



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2023 – 10:53 PM EDT

PDB ID : 7LNH  
Title : S-adenosylmethionine synthetase co-crystallized with UppNHp  
Authors : Tan, L.L.; Jackson, C.J.  
Deposited on : 2021-02-07  
Resolution : 2.50 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](mailto: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>.

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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

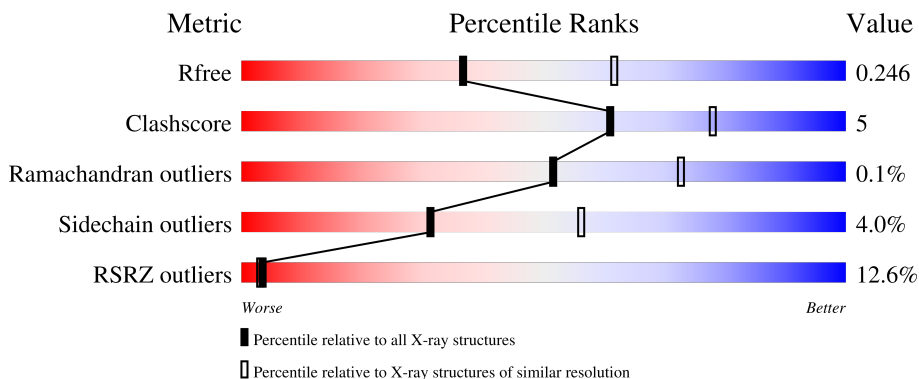
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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  $\geq 3$ , 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	395	
1	B	395	

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
2	YQP	B	502	X	-	-	-

## 2 Entry composition i

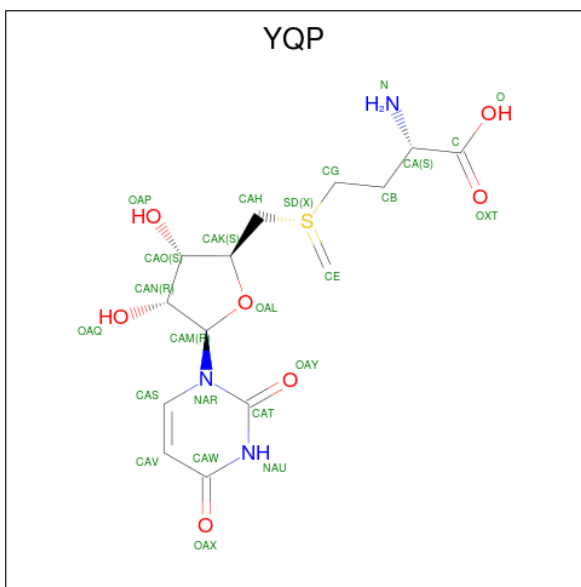
There are 4 unique types of molecules in this entry. The entry contains 6146 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 S-adenosylmethionine synthase isoform type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	381	Total 2963	C 1872	N 518	O 562	S 11	0	0	0
1	B	380	Total 3101	C 1956	N 543	O 590	S 12	0	19	0

- Molecule 2 is (2 {S})-2-azanyl-4-[[[(2 {S}),3 {S}),4 {R}),5 {R}]]-5-[2,4-bis(oxidanylidene)pyrimidin-1-yl]-3,4-bis(oxidanyl)oxolan-2-yl)methyl-methyl- $\text{S}^3$ -sulfanyl]butanoic acid (three-letter code: YQP) (formula:  $\text{C}_{14}\text{H}_{21}\text{N}_3\text{O}_7\text{S}$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	Total 25	C 14	N 3	O 7	S 1	0	1
2	B	1	Total 25	C 14	N 3	O 7	S 1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $\text{C}_2\text{H}_6\text{O}_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 4 2 2	0	0

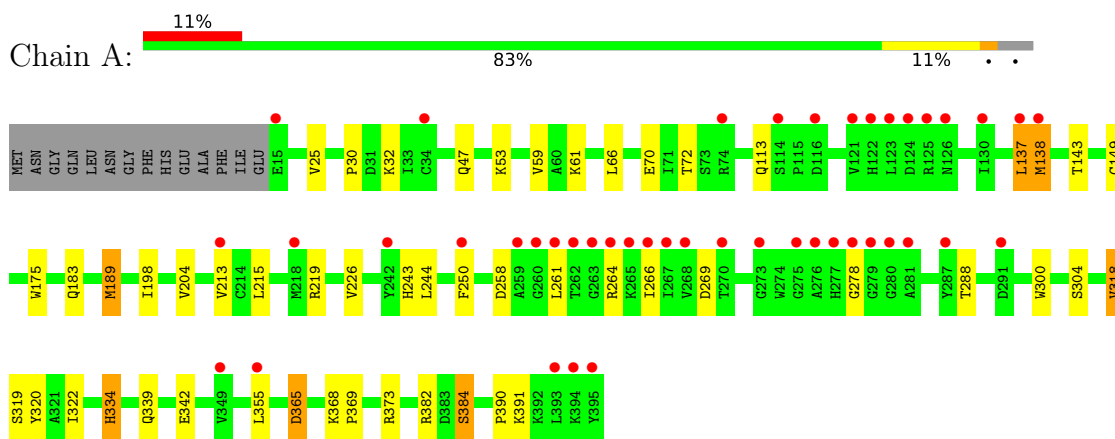
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	7	Total O 7 7	0	0
4	B	21	Total O 21 21	0	0

