



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2018 – 07:54 AM EDT

PDB ID : 6C9B
Title : The structure of MppP soaked with the products 4HKA and 2KA
Authors : Han, L.; Silvaggi, N.R.
Deposited on : 2018-01-26
Resolution : 1.69 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : rb-20031172
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031172

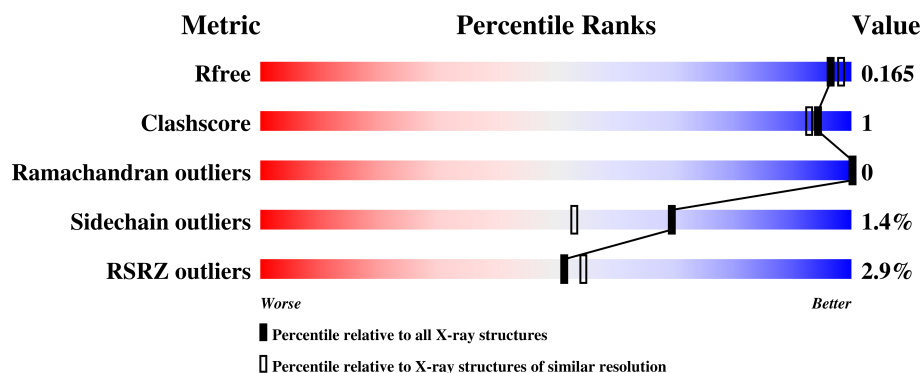
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 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}	111664	5816 (1.70-1.66)
Clashscore	122126	6305 (1.70-1.66)
Ramachandran outliers	120053	6198 (1.70-1.66)
Sidechain outliers	120020	6197 (1.70-1.66)
RSRZ outliers	108989	5700 (1.70-1.66)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	376	<div> <div>3%</div> <div>87% 7% 6%</div> </div>
1	B	376	<div> <div>3%</div> <div>94% 5%</div> </div>
1	C	376	<div> <div>%</div> <div>93% 6%</div> </div>
1	D	376	<div> <div>4%</div> <div>90% 6%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 23097 atoms, of which 10937 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.

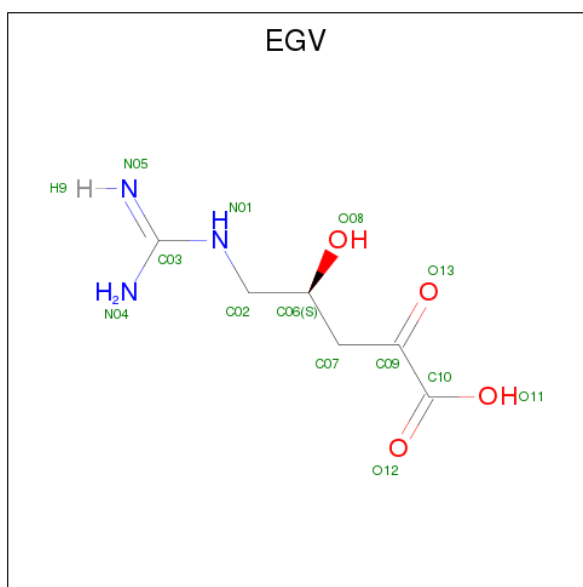
- Molecule 1 is a protein called PLP-Dependent L-Arginine Hydroxylase MppP.

