



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 8, 2024 – 07:12 am GMT

PDB ID : 6HE2
Title : Crystal structure of an open conformation of 2-Hydroxyisobutyryl-CoA Ligase (HCL) in complex with 2-HIB-AMP and CoA
Authors : Zahn, M.; Rohwerder, T.; Strater, N.
Deposited on : 2018-08-20
Resolution : 2.30 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

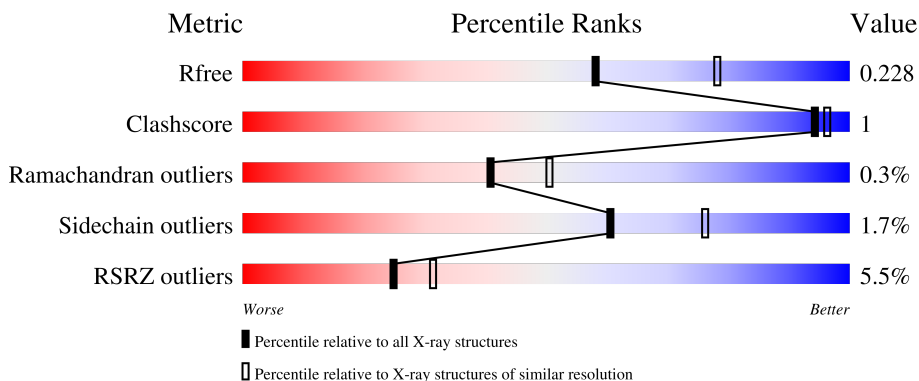
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

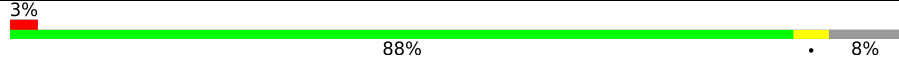

The reported resolution of this entry is 2.30 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	499	
1	B	499	

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 7501 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 2-hydroxyisobutyryl-CoA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	460	3630	2292	651	663	24	0	0	0
1	B	430	3380	2138	602	617	23	0	0	0

There are 44 discrepancies between the modelled and reference sequences:

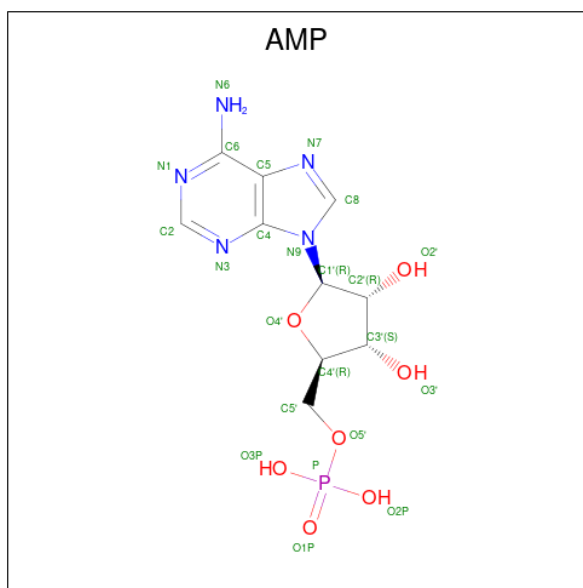
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	initiating methionine	UNP I3VE75
A	-9	ALA	-	expression tag	UNP I3VE75
A	-8	SER	-	expression tag	UNP I3VE75
A	-7	HIS	-	expression tag	UNP I3VE75
A	-6	HIS	-	expression tag	UNP I3VE75
A	-5	HIS	-	expression tag	UNP I3VE75
A	-4	HIS	-	expression tag	UNP I3VE75
A	-3	HIS	-	expression tag	UNP I3VE75
A	-2	HIS	-	expression tag	UNP I3VE75
A	-1	SER	-	expression tag	UNP I3VE75
A	0	GLY	-	expression tag	UNP I3VE75
A	478	GLY	-	expression tag	UNP I3VE75
A	479	SER	-	expression tag	UNP I3VE75
A	480	ALA	-	expression tag	UNP I3VE75
A	481	TRP	-	expression tag	UNP I3VE75
A	482	SER	-	expression tag	UNP I3VE75
A	483	HIS	-	expression tag	UNP I3VE75
A	484	PRO	-	expression tag	UNP I3VE75
A	485	GLN	-	expression tag	UNP I3VE75
A	486	PHE	-	expression tag	UNP I3VE75
A	487	GLU	-	expression tag	UNP I3VE75
A	488	LYS	-	expression tag	UNP I3VE75
B	-10	MET	-	initiating methionine	UNP I3VE75
B	-9	ALA	-	expression tag	UNP I3VE75
B	-8	SER	-	expression tag	UNP I3VE75

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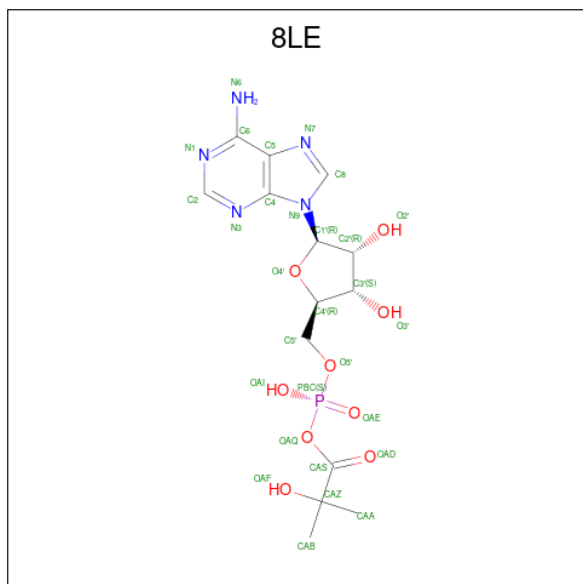
Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	HIS	-	expression tag	UNP I3VE75
B	-6	HIS	-	expression tag	UNP I3VE75
B	-5	HIS	-	expression tag	UNP I3VE75
B	-4	HIS	-	expression tag	UNP I3VE75
B	-3	HIS	-	expression tag	UNP I3VE75
B	-2	HIS	-	expression tag	UNP I3VE75
B	-1	SER	-	expression tag	UNP I3VE75
B	0	GLY	-	expression tag	UNP I3VE75
B	478	GLY	-	expression tag	UNP I3VE75
B	479	SER	-	expression tag	UNP I3VE75
B	480	ALA	-	expression tag	UNP I3VE75
B	481	TRP	-	expression tag	UNP I3VE75
B	482	SER	-	expression tag	UNP I3VE75
B	483	HIS	-	expression tag	UNP I3VE75
B	484	PRO	-	expression tag	UNP I3VE75
B	485	GLN	-	expression tag	UNP I3VE75
B	486	PHE	-	expression tag	UNP I3VE75
B	487	GLU	-	expression tag	UNP I3VE75
B	488	LYS	-	expression tag	UNP I3VE75

