



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 08:50 am GMT

PDB ID : 5CE8
Title : Crystal structure of branched-chain aminotransferase from thermophilic archaea *Thermoproteus uzoniensis*
Authors : Boyko, K.M.; Nikolaeva, A.Y.; Stekhanova, T.N.; Mardanov, A.V.; Rakitin, A.L.; Ravin, N.V.; Popov, V.O.
Deposited on : 2015-07-06
Resolution : 2.00 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

<http://wwpdb.org/validation/2016/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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

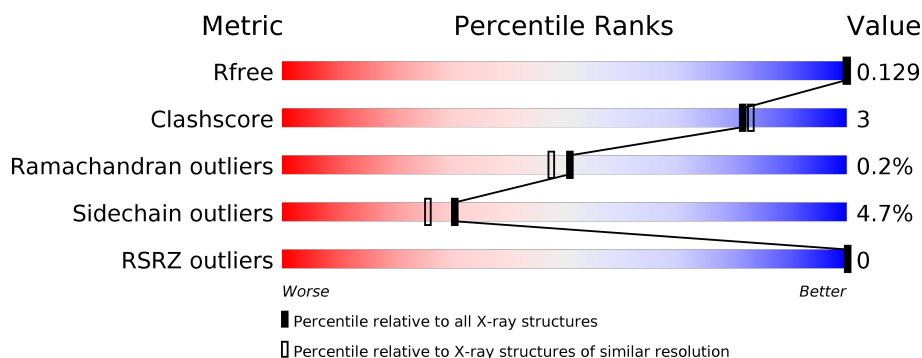
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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 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	307	
1	B	307	
1	C	307	

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	PEG	C	301	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7219 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 Branched-chain amino acid aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	0	0
			2281	1468	382	423	8			
1	B	296	Total	C	N	O	S	0	0	0
			2278	1465	382	424	7			
1	C	295	Total	C	N	O	S	0	1	0
			2275	1467	385	415	8			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP F2L0W0
A	-10	ARG	-	expression tag	UNP F2L0W0
A	-9	GLY	-	expression tag	UNP F2L0W0
A	-8	SER	-	expression tag	UNP F2L0W0
A	-7	HIS	-	expression tag	UNP F2L0W0
A	-6	HIS	-	expression tag	UNP F2L0W0
A	-5	HIS	-	expression tag	UNP F2L0W0
A	-4	HIS	-	expression tag	UNP F2L0W0
A	-3	HIS	-	expression tag	UNP F2L0W0
A	-2	HIS	-	expression tag	UNP F2L0W0
A	-1	GLY	-	expression tag	UNP F2L0W0
A	0	SER	-	expression tag	UNP F2L0W0
B	-11	MET	-	initiating methionine	UNP F2L0W0
B	-10	ARG	-	expression tag	UNP F2L0W0
B	-9	GLY	-	expression tag	UNP F2L0W0
B	-8	SER	-	expression tag	UNP F2L0W0
B	-7	HIS	-	expression tag	UNP F2L0W0
B	-6	HIS	-	expression tag	UNP F2L0W0
B	-5	HIS	-	expression tag	UNP F2L0W0
B	-4	HIS	-	expression tag	UNP F2L0W0
B	-3	HIS	-	expression tag	UNP F2L0W0
B	-2	HIS	-	expression tag	UNP F2L0W0
B	-1	GLY	-	expression tag	UNP F2L0W0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	SER	-	expression tag	UNP F2L0W0
C	-11	MET	-	initiating methionine	UNP F2L0W0
C	-10	ARG	-	expression tag	UNP F2L0W0
C	-9	GLY	-	expression tag	UNP F2L0W0
C	-8	SER	-	expression tag	UNP F2L0W0
C	-7	HIS	-	expression tag	UNP F2L0W0
C	-6	HIS	-	expression tag	UNP F2L0W0
C	-5	HIS	-	expression tag	UNP F2L0W0
C	-4	HIS	-	expression tag	UNP F2L0W0
C	-3	HIS	-	expression tag	UNP F2L0W0
C	-2	HIS	-	expression tag	UNP F2L0W0
C	-1	GLY	-	expression tag	UNP F2L0W0
C	0	SER	-	expression tag	UNP F2L0W0

- # PLP
-
- The diagram shows the chemical structure of PLP (Pyridoxal phosphate). It consists of a pyridine ring substituted with a hydroxyl group at the 3-position and a hydroxymethyl group at the 4-position. The hydroxyl group is shown in red with the label O3. The hydroxymethyl group is shown in green with the label C5A and O4P. The pyridine ring is shown in green with labels C2, C3, C4, C5, C6, and N1. The phosphate group is shown in purple with labels P, O1P, O2P, O3P, and O4P. The structure is labeled PLP at the top.

