



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 26, 2026 – 05:15 am BST

PDB ID : 2VPX / pdb_00002vpx
Title : Polysulfide reductase with bound quinone (UQ1)
Authors : Jormakka, M.; Yokoyama, K.; Yano, T.; Tamakoshi, M.; Akimoto, S.; Shimamura, T.; Curmi, P.; Iwata, S.
Deposited on : 2008-03-09
Resolution : 3.10 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 Phenix2.0
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

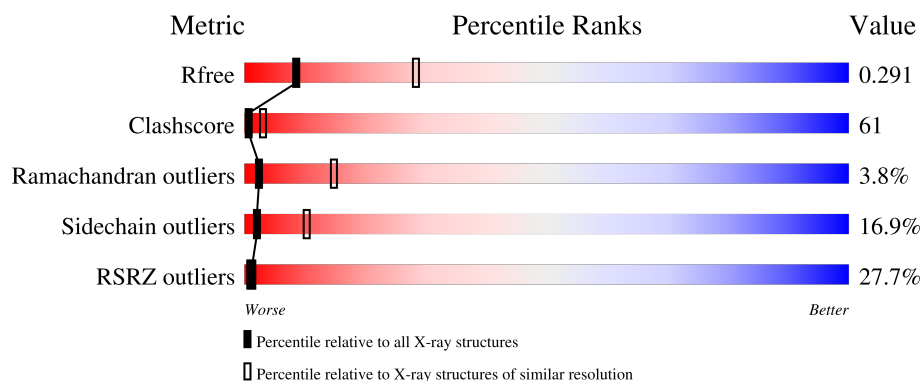
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	765	23% 27% 47% 18% 5% .
1	E	765	30% 29% 44% 17% 6% .
2	B	195	6% 35% 49% 12% ..
2	F	195	42% 33% 50% 13% ..
3	C	253	20% 46% 38% 14% ..

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Mol	Chain	Length	Quality of chain
3	G	253	42% 36% 45% 14% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SF4	A	1764	-	-	X	-
4	SF4	B	1194	-	-	X	-
4	SF4	B	1195	-	-	X	-
4	SF4	B	1196	-	-	X	-
4	SF4	F	1194	-	-	X	-
4	SF4	F	1195	-	-	X	-
7	UQ1	C	1252	-	-	X	-
7	UQ1	G	1251	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 20229 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 THIOSULFATE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	735	Total	C	N	O	S	0	0	1
			5896	3802	1032	1043	19			
1	E	735	Total	C	N	O	S	0	0	1
			5896	3802	1032	1043	19			

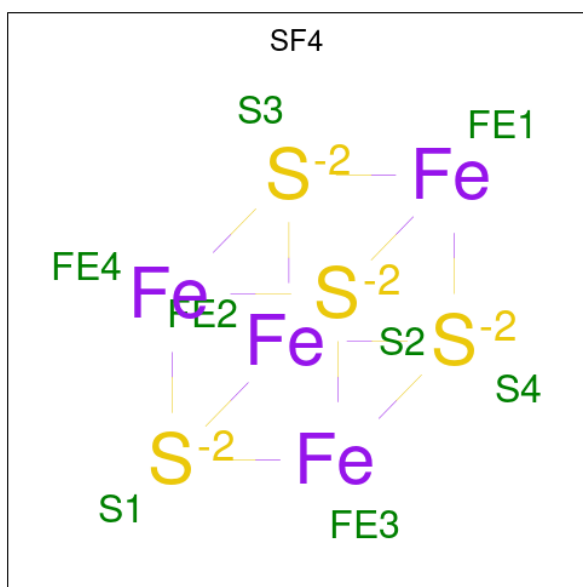
- Molecule 2 is a protein called NRFC PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	194	Total	C	N	O	S	0	0	1
			1475	930	256	269	20			
2	F	194	Total	C	N	O	S	0	0	1
			1475	930	256	269	20			

- Molecule 3 is a protein called HYPOTHETICAL MEMBRANE SPANNING PROTEIN.

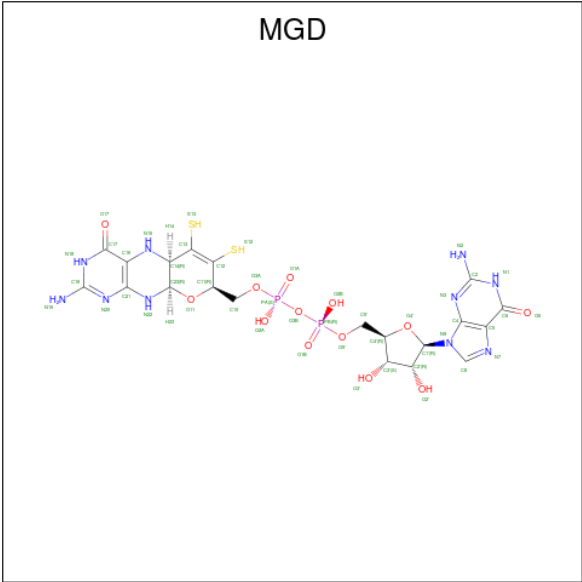
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	251	Total	C	N	O	S	0	0	1
			1948	1323	320	303	2			
3	G	251	Total	C	N	O	S	0	0	1
			1948	1323	320	303	2			

- Molecule 4 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	E	1	Total	Fe	S	0	0
			8	4	4		
4	F	1	Total	Fe	S	0	0
			8	4	4		
4	F	1	Total	Fe	S	0	0
			8	4	4		
4	F	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (CCD ID: MGD) (formula: C₂₀H₂₆N₁₀O₁₃P₂S₂).

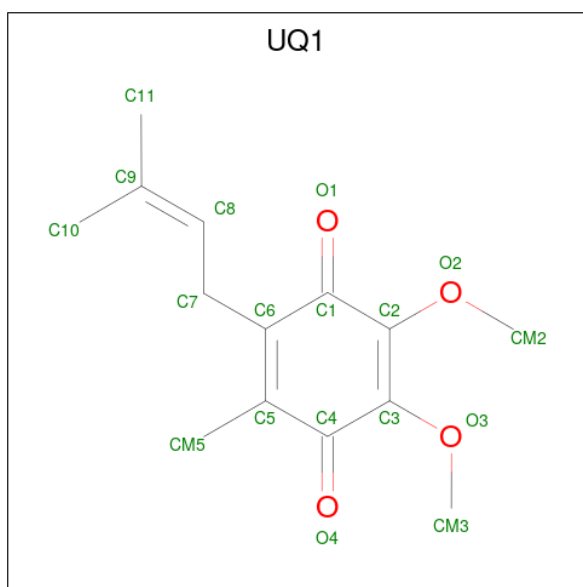


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
5	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
5	E	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
5	E	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- Molecule 6 is MOLYBDENUM ATOM (CCD ID: MO) (formula: Mo).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mo	0	0
			1	1		
6	E	1	Total	Mo	0	0
			1	1		

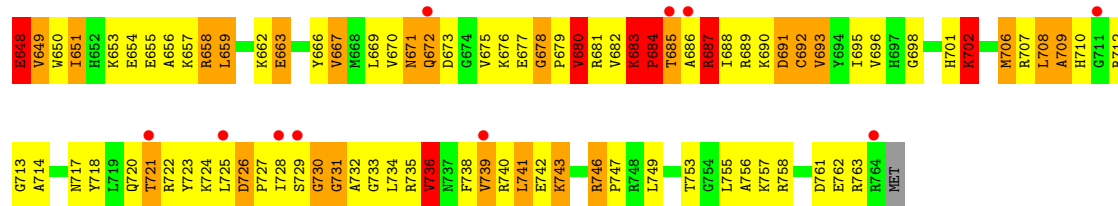
- Molecule 7 is UBIQUINONE-1 (CCD ID: UQ1) (formula: C₁₄H₁₈O₄).