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



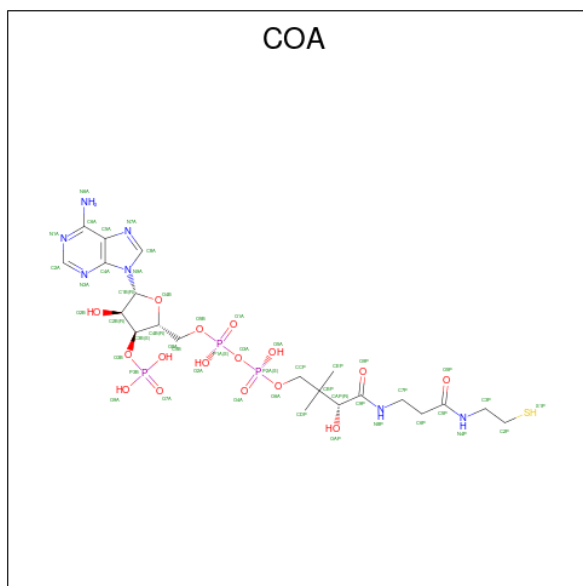
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	1
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	1
			23	10	5	7	1		

- Molecule 3 is [[(2 {R},3 {S},4 {R},5 {R})-5-(6-aminopurin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl] 2-methyl-2-oxidanyl-propanoate (three-letter code: 8LE) (formula: C₁₄H₂₀N₅O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	Total	C	N	O	P	0	1
			29	14	5	9	1		
3	B	1	Total	C	N	O	P	0	1
			29	14	5	9	1		

- Molecule 4 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
4	A	1	48	21	7	16	3	1	11	0
4	B	1	48	21	7	16	3	1	17	0

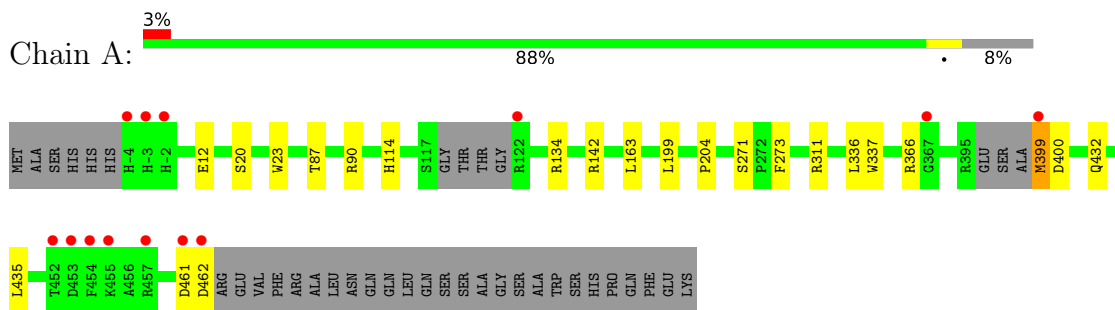
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	159	Total	O	0	0
			159	159		
5	B	132	Total	O	0	0
			132	132		

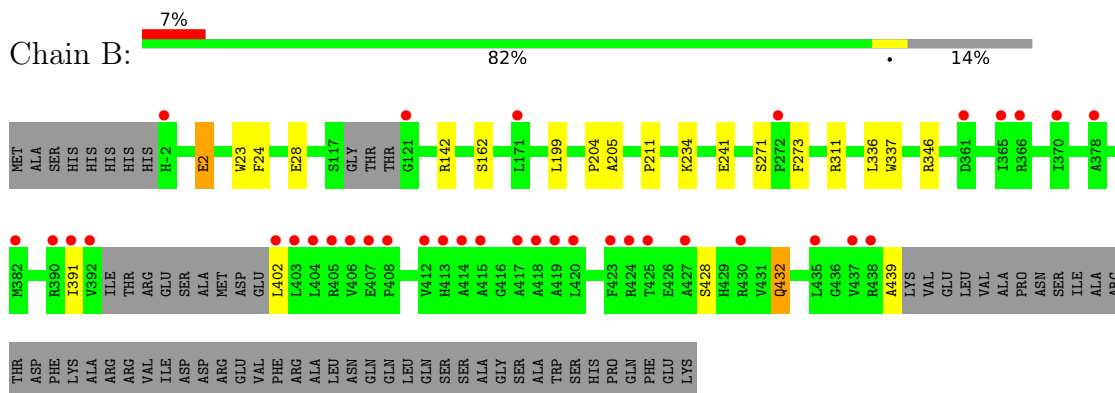
3 Residue-property plots [i](#)

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: 2-hydroxyisobutyryl-CoA synthetase



- Molecule 1: 2-hydroxyisobutyryl-CoA synthetase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.85Å 101.85Å 109.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.72 – 2.30 39.72 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.72-2.30) 99.8 (39.72-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 2.29Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.184 , 0.222 0.186 , 0.228	Depositor DCC
R_{free} test set	1467 reflections (3.11%)	wwPDB-VP
Wilson B-factor (Å ²)	35.9	Xtrriage
Anisotropy	0.568	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7501	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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: 8LE, AMP, COA

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	0.50	0/3728	0.65	0/5056
1	B	0.50	0/3474	0.66	0/4713
All	All	0.50	0/7202	0.65	0/9769

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

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	3630	0	3507	7	0
1	B	3380	0	3254	11	0
2	A	23	0	12	0	0
2	B	23	0	12	0	0
3	A	29	0	0	0	0
3	B	29	0	0	0	0
4	A	48	0	32	0	0
4	B	48	0	32	0	0
5	A	159	0	0	0	0
5	B	132	0	0	0	0
All	All	7501	0	6849	18	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 1.

