



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2020 – 02:19 PM JST

PDB ID : 6LTV  
Title : Crystal Structure of I122A/I330A variant of S-adenosylmethionine synthetase from *Cryptosporidium hominis* in complex with ONB-SAM (2-nitro benzoyl-S-adenosyl-methionine)  
Authors : Singh, R.K.; Michailidou, F.; Rentmeister, A.; Kuemmel, D.  
Deposited on : 2020-01-23  
Resolution : 1.87 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 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 : 2.14.6  
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) : 2.14.6

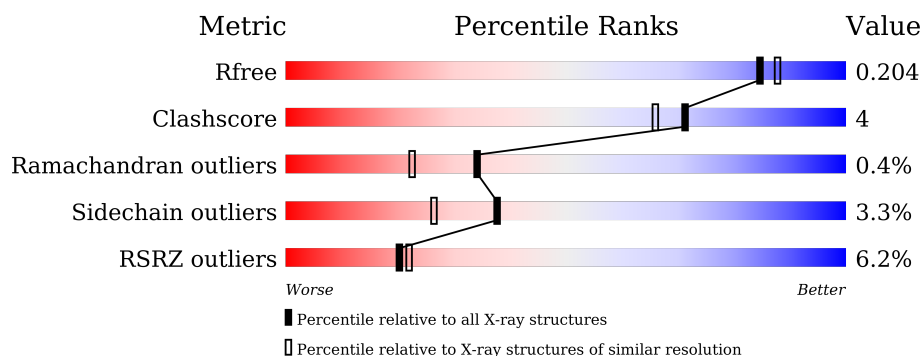
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.87 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	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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 on 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	414	
1	B	414	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6418 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.

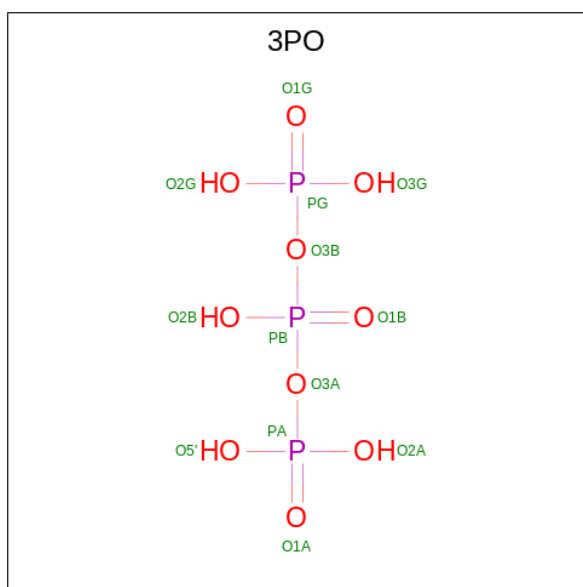
- Molecule 1 is a protein called S-adenosylmethionine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	381	Total	C	N	O	S	0	4	0
			2973	1876	506	572	19			
1	B	381	Total	C	N	O	S	0	5	0
			2978	1881	505	575	17			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP A0A0S4TKQ5
A	-6	ALA	-	expression tag	UNP A0A0S4TKQ5
A	-5	HIS	-	expression tag	UNP A0A0S4TKQ5
A	-4	HIS	-	expression tag	UNP A0A0S4TKQ5
A	-3	HIS	-	expression tag	UNP A0A0S4TKQ5
A	-2	HIS	-	expression tag	UNP A0A0S4TKQ5
A	-1	HIS	-	expression tag	UNP A0A0S4TKQ5
A	0	HIS	-	expression tag	UNP A0A0S4TKQ5
A	122	ALA	ILE	variant	UNP A0A0S4TKQ5
A	330	ALA	ILE	variant	UNP A0A0S4TKQ5
B	-7	MET	-	initiating methionine	UNP A0A0S4TKQ5
B	-6	ALA	-	expression tag	UNP A0A0S4TKQ5
B	-5	HIS	-	expression tag	UNP A0A0S4TKQ5
B	-4	HIS	-	expression tag	UNP A0A0S4TKQ5
B	-3	HIS	-	expression tag	UNP A0A0S4TKQ5
B	-2	HIS	-	expression tag	UNP A0A0S4TKQ5
B	-1	HIS	-	expression tag	UNP A0A0S4TKQ5
B	0	HIS	-	expression tag	UNP A0A0S4TKQ5
B	122	ALA	ILE	variant	UNP A0A0S4TKQ5
B	330	ALA	ILE	variant	UNP A0A0S4TKQ5

- Molecule 2 is TRIPHOSPHATE (three-letter code: 3PO) (formula:  $\text{H}_5\text{O}_{10}\text{P}_3$ ) (labeled as "Ligand of Interest" by author).

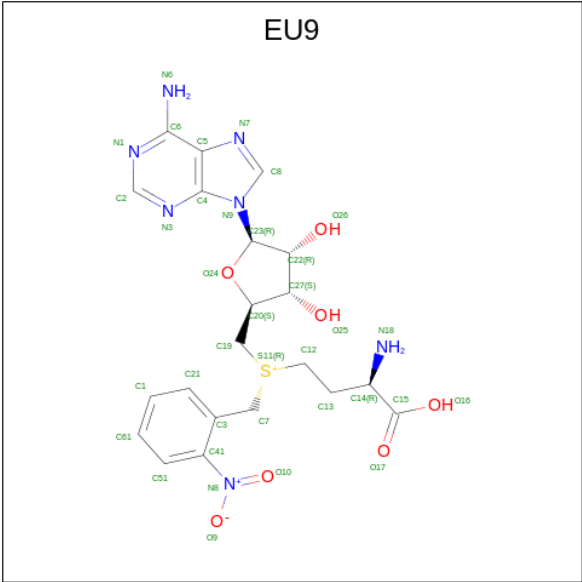


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			13	10	3		
2	B	1	Total	O	P	0	0
			13	10	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by author).

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

- Molecule 4 is [(2S,3S,4R,5R)-5-(6-aminopurin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methyl-[(3R)-3-azanyl-4-oxidanyl-4-oxidanylidene-butyl]-[(2-nitrophenyl)methyl]sulfanium (three-letter code: EU9) (formula: C<sub>21</sub>H<sub>26</sub>N<sub>7</sub>O<sub>7</sub>S) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			36	21	7	7	1		
4	B	1	Total	C	N	O	S	0	0
			36	21	7	7	1		