Mol	Chain	Residues	Atoms								ZeroOcc	AltConf	Trace
1	A	353	Total	C	H	N	O	P	S		0	0	0
			5435	1726	2690	487	524	1	7				
1	B	369	Total	C	H	N	O	P	S		0	4	0
			5733	1822	2838	510	555	1	7				
1	C	353	Total	C	H	N	O	P	S		0	1	0
			5436	1726	2691	487	524	1	7				
1	D	353	Total	C	H	N	O	P	S		0	4	0
			5470	1735	2708	492	527	1	7				

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		

- Molecule 3 is (4S)-5-carbamimidamido-4-hydroxy-2-oxopentanoic acid (three-letter code: EGV) (formula: C₆H₁₁N₃O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	0	0
			23	6	10	3	4		

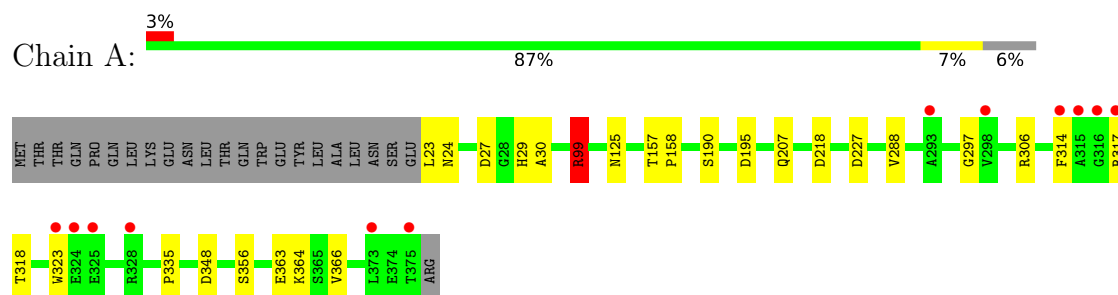
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	239	Total	O	0	0
			239	239		
4	B	256	Total	O	0	0
			256	256		
4	C	245	Total	O	0	0
			245	245		
4	D	257	Total	O	0	0
			257	257		

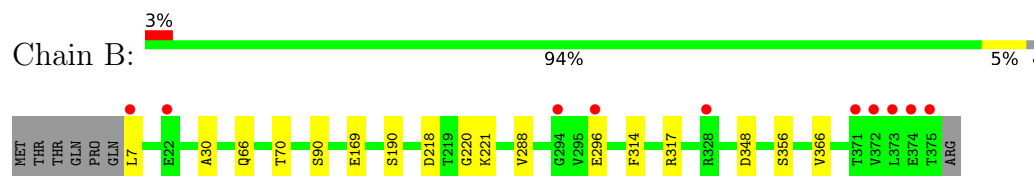
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

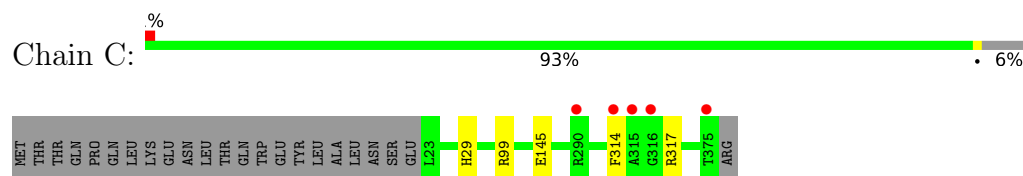
• Molecule 1: PLP-Dependent L-Arginine Hydroxylase MppP



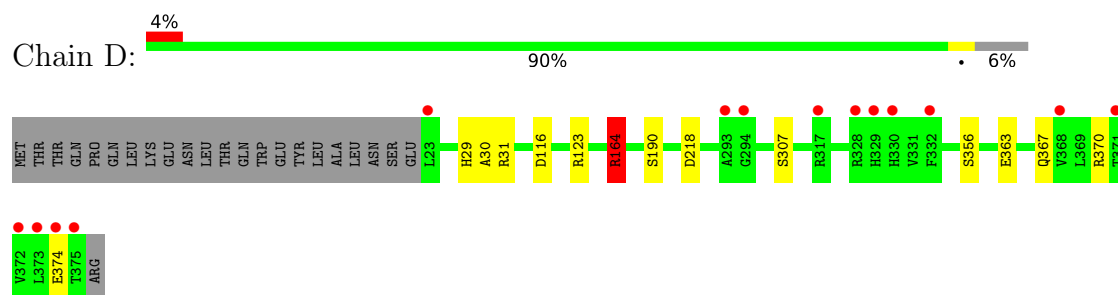
• Molecule 1: PLP-Dependent L-Arginine Hydroxylase MppP