All (18) 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:199:LEU:HD22	1:A:204:PRO:HG3	1.82	0.61
1:B:199:LEU:HD22	1:B:204:PRO:HG3	1.88	0.56
1:B:211:PRO:HD2	1:B:241:GLU:HG3	1.89	0.54
1:B:428:SER:O	1:B:432:GLN:HB2	2.11	0.50
1:A:87:THR:HG22	1:A:90:ARG:HH12	1.77	0.49
1:A:366:ARG:HG3	1:A:399:MET:HG2	1.97	0.46
1:B:2:GLU:HG3	1:B:24:PHE:CD1	2.51	0.46
1:A:114:HIS:HB3	1:A:163:LEU:O	2.16	0.46
1:A:271:SER:HA	1:A:273:PHE:N	2.31	0.45
1:B:271:SER:HA	1:B:273:PHE:N	2.31	0.45
1:B:402:LEU:HD21	1:B:439:ALA:HA	2.00	0.44
1:B:23:TRP:HB3	1:B:142:ARG:HG3	1.99	0.43
1:B:28:GLU:HB3	1:B:346:ARG:HG2	2.00	0.43
1:A:23:TRP:HB3	1:A:142:ARG:HG3	2.01	0.42
1:B:432:GLN:HE22	1:B:439:ALA:H	1.66	0.42
1:A:12:GLU:OE2	1:A:134:ARG:HD3	2.21	0.41
1:B:205:ALA:HB1	1:B:234:LYS:HE2	2.02	0.41
1:B:311:ARG:HG2	1:B:336:LEU:HD12	2.04	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	454/499 (91%)	434 (96%)	19 (4%)	1 (0%)	47	58
1	B	424/499 (85%)	408 (96%)	14 (3%)	2 (0%)	29	35
All	All	878/998 (88%)	842 (96%)	33 (4%)	3 (0%)	41	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	400	ASP
1	B	162	SER
1	B	391	ILE

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	374/405 (92%)	365 (98%)	9 (2%)	49 66
1	B	346/405 (85%)	343 (99%)	3 (1%)	78 89
All	All	720/810 (89%)	708 (98%)	12 (2%)	60 76

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	SER
1	A	311	ARG
1	A	336	LEU
1	A	337	TRP
1	A	399	MET
1	A	432	GLN
1	A	435	LEU
1	A	461	ASP
1	A	462	ASP
1	B	2	GLU
1	B	337	TRP
1	B	432	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	216	HIS
1	B	197	GLN

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Mol	Chain	Res	Type
1	B	230	ASN
1	B	353	GLN
1	B	432	GLN

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](#)

6 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
4	COA	B	503	-	41,50,50	0.56	0	52,75,75	0.63	1 (1%)
4	COA	A	503	-	41,50,50	0.58	0	52,75,75	0.72	1 (1%)
3	8LE	A	502[A]	-	26,31,31	0.80	1 (3%)	30,48,48	1.29	2 (6%)
3	8LE	B	502[A]	-	26,31,31	0.74	0	30,48,48	1.33	3 (10%)
2	AMP	A	501[B]	-	22,25,25	0.66	0	25,38,38	0.80	1 (4%)
2	AMP	B	501[B]	-	22,25,25	0.57	0	25,38,38	0.75	1 (4%)

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	COA	B	503	-	-	7/44/64/64	0/3/3/3
4	COA	A	503	-	-	13/44/64/64	0/3/3/3
3	8LE	A	502[A]	-	-	2/15/37/37	0/3/3/3
3	8LE	B	502[A]	-	-	2/15/37/37	0/3/3/3
2	AMP	A	501[B]	-	-	3/6/26/26	0/3/3/3
2	AMP	B	501[B]	-	-	4/6/26/26	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502[A]	8LE	O4'-C1'	2.28	1.44	1.41

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502[A]	8LE	N3-C2-N1	-5.02	120.83	128.68
3	B	502[A]	8LE	N3-C2-N1	-4.95	120.94	128.68
3	B	502[A]	8LE	OAI-PBC-OAQ	2.89	113.56	104.14
2	A	501[B]	AMP	C5-C6-N6	2.31	123.86	120.35
4	B	503	COA	C5A-C6A-N6A	2.30	123.85	120.35
4	A	503	COA	C5A-C6A-N6A	2.30	123.84	120.35
2	B	501[B]	AMP	C5-C6-N6	2.28	123.81	120.35
3	B	502[A]	8LE	C4-C5-N7	-2.18	107.12	109.40
3	A	502[A]	8LE	OAI-PBC-OAQ	2.14	111.12	104.14

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501[B]	AMP	C3'-C4'-C5'-O5'
2	B	501[B]	AMP	C5'-O5'-P-O1P
2	B	501[B]	AMP	C5'-O5'-P-O3P
2	B	501[B]	AMP	C3'-C4'-C5'-O5'
4	A	503	COA	P2A-O3A-P1A-O5B
4	A	503	COA	OAP-CAP-CBP-CCP
4	A	503	COA	C9P-CAP-CBP-CCP
4	A	503	COA	OAP-CAP-CBP-CDP
4	A	503	COA	C9P-CAP-CBP-CDP