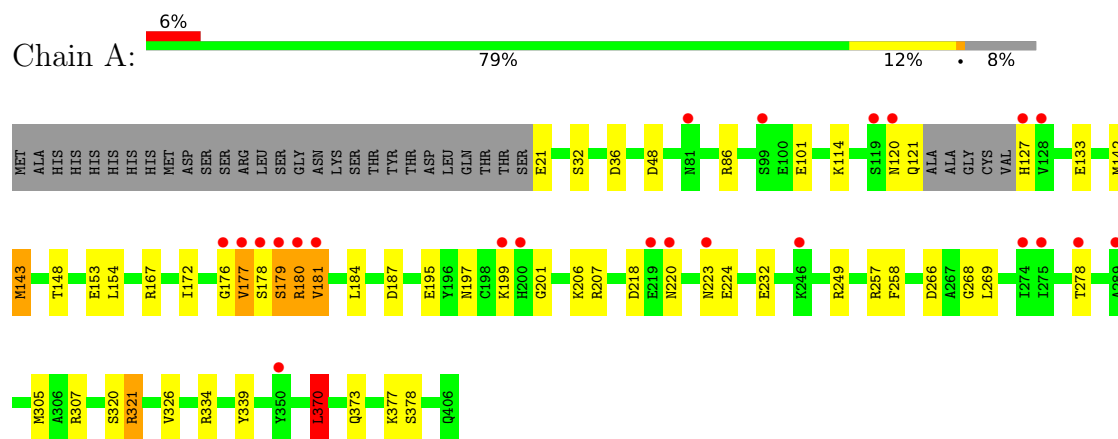
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	199	Total	O	0	0
			199	199		
5	B	168	Total	O	0	0
			168	168		

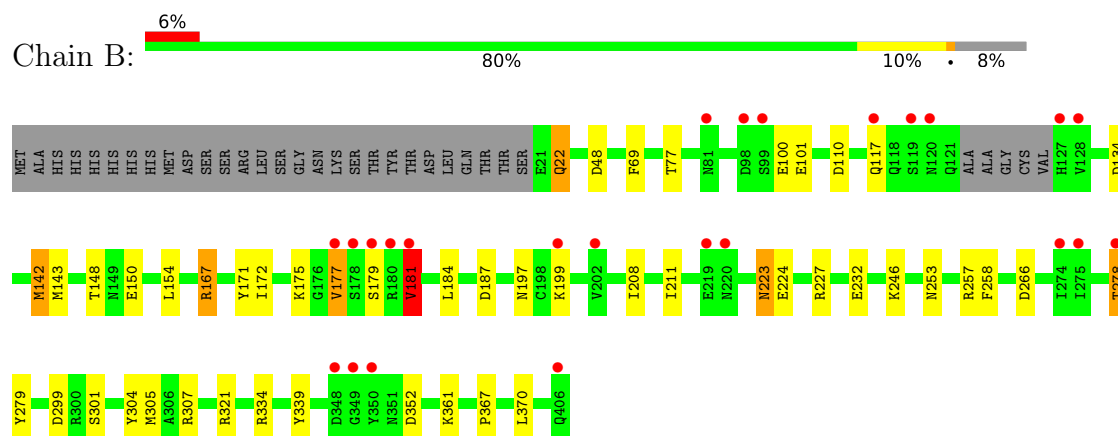
### 3 Residue-property plots [i](#)

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



- Molecule 1: S-adenosylmethionine synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.17Å 100.17Å 66.94Å 90.00° 95.99° 90.00°	Depositor
Resolution (Å)	48.28 – 1.87 43.48 – 1.88	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.28-1.87) 99.1 (43.48-1.88)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5.8.0218	Depositor
R, $R_{free}$	0.162 , 0.194 0.176 , 0.204	Depositor DCC
$R_{free}$ test set	3384 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.3	Xtriage
Anisotropy	0.692	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6418	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, EU9, 3PO

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	1.28	9/3030 (0.3%)	1.23	20/4087 (0.5%)
1	B	1.24	8/3031 (0.3%)	1.24	21/4088 (0.5%)
All	All	1.26	17/6061 (0.3%)	1.23	41/8175 (0.5%)

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	320	SER	CB-OG	-8.79	1.30	1.42
1	B	339	TYR	CE1-CZ	-6.81	1.29	1.38
1	A	32	SER	CB-OG	-6.17	1.34	1.42
1	A	195	GLU	CD-OE1	6.16	1.32	1.25
1	A	224	GLU	CG-CD	6.14	1.61	1.51
1	A	232	GLU	CD-OE1	6.07	1.32	1.25
1	B	304	TYR	CE1-CZ	-5.98	1.30	1.38
1	A	223	ASN	CB-CG	5.94	1.64	1.51
1	A	21	GLU	CD-OE2	5.73	1.31	1.25
1	B	167	ARG	CZ-NH1	5.48	1.40	1.33
1	B	100	GLU	CG-CD	5.43	1.60	1.51
1	A	339	TYR	CE1-CZ	-5.43	1.31	1.38
1	B	232	GLU	CD-OE1	5.33	1.31	1.25
1	B	339	TYR	CG-CD1	-5.26	1.32	1.39
1	B	150	GLU	CD-OE1	5.14	1.31	1.25
1	A	133	GLU	CD-OE2	5.12	1.31	1.25
1	B	224	GLU	CG-CD	5.06	1.59	1.51

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	142	MET	CG-SD-CE	-19.03	69.75	100.20
1	B	278	THR	N-CA-C	10.32	138.87	111.00

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	167	ARG	NE-CZ-NH2	-10.18	115.21	120.30
1	B	167	ARG	NE-CZ-NH1	9.79	125.19	120.30
1	A	207	ARG	NE-CZ-NH1	9.47	125.04	120.30
1	A	370	LEU	CB-CG-CD2	-9.34	95.12	111.00
1	B	321	ARG	NE-CZ-NH2	-8.70	115.95	120.30
1	A	48	ASP	CB-CG-OD2	-8.28	110.85	118.30
1	B	134	ASP	CB-CG-OD2	8.17	125.66	118.30
1	A	48	ASP	CB-CG-OD1	8.02	125.52	118.30
1	A	307	ARG	NE-CZ-NH1	-7.94	116.33	120.30
1	A	167	ARG	NE-CZ-NH2	-7.93	116.33	120.30
1	B	227	ARG	NE-CZ-NH1	7.83	124.22	120.30
1	A	184	LEU	CA-CB-CG	7.78	133.18	115.30
1	B	307	ARG	NE-CZ-NH1	-7.58	116.51	120.30
1	A	177	VAL	N-CA-C	7.53	131.34	111.00
1	A	321	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	A	167	ARG	NE-CZ-NH1	6.79	123.69	120.30
1	B	224	GLU	OE1-CD-OE2	-6.77	115.18	123.30
1	A	278	THR	N-CA-C	6.65	128.96	111.00
1	B	257	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	A	184	LEU	CB-CG-CD2	-6.63	99.72	111.00
1	A	218	ASP	CB-CG-OD1	6.62	124.26	118.30
1	A	249	ARG	NE-CZ-NH2	6.60	123.60	120.30
1	B	227	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	B	299	ASP	CB-CG-OD1	-6.46	112.48	118.30
1	A	257	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	A	36	ASP	CB-CG-OD1	6.28	123.95	118.30
1	B	48	ASP	CB-CG-OD2	-6.11	112.80	118.30
1	B	187	ASP	CB-CG-OD1	6.10	123.79	118.30
1	B	278	THR	CB-CA-C	-5.81	95.90	111.60
1	A	187	ASP	CB-CG-OD1	5.80	123.52	118.30
1	B	177	VAL	CB-CA-C	-5.74	100.50	111.40
1	A	377	LYS	CD-CE-NZ	-5.47	99.12	111.70
1	A	378	SER	N-CA-CB	-5.47	102.30	110.50
1	B	134	ASP	CB-CG-OD1	-5.43	113.41	118.30
1	B	110	ASP	CB-CG-OD2	-5.38	113.46	118.30
1	B	307	ARG	NE-CZ-NH2	5.29	122.95	120.30
1	B	352	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	176	GLY	N-CA-C	-5.10	100.34	113.10
1	B	184	LEU	CA-CB-CG	5.04	126.88	115.30

There are no chirality outliers.