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $\text{C}_4\text{H}_{10}\text{O}_3$).



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

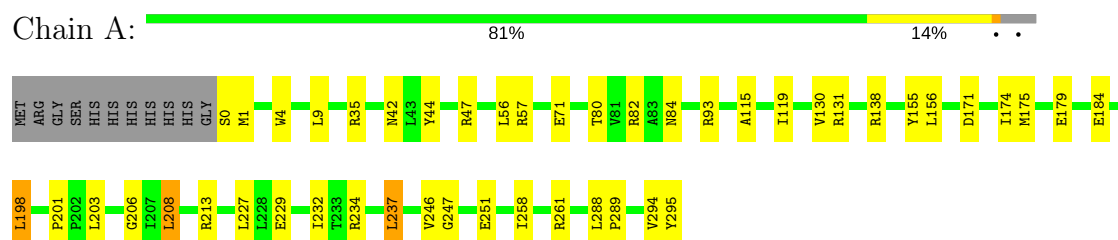
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	113	Total	O	0	0
			113	113		
4	B	104	Total	O	0	0
			104	104		
4	C	116	Total	O	0	0
			116	116		

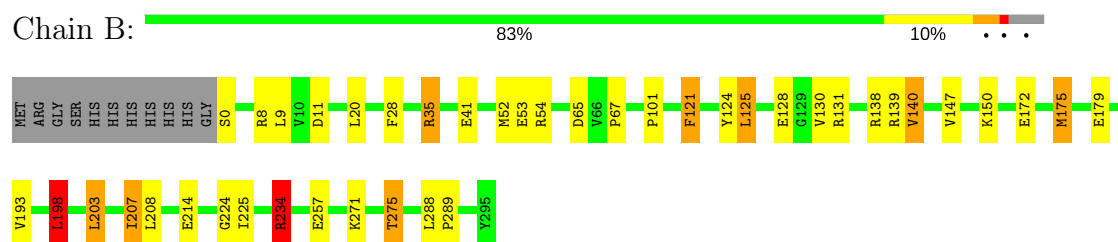
3 Residue-property plots [i](#)

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.

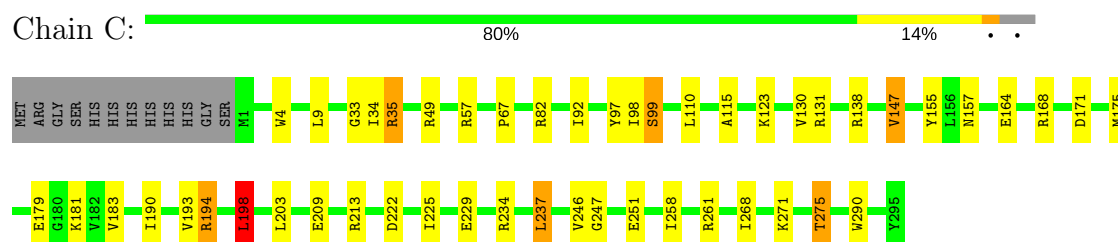
- Molecule 1: Branched-chain amino acid aminotransferase



- Molecule 1: Branched-chain amino acid aminotransferase



- Molecule 1: Branched-chain amino acid aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, α , β , γ	93.54Å 93.54Å 212.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	75.69 – 2.00 75.69 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (75.69-2.00) 99.9 (75.69-2.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.00Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.120 , 0.168 0.128 , 0.129	Depositor DCC
R_{free} test set	3602 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	26.9	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 19.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.460 for -h,-k,l	Xtriage
Reported twinning fraction	0.491 for H, K, L 0.509 for K, H, -L	Depositor
Outliers	0 of 72105 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7219	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% 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: PEG, 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	1.27	4/2324 (0.2%)	1.33	21/3158 (0.7%)
1	B	1.28	5/2320 (0.2%)	1.25	14/3151 (0.4%)
1	C	1.26	9/2323 (0.4%)	1.35	24/3156 (0.8%)
All	All	1.27	18/6967 (0.3%)	1.31	59/9465 (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	2

