



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 2, 2022 – 06:31 PM JST

PDB ID : 7FJK
Title : Tyrosine phenol-lyase from pantoea agglomerans
Authors : Katayama, T.; Mikamii, B.; Byun, Z.
Deposited on : 2021-08-04
Resolution : 1.30 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.29
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) : 2.29

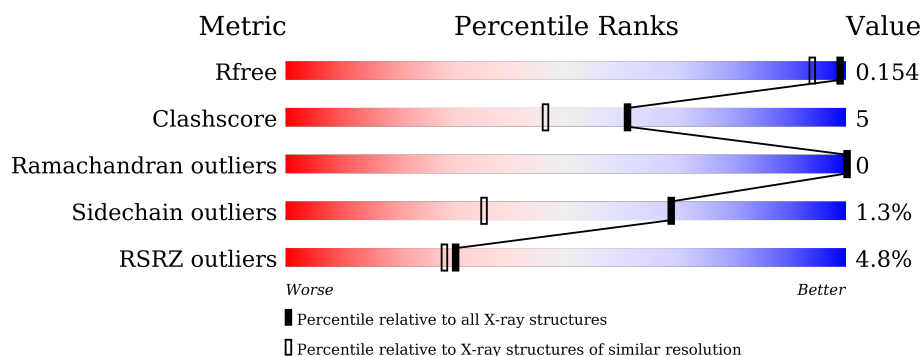
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)
RSRZ outliers	127900	1029 (1.30-1.30)

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	456	<div> <div>2%</div> <div>91%</div> <div>9%</div> </div>
1	B	456	<div> <div>7%</div> <div>92%</div> <div>8%</div> </div>
1	C	456	<div> <div>%</div> <div>91%</div> <div>9%</div> </div>
1	D	456	<div> <div>9%</div> <div>90%</div> <div>10%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	A	512	-	-	X	-
4	EDO	A	519	-	-	X	-
4	EDO	A	521	-	-	X	-
4	EDO	C	505	-	-	-	X
4	EDO	D	502	-	-	X	-
4	EDO	D	506	-	-	X	-
4	EDO	D	519	-	-	X	-

2 Entry composition [i](#)

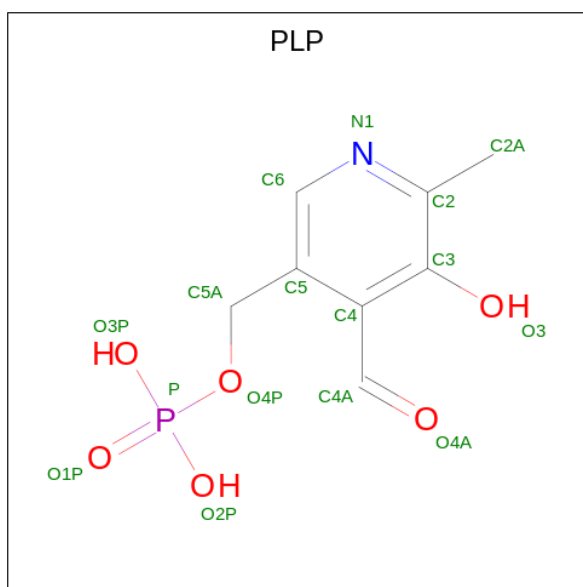
There are 6 unique types of molecules in this entry. The entry contains 17301 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Tyrosine phenol-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	456	Total	C	N	O	S	0	22	0
			3738	2378	629	702	29			
1	B	456	Total	C	N	O	S	0	19	0
			3708	2353	629	697	29			
1	C	456	Total	C	N	O	S	0	24	0
			3736	2378	631	698	29			
1	D	456	Total	C	N	O	S	5	20	0
			3731	2367	633	701	30			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P) (labeled as "Ligand of Interest" by depositor).



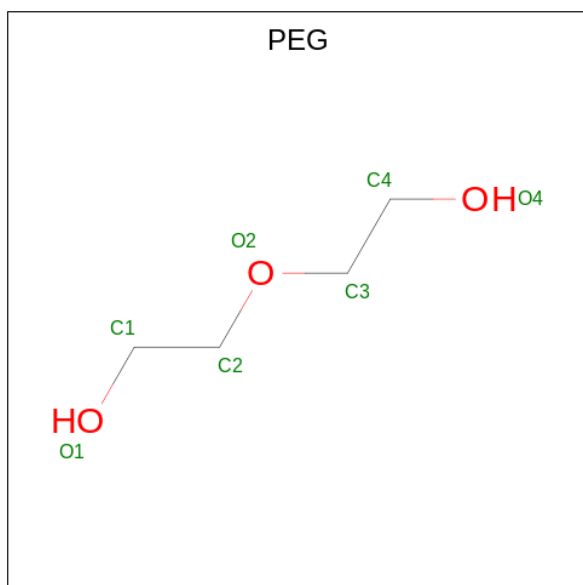
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			14	8	6		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	1
			8	4	4		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 8	C 4	O 4	0	1
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0

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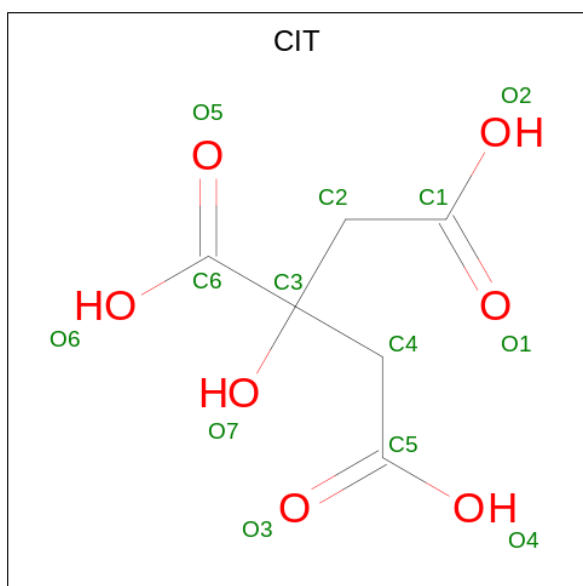
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 8 4 4	0	1
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 8 4 4	0	1
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0

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

- Molecule 5 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	6	7		

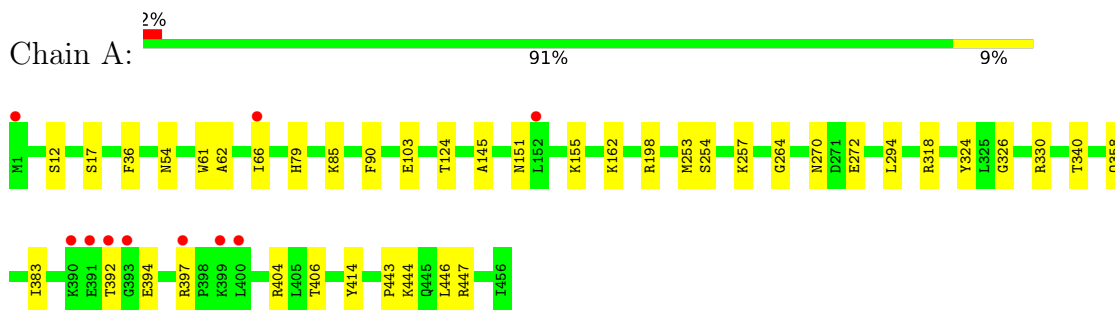
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	531	Total	O	0	2
			533	533		
6	B	466	Total	O	0	0
			466	466		
6	C	582	Total	O	0	4
			586	586		
6	D	463	Total	O	0	1
			464	464		

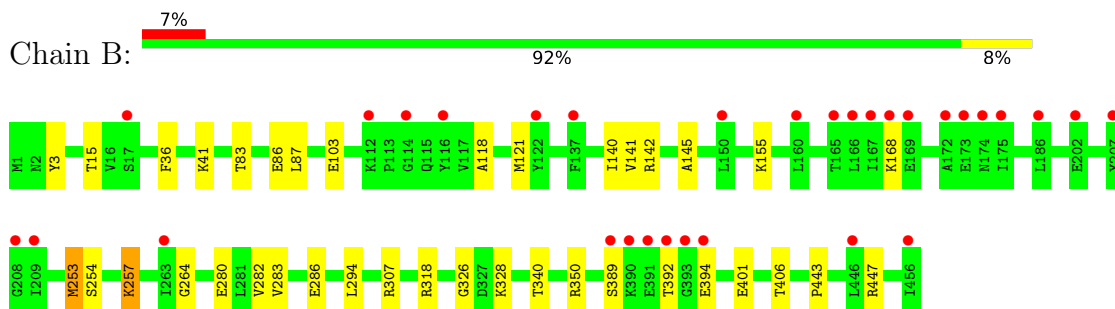
3 Residue-property plots [i](#)

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.