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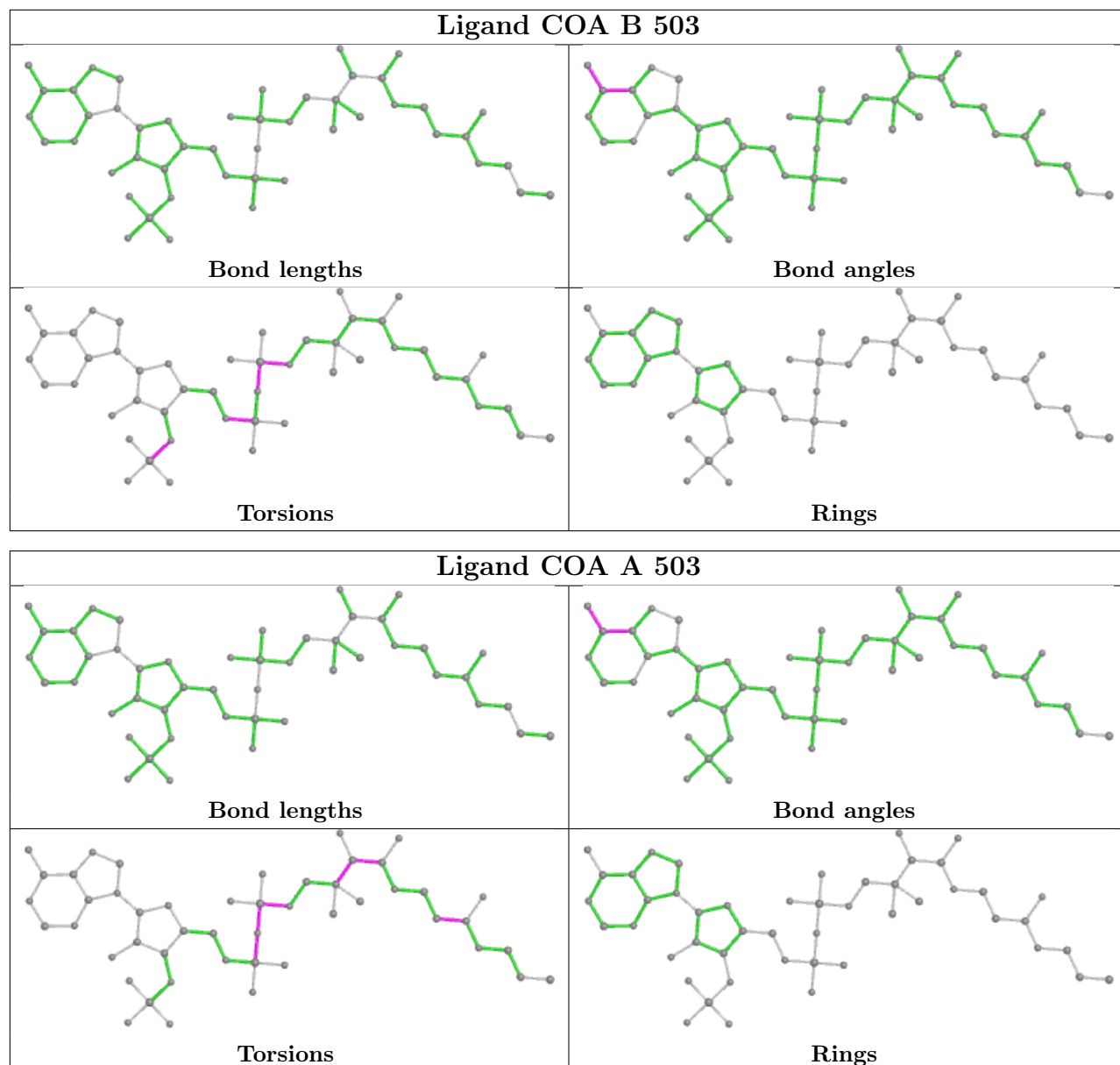
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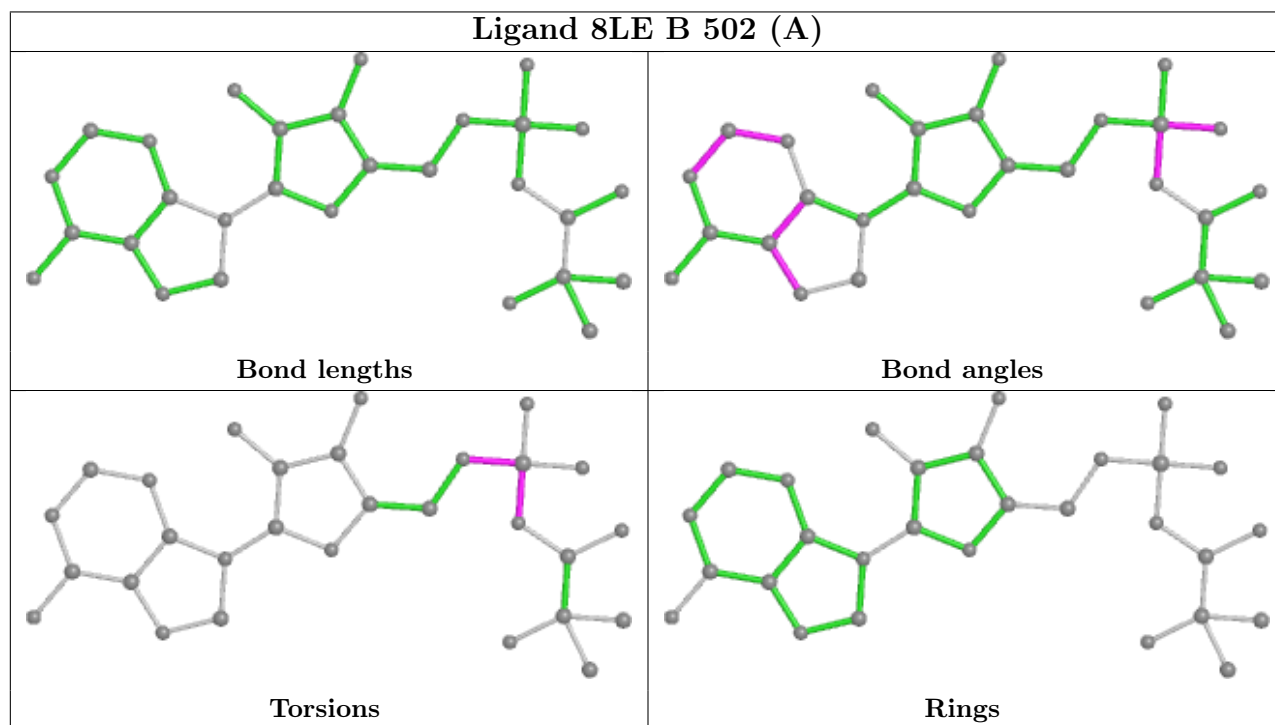
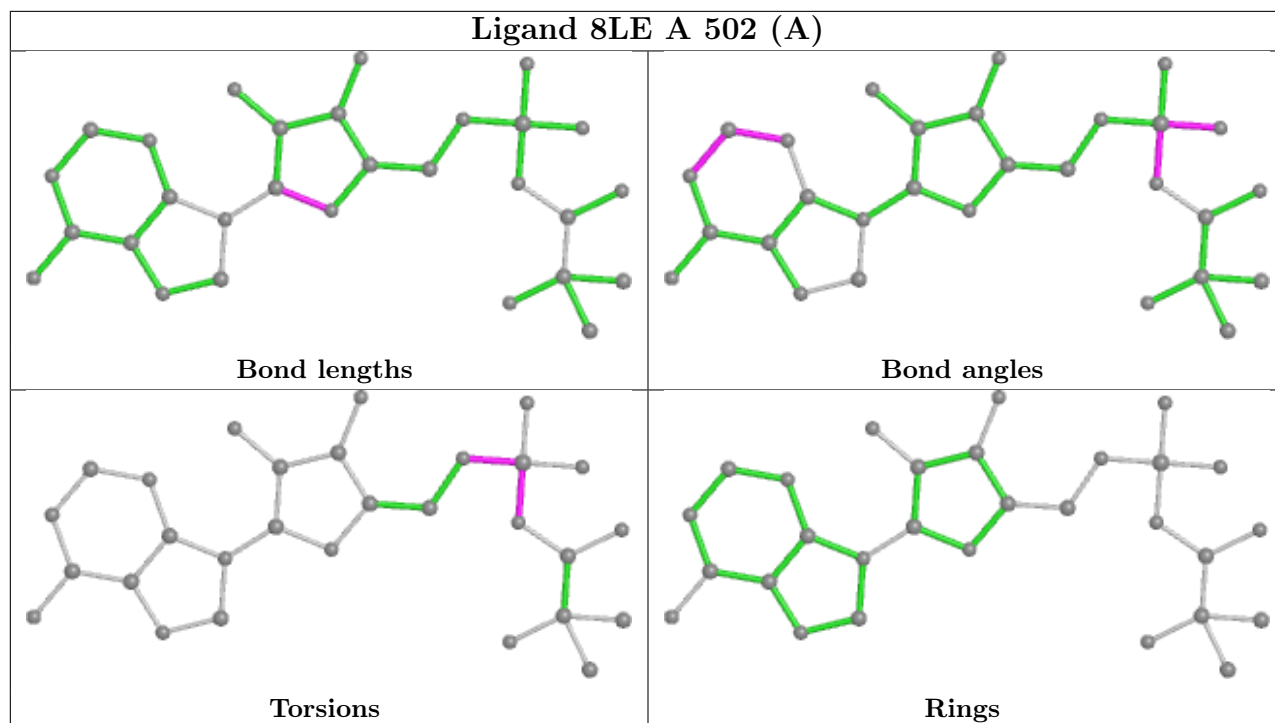
Mol	Chain	Res	Type	Atoms
4	A	503	COA	OAP-CAP-CBP-CEP
4	A	503	COA	O9P-C9P-CAP-CBP
4	B	503	COA	C3B-O3B-P3B-O9A
4	B	503	COA	C5B-O5B-P1A-O1A
2	A	501[B]	AMP	O4'-C4'-C5'-O5'
2	B	501[B]	AMP	O4'-C4'-C5'-O5'
3	A	502[A]	8LE	CAS-OAQ-PBC-OAI
4	A	503	COA	N8P-C9P-CAP-CBP
4	A	503	COA	P1A-O3A-P2A-O6A
4	A	503	COA	C9P-CAP-CBP-CEP
4	B	503	COA	C5B-O5B-P1A-O3A
4	B	503	COA	C5B-O5B-P1A-O2A
4	B	503	COA	P1A-O3A-P2A-O5A
3	B	502[A]	8LE	CAS-OAQ-PBC-OAE
2	A	501[B]	AMP	C5'-O5'-P-O3P
4	A	503	COA	N8P-C9P-CAP-OAP
4	B	503	COA	P1A-O3A-P2A-O4A
3	A	502[A]	8LE	C5'-O5'-PBC-OAE
3	B	502[A]	8LE	C5'-O5'-PBC-OAE
4	A	503	COA	CCP-O6A-P2A-O4A
4	B	503	COA	CCP-O6A-P2A-O4A
4	A	503	COA	O5P-C5P-C6P-C7P