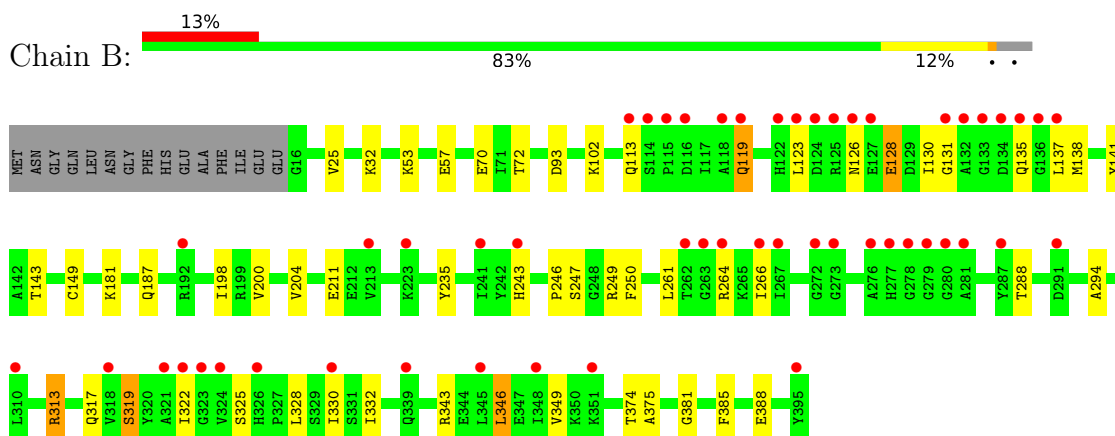
### 3 Residue-property plots [i](#)

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: S-adenosylmethionine synthase isoform type-2



- Molecule 1: S-adenosylmethionine synthase isoform type-2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	144.19Å 144.19Å 188.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.40 – 2.50 39.40 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (39.40-2.50) 99.5 (39.40-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.20 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.219 , 0.246 0.220 , 0.246	Depositor DCC
$R_{free}$ test set	2078 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	74.6	Xtrriage
Anisotropy	0.479	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 66.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6146	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	103.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: YQP, EDO

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	0.25	0/3022	0.43	0/4088
1	B	0.24	0/3162	0.43	0/4276
All	All	0.24	0/6184	0.43	0/8364

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	2963	0	2956	29	0
1	B	3101	0	3081	32	0
2	A	25	0	0	1	0
2	B	25	0	0	0	0
3	B	4	0	6	0	0
4	A	7	0	0	0	0
4	B	21	0	0	2	0
All	All	6146	0	6043	55	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 5.