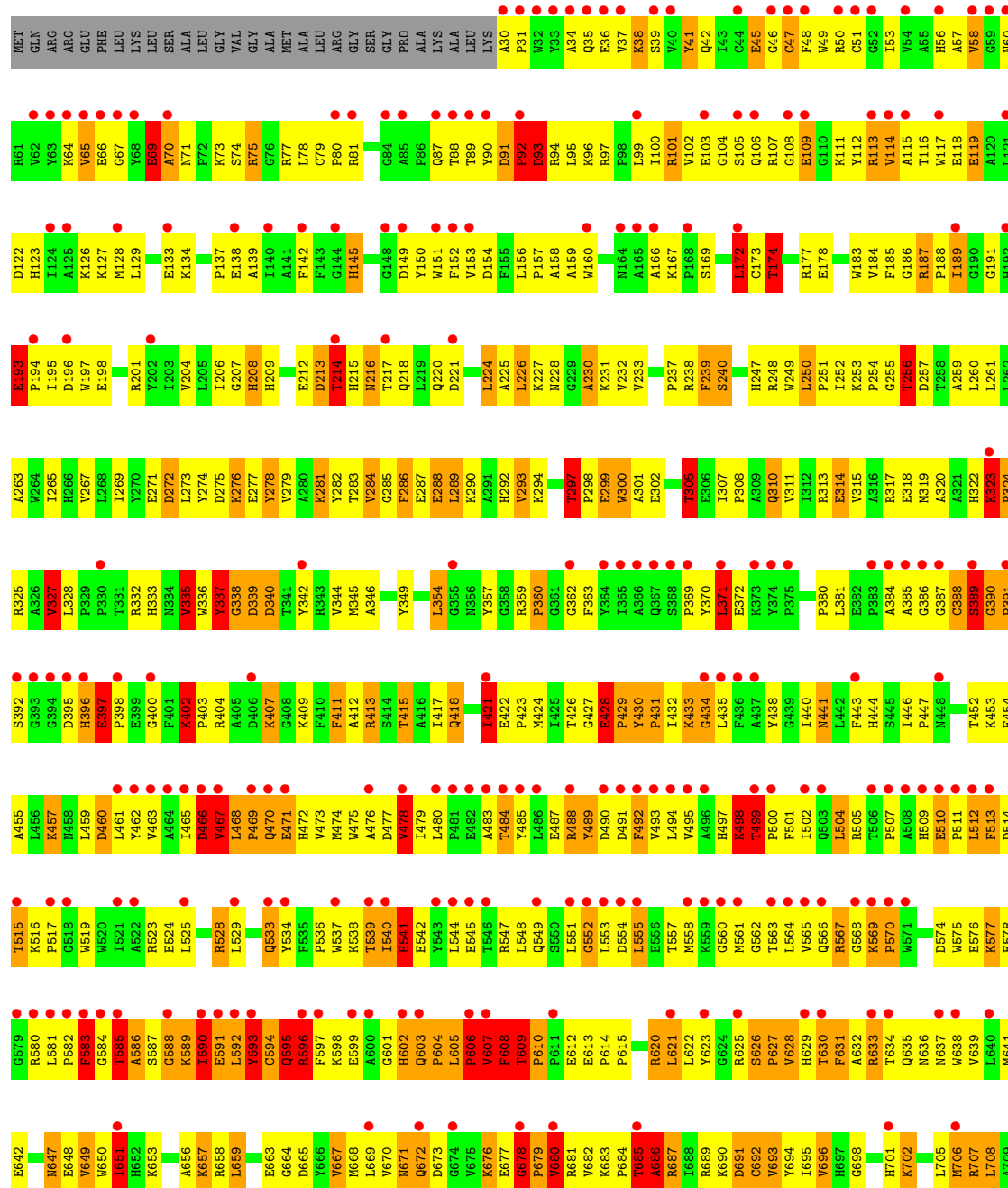
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			18	14	4		
7	G	1	Total	C	O	0	0
			18	14	4		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	387	Total	O	0	0
			387	387		
8	B	149	Total	O	0	0
			149	149		
8	C	90	Total	O	0	0
			90	90		
8	E	452	Total	O	0	0
			452	452		
8	F	130	Total	O	0	0
			130	130		
8	G	77	Total	O	0	0
			77	77		