There are no planarity outliers.

## 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	2973	0	2959	24	0
1	B	2978	0	2967	19	0
2	A	13	0	0	0	0
2	B	13	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	36	0	0	1	0
4	B	36	0	0	1	0
5	A	199	0	0	4	0
5	B	168	0	0	1	0
All	All	6418	0	5926	42	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 4.

All (42) 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:223:ASN:HD21	1:B:253:ASN:HB2	1.37	0.90
1:A:143[B]:MET:CE	1:A:326:VAL:HG13	2.03	0.88
1:A:143[B]:MET:HE1	1:A:326:VAL:HG13	1.64	0.79
1:A:178:SER:O	1:A:180:ARG:N	2.25	0.70
1:A:143[B]:MET:N	1:A:143[B]:MET:HE2	2.08	0.68
1:B:167:ARG:HD3	5:B:755:HOH:O	1.96	0.64
1:B:370[B]:LEU:C	1:B:370[B]:LEU:HD12	2.18	0.64
1:A:177:VAL:O	1:A:177:VAL:HG22	2.01	0.59
1:A:373[A]:GLN:NE2	5:A:602:HOH:O	2.35	0.58
1:B:301:SER:HB2	1:B:370[B]:LEU:HD11	1.86	0.57
1:A:334:ARG:NH1	5:A:603:HOH:O	2.37	0.57
1:A:143[B]:MET:CE	1:A:326:VAL:CG1	2.81	0.57
1:A:114:LYS:HD3	1:B:69:PHE:CE1	2.40	0.56
1:A:172:ILE:CG2	1:A:181:VAL:HG11	2.36	0.55
1:B:77:THR:OG1	1:B:117:GLN:NE2	2.42	0.52
1:A:197:ASN:HD21	1:A:206:LYS:HD2	1.76	0.51
1:B:278:THR:O	1:B:279:TYR:CD1	2.63	0.51

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ARG:NH2	5:A:607:HOH:O	2.44	0.50
1:B:305:MET:HE2	1:B:370[B]:LEU:HB2	1.94	0.50
1:A:266:ASP:OD1	4:A:503:EU9:N18	2.45	0.50
1:A:178:SER:C	1:A:180:ARG:N	2.64	0.49
1:B:278:THR:O	1:B:279:TYR:CG	2.65	0.49
1:A:178:SER:O	1:A:179:SER:C	2.51	0.49
1:B:117:GLN:HE21	1:B:117:GLN:HA	1.77	0.48
1:B:266:ASP:OD1	4:B:503:EU9:N18	2.49	0.45
1:B:22:GLN:HG3	1:B:197:ASN:OD1	2.16	0.45
1:A:305:MET:HB2	1:A:370:LEU:HD21	1.98	0.44
1:B:172:ILE:CG2	1:B:181:VAL:HG11	2.48	0.44
1:B:367:PRO:HA	1:B:370[A]:LEU:HD12	2.00	0.44
1:B:148:THR:O	1:B:154:LEU:HA	2.18	0.43
1:A:201:GLY:O	1:A:321:ARG:CD	2.67	0.43
1:B:208:ILE:HG21	1:B:211:ILE:HD11	2.01	0.43
1:A:143[B]:MET:HE2	1:A:143[B]:MET:CA	2.39	0.42
1:A:197:ASN:ND2	1:A:206:LYS:HD2	2.34	0.42
1:B:171:TYR:CE1	1:B:175:LYS:HG3	2.55	0.42
1:A:172:ILE:HG22	1:A:181:VAL:HG11	2.02	0.41
1:A:153:GLU:HG2	5:A:745:HOH:O	2.20	0.41
1:A:268:GLY:C	1:A:269:LEU:HD12	2.40	0.41
1:B:334:ARG:HG2	1:B:334:ARG:HH11	1.86	0.41
1:B:77:THR:HA	1:B:117:GLN:NE2	2.36	0.41
1:A:120:ASN:O	1:A:121:GLN:CB	2.68	0.41
1:A:148:THR:O	1:A:154:LEU:HA	2.20	0.40

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	381/414 (92%)	363 (95%)	16 (4%)	2 (0%)	29 17

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	382/414 (92%)	371 (97%)	10 (3%)	1 (0%)	41	30
All	All	763/828 (92%)	734 (96%)	26 (3%)	3 (0%)	34	22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	179	SER
1	A	180	ARG
1	B	181	VAL

### 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	327/354 (92%)	317 (97%)	10 (3%)	40	29
1	B	327/354 (92%)	315 (96%)	12 (4%)	34	22
All	All	654/708 (92%)	632 (97%)	22 (3%)	38	25

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	GLU
1	A	127	HIS
1	A	142	MET
1	A	143[A]	MET
1	A	143[B]	MET
1	A	181	VAL
1	A	199	LYS
1	A	220	ASN
1	A	258	PHE
1	A	370	LEU
1	B	22	GLN
1	B	101	GLU
1	B	142	MET

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	143	MET
1	B	177	VAL
1	B	179	SER
1	B	181	VAL
1	B	199	LYS
1	B	223	ASN
1	B	246	LYS
1	B	258	PHE
1	B	361	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	197	ASN
1	A	220	ASN
1	B	117	GLN
1	B	118	GLN
1	B	223	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 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	EU9	B	503	-	29,39,39	2.21	6 (20%)	27,56,56	1.47	5 (18%)
2	3PO	B	501	3	8,12,12	0.80	0	15,20,20	1.54	3 (20%)
2	3PO	A	501	3	8,12,12	1.12	0	15,20,20	1.30	1 (6%)
4	EU9	A	503	-	29,39,39	2.19	7 (24%)	27,56,56	1.49	4 (14%)

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	EU9	B	503	-	-	5/15/41/41	0/4/4/4
2	3PO	B	501	3	-	2/12/12/12	-
2	3PO	A	501	3	-	3/12/12/12	-
4	EU9	A	503	-	-	3/15/41/41	0/4/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	503	EU9	O10-N8	9.47	1.38	1.22
4	A	503	EU9	O10-N8	9.33	1.38	1.22
4	B	503	EU9	C41-N8	-2.56	1.41	1.45
4	A	503	EU9	C2-N3	2.55	1.36	1.32
4	B	503	EU9	C5-C4	2.52	1.47	1.40
4	B	503	EU9	C2-N3	2.52	1.36	1.32
4	B	503	EU9	C7-C3	2.51	1.54	1.50
4	A	503	EU9	O24-C23	2.37	1.44	1.41
4	B	503	EU9	C21-C3	2.35	1.43	1.39
4	A	503	EU9	C5-C4	2.33	1.47	1.40
4	A	503	EU9	O24-C20	-2.21	1.40	1.45
4	A	503	EU9	C41-N8	-2.20	1.41	1.45
4	A	503	EU9	C41-C3	2.05	1.43	1.40