All (55) 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:72:THR:HG23	1:B:113:GLN:H	1.53	0.74
1:B:211:GLU:OE2	1:B:249:ARG:NH2	2.30	0.64
1:B:330:ILE:HB	1:B:346:LEU:HD11	1.80	0.62
1:A:30:PRO:HG2	1:A:258:ASP:HB3	1.81	0.61
1:B:25:VAL:HG12	1:B:181:LYS:HG2	1.82	0.60
1:A:261:LEU:HD22	1:B:261:LEU:HD22	1.85	0.58
1:B:200:VAL:HG23	1:B:235:TYR:HB3	1.86	0.57
1:A:70:GLU:HB3	1:A:113:GLN:HA	1.86	0.57
1:B:131[A]:GLY:HA2	1:B:325:SER:HA	1.87	0.56
1:B:53:LYS:HE3	1:B:288:THR:HG21	1.87	0.56
1:A:72:THR:HG23	1:A:113:GLN:H	1.72	0.55
1:A:53:LYS:HE3	1:A:288:THR:HG21	1.90	0.53
1:A:189:MET:HB2	1:A:198:ILE:HD11	1.91	0.52
1:A:204:VAL:HG21	1:B:135[A]:GLN:NE2	2.26	0.51
1:A:215:LEU:HD21	1:A:219:ARG:CZ	2.41	0.51
1:A:138:MET:HE1	1:A:320:TYR:CD1	2.46	0.50
1:A:322:ILE:HG23	1:B:246:PRO:HG2	1.91	0.50
2:A:601[B]:YQP:OXT	1:B:113:GLN:NE2	2.44	0.50
1:A:137:LEU:O	1:A:278:GLY:HA3	2.11	0.50
1:B:204:VAL:HG22	1:B:243:HIS:HB2	1.94	0.49
1:A:266:ILE:HD11	1:B:266:ILE:HD11	1.95	0.48
1:A:47:GLN:HG3	1:A:369:PRO:HG3	1.95	0.48
1:B:141:TYR:OH	1:B:313:ARG:HD3	2.13	0.48
1:B:138[A]:MET:HG2	1:B:294:ALA:HB3	1.95	0.48
1:A:61:LYS:HD2	1:A:61:LYS:HA	1.63	0.47
1:B:187:GLN:HG2	1:B:198:ILE:HD11	1.95	0.47
1:A:138:MET:HE1	1:A:320:TYR:HD1	1.78	0.47
1:A:304:SER:HA	1:A:390:PRO:HB3	1.97	0.47
1:B:374:THR:HG22	1:B:385:PHE:CE1	2.50	0.46
1:B:119:GLN:HA	1:B:123[B]:LEU:HB2	1.98	0.45
1:B:32:LYS:HD2	1:B:375:ALA:O	2.16	0.45
1:A:143:THR:O	1:A:149:CYS:HA	2.17	0.45
1:A:219:ARG:NE	1:A:244:LEU:O	2.50	0.45
1:A:365:ASP:HB3	1:A:368:LYS:HE2	1.97	0.45
1:B:70:GLU:HB3	1:B:113:GLN:HA	1.99	0.44
1:A:261:LEU:HD11	1:B:57:GLU:HB3	1.99	0.44
1:B:247:SER:OG	4:B:601:HOH:O	2.21	0.44
1:B:126[A]:ASN:O	1:B:128[A]:GLU:N	2.51	0.44
1:B:135[A]:GLN:O	4:B:602:HOH:O	2.21	0.44
1:B:135[B]:GLN:H	1:B:135[B]:GLN:HG3	1.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:ARG:HH22	1:A:384:SER:HB3	1.84	0.43
1:B:319:SER:O	1:B:328:LEU:HB3	2.18	0.43
1:A:59:VAL:HB	1:A:66:LEU:HB3	2.00	0.43
1:A:243:HIS:CG	1:B:322:ILE:HD12	2.53	0.42
1:B:332:ILE:HD11	1:B:349:VAL:HG21	2.01	0.42
1:B:381:GLY:H	1:B:388:GLU:CD	2.23	0.42
1:A:300:TRP:CZ2	1:A:391:LYS:HB2	2.53	0.42
1:A:261:LEU:HD12	1:A:264:ARG:HH11	1.85	0.42
1:A:318:VAL:HG11	1:A:355:LEU:HD13	2.02	0.41
1:A:334:HIS:CE1	1:A:342:GLU:HG3	2.55	0.41
1:B:93:ASP:O	1:B:102:LYS:NZ	2.53	0.41
1:B:261:LEU:HB2	1:B:264:ARG:HG3	2.03	0.41
1:B:32:LYS:HD3	1:B:32:LYS:HA	1.83	0.41
1:A:175:TRP:HB3	1:A:213:VAL:HG21	2.02	0.41
1:A:32:LYS:NZ	1:A:269:ASP:OD1	2.51	0.41

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	379/395 (96%)	357 (94%)	21 (6%)	1 (0%)	41	61
1	B	397/395 (100%)	373 (94%)	24 (6%)	0	100	100
All	All	776/790 (98%)	730 (94%)	45 (6%)	1 (0%)	51	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	SER

### 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	316/327 (97%)	303 (96%)	13 (4%)	30	55
1	B	330/327 (101%)	315 (96%)	15 (4%)	27	51
All	All	646/654 (99%)	618 (96%)	28 (4%)	31	53

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	VAL
1	A	137	LEU
1	A	138	MET
1	A	183	GLN
1	A	189	MET
1	A	226	VAL
1	A	250	PHE
1	A	318	VAL
1	A	319	SER
1	A	334	HIS
1	A	339	GLN
1	A	365	ASP
1	A	382	ARG
1	B	119	GLN
1	B	128[A]	GLU
1	B	128[B]	GLU
1	B	130[A]	ILE
1	B	130[B]	ILE
1	B	137[A]	LEU
1	B	137[B]	LEU
1	B	143	THR
1	B	149	CYS
1	B	250	PHE
1	B	313	ARG
1	B	317	GLN
1	B	319	SER
1	B	343	ARG

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Mol	Chain	Res	Type
1	B	346	LEU

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

### 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](#)

3 ligands are modelled in this entry.