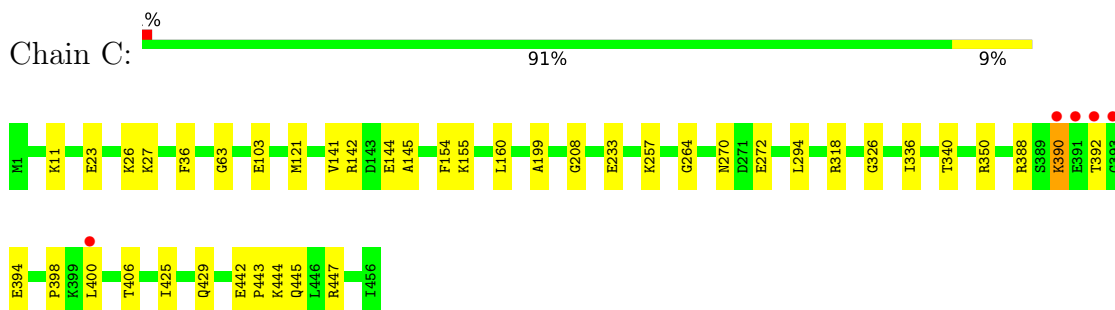
- Molecule 1: Tyrosine phenol-lyase



- Molecule 1: Tyrosine phenol-lyase

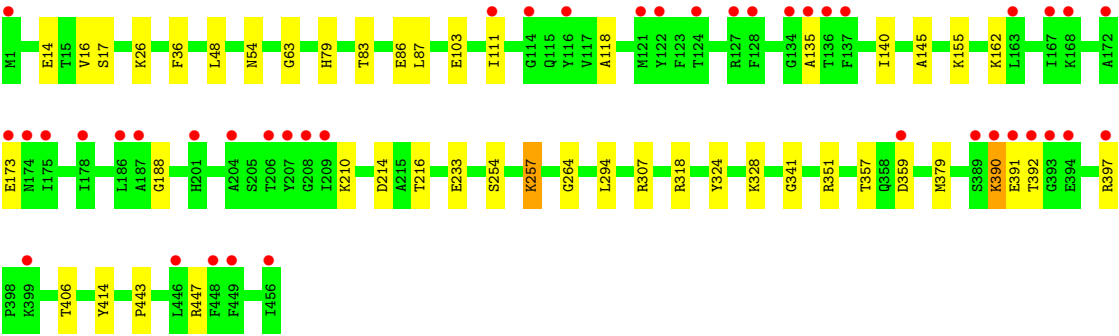


- Molecule 1: Tyrosine phenol-lyase



- Molecule 1: Tyrosine phenol-lyase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	111.52Å 161.08Å 100.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.84 – 1.30 45.84 – 1.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.84-1.30) 99.6 (45.84-1.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.30Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.128 , 0.155 0.128 , 0.154	Depositor DCC
R_{free} test set	22119 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	12.9	Xtriage
Anisotropy	0.338	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	17301	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, EDO, PLP, CIT

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	0.31	0/3876	0.57	0/5212
1	B	0.30	0/3838	0.55	0/5167
1	C	0.32	0/3884	0.57	0/5225
1	D	0.30	0/3850	0.55	0/5181
All	All	0.31	0/15448	0.56	0/20785

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	A	3738	0	3749	36	0
1	B	3708	0	3695	25	0
1	C	3736	0	3759	28	0
1	D	3731	0	3706	40	1
2	A	15	0	7	2	0
2	B	15	0	7	2	0
2	C	15	0	7	2	0
2	D	15	0	7	2	0
3	A	14	0	20	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	84	0	126	19	0
4	B	28	0	42	3	0
4	C	60	0	90	6	0
4	D	80	0	120	17	1
5	A	13	0	5	1	0
6	A	533	0	0	9	0
6	B	466	0	0	4	0
6	C	586	0	0	3	0
6	D	464	0	0	5	0
All	All	17301	0	15340	139	1

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 5.