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	EU9	N3-C2-N1	-4.08	122.30	128.68
4	B	503	EU9	N3-C2-N1	-4.00	122.43	128.68
2	B	501	3PO	PB-O3A-PA	-3.34	121.36	132.83
2	A	501	3PO	PB-O3B-PG	-3.19	121.90	132.83
4	A	503	EU9	C4-C5-N7	-2.90	106.38	109.40
4	B	503	EU9	C4-C5-N7	-2.48	106.82	109.40
2	B	501	3PO	O2A-PA-O1A	2.33	119.81	110.68
4	A	503	EU9	C23-N9-C4	-2.26	122.68	126.64
4	A	503	EU9	C7-C3-C21	-2.25	116.03	120.43
2	B	501	3PO	O3G-PG-O3B	2.24	112.15	104.64
4	B	503	EU9	C7-C3-C21	-2.22	116.09	120.43
4	B	503	EU9	C22-C27-C20	-2.20	98.37	102.64
4	B	503	EU9	C2-N1-C6	2.08	122.31	118.75

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	3PO	PB-O3A-PA-O5'
2	B	501	3PO	PB-O3B-PG-O3G
4	B	503	EU9	C12-C13-C14-N18
4	A	503	EU9	C12-C13-C14-N18
4	A	503	EU9	C3-C7-S11-C19
4	B	503	EU9	C21-C3-C7-S11
2	A	501	3PO	PB-O3A-PA-O2A
4	B	503	EU9	C3-C7-S11-C19
4	B	503	EU9	S11-C12-C13-C14
4	A	503	EU9	S11-C12-C13-C14
2	B	501	3PO	PB-O3B-PG-O2G
4	B	503	EU9	C3-C7-S11-C12
2	A	501	3PO	PB-O3A-PA-O1A

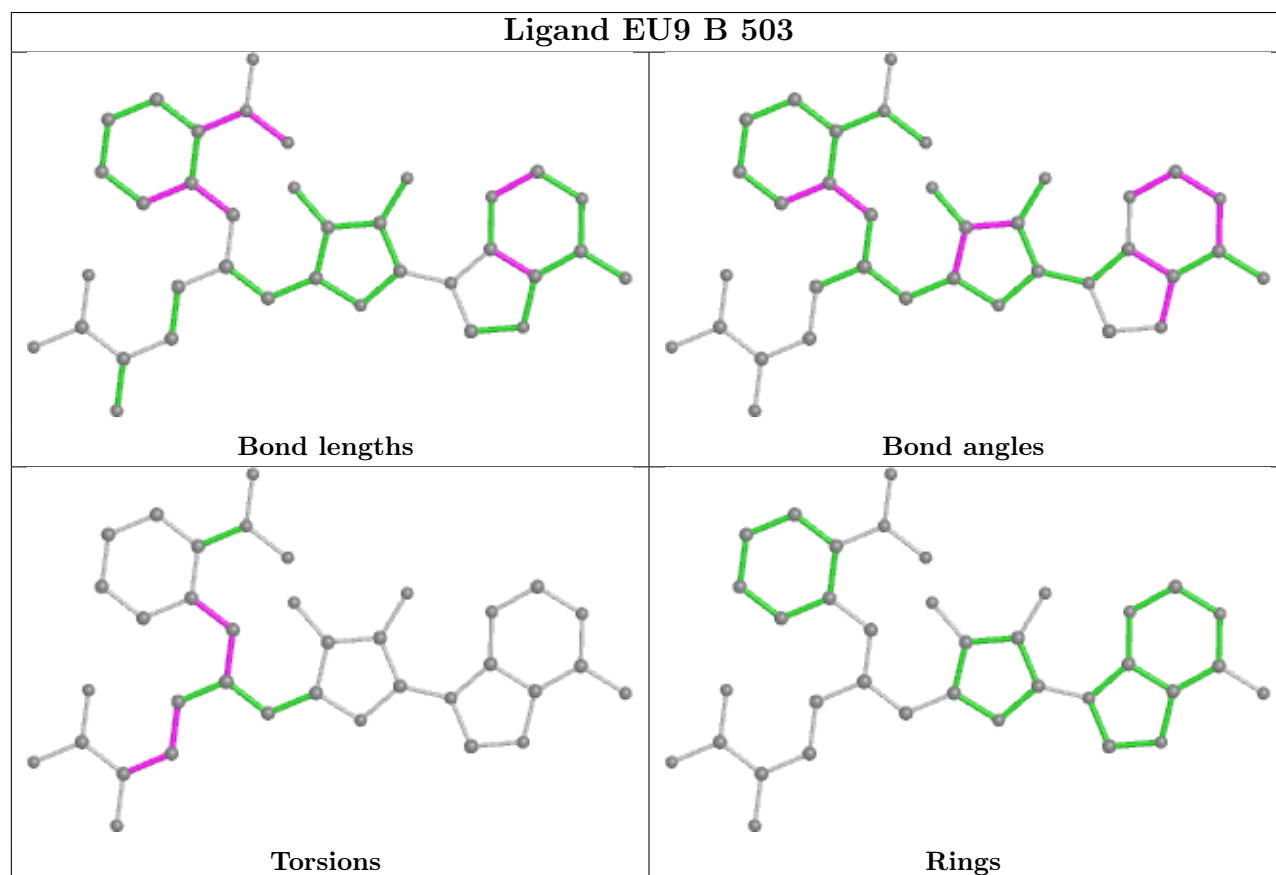
There are no ring outliers.

2 monomers are involved in 2 short contacts:

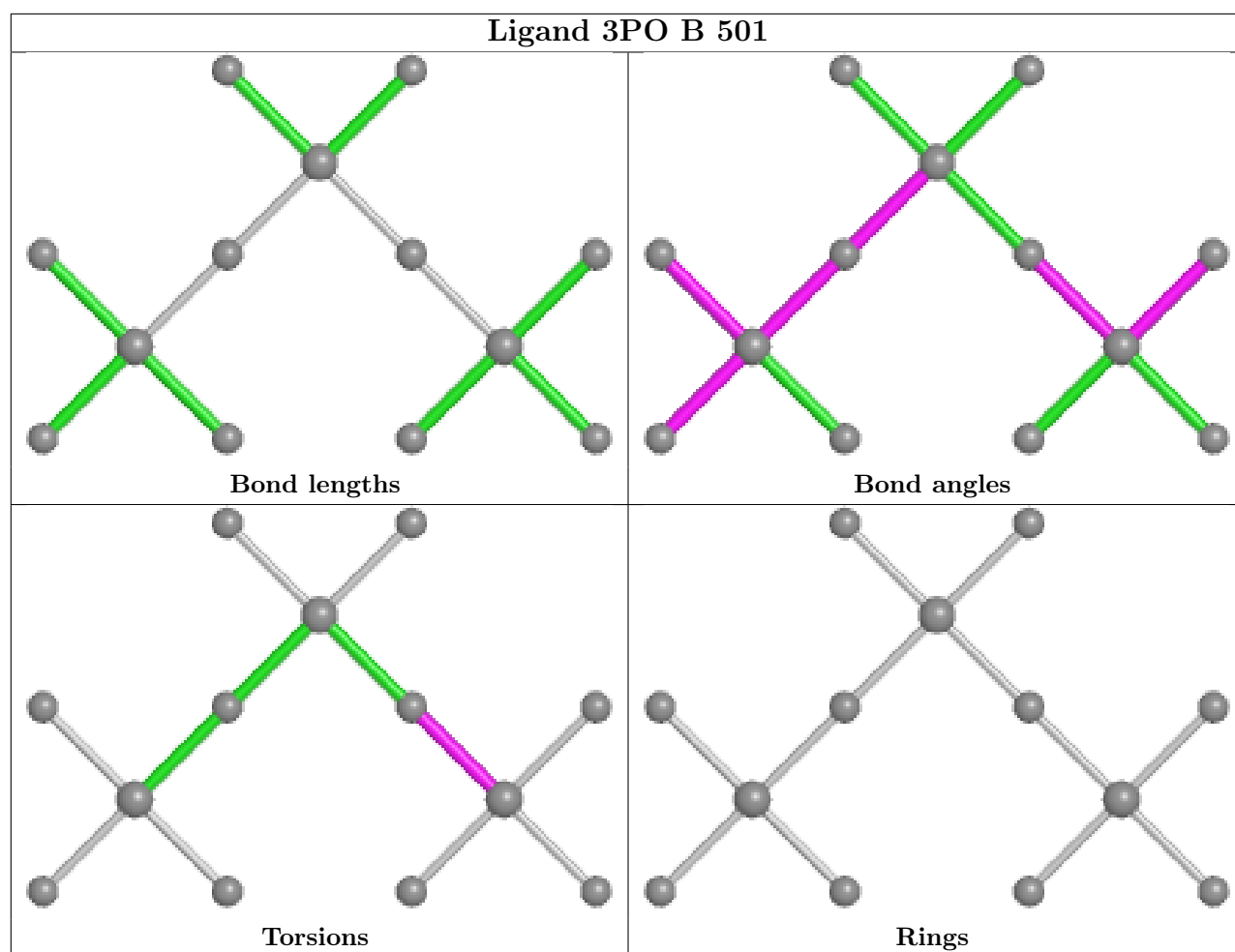
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	503	EU9	1	0
4	A	503	EU9	1	0

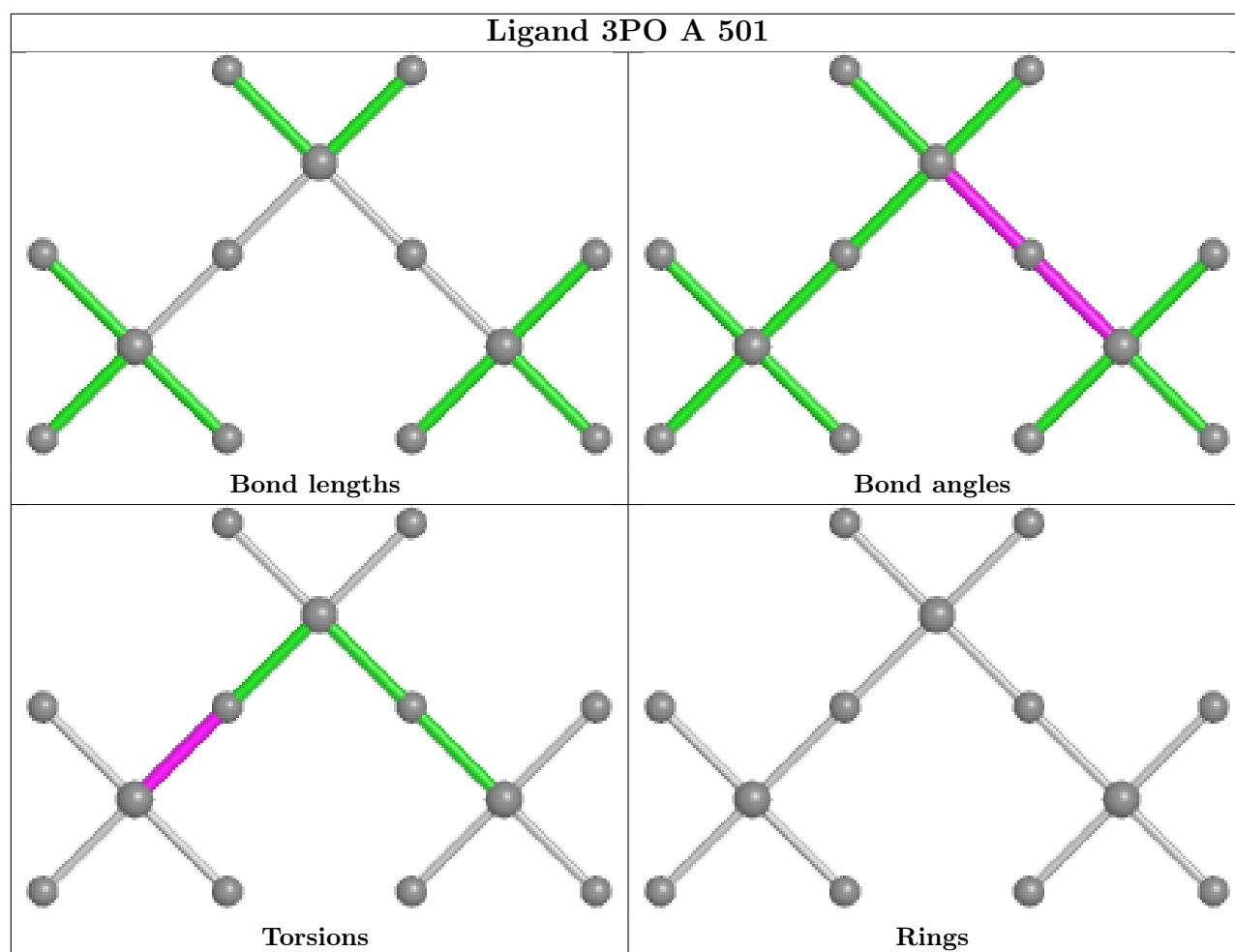
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

