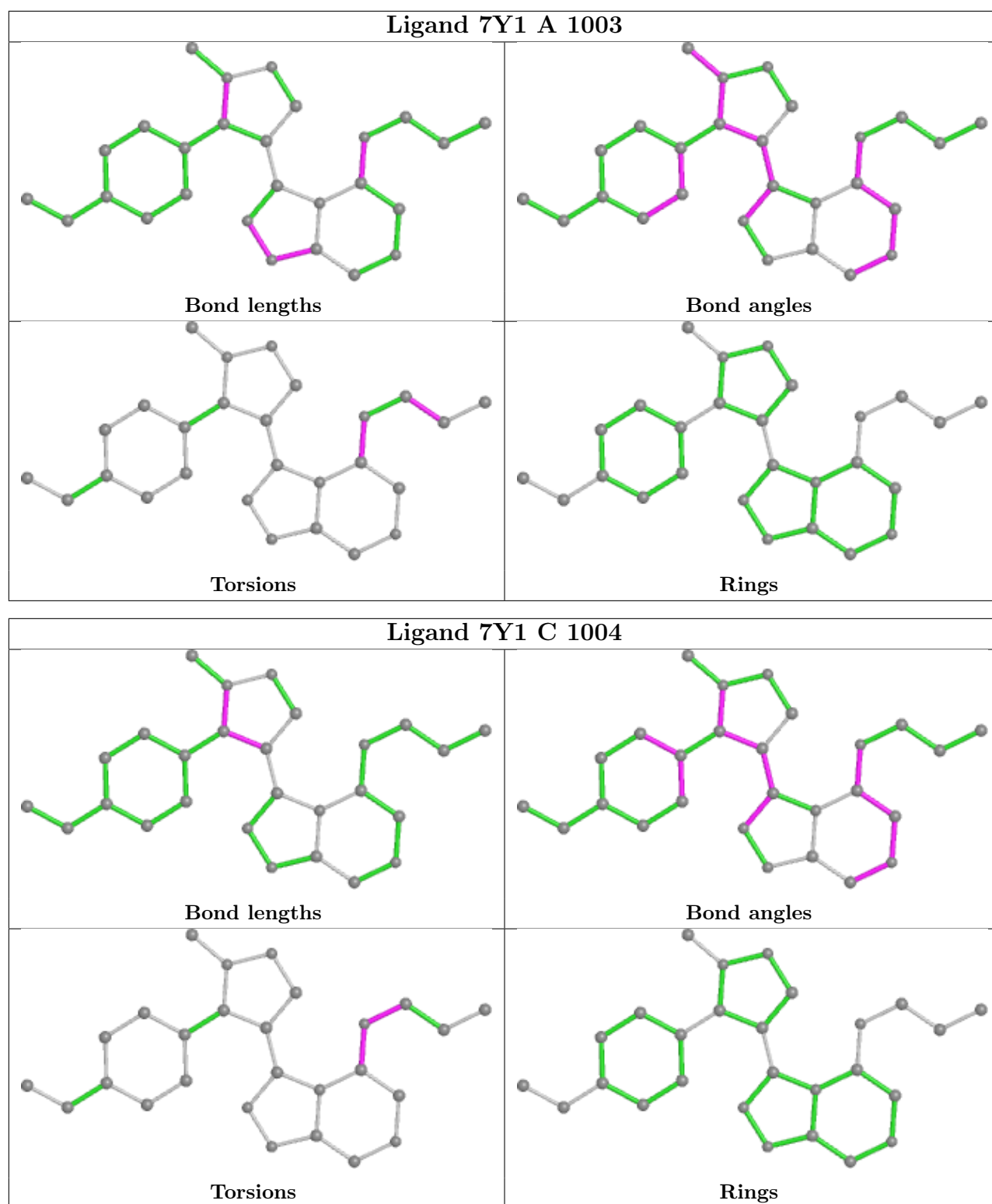
5.7   Other polymers ⓘ

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	340/345 (98%)	-0.07	8 (2%)	59	61	17, 35, 57, 92	2 (0%)
1	B	343/345 (99%)	-0.07	6 (1%)	70	71	17, 33, 53, 85	6 (1%)
1	C	339/345 (98%)	0.00	12 (3%)	44	46	18, 34, 60, 116	7 (2%)
1	D	327/345 (94%)	0.14	12 (3%)	41	43	18, 38, 59, 77	3 (0%)
All	All	1349/1380 (97%)	-0.00	38 (2%)	53	56	17, 35, 59, 116	18 (1%)