• Molecule 1: PLP-Dependent L-Arginine Hydroxylase MppP



• Molecule 1: PLP-Dependent L-Arginine Hydroxylase MppP



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.11Å 108.83Å 195.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.79 – 1.69 48.79 – 1.69	Depositor EDS
% Data completeness (in resolution range)	97.0 (48.79-1.69) 97.0 (48.79-1.69)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 1.69Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.151 , 0.165 0.151 , 0.165	Depositor DCC
R_{free} test set	1998 reflections (1.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.7	Xtriage
Anisotropy	0.376	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	23097	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LLP, EGV, CL

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	0.43	0/2778	0.62	1/3782 (0.0%)
1	B	0.43	0/2949	0.62	0/4015
1	C	0.44	0/2787	0.63	1/3794 (0.0%)
1	D	0.44	0/2813	0.66	1/3828 (0.0%)
All	All	0.43	0/11327	0.63	3/15419 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	164	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	A	99	ARG	NE-CZ-NH1	-5.98	117.31	120.30
1	C	99	ARG	NE-CZ-NH2	-5.14	117.73	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2745	2690	2690	13	0
1	B	2895	2838	2823	9	0
1	C	2745	2691	2684	1	0
1	D	2762	2708	2696	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	B	13	10	0	0	0
4	A	239	0	0	3	0
4	B	256	0	0	4	0
4	C	245	0	0	1	0
4	D	257	0	0	2	0
All	All	12160	10937	10893	31	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (31) 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:27:ASP:OD2	4:A:501:HOH:O	2.13	0.66
1:B:90:SER:HB3	1:B:221:LLP:H5'2	1.81	0.62
1:C:145:GLU:OE2	4:C:501:HOH:O	2.17	0.59
1:A:99:ARG:HG2	1:A:125:ASN:OD1	2.07	0.55
1:B:169:GLU:HG2	4:B:663:HOH:O	2.08	0.54
1:D:164:ARG:HH11	1:D:164:ARG:HG3	1.76	0.50
1:D:370:ARG:O	1:D:374:GLU:HG3	2.13	0.49
1:D:363:GLU:O	1:D:367:GLN:HG2	2.14	0.47
1:D:116:ASP:OD2	4:D:501:HOH:O	2.20	0.47
1:D:30:ALA:HA	1:D:356:SER:HB3	1.96	0.47
1:A:30:ALA:HA	1:A:356:SER:HB3	1.97	0.46
1:D:190:SER:HA	1:D:218:ASP:HB3	1.98	0.46
1:A:297:GLY:O	1:A:314:PHE:HA	2.16	0.45
1:A:318:THR:HA	1:A:348:ASP:O	2.16	0.44
1:B:220:GLY:O	4:B:502:HOH:O	2.21	0.44
1:B:30:ALA:HA	1:B:356:SER:HB3	1.99	0.44
1:D:123:ARG:NH2	4:D:515:HOH:O	2.51	0.42
1:B:169:GLU:CG	4:B:663:HOH:O	2.64	0.42
1:A:27:ASP:HB3	4:A:501:HOH:O	2.18	0.42
1:B:288:VAL:HG22	1:B:366:VAL:HG11	2.02	0.42
1:B:7:LEU:N	4:B:512:HOH:O	2.52	0.42
1:B:190:SER:HA	1:B:218:ASP:HB3	2.02	0.42
1:A:207:GLN:NE2	4:A:504:HOH:O	2.41	0.41
1:B:66:GLN:O	1:B:70:THR:HG23	2.20	0.41
1:A:195:ASP:OD1	1:A:306:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:VAL:HG22	1:A:366:VAL:HG21	2.02	0.41
1:A:323:TRP:CD1	1:A:335:PRO:HD3	2.56	0.41
1:A:190:SER:HA	1:A:218:ASP:HB3	2.03	0.41
1:A:157:THR:HA	1:A:158:PRO:C	2.41	0.41
1:A:23:LEU:HB3	1:A:24:ASN:H	1.78	0.40
1:D:164:ARG:NH1	1:D:164:ARG:HG3	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	350/376 (93%)	344 (98%)	6 (2%)	0	100	100
1	B	370/376 (98%)	360 (97%)	10 (3%)	0	100	100
1	C	351/376 (93%)	345 (98%)	6 (2%)	0	100	100
1	D	354/376 (94%)	349 (99%)	5 (1%)	0	100	100
All	All	1425/1504 (95%)	1398 (98%)	27 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	292/314 (93%)	286 (98%)	6 (2%)	56	35
1	B	311/314 (99%)	307 (99%)	4 (1%)	71	56
1	C	293/314 (93%)	290 (99%)	3 (1%)	78	67
1	D	296/314 (94%)	292 (99%)	4 (1%)	69	53
All	All	1192/1256 (95%)	1175 (99%)	17 (1%)	69	53

