



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 12:12 AM UTC

PDB ID : 7KZD / pdb_00007kzd
Title : Crystal structure of KabA from Bacillus cereus UW85 in complex with the reduced internal aldimine and with bound Glutarate
Authors : Prasertanan, T.; Palmer, D.R.J.; Sanders, D.A.R.
Deposited on : 2020-12-10
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 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

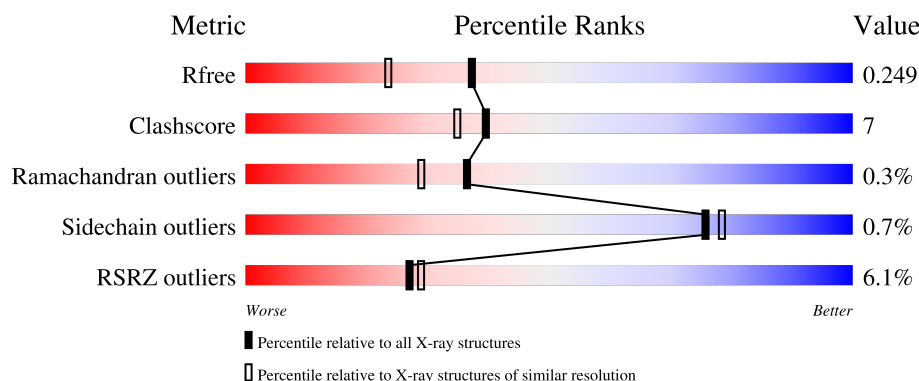
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	445	3% 83% 15% ..
1	B	445	4% 84% 15% .
1	C	445	15% 82% 16% .
1	D	445	6% 82% 16% .
1	E	445	4% 83% 15% .

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Mol	Chain	Length	Quality of chain
1	F	445	 5% 85% 13% .
1	G	445	 4% 85% 13% .
1	H	445	 8% 81% 18% .

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 30275 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 Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	1	0
			3539	2263	603	658	15			
1	B	439	Total	C	N	O	S	0	2	0
			3551	2269	605	662	15			
1	C	438	Total	C	N	O	S	0	1	0
			3539	2263	603	658	15			
1	D	438	Total	C	N	O	S	0	2	0
			3542	2264	604	659	15			
1	E	437	Total	C	N	O	S	0	2	0
			3540	2264	603	658	15			
1	F	437	Total	C	N	O	S	0	0	0
			3522	2252	601	654	15			
1	G	439	Total	C	N	O	S	0	0	0
			3537	2262	603	657	15			
1	H	438	Total	C	N	O	S	0	1	0
			3538	2262	603	658	15			

There are 32 discrepancies between the modelled and reference sequences:

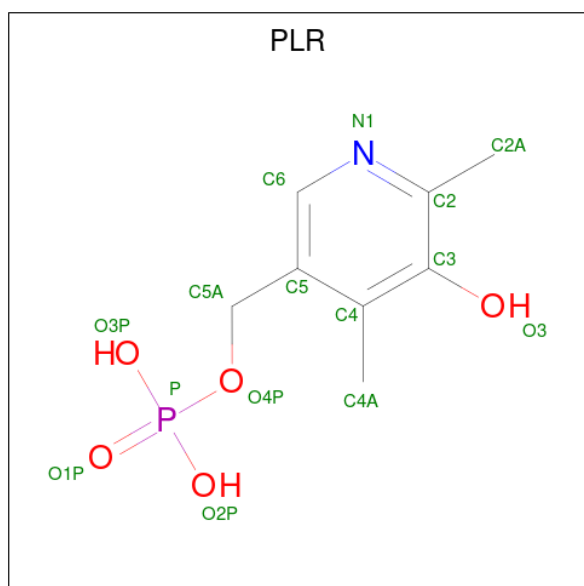
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP C0JRF5
A	0	ALA	-	expression tag	UNP C0JRF5
A	1	MET	-	expression tag	UNP C0JRF5
A	2	ASP	-	expression tag	UNP C0JRF5
B	-1	GLY	-	expression tag	UNP C0JRF5
B	0	ALA	-	expression tag	UNP C0JRF5
B	1	MET	-	expression tag	UNP C0JRF5
B	2	ASP	-	expression tag	UNP C0JRF5
C	-1	GLY	-	expression tag	UNP C0JRF5
C	0	ALA	-	expression tag	UNP C0JRF5
C	1	MET	-	expression tag	UNP C0JRF5
C	2	ASP	-	expression tag	UNP C0JRF5

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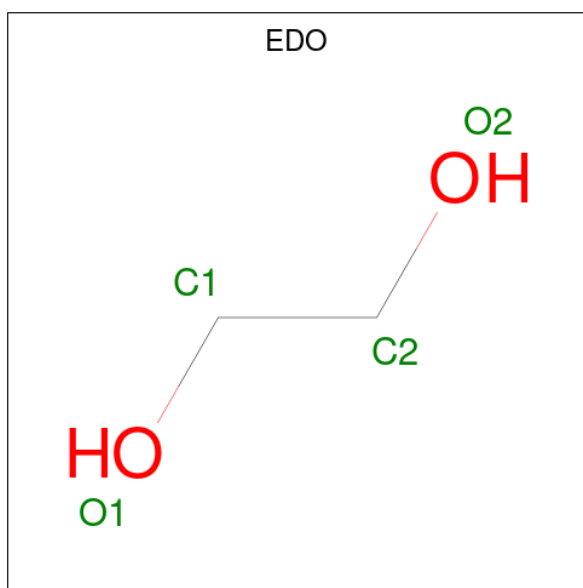
Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	GLY	-	expression tag	UNP C0JRF5
D	0	ALA	-	expression tag	UNP C0JRF5
D	1	MET	-	expression tag	UNP C0JRF5
D	2	ASP	-	expression tag	UNP C0JRF5
E	-1	GLY	-	expression tag	UNP C0JRF5
E	0	ALA	-	expression tag	UNP C0JRF5
E	1	MET	-	expression tag	UNP C0JRF5
E	2	ASP	-	expression tag	UNP C0JRF5
F	-1	GLY	-	expression tag	UNP C0JRF5
F	0	ALA	-	expression tag	UNP C0JRF5
F	1	MET	-	expression tag	UNP C0JRF5
F	2	ASP	-	expression tag	UNP C0JRF5
G	-1	GLY	-	expression tag	UNP C0JRF5
G	0	ALA	-	expression tag	UNP C0JRF5
G	1	MET	-	expression tag	UNP C0JRF5
G	2	ASP	-	expression tag	UNP C0JRF5
H	-1	GLY	-	expression tag	UNP C0JRF5
H	0	ALA	-	expression tag	UNP C0JRF5
H	1	MET	-	expression tag	UNP C0JRF5
H	2	ASP	-	expression tag	UNP C0JRF5

- Molecule 2 is (5-HYDROXY-4,6-DIMETHYLPYRIDIN-3-YL)METHYL DIHYDROGEN PHOSPHATE (CCD ID: PLR) (formula: C₈H₁₂NO₅P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	E	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	F	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	G	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	H	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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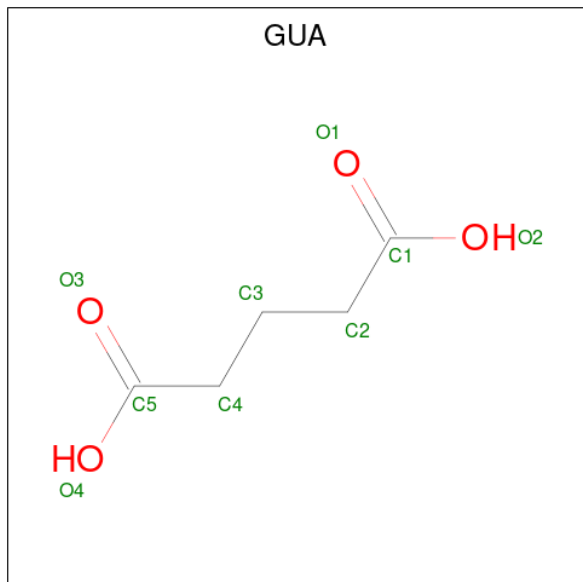
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 2	0	0
3	A	1	Total 4	C 2	O 2	0	0
3	A	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0

- Molecule 4 is GLUTARIC ACID (CCD ID: GUA) (formula: $C_5H_8O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			9	5	4		
4	D	1	Total	C	O	0	0
			9	5	4		
4	E	1	Total	C	O	0	0
			9	5	4		
4	F	1	Total	C	O	0	0
			9	5	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	200	Total	O	0	0
			200	200		
5	B	226	Total	O	0	0
			226	226		
5	C	158	Total	O	0	0
			158	158		
5	D	207	Total	O	0	0
			207	207		
5	E	218	Total	O	0	0
			218	218		
5	F	220	Total	O	0	0
			220	220		

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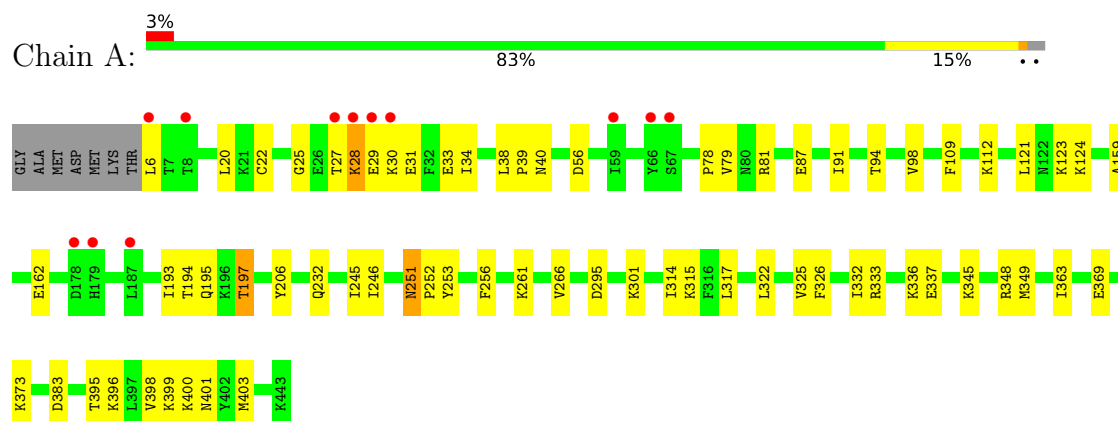
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	219	Total 219	O 219	0	0
5	H	179	Total 179	O 179	0	0

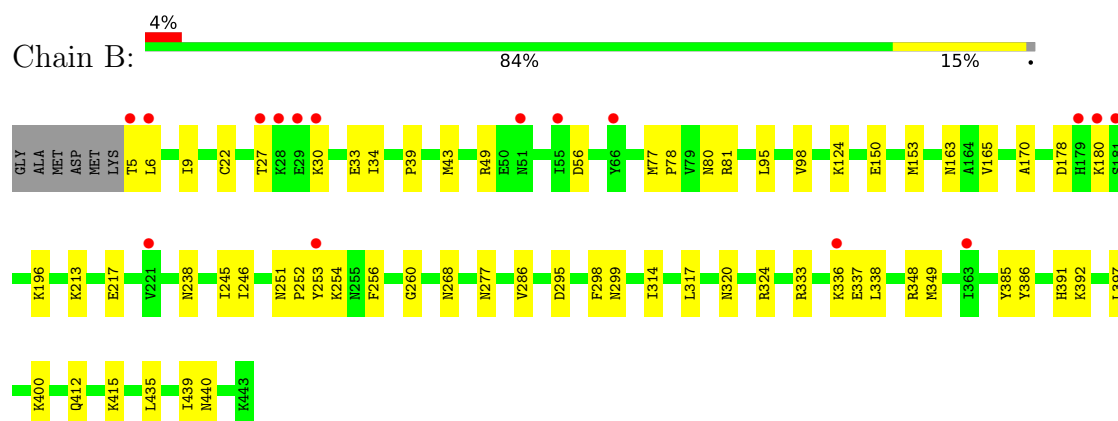
3 Residue-property plots [i](#)

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.