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	YQP	B	502	-	21,26,26	3.84	10 (47%)	31,37,37	2.05	8 (25%)
3	EDO	B	501	-	3,3,3	0.46	0	2,2,2	0.32	0
2	YQP	A	601[B]	-	21,26,26	3.83	11 (52%)	31,37,37	2.03	7 (22%)

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	YQP	B	502	-	1/1/7/7	11/15/33/33	0/2/2/2
3	EDO	B	501	-	-	0/1/1/1	-
2	YQP	A	601[B]	-	-	8/15/33/33	0/2/2/2

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	YQP	OAY-CAT	9.72	1.40	1.23
2	A	601[B]	YQP	OAY-CAT	9.62	1.40	1.23
2	B	502	YQP	OAX-CAW	8.58	1.41	1.24
2	A	601[B]	YQP	OAX-CAW	8.56	1.41	1.24
2	B	502	YQP	OAL-CAM	6.56	1.57	1.42
2	A	601[B]	YQP	OAL-CAM	6.45	1.57	1.42
2	A	601[B]	YQP	OAL-CAK	4.76	1.55	1.45
2	B	502	YQP	OAL-CAK	4.65	1.55	1.45
2	A	601[B]	YQP	CAT-NAU	4.44	1.45	1.38
2	B	502	YQP	CAT-NAU	4.41	1.45	1.38
2	A	601[B]	YQP	CAO-CAN	-3.87	1.42	1.53
2	B	502	YQP	CAO-CAN	-3.71	1.43	1.53
2	A	601[B]	YQP	OAQ-CAN	2.72	1.49	1.43
2	B	502	YQP	OAQ-CAN	2.67	1.49	1.43
2	B	502	YQP	CAS-CAV	2.60	1.41	1.35
2	A	601[B]	YQP	CAS-CAV	2.55	1.40	1.35
2	A	601[B]	YQP	CAO-CAK	-2.35	1.47	1.53
2	B	502	YQP	CAO-CAK	-2.18	1.47	1.53
2	B	502	YQP	OAP-CAO	2.12	1.48	1.43
2	A	601[B]	YQP	CAM-NAR	-2.02	1.41	1.47
2	A	601[B]	YQP	OAP-CAO	2.01	1.47	1.43

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	502	YQP	CAK-OAL-CAM	-5.26	97.87	109.47
2	A	601[B]	YQP	CAK-OAL-CAM	-5.06	98.31	109.47
2	A	601[B]	YQP	CAW-NAU-CAT	-4.71	120.37	126.58
2	B	502	YQP	CAW-NAU-CAT	-4.23	121.00	126.58
2	B	502	YQP	CAM-NAR-CAT	3.83	124.51	117.57
2	A	601[B]	YQP	NAU-CAT-NAR	3.72	119.83	114.89
2	A	601[B]	YQP	CAO-CAN-CAM	3.39	107.86	101.43
2	B	502	YQP	CAV-CAW-NAU	3.37	119.88	114.84
2	B	502	YQP	CAO-CAN-CAM	3.37	107.83	101.43
2	A	601[B]	YQP	CAV-CAW-NAU	3.36	119.86	114.84
2	B	502	YQP	NAU-CAT-NAR	3.34	119.32	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601[B]	YQP	OAX-CAW-CAV	-3.22	119.50	125.16
2	A	601[B]	YQP	CAM-NAR-CAT	3.01	123.02	117.57
2	B	502	YQP	OAX-CAW-CAV	-2.95	119.98	125.16
2	B	502	YQP	CAM-NAR-CAS	-2.02	116.43	120.84

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	502	YQP	CA

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601[B]	YQP	N-CA-CB-CG
2	A	601[B]	YQP	CB-CG-SD-CAH
2	A	601[B]	YQP	SD-CAH-CAK-CAO
2	A	601[B]	YQP	SD-CAH-CAK-OAL
2	B	502	YQP	OXT-C-CA-N
2	B	502	YQP	O-C-CA-N
2	B	502	YQP	CAN-CAM-NAR-CAT
2	A	601[B]	YQP	C-CA-CB-CG
2	B	502	YQP	O-C-CA-CB
2	B	502	YQP	OXT-C-CA-CB
2	B	502	YQP	CAN-CAM-NAR-CAS
2	B	502	YQP	OAL-CAM-NAR-CAS
2	B	502	YQP	CA-CB-CG-SD
2	B	502	YQP	OAL-CAM-NAR-CAT
2	A	601[B]	YQP	OAL-CAM-NAR-CAS
2	B	502	YQP	CB-CG-SD-CAH
2	B	502	YQP	N-CA-CB-CG
2	A	601[B]	YQP	CAN-CAM-NAR-CAT
2	A	601[B]	YQP	OAL-CAM-NAR-CAT