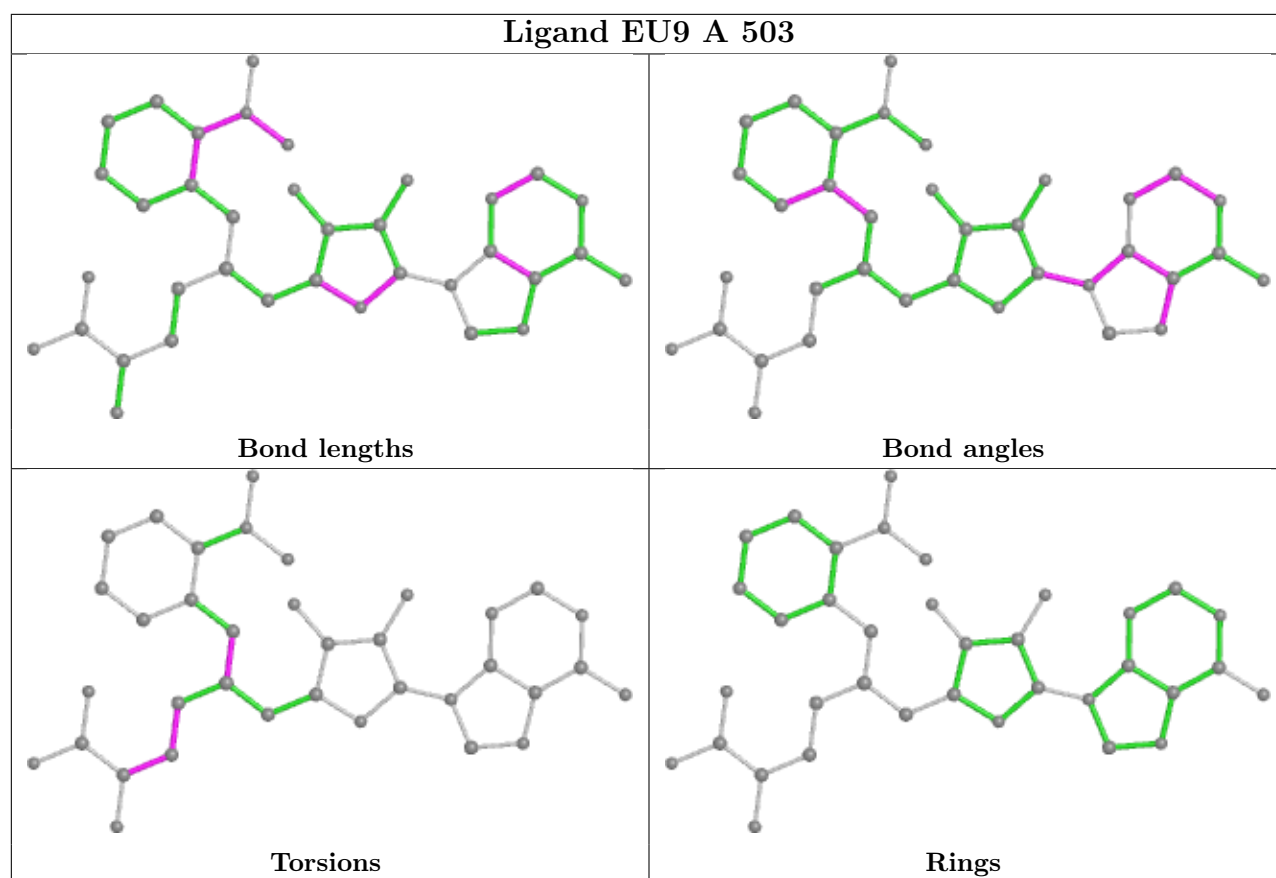
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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, 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	381/414 (92%)	0.39	23 (6%) 21 23	13, 26, 51, 84	0
1	B	381/414 (92%)	0.43	24 (6%) 20 21	15, 29, 54, 111	0
All	All	762/828 (92%)	0.41	47 (6%) 20 22	13, 27, 53, 111	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	177	VAL	13.1
1	B	179	SER	10.3
1	A	179	SER	8.7
1	A	177	VAL	8.7
1	B	120	ASN	4.6
1	B	127	HIS	4.5
1	A	120	ASN	4.3
1	B	128	VAL	4.3
1	A	200	HIS	4.0
1	B	202	VAL	4.0
1	A	128	VAL	3.8
1	A	220	ASN	3.5
1	A	127	HIS	3.5
1	B	220	ASN	3.4
1	B	99	SER	3.4
1	A	274	ILE	3.4
1	B	274	ILE	3.4
1	A	119	SER	3.2
1	B	119	SER	3.2
1	B	199	LYS	3.2
1	B	350	TYR	3.1
1	A	180	ARG	3.0
1	A	278	THR	2.9
1	B	278	THR	2.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	181	VAL	2.8
1	B	406	GLN	2.8
1	B	348	ASP	2.8
1	B	181	VAL	2.5
1	A	81	ASN	2.5
1	A	275	ILE	2.5
1	B	81	ASN	2.5
1	A	199	LYS	2.4
1	B	178	SER	2.4
1	A	219	GLU	2.4
1	A	178	SER	2.3
1	B	180	ARG	2.3
1	B	219	GLU	2.3
1	B	349	GLY	2.3
1	A	176	GLY	2.2
1	A	99	SER	2.2
1	A	223	ASN	2.2
1	A	289	ALA	2.2
1	B	275	ILE	2.1
1	B	98	ASP	2.1
1	B	117	GLN	2.0
1	A	246	LYS	2.0
1	A	350	TYR	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.

*Continued on next page...*

*Continued from previous page...*

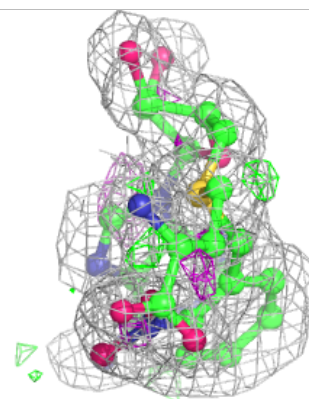
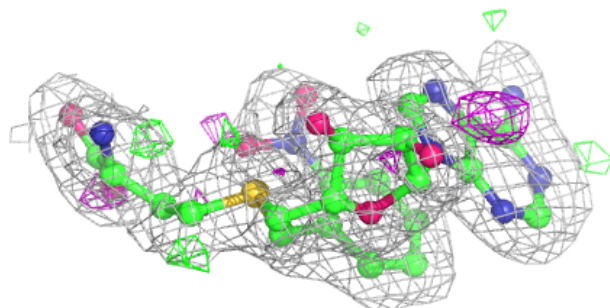
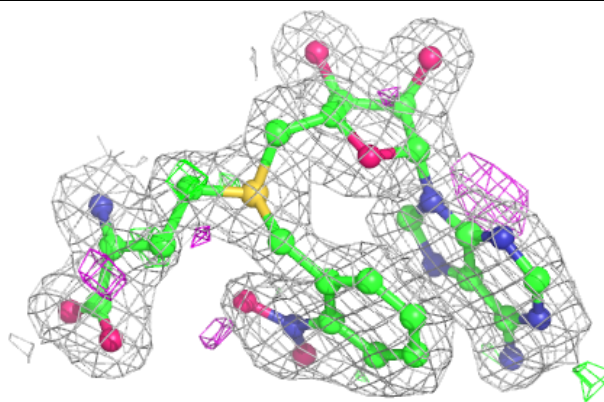
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
-----	------	-------	-----	-------	------	-----	-----------------------------	-------

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EU9	B	503	36/36	0.93	0.12	21,25,45,56	0
4	EU9	A	503	36/36	0.93	0.12	19,25,43,58	0
3	MG	A	502	1/1	0.97	0.08	16,16,16,16	0
2	3PO	B	501	13/13	0.98	0.11	15,18,19,20	0
3	MG	B	502	1/1	0.98	0.09	17,17,17,17	0
2	3PO	A	501	13/13	0.99	0.12	15,17,19,19	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.