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	172	GLU	CD-OE2	7.01	1.33	1.25
1	A	179	GLU	CD-OE2	6.49	1.32	1.25
1	A	206	GLY	C-O	-6.45	1.13	1.23
1	C	290	TRP	CB-CG	-6.43	1.38	1.50
1	B	28	PHE	C-O	6.43	1.35	1.23
1	C	234	ARG	CD-NE	-5.84	1.36	1.46
1	A	229	GLU	CD-OE1	-5.71	1.19	1.25
1	C	97	TYR	CE1-CZ	-5.68	1.31	1.38
1	B	224	GLY	N-CA	5.67	1.54	1.46
1	C	229	GLU	CD-OE1	-5.48	1.19	1.25
1	A	234	ARG	CD-NE	-5.45	1.37	1.46
1	C	33	GLY	N-CA	5.43	1.54	1.46
1	B	179	GLU	CD-OE2	5.29	1.31	1.25
1	C	155	TYR	CE1-CZ	-5.23	1.31	1.38
1	C	164	GLU	CD-OE1	5.22	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	140	VAL	C-O	5.20	1.33	1.23
1	C	157	ASN	C-O	5.10	1.33	1.23
1	C	179	GLU	CD-OE2	5.10	1.31	1.25

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	234	ARG	NE-CZ-NH2	-22.68	108.96	120.30
1	C	234	ARG	NE-CZ-NH2	-19.43	110.58	120.30
1	B	234	ARG	NE-CZ-NH2	-16.50	112.05	120.30
1	B	234	ARG	NE-CZ-NH1	13.01	126.81	120.30
1	C	234	ARG	NE-CZ-NH1	11.46	126.03	120.30
1	A	35	ARG	NE-CZ-NH2	-11.14	114.73	120.30
1	C	138[A]	ARG	NE-CZ-NH1	10.47	125.54	120.30
1	C	138[B]	ARG	NE-CZ-NH1	10.47	125.54	120.30
1	A	234	ARG	NE-CZ-NH1	10.32	125.46	120.30
1	C	213	ARG	NE-CZ-NH1	8.63	124.61	120.30
1	A	93	ARG	NE-CZ-NH1	8.27	124.44	120.30
1	C	213	ARG	NE-CZ-NH2	-7.37	116.61	120.30
1	B	11	ASP	CB-CG-OD2	-7.24	111.79	118.30
1	C	35	ARG	NE-CZ-NH2	-7.13	116.73	120.30
1	C	138[A]	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	C	138[B]	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	C	222	ASP	CB-CG-OD1	6.89	124.50	118.30
1	A	82	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	B	8	ARG	NE-CZ-NH1	6.74	123.67	120.30
1	B	35	ARG	NE-CZ-NH2	-6.58	117.01	120.30
1	A	138	ARG	NE-CZ-NH1	6.49	123.54	120.30
1	C	131	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	A	35	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	A	47	ARG	NE-CZ-NH1	6.32	123.46	120.30
1	C	198	LEU	CA-CB-CG	6.29	129.76	115.30
1	B	11	ASP	CB-CG-OD1	6.24	123.92	118.30
1	A	131	ARG	NE-CZ-NH1	6.21	123.41	120.30
1	A	261	ARG	NE-CZ-NH2	6.21	123.40	120.30
1	A	213	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	A	57	ARG	NE-CZ-NH1	6.14	123.37	120.30
1	B	138	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	B	138	ARG	NE-CZ-NH2	-5.99	117.30	120.30
1	C	131	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	C	57	ARG	NE-CZ-NH1	5.89	123.24	120.30
1	C	198	LEU	CB-CG-CD1	5.78	120.82	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	175	MET	CG-SD-CE	-5.74	91.01	100.20
1	A	261	ARG	CG-CD-NE	5.73	123.83	111.80
1	C	261	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	B	54	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	B	175	MET	CG-SD-CE	-5.63	91.18	100.20
1	B	35	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	A	93	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	C	198	LEU	CB-CG-CD2	-5.44	101.76	111.00
1	C	147	VAL	CG1-CB-CG2	5.43	119.58	110.90
1	B	52	MET	CG-SD-CE	-5.38	91.60	100.20
1	C	222	ASP	CB-CG-OD2	-5.36	113.48	118.30
1	A	156	LEU	CB-CG-CD2	5.32	120.04	111.00
