



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 07:25 am BST

PDB ID : 3UYY  
Title : Crystal Structures of Branched-Chain Aminotransferase from *Deinococcus radiodurans* Complexes with alpha-Ketoisocaproate and L-Glutamate Suggest Its Radio-Resistance for Catalysis  
Authors : Chen, C.D.; Huang, Y.C.; Chuankhayan, P.; Hsieh, Y.C.; Huang, T.F.; Lin, C.H.; Guan, H.H.; Liu, M.Y.; Chang, W.C.; Chen, C.J.  
Deposited on : 2011-12-07  
Resolution : 2.50 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](mailto: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.

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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	:	2.11
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)	:	2.11

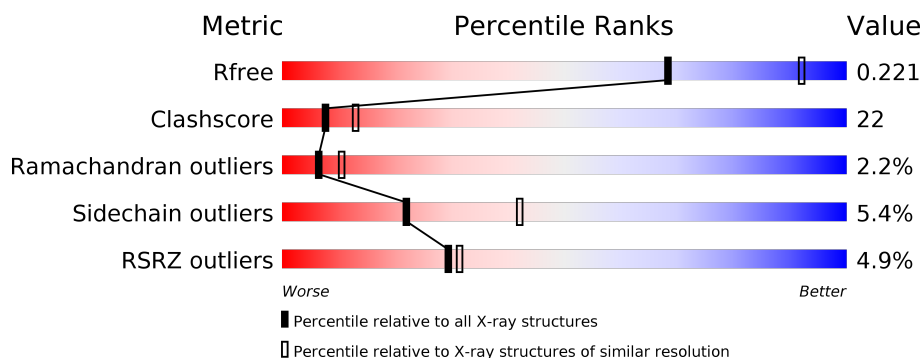
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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  $\geq 3$ , 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	358	<div> <div>6%</div> <div> <div></div> <div>59%</div> <div>29%</div> <div>5% • 6%</div> </div> </div>
1	B	358	<div> <div>4%</div> <div> <div></div> <div>59%</div> <div>31%</div> <div>• 6%</div> </div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5316 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	335	Total	C	N	O	S	0	0	0
			2605	1662	439	495	9			
1	B	337	Total	C	N	O	S	0	0	0
			2618	1669	441	499	9			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula:  $C_8H_{10}NO_6P$ ).



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		

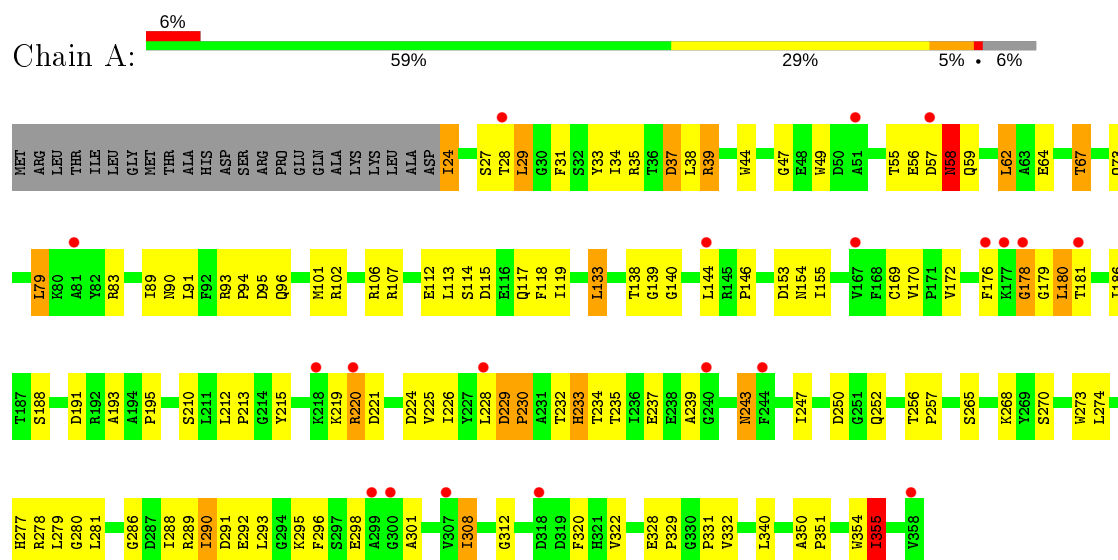
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total 18	O 18	0	0
3	B	45	Total 45	O 45	0	0