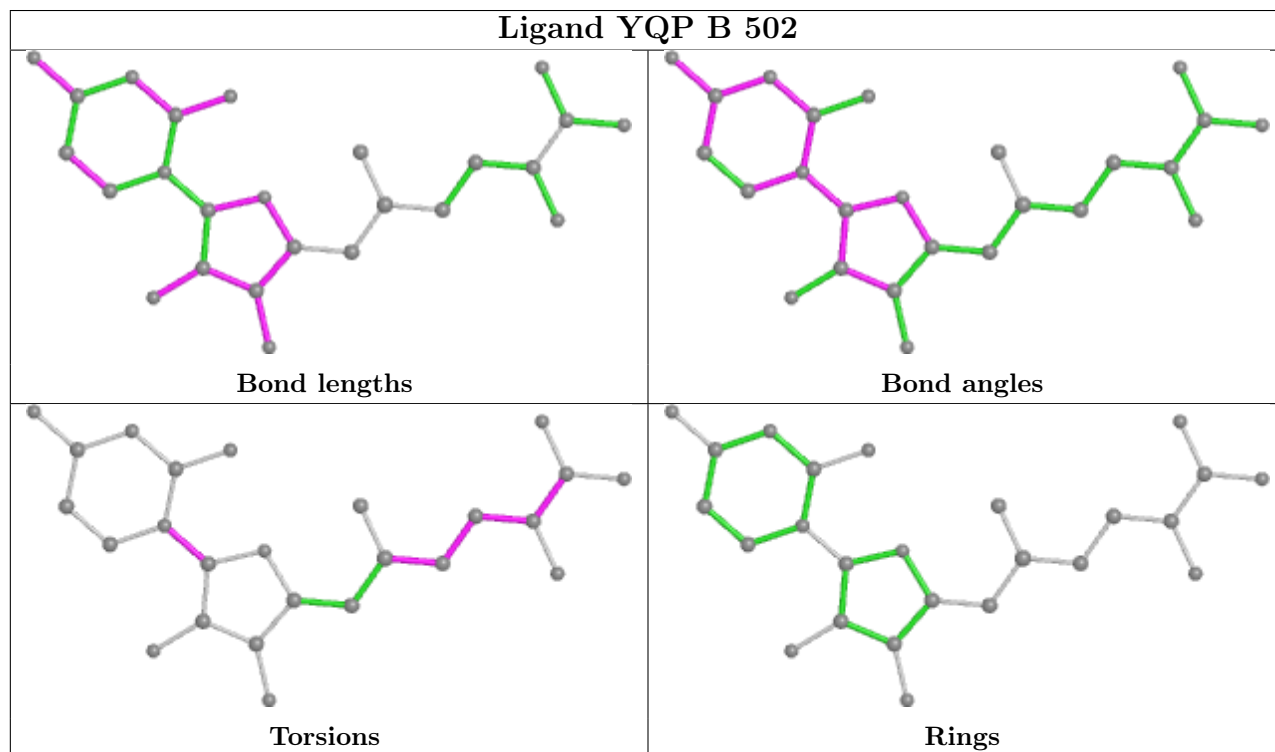
There are no ring outliers.

