



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:59 PM UTC

PDB ID : 7Q9X / pdb_00007q9x
Title : Crystal structure of Chromobacterium violaceum aminotransferase in complex with PLP-pyruvate adduct
Authors : Isupov, M.N.; Mitchell, D.; Sayer, C.; Littlechild, J.A.
Deposited on : 2021-11-15
Resolution : 1.60 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

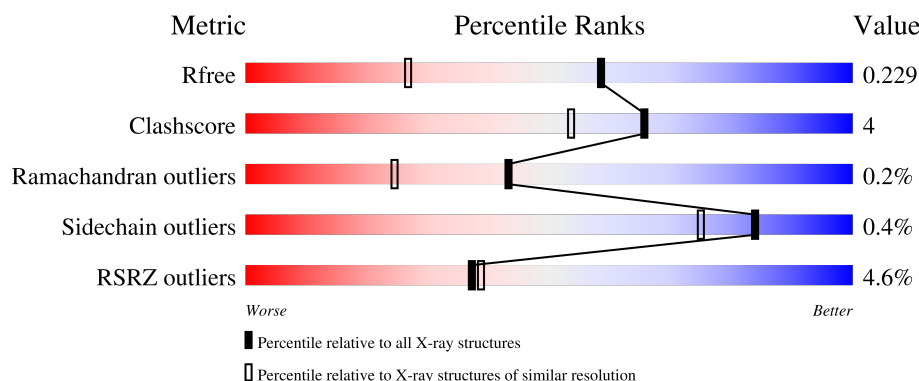
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

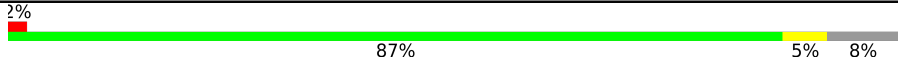
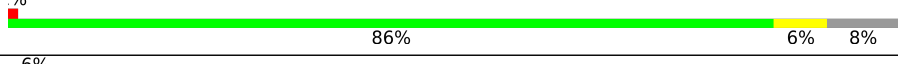
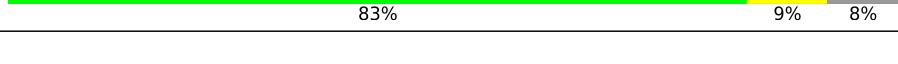
The reported resolution of this entry is 1.60 Å.

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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	AAA	493	
1	BBB	493	
1	CCC	493	
1	DDD	493	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PLP	BBB	503[B]	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17188 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 Probable aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	455	Total	C	N	O	S	0	27	0
			3728	2387	647	673	21			
1	BBB	455	Total	C	N	O	S	0	34	0
			3771	2425	647	678	21			
1	CCC	455	Total	C	N	O	S	0	29	0
			3734	2399	644	670	21			
1	DDD	455	Total	C	N	O	S	0	22	0
			3711	2378	643	669	21			

There are 136 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-33	MET	-	initiating methionine	UNP Q7NWG4
AAA	-32	GLY	-	expression tag	UNP Q7NWG4
AAA	-31	SER	-	expression tag	UNP Q7NWG4
AAA	-30	SER	-	expression tag	UNP Q7NWG4
AAA	-29	HIS	-	expression tag	UNP Q7NWG4
AAA	-28	HIS	-	expression tag	UNP Q7NWG4
AAA	-27	HIS	-	expression tag	UNP Q7NWG4
AAA	-26	HIS	-	expression tag	UNP Q7NWG4
AAA	-25	HIS	-	expression tag	UNP Q7NWG4
AAA	-24	HIS	-	expression tag	UNP Q7NWG4
AAA	-23	SER	-	expression tag	UNP Q7NWG4
AAA	-22	SER	-	expression tag	UNP Q7NWG4
AAA	-21	GLY	-	expression tag	UNP Q7NWG4
AAA	-20	LEU	-	expression tag	UNP Q7NWG4
AAA	-19	VAL	-	expression tag	UNP Q7NWG4
AAA	-18	PRO	-	expression tag	UNP Q7NWG4
AAA	-17	ARG	-	expression tag	UNP Q7NWG4
AAA	-16	GLY	-	expression tag	UNP Q7NWG4
AAA	-15	SER	-	expression tag	UNP Q7NWG4
AAA	-14	HIS	-	expression tag	UNP Q7NWG4
AAA	-13	MET	-	expression tag	UNP Q7NWG4

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Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-12	ALA	-	expression tag	UNP Q7NWX4
AAA	-11	SER	-	expression tag	UNP Q7NWX4
AAA	-10	MET	-	expression tag	UNP Q7NWX4
AAA	-9	THR	-	expression tag	UNP Q7NWX4
AAA	-8	GLY	-	expression tag	UNP Q7NWX4
AAA	-7	GLY	-	expression tag	UNP Q7NWX4
AAA	-6	GLN	-	expression tag	UNP Q7NWX4
AAA	-5	GLN	-	expression tag	UNP Q7NWX4
AAA	-4	MET	-	expression tag	UNP Q7NWX4
AAA	-3	GLY	-	expression tag	UNP Q7NWX4
AAA	-2	ARG	-	expression tag	UNP Q7NWX4
AAA	-1	GLY	-	expression tag	UNP Q7NWX4
AAA	0	SER	-	expression tag	UNP Q7NWX4
BBB	-33	MET	-	initiating methionine	UNP Q7NWX4
BBB	-32	GLY	-	expression tag	UNP Q7NWX4
BBB	-31	SER	-	expression tag	UNP Q7NWX4
BBB	-30	SER	-	expression tag	UNP Q7NWX4
BBB	-29	HIS	-	expression tag	UNP Q7NWX4
BBB	-28	HIS	-	expression tag	UNP Q7NWX4
BBB	-27	HIS	-	expression tag	UNP Q7NWX4
BBB	-26	HIS	-	expression tag	UNP Q7NWX4
BBB	-25	HIS	-	expression tag	UNP Q7NWX4
BBB	-24	HIS	-	expression tag	UNP Q7NWX4
BBB	-23	SER	-	expression tag	UNP Q7NWX4
BBB	-22	SER	-	expression tag	UNP Q7NWX4
BBB	-21	GLY	-	expression tag	UNP Q7NWX4
BBB	-20	LEU	-	expression tag	UNP Q7NWX4
BBB	-19	VAL	-	expression tag	UNP Q7NWX4
BBB	-18	PRO	-	expression tag	UNP Q7NWX4
BBB	-17	ARG	-	expression tag	UNP Q7NWX4
BBB	-16	GLY	-	expression tag	UNP Q7NWX4
BBB	-15	SER	-	expression tag	UNP Q7NWX4
BBB	-14	HIS	-	expression tag	UNP Q7NWX4
BBB	-13	MET	-	expression tag	UNP Q7NWX4
BBB	-12	ALA	-	expression tag	UNP Q7NWX4
BBB	-11	SER	-	expression tag	UNP Q7NWX4
BBB	-10	MET	-	expression tag	UNP Q7NWX4
BBB	-9	THR	-	expression tag	UNP Q7NWX4
BBB	-8	GLY	-	expression tag	UNP Q7NWX4
BBB	-7	GLY	-	expression tag	UNP Q7NWX4
BBB	-6	GLN	-	expression tag	UNP Q7NWX4
BBB	-5	GLN	-	expression tag	UNP Q7NWX4

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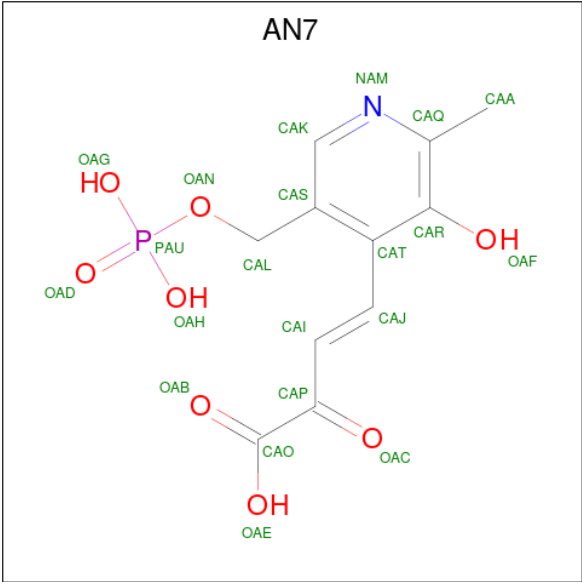
Chain	Residue	Modelled	Actual	Comment	Reference
BBB	-4	MET	-	expression tag	UNP Q7NWX4
BBB	-3	GLY	-	expression tag	UNP Q7NWX4
BBB	-2	ARG	-	expression tag	UNP Q7NWX4
BBB	-1	GLY	-	expression tag	UNP Q7NWX4
BBB	0	SER	-	expression tag	UNP Q7NWX4
CCC	-33	MET	-	initiating methionine	UNP Q7NWX4
CCC	-32	GLY	-	expression tag	UNP Q7NWX4
CCC	-31	SER	-	expression tag	UNP Q7NWX4
CCC	-30	SER	-	expression tag	UNP Q7NWX4
CCC	-29	HIS	-	expression tag	UNP Q7NWX4
CCC	-28	HIS	-	expression tag	UNP Q7NWX4
CCC	-27	HIS	-	expression tag	UNP Q7NWX4
CCC	-26	HIS	-	expression tag	UNP Q7NWX4
CCC	-25	HIS	-	expression tag	UNP Q7NWX4
CCC	-24	HIS	-	expression tag	UNP Q7NWX4
CCC	-23	SER	-	expression tag	UNP Q7NWX4
CCC	-22	SER	-	expression tag	UNP Q7NWX4
CCC	-21	GLY	-	expression tag	UNP Q7NWX4
CCC	-20	LEU	-	expression tag	UNP Q7NWX4
CCC	-19	VAL	-	expression tag	UNP Q7NWX4
CCC	-18	PRO	-	expression tag	UNP Q7NWX4
CCC	-17	ARG	-	expression tag	UNP Q7NWX4
CCC	-16	GLY	-	expression tag	UNP Q7NWX4
CCC	-15	SER	-	expression tag	UNP Q7NWX4
CCC	-14	HIS	-	expression tag	UNP Q7NWX4
CCC	-13	MET	-	expression tag	UNP Q7NWX4
CCC	-12	ALA	-	expression tag	UNP Q7NWX4
CCC	-11	SER	-	expression tag	UNP Q7NWX4
CCC	-10	MET	-	expression tag	UNP Q7NWX4
CCC	-9	THR	-	expression tag	UNP Q7NWX4
CCC	-8	GLY	-	expression tag	UNP Q7NWX4
CCC	-7	GLY	-	expression tag	UNP Q7NWX4
CCC	-6	GLN	-	expression tag	UNP Q7NWX4
CCC	-5	GLN	-	expression tag	UNP Q7NWX4
CCC	-4	MET	-	expression tag	UNP Q7NWX4
CCC	-3	GLY	-	expression tag	UNP Q7NWX4
CCC	-2	ARG	-	expression tag	UNP Q7NWX4
CCC	-1	GLY	-	expression tag	UNP Q7NWX4
CCC	0	SER	-	expression tag	UNP Q7NWX4
DDD	-33	MET	-	initiating methionine	UNP Q7NWX4
DDD	-32	GLY	-	expression tag	UNP Q7NWX4
DDD	-31	SER	-	expression tag	UNP Q7NWX4