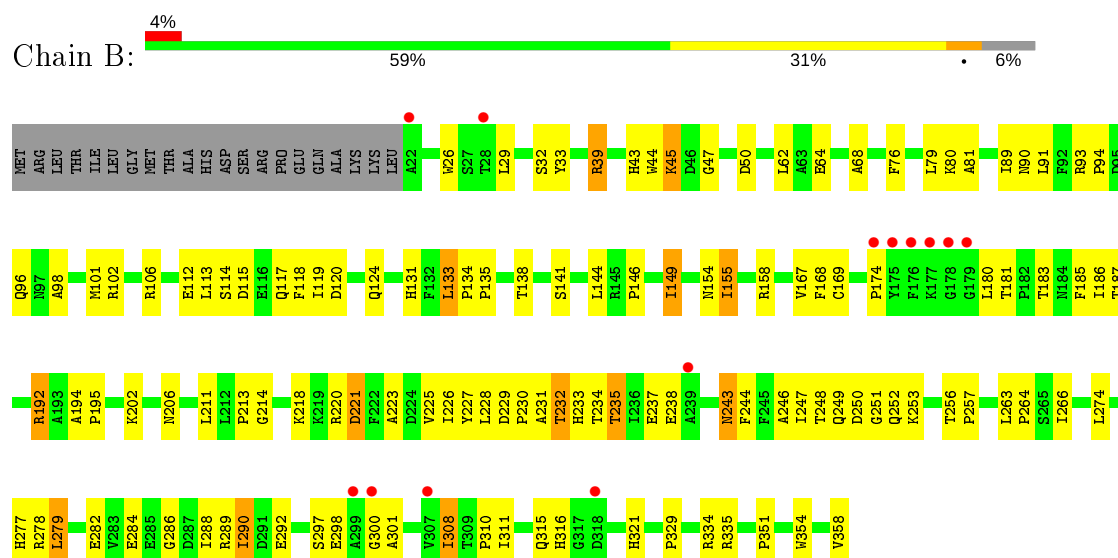
### 3 Residue-property plots [i](#)

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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.37Å 90.70Å 155.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50 25.20 – 2.41	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.50) 98.6 (25.20-2.41)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.71 (at 2.41Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.233 , 0.283 0.227 , 0.221	Depositor DCC
$R_{free}$ test set	1567 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.2	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 38.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5316	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.36	0/2675	0.61	0/3636
1	B	0.39	0/2688	0.64	0/3654
All	All	0.38	0/5363	0.62	0/7290

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

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	2605	0	2500	122	0
1	B	2618	0	2509	108	0
2	A	15	0	6	0	0
2	B	15	0	6	1	0
3	A	18	0	0	0	0
3	B	45	0	0	2	0
All	All	5316	0	5021	225	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 22.