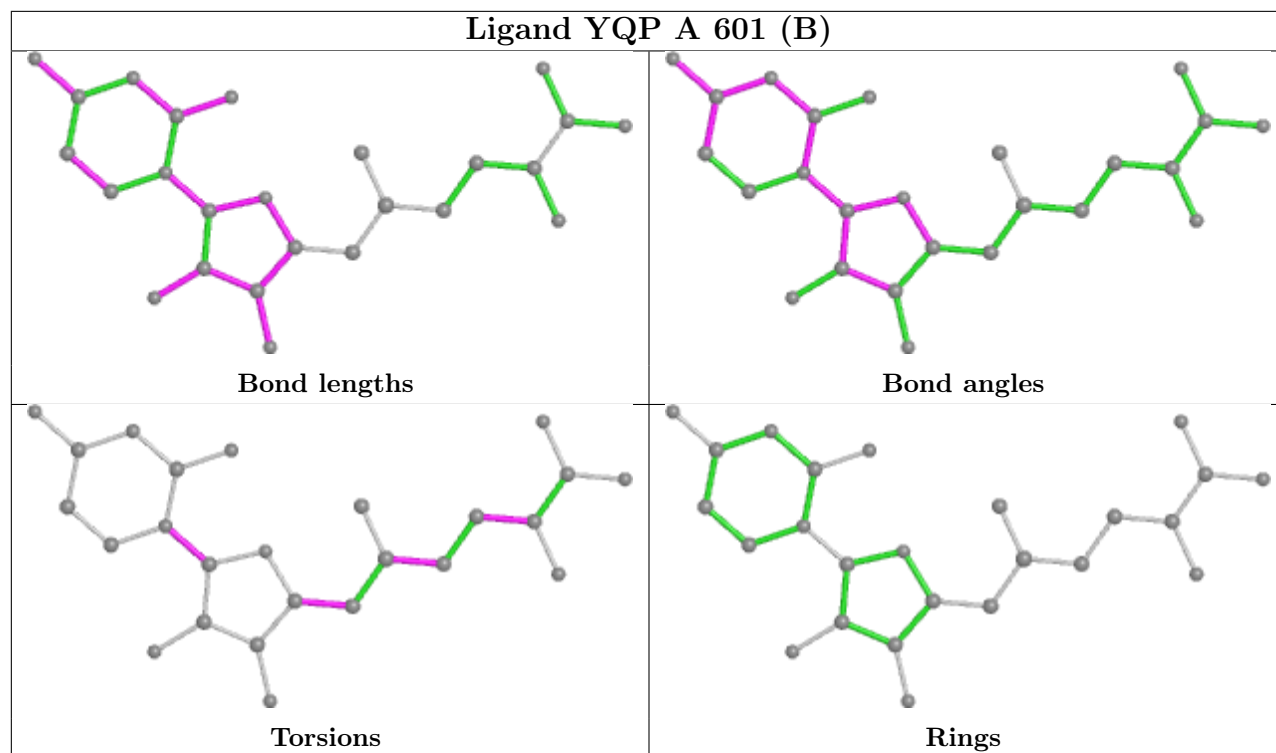
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601[B]	YQP	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	381/395 (96%)	0.57	44 (11%) 4 4	72, 100, 147, 187	0
1	B	380/395 (96%)	0.76	52 (13%) 3 2	69, 93, 147, 231	0
All	All	761/790 (96%)	0.67	96 (12%) 3 3	69, 97, 147, 231	0

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	133[A]	GLY	8.5
1	A	278	GLY	7.3
1	B	118	ALA	6.4
1	B	132[A]	ALA	6.0
1	B	124[A]	ASP	6.0
1	B	136[A]	GLY	6.0
1	B	122[A]	HIS	5.9
1	B	279	GLY	5.5
1	B	345	LEU	5.5
1	A	125	ARG	4.8
1	B	267	ILE	4.8
1	B	115	PRO	4.5
1	B	323	GLY	4.5
1	B	113	GLN	4.3
1	B	134[A]	ASP	4.3
1	A	279	GLY	4.2
1	B	123[A]	LEU	4.1
1	A	267	ILE	4.0
1	B	135[A]	GLN	3.9
1	B	280	GLY	3.9
1	B	322	ILE	3.8
1	B	310	LEU	3.8
1	A	280	GLY	3.8
1	B	273	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	114	SER	3.7
1	B	321	ALA	3.7
1	A	122	HIS	3.5
1	A	266	ILE	3.5
1	B	266	ILE	3.5
1	A	126	ASN	3.5
1	A	121	VAL	3.5
1	B	277	HIS	3.5
1	B	119	GLN	3.5
1	A	123	LEU	3.5
1	B	318	VAL	3.4
1	B	324	VAL	3.4
1	B	395	TYR	3.4
1	B	281	ALA	3.4
1	A	291	ASP	3.4
1	B	278	GLY	3.3
1	B	213	VAL	3.3
1	B	276	ALA	3.3
1	B	137[A]	LEU	3.3
1	B	326	HIS	3.2
1	B	116	ASP	3.1
1	A	74	ARG	3.1
1	A	395	TYR	3.1
1	B	125[A]	ARG	3.0
1	A	393	LEU	3.0
1	A	137	LEU	3.0
1	A	273	GLY	3.0
1	B	348	ILE	2.9
1	A	260	GLY	2.9
1	B	330	ILE	2.9
1	B	243	HIS	2.8
1	A	130	ILE	2.8
1	A	277	HIS	2.8
1	A	262	THR	2.8
1	B	126[A]	ASN	2.8
1	A	261	LEU	2.7
1	A	275	GLY	2.7
1	A	276	ALA	2.7
1	B	127[A]	GLU	2.7
1	B	241	ILE	2.7
1	A	265	LYS	2.6
1	A	281	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	263	GLY	2.6
1	A	138	MET	2.6
1	A	242	TYR	2.6
1	A	264	ARG	2.5
1	B	272	GLY	2.5
1	A	349	VAL	2.5
1	A	124	ASP	2.5
1	B	264	ARG	2.5
1	A	116	ASP	2.4
1	A	218	MET	2.4
1	A	394	LYS	2.3
1	A	270	THR	2.3
1	A	114	SER	2.3
1	B	291	ASP	2.3
1	B	192	ARG	2.3
1	B	223	LYS	2.3
1	A	263	GLY	2.3
1	A	287	TYR	2.2
1	B	339	GLN	2.2
1	A	268	VAL	2.2
1	A	15	GLU	2.2
1	A	250	PHE	2.2
1	A	259	ALA	2.1
1	B	262	THR	2.1
1	A	355	LEU	2.1
1	B	287	TYR	2.1
1	A	34	CYS	2.1
1	B	351	LYS	2.0
1	B	131[A]	GLY	2.0
1	A	213	VAL	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](#)

