



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:36 AM UTC

PDB ID : 3B8T / pdb_00003b8t
Title : Crystal structure of Escherichia coli alaine racemase mutant P219A
Authors : Wu, D.; Hu, T.; Zhang, L.; Jiang, H.; Shen, X.
Deposited on : 2007-11-02
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

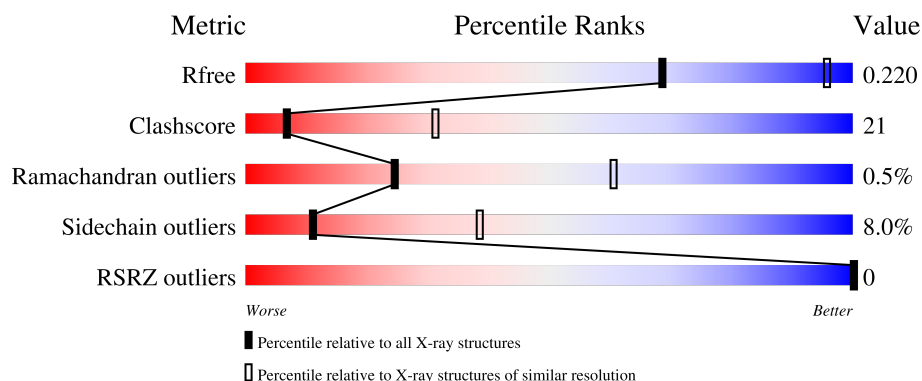
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	379	 66% 25% 5% 5%
1	B	379	 65% 27% 5% 5%
1	C	379	 54% 32% 6% 8%
1	D	379	 50% 36% 6% 7%

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
3	PLP	C	1001	-	X	-	-
3	PLP	D	1001	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11336 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 Alanine racemase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	0	0
			2752	1732	498	507	15			
1	B	359	Total	C	N	O	S	0	0	0
			2752	1732	498	507	15			
1	C	350	Total	C	N	O	S	0	0	0
			2682	1692	485	492	13			
1	D	351	Total	C	N	O	S	0	0	0
			2690	1693	487	495	15			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P0A6B4
A	-18	GLY	-	expression tag	UNP P0A6B4
A	-17	SER	-	expression tag	UNP P0A6B4
A	-16	SER	-	expression tag	UNP P0A6B4
A	-15	HIS	-	expression tag	UNP P0A6B4
A	-14	HIS	-	expression tag	UNP P0A6B4
A	-13	HIS	-	expression tag	UNP P0A6B4
A	-12	HIS	-	expression tag	UNP P0A6B4
A	-11	HIS	-	expression tag	UNP P0A6B4
A	-10	HIS	-	expression tag	UNP P0A6B4
A	-9	SER	-	expression tag	UNP P0A6B4
A	-8	SER	-	expression tag	UNP P0A6B4
A	-7	GLY	-	expression tag	UNP P0A6B4
A	-6	LEU	-	expression tag	UNP P0A6B4
A	-5	VAL	-	expression tag	UNP P0A6B4
A	-4	PRO	-	expression tag	UNP P0A6B4
A	-3	ARG	-	expression tag	UNP P0A6B4
A	-2	GLY	-	expression tag	UNP P0A6B4
A	-1	SER	-	expression tag	UNP P0A6B4
A	0	HIS	-	expression tag	UNP P0A6B4
A	219	ALA	PRO	engineered mutation	UNP P0A6B4

