



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:01 PM UTC

PDB ID : 6LTV / pdb_00006ltv
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

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	:	2022.3.0, CSD as543be (2022)
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	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

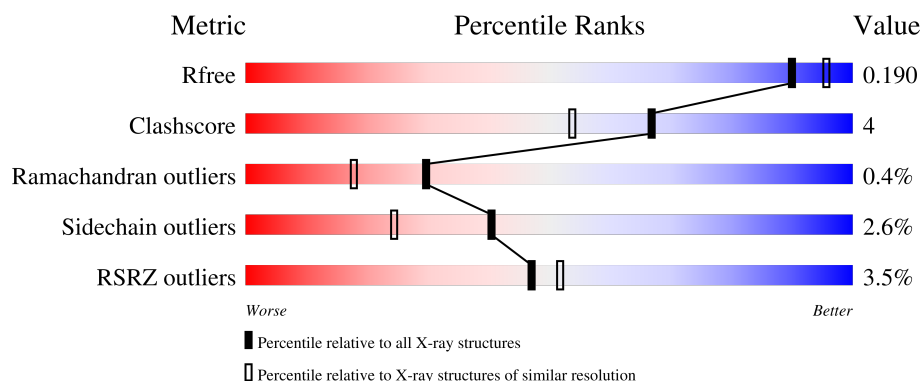
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

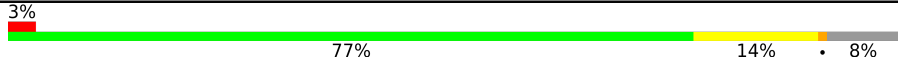
The reported resolution of this entry is 1.87 Å.

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}	180053	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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	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.

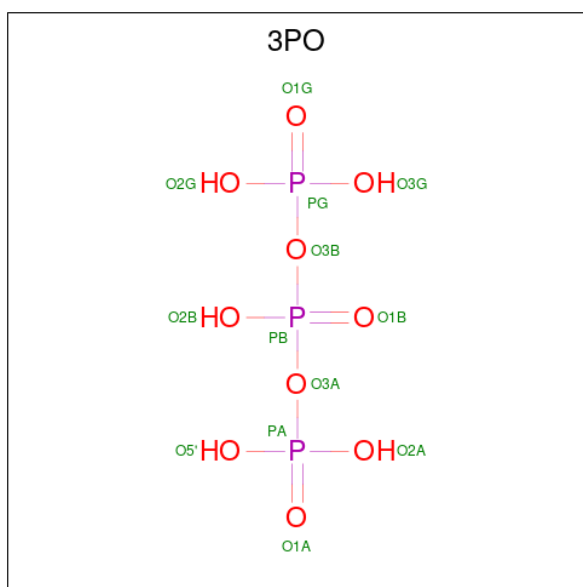
- Molecule 1 is a protein called S-adenosylmethionine synthase.

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 (CCD ID: 3PO) (formula: $\text{H}_5\text{O}_{10}\text{P}_3$) (labeled as "Ligand of Interest" by depositor).

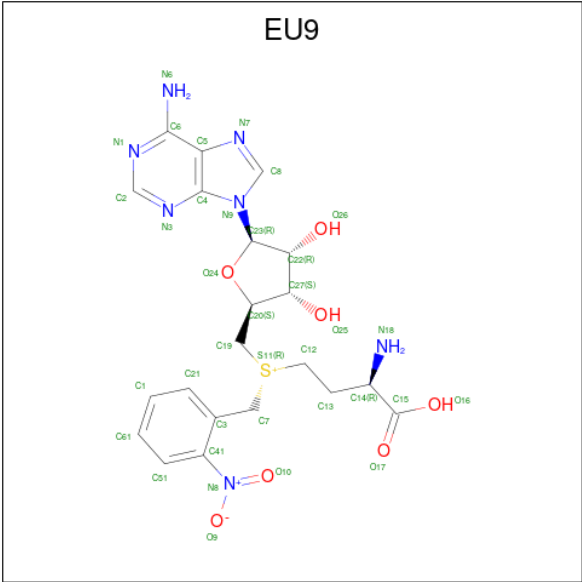


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			13	10	3		
2	B	1	Total	O	P	0	0
			13	10	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	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 (CCD ID: EU9) (formula: C₂₁H₂₆N₇O₇S) (labeled as "Ligand of Interest" by depositor).



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		

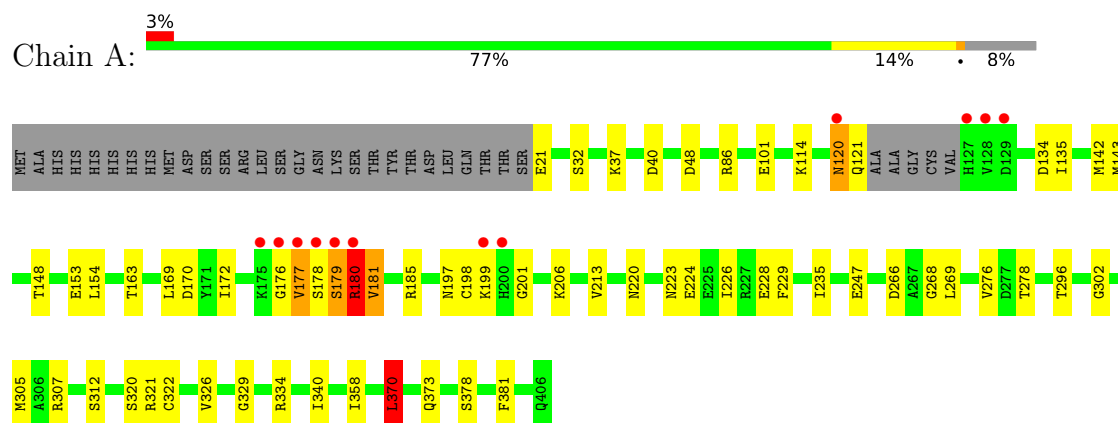
- Molecule 5 is water.