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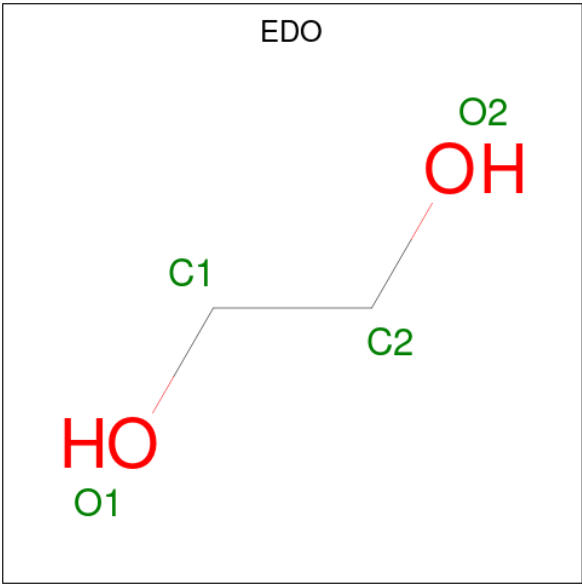
Chain	Residue	Modelled	Actual	Comment	Reference
DDD	-30	SER	-	expression tag	UNP Q7NWX4
DDD	-29	HIS	-	expression tag	UNP Q7NWX4
DDD	-28	HIS	-	expression tag	UNP Q7NWX4
DDD	-27	HIS	-	expression tag	UNP Q7NWX4
DDD	-26	HIS	-	expression tag	UNP Q7NWX4
DDD	-25	HIS	-	expression tag	UNP Q7NWX4
DDD	-24	HIS	-	expression tag	UNP Q7NWX4
DDD	-23	SER	-	expression tag	UNP Q7NWX4
DDD	-22	SER	-	expression tag	UNP Q7NWX4
DDD	-21	GLY	-	expression tag	UNP Q7NWX4
DDD	-20	LEU	-	expression tag	UNP Q7NWX4
DDD	-19	VAL	-	expression tag	UNP Q7NWX4
DDD	-18	PRO	-	expression tag	UNP Q7NWX4
DDD	-17	ARG	-	expression tag	UNP Q7NWX4
DDD	-16	GLY	-	expression tag	UNP Q7NWX4
DDD	-15	SER	-	expression tag	UNP Q7NWX4
DDD	-14	HIS	-	expression tag	UNP Q7NWX4
DDD	-13	MET	-	expression tag	UNP Q7NWX4
DDD	-12	ALA	-	expression tag	UNP Q7NWX4
DDD	-11	SER	-	expression tag	UNP Q7NWX4
DDD	-10	MET	-	expression tag	UNP Q7NWX4
DDD	-9	THR	-	expression tag	UNP Q7NWX4
DDD	-8	GLY	-	expression tag	UNP Q7NWX4
DDD	-7	GLY	-	expression tag	UNP Q7NWX4
DDD	-6	GLN	-	expression tag	UNP Q7NWX4
DDD	-5	GLN	-	expression tag	UNP Q7NWX4
DDD	-4	MET	-	expression tag	UNP Q7NWX4
DDD	-3	GLY	-	expression tag	UNP Q7NWX4
DDD	-2	ARG	-	expression tag	UNP Q7NWX4
DDD	-1	GLY	-	expression tag	UNP Q7NWX4
DDD	0	SER	-	expression tag	UNP Q7NWX4

- Molecule 2 is (3E)-4-{3-hydroxy-2-methyl-5-[(phosphonooxy)methyl]pyridin-4-yl}-2-oxobut-3-enoic acid (CCD ID: AN7) (formula: C₁₁H₁₂NO₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	AAA	1	Total	C	N	O	P	0	0
			21	11	1	8	1		
2	BBB	1	Total	C	N	O	P	0	1
			21	11	1	8	1		
2	CCC	1	Total	C	N	O	P	0	0
			21	11	1	8	1		
2	DDD	1	Total	C	N	O	P	0	0
			21	11	1	8	1		

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

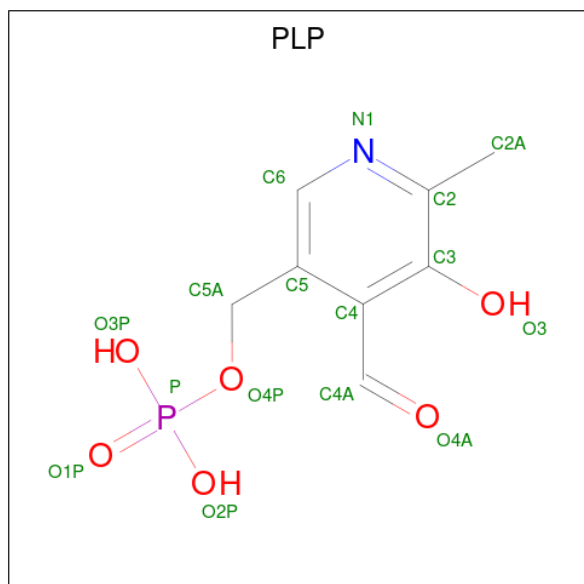


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	AAA	1	Total 4	C 2	O 2	0	0
3	AAA	1	Total 4	C 2	O 2	0	0
3	BBB	1	Total 4	C 2	O 2	0	0
3	CCC	1	Total 4	C 2	O 2	0	0
3	DDD	1	Total 4	C 2	O 2	0	0

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

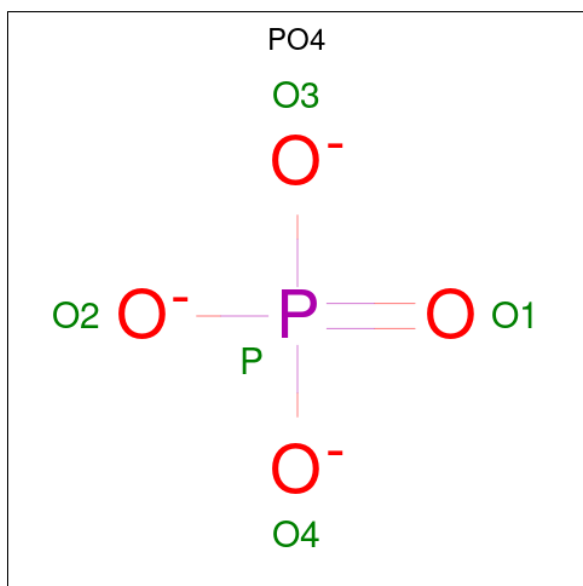
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	13	Total Na 13 13	0	0
4	BBB	26	Total Na 26 26	0	0
4	CCC	17	Total Na 17 17	0	0
4	DDD	21	Total Na 21 21	0	0

- Molecule 5 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $\text{C}_8\text{H}_{10}\text{NO}_6\text{P}$) (labeled as "Ligand of Interest" by depositor).



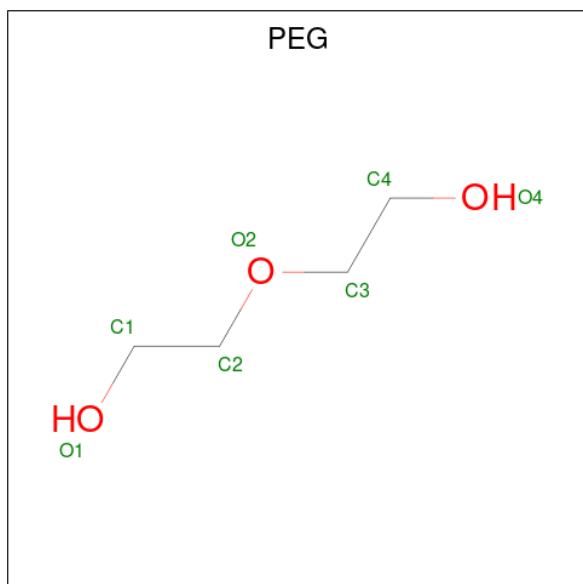
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	BBB	1	Total	C	N	O	P	0	1
			15	8	1	5	1		

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	BBB	1	Total	O	P	0	0
			5	4	1		
6	DDD	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	CCC	1	Total	C	O	0	0
			7	4	3		

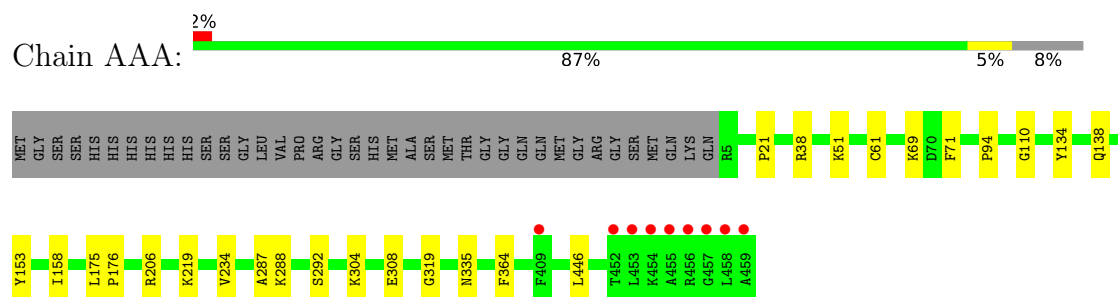
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	AAA	526	Total	O	0	0
			526	526		
8	BBB	567	Total	O	0	0
			567	567		
8	CCC	453	Total	O	0	0
			453	453		
8	DDD	485	Total	O	0	0
			485	485		

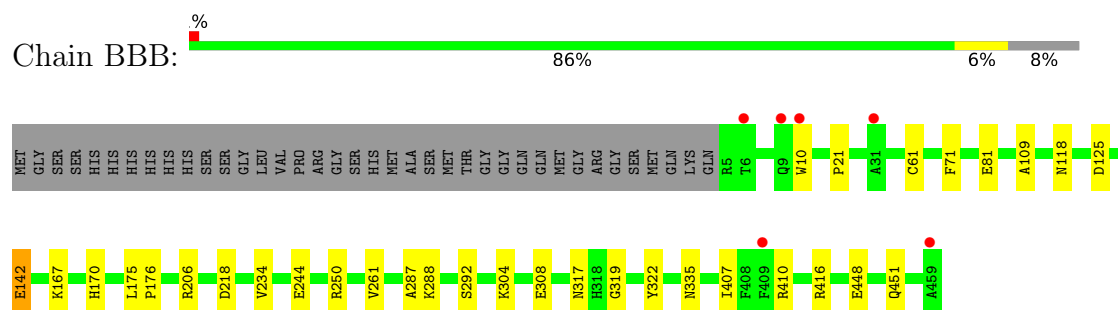
3 Residue-property plots [i](#)

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.

