



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:50 PM UTC

PDB ID : 2Z1Y / pdb_00002z1y
Title : Crystal structure of LysN, alpha-aminoadipate aminotransferase (complexed with N-(5'-phosphopyridoxyl)-L-leucine), from *Thermus thermophilus* HB27
Authors : Tomita, T.; Miyazaki, T.; Miyagawa, T.; Fushinobu, S.; Kuzuyama, T.; Nishiyama, M.
Deposited on : 2007-05-16
Resolution : 1.75 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
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

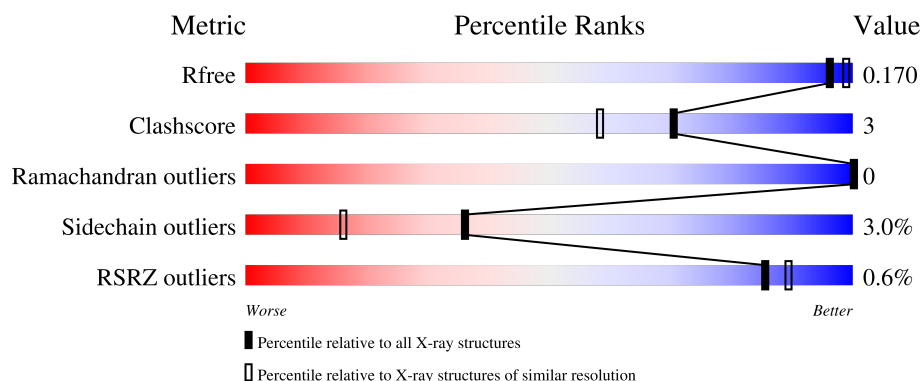
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	397	% 88% 10% ..
1	B	397	88% 9% ..

2 Entry composition [i](#)

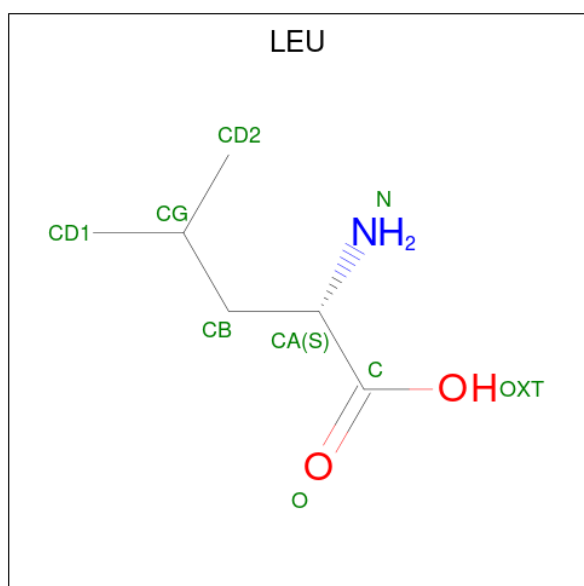
There are 4 unique types of molecules in this entry. The entry contains 6946 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 2-aminoadipate transaminase.

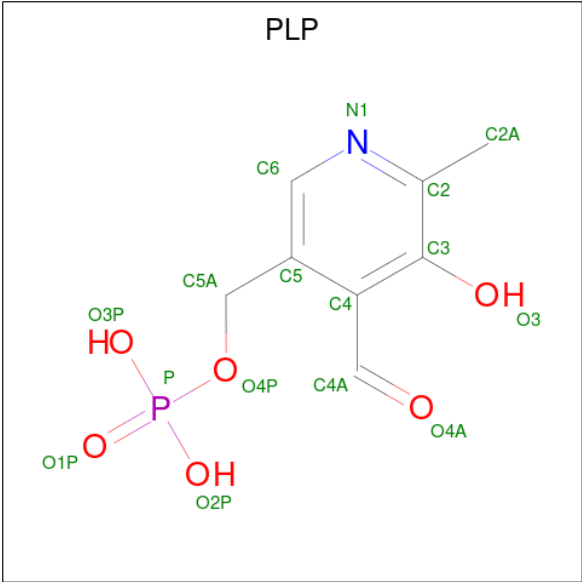
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	1	0
			3058	1963	538	549	8			
1	B	395	Total	C	N	O	S	0	1	0
			3086	1980	546	552	8			

- Molecule 2 is LEUCINE (CCD ID: LEU) (formula: $C_6H_{13}NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			9	6	1	2		
2	B	1	Total	C	N	O	0	0
			9	6	1	2		