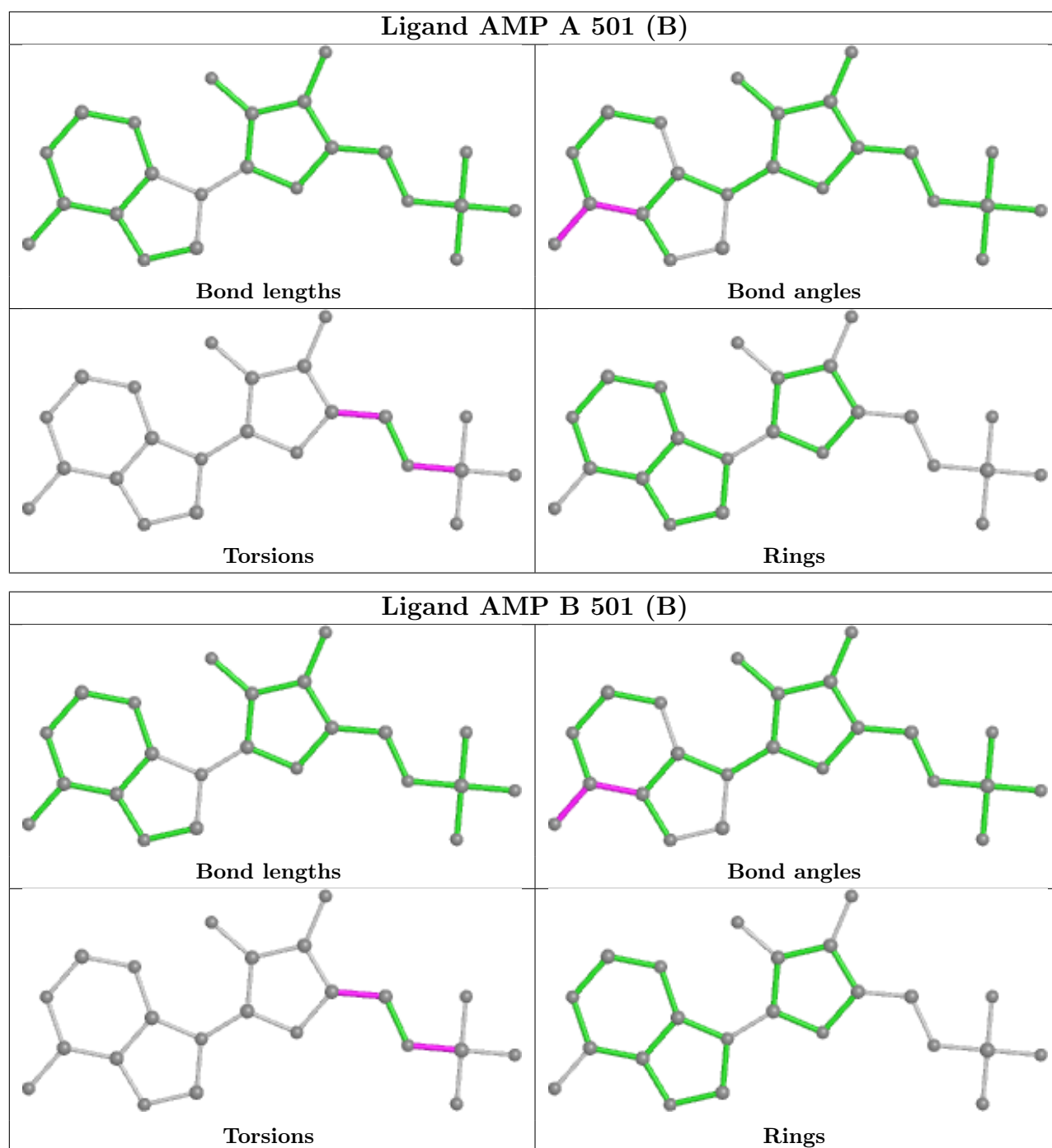
There are no ring outliers.