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	580	ASP	5.1
1	B	577	ALA	4.8
1	D	590	ILE	4.8
1	A	577	ALA	4.3
1	A	630	ASN	4.3

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

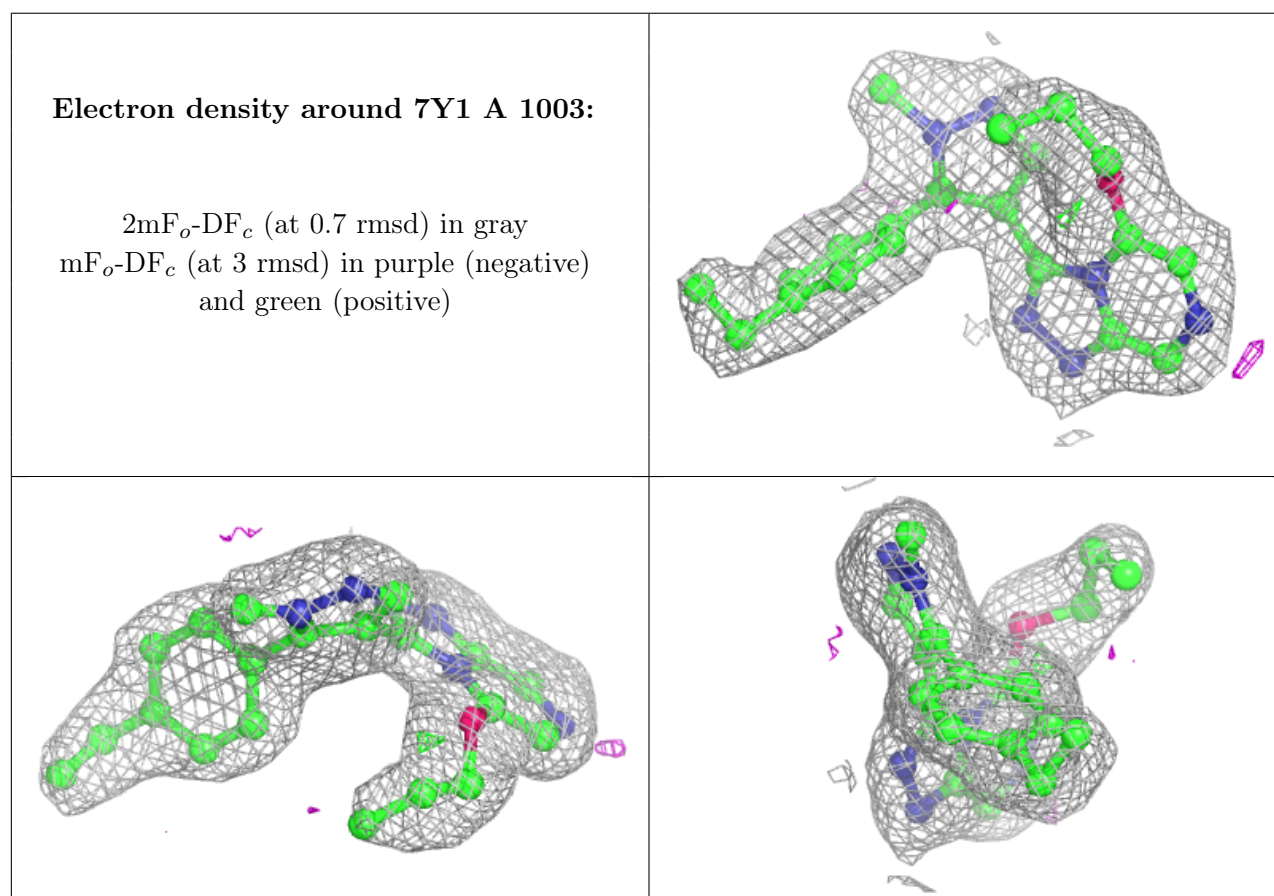There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	CL	C	1003	1/1	0.91	0.12	61,61,61,61	0
3	MG	D	1002	1/1	0.96	0.15	19,19,19,19	0
4	7Y1	A	1003	27/27	0.96	0.14	23,28,32,38	0
4	7Y1	C	1004	27/27	0.96	0.17	20,26,30,32	0
4	7Y1	D	1003	27/27	0.96	0.16	25,30,35,36	0
3	MG	B	1002	1/1	0.96	0.18	20,20,20,20	0