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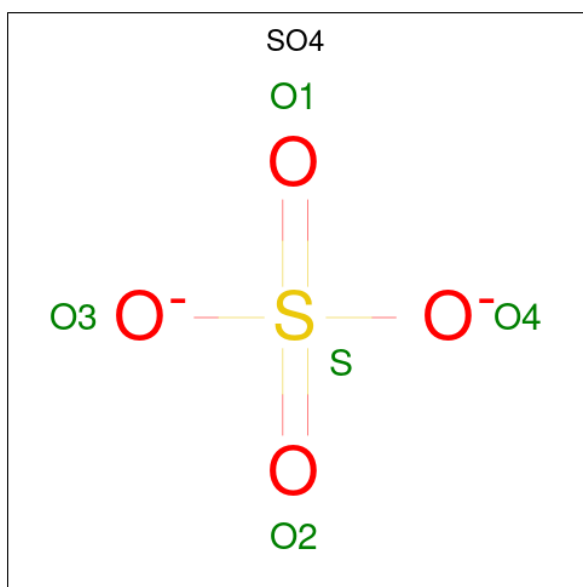
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	expression tag	UNP P0A6B4
B	-18	GLY	-	expression tag	UNP P0A6B4
B	-17	SER	-	expression tag	UNP P0A6B4
B	-16	SER	-	expression tag	UNP P0A6B4
B	-15	HIS	-	expression tag	UNP P0A6B4
B	-14	HIS	-	expression tag	UNP P0A6B4
B	-13	HIS	-	expression tag	UNP P0A6B4
B	-12	HIS	-	expression tag	UNP P0A6B4
B	-11	HIS	-	expression tag	UNP P0A6B4
B	-10	HIS	-	expression tag	UNP P0A6B4
B	-9	SER	-	expression tag	UNP P0A6B4
B	-8	SER	-	expression tag	UNP P0A6B4
B	-7	GLY	-	expression tag	UNP P0A6B4
B	-6	LEU	-	expression tag	UNP P0A6B4
B	-5	VAL	-	expression tag	UNP P0A6B4
B	-4	PRO	-	expression tag	UNP P0A6B4
B	-3	ARG	-	expression tag	UNP P0A6B4
B	-2	GLY	-	expression tag	UNP P0A6B4
B	-1	SER	-	expression tag	UNP P0A6B4
B	0	HIS	-	expression tag	UNP P0A6B4
B	219	ALA	PRO	engineered mutation	UNP P0A6B4
C	-19	MET	-	expression tag	UNP P0A6B4
C	-18	GLY	-	expression tag	UNP P0A6B4
C	-17	SER	-	expression tag	UNP P0A6B4
C	-16	SER	-	expression tag	UNP P0A6B4
C	-15	HIS	-	expression tag	UNP P0A6B4
C	-14	HIS	-	expression tag	UNP P0A6B4
C	-13	HIS	-	expression tag	UNP P0A6B4
C	-12	HIS	-	expression tag	UNP P0A6B4
C	-11	HIS	-	expression tag	UNP P0A6B4
C	-10	HIS	-	expression tag	UNP P0A6B4
C	-9	SER	-	expression tag	UNP P0A6B4
C	-8	SER	-	expression tag	UNP P0A6B4
C	-7	GLY	-	expression tag	UNP P0A6B4
C	-6	LEU	-	expression tag	UNP P0A6B4
C	-5	VAL	-	expression tag	UNP P0A6B4
C	-4	PRO	-	expression tag	UNP P0A6B4
C	-3	ARG	-	expression tag	UNP P0A6B4
C	-2	GLY	-	expression tag	UNP P0A6B4
C	-1	SER	-	expression tag	UNP P0A6B4
C	0	HIS	-	expression tag	UNP P0A6B4
C	219	ALA	PRO	engineered mutation	UNP P0A6B4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MET	-	expression tag	UNP P0A6B4
D	-18	GLY	-	expression tag	UNP P0A6B4
D	-17	SER	-	expression tag	UNP P0A6B4
D	-16	SER	-	expression tag	UNP P0A6B4
D	-15	HIS	-	expression tag	UNP P0A6B4
D	-14	HIS	-	expression tag	UNP P0A6B4
D	-13	HIS	-	expression tag	UNP P0A6B4
D	-12	HIS	-	expression tag	UNP P0A6B4
D	-11	HIS	-	expression tag	UNP P0A6B4
D	-10	HIS	-	expression tag	UNP P0A6B4
D	-9	SER	-	expression tag	UNP P0A6B4
D	-8	SER	-	expression tag	UNP P0A6B4
D	-7	GLY	-	expression tag	UNP P0A6B4
D	-6	LEU	-	expression tag	UNP P0A6B4
D	-5	VAL	-	expression tag	UNP P0A6B4
D	-4	PRO	-	expression tag	UNP P0A6B4
D	-3	ARG	-	expression tag	UNP P0A6B4
D	-2	GLY	-	expression tag	UNP P0A6B4
D	-1	SER	-	expression tag	UNP P0A6B4
D	0	HIS	-	expression tag	UNP P0A6B4
D	219	ALA	PRO	engineered mutation	UNP P0A6B4

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



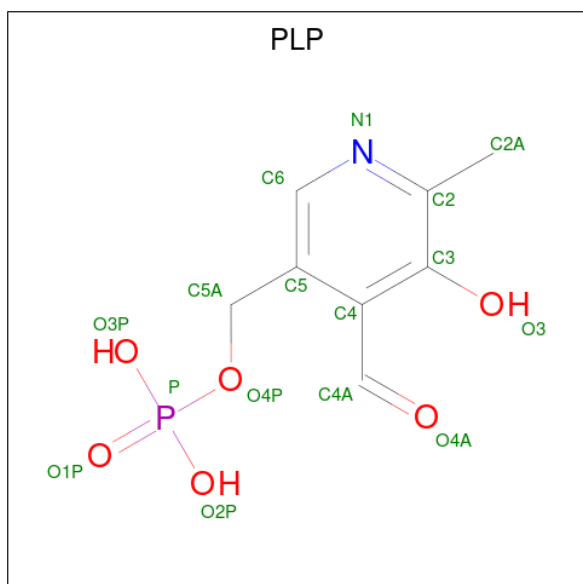
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