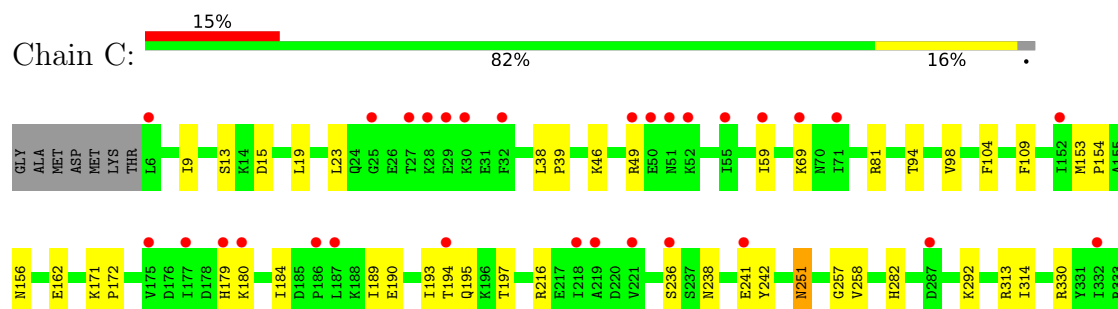
- Molecule 1: Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme

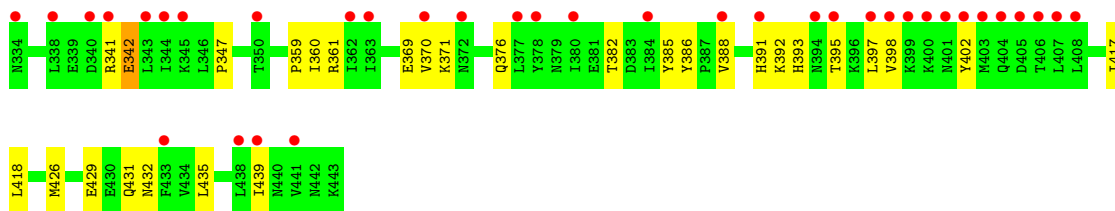


- Molecule 1: Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme

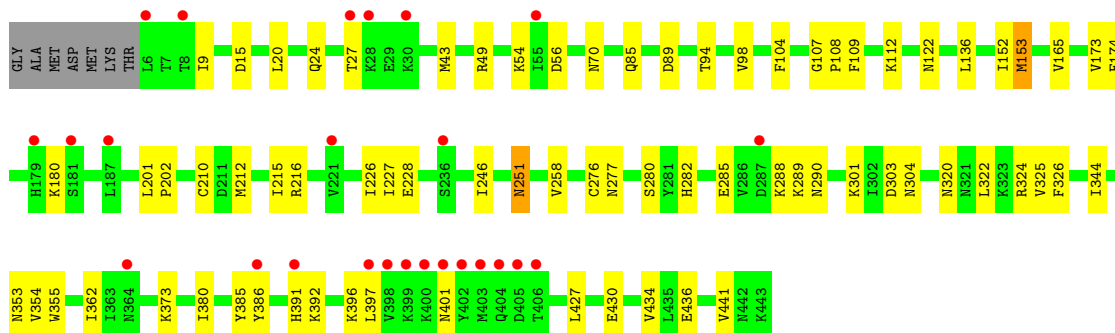
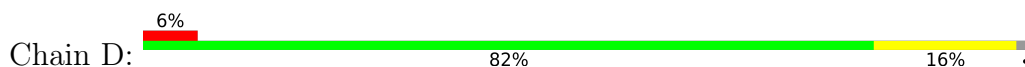


- Molecule 1: Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme

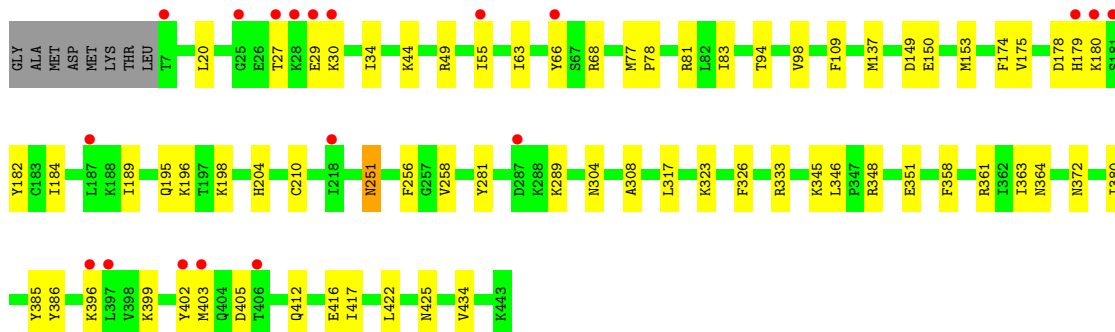
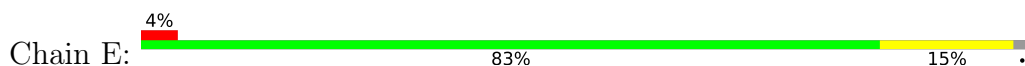




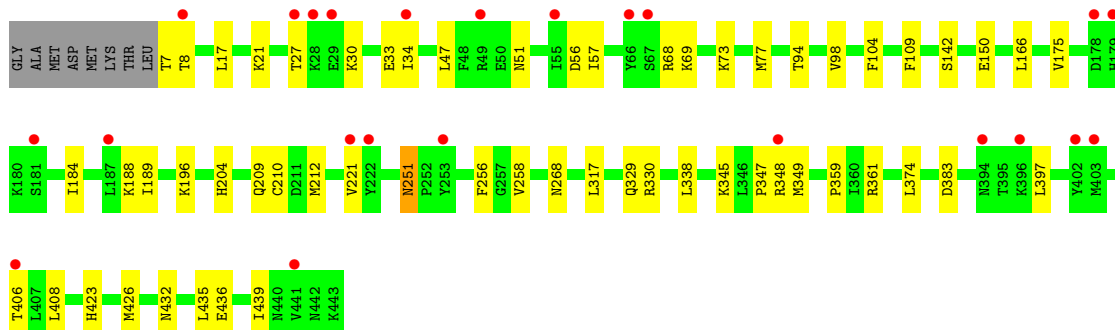
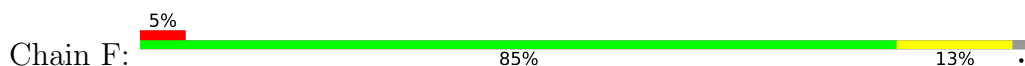
- Molecule 1: Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme



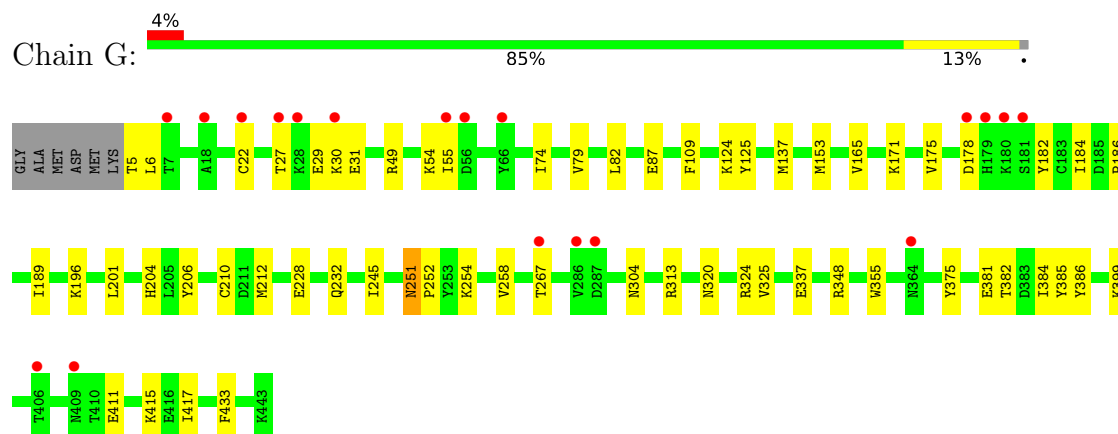
- Molecule 1: Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme



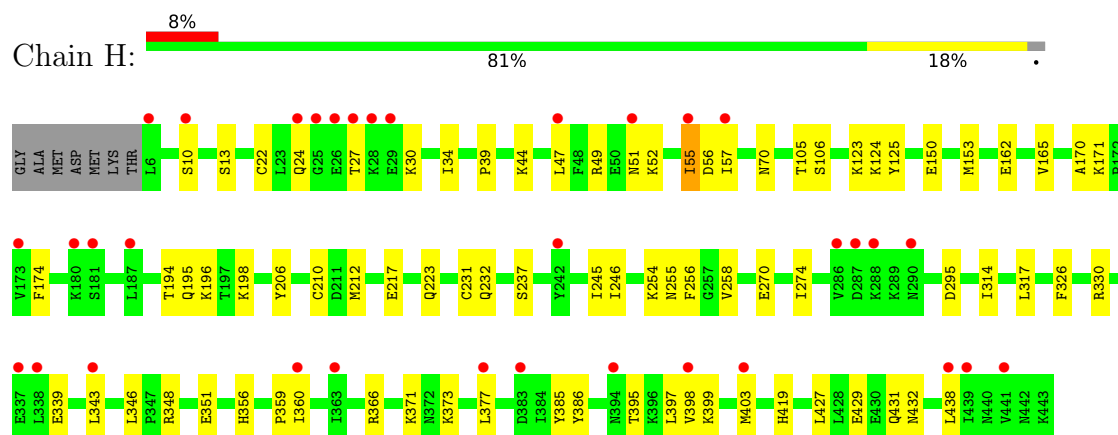
- Molecule 1: Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme



- Molecule 1: Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme



- Molecule 1: Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	92.94Å 93.58Å 106.89Å 108.84° 92.33° 90.08°	Depositor
Resolution (Å)	48.41 – 1.90 48.41 – 1.90	Depositor EDS
% Data completeness (in resolution range)	95.9 (48.41-1.90) 96.1 (48.41-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 1.90Å)	Xtriage
Refinement program	PHENIX dev_2398	Depositor
R, R_{free}	0.207 , 0.249 0.209 , 0.249	Depositor DCC
R_{free} test set	12893 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 52.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.045 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	30275	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 79.47 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.5374e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, PLR, GUA

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	0.37	0/3600	0.55	0/4852
1	B	0.37	1/3612 (0.0%)	0.53	0/4869
1	C	0.34	0/3600	0.53	0/4852
1	D	0.36	0/3603	0.53	0/4856
1	E	0.38	0/3602	0.55	2/4855 (0.0%)
1	F	0.39	0/3583	0.55	1/4829 (0.0%)
1	G	0.36	0/3598	0.55	0/4850
1	H	0.31	0/3599	0.49	0/4851
All	All	0.36	1/28797 (0.0%)	0.54	3/38814 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	80	ASN	C-O	-5.99	1.16	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	346	LEU	CA-C-N	-6.30	114.13	120.31
1	E	346	LEU	C-N-CA	-6.30	114.13	120.31
1	F	212	MET	N-CA-C	5.94	118.71	111.82

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	3539	0	3624	46	0
1	B	3551	0	3633	45	0
1	C	3539	0	3623	51	0
1	D	3542	0	3627	58	0
1	E	3540	0	3619	45	0
1	F	3522	0	3608	38	0
1	G	3537	0	3626	48	0
1	H	3538	0	3621	67	0
2	A	15	0	9	0	0
2	B	15	0	9	0	0
2	C	15	0	9	0	0
2	D	15	0	9	0	0
2	E	15	0	9	0	0
2	F	15	0	9	0	0
2	G	15	0	8	1	0
2	H	15	0	9	0	0
3	A	28	0	42	3	0
3	B	44	0	66	8	0
3	C	20	0	30	0	0
3	D	20	0	30	2	0
3	E	24	0	36	0	0
3	F	12	0	18	1	0
3	G	24	0	36	3	0
3	H	12	0	18	0	0
4	C	9	0	0	0	0
4	D	9	0	0	0	0
4	E	9	0	0	1	0
4	F	9	0	0	0	0
5	A	200	0	0	3	0
5	B	226	0	0	6	0
5	C	158	0	0	4	0
5	D	207	0	0	6	0
5	E	218	0	0	7	0
5	F	220	0	0	4	0
5	G	219	0	0	6	0
5	H	179	0	0	5	0
All	All	30275	0	29328	391	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 7.