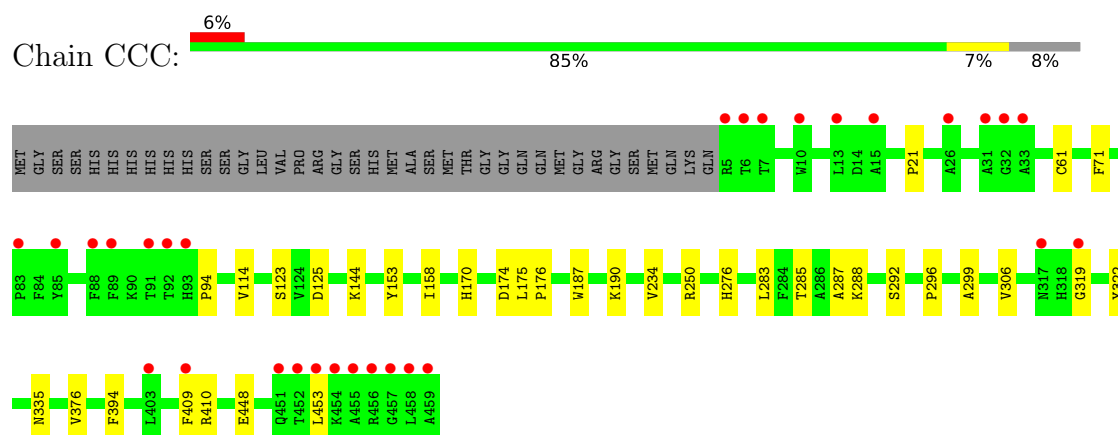
- Molecule 1: Probable aminotransferase



- Molecule 1: Probable aminotransferase

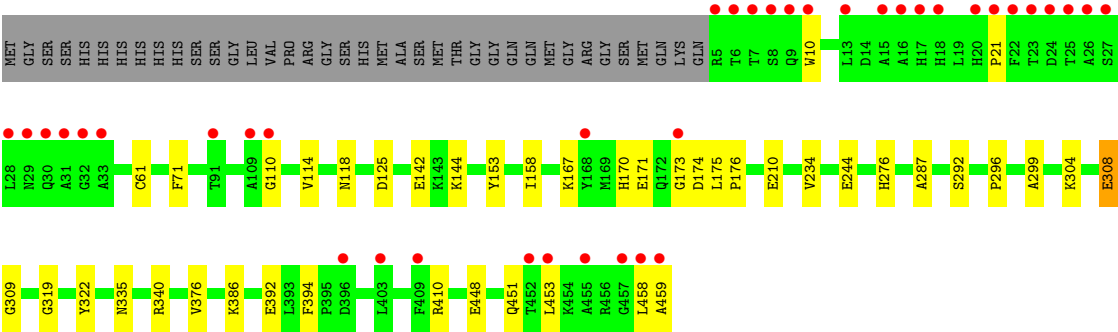


- Molecule 1: Probable aminotransferase



- Molecule 1: Probable aminotransferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.33Å 61.38Å 116.48Å 103.56° 89.38° 105.42°	Depositor
Resolution (Å)	39.43 – 1.60 39.43 – 1.60	Depositor EDS
% Data completeness (in resolution range)	76.1 (39.43-1.60) 76.1 (39.43-1.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.227 , 0.261 (Not available) , 0.229	Depositor DCC
R_{free} test set	7878 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	13.9	Xtriage
Anisotropy	0.277	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17188	wwPDB-VP
Average B, all atoms (Å ²)	17.0	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 89.82 % 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 2.9432e-08. 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: PLP, NA, PO4, AN7, EDO, PEG

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	AAA	0.93	0/3901	1.27	0/5271
1	BBB	0.93	0/3973	1.24	0/5367
1	CCC	0.93	0/3913	1.24	0/5286
1	DDD	0.93	0/3871	1.22	0/5235
All	All	0.93	0/15658	1.24	0/21159

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AAA	3728	0	3697	29	0
1	BBB	3771	0	3768	39	0
1	CCC	3734	0	3728	27	0
1	DDD	3711	0	3659	38	0
2	AAA	21	0	8	6	0
2	BBB	21	0	8	1	0
2	CCC	21	0	8	4	0
2	DDD	21	0	8	4	0
3	AAA	8	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BBB	4	0	6	0	0
3	CCC	4	0	6	0	0
3	DDD	4	0	6	0	0
4	AAA	13	0	0	0	0
4	BBB	26	0	0	0	0
4	CCC	17	0	0	1	0
4	DDD	21	0	0	0	0
5	BBB	15	0	6	6	0
6	BBB	5	0	0	0	0
6	DDD	5	0	0	0	0
7	CCC	7	0	10	0	0
8	AAA	526	0	0	5	0
8	BBB	567	0	0	7	0
8	CCC	453	0	0	3	0
8	DDD	485	0	0	5	0
All	All	17188	0	14930	114	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 (114) 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:BBB:288[B]:LYS:NZ	5:BBB:503[B]:PLP:C4A	2.11	1.13
1:BBB:288[B]:LYS:HZ1	5:BBB:503[B]:PLP:C4A	1.68	1.04
1:DDD:167[B]:LYS:HG2	1:DDD:171[B]:GLU:OE2	1.72	0.90
1:AAA:288[B]:LYS:NZ	2:AAA:501:AN7:CAJ	2.39	0.86
1:BBB:288[B]:LYS:HZ2	5:BBB:503[B]:PLP:C4A	1.84	0.84
1:AAA:288[B]:LYS:HZ1	2:AAA:501:AN7:CAJ	1.93	0.81
1:CCC:288[B]:LYS:HZ1	2:CCC:501:AN7:CAJ	1.95	0.80
1:CCC:288[B]:LYS:NZ	2:CCC:501:AN7:CAJ	2.52	0.72
1:AAA:38[B]:ARG:CG	1:BBB:81[B]:GLU:OE2	2.40	0.70
1:AAA:94:PRO:HB3	1:BBB:10[A]:TRP:CH2	2.27	0.70
1:BBB:288[B]:LYS:NZ	5:BBB:503[B]:PLP:C4	2.57	0.67
1:AAA:288[B]:LYS:HZ2	2:AAA:501:AN7:CAJ	2.09	0.66
1:DDD:167[B]:LYS:CG	1:DDD:171[B]:GLU:OE2	2.45	0.65
1:CCC:176:PRO:O	8:CCC:603:HOH:O	2.14	0.65
1:AAA:110:GLY:HA2	1:AAA:304[B]:LYS:HE2	1.80	0.64
1:DDD:386[B]:LYS:HD3	1:DDD:392:GLU:CD	2.24	0.63
1:DDD:153:TYR:CE2	2:DDD:501:AN7:HAI	2.34	0.63
1:AAA:308[A]:GLU:HG3	8:AAA:677:HOH:O	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:407[B]:ILE:HD12	1:BBB:410:ARG:HH12	1.65	0.61
4:CCC:509:NA:NA	8:CCC:818:HOH:O	1.74	0.59
1:DDD:110:GLY:HA2	1:DDD:304:LYS:HE3	1.84	0.58
1:DDD:410:ARG:NH1	1:DDD:448:GLU:OE2	2.37	0.58
1:BBB:118:ASN:HD21	1:BBB:322:TYR:HB2	1.68	0.58
1:BBB:410:ARG:NH1	1:BBB:448:GLU:OE2	2.36	0.58
1:AAA:51[B]:LYS:NZ	8:AAA:609:HOH:O	2.37	0.57
1:AAA:288[B]:LYS:HZ1	2:AAA:501:AN7:CAI	2.18	0.56
1:DDD:153:TYR:CE2	2:DDD:501:AN7:CAI	2.88	0.56
1:CCC:410:ARG:NH2	1:CCC:448:GLU:OE2	2.40	0.55
1:BBB:407[B]:ILE:HD12	1:BBB:410:ARG:NH1	2.22	0.54
1:CCC:174:ASP:OD2	1:DDD:144:LYS:HG3	2.07	0.54
1:CCC:288[B]:LYS:HZ1	2:CCC:501:AN7:CAI	2.21	0.54
1:BBB:250:ARG:HG3	1:CCC:250:ARG:HB3	1.90	0.54
1:AAA:206[B]:ARG:HG3	8:AAA:957:HOH:O	2.08	0.53
1:BBB:142[B]:GLU:H	1:BBB:142[B]:GLU:CD	2.17	0.53
1:CCC:94:PRO:HB3	1:DDD:10[B]:TRP:CH2	2.44	0.53
1:BBB:288[B]:LYS:HZ2	5:BBB:503[B]:PLP:C4	2.21	0.53
1:CCC:322:TYR:CD2	1:DDD:296:PRO:HA	2.44	0.53
1:DDD:173:GLY:N	8:DDD:620:HOH:O	2.43	0.52
1:CCC:125[B]:ASP:OD2	1:DDD:158:ILE:N	2.43	0.52
1:BBB:261:VAL:HG12	1:BBB:288[B]:LYS:HZ3	1.75	0.51
1:AAA:38[B]:ARG:HG3	1:BBB:81[B]:GLU:OE2	2.08	0.51
1:DDD:153:TYR:HE2	2:DDD:501:AN7:CAI	2.24	0.50
1:AAA:38[B]:ARG:HG2	1:BBB:81[B]:GLU:OE2	2.12	0.50
1:BBB:109:ALA:HB2	8:CCC:877:HOH:O	2.10	0.50
1:CCC:276:HIS:CE1	1:CCC:376[B]:VAL:HG21	2.46	0.50
1:DDD:386[B]:LYS:HD3	1:DDD:392:GLU:OE2	2.11	0.49
1:BBB:308[A]:GLU:HG3	8:BBB:826:HOH:O	2.12	0.49
1:DDD:175:LEU:HB3	1:DDD:176:PRO:HA	1.94	0.49
1:AAA:219:LYS:NZ	8:AAA:612:HOH:O	2.42	0.49
1:DDD:340:ARG:NH2	8:DDD:623:HOH:O	2.44	0.48
1:AAA:158:ILE:N	1:BBB:125[B]:ASP:OD1	2.47	0.48
1:BBB:61:CYS:O	1:BBB:292:SER:HA	2.14	0.48
1:AAA:319:GLY:HA3	1:BBB:21:PRO:HB3	1.96	0.48
1:CCC:296:PRO:HA	1:DDD:322:TYR:CD2	2.49	0.48
1:DDD:61:CYS:O	1:DDD:292:SER:HA	2.14	0.48
1:BBB:175:LEU:HB3	1:BBB:176:PRO:HA	1.96	0.48
1:AAA:158:ILE:HG13	1:BBB:125[B]:ASP:OD1	2.13	0.47
1:AAA:69:LYS:NZ	8:AAA:616:HOH:O	2.47	0.47
1:CCC:61:CYS:O	1:CCC:292:SER:HA	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DDD:308:GLU:HG3	8:DDD:666:HOH:O	2.14	0.47
1:AAA:61:CYS:O	1:AAA:292:SER:HA	2.15	0.47
1:AAA:175:LEU:HB3	1:AAA:176:PRO:HA	1.97	0.47
1:CCC:175:LEU:HB3	1:CCC:176:PRO:HA	1.97	0.47
1:CCC:144:LYS:HG3	1:DDD:174:ASP:OD2	2.15	0.46
1:BBB:317:ASN:ND2	8:BBB:624:HOH:O	2.46	0.46
1:DDD:244:GLU:HG2	8:DDD:619:HOH:O	2.16	0.46
1:CCC:187:TRP:CZ3	1:CCC:190[B]:LYS:HD2	2.51	0.46
1:DDD:118:ASN:HD21	1:DDD:322:TYR:HB2	1.81	0.46
1:BBB:234:VAL:HG12	1:BBB:234:VAL:O	2.15	0.45
1:DDD:234:VAL:O	1:DDD:234:VAL:HG12	2.15	0.45
1:BBB:142[B]:GLU:HG2	1:BBB:218:ASP:O	2.16	0.45
1:DDD:276:HIS:CE1	1:DDD:376[B]:VAL:HG21	2.51	0.45
1:AAA:38[B]:ARG:NE	1:BBB:81[B]:GLU:OE2	2.50	0.45
1:BBB:167[B]:LYS:NZ	8:BBB:632:HOH:O	2.49	0.45
1:CCC:158:ILE:N	1:DDD:125[B]:ASP:OD1	2.48	0.45
1:DDD:451[A]:GLN:HA	1:DDD:451[A]:GLN:OE1	2.16	0.45
1:CCC:319:GLY:HA3	1:DDD:21:PRO:HB3	1.99	0.45
1:AAA:153:TYR:CE2	2:AAA:501:AN7:CAI	3.00	0.44
1:AAA:288[B]:LYS:NZ	2:AAA:501:AN7:CAT	2.80	0.44
1:BBB:288[A]:LYS:HZ3	2:BBB:501[A]:AN7:HAJ	1.83	0.44
1:AAA:158:ILE:H	1:BBB:125[B]:ASP:CG	2.26	0.44
1:CCC:71:PHE:CZ	1:CCC:335:ASN:HA	2.52	0.44
1:AAA:234:VAL:HG12	1:AAA:234:VAL:O	2.18	0.44
1:CCC:123[B]:SER:OG	1:CCC:285:THR:HB	2.18	0.43
1:CCC:234:VAL:O	1:CCC:234:VAL:HG12	2.18	0.43
1:CCC:21:PRO:HB3	1:DDD:319:GLY:HA3	1.98	0.43
1:DDD:114[B]:VAL:HG23	1:DDD:299:ALA:HB1	1.99	0.43
1:AAA:446[B]:LEU:HD23	1:AAA:446[B]:LEU:HA	1.89	0.43
1:DDD:71:PHE:CZ	1:DDD:335:ASN:HA	2.53	0.43
1:CCC:283[B]:LEU:HD21	1:CCC:306:VAL:HG11	1.99	0.43
1:DDD:170:HIS:HA	1:DDD:175:LEU:HB2	2.01	0.42
1:CCC:114[B]:VAL:HG23	1:CCC:299:ALA:HB1	2.01	0.42
1:BBB:261:VAL:HG12	1:BBB:288[B]:LYS:NZ	2.34	0.42
1:BBB:288[B]:LYS:NZ	5:BBB:503[B]:PLP:C3	2.82	0.42
1:DDD:167[B]:LYS:HE2	1:DDD:171[B]:GLU:OE2	2.18	0.42
1:AAA:71:PHE:CZ	1:AAA:335:ASN:HA	2.54	0.42
1:BBB:81[A]:GLU:OE2	8:BBB:606:HOH:O	2.21	0.42
1:BBB:170:HIS:HA	1:BBB:175:LEU:HB2	2.02	0.42
1:BBB:71:PHE:CZ	1:BBB:335:ASN:HA	2.55	0.41
1:BBB:304[A]:LYS:NZ	8:BBB:622:HOH:O	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:21:PRO:HB3	1:BBB:319:GLY:HA3	2.01	0.41
1:CCC:153:TYR:CE2	2:CCC:501:AN7:CAI	3.04	0.41
1:CCC:170:HIS:HA	1:CCC:175:LEU:HB2	2.03	0.41
1:DDD:458:LEU:O	1:DDD:459:ALA:HB2	2.20	0.41
1:AAA:364:PHE:CD1	1:AAA:446[B]:LEU:HD12	2.56	0.41
1:DDD:394:PHE:HZ	1:DDD:453:LEU:HD21	1.85	0.41
1:BBB:416:ARG:NH2	8:BBB:648:HOH:O	2.54	0.41
1:DDD:153:TYR:CD2	2:DDD:501:AN7:HAI	2.56	0.41
1:DDD:210[B]:GLU:HG2	1:DDD:210[B]:GLU:H	1.74	0.40
1:CCC:394:PHE:HZ	1:CCC:453:LEU:HD21	1.86	0.40
1:DDD:309:GLY:HA2	8:DDD:830:HOH:O	2.20	0.40
1:AAA:134:TYR:O	1:AAA:138:GLN:HG2	2.21	0.40
1:BBB:206[B]:ARG:NH1	8:BBB:650:HOH:O	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AAA	480/493 (97%)	461 (96%)	18 (4%)	1 (0%)	43	24
1	BBB	488/493 (99%)	471 (96%)	16 (3%)	1 (0%)	43	24
1	CCC	482/493 (98%)	465 (96%)	16 (3%)	1 (0%)	43	24
1	DDD	476/493 (97%)	460 (97%)	15 (3%)	1 (0%)	43	24
All	All	1926/1972 (98%)	1857 (96%)	65 (3%)	4 (0%)	43	24