- 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		

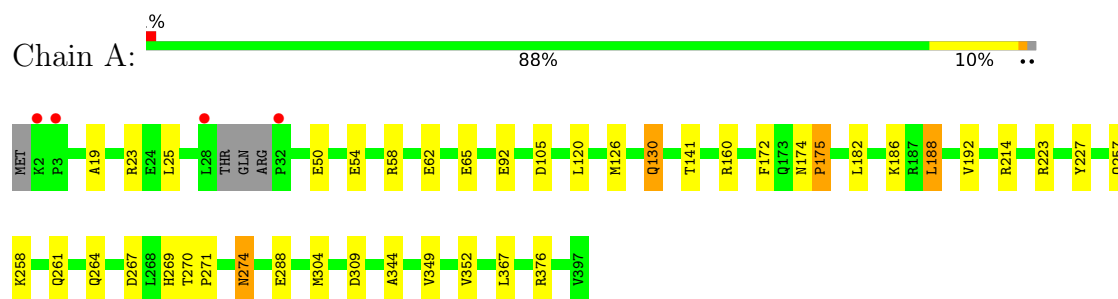
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	390	Total	O	0	0
			390	390		
4	B	364	Total	O	0	0
			364	364		

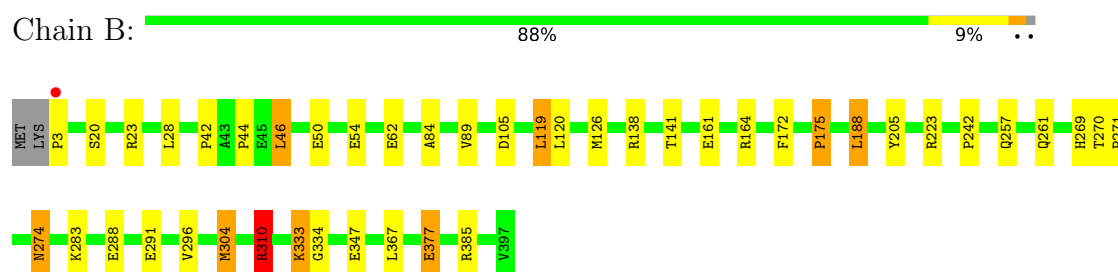
3 Residue-property plots

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: 2-aminoadipate transaminase



• Molecule 1: 2-aminoadipate transaminase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	137.11Å 62.23Å 107.44Å 90.00° 116.34° 90.00°	Depositor
Resolution (Å)	36.86 – 1.75 36.86 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.7 (36.86-1.75) 99.7 (36.86-1.75)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.153 , 0.194 0.166 , 0.170	Depositor DCC
R_{free} test set	4097 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	15.2	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6946	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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

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	0.94	2/3124 (0.1%)	1.29	11/4222 (0.3%)
1	B	0.92	1/3156 (0.0%)	1.29	14/4265 (0.3%)
All	All	0.93	3/6280 (0.0%)	1.29	25/8487 (0.3%)

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	A	0	1
1	B	0	3
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	105	ASP	CG-OD2	-6.70	1.12	1.25
1	B	105	ASP	CG-OD2	-6.48	1.13	1.25
1	A	227	TYR	C-N	5.33	1.37	1.33

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	304	MET	CG-SD-CE	-14.77	68.40	100.90
1	A	304	MET	CG-SD-CE	-8.41	82.39	100.90
1	A	214	ARG	N-CA-CB	-7.60	98.74	110.29
1	B	288	GLU	CB-CG-CD	7.31	125.03	112.60
1	B	283	LYS	CB-CA-C	-6.61	99.83	110.79
1	B	377	GLU	CB-CG-CD	6.57	123.77	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	172	PHE	CA-CB-CG	-6.29	107.51	113.80
1	A	223	ARG	NE-CZ-NH2	6.07	124.67	119.20
1	A	172	PHE	CA-CB-CG	-5.96	107.84	113.80
1	B	3	PRO	N-CA-CB	5.95	109.54	103.00
1	B	164	ARG	NE-CZ-NH2	5.84	124.46	119.20
1	A	288	GLU	CB-CG-CD	5.77	122.41	112.60
1	A	258	LYS	N-CA-CB	5.77	118.70	110.16
1	A	92	GLU	CB-CG-CD	5.69	122.28	112.60
1	B	205	TYR	CA-C-N	5.52	129.10	120.82
1	B	205	TYR	C-N-CA	5.52	129.10	120.82
1	A	376	ARG	CA-CB-CG	-5.43	103.24	114.10
1	B	310	ARG	N-CA-CB	5.32	118.31	110.33
1	A	62	GLU	CB-CG-CD	5.17	121.39	112.60
1	B	161	GLU	CB-CA-C	-5.13	99.01	109.94
1	B	175	PRO	N-CA-CB	-5.12	96.97	102.60
1	A	267	ASP	CA-CB-CG	5.11	117.71	112.60
1	B	161	GLU	CG-CD-OE2	-5.10	106.67	118.40
1	B	310	ARG	CB-CA-C	-5.08	99.46	109.67
1	A	309	ASP	CA-CB-CG	5.03	117.62	112.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	160	ARG	Sidechain
1	B	138	ARG	Sidechain
1	B	223	ARG	Sidechain
1	B	310	ARG	Sidechain