The worst 5 of 391 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:E:345:LYS:HG3	1:E:363:ILE:HD11	1.37	1.04
1:H:270:GLU:O	1:H:274:ILE:HD13	1.64	0.97
1:G:210:CYS:HB2	1:G:212:MET:HE2	1.57	0.86
1:C:23:LEU:HB3	1:C:59:ILE:HD11	1.58	0.85
1:G:49:ARG:HG3	1:G:54:LYS:HG2	1.56	0.84

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	437/445 (98%)	420 (96%)	17 (4%)	0	100	100
1	B	439/445 (99%)	424 (97%)	15 (3%)	0	100	100
1	C	437/445 (98%)	420 (96%)	15 (3%)	2 (0%)	24	16
1	D	438/445 (98%)	422 (96%)	14 (3%)	2 (0%)	24	16
1	E	437/445 (98%)	418 (96%)	17 (4%)	2 (0%)	24	16
1	F	435/445 (98%)	417 (96%)	17 (4%)	1 (0%)	43	36
1	G	437/445 (98%)	421 (96%)	15 (3%)	1 (0%)	43	36
1	H	437/445 (98%)	420 (96%)	15 (3%)	2 (0%)	24	16
All	All	3497/3560 (98%)	3362 (96%)	125 (4%)	10 (0%)	36	29

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	342	GLU
1	D	180	LYS
1	E	180	LYS
1	H	55	ILE

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Mol	Chain	Res	Type
1	C	258	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	397/401 (99%)	390 (98%)	7 (2%)	51	50
1	B	399/401 (100%)	399 (100%)	0	100	100
1	C	397/401 (99%)	394 (99%)	3 (1%)	73	75
1	D	398/401 (99%)	396 (100%)	2 (0%)	81	84
1	E	397/401 (99%)	394 (99%)	3 (1%)	73	75
1	F	395/401 (98%)	389 (98%)	6 (2%)	57	56
1	G	397/401 (99%)	396 (100%)	1 (0%)	86	88
1	H	397/401 (99%)	396 (100%)	1 (0%)	86	88
All	All	3177/3208 (99%)	3154 (99%)	23 (1%)	76	78

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	348	ARG
1	F	73	LYS
1	F	69	LYS
1	F	142	SER
1	A	383	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	204	HIS
1	F	432	ASN
1	E	209	GLN
1	F	290	ASN

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Mol	Chain	Res	Type
1	G	304	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

58 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	$\# Z > 2$
3	EDO	C	507	-	3,3,3	0.27	0	2,2,2	0.54	0
3	EDO	B	502	-	3,3,3	0.30	0	2,2,2	0.32	0
4	GUA	C	501	-	8,8,8	1.12	0	9,9,9	1.18	0
3	EDO	B	504	-	3,3,3	0.30	0	2,2,2	0.34	0
2	PLR	B	501	1	15,15,15	1.18	0	21,22,22	1.42	3 (14%)
3	EDO	D	504	-	3,3,3	0.29	0	2,2,2	0.44	0
3	EDO	C	506	-	3,3,3	0.30	0	2,2,2	0.58	0
3	EDO	F	505	-	3,3,3	0.29	0	2,2,2	0.47	0
3	EDO	H	502	-	3,3,3	0.30	0	2,2,2	0.54	0
2	PLR	F	501	1	15,15,15	1.25	3 (20%)	21,22,22	1.72	4 (19%)
3	EDO	B	503	-	3,3,3	0.30	0	2,2,2	0.37	0
3	EDO	A	508	-	3,3,3	0.28	0	2,2,2	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	G	504	-	3,3,3	0.27	0	2,2,2	0.46	0
2	PLR	C	502	1	15,15,15	1.21	1 (6%)	21,22,22	1.28	3 (14%)
3	EDO	B	505	-	3,3,3	0.29	0	2,2,2	0.52	0
3	EDO	D	503	-	3,3,3	0.28	0	2,2,2	0.35	0
3	EDO	G	502	-	3,3,3	0.29	0	2,2,2	0.30	0
2	PLR	E	501	1	15,15,15	1.13	0	21,22,22	1.44	3 (14%)
2	PLR	H	501	1	15,15,15	1.33	1 (6%)	21,22,22	1.63	5 (23%)
2	PLR	D	502	1	15,15,15	1.42	1 (6%)	21,22,22	1.68	3 (14%)
3	EDO	G	506	-	3,3,3	0.41	0	2,2,2	0.20	0
3	EDO	E	503	-	3,3,3	0.28	0	2,2,2	0.40	0
4	GUA	F	502	-	8,8,8	1.07	0	9,9,9	1.39	1 (11%)
3	EDO	A	506	-	3,3,3	0.27	0	2,2,2	0.56	0
3	EDO	B	508	-	3,3,3	0.29	0	2,2,2	0.45	0
3	EDO	E	508	-	3,3,3	0.29	0	2,2,2	0.38	0
3	EDO	G	503	-	3,3,3	0.29	0	2,2,2	0.43	0
3	EDO	A	504	-	3,3,3	0.30	0	2,2,2	0.41	0
4	GUA	E	502	-	8,8,8	1.10	0	9,9,9	1.24	1 (11%)
3	EDO	B	509	-	3,3,3	0.29	0	2,2,2	0.35	0
3	EDO	B	511	-	3,3,3	0.33	0	2,2,2	0.32	0
3	EDO	D	507	-	3,3,3	0.29	0	2,2,2	0.55	0
3	EDO	H	504	-	3,3,3	0.30	0	2,2,2	0.49	0
3	EDO	B	506	-	3,3,3	0.30	0	2,2,2	0.43	0
3	EDO	F	504	-	3,3,3	0.28	0	2,2,2	0.46	0
3	EDO	D	505	-	3,3,3	0.28	0	2,2,2	0.40	0
3	EDO	B	507	-	3,3,3	0.36	0	2,2,2	0.27	0
3	EDO	A	507	-	3,3,3	0.28	0	2,2,2	0.79	0
4	GUA	D	501	-	8,8,8	1.08	0	9,9,9	1.34	2 (22%)
3	EDO	D	506	-	3,3,3	0.30	0	2,2,2	0.59	0
3	EDO	E	506	-	3,3,3	0.29	0	2,2,2	0.49	0
3	EDO	F	503	-	3,3,3	0.27	0	2,2,2	0.47	0
3	EDO	G	505	-	3,3,3	0.29	0	2,2,2	0.43	0
3	EDO	C	505	-	3,3,3	0.32	0	2,2,2	0.39	0
3	EDO	E	504	-	3,3,3	0.28	0	2,2,2	0.54	0
3	EDO	E	505	-	3,3,3	0.30	0	2,2,2	0.45	0
3	EDO	C	503	-	3,3,3	0.28	0	2,2,2	0.50	0
3	EDO	G	507	-	3,3,3	0.29	0	2,2,2	0.74	0
3	EDO	B	512	-	3,3,3	0.28	0	2,2,2	0.64	0
3	EDO	H	503	-	3,3,3	0.29	0	2,2,2	0.49	0
2	PLR	A	501	1	15,15,15	1.30	2 (13%)	21,22,22	1.40	3 (14%)
3	EDO	A	502	-	3,3,3	0.32	0	2,2,2	0.41	0
3	EDO	A	505	-	3,3,3	0.29	0	2,2,2	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	C	504	-	3,3,3	0.28	0	2,2,2	0.61	0
3	EDO	E	507	-	3,3,3	0.31	0	2,2,2	0.39	0
3	EDO	A	503	-	3,3,3	0.29	0	2,2,2	0.58	0
2	PLR	G	501	1	15,15,15	1.38	1 (6%)	21,22,22	1.73	4 (19%)
3	EDO	B	510	-	3,3,3	0.31	0	2,2,2	0.33	0

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
3	EDO	C	507	-	-	0/1/1/1	-
3	EDO	B	502	-	-	0/1/1/1	-
4	GUA	C	501	-	-	5/6/6/6	-
3	EDO	B	504	-	-	1/1/1/1	-
2	PLR	B	501	1	-	0/6/6/6	0/1/1/1
3	EDO	D	504	-	-	0/1/1/1	-
3	EDO	C	506	-	-	0/1/1/1	-
3	EDO	F	505	-	-	1/1/1/1	-
3	EDO	H	502	-	-	1/1/1/1	-
2	PLR	F	501	1	-	0/6/6/6	0/1/1/1
3	EDO	B	503	-	-	1/1/1/1	-
3	EDO	A	508	-	-	0/1/1/1	-
3	EDO	G	504	-	-	1/1/1/1	-
2	PLR	C	502	1	-	0/6/6/6	0/1/1/1
3	EDO	B	505	-	-	0/1/1/1	-
3	EDO	D	503	-	-	1/1/1/1	-
3	EDO	G	502	-	-	1/1/1/1	-
2	PLR	E	501	1	-	0/6/6/6	0/1/1/1
2	PLR	H	501	1	-	0/6/6/6	0/1/1/1
2	PLR	D	502	1	-	0/6/6/6	0/1/1/1
3	EDO	G	506	-	-	1/1/1/1	-
3	EDO	E	503	-	-	1/1/1/1	-
4	GUA	F	502	-	-	4/6/6/6	-
3	EDO	A	506	-	-	0/1/1/1	-
3	EDO	B	508	-	-	0/1/1/1	-
3	EDO	E	508	-	-	0/1/1/1	-
3	EDO	G	503	-	-	1/1/1/1	-
3	EDO	A	504	-	-	1/1/1/1	-
4	GUA	E	502	-	-	6/6/6/6	-
3	EDO	B	509	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	511	-	-	0/1/1/1	-
3	EDO	D	507	-	-	1/1/1/1	-
3	EDO	H	504	-	-	1/1/1/1	-
3	EDO	B	506	-	-	0/1/1/1	-
3	EDO	F	504	-	-	1/1/1/1	-
3	EDO	D	505	-	-	0/1/1/1	-
3	EDO	B	507	-	-	1/1/1/1	-
3	EDO	A	507	-	-	1/1/1/1	-
4	GUA	D	501	-	-	5/6/6/6	-
3	EDO	D	506	-	-	0/1/1/1	-
3	EDO	E	506	-	-	1/1/1/1	-
3	EDO	F	503	-	-	1/1/1/1	-
3	EDO	G	505	-	-	0/1/1/1	-
3	EDO	C	505	-	-	0/1/1/1	-
3	EDO	E	504	-	-	0/1/1/1	-
3	EDO	E	505	-	-	0/1/1/1	-
3	EDO	C	503	-	-	0/1/1/1	-
3	EDO	G	507	-	-	1/1/1/1	-
3	EDO	B	512	-	-	1/1/1/1	-
3	EDO	H	503	-	-	1/1/1/1	-
2	PLR	A	501	1	-	0/6/6/6	0/1/1/1
3	EDO	A	502	-	-	0/1/1/1	-
3	EDO	A	505	-	-	1/1/1/1	-
3	EDO	C	504	-	-	0/1/1/1	-
3	EDO	E	507	-	-	1/1/1/1	-
3	EDO	A	503	-	-	1/1/1/1	-
2	PLR	G	501	1	-	0/6/6/6	0/1/1/1
3	EDO	B	510	-	-	1/1/1/1	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	502	PLR	C2A-C2	3.06	1.55	1.50
2	G	501	PLR	C2A-C2	2.51	1.54	1.50
2	H	501	PLR	P-O4P	2.27	1.67	1.60
2	A	501	PLR	C2A-C2	2.20	1.53	1.50
2	F	501	PLR	C2A-C2	2.20	1.53	1.50