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	287	ALA
1	DDD	287	ALA

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Mol	Chain	Res	Type
1	AAA	287	ALA
1	CCC	287	ALA

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	AAA	391/394 (99%)	391 (100%)	0	100	100
1	BBB	399/394 (101%)	395 (99%)	4 (1%)	68	50
1	CCC	393/394 (100%)	391 (100%)	2 (0%)	81	70
1	DDD	387/394 (98%)	385 (100%)	2 (0%)	81	70
All	All	1570/1576 (100%)	1562 (100%)	8 (0%)	84	70

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BBB	142[A]	GLU
1	BBB	142[B]	GLU
1	BBB	244	GLU
1	BBB	451	GLN
1	CCC	409[A]	PHE
1	CCC	409[B]	PHE
1	DDD	142	GLU
1	DDD	308	GLU

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

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 90 ligands modelled in this entry, 77 are monoatomic - leaving 13 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	AN7	CCC	501	4	20,21,21	0.92	1 (5%)	24,30,30	1.11	1 (4%)
3	EDO	AAA	502	-	3,3,3	0.17	0	2,2,2	0.22	0
2	AN7	BBB	501[A]	4	20,21,21	0.92	1 (5%)	24,30,30	0.89	1 (4%)
3	EDO	CCC	503	-	3,3,3	0.07	0	2,2,2	0.32	0
2	AN7	AAA	501	4	20,21,21	0.74	1 (5%)	24,30,30	0.96	1 (4%)
2	AN7	DDD	501	4	20,21,21	0.77	1 (5%)	24,30,30	1.04	1 (4%)
3	EDO	AAA	503	-	3,3,3	0.07	0	2,2,2	0.15	0
3	EDO	DDD	502	-	3,3,3	0.10	0	2,2,2	0.12	0
6	PO4	BBB	504	-	4,4,4	0.78	0	6,6,6	0.50	0
6	PO4	DDD	503	-	4,4,4	0.78	0	6,6,6	0.46	0
7	PEG	CCC	502	-	6,6,6	0.20	0	5,5,5	0.21	0
3	EDO	BBB	502	-	3,3,3	0.07	0	2,2,2	0.33	0
5	PLP	BBB	503[B]	-	15,15,16	0.63	0	21,22,23	1.49	4 (19%)

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	AN7	CCC	501	4	-	1/15/15/15	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	AAA	502	-	-	1/1/1/1	-
2	AN7	BBB	501[A]	4	-	7/15/15/15	0/1/1/1
3	EDO	CCC	503	-	-	1/1/1/1	-
2	AN7	AAA	501	4	-	5/15/15/15	0/1/1/1
2	AN7	DDD	501	4	-	7/15/15/15	0/1/1/1
3	EDO	AAA	503	-	-	1/1/1/1	-
3	EDO	DDD	502	-	-	0/1/1/1	-
7	PEG	CCC	502	-	-	2/4/4/4	-
3	EDO	BBB	502	-	-	1/1/1/1	-
5	PLP	BBB	503[B]	-	-	0/6/6/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	501[A]	AN7	OAE-CAO	-3.55	1.20	1.30
2	CCC	501	AN7	OAE-CAO	-2.81	1.22	1.30
2	DDD	501	AN7	OAE-CAO	-2.27	1.24	1.30
2	AAA	501	AN7	OAE-CAO	-2.00	1.25	1.30

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	BBB	503[B]	PLP	C4A-C4-C5	4.18	125.25	120.94
2	CCC	501	AN7	CAJ-CAI-CAP	3.90	127.19	121.50
2	DDD	501	AN7	CAJ-CAI-CAP	3.53	126.66	121.50
2	AAA	501	AN7	CAJ-CAI-CAP	2.90	125.74	121.50
5	BBB	503[B]	PLP	C3-C4-C5	-2.85	115.16	118.59
5	BBB	503[B]	PLP	C6-C5-C4	2.69	120.30	118.10
5	BBB	503[B]	PLP	O3P-P-O2P	2.29	116.41	107.80
2	BBB	501[A]	AN7	CAJ-CAI-CAP	2.29	124.84	121.50

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AAA	501	AN7	CAJ-CAI-CAP-CAO
2	AAA	501	AN7	OAB-CAO-CAP-CAI
2	AAA	501	AN7	OAE-CAO-CAP-CAI
2	BBB	501[A]	AN7	CAJ-CAI-CAP-CAO
2	BBB	501[A]	AN7	OAB-CAO-CAP-OAC