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	3058	0	3109	25	0
1	B	3086	0	3157	28	0
2	A	9	0	10	0	0
2	B	9	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	15	0	7	0	0
3	B	15	0	7	0	0
4	A	390	0	0	0	0
4	B	364	0	0	3	0
All	All	6946	0	6300	43	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 3.

All (43) 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:B:377:GLU:HG2	4:B:692:HOH:O	1.78	0.82
1:A:23:ARG:HE	1:B:261:GLN:HE22	1.28	0.81
1:A:264:GLN:HE21	1:B:23:ARG:H	1.24	0.81
1:B:257:GLN:HE21	1:B:261:GLN:HE21	1.36	0.71
1:B:62:GLU:OE2	4:B:501:HOH:O	2.08	0.71
1:A:274:ASN:H	1:A:274:ASN:HD22	1.38	0.70
1:B:42:PRO:HG2	1:B:242:PRO:HG3	1.75	0.67
1:A:54[A]:GLU:OE1	1:A:58:ARG:NH1	2.28	0.66
1:A:261:GLN:HE21	1:B:23:ARG:HH21	1.47	0.61
1:A:23:ARG:HE	1:B:261:GLN:NE2	2.00	0.58
1:B:269:HIS:HD2	1:B:270:THR:O	1.87	0.57
1:B:274:ASN:H	1:B:274:ASN:HD22	1.51	0.57
1:A:274:ASN:HD22	1:A:274:ASN:N	2.05	0.54
1:A:269:HIS:HD2	1:A:270:THR:O	1.91	0.53
1:A:257:GLN:CD	1:B:23:ARG:HH22	2.18	0.52
1:A:261:GLN:NE2	1:B:23:ARG:HH21	2.07	0.52
1:B:46:LEU:HD11	1:B:296:VAL:HG21	1.92	0.51
1:A:344:ALA:HB1	1:A:349:VAL:HG13	1.92	0.51
1:A:264:GLN:NE2	1:B:23:ARG:H	2.02	0.50
1:A:188:LEU:C	1:A:188:LEU:HD13	2.37	0.48
1:B:119:LEU:C	1:B:119:LEU:HD13	2.38	0.48
1:A:19:ALA:HB3	1:A:130:GLN:HE22	1.78	0.47
1:A:50:GLU:OE2	1:A:54[B]:GLU:OE2	2.32	0.47
1:B:274:ASN:HD22	1:B:274:ASN:N	2.12	0.47
1:A:271:PRO:HB2	1:A:274:ASN:ND2	2.31	0.46
1:B:347:GLU:O	1:B:385:ARG:HD3	2.16	0.46
1:B:120:LEU:O	1:B:141:THR:HA	2.16	0.45
1:A:120:LEU:O	1:A:141:THR:HA	2.15	0.45
1:A:274:ASN:N	1:A:274:ASN:ND2	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:GLU:HG3	1:B:44:PRO:HB2	1.99	0.44
1:B:333:LYS:HD3	1:B:334:GLY:N	2.32	0.43
1:A:182:LEU:HG	1:A:186:LYS:HE3	1.99	0.43
1:B:42:PRO:CG	1:B:242:PRO:HG3	2.46	0.43
1:A:54[A]:GLU:CD	1:A:58:ARG:NH1	2.77	0.42
1:A:264:GLN:HE21	1:B:23:ARG:N	2.05	0.42
1:B:188:LEU:C	1:B:188:LEU:HD13	2.43	0.42
1:B:271:PRO:HB2	1:B:274:ASN:ND2	2.34	0.42
1:B:271:PRO:HG2	4:B:527:HOH:O	2.20	0.41
1:A:264:GLN:HE22	1:B:20:SER:HA	1.85	0.41
1:A:25:LEU:HD21	1:A:352:VAL:HG22	2.03	0.41
1:B:84:ALA:HB1	1:B:89:VAL:O	2.21	0.41
1:A:174:ASN:HA	1:A:175:PRO:HA	1.93	0.41
1:B:50:GLU:OE2	1:B:54:GLU:OE1	2.39	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	390/397 (98%)	380 (97%)	10 (3%)	0	100	100
1	B	394/397 (99%)	384 (98%)	10 (2%)	0	100	100
All	All	784/794 (99%)	764 (97%)	20 (3%)	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	310/316 (98%)	303 (98%)	7 (2%)	44	24
1	B	315/316 (100%)	303 (96%)	12 (4%)	29	10
All	All	625/632 (99%)	606 (97%)	19 (3%)	36	16