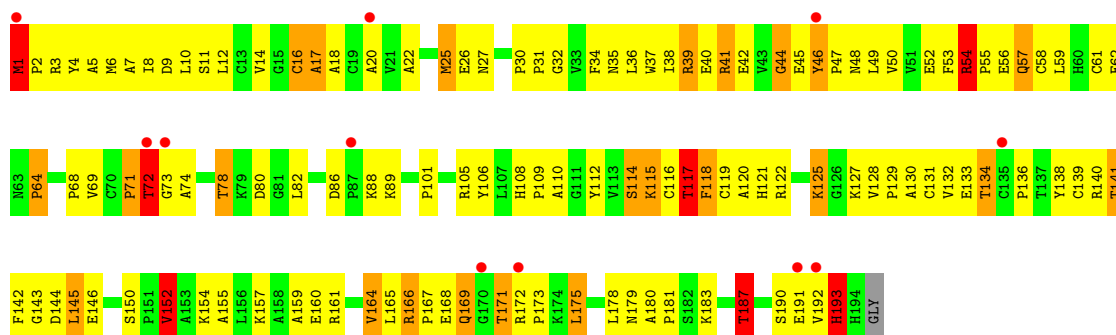


Molecule 1: THIOSULFATE REDUCTASE

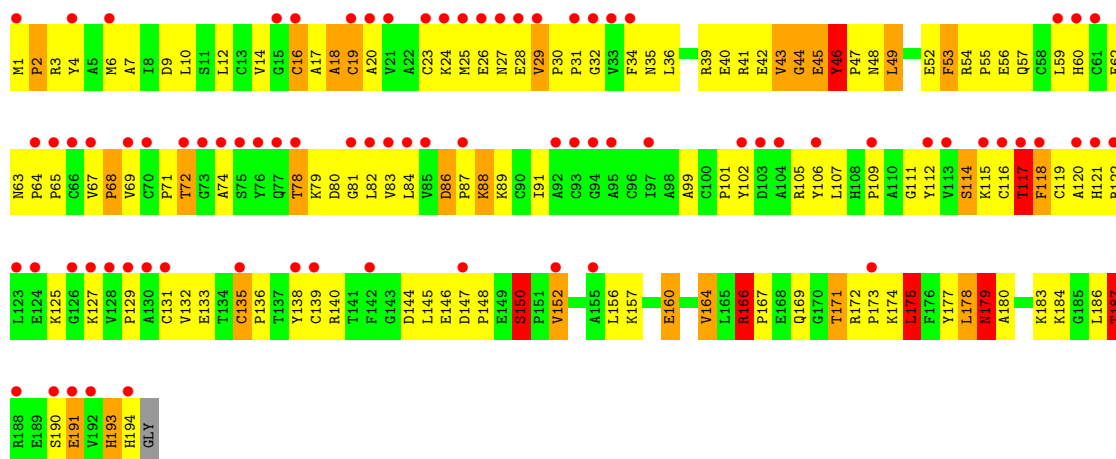




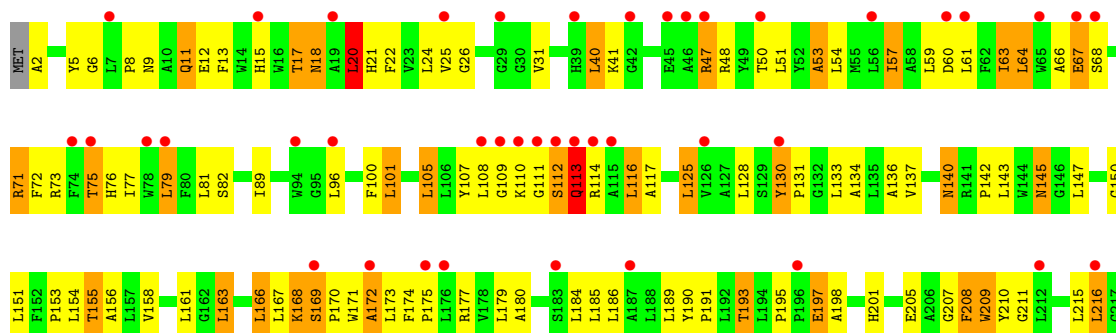
• Molecule 2: NRFC PROTEIN

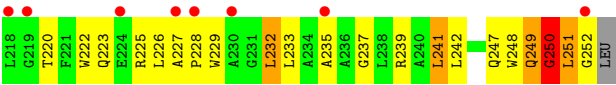


• Molecule 2: NRFC PROTEIN

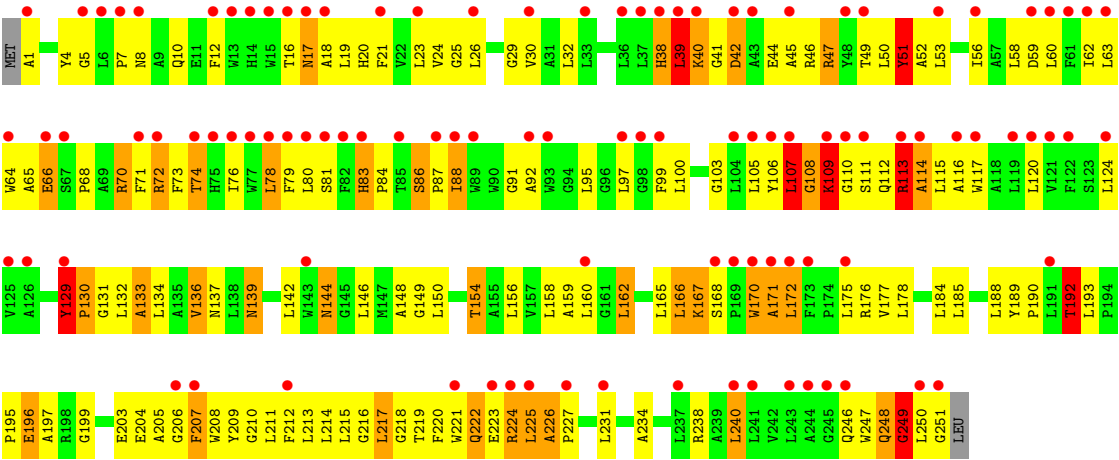


• Molecule 3: HYPOTHETICAL MEMBRANE SPANNING PROTEIN





● Molecule 3: HYPOTHETICAL MEMBRANE SPANNING PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	114.59Å 161.16Å 239.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.10 40.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (40.00-3.10) 99.2 (40.00-3.10)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 3.12Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.301 , 0.314 0.293 , 0.291	Depositor DCC
R_{free} test set	1642 reflections (2.04%)	wwPDB-VP
Wilson B-factor (Å ²)	75.2	Xtriage
Anisotropy	0.484	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 97.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	20229	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% 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: SF4, UQ1, MGD, MO

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	1.01	3/6079 (0.0%)	1.58	128/8267 (1.5%)
1	E	1.16	17/6079 (0.3%)	1.73	167/8267 (2.0%)
2	B	1.18	1/1512 (0.1%)	1.63	29/2058 (1.4%)
2	F	1.18	5/1512 (0.3%)	1.75	43/2058 (2.1%)
3	C	0.93	4/2016 (0.2%)	1.33	26/2764 (0.9%)
3	G	0.97	1/2016 (0.0%)	1.55	45/2764 (1.6%)
All	All	1.08	31/19214 (0.2%)	1.62	438/26178 (1.7%)

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	E	0	1

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	592	LEU	CG-CD1	15.83	2.04	1.52
1	E	387	GLY	C-N	-11.44	1.17	1.33
3	C	114	ARG	NE-CZ	9.20	1.43	1.33
1	E	593	TYR	CA-C	-8.97	1.40	1.52
1	A	364	TYR	C-O	-8.82	1.12	1.24

The worst 5 of 438 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	401	PHE	N-CA-C	22.60	140.98	113.41
2	F	171	THR	N-CA-C	22.29	137.68	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	114	ALA	N-CA-C	-19.80	89.41	114.56
1	E	467	VAL	N-CA-C	17.70	128.94	110.36
1	A	189	ILE	N-CA-C	-17.26	96.96	111.81

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	323	LYS	Mainchain

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	5896	0	5814	830	3
1	E	5896	0	5815	786	3
2	B	1475	0	1453	185	0
2	F	1475	0	1453	159	0
3	C	1948	0	2001	181	0
3	G	1948	0	2004	208	0
4	A	8	0	0	2	0
4	B	32	0	0	8	0
4	E	8	0	0	1	0
4	F	32	0	0	6	0
5	A	94	0	43	12	0
5	E	94	0	43	23	0
6	A	1	0	0	0	0
6	E	1	0	0	1	0
7	C	18	0	18	27	0
7	G	18	0	18	22	0
8	A	387	0	0	104	0
8	B	149	0	0	41	0
8	C	90	0	0	11	0
8	E	452	0	0	141	0
8	F	130	0	0	31	0
8	G	77	0	0	35	0
All	All	20229	0	18662	2297	3

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 61.