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	501	PLR	C4A-C4-C5	5.24	126.34	120.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	502	PLR	C4A-C4-C5	4.82	125.91	120.94
2	F	501	PLR	C4A-C4-C5	4.75	125.84	120.94
2	G	501	PLR	C4A-C4-C5	4.55	125.63	120.94
2	G	501	PLR	C6-C5-C4	3.63	121.07	118.10

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	502	GUA	C1-C2-C3-C4
4	E	502	GUA	C2-C3-C4-C5
4	C	501	GUA	C2-C3-C4-C5
4	D	501	GUA	C1-C2-C3-C4
3	B	507	EDO	O1-C1-C2-O2

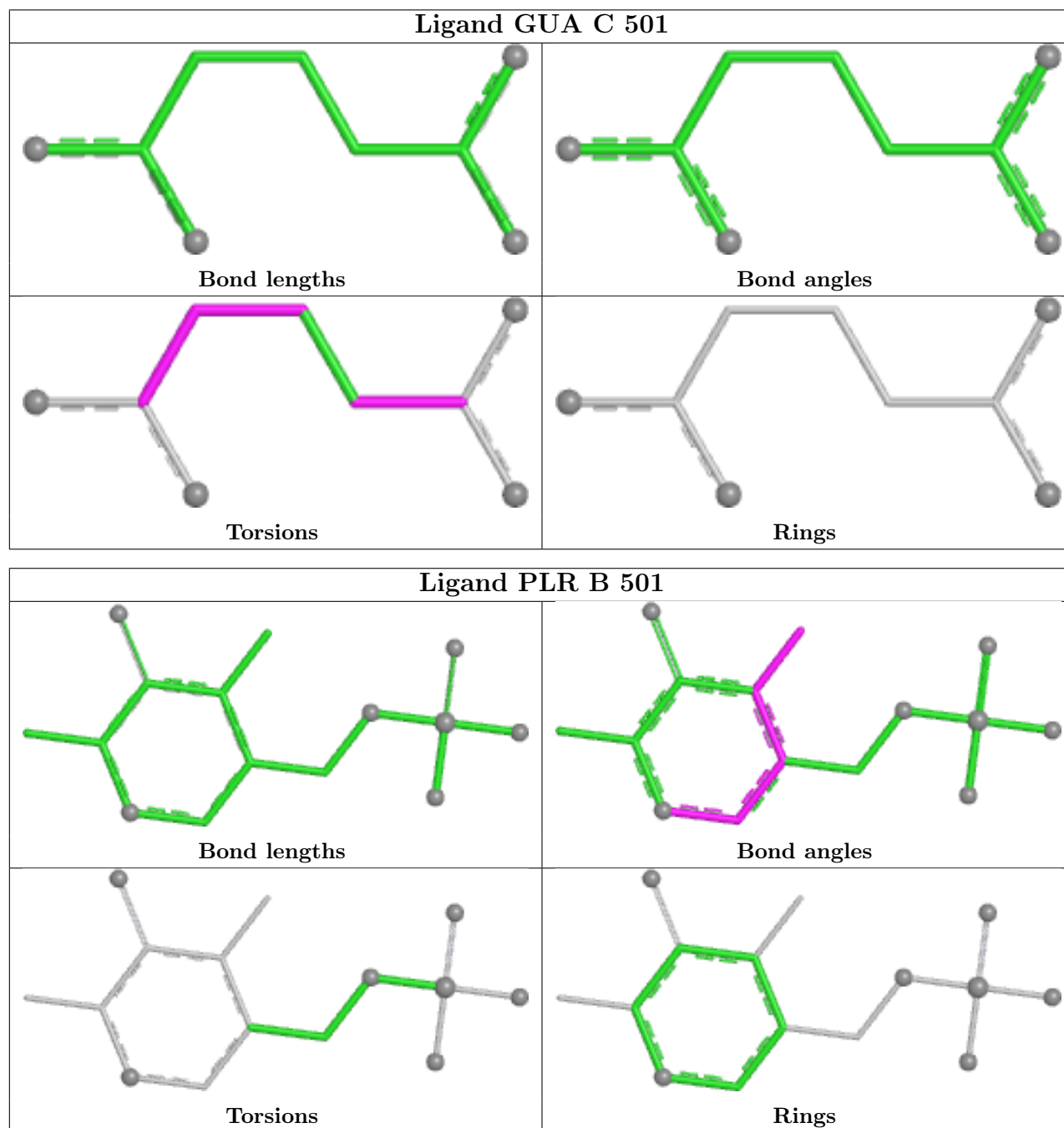
There are no ring outliers.

14 monomers are involved in 19 short contacts:

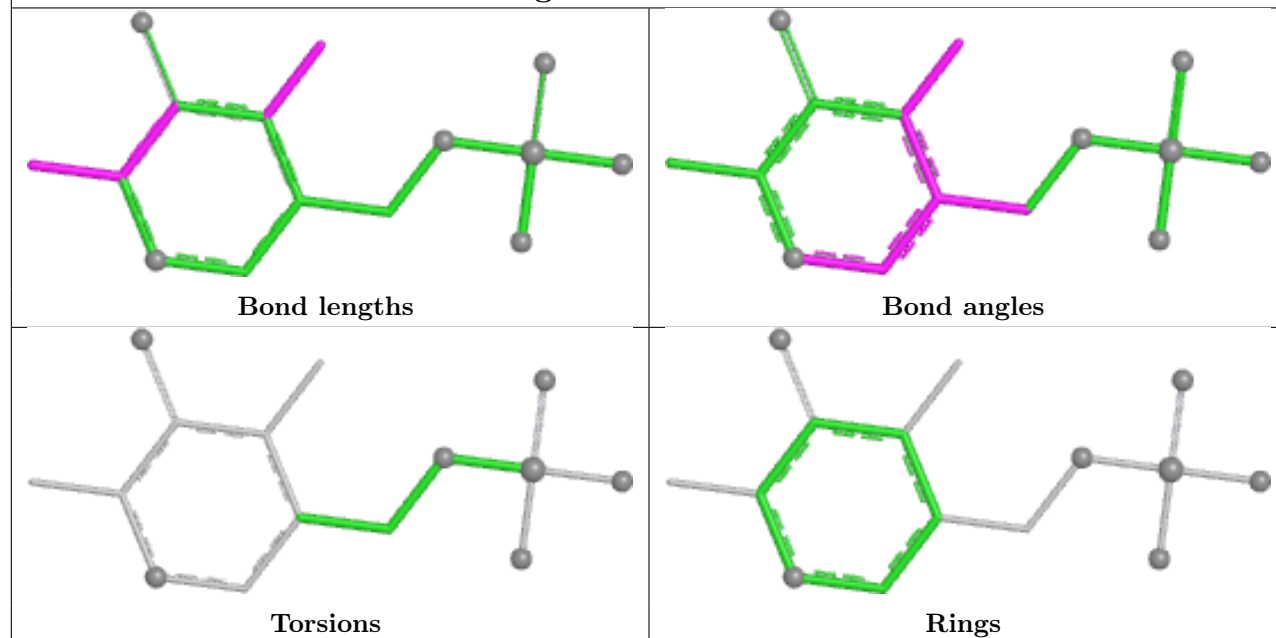
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	504	EDO	3	0
3	D	504	EDO	1	0
3	B	503	EDO	1	0
3	A	508	EDO	1	0
3	G	506	EDO	3	0
4	E	502	GUA	1	0
3	B	509	EDO	2	0
3	D	507	EDO	1	0
3	B	507	EDO	2	0
3	A	507	EDO	1	0
3	F	503	EDO	1	0
3	A	505	EDO	1	0
3	A	503	EDO	1	0
2	G	501	PLR	1	0

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

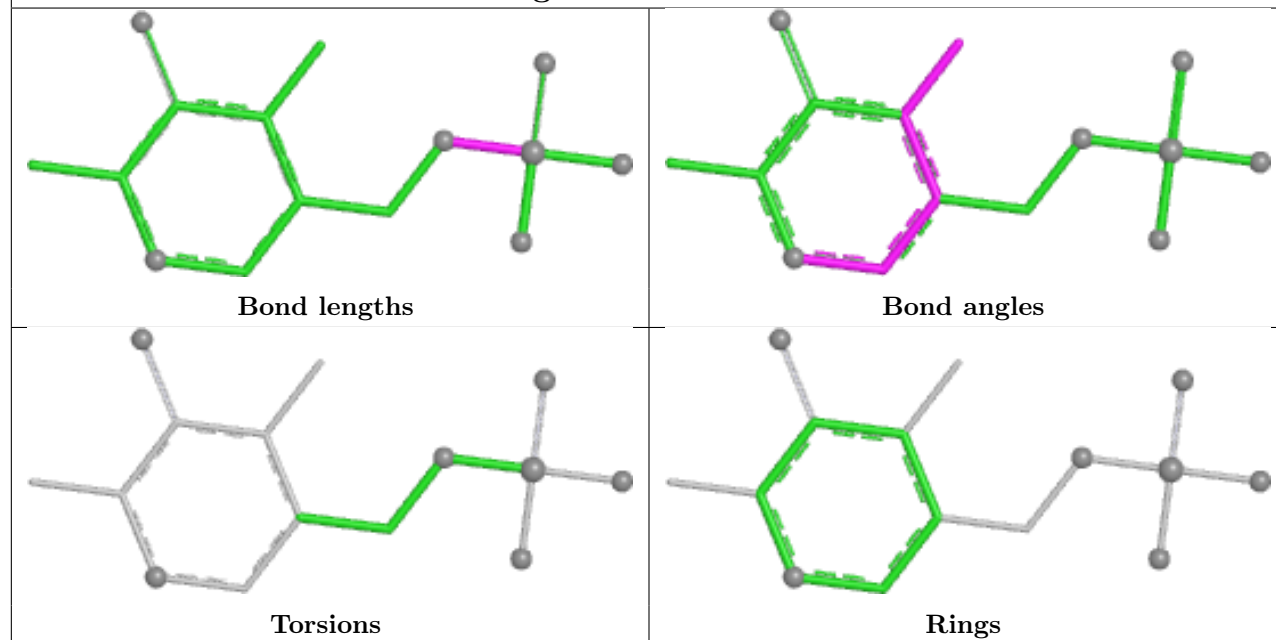
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents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