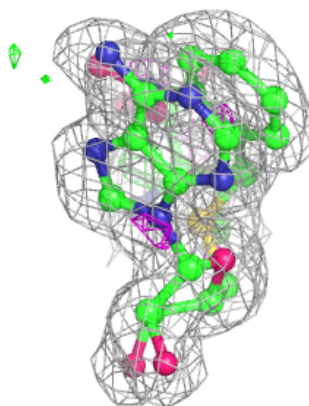
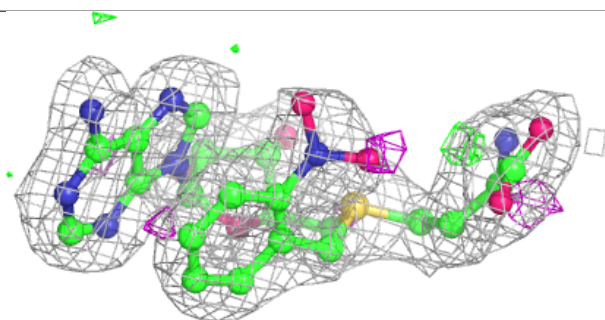
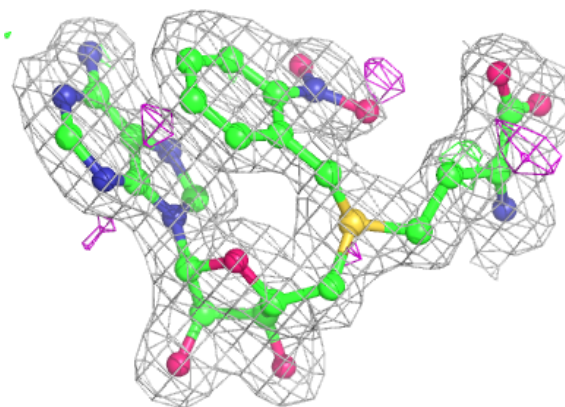
**Electron density around EU9 B 503:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



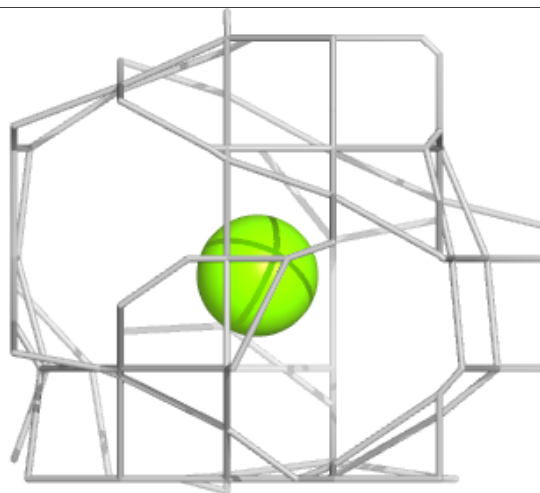
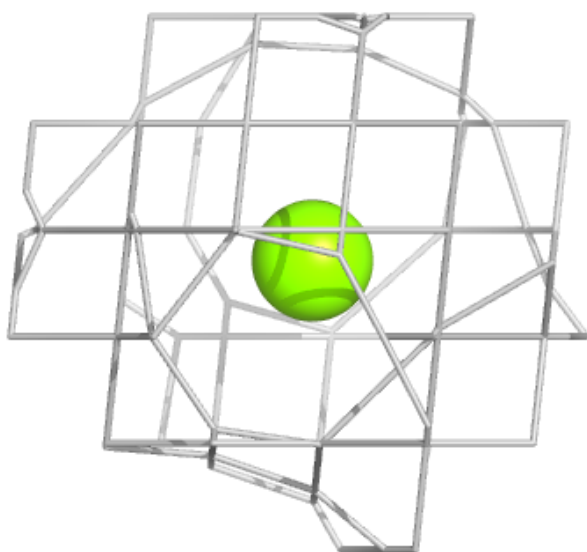
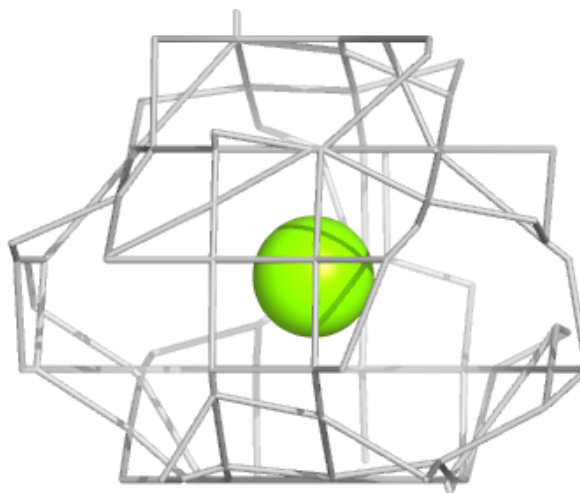
**Electron density around EU9 A 503:**

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



**Electron density around MG A 502:**

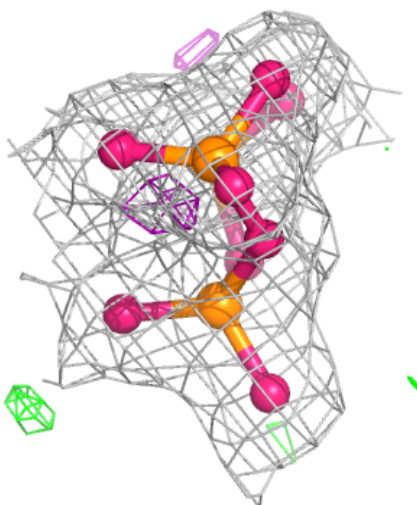
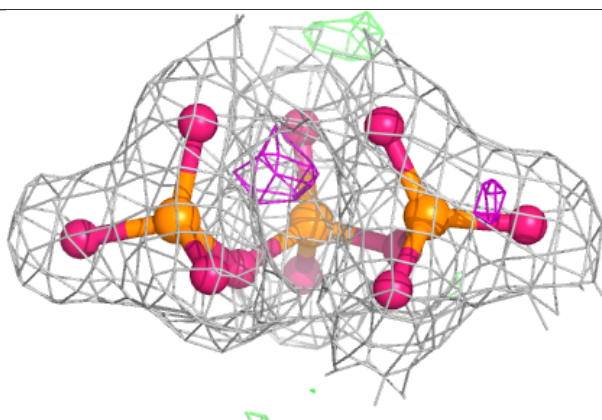
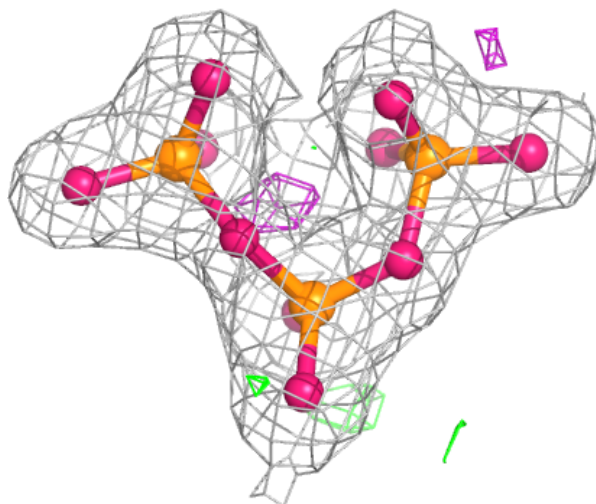
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