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

Mol	Chain	Res	Type
1	A	29	HIS
1	A	99	ARG
1	A	227	ASP
1	A	317	ARG
1	A	363	GLU
1	A	364	LYS
1	B	296	GLU
1	B	314	PHE
1	B	317	ARG
1	B	348	ASP
1	C	29	HIS
1	C	314	PHE
1	C	317	ARG
1	D	29	HIS
1	D	31	ARG
1	D	164	ARG
1	D	307	SER

Some 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 ⓘ

4 non-standard protein/DNA/RNA residues 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
1	LLP	A	221	1	24,24,25	1.35	2 (8%)	28,32,34	1.37	6 (21%)
1	LLP	B	221	1	24,24,25	1.09	2 (8%)	28,32,34	1.96	6 (21%)
1	LLP	C	221	1	24,24,25	1.24	3 (12%)	28,32,34	1.54	5 (17%)
1	LLP	D	221	1	24,24,25	1.12	2 (8%)	28,32,34	1.50	5 (17%)

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
1	LLP	A	221	1	-	0/15/17/19	0/1/1/1
1	LLP	B	221	1	-	0/15/17/19	0/1/1/1
1	LLP	C	221	1	-	0/15/17/19	0/1/1/1
1	LLP	D	221	1	-	0/15/17/19	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	221	LLP	OP4-C5'	-2.98	1.33	1.44
1	D	221	LLP	OP4-C5'	-2.33	1.35	1.44
1	C	221	LLP	CA-C	2.43	1.53	1.50
1	B	221	LLP	C3-C2	2.93	1.42	1.40
1	C	221	LLP	C3-C2	3.16	1.42	1.40
1	C	221	LLP	O-C	3.50	1.34	1.19
1	D	221	LLP	O-C	3.69	1.35	1.19
1	A	221	LLP	O-C	3.72	1.35	1.19
1	A	221	LLP	C3-C2	4.04	1.43	1.40