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Mol	Chain	Res	Type	Atoms
2	BBB	501[A]	AN7	OAB-CAO-CAP-CAI
2	BBB	501[A]	AN7	OAE-CAO-CAP-OAC
2	BBB	501[A]	AN7	OAE-CAO-CAP-CAI
2	DDD	501	AN7	CAJ-CAI-CAP-CAO
2	DDD	501	AN7	OAB-CAO-CAP-OAC
2	DDD	501	AN7	OAB-CAO-CAP-CAI
2	DDD	501	AN7	OAE-CAO-CAP-OAC
2	DDD	501	AN7	OAE-CAO-CAP-CAI
7	CCC	502	PEG	O2-C3-C4-O4
2	AAA	501	AN7	CAJ-CAI-CAP-OAC
2	DDD	501	AN7	CAJ-CAI-CAP-OAC
2	CCC	501	AN7	CAI-CAJ-CAT-CAR
3	CCC	503	EDO	O1-C1-C2-O2
2	BBB	501[A]	AN7	CAJ-CAI-CAP-OAC
2	AAA	501	AN7	CAI-CAJ-CAT-CAR
2	BBB	501[A]	AN7	CAI-CAJ-CAT-CAR
2	DDD	501	AN7	CAI-CAJ-CAT-CAR
3	AAA	503	EDO	O1-C1-C2-O2
3	BBB	502	EDO	O1-C1-C2-O2
7	CCC	502	PEG	C4-C3-O2-C2
3	AAA	502	EDO	O1-C1-C2-O2

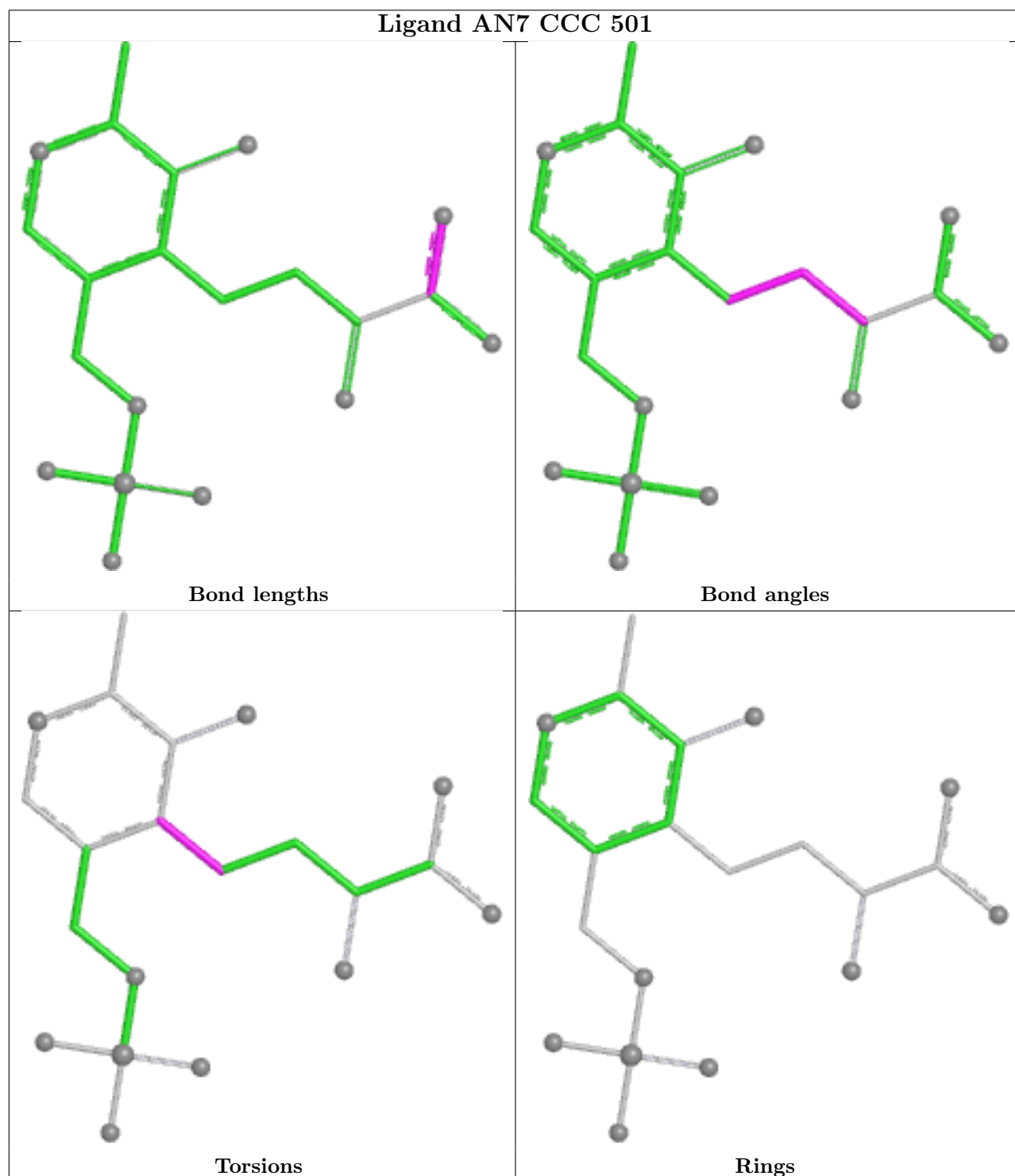
There are no ring outliers.

5 monomers are involved in 21 short contacts:

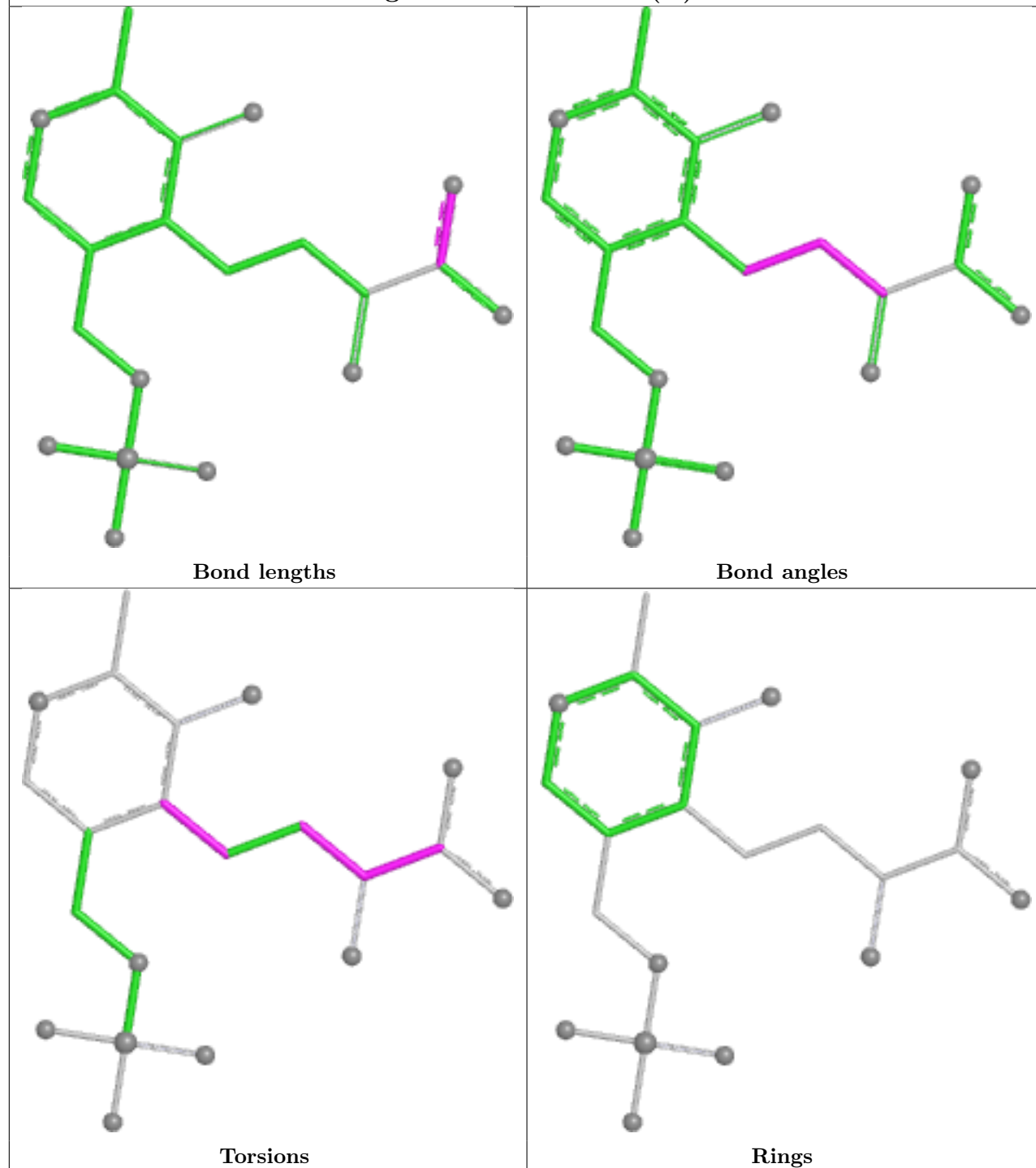
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	CCC	501	AN7	4	0
2	BBB	501[A]	AN7	1	0
2	AAA	501	AN7	6	0
2	DDD	501	AN7	4	0
5	BBB	503[B]	PLP	6	0

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.

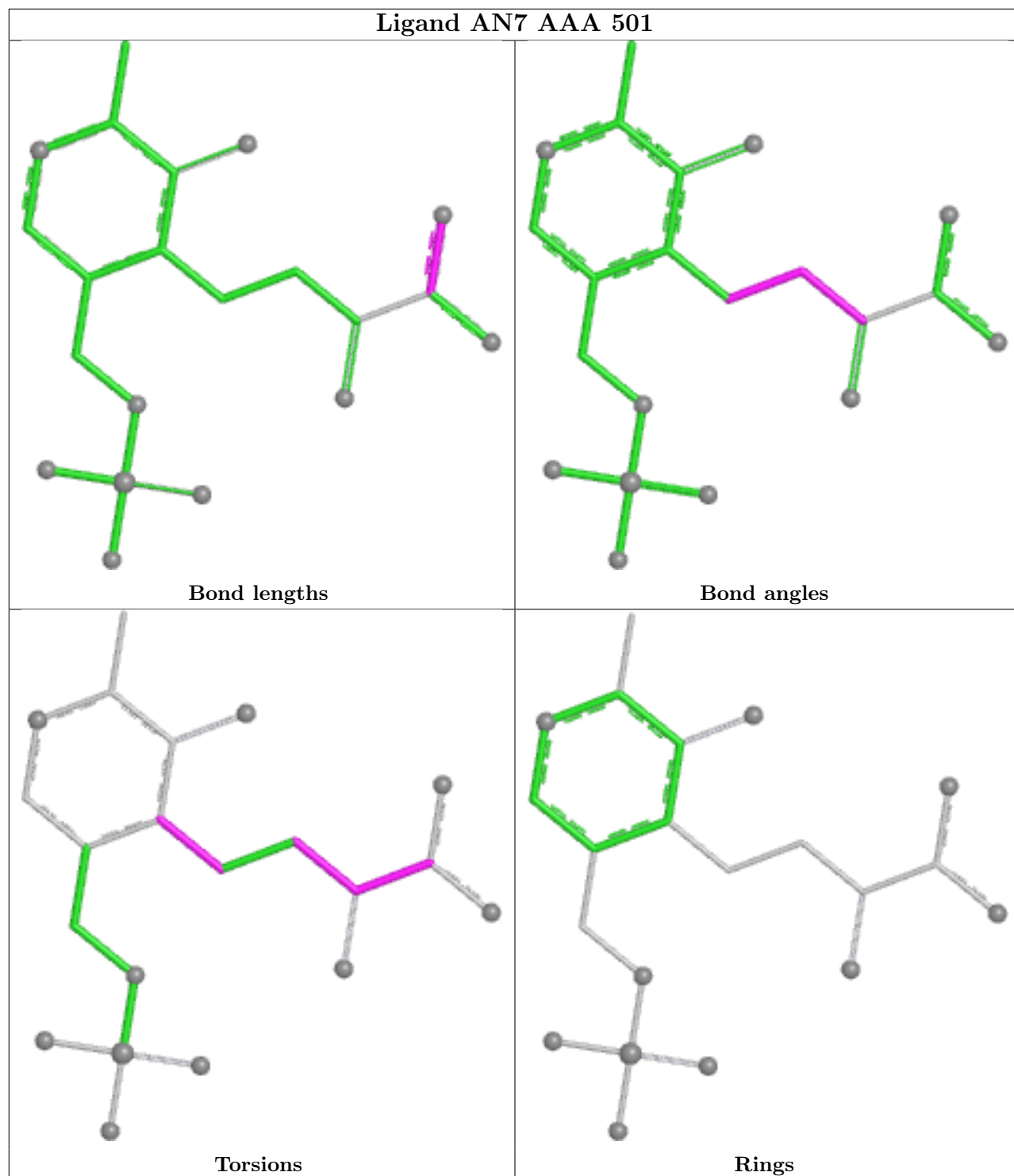
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