All (139) 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:392:THR:HG23	1:A:394:GLU:H	1.52	0.75
1:D:16[A]:VAL:HA	4:D:506:EDO:H21	1.69	0.74
1:D:359[A]:ASP:OD1	1:D:397:ARG:NH1	2.21	0.74
1:B:328:LYS:HB3	4:B:507:EDO:H12	1.74	0.69
1:B:443:PRO:HG2	1:B:447:ARG:HA	1.74	0.69
1:B:392:THR:HG23	1:B:394:GLU:H	1.59	0.67
1:D:63:GLY:HA2	4:D:519:EDO:H21	1.77	0.66
1:C:145:ALA:HA	1:C:155[A]:LYS:HG2	1.78	0.65
1:C:443:PRO:HG2	1:C:447:ARG:HA	1.78	0.65
1:D:391:GLU:HG3	1:D:392:THR:HG23	1.79	0.64
4:A:504:EDO:O1	4:A:519:EDO:O2	2.15	0.64
4:C:509:EDO:H21	1:D:414:TYR:HB2	1.79	0.64
1:A:79:HIS:HB3	4:A:522:EDO:H22	1.80	0.64
1:A:358[A]:GLN:HG2	1:A:383:ILE:HD12	1.81	0.63
1:B:86:GLU:OE1	1:B:307[B]:ARG:NH2	2.31	0.63
1:B:83:THR:OG1	1:B:307[B]:ARG:NH1	2.32	0.62
4:D:502:EDO:H12	4:D:503:EDO:C1	2.31	0.61
1:C:160[B]:LEU:HD21	1:C:199:ALA:HB1	1.81	0.60
1:D:16[B]:VAL:HA	4:D:506:EDO:H21	1.81	0.60
1:D:79:HIS:HB3	4:D:518:EDO:H11	1.83	0.60
1:A:162:LYS:HA	4:A:518:EDO:H12	1.84	0.59
1:A:414:TYR:HB2	4:B:502:EDO:H12	1.84	0.59
1:D:86:GLU:OE1	1:D:307[B]:ARG:NH2	2.35	0.58
1:A:85[C]:LYS:HG3	6:A:893:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:307[B]:ARG:NH1	6:B:607:HOH:O	2.36	0.58
1:B:142[A]:ARG:HG2	1:B:142[A]:ARG:HH21	1.67	0.58
1:A:270:ASN:HD21	4:A:519:EDO:H21	1.69	0.57
4:A:512:EDO:H12	4:A:521:EDO:C2	2.34	0.57
1:A:90:PHE:CD1	4:A:519:EDO:H22	2.40	0.57
1:A:270:ASN:HD21	4:A:519:EDO:C2	2.19	0.56
1:A:145:ALA:HA	1:A:155[B]:LYS:HG2	1.87	0.56
1:A:62:ALA:HB1	4:D:519:EDO:H12	1.87	0.56
1:B:103:GLU:OE2	2:B:501:PLP:H6	2.07	0.55
1:A:66[B]:ILE:HD11	4:A:520:EDO:H12	1.89	0.55
1:B:41:LYS:NZ	6:B:606:HOH:O	2.35	0.54
4:D:502:EDO:H12	4:D:503:EDO:H11	1.90	0.54
1:A:103:GLU:OE1	2:A:501:PLP:H6	2.07	0.54
1:D:443:PRO:HG2	1:D:447:ARG:HA	1.90	0.54
1:A:54:ASN:O	4:A:512:EDO:H11	2.09	0.53
1:A:85[A]:LYS:HG3	6:A:893:HOH:O	2.07	0.53
1:A:198:ARG:NH1	6:A:608:HOH:O	2.35	0.53
1:D:63:GLY:CA	4:D:519:EDO:H21	2.38	0.53
1:B:142[A]:ARG:HD2	6:B:754:HOH:O	2.09	0.52
4:D:519:EDO:H22	6:D:782:HOH:O	2.09	0.52
1:D:210:LYS:NZ	6:D:611:HOH:O	2.38	0.52
1:C:392:THR:HG23	1:C:394:GLU:H	1.75	0.51
1:A:90:PHE:CE1	4:A:519:EDO:H22	2.46	0.51
1:B:389:SER:HB3	1:B:392:THR:HG22	1.93	0.51
1:D:390:LYS:H	1:D:390:LYS:HE3	1.76	0.51
1:C:121:MET:HE2	1:C:141:VAL:HG11	1.93	0.50
1:D:351:ARG:NH1	4:D:507[B]:EDO:O1	2.34	0.50
1:A:17[B]:SER:O	6:A:601:HOH:O	2.18	0.50
1:D:188:GLY:O	1:D:341:GLY:HA3	2.12	0.49
1:D:17[B]:SER:HB3	4:D:506:EDO:H12	1.94	0.49
1:D:26[A]:LYS:NZ	6:D:613:HOH:O	2.45	0.49
1:A:443:PRO:HG2	1:A:447:ARG:HA	1.95	0.49
1:A:61:TRP:CE2	3:A:502[B]:PEG:H11	2.48	0.49
1:D:54:ASN:O	4:D:502:EDO:H11	2.13	0.48
1:A:324:TYR:CE1	4:A:507[A]:EDO:H12	2.49	0.48
1:D:264:GLY:HA2	1:D:294:LEU:HD21	1.95	0.48
1:B:264:GLY:HA2	1:B:294:LEU:HD21	1.96	0.48
1:B:145:ALA:HA	1:B:155[B]:LYS:HG2	1.96	0.48
1:C:103:GLU:OE2	2:C:501:PLP:H6	2.13	0.48
1:C:264:GLY:HA2	1:C:294:LEU:HD21	1.96	0.48
1:C:326:GLY:HA3	1:C:340[B]:THR:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:GLU:O	1:B:283[B]:VAL:HG22	2.14	0.47
4:A:508:EDO:H22	6:A:1000:HOH:O	2.14	0.47
1:D:103:GLU:OE2	2:D:501:PLP:H6	2.14	0.47
1:A:272:GLU:OE1	6:A:602:HOH:O	2.20	0.47
1:D:324:TYR:CE1	1:D:328[A]:LYS:HE2	2.50	0.47
4:D:504[A]:EDO:H11	4:D:506:EDO:H22	1.96	0.47
1:B:121:MET:HE2	1:B:141:VAL:HG11	1.96	0.47
1:D:216[B]:THR:HG23	1:D:254:SER:HB3	1.97	0.47
1:A:326:GLY:HA3	1:A:340[B]:THR:HG21	1.95	0.47
1:A:124[B]:THR:HG23	6:A:963:HOH:O	2.15	0.47
1:C:272[A]:GLU:HG2	6:C:893:HOH:O	2.14	0.47
1:D:145:ALA:HA	1:D:155:LYS:HG2	1.96	0.46
1:A:257:LYS:NZ	2:A:501:PLP:O3	2.48	0.46
1:A:404:ARG:HD3	4:A:511:EDO:H12	1.98	0.46
1:C:23:GLU:HG3	1:C:27:LYS:HE2	1.98	0.46
5:A:523:CIT:O3	5:A:523:CIT:O7	2.27	0.46
1:A:253[B]:MET:HG3	1:A:254:SER:N	2.31	0.46
1:C:11:LYS:HB2	1:D:14[B]:GLU:HG3	1.98	0.45
1:C:26[B]:LYS:HA	1:C:26[B]:LYS:HD3	1.84	0.45
1:D:83:THR:OG1	1:D:307[B]:ARG:NH1	2.50	0.45
1:D:257:LYS:NZ	2:D:501:PLP:O3	2.47	0.45
1:C:208:GLY:O	4:C:510:EDO:H22	2.16	0.45
1:B:257:LYS:NZ	2:B:501:PLP:O3	2.50	0.45
1:D:118:ALA:HB1	1:D:140:ILE:HD13	1.98	0.45
1:D:357:THR:OG1	1:D:359[B]:ASP:OD1	2.25	0.45
1:B:253[A]:MET:HG3	1:B:254:SER:N	2.32	0.44
1:B:350:ARG:HG3	1:B:401:GLU:HB3	1.97	0.44
1:C:390:LYS:H	1:C:390:LYS:CD	2.30	0.44
1:D:14[B]:GLU:OE2	4:D:502:EDO:O2	2.29	0.44
1:D:173:GLU:H	1:D:173:GLU:CD	2.21	0.44
1:C:425:ILE:O	1:C:429[B]:GLN:HG2	2.16	0.44
1:C:233[A]:GLU:HG3	6:C:796:HOH:O	2.17	0.44
1:C:63:GLY:HA2	4:C:514:EDO:H12	2.00	0.44
1:B:87:LEU:HD11	1:B:307[B]:ARG:HG2	2.00	0.43
1:D:17[A]:SER:HB2	4:D:506:EDO:H12	2.01	0.43
1:A:151:ASN:ND2	4:A:508:EDO:H21	2.33	0.43
1:C:270:ASN:ND2	4:C:515:EDO:O1	2.48	0.43
4:A:521:EDO:H11	6:A:655:HOH:O	2.18	0.43
1:B:142[B]:ARG:HB2	6:B:647:HOH:O	2.17	0.43
1:C:257:LYS:NZ	2:C:501:PLP:O3	2.50	0.43
1:C:233[B]:GLU:HG3	4:C:512:EDO:H11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:444:LYS:HG3	1:C:445:GLN:HG3	2.00	0.43
1:D:48:LEU:HD12	1:D:379:MET:HB2	2.01	0.43
1:C:444:LYS:NZ	6:C:616:HOH:O	2.51	0.43
1:B:168:LYS:HB2	1:B:168:LYS:HE2	1.85	0.43
1:D:233:GLU:HG3	6:D:723:HOH:O	2.18	0.42
1:C:336:ILE:H	4:C:505:EDO:H12	1.83	0.42
1:D:63:GLY:N	4:D:519:EDO:H21	2.34	0.42
1:D:214:ASP:OD1	1:D:216[A]:THR:HG23	2.20	0.42
1:D:328[A]:LYS:HA	1:D:328[A]:LYS:HD3	1.90	0.42
1:A:162:LYS:HG2	4:A:518:EDO:H11	2.01	0.42
4:A:512:EDO:H12	4:A:521:EDO:H22	2.01	0.42
1:A:330:ARG:NH2	4:A:508:EDO:H11	2.35	0.42
1:B:282:VAL:HG22	1:B:286:GLU:HB2	2.02	0.42
1:C:350:ARG:NH1	1:C:398:PRO:O	2.53	0.42
1:D:111:ILE:HG21	1:D:135:ALA:HB2	2.02	0.42
1:A:358[A]:GLN:HB3	1:A:397:ARG:HH12	1.85	0.41
1:C:390:LYS:H	1:C:390:LYS:HD3	1.85	0.41
1:D:17[B]:SER:OG	1:D:17[B]:SER:O	2.32	0.41
1:A:444:LYS:HB2	1:A:444:LYS:HE3	1.89	0.41
1:B:118:ALA:HB1	1:B:140:ILE:HD13	2.02	0.41
1:A:264:GLY:HA2	1:A:294:LEU:HD21	2.02	0.41
1:D:87:LEU:HD11	1:D:307[B]:ARG:HG2	2.03	0.41
1:A:358[B]:GLN:HB2	1:A:397:ARG:HH12	1.86	0.41
1:D:16[A]:VAL:HG12	4:D:504[A]:EDO:O1	2.21	0.41
1:A:12:SER:OG	3:A:502[A]:PEG:H22	2.21	0.41
1:D:162:LYS:NZ	6:D:624:HOH:O	2.54	0.41
1:A:124[B]:THR:HG22	6:A:1039:HOH:O	2.20	0.41
1:B:3:TYR:HB2	4:B:505:EDO:H22	2.02	0.40
1:C:388[A]:ARG:HD2	1:C:442:GLU:OE2	2.22	0.40
1:B:326:GLY:HA3	1:B:340[B]:THR:HG21	2.04	0.40
4:A:512:EDO:H12	4:A:521:EDO:H21	2.02	0.40
1:C:142[A]:ARG:NH1	1:C:154:PHE:O	2.55	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:26[A]:LYS:NZ	4:D:512:EDO:O2[2_655]	1.30	0.90

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	477/456 (105%)	465 (98%)	12 (2%)	0	100	100
1	B	473/456 (104%)	465 (98%)	8 (2%)	0	100	100
1	C	479/456 (105%)	471 (98%)	8 (2%)	0	100	100
1	D	474/456 (104%)	466 (98%)	8 (2%)	0	100	100
All	All	1903/1824 (104%)	1867 (98%)	36 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	404/380 (106%)	400 (99%)	4 (1%)	76	48
1	B	399/380 (105%)	392 (98%)	7 (2%)	59	24
1	C	405/380 (107%)	400 (99%)	5 (1%)	71	40
1	D	400/380 (105%)	395 (99%)	5 (1%)	69	35
All	All	1608/1520 (106%)	1587 (99%)	21 (1%)	69	35

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	PHE
1	A	318	ARG

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Mol	Chain	Res	Type
1	A	406	THR
1	A	446	LEU
1	B	15	THR
1	B	36	PHE
1	B	253[A]	MET
1	B	253[B]	MET
1	B	257	LYS
1	B	318	ARG
1	B	406	THR
1	C	36	PHE
1	C	318	ARG
1	C	390	LYS
1	C	400	LEU
1	C	406	THR
1	D	36	PHE
1	D	257	LYS
1	D	318	ARG
1	D	390	LYS
1	D	406	THR

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

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](#)