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	221	LLP	C5'-C5-C6	-5.51	110.08	119.34
1	B	221	LLP	OP3-P-OP4	-3.68	96.94	106.73
1	B	221	LLP	C3-C4-C5	-3.65	115.46	118.24
1	D	221	LLP	C5'-C5-C6	-3.31	113.78	119.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	221	LLP	CB-CA-C	-3.28	105.59	111.85
1	D	221	LLP	C3-C4-C5	-3.18	115.82	118.24
1	C	221	LLP	O-C-CA	-3.05	116.60	124.96
1	A	221	LLP	C5'-C5-C6	-2.99	114.31	119.34
1	C	221	LLP	OP2-P-OP4	-2.91	98.98	106.73
1	D	221	LLP	CB-CA-C	-2.80	106.51	111.85
1	C	221	LLP	C5'-C5-C6	-2.45	115.22	119.34
1	D	221	LLP	O-C-CA	-2.42	118.32	124.96
1	B	221	LLP	CB-CA-C	-2.18	107.70	111.85
1	A	221	LLP	O-C-CA	-2.16	119.03	124.96
1	A	221	LLP	OP2-P-OP4	-2.13	101.07	106.73
1	A	221	LLP	CB-CA-C	-2.05	107.94	111.85
1	D	221	LLP	C5'-C5-C4	2.06	125.26	121.66
1	A	221	LLP	OP4-C5'-C5	2.36	113.92	109.39
1	B	221	LLP	OP4-C5'-C5	2.42	114.04	109.39
1	C	221	LLP	C5'-C5-C4	2.56	126.14	121.66
1	A	221	LLP	C5'-C5-C4	3.26	127.36	121.66
1	B	221	LLP	C5'-C5-C4	4.33	129.24	121.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	221	LLP	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	$\# Z > 2$
3	EGV	B	401	-	9,12,12	2.21	3 (33%)	8,15,15	0.71	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	EGV	B	401	-	-	0/9/13/13	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	EGV	O08-C06	-2.04	1.37	1.43
3	B	401	EGV	C07-C09	3.21	1.55	1.51
3	B	401	EGV	C03-N01	5.05	1.43	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	352/376 (93%)	-0.10	12 (3%) 45 48	16, 28, 58, 75	0
1	B	368/376 (97%)	-0.19	10 (2%) 54 57	16, 26, 59, 89	0
1	C	352/376 (93%)	-0.25	5 (1%) 75 79	14, 27, 52, 82	0
1	D	352/376 (93%)	-0.19	14 (3%) 38 41	13, 27, 60, 81	0
All	All	1424/1504 (94%)	-0.18	41 (2%) 51 54	13, 27, 58, 89	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	375	THR	7.2
1	A	315	ALA	6.4
1	D	375	THR	6.1
1	B	294	GLY	5.2
1	A	316	GLY	5.1
1	D	373	LEU	4.9
1	B	372	VAL	4.8
1	A	293	ALA	4.6
1	C	315	ALA	4.5
1	B	7	LEU	4.4
1	A	375	THR	4.2
1	B	373	LEU	4.2
1	D	372	VAL	3.9
1	A	314	PHE	3.7
1	D	328	ARG	3.2
1	B	371	THR	3.1
1	C	375	THR	3.0
1	A	328	ARG	3.0
1	B	296	GLU	2.9
1	D	368	VAL	2.8
1	A	298	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	314	PHE	2.8
1	D	317	ARG	2.7
1	B	374	GLU	2.7
1	D	332	PHE	2.7
1	A	325	GLU	2.6
1	C	316	GLY	2.6
1	D	293	ALA	2.6
1	D	371	THR	2.6
1	D	374	GLU	2.5
1	D	329	HIS	2.4
1	D	294	GLY	2.4
1	C	290	ARG	2.3
1	D	23	LEU	2.3
1	D	330	HIS	2.3
1	A	373	LEU	2.2
1	B	328	ARG	2.2
1	B	22	GLU	2.2
1	A	317	ARG	2.1
1	A	323	TRP	2.1
1	A	324	GLU	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	LLP	A	221	24/25	0.98	0.09	18,29,37,43	0
1	LLP	C	221	24/25	0.98	0.09	19,27,41,44	0
1	LLP	B	221	24/25	0.98	0.09	17,26,41,45	0
1	LLP	D	221	24/25	0.98	0.10	16,25,38,40	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CL	C	401	1/1	0.92	0.21	33,33,33,33	0
3	EGV	B	401	13/13	0.94	0.13	19,49,62,66	0
2	CL	A	401	1/1	0.94	0.16	36,36,36,36	0
2	CL	D	401	1/1	0.98	0.08	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.