No monomer is involved in short contacts.

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, 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	460/499 (92%)	-0.25	13 (2%) 53 60	25, 37, 63, 114	0
1	B	430/499 (86%)	0.19	36 (8%) 11 15	25, 39, 86, 106	0
All	All	890/998 (89%)	-0.03	49 (5%) 25 31	25, 38, 81, 114	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	405	ARG	9.4
1	B	391	ILE	8.6
1	A	-4	HIS	8.4
1	B	427	ALA	8.2
1	B	402	LEU	7.5
1	B	403	LEU	7.4
1	A	454	PHE	7.2
1	B	415	ALA	6.1
1	A	-3	HIS	5.7
1	B	404	LEU	5.5
1	B	-2	HIS	4.9
1	B	423	PHE	4.6
1	B	412	VAL	4.5
1	A	-2	HIS	4.3
1	A	399	MET	4.2
1	A	462	ASP	4.1
1	A	453	ASP	4.1
1	B	430	ARG	4.0
1	B	365	ILE	3.8
1	B	382	MET	3.5
1	B	366	ARG	3.2
1	B	378	ALA	3.2
1	B	406	VAL	3.1
1	B	407	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	390	ARG	3.1
1	A	367	GLY	3.0
1	A	457	ARG	2.9
1	B	370	ILE	2.8
1	A	122	ARG	2.7
1	B	392	VAL	2.7
1	B	413	HIS	2.6
1	B	420	LEU	2.6
1	B	425	THR	2.6
1	B	437	VAL	2.5
1	B	408	PRO	2.5
1	B	272	PRO	2.4
1	B	435	LEU	2.4
1	B	438	ARG	2.3
1	A	452	THR	2.3
1	B	417	ALA	2.3
1	B	361	ASP	2.3
1	B	419	ALA	2.2
1	B	414	ALA	2.2
1	B	418	ALA	2.1
1	B	424	ARG	2.1
1	B	171	LEU	2.1
1	A	461	ASP	2.0
1	A	455	LYS	2.0
1	B	121	GLY	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](#)

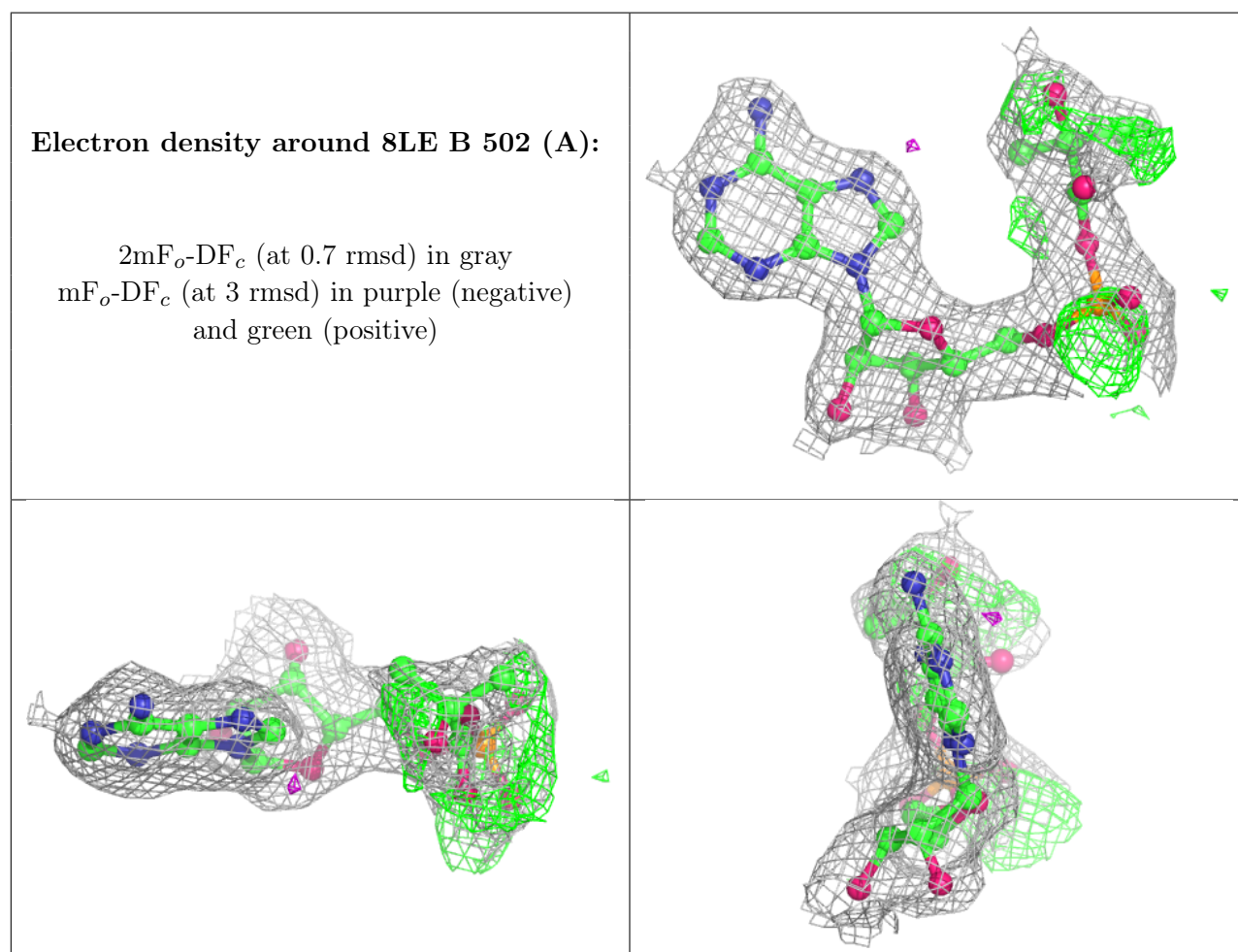
There are no monosaccharides in this entry.