70 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	EDO	D	508	-	3,3,3	0.49	0	2,2,2	0.24	0
4	EDO	D	515	-	3,3,3	0.42	0	2,2,2	0.52	0
4	EDO	A	516	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	A	506	-	3,3,3	0.48	0	2,2,2	0.40	0
4	EDO	B	508	-	3,3,3	0.60	0	2,2,2	0.14	0
4	EDO	C	515	-	3,3,3	0.37	0	2,2,2	0.58	0
4	EDO	D	502	-	3,3,3	0.64	0	2,2,2	0.54	0
4	EDO	C	509	-	3,3,3	0.45	0	2,2,2	0.54	0
4	EDO	D	503	-	3,3,3	0.56	0	2,2,2	0.48	0
4	EDO	A	503	-	3,3,3	0.47	0	2,2,2	0.12	0
2	PLP	A	501	1	15,15,16	0.97	1 (6%)	20,22,23	1.16	3 (15%)
4	EDO	C	511	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	D	511	-	3,3,3	0.47	0	2,2,2	0.28	0
4	EDO	A	509	-	3,3,3	0.46	0	2,2,2	0.18	0
4	EDO	B	502	-	3,3,3	0.50	0	2,2,2	0.13	0
4	EDO	C	502	-	3,3,3	0.45	0	2,2,2	0.25	0
5	CIT	A	523	-	12,12,12	1.05	0	17,17,17	1.63	3 (17%)
4	EDO	A	514	-	3,3,3	0.48	0	2,2,2	0.28	0
4	EDO	C	503[A]	-	3,3,3	0.48	0	2,2,2	0.36	0
4	EDO	C	503[B]	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	C	510	-	3,3,3	0.40	0	2,2,2	0.31	0
4	EDO	A	520	-	3,3,3	0.52	0	2,2,2	0.24	0
4	EDO	B	505	-	3,3,3	0.42	0	2,2,2	0.47	0
4	EDO	A	522	-	3,3,3	0.46	0	2,2,2	0.16	0
4	EDO	C	505	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	C	508	-	3,3,3	0.50	0	2,2,2	0.34	0
4	EDO	A	517	-	3,3,3	0.45	0	2,2,2	0.31	0
4	EDO	D	513	-	3,3,3	0.41	0	2,2,2	0.37	0
4	EDO	A	518	-	3,3,3	0.43	0	2,2,2	0.34	0
4	EDO	D	504[A]	-	3,3,3	0.39	0	2,2,2	0.42	0
4	EDO	D	504[B]	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	A	505	-	3,3,3	0.48	0	2,2,2	0.28	0
4	EDO	A	512	-	3,3,3	0.69	0	2,2,2	0.75	0
4	EDO	D	506	-	3,3,3	0.43	0	2,2,2	0.40	0
4	EDO	D	516	-	3,3,3	0.46	0	2,2,2	0.33	0
4	EDO	D	517	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	B	506	-	3,3,3	0.47	0	2,2,2	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	C	506	-	3,3,3	0.47	0	2,2,2	0.32	0
2	PLP	B	501	1	15,15,16	0.97	1 (6%)	20,22,23	1.01	1 (5%)
2	PLP	D	501	1	15,15,16	0.98	1 (6%)	20,22,23	0.98	1 (5%)
4	EDO	A	513	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	A	519	-	3,3,3	0.31	0	2,2,2	0.46	0
4	EDO	B	503	-	3,3,3	0.49	0	2,2,2	0.27	0
2	PLP	C	501	1	15,15,16	1.01	1 (6%)	20,22,23	1.40	4 (20%)
4	EDO	C	514	-	3,3,3	0.51	0	2,2,2	0.19	0
4	EDO	D	509	-	3,3,3	0.47	0	2,2,2	0.30	0
4	EDO	D	519	-	3,3,3	0.41	0	2,2,2	0.35	0
4	EDO	C	507	-	3,3,3	0.47	0	2,2,2	0.36	0
4	EDO	A	507[B]	-	3,3,3	0.46	0	2,2,2	0.30	0
4	EDO	D	514	-	3,3,3	0.38	0	2,2,2	0.47	0
4	EDO	A	511	-	3,3,3	0.41	0	2,2,2	0.30	0
4	EDO	D	512	-	3,3,3	0.47	0	2,2,2	0.32	0
4	EDO	A	507[A]	-	3,3,3	0.44	0	2,2,2	0.39	0
4	EDO	D	507[A]	-	3,3,3	0.45	0	2,2,2	0.35	0
4	EDO	D	507[B]	-	3,3,3	0.44	0	2,2,2	0.32	0
3	PEG	A	502[A]	-	6,6,6	1.46	0	5,5,5	0.77	0
3	PEG	A	502[B]	-	6,6,6	0.49	0	5,5,5	0.59	0
4	EDO	B	507	-	3,3,3	0.45	0	2,2,2	0.20	0
4	EDO	D	505	-	3,3,3	0.46	0	2,2,2	0.25	0
4	EDO	B	504	-	3,3,3	0.47	0	2,2,2	0.30	0
4	EDO	A	510	-	3,3,3	0.42	0	2,2,2	0.38	0
4	EDO	D	510	-	3,3,3	0.52	0	2,2,2	0.18	0
4	EDO	A	504	-	3,3,3	0.46	0	2,2,2	0.33	0
4	EDO	A	508	-	3,3,3	0.44	0	2,2,2	0.13	0
4	EDO	A	521	-	3,3,3	0.53	0	2,2,2	0.45	0
4	EDO	C	504	-	3,3,3	0.48	0	2,2,2	0.26	0
4	EDO	D	518	-	3,3,3	0.45	0	2,2,2	0.19	0
4	EDO	C	513	-	3,3,3	0.48	0	2,2,2	0.29	0
4	EDO	A	515	-	3,3,3	0.45	0	2,2,2	0.35	0
4	EDO	C	512	-	3,3,3	0.44	0	2,2,2	0.30	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
4	EDO	D	508	-	-	0/1/1/1	-
4	EDO	D	515	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	516	-	-	0/1/1/1	-
4	EDO	A	506	-	-	1/1/1/1	-
4	EDO	B	508	-	-	0/1/1/1	-
4	EDO	C	515	-	-	0/1/1/1	-
4	EDO	D	502	-	-	0/1/1/1	-
4	EDO	C	509	-	-	1/1/1/1	-
4	EDO	D	503	-	-	0/1/1/1	-
4	EDO	A	503	-	-	0/1/1/1	-
2	PLP	A	501	1	-	0/6/6/8	0/1/1/1
4	EDO	C	511	-	-	1/1/1/1	-
4	EDO	D	511	-	-	0/1/1/1	-
4	EDO	A	509	-	-	0/1/1/1	-
4	EDO	B	502	-	-	0/1/1/1	-
4	EDO	C	502	-	-	0/1/1/1	-
5	CIT	A	523	-	-	8/16/16/16	-
4	EDO	A	514	-	-	0/1/1/1	-
4	EDO	C	503[A]	-	-	0/1/1/1	-
4	EDO	C	503[B]	-	-	0/1/1/1	-
4	EDO	C	510	-	-	0/1/1/1	-
4	EDO	A	520	-	-	1/1/1/1	-
4	EDO	B	505	-	-	0/1/1/1	-
4	EDO	A	522	-	-	0/1/1/1	-
4	EDO	C	505	-	-	0/1/1/1	-
4	EDO	C	508	-	-	0/1/1/1	-
4	EDO	A	517	-	-	0/1/1/1	-
4	EDO	D	513	-	-	1/1/1/1	-
4	EDO	A	518	-	-	0/1/1/1	-
4	EDO	D	504[A]	-	-	0/1/1/1	-
4	EDO	D	504[B]	-	-	1/1/1/1	-
4	EDO	A	505	-	-	0/1/1/1	-
4	EDO	A	512	-	-	0/1/1/1	-
4	EDO	D	506	-	-	0/1/1/1	-
4	EDO	D	516	-	-	0/1/1/1	-
4	EDO	D	517	-	-	0/1/1/1	-
4	EDO	B	506	-	-	0/1/1/1	-
4	EDO	C	506	-	-	0/1/1/1	-
2	PLP	B	501	1	-	0/6/6/8	0/1/1/1
2	PLP	D	501	1	-	0/6/6/8	0/1/1/1
4	EDO	A	513	-	-	0/1/1/1	-
4	EDO	A	519	-	-	1/1/1/1	-
4	EDO	B	503	-	-	0/1/1/1	-
2	PLP	C	501	1	-	0/6/6/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	C	514	-	-	1/1/1/1	-
4	EDO	D	509	-	-	0/1/1/1	-
4	EDO	D	519	-	-	0/1/1/1	-
4	EDO	C	507	-	-	1/1/1/1	-
4	EDO	A	507[B]	-	-	0/1/1/1	-
4	EDO	D	514	-	-	1/1/1/1	-
4	EDO	A	511	-	-	0/1/1/1	-
4	EDO	D	512	-	-	0/1/1/1	-
4	EDO	A	507[A]	-	-	0/1/1/1	-
4	EDO	D	507[A]	-	-	0/1/1/1	-
4	EDO	D	507[B]	-	-	0/1/1/1	-
3	PEG	A	502[A]	-	-	0/4/4/4	-
3	PEG	A	502[B]	-	-	0/4/4/4	-
4	EDO	B	507	-	-	0/1/1/1	-
4	EDO	D	505	-	-	0/1/1/1	-
4	EDO	B	504	-	-	0/1/1/1	-
4	EDO	A	510	-	-	0/1/1/1	-
4	EDO	D	510	-	-	0/1/1/1	-
4	EDO	A	504	-	-	1/1/1/1	-
4	EDO	A	508	-	-	1/1/1/1	-
4	EDO	A	521	-	-	0/1/1/1	-
4	EDO	C	504	-	-	0/1/1/1	-
4	EDO	D	518	-	-	0/1/1/1	-
4	EDO	C	513	-	-	0/1/1/1	-
4	EDO	A	515	-	-	0/1/1/1	-
4	EDO	C	512	-	-	0/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	PLP	C2-N1	2.24	1.38	1.33
2	D	501	PLP	C2-N1	2.15	1.37	1.33
2	A	501	PLP	C2-N1	2.08	1.37	1.33
2	C	501	PLP	C2-N1	2.04	1.37	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	523	CIT	O6-C6-C3	4.45	120.78	113.05
2	C	501	PLP	O4P-C5A-C5	3.32	115.67	109.35
2	C	501	PLP	C4A-C4-C5	-2.77	118.08	120.94
2	A	501	PLP	O4P-C5A-C5	2.58	114.27	109.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	PLP	C5-C6-N1	-2.51	119.64	123.82
5	A	523	CIT	O2-C1-C2	2.24	121.53	114.35
2	B	501	PLP	O4P-C5A-C5	2.16	113.46	109.35
2	C	501	PLP	C6-C5-C4	2.10	119.81	118.16
2	A	501	PLP	C4A-C4-C5	-2.08	118.79	120.94
2	D	501	PLP	O4P-C5A-C5	2.08	113.31	109.35
2	A	501	PLP	C5-C6-N1	-2.04	120.41	123.82
5	A	523	CIT	O5-C6-C3	-2.00	119.42	122.25

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	523	CIT	O7-C3-C6-O5
5	A	523	CIT	O7-C3-C6-O6
5	A	523	CIT	C4-C3-C6-O5
5	A	523	CIT	C4-C3-C6-O6
4	A	506	EDO	O1-C1-C2-O2
4	A	508	EDO	O1-C1-C2-O2
4	A	520	EDO	O1-C1-C2-O2
4	C	509	EDO	O1-C1-C2-O2
4	C	511	EDO	O1-C1-C2-O2
4	C	514	EDO	O1-C1-C2-O2
4	A	519	EDO	O1-C1-C2-O2
4	D	513	EDO	O1-C1-C2-O2
4	D	504[B]	EDO	O1-C1-C2-O2
4	D	514	EDO	O1-C1-C2-O2
4	D	515	EDO	O1-C1-C2-O2
5	A	523	CIT	C1-C2-C3-O7
5	A	523	CIT	O7-C3-C4-C5
5	A	523	CIT	C6-C3-C4-C5
5	A	523	CIT	C2-C3-C4-C5
4	C	507	EDO	O1-C1-C2-O2
4	A	504	EDO	O1-C1-C2-O2

There are no ring outliers.