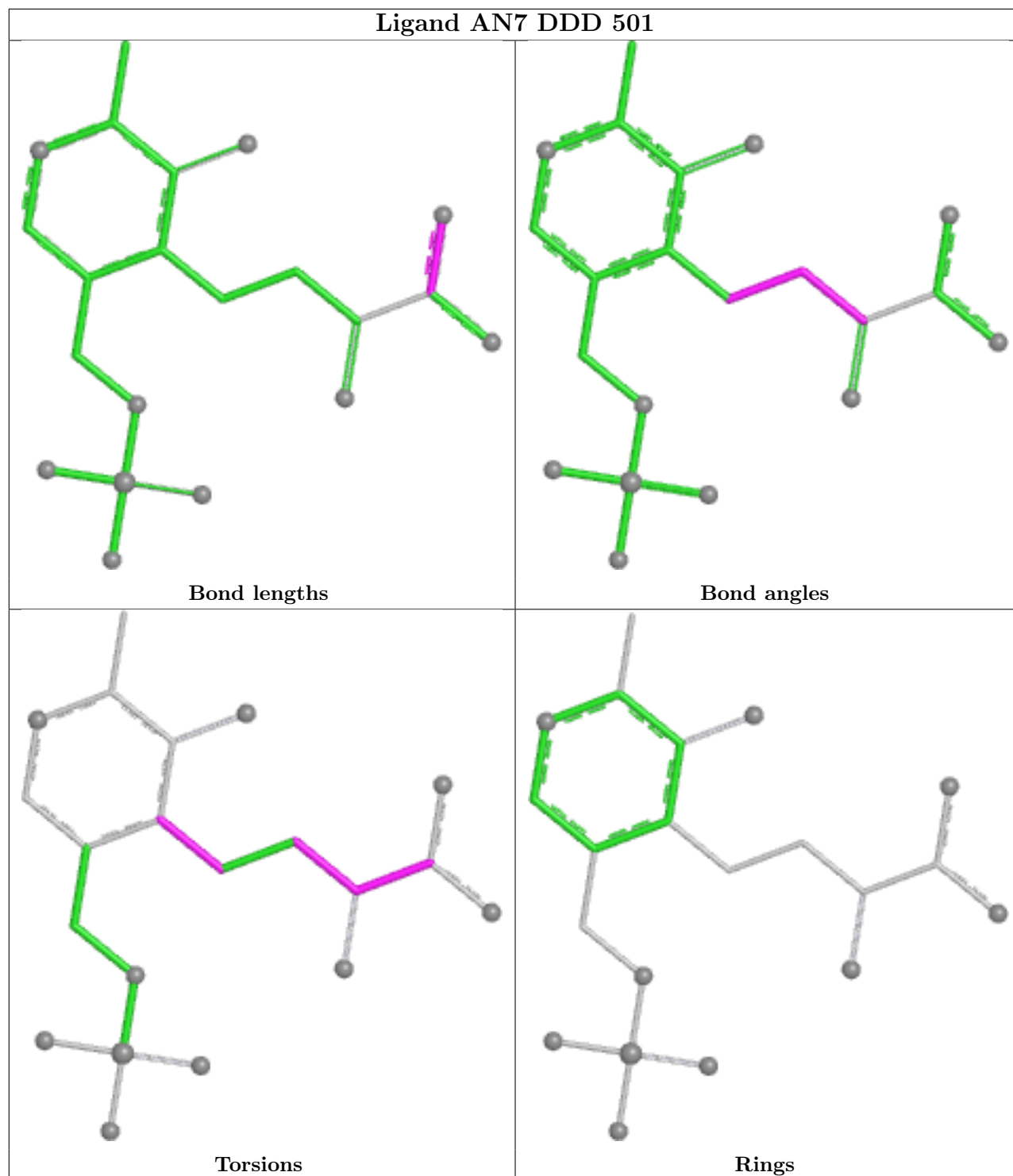
Ligand AN7 BBB 501 (A)

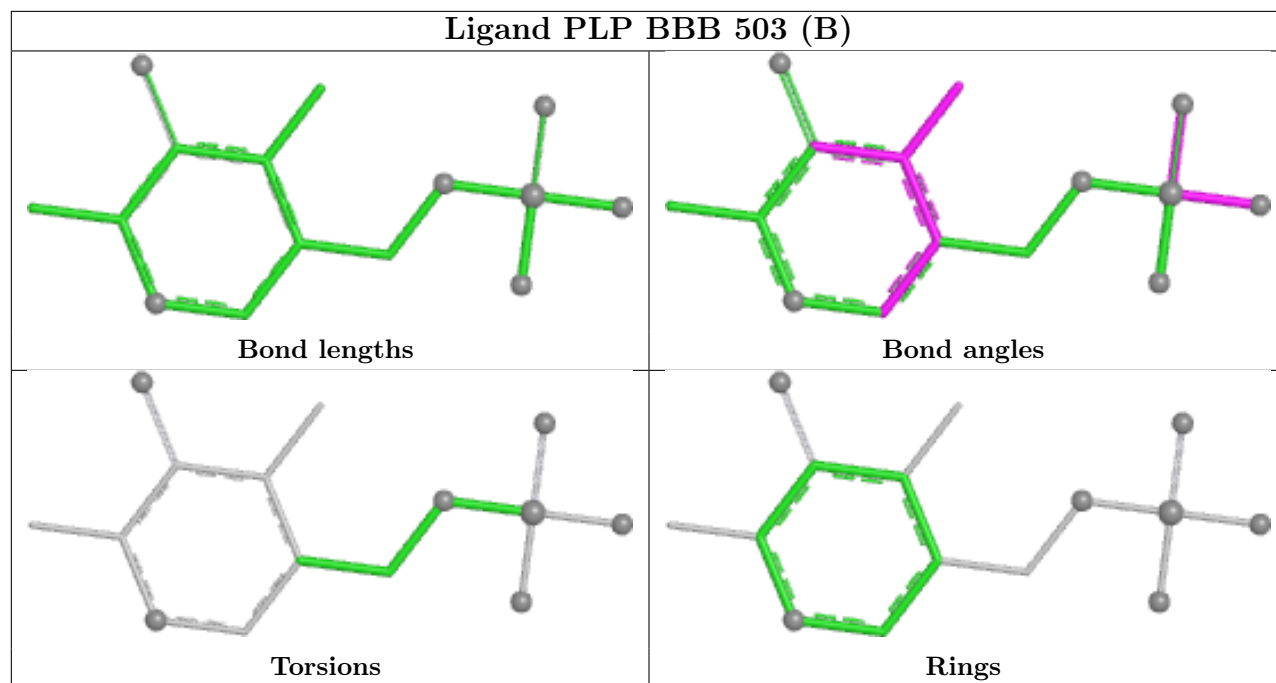


Ligand AN7 AAA 501



Ligand AN7 DDD 501





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	AAA	455/493 (92%)	-0.03	9 (1%) 65 69	5, 12, 23, 58	27 (5%)
1	BBB	455/493 (92%)	-0.06	6 (1%) 75 79	3, 11, 24, 40	34 (7%)
1	CCC	455/493 (92%)	0.28	30 (6%) 24 25	5, 14, 33, 77	29 (6%)
1	DDD	455/493 (92%)	0.47	39 (8%) 16 16	5, 15, 45, 111	22 (4%)
All	All	1820/1972 (92%)	0.17	84 (4%) 37 39	3, 13, 31, 111	112 (6%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	DDD	28	LEU	6.3
1	DDD	7	THR	5.7
1	DDD	10[A]	TRP	5.3
1	CCC	453	LEU	5.2
1	CCC	458	LEU	5.1
1	DDD	6	THR	4.9
1	DDD	26	ALA	4.8
1	DDD	458	LEU	4.7
1	DDD	8	SER	4.7
1	CCC	409[A]	PHE	4.6
1	DDD	453	LEU	4.5
1	CCC	455	ALA	4.5
1	DDD	29	ASN	4.5
1	CCC	459	ALA	4.3
1	DDD	22	PHE	4.1
1	CCC	6	THR	4.1
1	DDD	21	PRO	4.0
1	AAA	455	ALA	4.0
1	DDD	31	ALA	3.9
1	CCC	31	ALA	3.9
1	DDD	33	ALA	3.8