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

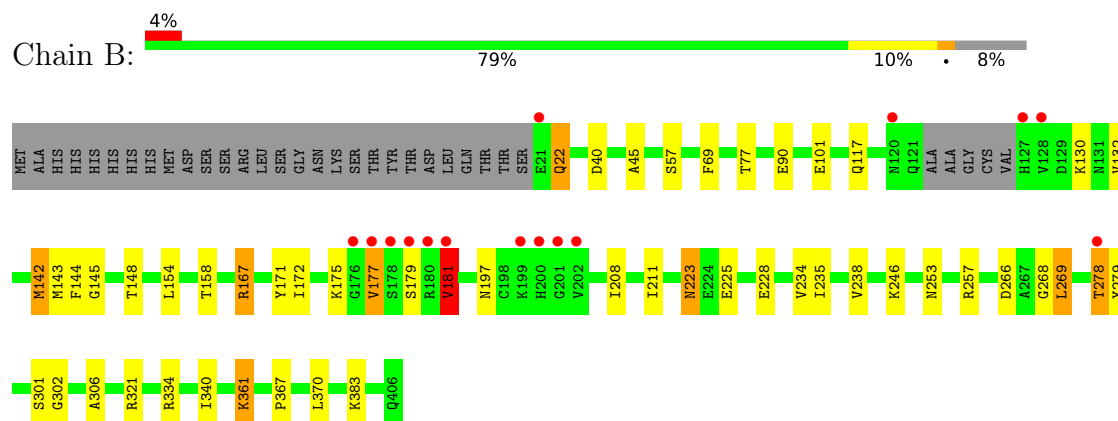
3 Residue-property plots [i](#)

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, α , β , γ	63.17Å 100.17Å 66.94Å 90.00° 95.99° 90.00°	Depositor
Resolution (Å)	48.28 – 1.87 48.28 – 1.88	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.28-1.87) 99.1 (48.28-1.88)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5.8.0218	Depositor
R, R_{free}	0.162 , 0.194 (Not available) , 0.190	Depositor DCC
R_{free} test set	3384 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	23.3	Xtriage
Anisotropy	0.692	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	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 ²)	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.*

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

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	1.62	26/3030 (0.9%)	1.39	17/4087 (0.4%)
1	B	1.55	15/3031 (0.5%)	1.36	13/4088 (0.3%)
All	All	1.58	41/6061 (0.7%)	1.37	30/8175 (0.4%)

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	278	THR	N-CA	-7.99	1.38	1.46
1	B	57	SER	CA-C	6.82	1.61	1.52
1	A	169	LEU	C-O	6.77	1.31	1.24
1	A	312	SER	N-CA	6.66	1.54	1.46
1	B	383	LYS	C-O	-6.57	1.15	1.24
1	A	37	LYS	CA-C	6.52	1.61	1.52
1	A	276	VAL	N-CA	6.51	1.54	1.46
1	A	224	GLU	CA-C	6.51	1.61	1.52
1	B	45	ALA	C-O	6.34	1.31	1.24
1	B	228	GLU	C-O	-6.20	1.17	1.24
1	A	223	ASN	CA-C	6.01	1.61	1.52
1	A	180	ARG	N-CA	5.93	1.53	1.46
1	B	132	VAL	CA-CB	5.91	1.61	1.54
1	B	145	GLY	N-CA	5.91	1.52	1.45
1	A	170	ASP	C-O	-5.87	1.17	1.24
1	A	226	ILE	N-CA	5.87	1.53	1.46
1	B	306	ALA	C-O	-5.86	1.17	1.24
1	A	163	THR	CA-C	5.74	1.60	1.52
1	B	269	LEU	C-O	-5.74	1.16	1.23
1	A	320	SER	CB-OG	-5.67	1.30	1.42
1	A	296	THR	N-CA	5.61	1.53	1.46
1	B	130	LYS	N-CA	5.58	1.52	1.46
1	B	321	ARG	CD-NE	-5.46	1.38	1.46
1	A	185	ARG	C-O	-5.46	1.19	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	329	GLY	CA-C	-5.45	1.47	1.52
1	B	302	GLY	N-CA	5.45	1.52	1.45
1	A	32	SER	C-O	-5.45	1.17	1.24
1	A	48	ASP	N-CA	5.38	1.52	1.46
1	A	40	ASP	N-CA	5.37	1.52	1.46
1	A	340	ILE	N-CA	5.37	1.52	1.46
1	A	213	VAL	C-O	5.35	1.29	1.24
1	B	145	GLY	CA-C	-5.35	1.47	1.52
1	A	228	GLU	N-CA	-5.32	1.40	1.46
1	B	167	ARG	CZ-NH1	5.30	1.40	1.32
1	A	322	CYS	C-O	-5.24	1.17	1.23
1	A	134	ASP	C-O	-5.21	1.17	1.24
1	B	40	ASP	N-CA	5.17	1.52	1.46
1	A	302	GLY	N-CA	5.17	1.52	1.45
1	A	223	ASN	CB-CG	5.07	1.64	1.52
1	B	90	GLU	C-O	-5.06	1.18	1.24
1	A	247	GLU	C-O	-5.03	1.17	1.24

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	278	THR	N-CA-C	20.43	138.87	112.72
1	B	142	MET	CG-SD-CE	-14.16	69.75	100.90
1	A	278	THR	N-CA-C	11.83	128.96	111.34
1	A	177	VAL	N-CA-C	10.57	131.34	109.34
1	B	177	VAL	CB-CA-C	-10.36	100.50	110.65
1	B	278	THR	CB-CA-C	-8.82	95.90	110.37
1	A	278	THR	CB-CA-C	-8.09	99.93	112.31
1	A	120	ASN	N-CA-C	-6.19	101.12	110.28
1	A	235	ILE	N-CA-C	5.91	116.38	110.23
1	B	225	GLU	N-CA-C	-5.91	104.92	111.36
1	A	378	SER	N-CA-CB	-5.56	102.30	110.14
1	B	144	PHE	CA-C-N	5.56	126.02	122.18
1	B	144	PHE	C-N-CA	5.56	126.02	122.18
1	A	135	ILE	CA-C-N	5.55	125.61	120.34
1	A	135	ILE	C-N-CA	5.55	125.61	120.34
1	A	381	PHE	N-CA-C	5.54	119.30	112.54
1	A	176	GLY	N-CA-C	-5.42	100.34	113.18
1	B	238	VAL	N-CA-C	5.37	119.83	113.22
1	A	224	GLU	CB-CG-CD	5.35	121.69	112.60
1	B	340	ILE	CB-CA-C	-5.27	102.63	110.33
1	A	224	GLU	CA-C-O	5.27	126.01	120.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	361	LYS	N-CA-C	5.23	117.89	111.82
1	A	169	LEU	N-CA-C	5.22	117.37	111.11
1	A	358	ILE	N-CA-C	5.20	115.93	110.62
1	A	370	LEU	CB-CG-CD2	-5.19	95.12	110.70
1	A	307	ARG	NE-CZ-NH1	-5.17	116.33	121.50
1	A	198	CYS	N-CA-CB	5.14	118.64	110.57
1	B	158	THR	CA-C-N	5.12	127.14	120.28
1	B	158	THR	C-N-CA	5.12	127.14	120.28
1	B	257	ARG	N-CA-C	5.01	117.49	110.23