34 monomers are involved in 57 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	515	EDO	1	0
4	D	502	EDO	4	0

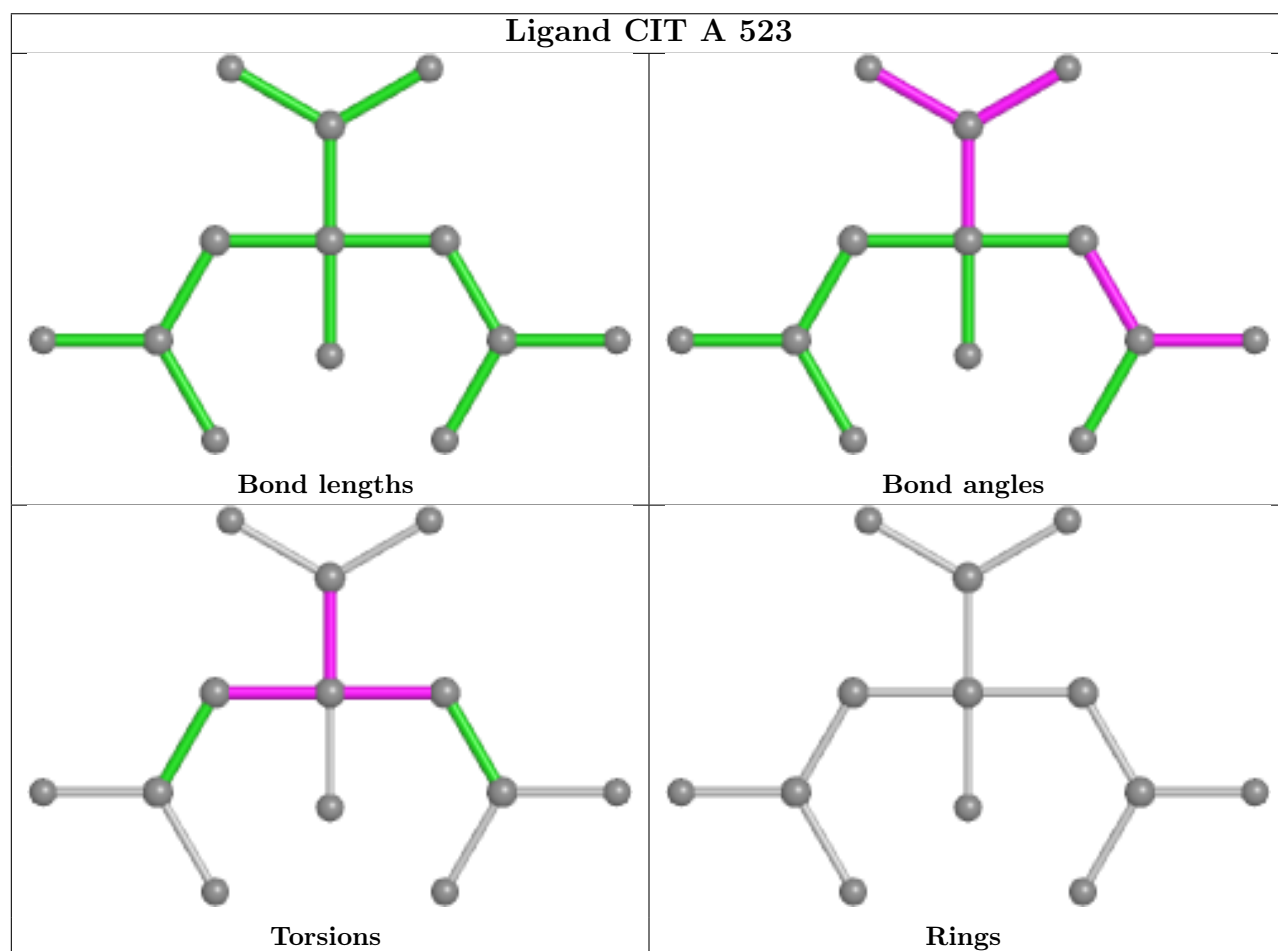
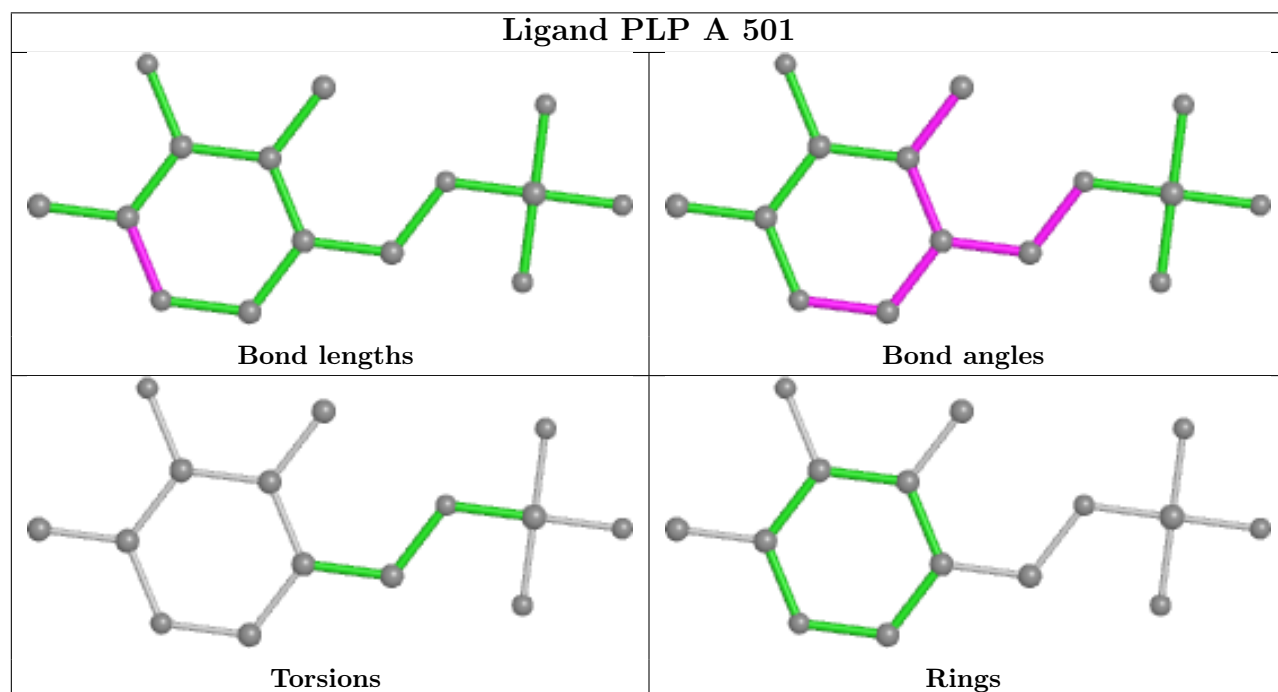
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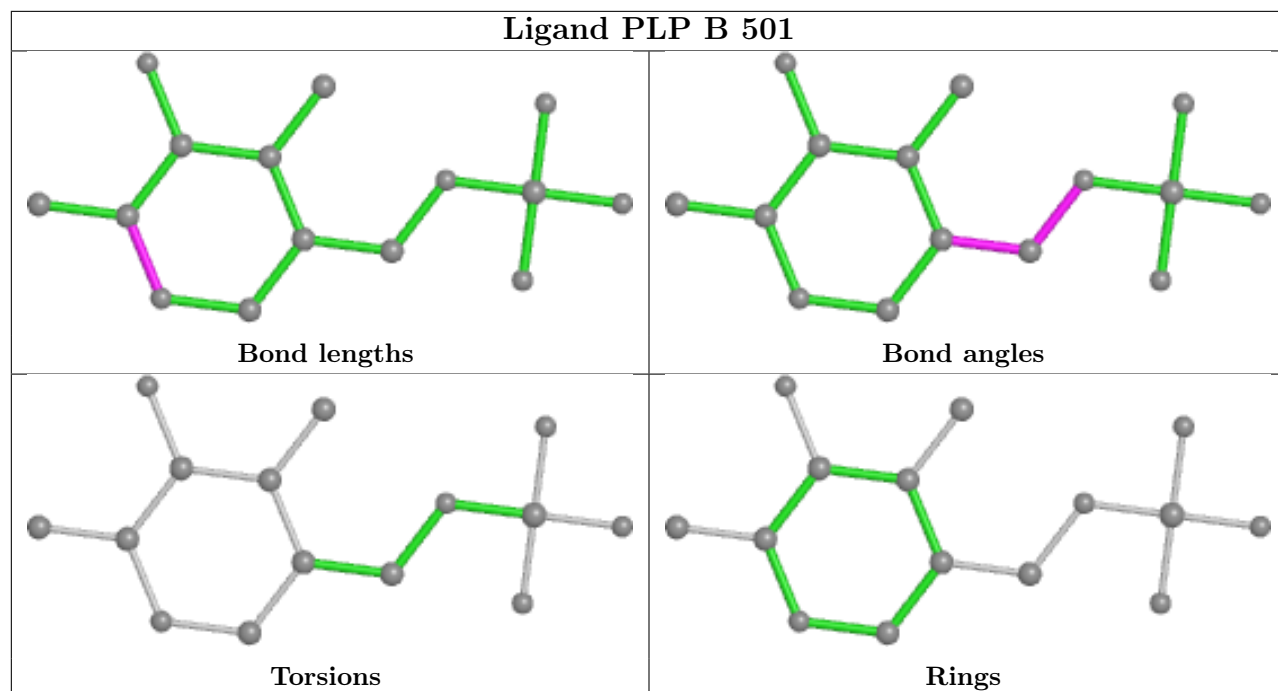
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	509	EDO	1	0
4	D	503	EDO	2	0
2	A	501	PLP	2	0
4	B	502	EDO	1	0
5	A	523	CIT	1	0
4	C	510	EDO	1	0
4	A	520	EDO	1	0
4	B	505	EDO	1	0
4	A	522	EDO	1	0
4	C	505	EDO	1	0
4	A	518	EDO	2	0
4	D	504[A]	EDO	2	0
4	A	512	EDO	4	0
4	D	506	EDO	5	0
2	B	501	PLP	2	0
2	D	501	PLP	2	0
4	A	519	EDO	5	0
2	C	501	PLP	2	0
4	C	514	EDO	1	0
4	D	519	EDO	5	0
4	A	511	EDO	1	0
4	D	512	EDO	0	1
4	A	507[A]	EDO	1	0
4	D	507[B]	EDO	1	0
3	A	502[A]	PEG	1	0
3	A	502[B]	PEG	1	0
4	B	507	EDO	1	0
4	A	504	EDO	1	0
4	A	508	EDO	3	0
4	A	521	EDO	4	0
4	D	518	EDO	1	0
4	C	512	EDO	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.