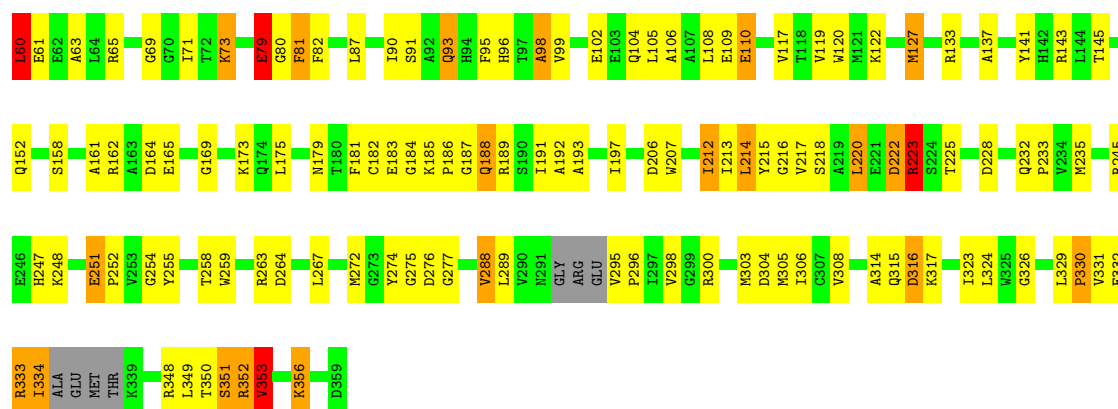
- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



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

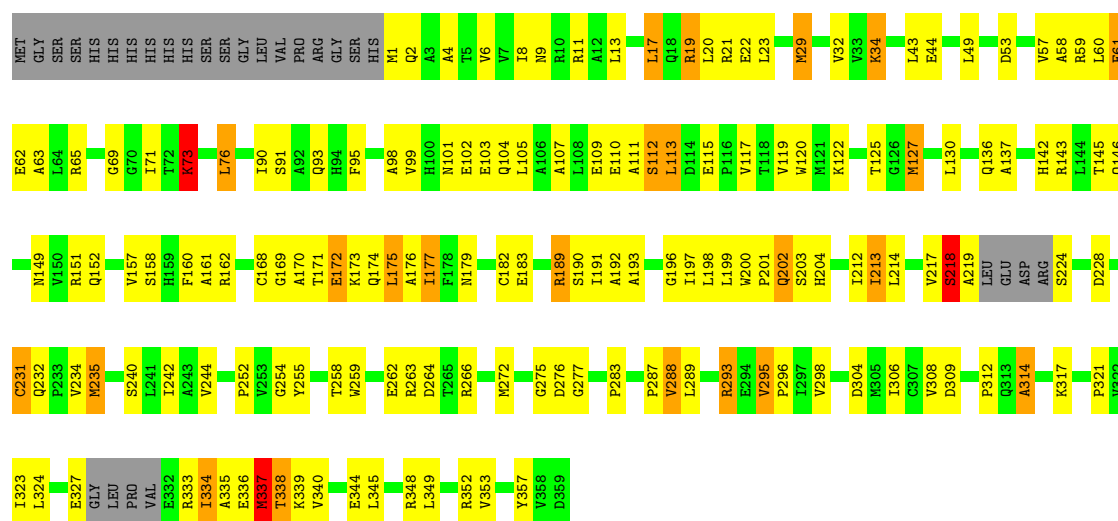
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	96	Total 96	O 96	0	0
4	B	122	Total 122	O 122	0	0
4	C	71	Total 71	O 71	0	0
4	D	76	Total 76	O 76	0	0



• Molecule 1: Alanine racemase

Chain D: 50% 36% 6% • 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 6	Depositor
Cell constants a, b, c, α , β , γ	147.92Å 147.92Å 163.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	15.00 – 3.00 15.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.7 (15.00-3.00) 98.7 (15.00-3.00)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 3.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.219 , 0.226 0.212 , 0.220	Depositor DCC
R_{free} test set	3804 reflections (9.48%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 11.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.457 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11336	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: PLP, KCX, SO4