1	C	168	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	C	261	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	A	208	LEU	CA-CB-CG	-5.28	103.15	115.30
1	A	131	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	C	35	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	B	65	ASP	CB-CG-OD1	5.24	123.01	118.30
1	C	82	ARG	NE-CZ-NH2	-5.23	117.69	120.30
1	A	198	LEU	CA-CB-CG	5.18	127.22	115.30
1	A	234	ARG	CG-CD-NE	-5.10	101.08	111.80
1	A	234	ARG	NH1-CZ-NH2	5.06	124.96	119.40
1	C	209	GLU	OE1-CD-OE2	-5.05	117.23	123.30
1	B	198	LEU	CB-CG-CD1	5.04	119.56	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	121	PHE	Peptide
1	B	207	ILE	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	2281	0	2299	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2278	0	2296	14	0
1	C	2275	0	2300	13	0
2	A	15	0	7	2	0
2	B	15	0	7	1	0
2	C	15	0	7	0	0
3	C	7	0	10	0	0
4	A	113	0	0	0	0
4	B	104	0	0	1	0
4	C	116	0	0	3	0
All	All	7219	0	6926	42	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 (42) 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:4:TRP:O	1:A:115:ALA:HA	1.99	0.63
1:B:203:LEU:HD12	1:B:207:ILE:HD11	1.82	0.60
1:C:99:SER:HB2	4:C:445:HOH:O	2.05	0.57
1:A:155:TYR:HE2	2:A:301:PLP:HO3	1.57	0.51
1:B:234:ARG:HD2	4:C:479:HOH:O	2.09	0.51
1:C:34:ILE:HB	1:C:92:ILE:HB	1.91	0.51
1:B:139:ARG:HA	1:B:175:MET:HE2	1.93	0.50
1:B:140:VAL:HG13	1:B:147:VAL:CG1	2.40	0.50
1:B:198:LEU:HD22	1:B:225:ILE:HG21	1.94	0.49
1:B:150:LYS:NZ	2:B:301:PLP:O3	2.45	0.49
1:A:174:ILE:HD13	1:A:237:LEU:HD11	1.94	0.47
1:A:246:VAL:HA	1:A:251:GLU:O	2.15	0.47
1:B:124:TYR:O	1:B:125:LEU:HD13	2.15	0.47
1:B:193:VAL:HG22	1:B:198:LEU:HD13	1.97	0.46
1:B:214:GLU:HG2	4:B:439:HOH:O	2.16	0.46
1:C:247:GLY:O	1:C:251:GLU:N	2.49	0.46
1:C:98:ILE:HD13	1:C:110:LEU:HD13	1.98	0.45
1:C:130:VAL:HB	1:C:171:ASP:HB2	1.98	0.45
1:B:20:LEU:HB2	1:B:101:PRO:HB3	1.99	0.45
1:C:193:VAL:HG22	1:C:198:LEU:HD13	1.99	0.45
1:C:271:LYS:O	1:C:275:THR:HG23	2.17	0.44
1:C:246:VAL:HA	1:C:251:GLU:O	2.17	0.44
1:B:125:LEU:HG	1:B:130:VAL:HG11	1.99	0.44
1:A:247:GLY:O	1:A:251:GLU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:VAL:HB	1:A:171:ASP:HB2	1.99	0.43
1:A:294:VAL:HG12	1:A:295:TYR:CD2	2.53	0.43
1:A:201:PRO:HD3	1:A:232:ILE:HD12	2.00	0.43
1:A:42:ASN:HB3	1:A:44:TYR:CE2	2.54	0.43
1:B:271:LYS:O	1:B:275:THR:HG23	2.19	0.43
1:B:288:LEU:N	1:B:289:PRO:CD	2.82	0.42
1:C:237:LEU:HD22	1:C:258:ILE:CG1	2.49	0.42
1:A:237:LEU:HD13	1:A:258:ILE:HG21	2.01	0.42
1:C:225:ILE:HD13	1:C:268:ILE:HG23	2.02	0.42
1:C:194:ARG:HG3	4:C:473:HOH:O	2.20	0.42
1:A:198:LEU:HD23	1:A:227:LEU:HD12	2.02	0.41
1:A:288:LEU:N	1:A:289:PRO:CD	2.83	0.41
1:A:184:GLU:OE1	2:A:301:PLP:N1	2.53	0.41
1:C:4:TRP:O	1:C:115:ALA:HA	2.20	0.41
1:A:0:SER:O	1:A:1:MET:HG2	2.21	0.41
1:A:80:THR:O	1:A:84:ASN:ND2	2.45	0.40
1:B:131:ARG:HG2	1:B:257:GLU:HB3	2.03	0.40
1:C:175:MET:O	1:C:183:VAL:HG12	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	294/307 (96%)	287 (98%)	7 (2%)	0	100	100
1	B	294/307 (96%)	281 (96%)	11 (4%)	2 (1%)	25	18
1	C	294/307 (96%)	282 (96%)	12 (4%)	0	100	100
All	All	882/921 (96%)	850 (96%)	30 (3%)	2 (0%)	51	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	121	PHE
1	B	67	PRO