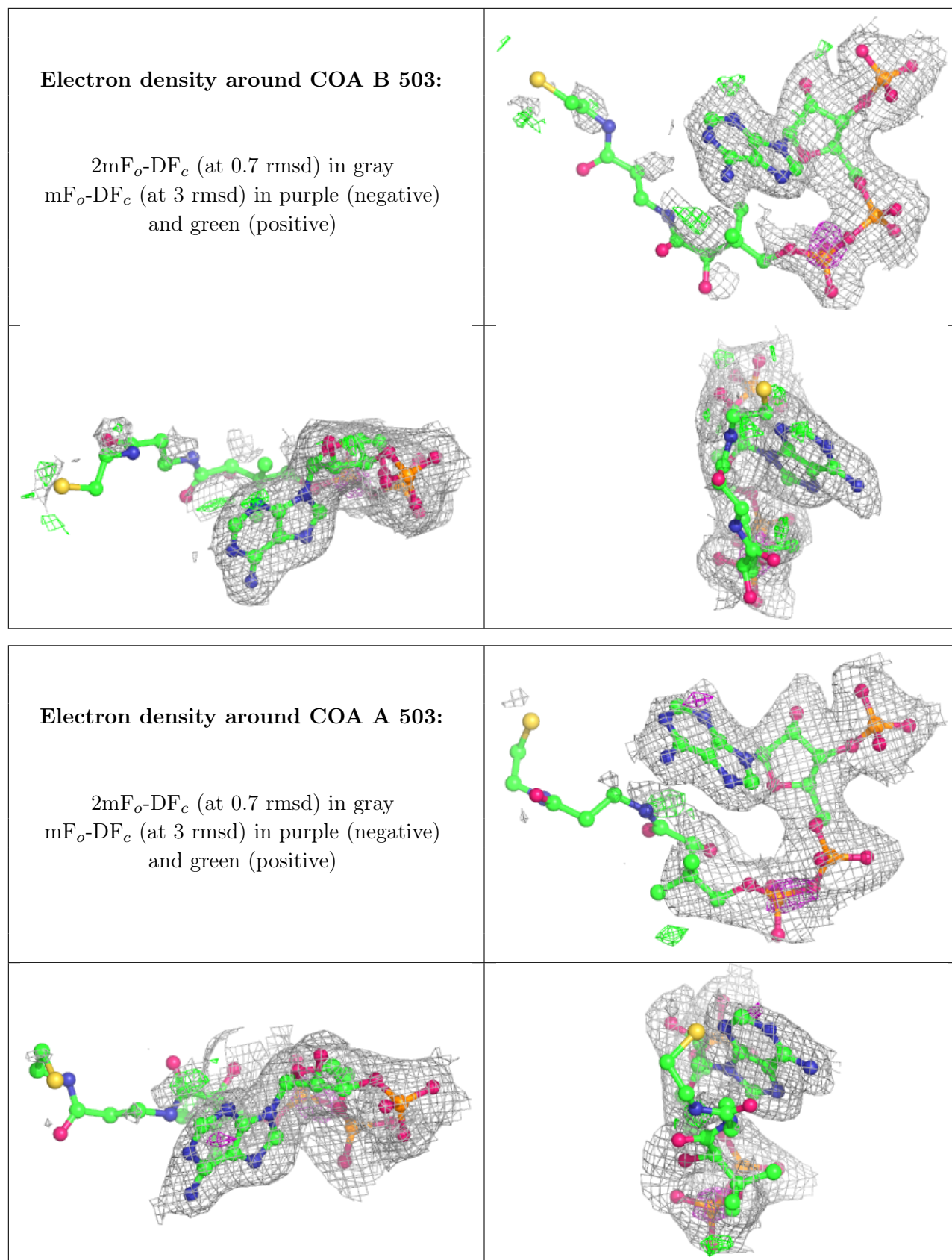
6.4 Ligands [i](#)

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, 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(\AA^2)	Q<0.9
3	8LE	B	502[A]	29/29	0.90	0.31	23,38,40,41	29
4	COA	B	503	48/48	0.92	0.12	42,74,98,98	17
4	COA	A	503	48/48	0.93	0.15	38,76,95,95	11
2	AMP	B	501[B]	23/23	0.94	0.22	25,38,40,41	23
3	8LE	A	502[A]	29/29	0.95	0.23	23,31,39,44	29
2	AMP	A	501[B]	23/23	0.97	0.19	13,30,32,32	23

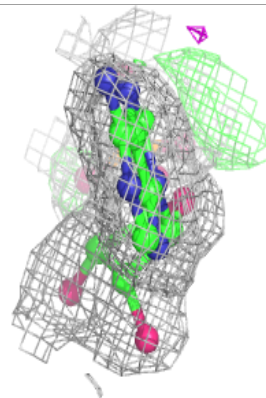
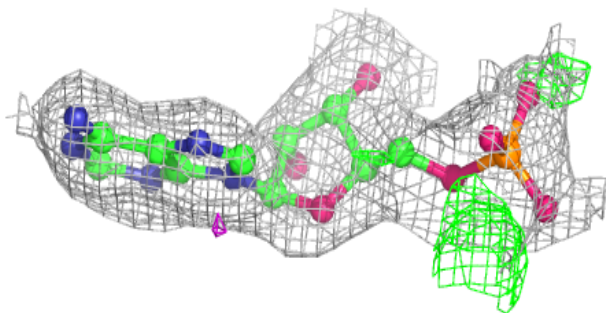
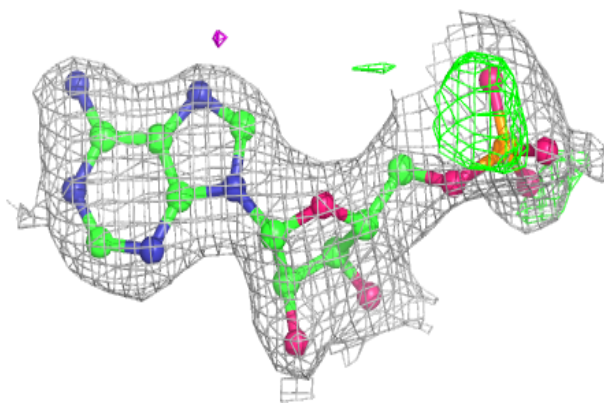
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