4	7Y1	B	1003	27/27	0.97	0.17	18,26,32,32	0
3	MG	A	1002	1/1	0.98	0.12	17,17,17,17	0
3	MG	C	1002	1/1	0.98	0.16	15,15,15,15	0
2	ZN	D	1001	1/1	0.99	0.11	29,29,29,29	0
2	ZN	B	1001	1/1	1.00	0.11	29,29,29,29	0
2	ZN	C	1001	1/1	1.00	0.10	29,29,29,29	0
2	ZN	A	1001	1/1	1.00	0.09	28,28,28,28	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.
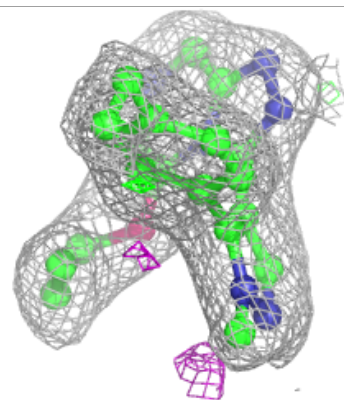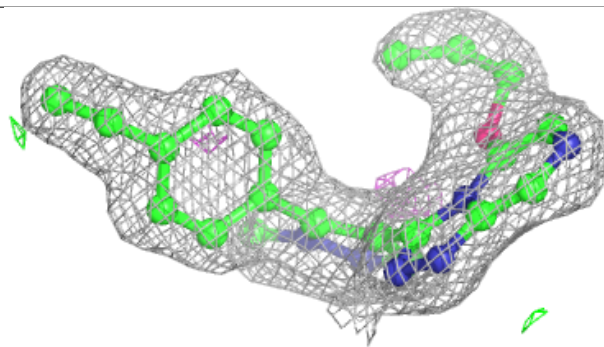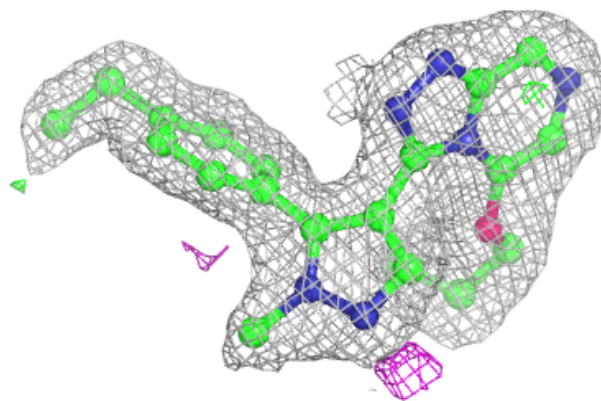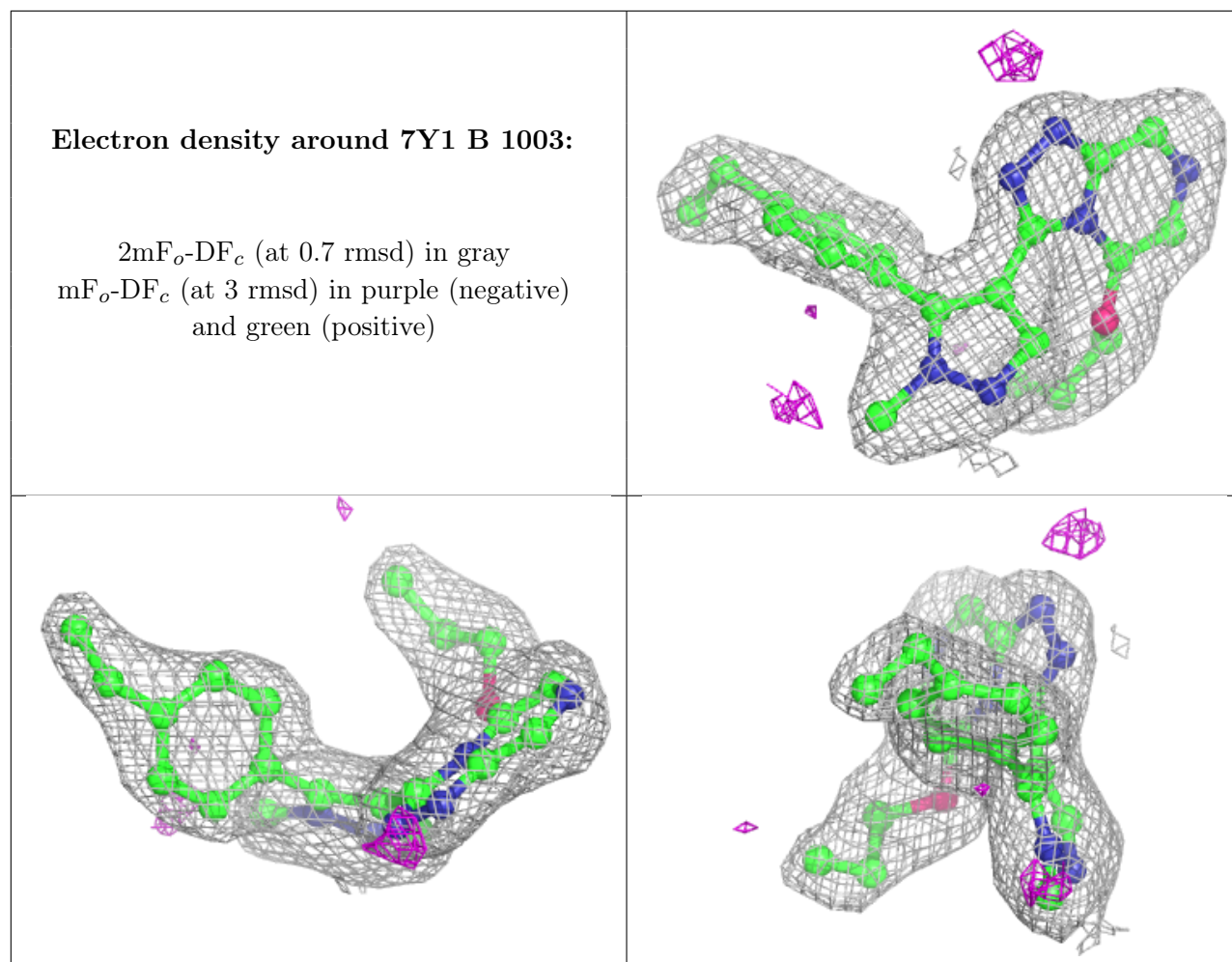