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	25	0
1	B	2978	0	2967	20	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	44	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 (44) 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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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	0.78
1:A:143[B]:MET:N	1:A:143[B]:MET:HE2	2.05	0.71
1:A:178:SER:O	1:A:180:ARG:N	2.25	0.70
1:B:370[B]:LEU:C	1:B:370[B]:LEU:HD12	2.18	0.69
1:B:167:ARG:HD3	5:B:755:HOH:O	1.96	0.64
1:A:177:VAL:HG22	1:A:177:VAL:O	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:A:178:SER:C	1:A:180:ARG:N	2.64	0.54
1:A:178:SER:O	1:A:179:SER:C	2.51	0.54
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
1:A:86:ARG:NH2	5:A:607:HOH:O	2.44	0.50
1:A:266:ASP:OD1	4:A:503:EU9:N18	2.45	0.50
1:B:278:THR:O	1:B:279:TYR:CG	2.65	0.49
1:B:117:GLN:HE21	1:B:117:GLN:HA	1.77	0.48
1:A:143[B]:MET:HE2	1:A:143[B]:MET:H	1.80	0.46
1:A:268:GLY:C	1:A:269:LEU:HD12	2.40	0.45
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: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:229:PHE:CD1	1:A:229:PHE:C	2.99	0.41
1:B:234:VAL:O	1:B:235:ILE:C	2.63	0.41
1:B:334:ARG:HH11	1:B:334:ARG:HG2	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:GLY:C	1:B:269:LEU:HD12	2.45	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 [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	381/414 (92%)	363 (95%)	16 (4%)	2 (0%)	24	13
1	B	382/414 (92%)	371 (97%)	10 (3%)	1 (0%)	36	26
All	All	763/828 (92%)	734 (96%)	26 (3%)	3 (0%)	30	18

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%)	320 (98%)	7 (2%)	47	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	327/354 (92%)	317 (97%)	10 (3%)	35	18
All	All	654/708 (92%)	637 (97%)	17 (3%)	40	24

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	GLU
1	A	101	GLU
1	A	142	MET
1	A	181	VAL
1	A	199	LYS
1	A	220	ASN
1	A	370	LEU
1	B	22	GLN
1	B	101	GLU
1	B	142	MET
1	B	143	MET
1	B	177	VAL
1	B	179	SER
1	B	181	VAL
1	B	223	ASN
1	B	246	LYS
1	B	361	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	118	GLN
1	A	197	ASN
1	A	220	ASN
1	A	406	GLN
1	B	41	GLN
1	B	117	GLN
1	B	223	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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$
2	3PO	A	501	3	10,12,12	1.28	1 (10%)	17,20,20	1.24	1 (5%)
2	3PO	B	501	3	10,12,12	1.60	1 (10%)	17,20,20	1.19	2 (11%)
4	EU9	B	503	-	36,39,39	2.19	9 (25%)	42,56,56	2.08	12 (28%)
4	EU9	A	503	-	36,39,39	2.17	9 (25%)	42,56,56	2.03	12 (28%)

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	3PO	A	501	3	-	3/12/12/12	-
2	3PO	B	501	3	-	2/12/12/12	-
4	EU9	B	503	-	-	8/23/41/41	0/4/4/4
4	EU9	A	503	-	-	6/23/41/41	0/4/4/4

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	503	EU9	O10-N8	9.32	1.38	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	EU9	O10-N8	9.19	1.38	1.22
4	B	503	EU9	C5-C4	4.78	1.47	1.39
4	A	503	EU9	C5-C4	4.49	1.47	1.39
2	B	501	3PO	PB-O3B	4.27	1.64	1.59
4	A	503	EU9	O16-C15	-2.97	1.21	1.30
4	A	503	EU9	C8-N7	2.77	1.37	1.31
4	B	503	EU9	C4-N9	-2.69	1.32	1.37
4	B	503	EU9	C5-N7	-2.67	1.34	1.39
4	B	503	EU9	C41-N8	-2.56	1.41	1.45
4	B	503	EU9	C8-N7	2.52	1.36	1.31
4	B	503	EU9	C7-C3	2.48	1.54	1.50
4	B	503	EU9	C21-C3	2.45	1.43	1.39
4	A	503	EU9	C4-N9	-2.35	1.32	1.37
4	A	503	EU9	O24-C20	-2.22	1.40	1.45
4	A	503	EU9	C41-N8	-2.20	1.41	1.45
4	A	503	EU9	C41-C3	2.18	1.43	1.40
4	A	503	EU9	C5-N7	-2.15	1.35	1.39
4	B	503	EU9	O16-C15	-2.10	1.23	1.30
2	A	501	3PO	PG-O3G	-2.04	1.47	1.54

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	503	EU9	C5-C4-N3	-5.57	119.05	126.72
4	A	503	EU9	C5-C4-N3	-5.24	119.50	126.72
4	B	503	EU9	N3-C4-N9	4.71	135.19	127.17
4	A	503	EU9	C13-C14-N18	4.43	121.66	110.12
4	A	503	EU9	N3-C2-N1	-4.15	122.30	128.58
4	B	503	EU9	N3-C2-N1	-4.06	122.43	128.58
4	B	503	EU9	C4-N9-C8	4.01	109.94	105.74
4	A	503	EU9	N3-C4-N9	3.90	133.80	127.17
4	B	503	EU9	C13-C14-N18	3.73	119.85	110.12
4	A	503	EU9	C4-C5-N7	-3.68	106.38	110.58
4	B	503	EU9	C4-C5-N7	-3.29	106.82	110.58
4	A	503	EU9	C4-N9-C8	3.20	109.10	105.74
4	B	503	EU9	N9-C8-N7	-3.16	109.45	113.94
4	A	503	EU9	C2-N3-C4	2.98	119.11	111.83
4	B	503	EU9	C2-N3-C4	2.91	118.94	111.83
4	B	503	EU9	C5-N7-C8	2.90	108.00	103.45
4	A	503	EU9	N9-C8-N7	-2.68	110.13	113.94
4	A	503	EU9	C5-N7-C8	2.67	107.65	103.45
2	B	501	3PO	O2A-PA-O1A	2.30	119.81	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	EU9	C7-C3-C21	-2.25	116.03	120.41
2	A	501	3PO	O2B-PB-O3B	2.25	113.36	107.27
2	B	501	3PO	O3G-PG-O3B	2.24	112.15	104.64
4	B	503	EU9	C7-C3-C21	-2.22	116.09	120.41
4	B	503	EU9	C22-C27-C20	-2.19	98.37	102.61
4	B	503	EU9	C2-N1-C6	2.18	122.31	118.73
4	A	503	EU9	C6-C5-N7	2.13	136.19	132.09
4	A	503	EU9	C2-N1-C6	2.07	122.14	118.73

There are no chirality outliers.