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Mol	Chain	Res	Type	RSRZ
1	AAA	452	THR	3.7
1	DDD	32	GLY	3.7
1	DDD	457	GLY	3.6
1	CCC	452	THR	3.5
1	AAA	453	LEU	3.5
1	DDD	9	GLN	3.5
1	DDD	452	THR	3.5
1	DDD	5	ARG	3.5
1	DDD	459	ALA	3.4
1	CCC	454	LYS	3.4
1	DDD	168	TYR	3.3
1	DDD	109	ALA	3.2
1	DDD	13	LEU	3.1
1	DDD	30	GLN	3.0
1	CCC	457	GLY	3.0
1	BBB	409[A]	PHE	2.9
1	DDD	409[A]	PHE	2.9
1	DDD	17	HIS	2.8
1	CCC	33	ALA	2.8
1	CCC	93	HIS	2.8
1	BBB	459	ALA	2.8
1	DDD	455	ALA	2.7
1	CCC	10	TRP	2.7
1	AAA	458	LEU	2.7
1	CCC	13	LEU	2.7
1	CCC	5	ARG	2.7
1	DDD	27	SER	2.7
1	DDD	18	HIS	2.6
1	CCC	92	THR	2.5
1	CCC	403	LEU	2.5
1	CCC	32	GLY	2.4
1	CCC	15	ALA	2.4
1	DDD	110	GLY	2.4
1	DDD	396	ASP	2.4
1	CCC	456	ARG	2.4
1	BBB	6	THR	2.3
1	CCC	7	THR	2.3
1	CCC	91	THR	2.3
1	CCC	85	TYR	2.3
1	AAA	409[A]	PHE	2.3
1	AAA	459	ALA	2.2
1	CCC	26	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	CCC	83	PRO	2.2
1	CCC	317	ASN	2.2
1	DDD	403	LEU	2.2
1	AAA	457	GLY	2.2
1	CCC	319	GLY	2.2
1	BBB	9	GLN	2.2
1	CCC	88	PHE	2.2
1	DDD	23	THR	2.2
1	BBB	31	ALA	2.2
1	BBB	10[A]	TRP	2.2
1	CCC	451	GLN	2.1
1	DDD	25	THR	2.1
1	DDD	24	ASP	2.1
1	AAA	456	ARG	2.1
1	DDD	91	THR	2.1
1	DDD	20	HIS	2.1
1	CCC	89	PHE	2.1
1	DDD	173	GLY	2.0
1	DDD	16	ALA	2.0
1	DDD	15	ALA	2.0
1	AAA	454	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

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($\text{\AA}^2$)	Q<0.9
4	NA	DDD	508	1/1	0.30	0.37	57,57,57,57	0
4	NA	DDD	505	1/1	0.54	0.34	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NA	DDD	510	1/1	0.54	0.34	51,51,51,51	0
4	NA	BBB	527	1/1	0.59	0.23	54,54,54,54	0
4	NA	BBB	529	1/1	0.67	0.19	48,48,48,48	0
4	NA	BBB	525	1/1	0.67	0.24	55,55,55,55	0
4	NA	CCC	511	1/1	0.72	0.17	43,43,43,43	0
4	NA	DDD	516	1/1	0.72	0.21	49,49,49,49	0
4	NA	CCC	509	1/1	0.74	0.21	44,44,44,44	0
4	NA	BBB	514	1/1	0.74	0.27	36,36,36,36	0
4	NA	DDD	514	1/1	0.76	0.19	70,70,70,70	0
4	NA	DDD	515	1/1	0.76	0.13	49,49,49,49	0
4	NA	BBB	519	1/1	0.76	0.15	47,47,47,47	0
4	NA	CCC	516	1/1	0.77	0.13	42,42,42,42	0
4	NA	CCC	519	1/1	0.77	0.15	26,26,26,26	1
4	NA	BBB	530	1/1	0.77	0.15	47,47,47,47	0
4	NA	CCC	504	1/1	0.77	0.15	42,42,42,42	0
4	NA	BBB	509	1/1	0.78	0.15	41,41,41,41	0
3	EDO	AAA	503	4/4	0.78	0.12	34,35,36,36	0
4	NA	CCC	510	1/1	0.79	0.23	39,39,39,39	0
4	NA	AAA	509	1/1	0.79	0.12	46,46,46,46	0
4	NA	DDD	517	1/1	0.79	0.26	39,39,39,39	0
4	NA	DDD	520	1/1	0.79	0.20	62,62,62,62	0
4	NA	DDD	513	1/1	0.80	0.15	41,41,41,41	0
4	NA	BBB	511	1/1	0.80	0.19	36,36,36,36	0
3	EDO	AAA	502	4/4	0.80	0.15	34,35,35,36	0
4	NA	AAA	514	1/1	0.80	0.12	47,47,47,47	0
3	EDO	BBB	502	4/4	0.80	0.14	41,41,42,44	0
4	NA	DDD	512	1/1	0.80	0.16	46,46,46,46	0
4	NA	BBB	524	1/1	0.81	0.17	33,33,33,33	0
7	PEG	CCC	502	7/7	0.82	0.12	27,33,37,37	0
4	NA	BBB	515	1/1	0.83	0.11	39,39,39,39	0
4	NA	BBB	523	1/1	0.85	0.11	44,44,44,44	0
4	NA	CCC	520	1/1	0.85	0.12	44,44,44,44	0
4	NA	DDD	523	1/1	0.85	0.10	41,41,41,41	0
4	NA	DDD	509	1/1	0.85	0.11	37,37,37,37	0
3	EDO	DDD	502	4/4	0.86	0.12	32,32,32,33	0
4	NA	AAA	516	1/1	0.86	0.12	48,48,48,48	0
4	NA	AAA	512	1/1	0.86	0.20	42,42,42,42	0
4	NA	DDD	511	1/1	0.87	0.15	39,39,39,39	0
4	NA	BBB	520	1/1	0.87	0.09	37,37,37,37	0
4	NA	DDD	518	1/1	0.87	0.09	31,31,31,31	0
4	NA	BBB	521	1/1	0.87	0.09	37,37,37,37	0
4	NA	BBB	513	1/1	0.87	0.11	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NA	DDD	504	1/1	0.87	0.11	25,25,25,25	0
4	NA	BBB	517	1/1	0.88	0.10	42,42,42,42	0
4	NA	CCC	506	1/1	0.88	0.16	45,45,45,45	0
4	NA	AAA	510	1/1	0.88	0.16	38,38,38,38	0
4	NA	BBB	526	1/1	0.88	0.13	37,37,37,37	0
4	NA	AAA	506	1/1	0.88	0.18	32,32,32,32	0
4	NA	BBB	528	1/1	0.88	0.11	47,47,47,47	0
4	NA	BBB	507	1/1	0.88	0.10	37,37,37,37	0
4	NA	AAA	513	1/1	0.88	0.09	43,43,43,43	0
4	NA	BBB	510	1/1	0.89	0.14	37,37,37,37	0
4	NA	DDD	519	1/1	0.89	0.08	24,24,24,24	0
4	NA	CCC	507	1/1	0.89	0.18	27,27,27,27	0
4	NA	BBB	516	1/1	0.89	0.14	41,41,41,41	0
4	NA	AAA	508	1/1	0.89	0.10	39,39,39,39	0
4	NA	AAA	505	1/1	0.90	0.13	31,31,31,31	0
3	EDO	CCC	503	4/4	0.90	0.12	27,28,28,29	0
4	NA	BBB	508	1/1	0.90	0.15	39,39,39,39	0
4	NA	AAA	507	1/1	0.90	0.14	39,39,39,39	0
4	NA	CCC	514	1/1	0.91	0.09	42,42,42,42	0
4	NA	BBB	518	1/1	0.91	0.07	36,36,36,36	0
4	NA	DDD	524	1/1	0.91	0.09	39,39,39,39	0
4	NA	BBB	522	1/1	0.91	0.09	37,37,37,37	0
4	NA	DDD	522	1/1	0.92	0.09	32,32,32,32	0
2	AN7	BBB	501[A]	21/21	0.92	0.10	8,13,16,17	21
4	NA	DDD	506	1/1	0.92	0.17	36,36,36,36	0
4	NA	BBB	505	1/1	0.92	0.10	47,47,47,47	0
4	NA	BBB	512	1/1	0.93	0.09	33,33,33,33	0
4	NA	DDD	521	1/1	0.93	0.12	47,47,47,47	0
2	AN7	DDD	501	21/21	0.93	0.10	14,20,35,35	0
4	NA	CCC	508	1/1	0.93	0.08	35,35,35,35	0
4	NA	AAA	515	1/1	0.93	0.11	41,41,41,41	0
4	NA	AAA	511	1/1	0.93	0.08	43,43,43,43	0
4	NA	CCC	518	1/1	0.94	0.05	24,24,24,24	0
2	AN7	CCC	501	21/21	0.94	0.09	12,18,33,36	0
4	NA	BBB	506	1/1	0.94	0.15	30,30,30,30	0
4	NA	CCC	513	1/1	0.94	0.10	35,35,35,35	0
4	NA	AAA	504	1/1	0.94	0.13	33,33,33,33	0
4	NA	CCC	515	1/1	0.94	0.09	37,37,37,37	0
4	NA	CCC	505	1/1	0.94	0.21	26,26,26,26	0
6	PO4	DDD	503	5/5	0.94	0.10	32,37,38,38	0
4	NA	CCC	517	1/1	0.94	0.10	33,33,33,33	0
6	PO4	BBB	504	5/5	0.95	0.10	26,26,30,30	0

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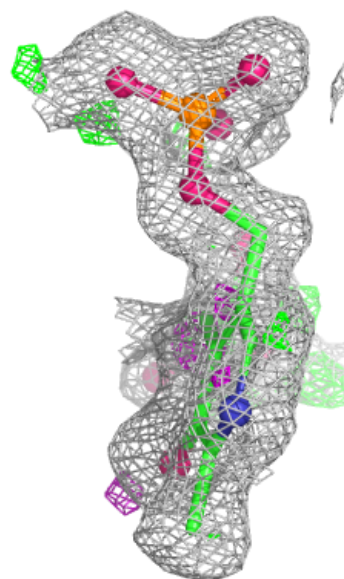
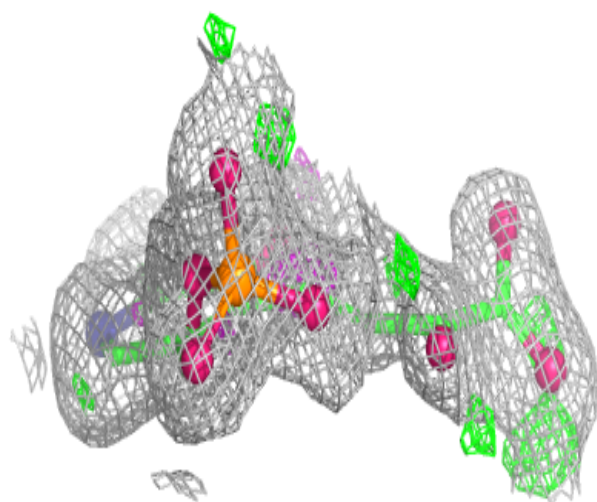
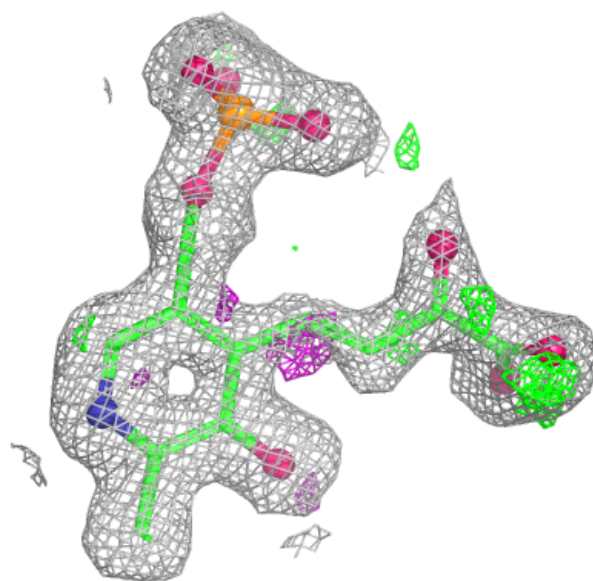
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NA	CCC	512	1/1	0.95	0.09	40,40,40,40	0
5	PLP	BBB	503[B]	15/16	0.95	0.07	4,8,9,11	15
4	NA	DDD	507	1/1	0.96	0.13	31,31,31,31	0
2	AN7	AAA	501	21/21	0.96	0.08	9,14,26,28	0

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.