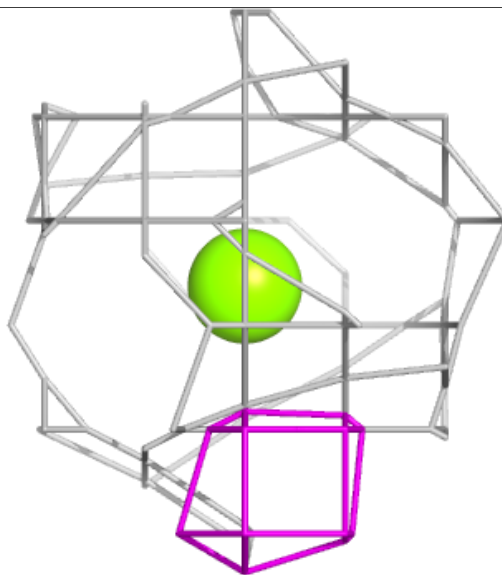
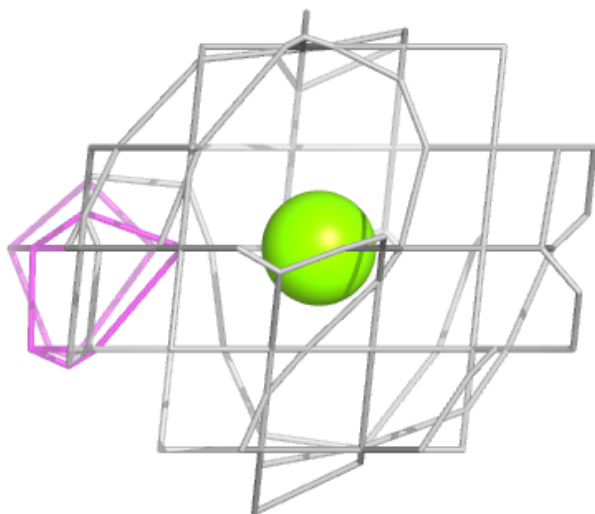
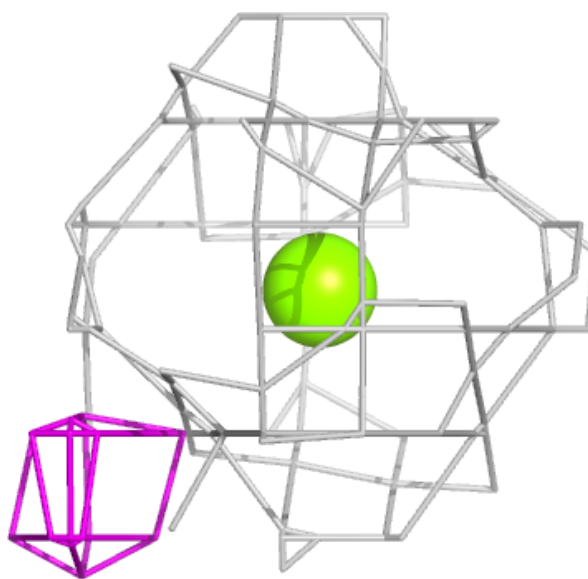
**Electron density around 3PO B 501:**

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



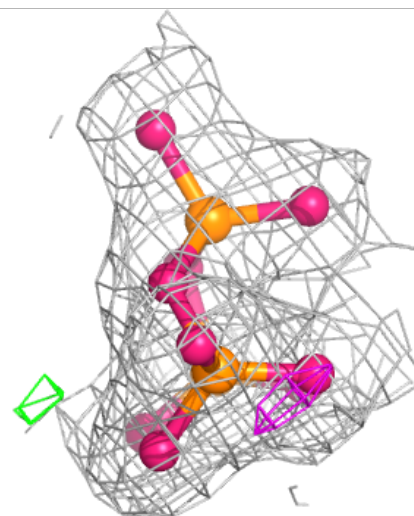
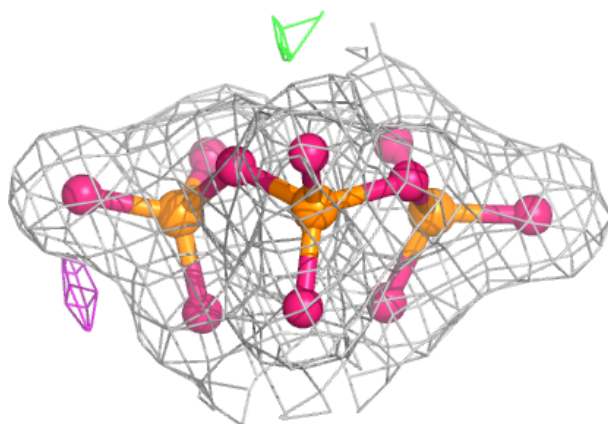
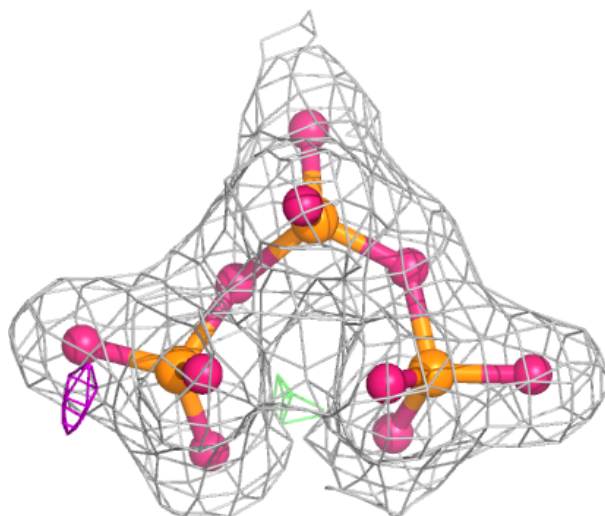
**Electron density around MG B 502:**

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



**Electron density around 3PO A 501:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.