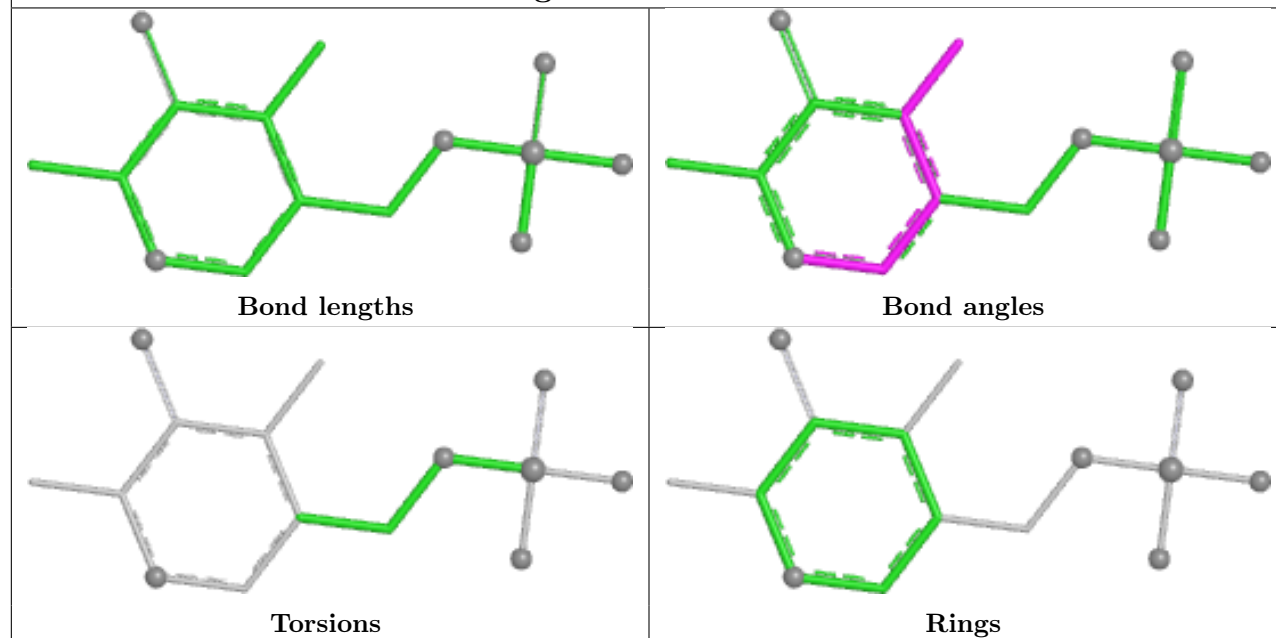
Ligand PLR F 501



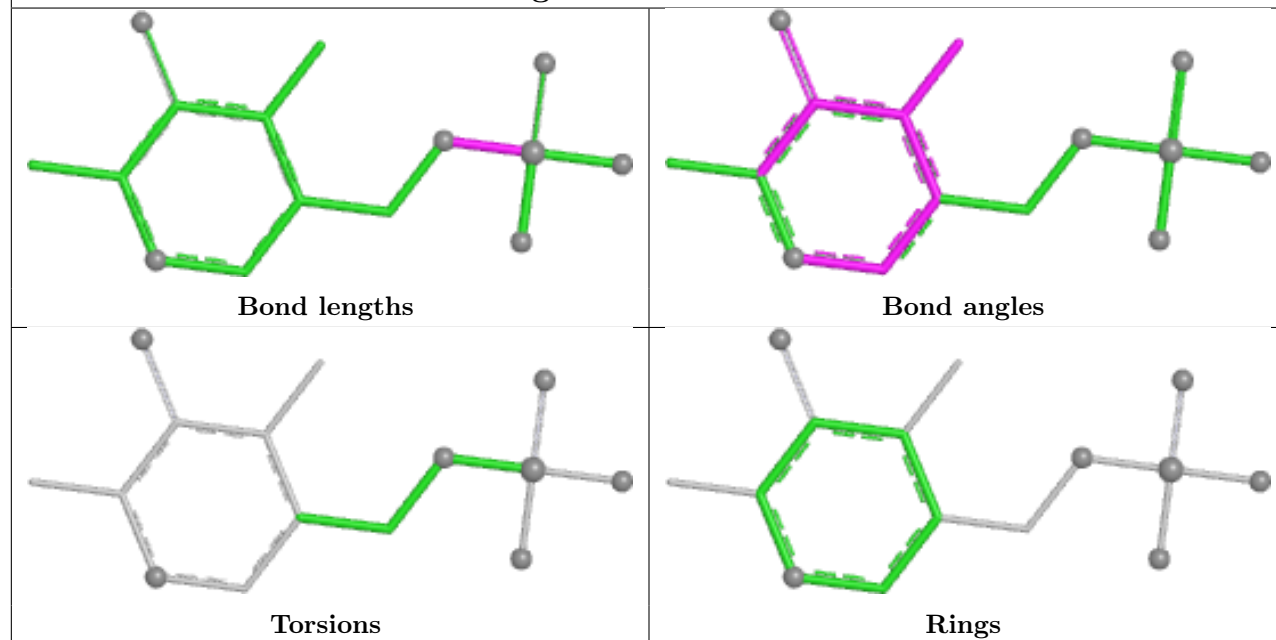
Ligand PLR C 502



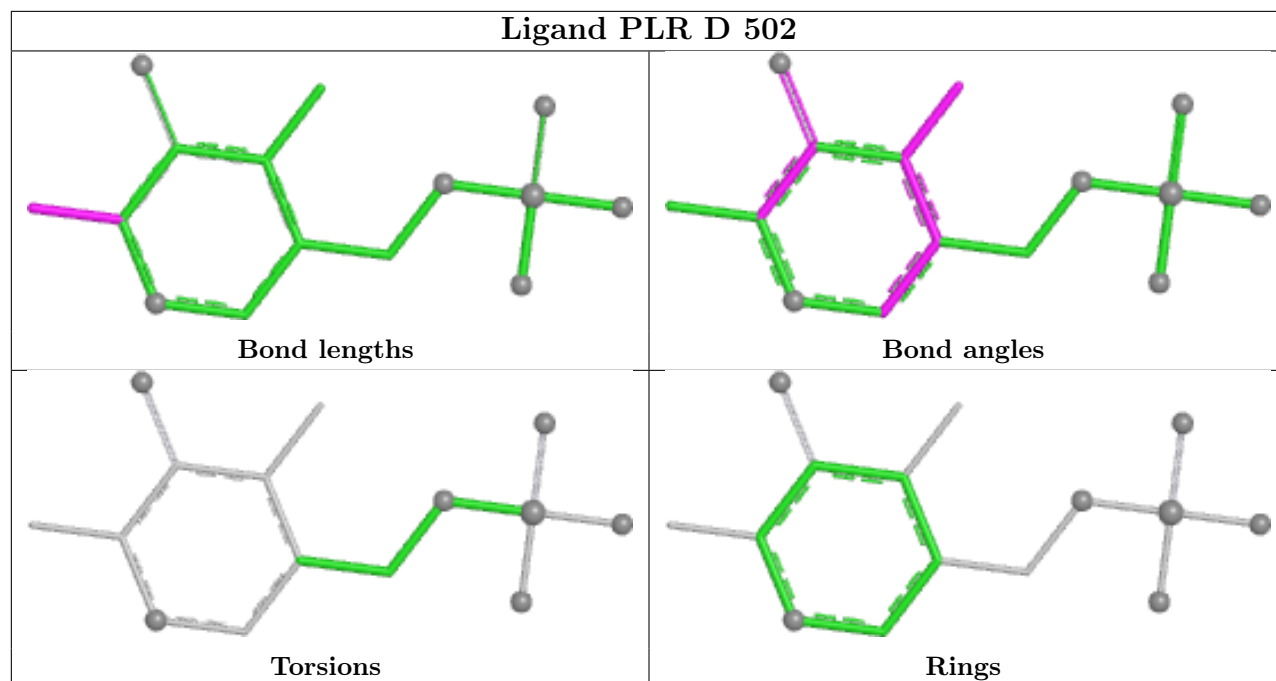
Ligand PLR E 501



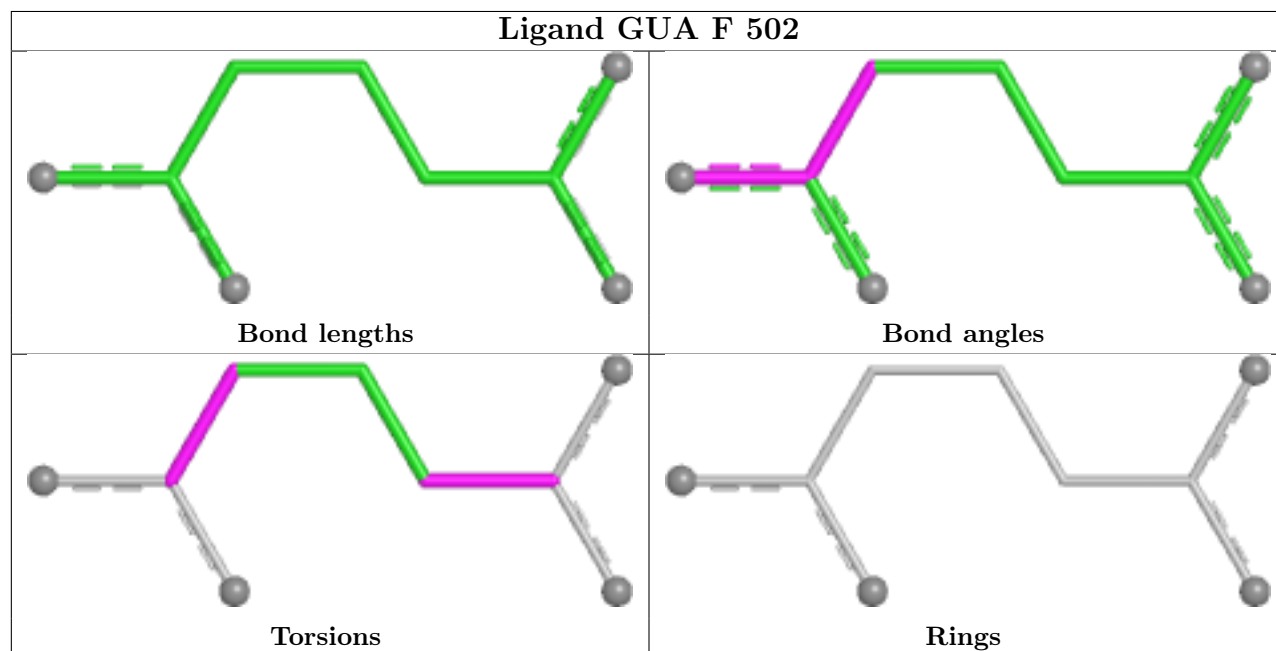
Ligand PLR H 501

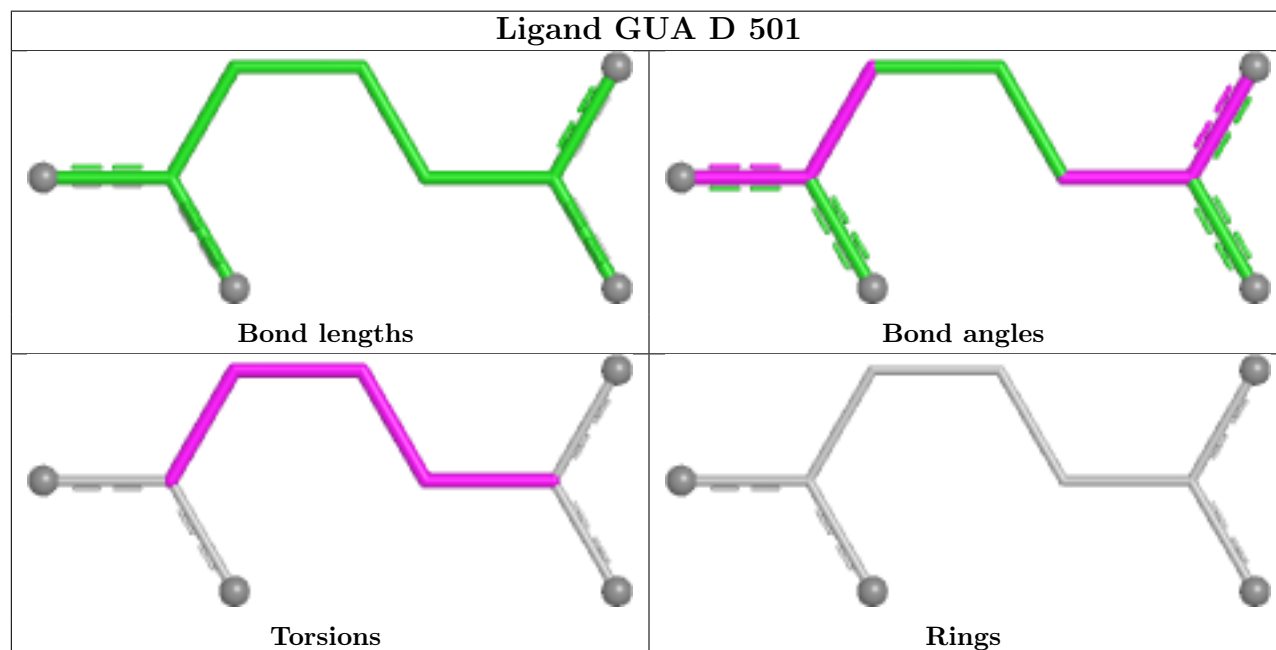
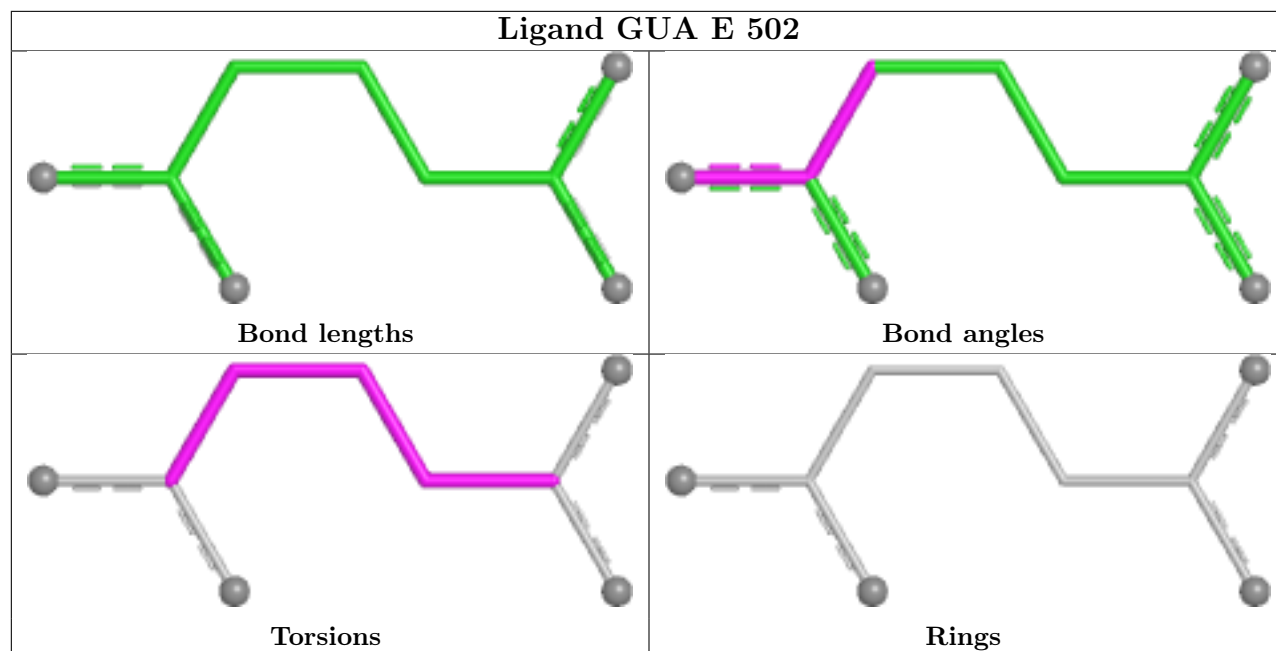


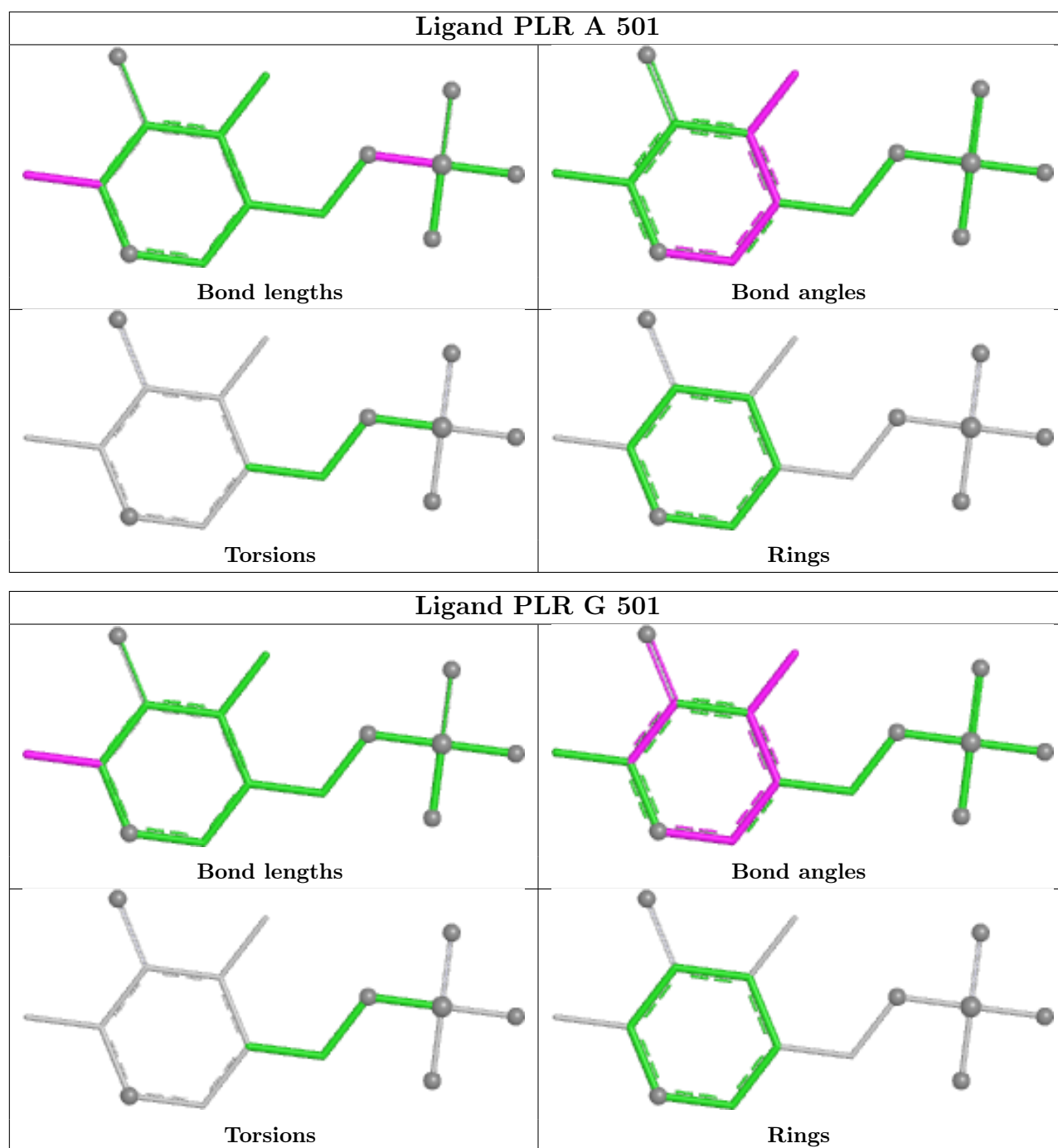
Ligand PLR D 502



Ligand GUA F 502







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, 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	438/445 (98%)	0.34	12 (2%)	56	60	16, 34, 59, 119	1 (0%)
1	B	439/445 (98%)	0.28	16 (3%)	46	49	11, 32, 60, 101	2 (0%)
1	C	438/445 (98%)	0.92	66 (15%)	5	5	21, 42, 79, 164	1 (0%)
1	D	438/445 (98%)	0.51	25 (5%)	29	31	14, 35, 66, 132	2 (0%)
1	E	437/445 (98%)	0.36	19 (4%)	40	42	12, 33, 64, 121	2 (0%)
1	F	437/445 (98%)	0.38	23 (5%)	32	34	18, 34, 66, 106	0
1	G	439/445 (98%)	0.39	19 (4%)	40	42	20, 32, 61, 106	0
1	H	438/445 (98%)	0.72	34 (7%)	19	20	20, 40, 69, 122	1 (0%)
All	All	3504/3560 (98%)	0.49	214 (6%)	27	29	11, 35, 67, 164	9 (0%)

The worst 5 of 214 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	55	ILE	5.7
1	D	402	TYR	5.5
1	C	402	TYR	5.1
1	F	187	LEU	4.8
1	C	55	ILE	4.7

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	EDO	G	505	4/4	0.55	0.18	71,71,72,72	0
3	EDO	A	505	4/4	0.59	0.25	74,75,76,77	0
3	EDO	B	505	4/4	0.60	0.16	83,83,84,84	0