All (19) 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	A	503	EU9	C12-C13-C14-N18
4	B	503	EU9	C12-C13-C14-N18
4	B	503	EU9	C21-C3-C7-S11
4	A	503	EU9	C3-C7-S11-C19
2	A	501	3PO	PB-O3A-PA-O2A
4	B	503	EU9	C13-C14-C15-O16
4	A	503	EU9	S11-C12-C13-C14
4	B	503	EU9	S11-C12-C13-C14
4	B	503	EU9	C13-C14-C15-O17
4	B	503	EU9	C3-C7-S11-C12
4	B	503	EU9	C3-C7-S11-C19
4	A	503	EU9	C13-C14-C15-O17
2	B	501	3PO	PB-O3B-PG-O2G
4	A	503	EU9	C22-C23-N9-C8
4	B	503	EU9	C22-C23-N9-C8
4	A	503	EU9	C13-C14-C15-O16
2	A	501	3PO	PB-O3A-PA-O1A

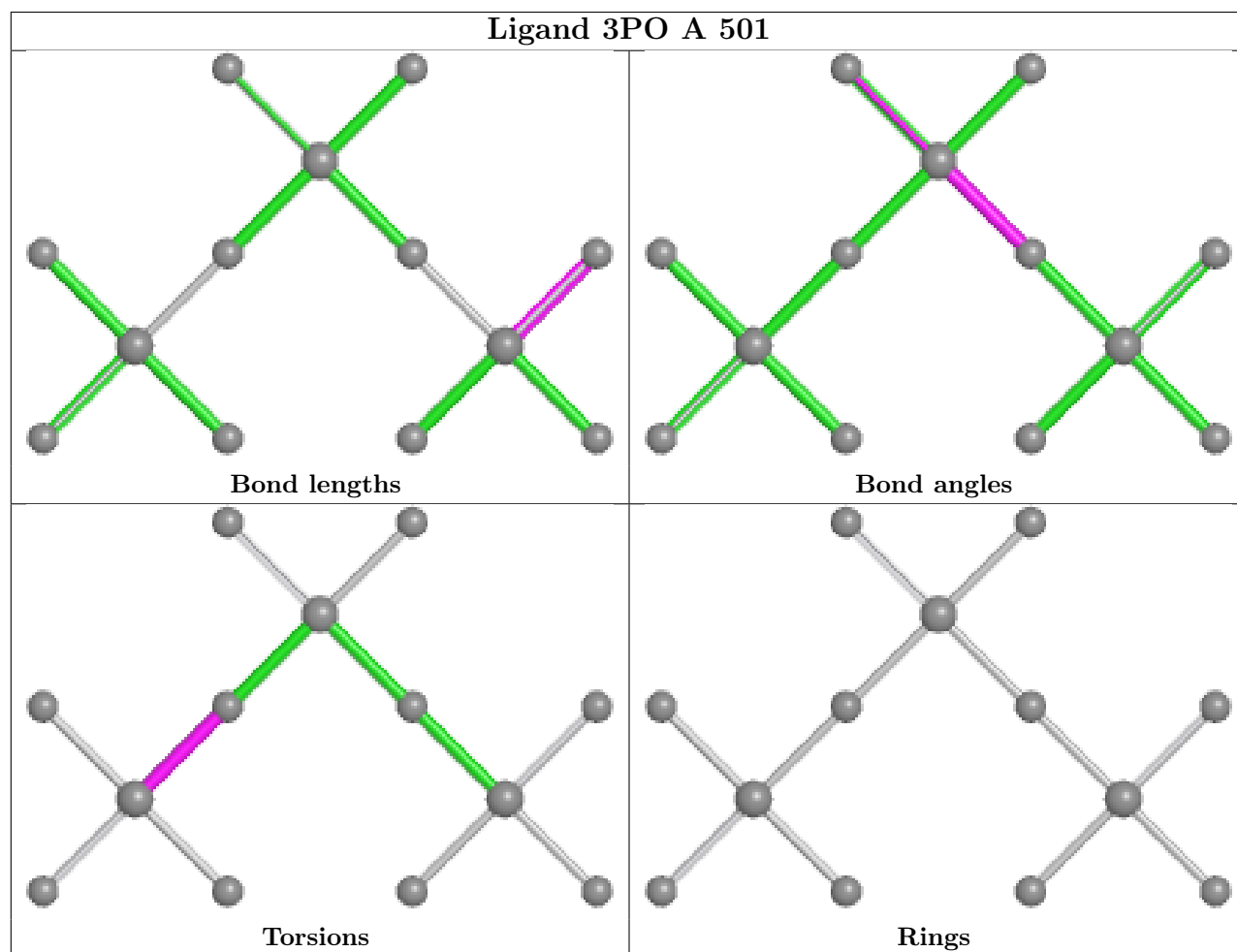
There are no ring outliers.