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	0.83	3/2796 (0.1%)	1.15	16/3795 (0.4%)
1	B	0.77	3/2796 (0.1%)	1.18	24/3795 (0.6%)
1	C	0.71	0/2724	1.17	26/3697 (0.7%)
1	D	0.66	0/2731	1.15	19/3703 (0.5%)
All	All	0.75	6/11047 (0.1%)	1.16	85/14990 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	3
1	D	0	1
All	All	0	5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1	MET	SD-CE	6.38	1.95	1.79
1	A	89	THR	C-O	-5.79	1.17	1.24
1	A	326	GLY	C-O	-5.67	1.19	1.23
1	B	89	THR	C-O	-5.55	1.17	1.24
1	B	151	ARG	C-O	-5.32	1.17	1.24

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	314	ALA	N-CA-C	-13.30	91.75	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	315	GLN	N-CA-CB	-12.45	90.99	110.92
1	B	315	GLN	N-CA-CB	-11.97	91.77	110.92
1	B	85	ARG	NE-CZ-NH2	11.68	129.71	119.20
1	A	314	ALA	N-CA-C	-11.45	93.53	110.48

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	257	GLY	Peptide
1	C	60	LEU	Peptide
1	C	79	GLU	Peptide
1	C	80	GLY	Peptide
1	D	112	SER	Peptide

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	2752	0	2756	77	0
1	B	2752	0	2756	73	0
1	C	2682	0	2685	162	0
1	D	2690	0	2690	181	0
2	A	15	0	0	0	0
2	B	10	0	0	0	0
2	C	10	0	0	0	0
3	A	15	0	7	0	0
3	B	15	0	7	0	0
3	C	15	0	7	0	0
3	D	15	0	7	2	0
4	A	96	0	0	4	0
4	B	122	0	0	3	0
4	C	71	0	0	17	0
4	D	76	0	0	21	0
All	All	11336	0	10915	469	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 21.

The worst 5 of 469 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:C:164:ASP:HB2	1:C:220:LEU:HD21	1.25	1.13
1:D:176:ALA:HB2	4:D:1062:HOH:O	1.47	1.11
1:D:338:THR:HG22	1:D:340:VAL:CG1	1.80	1.11
1:D:113:LEU:HD12	1:D:115:GLU:O	1.51	1.10
1:D:169:GLY:O	1:D:173:LYS:HB2	1.51	1.08

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	356/379 (94%)	340 (96%)	15 (4%)	1 (0%)	36	70
1	B	356/379 (94%)	341 (96%)	14 (4%)	1 (0%)	36	70
1	C	343/379 (90%)	320 (93%)	20 (6%)	3 (1%)	14	48
1	D	344/379 (91%)	320 (93%)	22 (6%)	2 (1%)	21	56
All	All	1399/1516 (92%)	1321 (94%)	71 (5%)	7 (0%)	24	60

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	61	GLU
1	D	172	GLU
1	A	258	THR
1	C	223	ARG
1	B	257	GLY

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	285/302 (94%)	263 (92%)	22 (8%)	12	40
1	B	285/302 (94%)	265 (93%)	20 (7%)	14	44
1	C	278/302 (92%)	257 (92%)	21 (8%)	12	41
1	D	278/302 (92%)	251 (90%)	27 (10%)	8	30
All	All	1126/1208 (93%)	1036 (92%)	90 (8%)	11	38

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	288	VAL
1	D	103	GLU
1	C	333	ARG
1	D	19	ARG
1	D	151	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	93	GLN
1	D	146	GLN
1	D	96	HIS
1	D	152	GLN
1	B	94	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	KCX	D	122	1	10,11,12	1.72	2 (20%)	6,12,14	2.95	2 (33%)
1	KCX	C	122	1	10,11,12	1.57	2 (20%)	6,12,14	2.82	2 (33%)
1	KCX	A	122	1	10,11,12	1.64	2 (20%)	6,12,14	2.63	2 (33%)
1	KCX	B	122	1	10,11,12	1.58	2 (20%)	6,12,14	2.86	2 (33%)

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	KCX	D	122	1	-	0/9/10/12	-
1	KCX	C	122	1	-	0/9/10/12	-
1	KCX	A	122	1	-	0/9/10/12	-
1	KCX	B	122	1	-	0/9/10/12	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	122	KCX	CE-NZ	4.58	1.56	1.46
1	A	122	KCX	CE-NZ	4.34	1.55	1.46
1	B	122	KCX	CE-NZ	4.02	1.55	1.46
1	C	122	KCX	CE-NZ	3.91	1.55	1.46
1	A	122	KCX	OQ1-CX	2.04	1.25	1.21