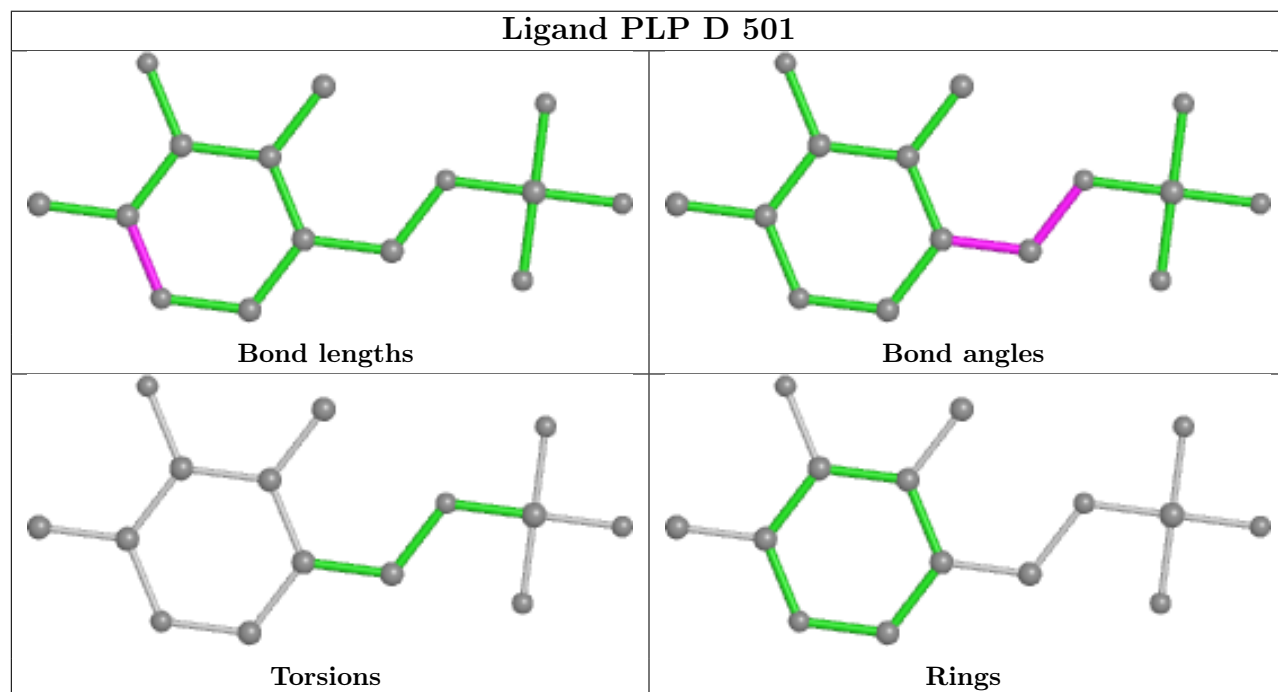
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

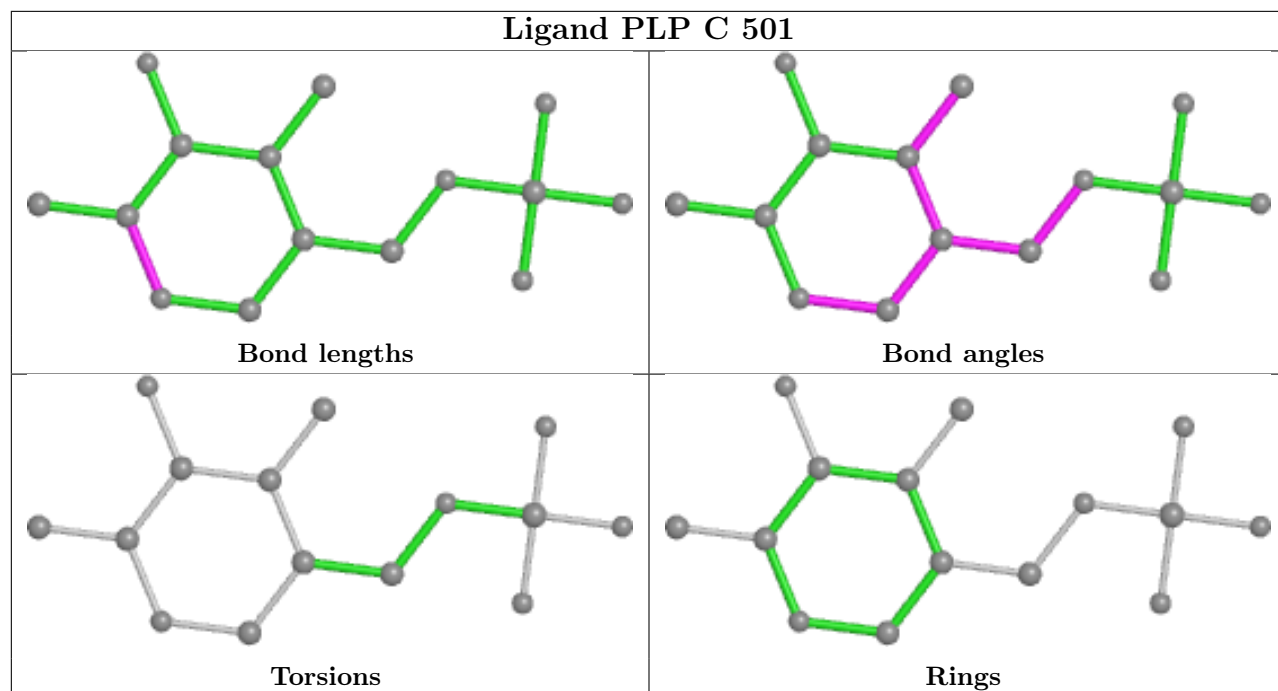


Ligand PLP B 501



Ligand PLP D 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	A	456/456 (100%)	-0.07	10 (2%) 62 61	9, 13, 25, 61	0
1	B	456/456 (100%)	0.29	31 (6%) 17 14	9, 18, 37, 58	0
1	C	456/456 (100%)	-0.09	5 (1%) 80 82	8, 13, 27, 67	0
1	D	456/456 (100%)	0.52	42 (9%) 9 6	9, 18, 37, 69	0
All	All	1824/1824 (100%)	0.16	88 (4%) 30 28	8, 16, 34, 69	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	207	TYR	7.4
1	D	390	LYS	7.1
1	C	392	THR	6.6
1	D	391	GLU	5.9
1	D	122	TYR	5.8
1	B	114	GLY	5.7
1	D	186	LEU	5.5
1	B	186	LEU	5.3
1	A	390	LYS	5.2
1	D	173	GLU	5.0
1	D	393	GLY	4.9
1	A	391	GLU	4.9
1	D	389	SER	4.8
1	A	399	LYS	4.8
1	D	135	ALA	4.8
1	B	168	LYS	4.6
1	D	392	THR	4.6
1	D	116	TYR	4.4
1	D	206	THR	4.3
1	C	391	GLU	4.3
1	D	397	ARG	4.3