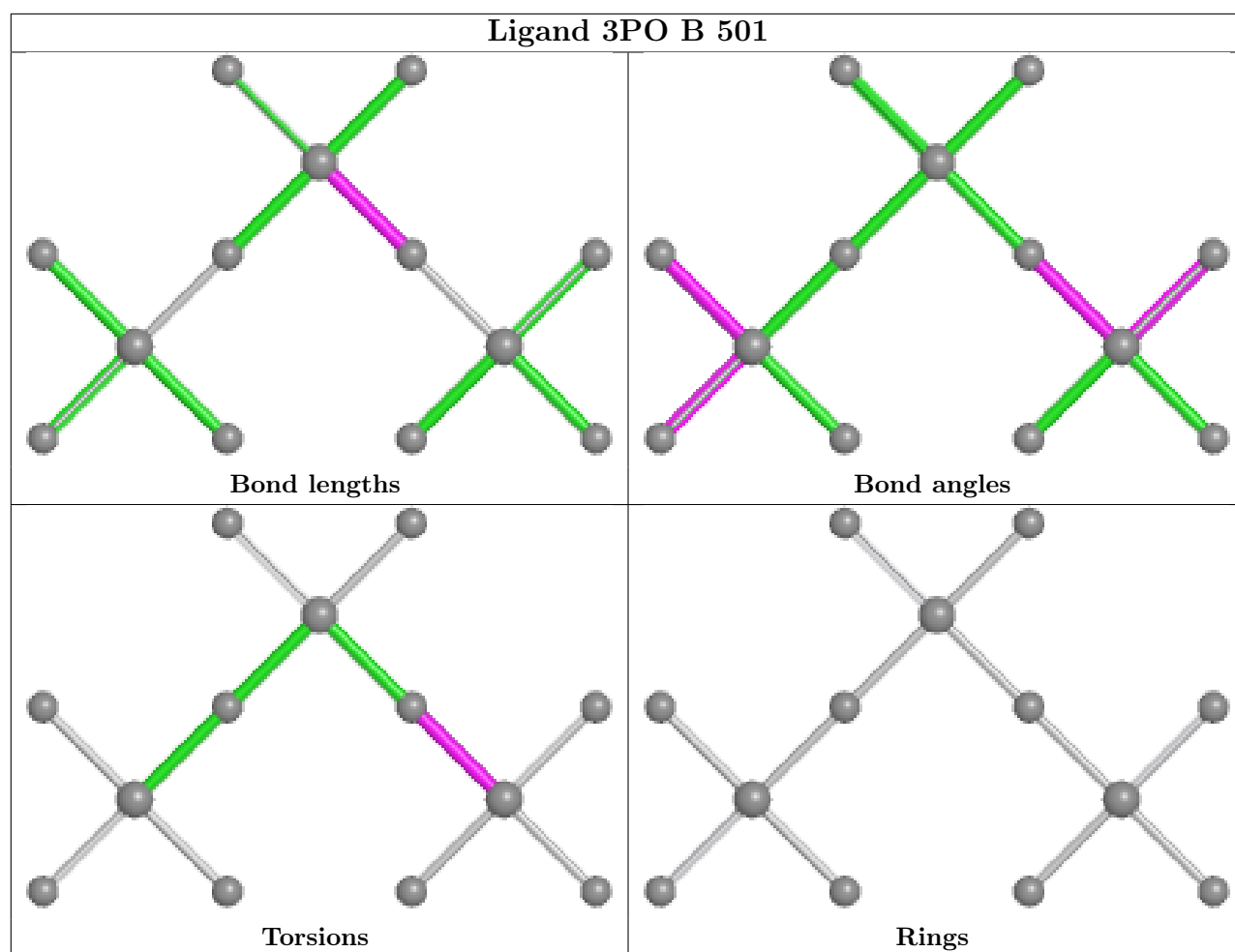
2 monomers are involved in 2 short contacts:

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

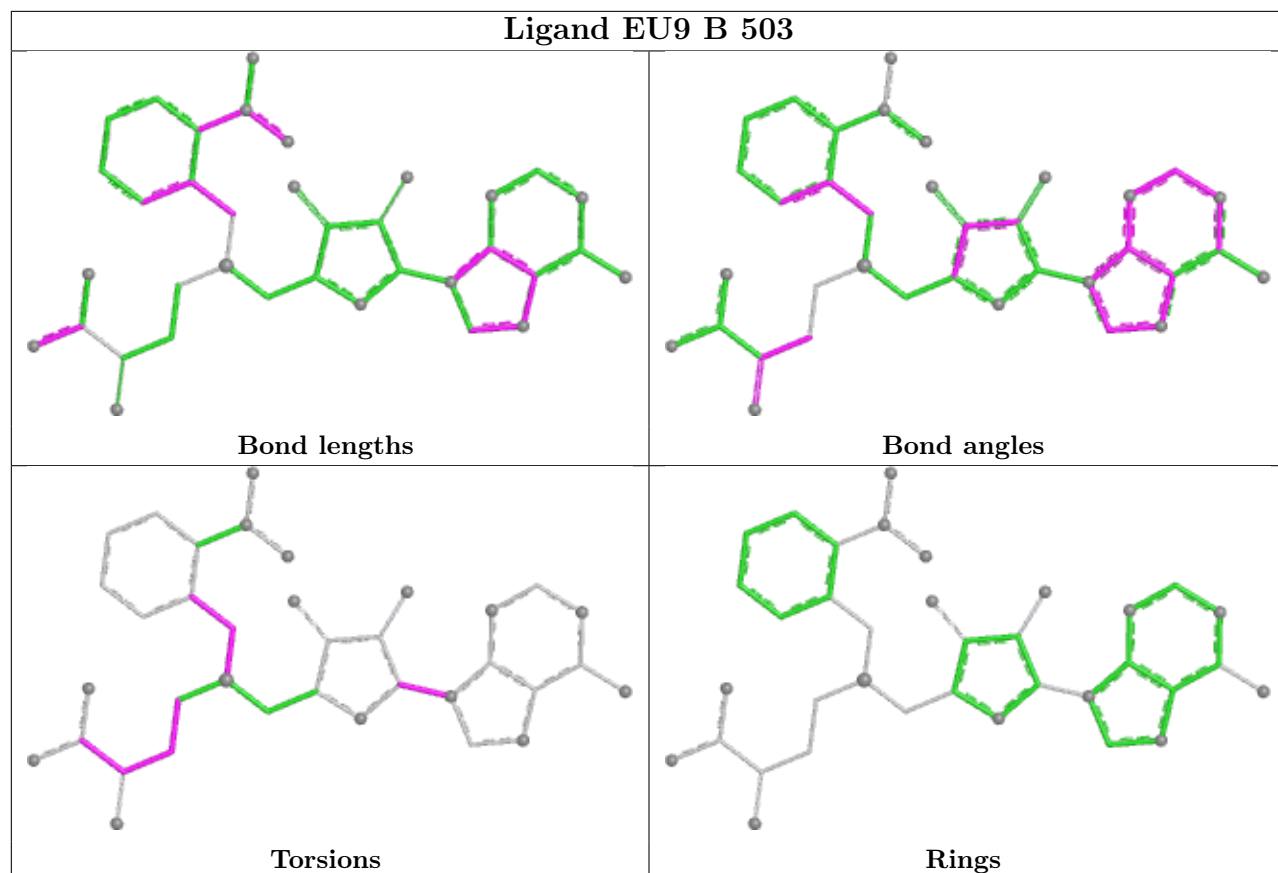
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.