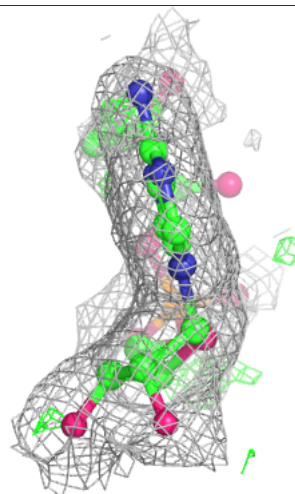
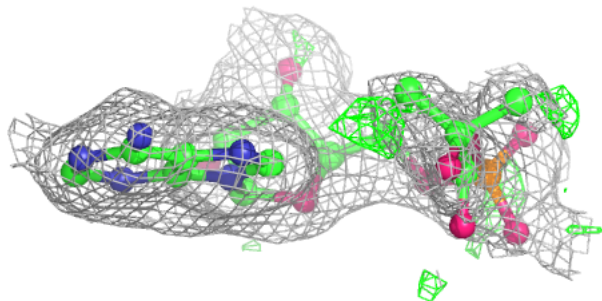
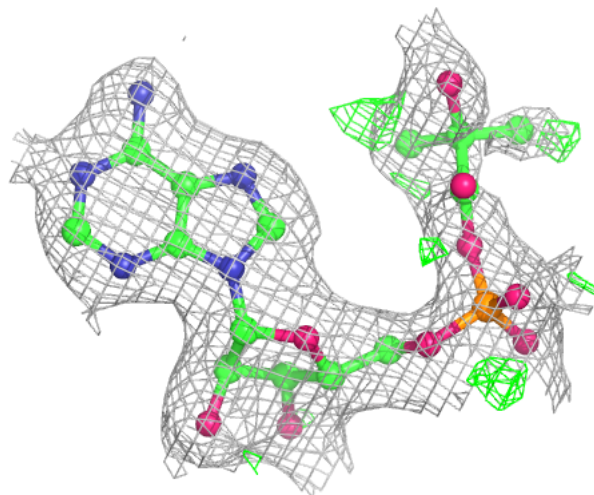
Electron density around AMP B 501 (B):

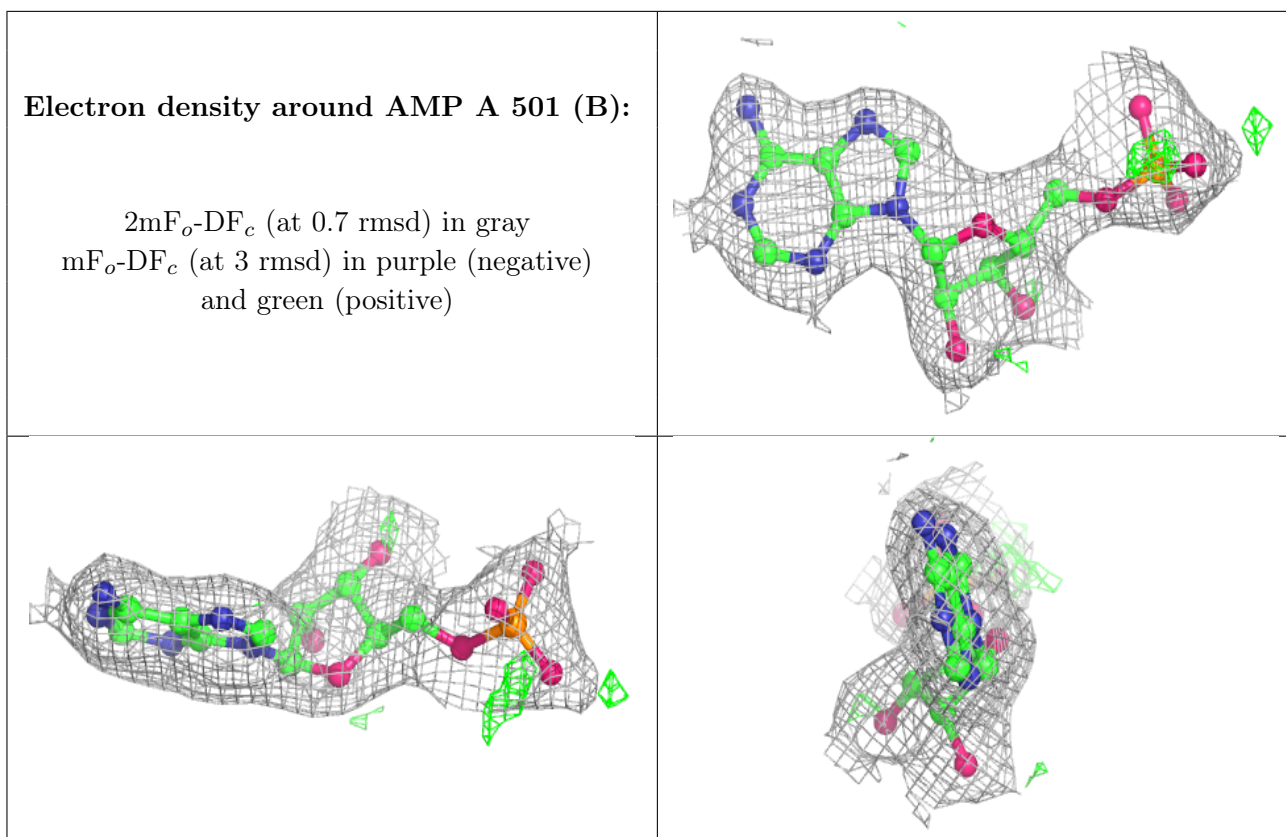
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 8LE A 502 (A):

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





6.5 Other polymers [i](#)

There are no such residues in this entry.