The worst 5 of 2297 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:602:HIS:CE1	1:A:606:PRO:HG3	1.48	1.46
3:G:78:LEU:HD21	7:G:1251:UQ1:C7	1.49	1.43
1:E:592:LEU:HA	1:E:603:GLN:NE2	1.19	1.41
1:A:186:GLY:HA3	1:A:583:PHE:C	1.40	1.41
1:E:605:LEU:H	1:E:605:LEU:CD2	1.30	1.39

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:GLU:OE2	1:E:133:GLU:C[2_674]	1.77	0.43
1:A:399:GLU:OE2	1:E:134:LYS:N[2_674]	1.83	0.37
1:A:399:GLU:OE2	1:E:133:GLU:O[2_674]	2.04	0.16

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	733/765 (96%)	653 (89%)	45 (6%)	35 (5%)	2	11
1	E	733/765 (96%)	639 (87%)	59 (8%)	35 (5%)	2	11
2	B	192/195 (98%)	178 (93%)	11 (6%)	3 (2%)	7	30
2	F	192/195 (98%)	179 (93%)	9 (5%)	4 (2%)	5	25
3	C	249/253 (98%)	233 (94%)	11 (4%)	5 (2%)	6	25
3	G	249/253 (98%)	220 (88%)	21 (8%)	8 (3%)	3	18
All	All	2348/2426 (97%)	2102 (90%)	156 (7%)	90 (4%)	2	15

5 of 90 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	336	TRP
1	A	340	ASP
1	A	428	GLU
1	A	429	PRO
1	A	431	PRO

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	610/632 (96%)	491 (80%)	119 (20%)	1	6
1	E	610/632 (96%)	494 (81%)	116 (19%)	1	7
2	B	162/163 (99%)	140 (86%)	22 (14%)	3	16
2	F	162/163 (99%)	143 (88%)	19 (12%)	5	22
3	C	185/187 (99%)	160 (86%)	25 (14%)	4	16
3	G	185/187 (99%)	162 (88%)	23 (12%)	4	19
All	All	1914/1964 (98%)	1590 (83%)	324 (17%)	2	10

5 of 324 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	541	GLU
2	F	78	THR
1	E	581	LEU
1	E	663	GLU
2	F	191	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	603	GLN
3	G	10	GLN

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Mol	Chain	Res	Type
1	E	647	ASN
2	F	48	ASN
3	G	139	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 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
7	UQ1	C	1252	-	18,18,18	1.09	2 (11%)	22,25,25	1.66	6 (27%)
4	SF4	B	1196	2	0,12,12	-	-	-		
5	MGD	E	1766	6	45,52,52	2.96	19 (42%)	54,81,81	2.64	18 (33%)
4	SF4	F	1195	2	0,12,12	-	-	-		
5	MGD	A	1766	6	45,52,52	2.86	22 (48%)	54,81,81	2.93	17 (31%)
4	SF4	E	1764	1	0,12,12	-	-	-		
4	SF4	A	1764	1	0,12,12	-	-	-		
4	SF4	B	1194	2	0,12,12	-	-	-		
4	SF4	F	1196	2	0,12,12	-	-	-		
5	MGD	E	1765	6	45,52,52	2.89	28 (62%)	54,81,81	2.81	18 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SF4	B	1195	2	0,12,12	-	-	-		
4	SF4	F	1194	2	0,12,12	-	-	-		
4	SF4	F	1197	2	0,12,12	-	-	-		
4	SF4	B	1197	2	0,12,12	-	-	-		
5	MGD	A	1765	6	45,52,52	2.81	20 (44%)	54,81,81	2.88	16 (29%)
7	UQ1	G	1251	-	18,18,18	1.09	2 (11%)	22,25,25	1.66	6 (27%)

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
7	UQ1	C	1252	-	-	3/9/33/33	0/1/1/1
4	SF4	B	1196	2	-	-	0/6/5/5
5	MGD	E	1766	6	-	1/22/66/66	0/6/6/6
4	SF4	B	1195	2	-	-	0/6/5/5
5	MGD	A	1766	6	-	1/22/66/66	0/6/6/6
4	SF4	F	1195	2	-	-	0/6/5/5
4	SF4	E	1764	1	-	-	0/6/5/5
4	SF4	A	1764	1	-	-	0/6/5/5
4	SF4	F	1196	2	-	-	0/6/5/5
5	MGD	E	1765	6	-	2/22/66/66	0/6/6/6
4	SF4	B	1194	2	-	-	0/6/5/5
4	SF4	F	1194	2	-	-	0/6/5/5
4	SF4	F	1197	2	-	-	0/6/5/5
4	SF4	B	1197	2	-	-	0/6/5/5
5	MGD	A	1765	6	-	6/22/66/66	0/6/6/6
7	UQ1	G	1251	-	-	3/9/33/33	0/1/1/1

The worst 5 of 93 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1765	MGD	C23-C14	-9.87	1.45	1.53
5	E	1766	MGD	C21-N22	-9.57	1.25	1.35
5	A	1766	MGD	C14-N15	-7.80	1.37	1.46
5	A	1766	MGD	C23-C14	-7.36	1.47	1.53
5	E	1765	MGD	C23-C14	-7.11	1.48	1.53

The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1766	MGD	O11-C23-C14	14.24	118.46	108.96
5	A	1765	MGD	O11-C23-C14	12.67	117.42	108.96
5	E	1766	MGD	O11-C23-C14	10.85	116.20	108.96
5	E	1765	MGD	O11-C23-N22	-9.77	98.53	108.57
5	E	1766	MGD	C5-C4-N3	-7.07	117.00	128.46

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1765	MGD	C5'-O5'-PB-O2B
5	E	1765	MGD	O4'-C4'-C5'-O5'
7	C	1252	UQ1	C1-C6-C7-C8
7	C	1252	UQ1	C5-C6-C7-C8
7	G	1251	UQ1	C1-C6-C7-C8