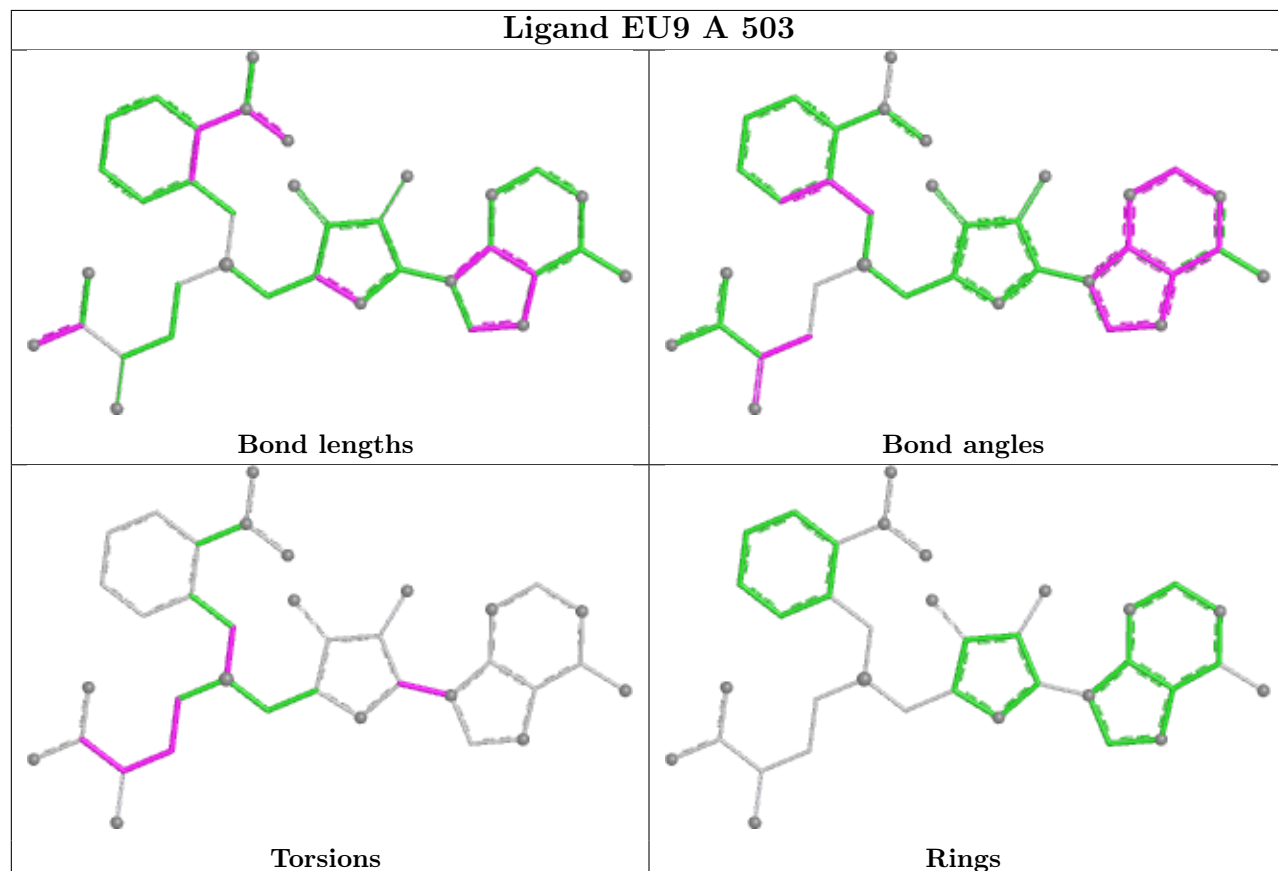




Ligand EU9 B 503



Ligand EU9 A 503



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	381/414 (92%)	-0.09	12 (3%) 51 56	9, 26, 51, 84	4 (1%)
1	B	381/414 (92%)	0.01	15 (3%) 43 47	9, 29, 54, 111	5 (1%)
All	All	762/828 (92%)	-0.04	27 (3%) 47 52	9, 27, 53, 111	9 (1%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	177	VAL	8.0
1	A	177	VAL	6.4
1	A	178	SER	4.4
1	B	179	SER	4.4
1	B	127	HIS	4.4
1	B	128	VAL	4.4
1	B	178	SER	4.3
1	A	179	SER	3.9
1	A	128	VAL	3.9
1	B	202	VAL	3.4
1	A	127	HIS	3.3
1	A	200	HIS	3.0
1	B	201	GLY	3.0
1	A	199	LYS	3.0
1	B	120	ASN	2.9
1	B	278	THR	2.8
1	B	180	ARG	2.7
1	A	180	ARG	2.6
1	A	176	GLY	2.6
1	A	175	LYS	2.6
1	B	181	VAL	2.5
1	B	200	HIS	2.4
1	B	199	LYS	2.4
1	B	176	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	120	ASN	2.2
1	B	21	GLU	2.1
1	A	129	ASP	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

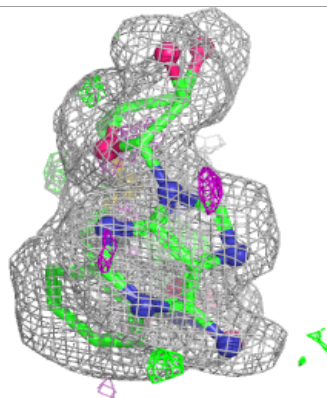
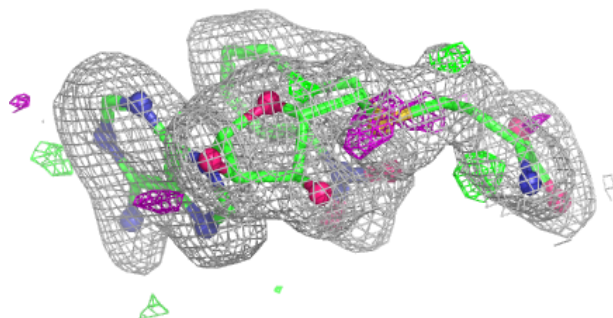
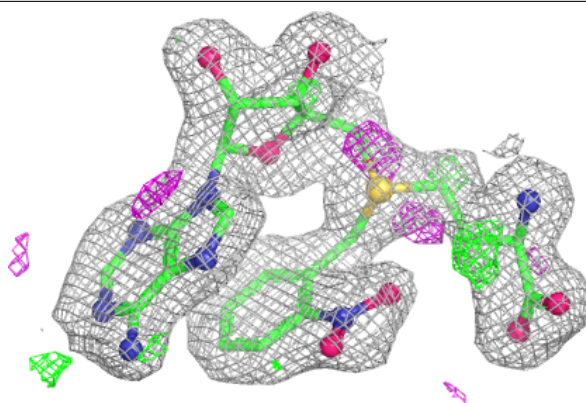
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EU9	B	503	36/36	0.94	0.09	21,25,45,56	0
4	EU9	A	503	36/36	0.95	0.08	19,25,43,58	0
3	MG	A	502	1/1	0.99	0.02	16,16,16,16	0
3	MG	B	502	1/1	0.99	0.02	17,17,17,17	0
2	3PO	A	501	13/13	0.99	0.03	15,17,19,19	0
2	3PO	B	501	13/13	0.99	0.04	15,18,19,20	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.