Electron density around 7Y1 A 1003:

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

Electron density around 7Y1 C 1004:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
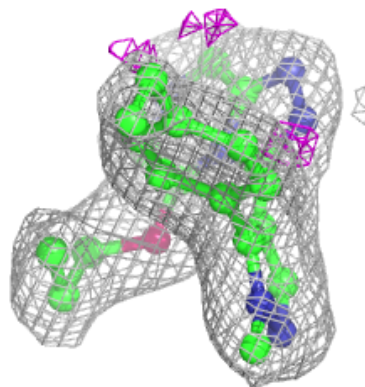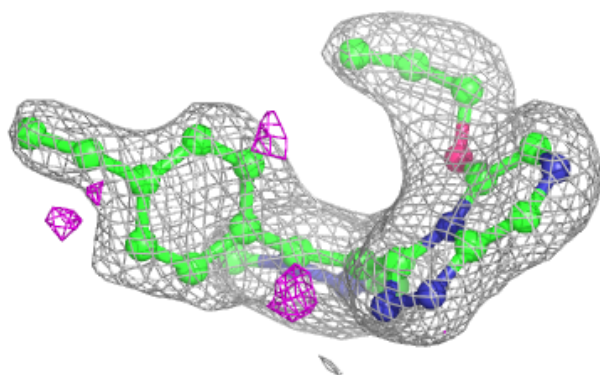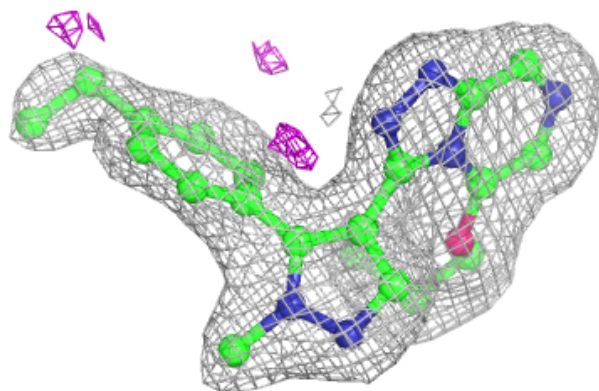
Electron density around 7Y1 D 1003:

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

Electron density around 7Y1 B 1003:

$2mF_o$-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 ⓘ

There are no such residues in this entry.