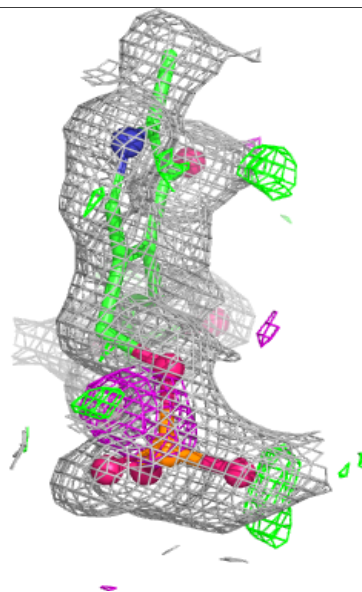
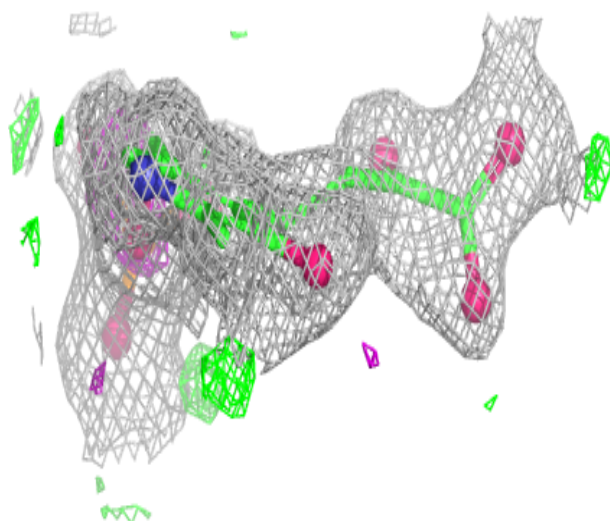
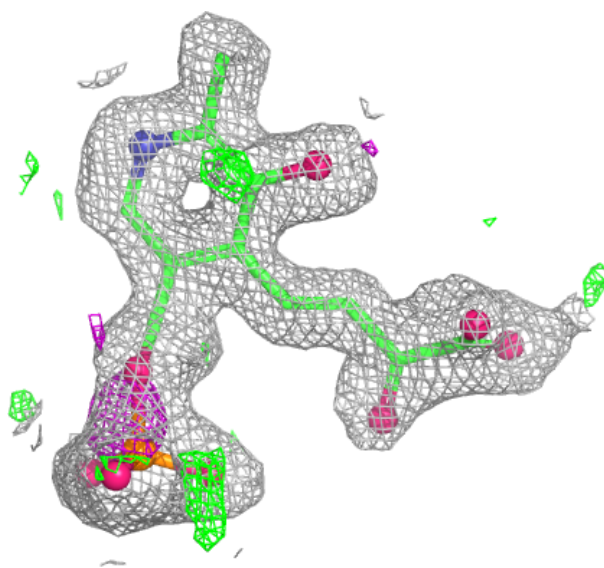
Electron density around AN7 BBB 501 (A):

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



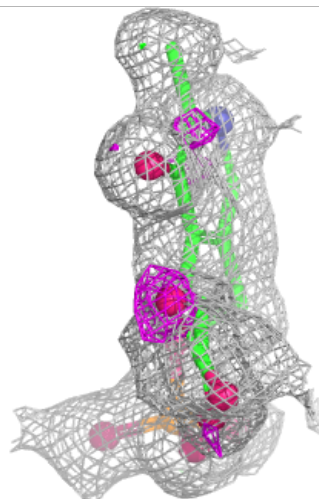
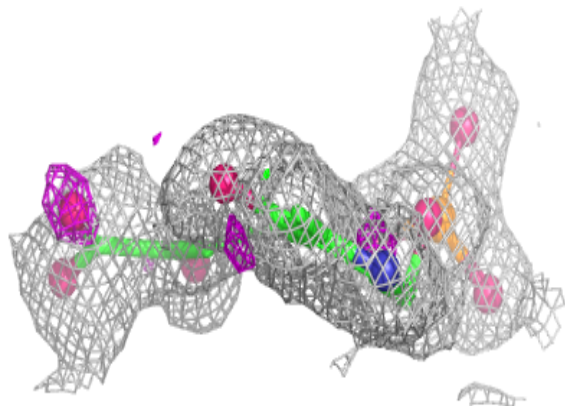
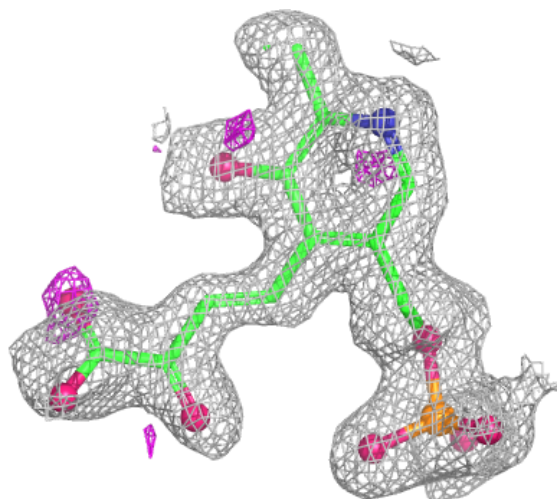
Electron density around AN7 DDD 501:

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



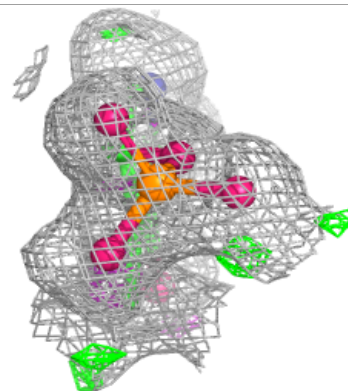
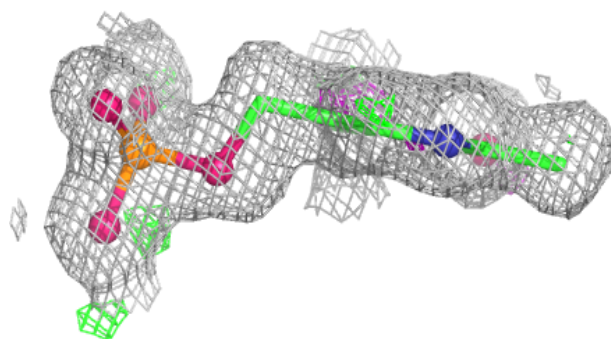
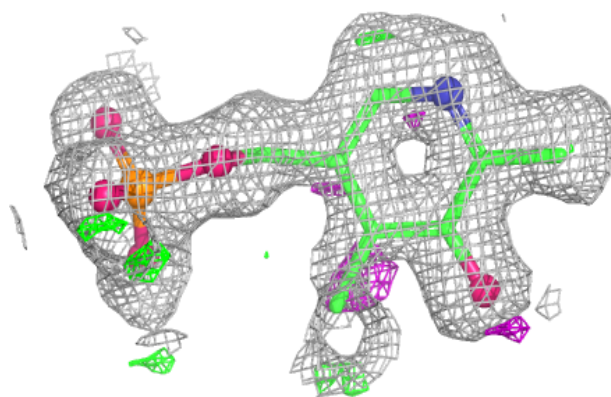
Electron density around AN7 CCC 501:

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



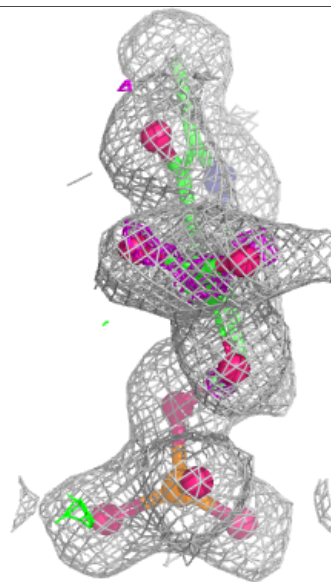
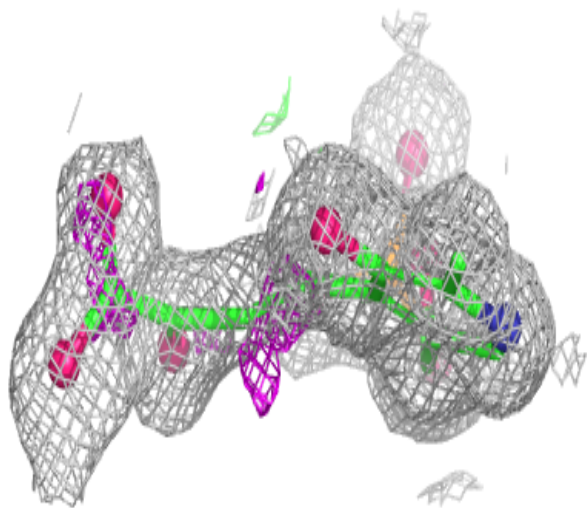
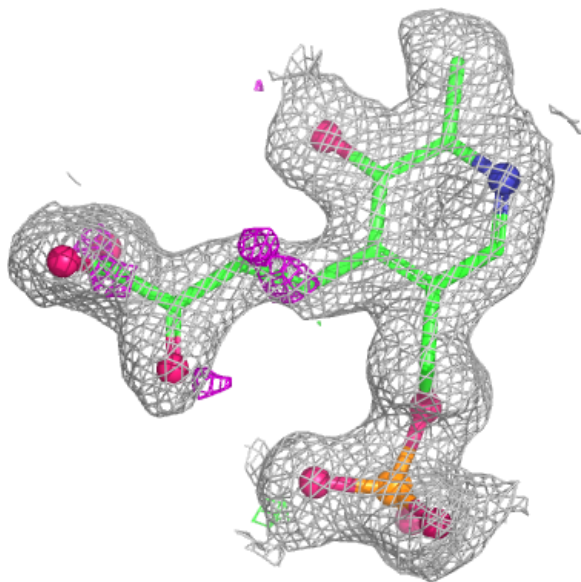
Electron density around PLP BBB 503 (B):

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



Electron density around AN7 AAA 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.