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	126	MET
1	A	130	GLN
1	A	175	PRO
1	A	188	LEU
1	A	192	VAL
1	A	274	ASN
1	A	367	LEU
1	B	28	LEU
1	B	46	LEU
1	B	119	LEU
1	B	126	MET
1	B	175	PRO
1	B	188	LEU
1	B	274	ASN
1	B	291	GLU
1	B	304	MET
1	B	310	ARG
1	B	333	LYS
1	B	367	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	GLN
1	A	135	GLN
1	A	261	GLN
1	A	264	GLN
1	A	269	HIS
1	A	274	ASN
1	B	30	GLN
1	B	101	GLN

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Mol	Chain	Res	Type
1	B	135	GLN
1	B	190	GLN
1	B	261	GLN
1	B	269	HIS
1	B	274	ASN
1	B	302	GLN
1	B	360	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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	$\# Z > 2$
2	LEU	B	401	3	6,8,8	1.49	2 (33%)	5,10,10	0.66	0
2	LEU	A	401	3	6,8,8	1.15	1 (16%)	5,10,10	0.72	0
3	PLP	B	402	2	15,15,16	0.72	0	21,22,23	1.14	1 (4%)
3	PLP	A	402	2	15,15,16	0.90	1 (6%)	21,22,23	1.06	2 (9%)

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	LEU	B	401	3	-	1/8/8/8	-
2	LEU	A	401	3	-	0/8/8/8	-
3	PLP	B	402	2	-	3/6/6/8	0/1/1/1
3	PLP	A	402	2	-	3/6/6/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	LEU	OXT-C	-2.87	1.21	1.30
3	A	402	PLP	C4A-C4	-2.27	1.47	1.51
2	A	401	LEU	OXT-C	-2.22	1.23	1.30
2	B	401	LEU	O-C	2.22	1.28	1.22

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	PLP	O3P-P-O2P	2.65	117.75	107.80
3	B	402	PLP	C4A-C4-C5	2.41	123.42	120.94
3	A	402	PLP	O3P-P-O4P	-2.31	100.64	106.67

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	PLP	C5A-O4P-P-O2P
3	A	402	PLP	C5A-O4P-P-O3P
3	B	402	PLP	C5A-O4P-P-O1P
3	B	402	PLP	C5A-O4P-P-O2P
3	B	402	PLP	C5A-O4P-P-O3P
3	A	402	PLP	C5A-O4P-P-O1P
2	B	401	LEU	OXT-C-CA-N

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 [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	393/397 (98%)	-0.31	4 (1%) 79 84	9, 14, 30, 63	1 (0%)
1	B	395/397 (99%)	-0.29	1 (0%) 90 92	9, 15, 32, 53	1 (0%)
All	All	788/794 (99%)	-0.30	5 (0%) 85 89	9, 15, 31, 63	2 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	28	LEU	5.4
1	A	2	LYS	4.4
1	A	32	PRO	4.3
1	A	3	PRO	3.3
1	B	3	PRO	3.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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	LEU	A	401	9/9	0.95	0.07	15,16,20,21	0
2	LEU	B	401	9/9	0.96	0.06	16,17,20,23	0
3	PLP	A	402	15/16	0.99	0.04	8,11,15,17	0
3	PLP	B	402	15/16	0.99	0.04	9,12,15,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.