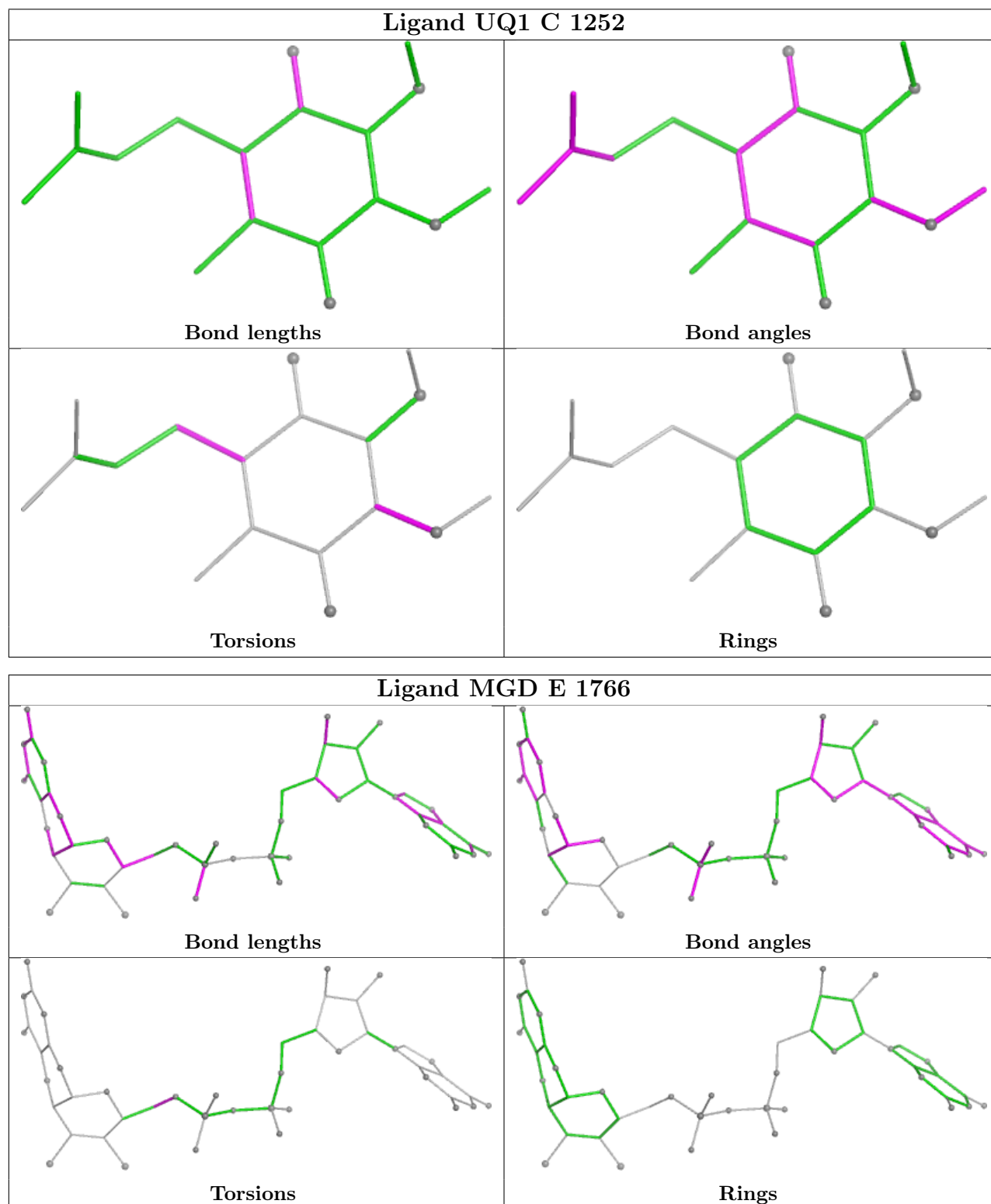
There are no ring outliers.

14 monomers are involved in 101 short contacts:

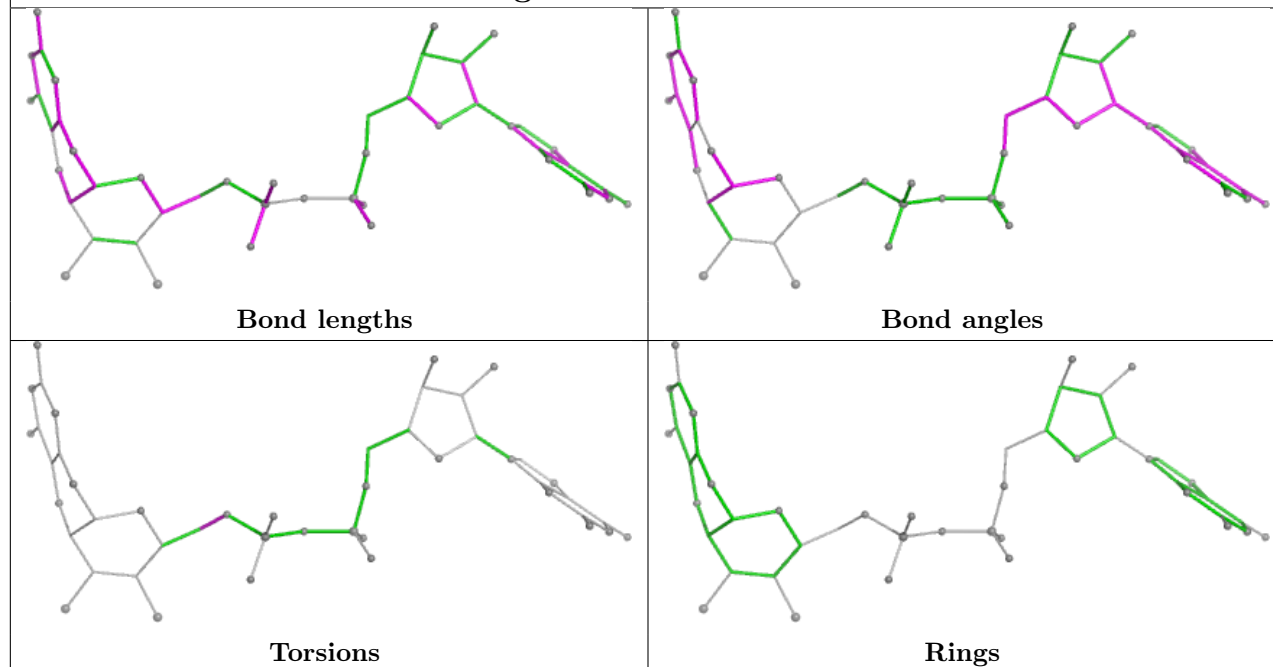
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	1252	UQ1	27	0
4	B	1196	SF4	2	0
5	E	1766	MGD	13	0
4	F	1195	SF4	2	0
5	A	1766	MGD	5	0
4	E	1764	SF4	1	0
4	A	1764	SF4	2	0
4	B	1194	SF4	3	0
4	F	1196	SF4	1	0
5	E	1765	MGD	10	0
4	B	1195	SF4	3	0
4	F	1194	SF4	3	0
5	A	1765	MGD	7	0
7	G	1251	UQ1	22	0

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

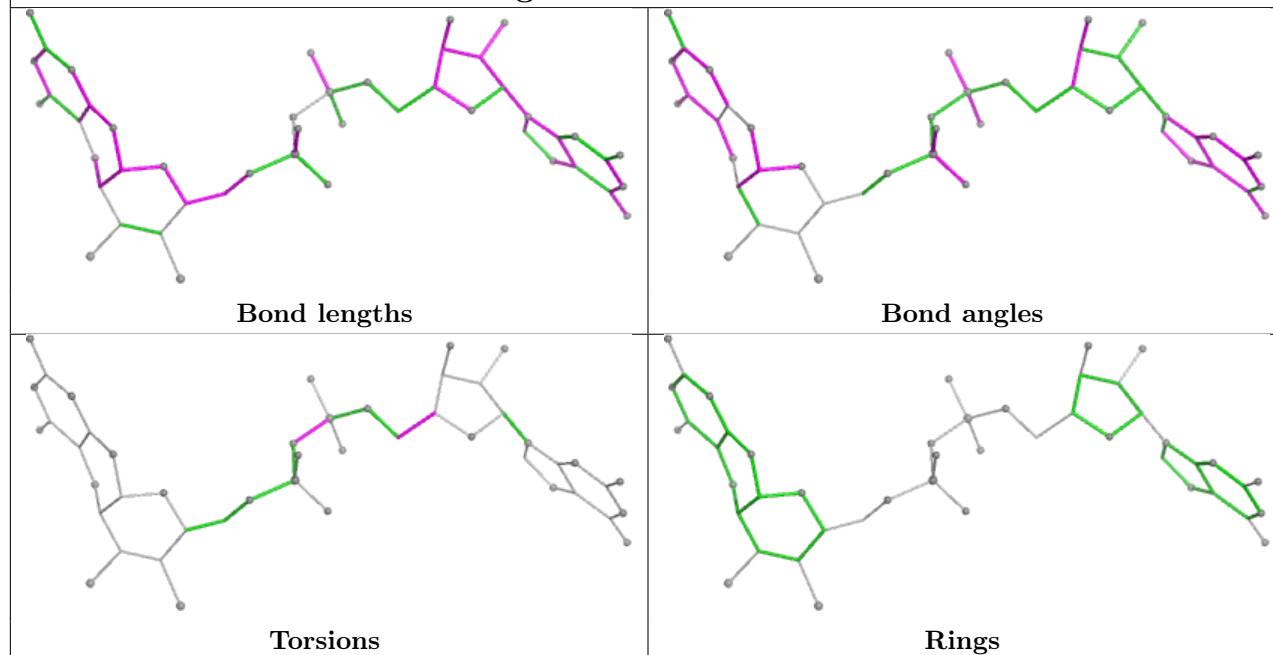
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