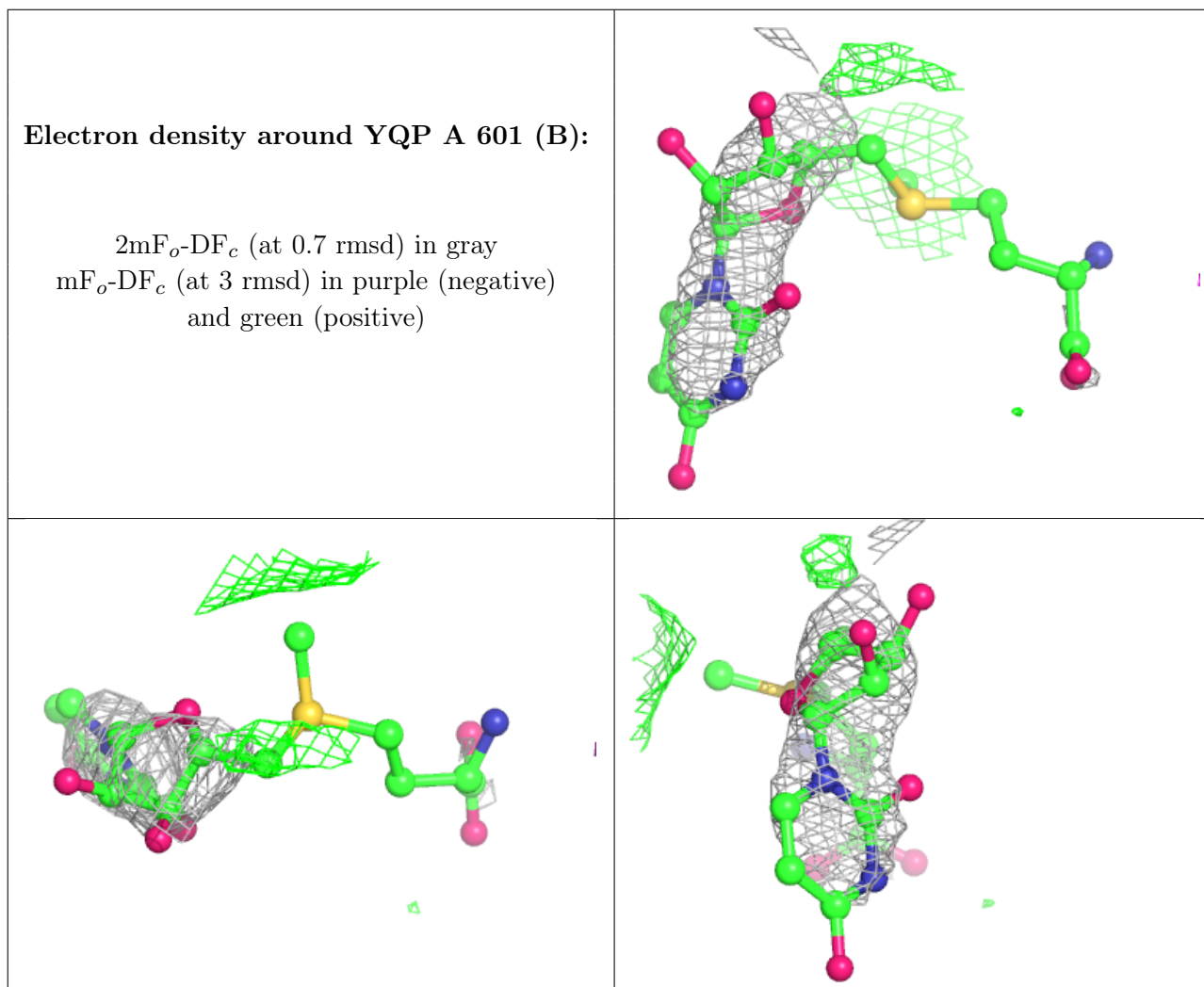
There are no monosaccharides in this entry.