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Mol	Chain	Res	Type	RSRZ
1	D	137	PHE	4.2
1	D	124	THR	4.2
1	A	400	LEU	4.2
1	D	134	GLY	3.8
1	D	399	LYS	3.8
1	D	128	PHE	3.8
1	D	207	TYR	3.6
1	D	172	ALA	3.5
1	A	393	GLY	3.4
1	D	208	GLY	3.4
1	D	359[A]	ASP	3.4
1	B	394	GLU	3.3
1	B	175	ILE	3.3
1	D	114	GLY	3.3
1	B	446	LEU	3.3
1	A	397	ARG	3.2
1	D	168	LYS	3.2
1	B	137	PHE	3.2
1	D	448	PHE	3.2
1	B	167	ILE	3.1
1	C	390	LYS	3.1
1	B	456	ILE	3.0
1	D	121	MET	2.9
1	B	208	GLY	2.9
1	B	116	TYR	2.8
1	D	136	THR	2.8
1	D	127	ARG	2.8
1	B	172	ALA	2.8
1	D	167	ILE	2.8
1	A	392	THR	2.8
1	D	394	GLU	2.8
1	B	390	LYS	2.8
1	D	178	ILE	2.7
1	B	165	THR	2.7
1	B	209	ILE	2.7
1	A	1	MET	2.7
1	D	456	ILE	2.7
1	B	112	LYS	2.6
1	B	389	SER	2.5
1	B	393	GLY	2.5
1	B	166	LEU	2.5
1	D	187	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	175	ILE	2.4
1	B	160	LEU	2.4
1	B	174	ASN	2.4
1	D	1	MET	2.4
1	B	173	GLU	2.4
1	D	446	LEU	2.4
1	D	209	ILE	2.3
1	D	163	LEU	2.3
1	B	122	TYR	2.3
1	C	400	LEU	2.3
1	B	169	GLU	2.3
1	D	174[A]	ASN	2.3
1	B	263	ILE	2.3
1	B	391	GLU	2.2
1	B	202[A]	GLU	2.2
1	A	66[A]	ILE	2.2
1	C	393	GLY	2.2
1	D	201	HIS	2.1
1	B	17	SER	2.1
1	B	150	LEU	2.1
1	D	111	ILE	2.1
1	A	152	LEU	2.0
1	D	204	ALA	2.0
1	B	392	THR	2.0
1	D	449	PHE	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 monosaccharides 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(\AA^2)	Q<0.9
4	EDO	D	511	4/4	0.23	0.24	54,55,55,55	0
4	EDO	A	509	4/4	0.45	0.25	44,45,46,47	0
4	EDO	C	505	4/4	0.51	0.73	62,62,62,63	0
4	EDO	B	506	4/4	0.54	0.34	53,54,54,54	0
4	EDO	D	515	4/4	0.54	0.19	44,44,44,44	0
4	EDO	D	507[B]	4/4	0.57	0.31	50,51,51,51	4
4	EDO	A	515	4/4	0.57	0.30	67,67,68,68	0
4	EDO	D	507[A]	4/4	0.57	0.31	49,49,49,49	4
4	EDO	C	507	4/4	0.59	0.15	44,44,44,45	0
4	EDO	A	520	4/4	0.60	0.33	40,40,40,40	0
4	EDO	B	505	4/4	0.62	0.19	46,46,47,48	0
4	EDO	A	514	4/4	0.62	0.16	52,53,53,53	0
4	EDO	C	513	4/4	0.62	0.15	44,45,46,46	0
4	EDO	C	515	4/4	0.62	0.25	28,31,32,35	0
4	EDO	B	502	4/4	0.66	0.26	37,38,40,42	0
4	EDO	B	507	4/4	0.66	0.17	48,48,48,49	0
4	EDO	C	514	4/4	0.67	0.23	30,32,32,32	0
4	EDO	A	504	4/4	0.68	0.22	40,41,42,43	0
4	EDO	D	506	4/4	0.68	0.26	51,53,54,55	0
4	EDO	A	508	4/4	0.68	0.22	50,50,51,51	0
3	PEG	A	502[B]	7/7	0.69	0.29	26,30,31,31	7
3	PEG	A	502[A]	7/7	0.69	0.29	15,19,21,24	7
4	EDO	C	506	4/4	0.69	0.20	47,48,49,49	0
4	EDO	D	519	4/4	0.70	0.17	33,33,33,34	0
4	EDO	D	509	4/4	0.71	0.20	51,52,52,53	0
4	EDO	D	518	4/4	0.71	0.20	43,43,44,45	0
4	EDO	A	517	4/4	0.71	0.20	52,53,54,54	0
4	EDO	D	504[B]	4/4	0.72	0.20	38,38,38,39	4
4	EDO	A	516	4/4	0.72	0.23	50,51,51,51	0
4	EDO	D	504[A]	4/4	0.72	0.20	36,36,37,37	4
4	EDO	A	513	4/4	0.73	0.15	55,55,56,56	0
4	EDO	C	512	4/4	0.74	0.27	52,52,53,53	0
4	EDO	A	506	4/4	0.74	0.13	32,33,33,34	0
4	EDO	D	512	4/4	0.76	0.28	66,66,67,67	0
4	EDO	C	511	4/4	0.76	0.24	52,52,52,52	0
4	EDO	D	516	4/4	0.78	0.18	54,55,55,56	0
4	EDO	A	511	4/4	0.78	0.23	38,38,39,40	0
4	EDO	A	510	4/4	0.78	0.22	59,59,59,60	0
4	EDO	A	522	4/4	0.79	0.16	30,32,32,35	0
4	EDO	A	519	4/4	0.80	0.29	32,32,34,34	0
5	CIT	A	523	13/13	0.80	0.17	28,32,37,38	0
4	EDO	B	504	4/4	0.83	0.16	31,34,35,35	0
4	EDO	D	503	4/4	0.83	0.14	15,16,18,18	0

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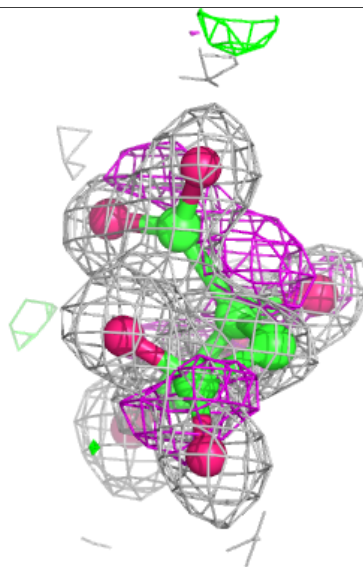
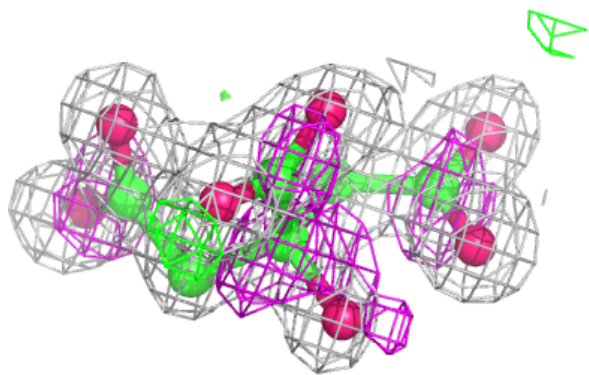
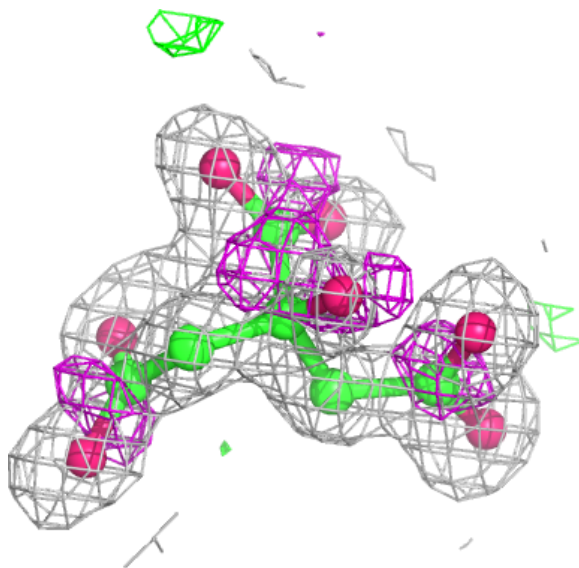
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	D	517	4/4	0.83	0.15	65,65,65,65	0
4	EDO	C	509	4/4	0.84	0.21	29,29,32,33	0
4	EDO	A	507[A]	4/4	0.84	0.12	36,37,38,39	4
4	EDO	A	507[B]	4/4	0.84	0.12	43,43,43,44	4
4	EDO	A	521	4/4	0.85	0.17	16,17,20,20	0
4	EDO	C	503[A]	4/4	0.85	0.17	15,19,19,20	4
4	EDO	C	503[B]	4/4	0.85	0.17	35,35,35,35	4
4	EDO	D	505	4/4	0.86	0.10	27,28,30,31	0
4	EDO	A	512	4/4	0.87	0.17	15,20,20,21	0
4	EDO	B	508	4/4	0.87	0.14	16,17,17,19	0
4	EDO	D	508	4/4	0.87	0.14	16,21,23,25	0
4	EDO	D	513	4/4	0.89	0.14	33,34,35,35	0
4	EDO	D	514	4/4	0.89	0.15	33,35,36,36	0
4	EDO	D	502	4/4	0.89	0.16	17,22,22,23	0
4	EDO	D	510	4/4	0.89	0.14	23,25,26,26	0
4	EDO	A	518	4/4	0.90	0.29	41,42,42,42	0
4	EDO	C	508	4/4	0.92	0.12	19,22,23,23	0
4	EDO	C	510	4/4	0.92	0.23	24,28,32,35	0
4	EDO	B	503	4/4	0.94	0.13	17,20,22,23	0
4	EDO	C	504	4/4	0.95	0.07	24,25,25,26	0
4	EDO	C	502	4/4	0.96	0.06	16,19,19,20	0
4	EDO	A	503	4/4	0.96	0.06	16,19,22,22	0
4	EDO	A	505	4/4	0.97	0.06	17,17,17,18	0
2	PLP	D	501	15/16	0.97	0.09	17,25,28,28	0
2	PLP	B	501	15/16	0.98	0.08	15,18,23,24	0
2	PLP	C	501	15/16	0.98	0.06	10,12,17,18	0
2	PLP	A	501	15/16	0.98	0.07	10,12,17,19	0