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	122	KCX	CD-CE-NZ	5.19	126.74	112.20
1	B	122	KCX	OQ1-CX-NZ	-4.87	117.53	124.92
1	B	122	KCX	CD-CE-NZ	4.87	125.84	112.20
1	D	122	KCX	OQ1-CX-NZ	-4.85	117.55	124.92
1	C	122	KCX	OQ1-CX-NZ	-4.84	117.57	124.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	PLP	A	1001	1	15,15,16	2.17	5 (33%)	21,22,23	2.82	11 (52%)
2	SO4	A	362	-	4,4,4	0.27	0	6,6,6	0.40	0
2	SO4	A	361	-	4,4,4	0.50	0	6,6,6	0.47	0
3	PLP	C	1001	1	15,15,16	2.22	8 (53%)	21,22,23	2.59	11 (52%)
2	SO4	A	360	-	4,4,4	0.60	0	6,6,6	0.37	0
3	PLP	D	1001	1	15,15,16	2.77	7 (46%)	21,22,23	3.21	12 (57%)
2	SO4	C	360	-	4,4,4	0.46	0	6,6,6	0.15	0
3	PLP	B	1001	1	15,15,16	2.78	6 (40%)	21,22,23	2.44	11 (52%)
2	SO4	B	360	-	4,4,4	0.54	0	6,6,6	0.45	0
2	SO4	B	361	-	4,4,4	0.57	0	6,6,6	0.44	0
2	SO4	C	361	-	4,4,4	0.34	0	6,6,6	0.37	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	PLP	A	1001	1	-	0/6/6/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PLP	B	1001	1	-	0/6/6/8	0/1/1/1
3	PLP	C	1001	1	-	0/6/6/8	0/1/1/1
3	PLP	D	1001	1	-	3/6/6/8	0/1/1/1

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1001	PLP	C3-C2	6.80	1.48	1.41
3	D	1001	PLP	P-O1P	5.00	1.66	1.50
3	A	1001	PLP	P-O4P	-4.84	1.45	1.60
3	D	1001	PLP	C2-N1	4.66	1.42	1.33
3	C	1001	PLP	P-O1P	4.30	1.63	1.50

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1001	PLP	O3P-P-O4P	6.98	124.87	106.67
3	D	1001	PLP	O2P-P-O4P	-6.27	90.33	106.67
3	A	1001	PLP	O4P-C5A-C5	5.61	119.87	109.36
3	A	1001	PLP	C4A-C4-C5	-4.74	116.06	120.94
3	B	1001	PLP	C5A-C5-C6	-4.69	111.72	119.36

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1001	PLP	C5A-O4P-P-O2P
3	D	1001	PLP	C5A-O4P-P-O1P
3	D	1001	PLP	C5A-O4P-P-O3P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1001	PLP	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	358/379 (94%)	-1.78	0 100 100	2, 12, 27, 46	0
1	B	358/379 (94%)	-1.78	0 100 100	2, 13, 26, 43	0
1	C	349/379 (92%)	-1.66	0 100 100	13, 31, 42, 51	0
1	D	350/379 (92%)	-1.61	0 100 100	15, 33, 47, 54	0
All	All	1415/1516 (93%)	-1.71	0 100 100	2, 23, 42, 54	0

There are no RSRZ outliers to report.

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	KCX	D	122	12/13	0.99	0.04	32,35,40,41	0
1	KCX	B	122	12/13	1.00	0.04	1,11,14,15	0
1	KCX	C	122	12/13	1.00	0.03	8,18,23,24	0
1	KCX	A	122	12/13	1.00	0.04	1,16,17,17	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	SO4	A	361	5/5	0.98	0.10	73,73,74,75	0
2	SO4	A	360	5/5	0.99	0.04	56,57,58,59	0
2	SO4	A	362	5/5	0.99	0.08	36,37,39,43	0
2	SO4	B	361	5/5	0.99	0.06	78,78,79,79	0
2	SO4	C	360	5/5	0.99	0.04	41,41,42,43	0
2	SO4	C	361	5/5	0.99	0.04	75,75,75,75	0
2	SO4	B	360	5/5	1.00	0.03	39,39,40,41	0
3	PLP	A	1001	15/16	1.00	0.03	12,22,24,26	0
3	PLP	B	1001	15/16	1.00	0.03	19,25,28,31	0
3	PLP	C	1001	15/16	1.00	0.04	37,39,40,41	0
3	PLP	D	1001	15/16	1.00	0.04	42,46,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.