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	233/253 (92%)	226 (97%)	7 (3%)	46	46
1	B	233/253 (92%)	221 (95%)	12 (5%)	27	22
1	C	231/253 (91%)	217 (94%)	14 (6%)	22	16
All	All	697/759 (92%)	664 (95%)	33 (5%)	30	26

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	56	LEU
1	A	71	GLU
1	A	119	ILE
1	A	203	LEU
1	A	208	LEU
1	A	237	LEU
1	B	0	SER
1	B	9	LEU
1	B	35	ARG
1	B	41	GLU
1	B	53	GLU
1	B	125	LEU
1	B	128	GLU
1	B	198	LEU
1	B	203	LEU
1	B	208	LEU
1	B	234	ARG
1	B	275	THR
1	C	9	LEU
1	C	35	ARG

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Mol	Chain	Res	Type
1	C	49	ARG
1	C	67	PRO
1	C	99	SER
1	C	123	LYS
1	C	147	VAL
1	C	181	LYS
1	C	190	ILE
1	C	194	ARG
1	C	198	LEU
1	C	203	LEU
1	C	237	LEU
1	C	275	THR

Some 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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	PLP	A	301	1	15,15,16	3.26	4 (26%)	20,22,23	1.46	3 (15%)
2	PLP	B	301	1	15,15,16	3.40	3 (20%)	20,22,23	1.70	4 (20%)
3	PEG	C	301	-	6,6,6	0.34	0	5,5,5	1.00	0
2	PLP	C	302	1	15,15,16	3.60	4 (26%)	20,22,23	2.09	8 (40%)

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	PLP	A	301	1	-	0/6/6/8	0/1/1/1
2	PLP	B	301	1	-	0/6/6/8	0/1/1/1
3	PEG	C	301	-	-	0/4/4/4	0/0/0/0
2	PLP	C	302	1	-	0/6/6/8	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	302	PLP	C4A-C4	2.16	1.56	1.51
2	A	301	PLP	C6-C5	2.41	1.42	1.37
2	B	301	PLP	C3-C4	3.08	1.46	1.40
2	C	302	PLP	C3-C4	3.77	1.48	1.40
2	A	301	PLP	C3-C4	4.28	1.49	1.40
2	B	301	PLP	C5-C4	4.85	1.46	1.40
2	C	302	PLP	C5-C4	7.20	1.48	1.40
2	A	301	PLP	C3-C2	7.69	1.46	1.40
2	A	301	PLP	C5-C4	7.76	1.49	1.40
2	C	302	PLP	C3-C2	10.55	1.48	1.40
2	B	301	PLP	C3-C2	11.16	1.48	1.40

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	PLP	O3P-P-O4P	-3.98	96.15	106.73
2	C	302	PLP	C2A-C2-C3	-3.28	117.06	120.96
2	A	301	PLP	C3-C4-C5	-2.68	115.58	118.63
2	C	302	PLP	O3P-P-O4P	-2.58	99.86	106.73
2	C	302	PLP	C5-C6-N1	-2.42	119.78	123.87
2	A	301	PLP	C2A-C2-C3	-2.40	118.11	120.96
2	C	302	PLP	O4P-P-O1P	-2.21	100.28	106.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	302	PLP	C3-C2-N1	-2.10	117.99	120.75
2	B	301	PLP	C4A-C4-C5	-2.03	118.81	120.86
2	A	301	PLP	C6-N1-C2	2.58	124.23	119.26
2	B	301	PLP	O4P-C5A-C5	2.71	114.77	109.32
2	C	302	PLP	O4P-C5A-C5	3.29	115.93	109.32
2	B	301	PLP	O3-C3-C2	3.36	124.81	117.78
2	C	302	PLP	C2A-C2-N1	3.42	124.73	117.89
2	C	302	PLP	C6-N1-C2	3.93	126.83	119.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	PLP	2	0
2	B	301	PLP	1	0

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	296/307 (96%)	-1.11	0 100 100	16, 24, 39, 47	0
1	B	296/307 (96%)	-1.06	0 100 100	16, 25, 40, 62	0
1	C	295/307 (96%)	-1.08	0 100 100	17, 26, 40, 51	0
All	All	887/921 (96%)	-1.08	0 100 100	16, 25, 40, 62	0

There are no RSRZ outliers to report.

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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	PEG	C	301	7/7	0.90	0.17	8.83	20,21,26,32	7
2	PLP	A	301	15/16	0.99	0.07	0.66	18,23,24,24	0
2	PLP	C	302	15/16	0.99	0.07	0.64	20,22,25,26	0
2	PLP	B	301	15/16	0.99	0.06	0.37	20,23,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.