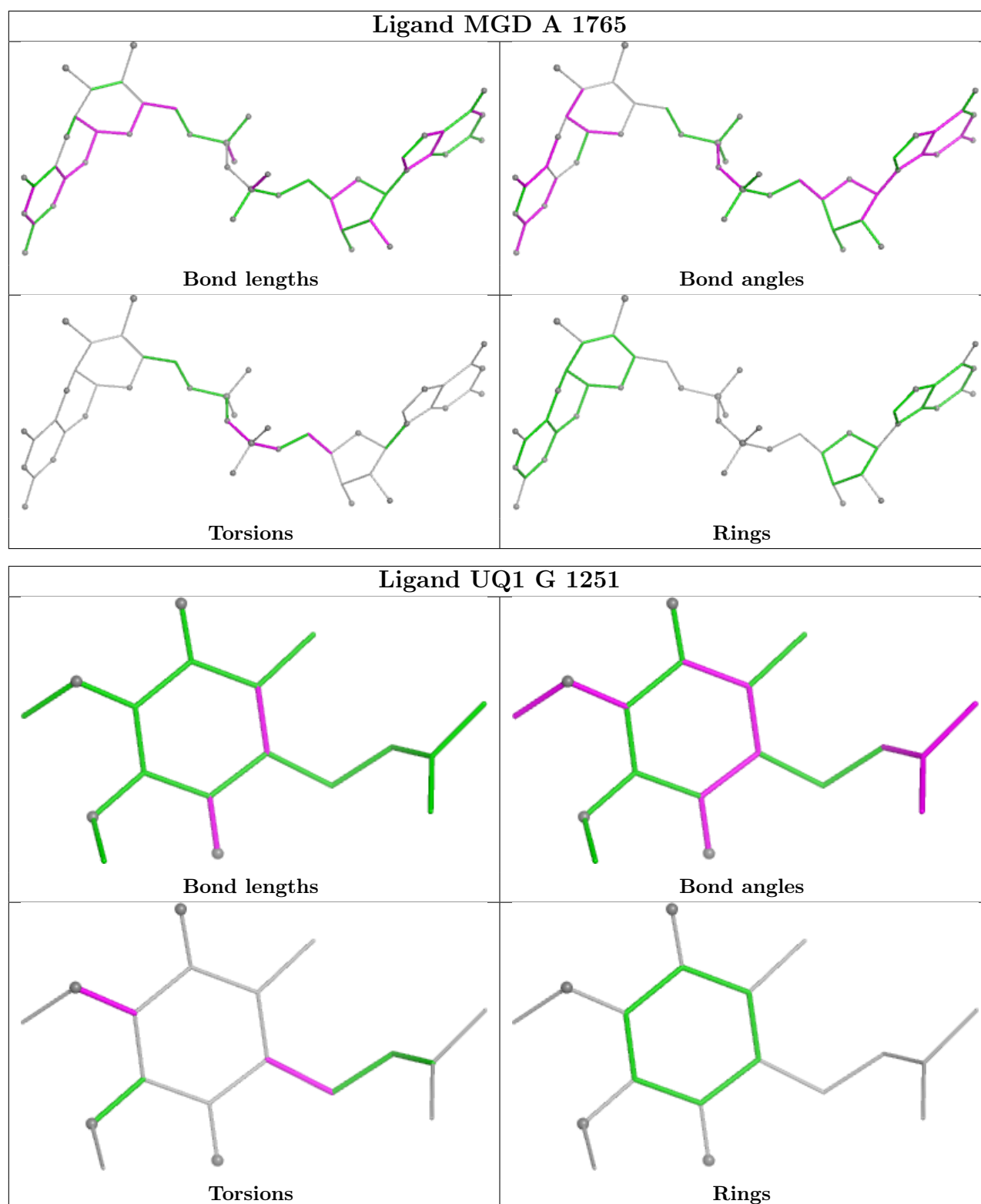


Ligand MGD A 1766



Ligand MGD E 1765





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	E	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	387:GLY	C	388:CYS	N	1.17

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	735/765 (96%)	1.44	175 (23%) 2 1	42, 73, 106, 157	0
1	E	735/765 (96%)	1.70	231 (31%) 1 1	44, 75, 104, 157	0
2	B	194/195 (99%)	0.74	11 (5%) 29 16	43, 61, 83, 106	0
2	F	194/195 (99%)	1.94	81 (41%) 0 0	50, 73, 91, 109	0
3	C	251/253 (99%)	1.34	50 (19%) 3 1	45, 75, 103, 119	0
3	G	251/253 (99%)	1.87	105 (41%) 0 0	55, 86, 115, 132	0
All	All	2360/2426 (97%)	1.54	653 (27%) 1 1	42, 74, 106, 157	0

The worst 5 of 653 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	251	GLY	13.8
3	C	252	GLY	9.8
1	E	518	GLY	8.5
1	A	362	GLY	7.7
1	A	570	PRO	7.4