3	EDO	A	502	4/4	0.60	0.15	64,66,66,66	0
3	EDO	H	503	4/4	0.61	0.15	69,69,70,70	0
3	EDO	B	503	4/4	0.62	0.21	62,63,63,64	0
3	EDO	A	506	4/4	0.62	0.17	63,65,66,66	0
3	EDO	B	504	4/4	0.64	0.19	54,54,54,55	0
3	EDO	H	504	4/4	0.69	0.14	49,49,52,54	0
3	EDO	B	511	4/4	0.72	0.20	42,45,47,48	0
3	EDO	B	502	4/4	0.72	0.14	61,62,62,63	0
3	EDO	E	504	4/4	0.73	0.13	55,55,56,57	0
3	EDO	B	510	4/4	0.74	0.17	47,48,51,53	0
3	EDO	C	505	4/4	0.74	0.12	58,60,60,60	0
3	EDO	E	505	4/4	0.75	0.15	61,63,65,67	0
3	EDO	D	506	4/4	0.75	0.12	48,49,52,53	0
3	EDO	E	507	4/4	0.76	0.16	40,42,44,45	0
3	EDO	B	508	4/4	0.76	0.17	67,68,70,71	0
3	EDO	B	512	4/4	0.76	0.19	44,46,48,49	0
3	EDO	E	506	4/4	0.76	0.17	68,68,68,68	0
4	GUA	C	501	9/9	0.76	0.21	79,82,85,87	0
3	EDO	B	509	4/4	0.77	0.17	65,66,68,68	0
3	EDO	F	505	4/4	0.77	0.12	58,60,61,62	0
3	EDO	C	507	4/4	0.77	0.14	56,58,60,61	0
3	EDO	B	506	4/4	0.78	0.15	66,66,66,67	0
3	EDO	D	507	4/4	0.79	0.13	48,48,49,50	0
3	EDO	A	508	4/4	0.80	0.14	39,42,45,47	0
3	EDO	C	503	4/4	0.80	0.12	54,54,54,54	0
3	EDO	A	504	4/4	0.80	0.13	53,53,54,54	0
4	GUA	E	502	9/9	0.80	0.22	83,84,87,87	0
4	GUA	F	502	9/9	0.80	0.19	76,80,85,90	0
3	EDO	H	502	4/4	0.81	0.20	66,67,67,67	0
3	EDO	D	505	4/4	0.81	0.14	52,53,53,54	0
3	EDO	F	503	4/4	0.82	0.21	37,39,39,43	0
3	EDO	D	503	4/4	0.83	0.14	39,39,43,43	0
3	EDO	G	506	4/4	0.84	0.16	29,39,43,46	0
3	EDO	B	507	4/4	0.85	0.21	35,38,41,45	0