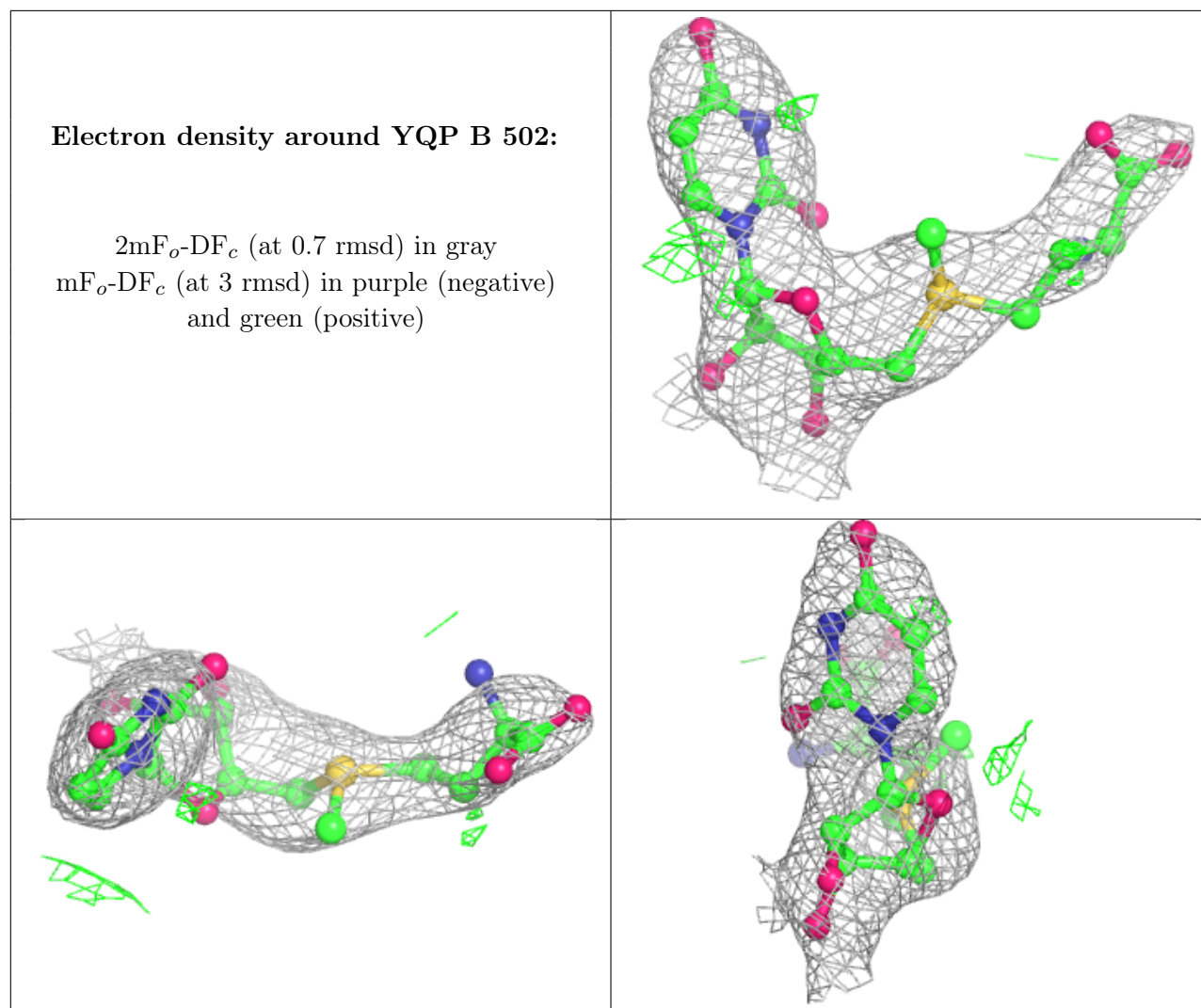
## 6.4 Ligands [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	EDO	B	501	4/4	0.74	0.14	93,99,109,113	0
2	YQP	A	601[B]	25/25	0.82	0.34	106,119,131,143	25
2	YQP	B	502	25/25	0.87	0.19	93,102,116,117	25

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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.