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

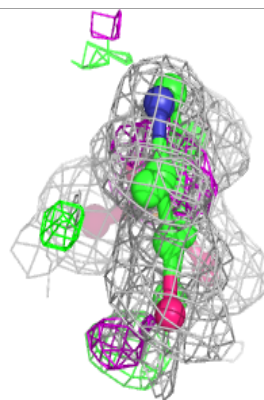
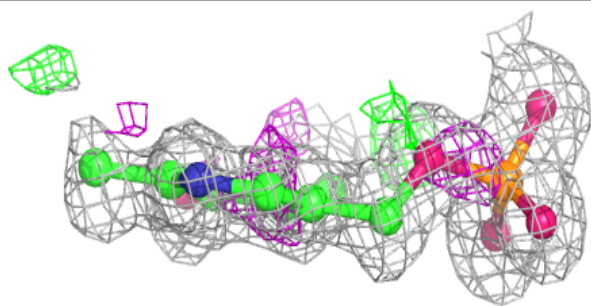
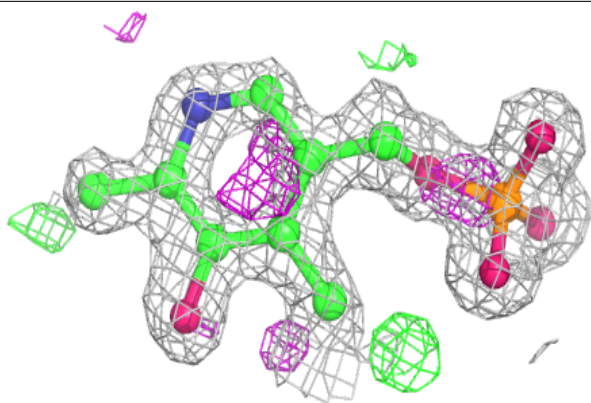
Electron density around CIT A 523:

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

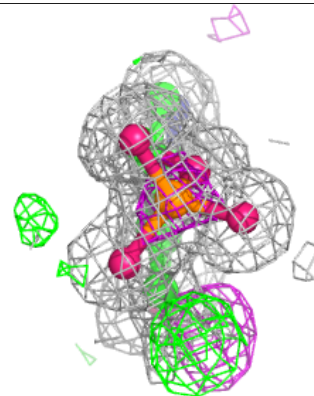
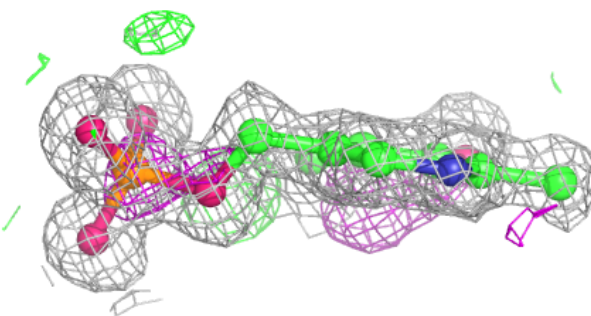
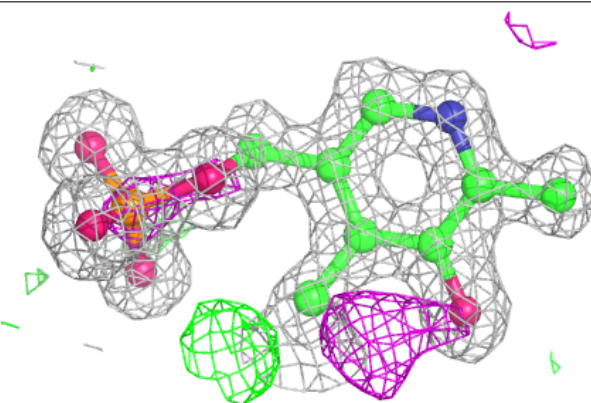


Electron density around PLP D 501:

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

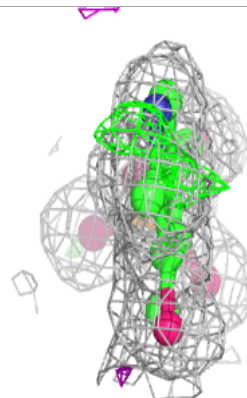
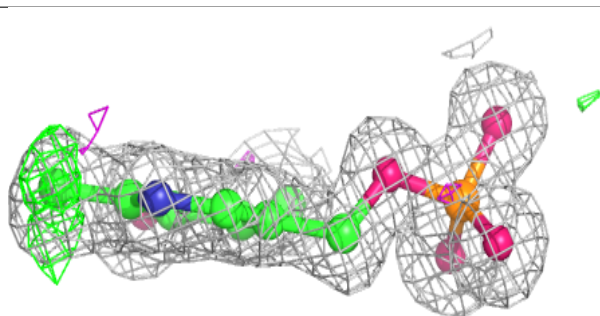
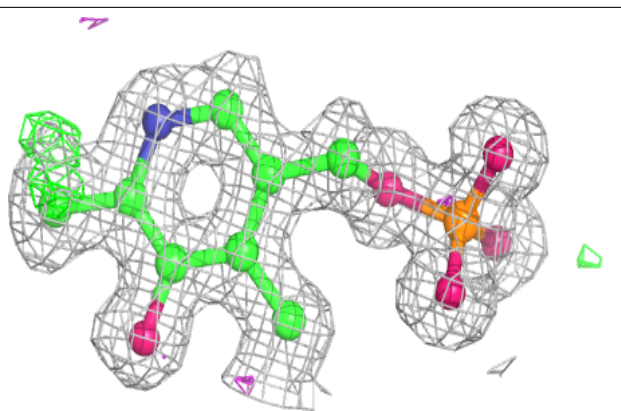
**Electron density around PLP B 501:**

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

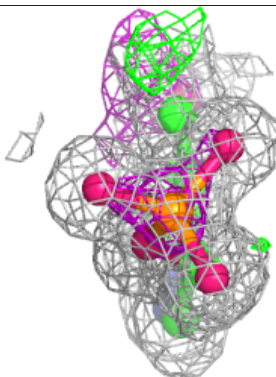
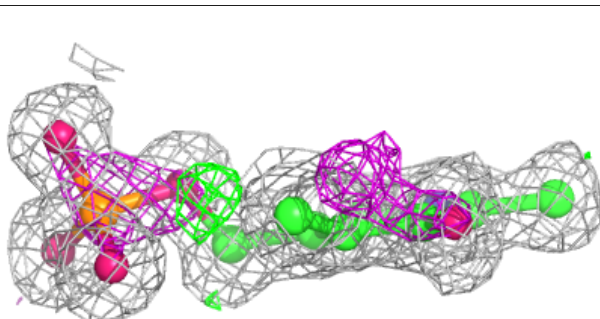
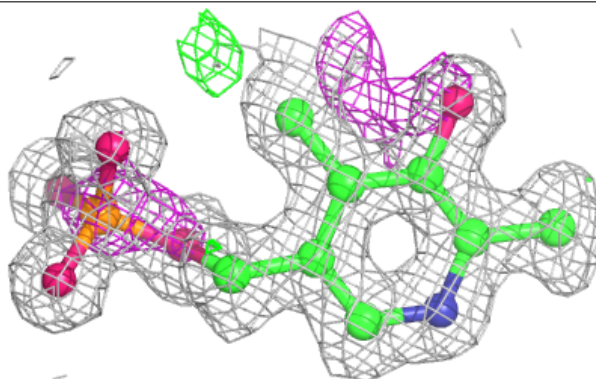


Electron density around PLP C 501:

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

**Electron density around PLP A 501:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.