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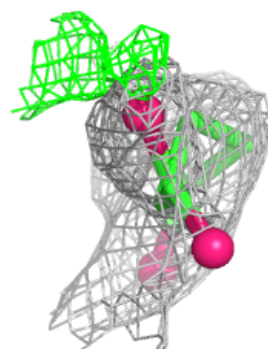
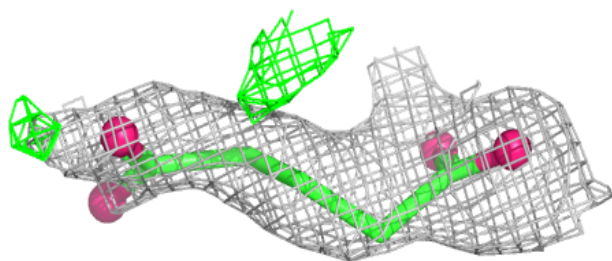
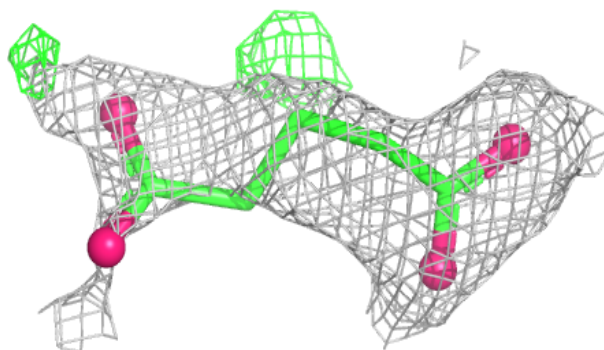
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	E	503	4/4	0.86	0.13	52,52,55,55	0
3	EDO	E	508	4/4	0.86	0.11	54,55,56,57	0
3	EDO	A	503	4/4	0.86	0.15	42,45,48,51	0
3	EDO	D	504	4/4	0.87	0.14	63,64,64,64	0
3	EDO	G	503	4/4	0.87	0.11	50,51,51,51	0
3	EDO	C	504	4/4	0.88	0.12	59,60,60,60	0
3	EDO	F	504	4/4	0.88	0.11	46,47,48,49	0
3	EDO	C	506	4/4	0.88	0.14	45,46,47,47	0
3	EDO	G	502	4/4	0.89	0.12	55,58,60,60	0
4	GUA	D	501	9/9	0.90	0.13	62,63,66,68	0
3	EDO	A	507	4/4	0.90	0.16	37,42,45,51	0
3	EDO	G	507	4/4	0.90	0.10	37,38,38,39	0
3	EDO	G	504	4/4	0.91	0.10	46,47,48,48	0
2	PLR	F	501	15/15	0.97	0.06	18,23,27,30	0
2	PLR	C	502	15/15	0.98	0.06	24,29,34,35	0
2	PLR	D	502	15/15	0.98	0.04	19,22,25,26	0
2	PLR	E	501	15/15	0.98	0.05	19,25,28,32	0
2	PLR	A	501	15/15	0.98	0.05	16,22,25,28	0
2	PLR	G	501	15/15	0.98	0.05	18,21,24,25	0
2	PLR	H	501	15/15	0.98	0.06	23,28,31,33	0
2	PLR	B	501	15/15	0.98	0.05	17,20,24,26	0

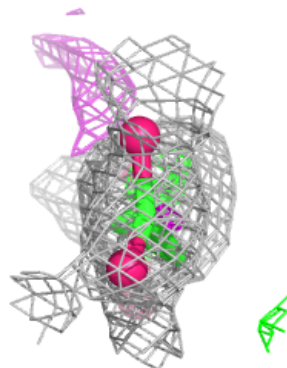
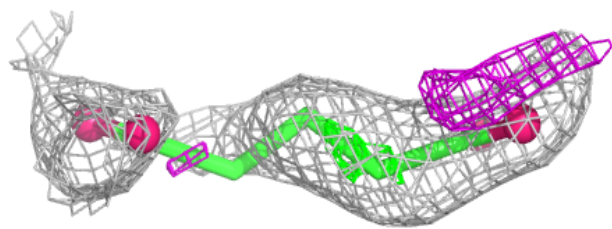
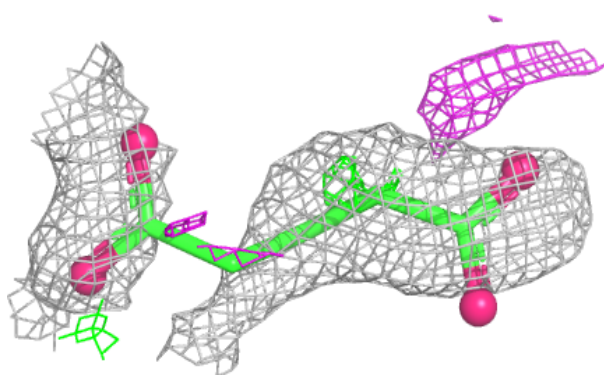
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GUA C 501:

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

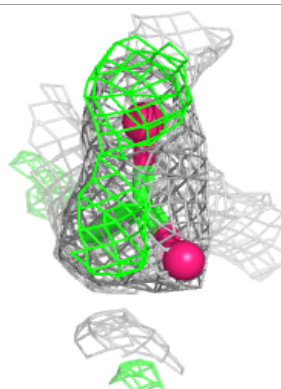
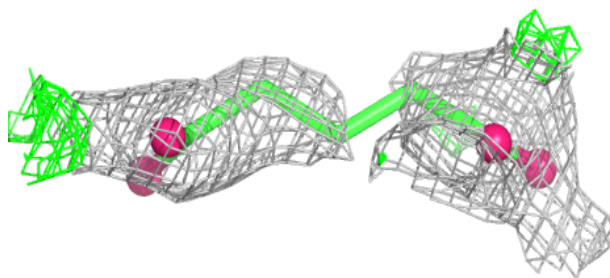
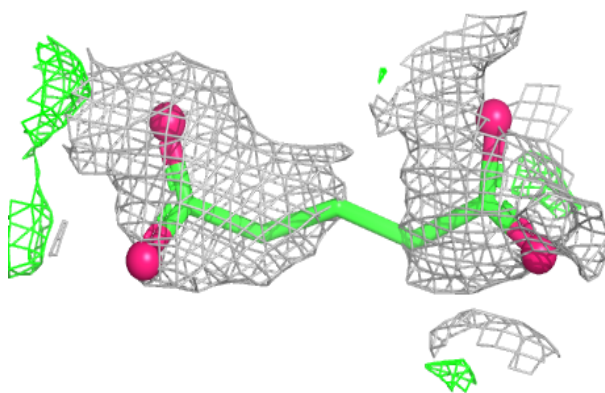
**Electron density around GUA E 502:**

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

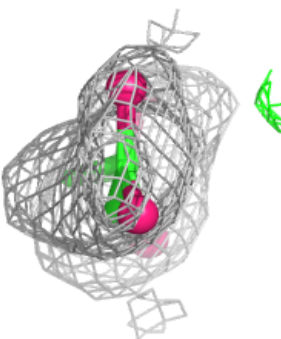
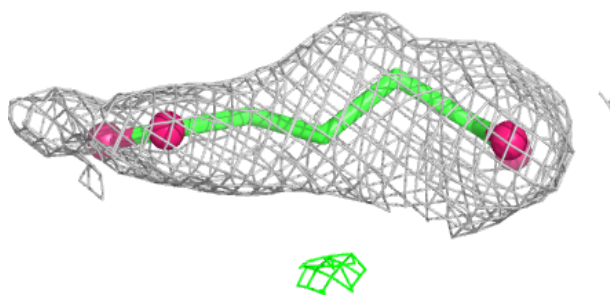
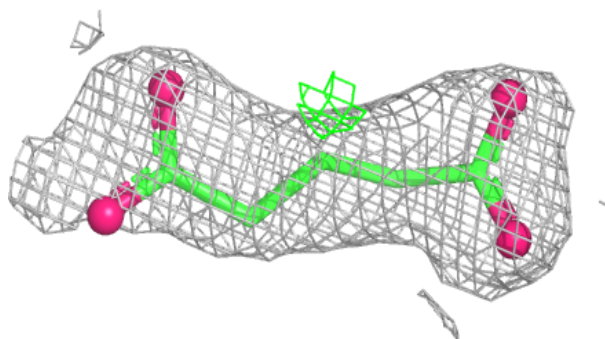


Electron density around GUA F 502:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

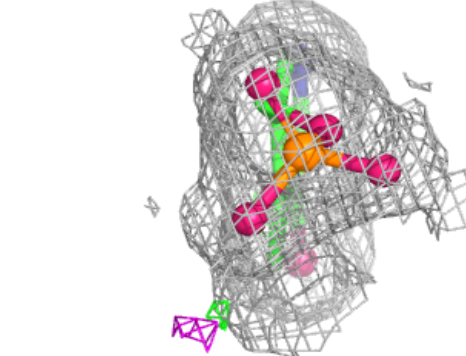
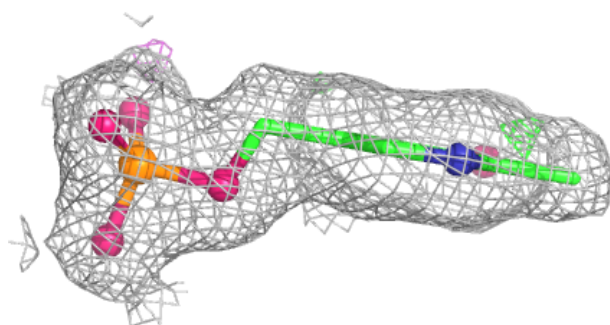
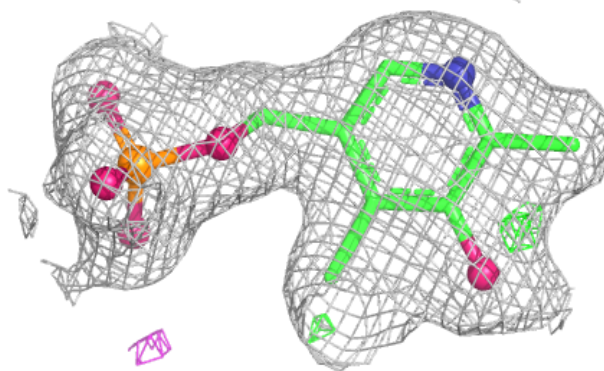
**Electron density around GUA D 501:**

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

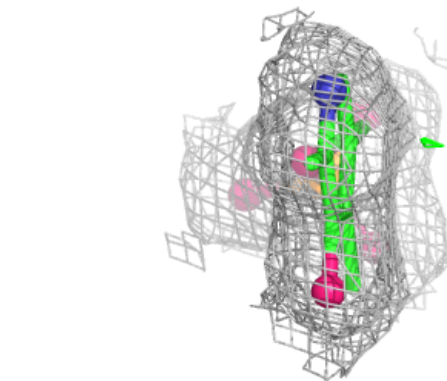
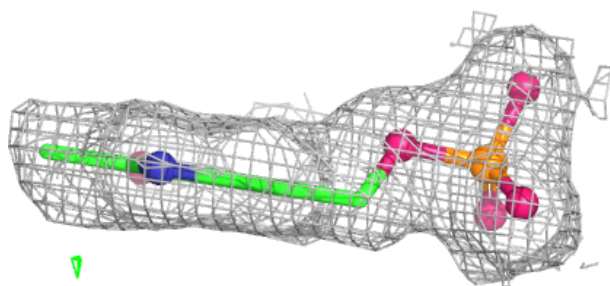
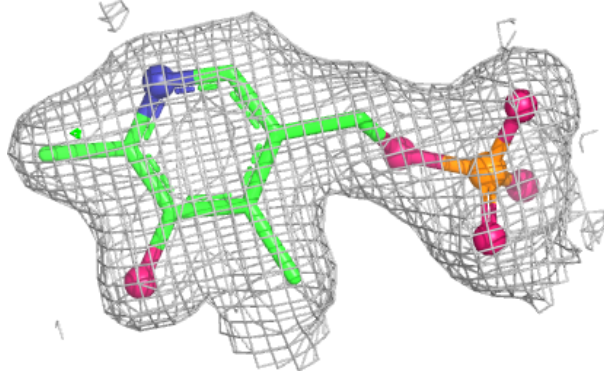