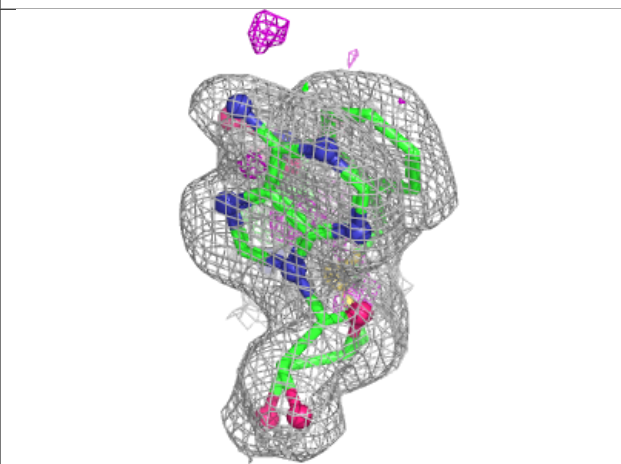
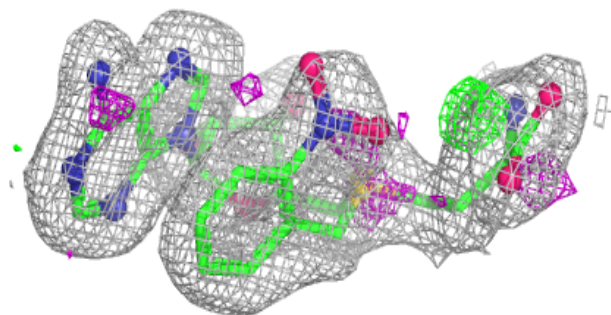
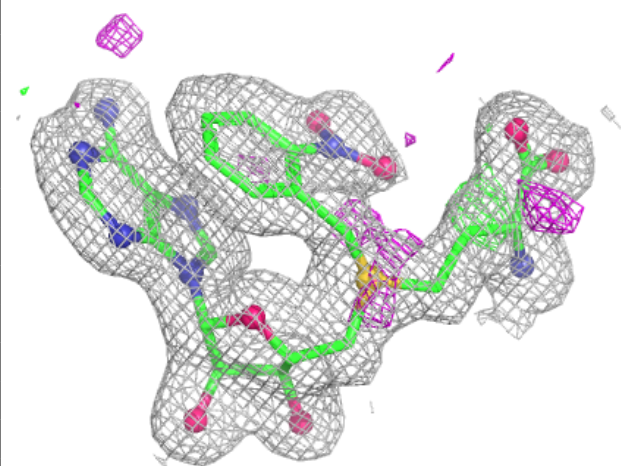
Electron density around EU9 B 503:

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



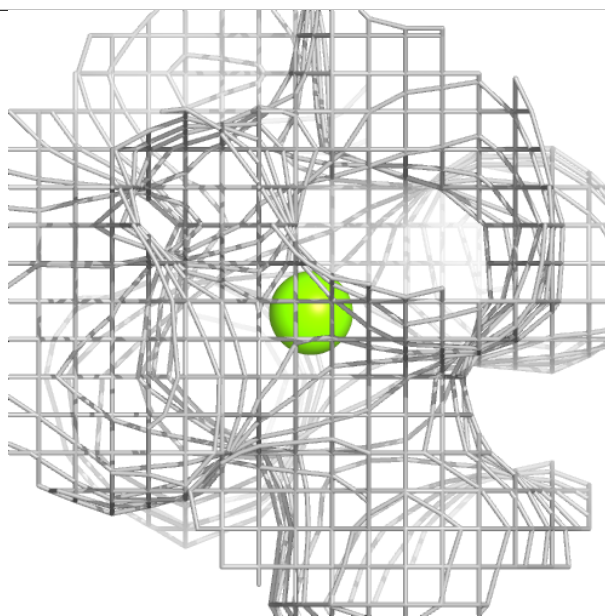
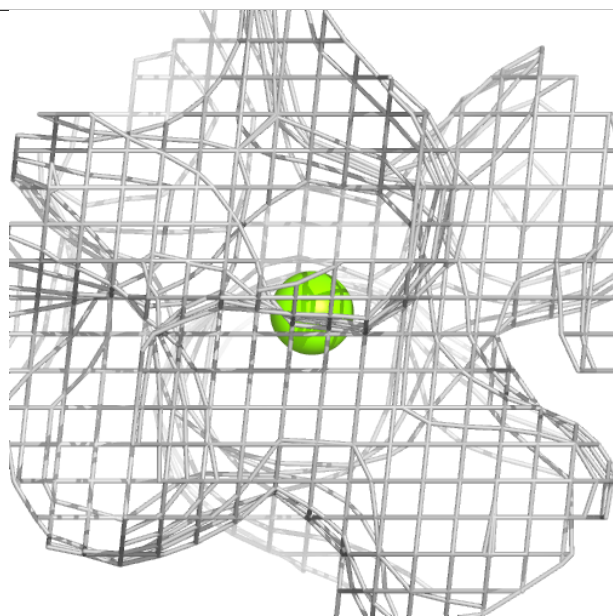
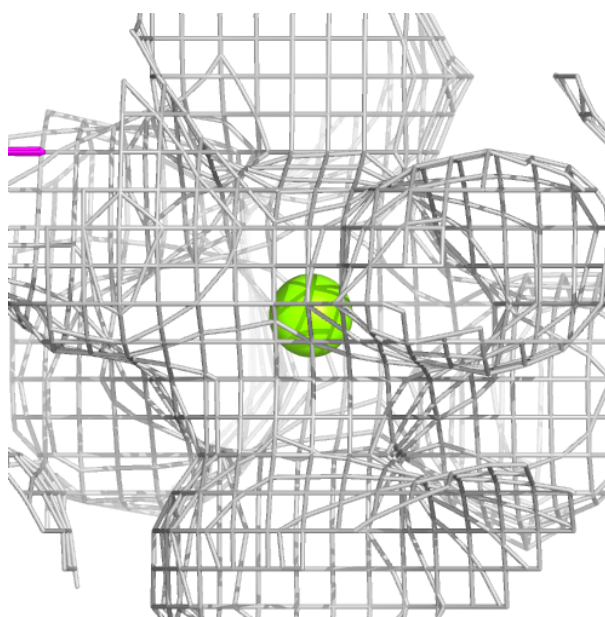
Electron density around EU9 A 503:

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



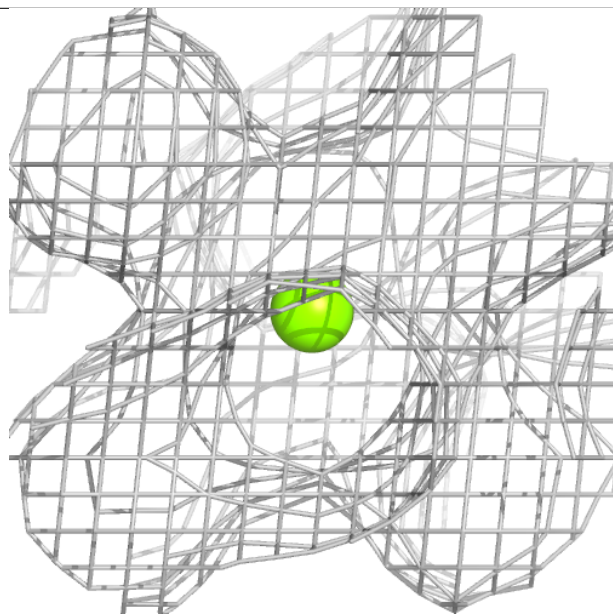
Electron density around MG A 502:

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



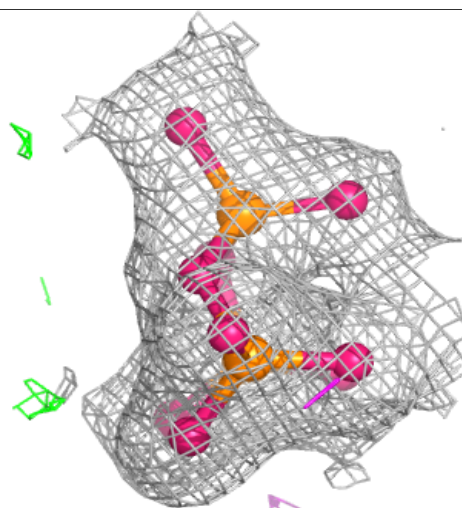
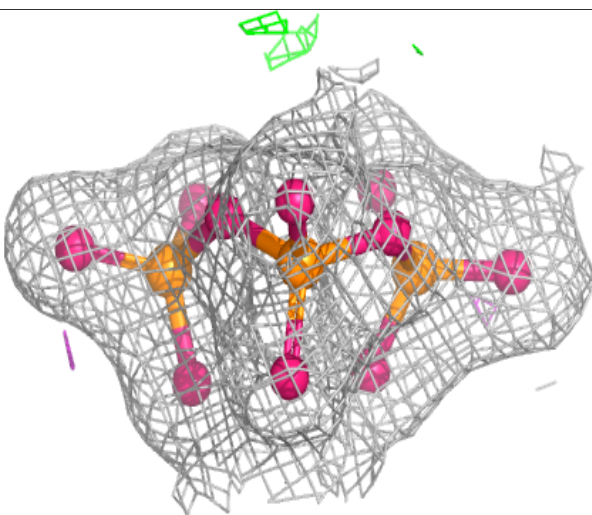
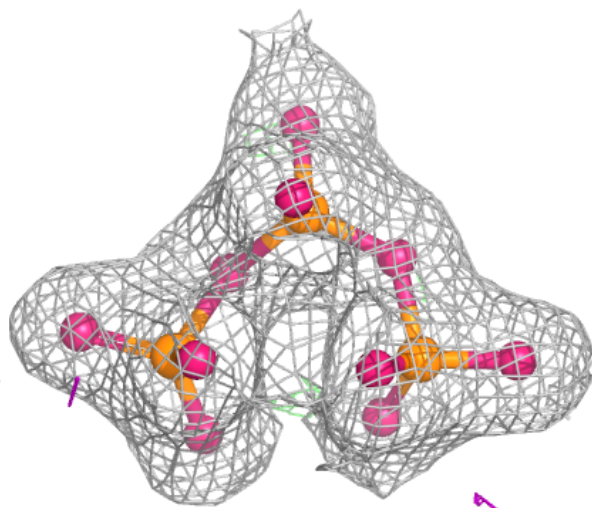
Electron density around MG B 502:

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and green (positive)



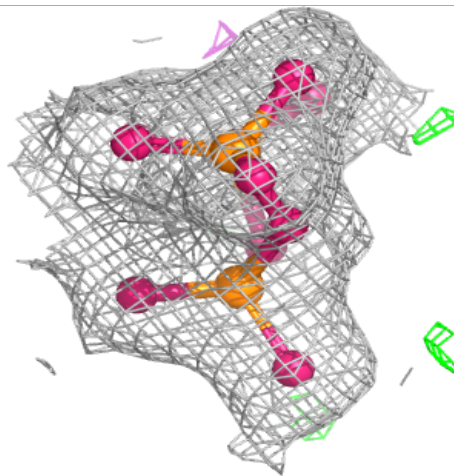
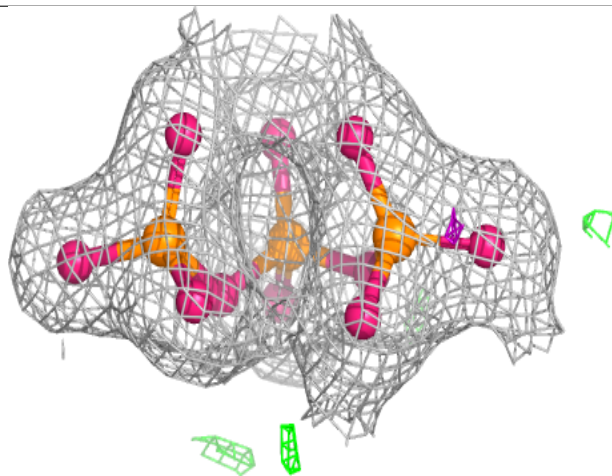
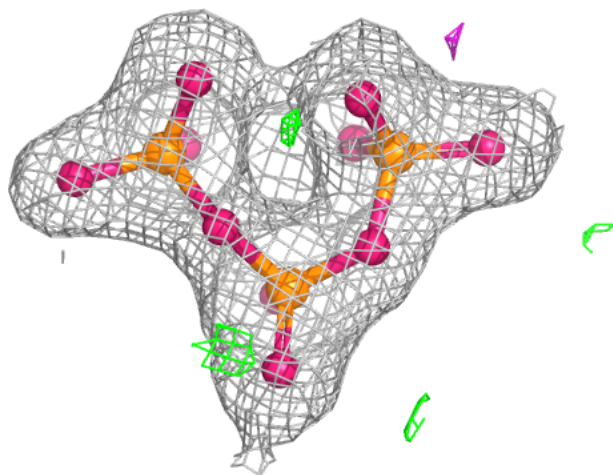
Electron density around 3PO A 501:

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



Electron density around 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)



6.5 Other polymers ⓘ

There are no such residues in this entry.