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

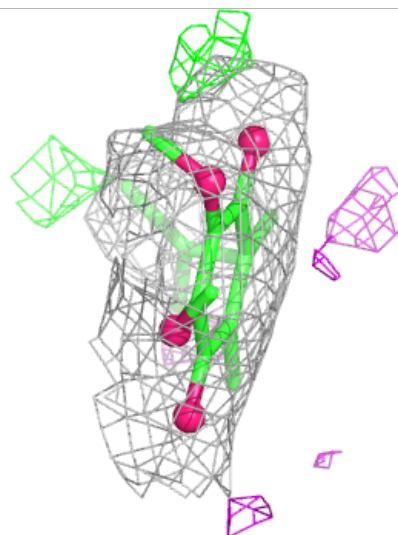
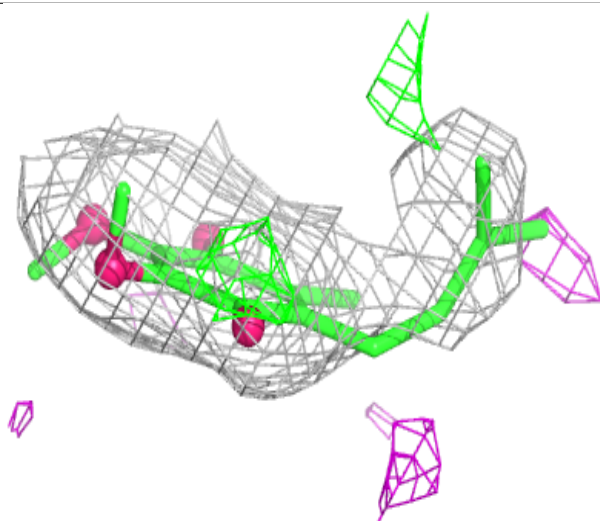
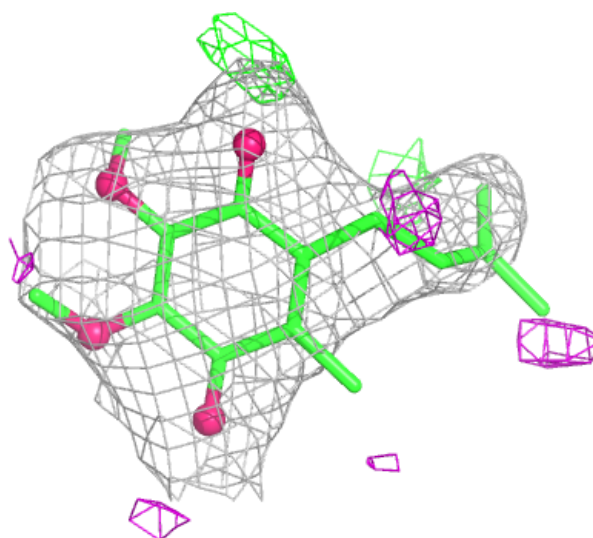
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	UQ1	G	1251	18/18	0.79	0.22	82,86,87,88	0
4	SF4	E	1764	8/8	0.88	0.15	60,69,74,77	0
4	SF4	F	1196	8/8	0.89	0.14	66,72,74,79	0
4	SF4	F	1197	8/8	0.89	0.13	77,82,85,86	0
5	MGD	E	1765	47/47	0.89	0.15	50,61,75,76	0
4	SF4	F	1195	8/8	0.89	0.15	56,63,69,69	0
5	MGD	E	1766	47/47	0.91	0.14	45,54,61,62	0
6	MO	A	1767	1/1	0.91	0.08	55,55,55,55	0
4	SF4	F	1194	8/8	0.91	0.13	67,71,72,73	0
5	MGD	A	1765	47/47	0.93	0.11	52,55,58,59	0
5	MGD	A	1766	47/47	0.93	0.13	46,50,63,64	0
4	SF4	B	1196	8/8	0.93	0.12	48,56,63,63	0
7	UQ1	C	1252	18/18	0.94	0.14	75,77,80,80	0
4	SF4	B	1194	8/8	0.96	0.08	62,65,67,68	0
6	MO	E	1767	1/1	0.96	0.07	60,60,60,60	0
4	SF4	A	1764	8/8	0.97	0.08	50,54,57,57	0
4	SF4	B	1195	8/8	0.97	0.07	60,61,63,65	0
4	SF4	B	1197	8/8	0.98	0.06	52,55,56,57	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.

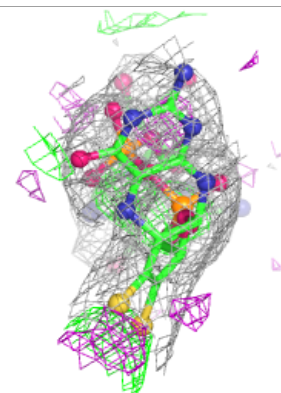
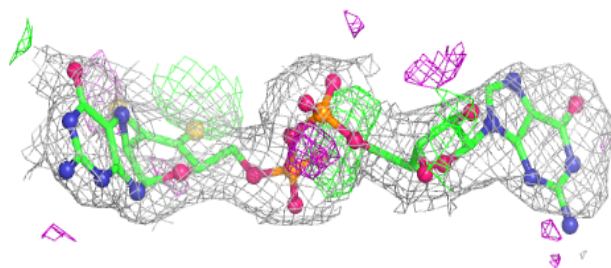
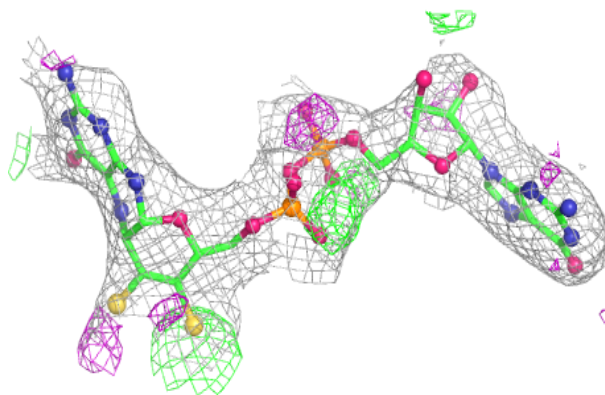
Electron density around UQ1 G 1251:

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

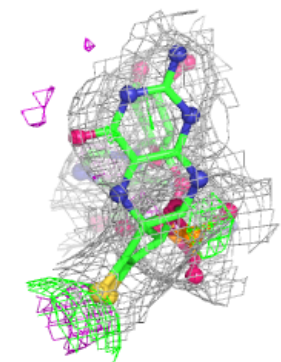
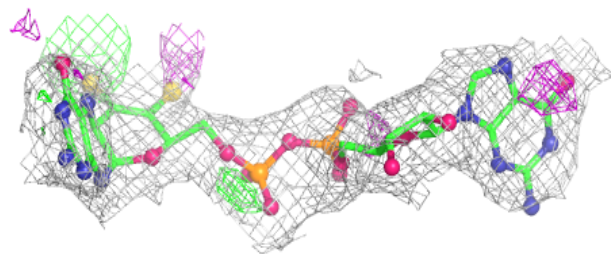
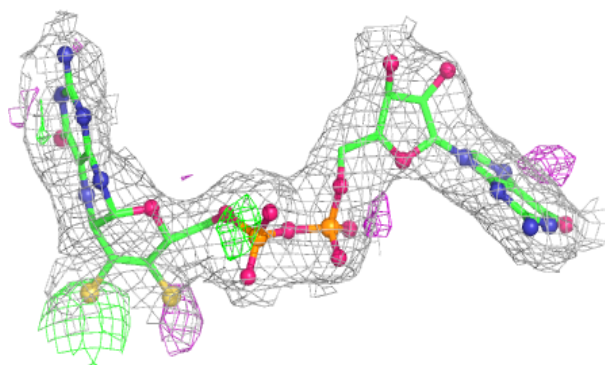


Electron density around MGD E 1765:

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

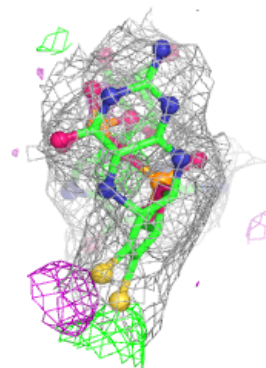
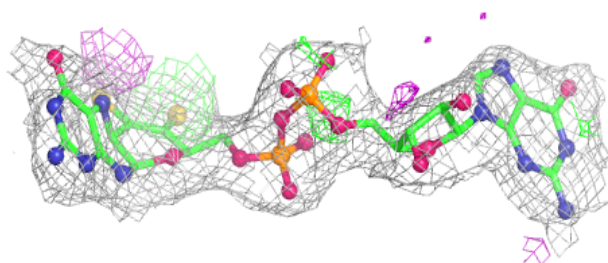
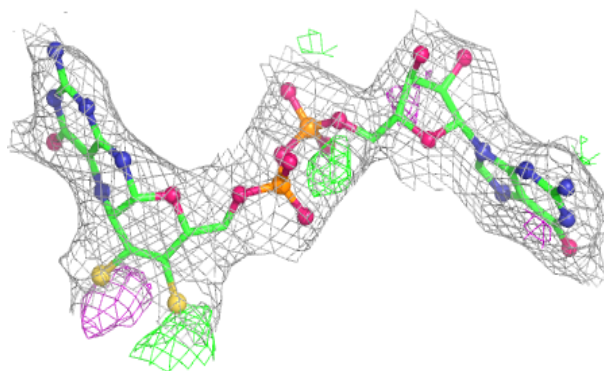
**Electron density around MGD E 1766:**

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

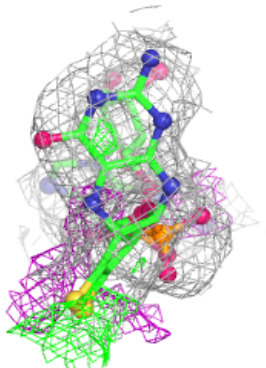
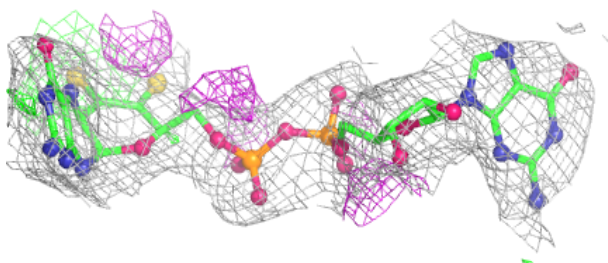
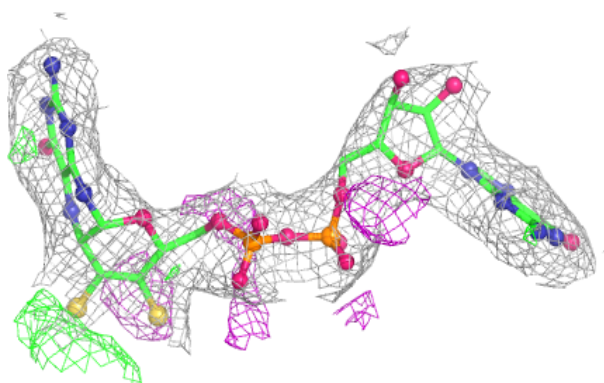


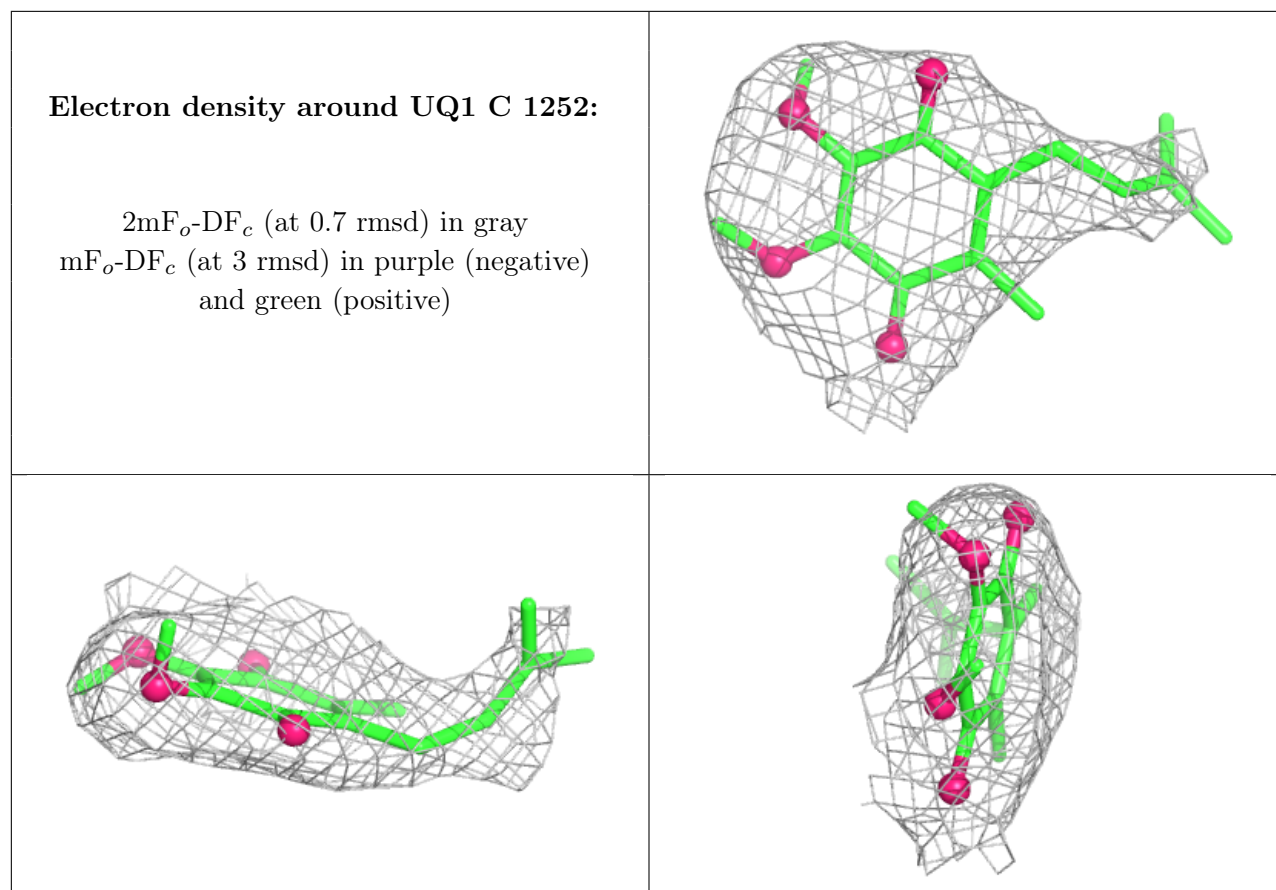
Electron density around MGD A 1765:

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

**Electron density around MGD A 1766:**

$2mF_o-DF_c$ (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.