Electron density around PLR F 501:

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

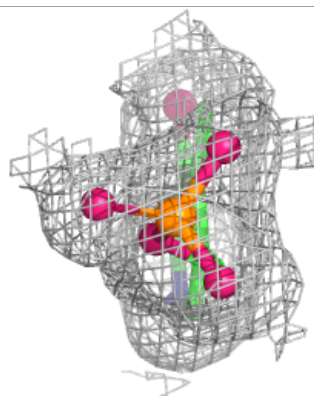
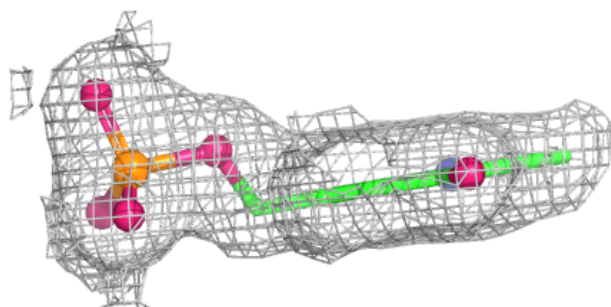
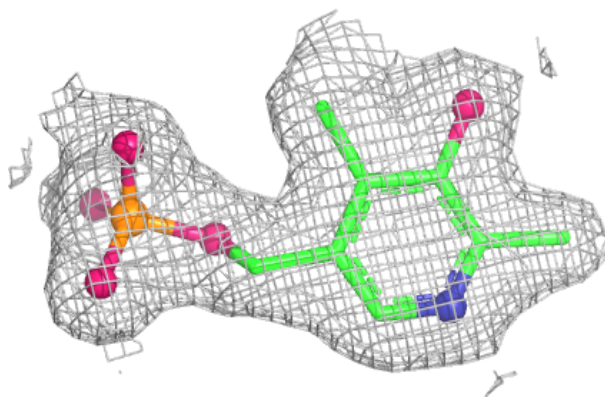
**Electron density around PLR C 502:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

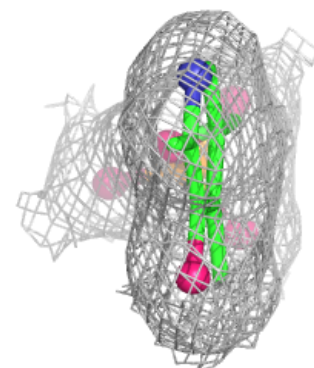
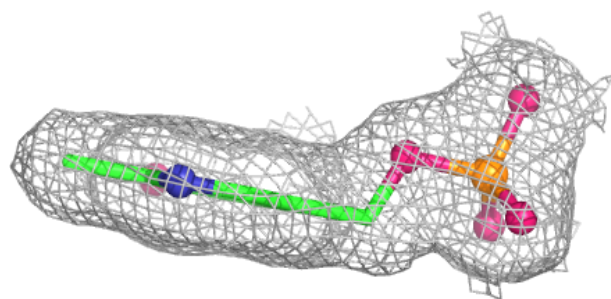
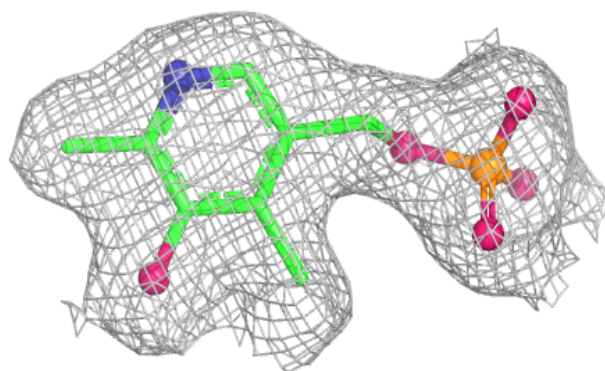


Electron density around PLR D 502:

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

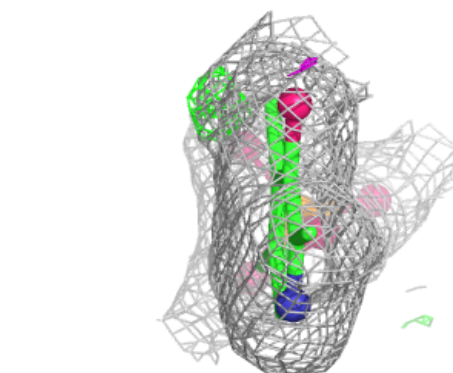
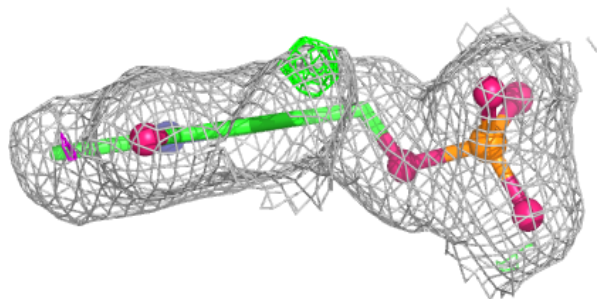
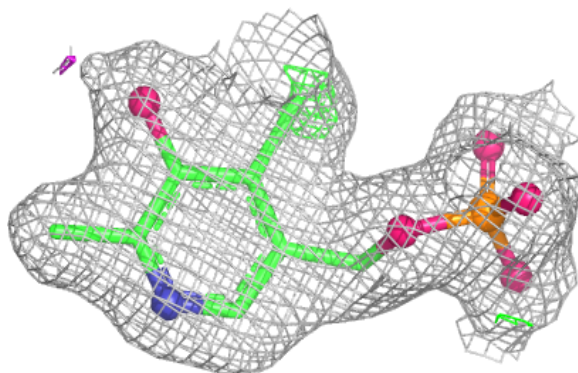
**Electron density around PLR E 501:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

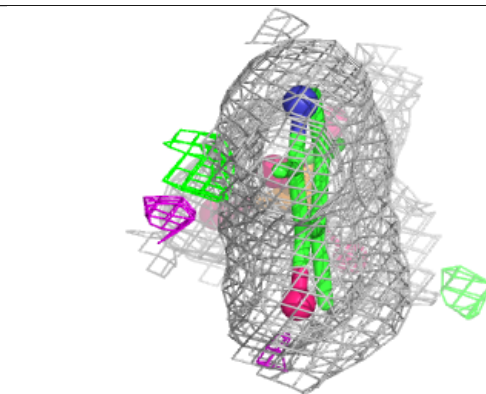
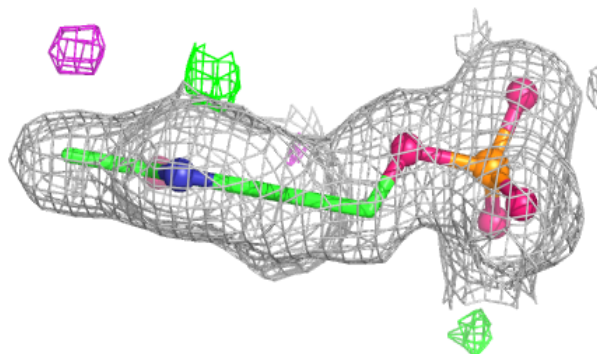
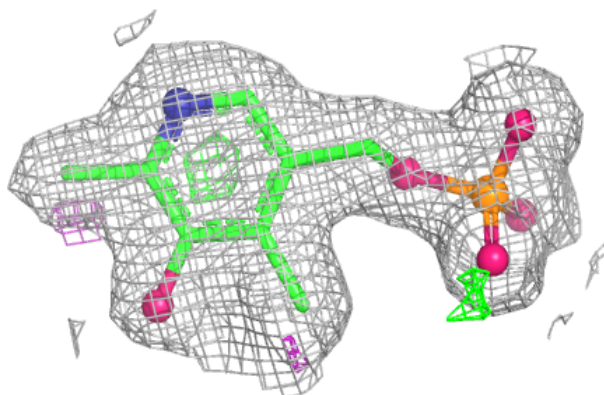


Electron density around PLR A 501:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

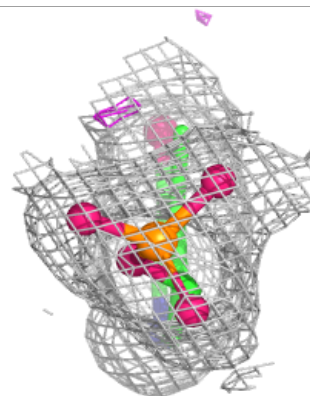
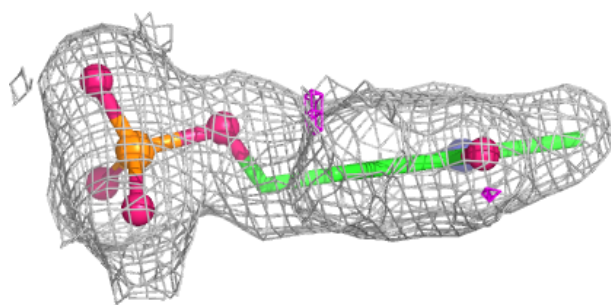
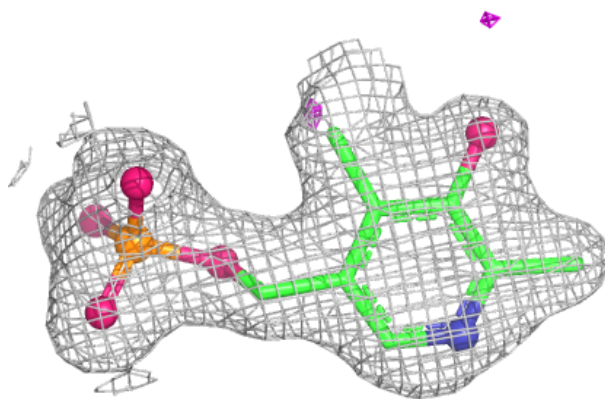
**Electron density around PLR G 501:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

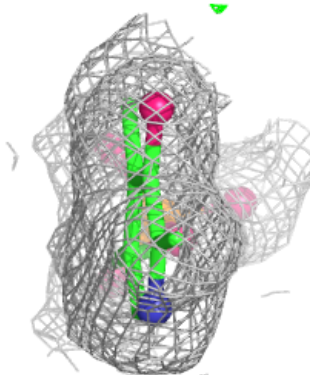
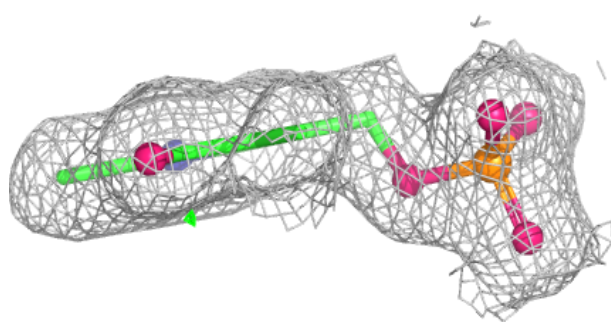
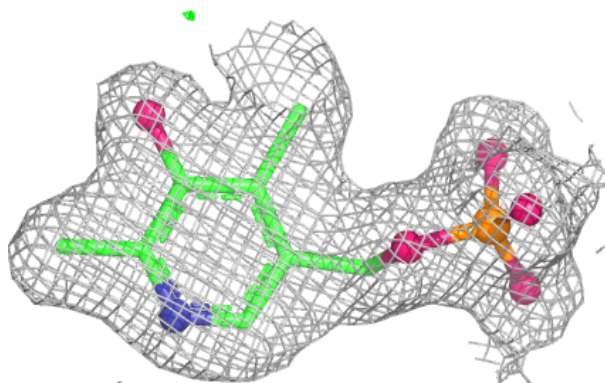


Electron density around PLR H 501:

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

**Electron density around PLR 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 [i](#)

There are no such residues in this entry.