All (225) 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:290:ILE:H	1:B:290:ILE:HD13	1.29	0.94
1:B:229:ASP:HB3	1:B:235:THR:HG22	1.52	0.91
1:A:67:THR:HG23	1:A:73:GLN:HB3	1.50	0.90
1:A:195:PRO:HG3	1:A:230:PRO:HB2	1.54	0.89
1:B:96:GLN:HB3	1:B:266:ILE:HD12	1.56	0.88
1:B:114:SER:H	1:B:117:GLN:HE21	1.25	0.83
1:A:67:THR:HG21	1:A:73:GLN:OE1	1.77	0.83
1:B:44:TRP:CZ2	1:B:47:GLY:HA2	2.15	0.81
1:A:67:THR:CG2	1:A:73:GLN:HB3	2.10	0.80
1:A:39:ARG:HG3	1:A:39:ARG:HH11	1.47	0.80
1:A:64:GLU:OE1	1:B:39:ARG:HD3	1.81	0.80
1:A:55:THR:HG22	1:A:57:ASP:H	1.44	0.79
1:A:91:LEU:HG	1:A:94:PRO:HG3	1.64	0.79
1:A:289:ARG:HH12	1:A:291:ASP:CG	1.89	0.76
1:A:94:PRO:HB2	1:A:119:ILE:HD12	1.69	0.74
1:A:106:ARG:HB3	1:A:106:ARG:HH11	1.52	0.74
1:A:278:ARG:O	1:A:279:LEU:HD12	1.88	0.73
1:A:115:ASP:O	1:A:119:ILE:HG12	1.88	0.72
1:B:114:SER:H	1:B:117:GLN:NE2	1.89	0.71
1:B:277:HIS:O	1:B:278:ARG:HB2	1.91	0.70
1:B:300:GLY:HA2	1:B:311:ILE:HG12	1.72	0.70
1:B:91:LEU:HG	1:B:94:PRO:HG3	1.72	0.70
1:B:257:PRO:HA	1:B:286:GLY:O	1.92	0.69
1:A:220:ARG:HB3	1:A:220:ARG:HH11	1.57	0.69
1:B:248:THR:HG22	1:B:250:ASP:H	1.56	0.69
1:A:228:LEU:O	1:A:237:GLU:HG2	1.93	0.69
1:B:329:PRO:HG2	1:B:334:ARG:HH12	1.58	0.68
1:A:39:ARG:NH1	1:A:39:ARG:HG3	2.07	0.67
1:A:67:THR:HG23	1:A:73:GLN:CB	2.23	0.66
1:B:192:ARG:HB2	1:B:192:ARG:HH11	1.61	0.66
1:B:290:ILE:H	1:B:290:ILE:CD1	2.07	0.66
1:A:83:ARG:HG3	1:A:83:ARG:HH11	1.59	0.66
1:B:114:SER:OG	1:B:117:GLN:HG3	1.95	0.65
1:B:351:PRO:HG2	1:B:354:TRP:CD2	2.30	0.65
1:B:158:ARG:HB3	1:B:158:ARG:HH11	1.61	0.65
1:B:45:LYS:H	1:B:45:LYS:HD3	1.61	0.64
1:A:228:LEU:HD12	1:A:233:HIS:HB3	1.79	0.63
1:B:249:GLN:HA	1:B:297:SER:HB3	1.78	0.63
1:A:180:LEU:HD12	1:A:180:LEU:H	1.63	0.63
1:A:101:MET:CE	1:A:113:LEU:HD12	2.29	0.62
1:A:144:LEU:HD23	1:A:169:CYS:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ARG:HG3	1:A:112:GLU:HB3	1.81	0.62
1:B:115:ASP:O	1:B:119:ILE:HD13	2.00	0.62
1:B:76:PHE:CE1	1:B:202:LYS:HE3	2.34	0.61
1:A:55:THR:HG22	1:A:56:GLU:N	2.16	0.61
1:A:290:ILE:HA	1:A:293:LEU:HD11	1.83	0.61
1:B:135:PRO:HG2	1:B:138:THR:CG2	2.31	0.60
1:A:273:TRP:HE3	1:A:274:LEU:HD12	1.66	0.60
1:B:192:ARG:HB2	1:B:192:ARG:NH1	2.15	0.60
1:A:24:ILE:HD13	1:A:24:ILE:N	2.16	0.60
1:B:231:ALA:C	1:B:232:THR:HG23	2.22	0.60
1:A:354:TRP:O	1:A:355:ILE:HG22	2.02	0.59
1:B:39:ARG:HG2	1:B:168:PHE:HB3	1.83	0.59
1:A:220:ARG:NH1	1:A:220:ARG:HB3	2.16	0.59
1:A:265:SER:HB3	1:A:268:LYS:CB	2.33	0.59
1:B:187:THR:OG1	1:B:316:HIS:HD2	1.85	0.59
1:A:278:ARG:C	1:A:279:LEU:HD12	2.23	0.59
1:A:57:ASP:OD2	1:A:59:GLN:HB2	2.02	0.59
1:B:185:PHE:HB3	1:B:226:ILE:HG13	1.85	0.58
1:A:265:SER:HB3	1:A:268:LYS:HB3	1.85	0.58
1:A:106:ARG:HB3	1:A:106:ARG:NH1	2.17	0.58
1:A:186:ILE:O	1:A:225:VAL:HG23	2.05	0.57
1:B:290:ILE:N	1:B:290:ILE:HD13	2.09	0.57
1:B:230:PRO:O	1:B:231:ALA:HB3	2.05	0.57
1:A:195:PRO:HG3	1:A:230:PRO:CB	2.32	0.56
1:B:232:THR:O	1:B:234:THR:N	2.38	0.56
1:A:292:GLU:HB2	1:A:295:LYS:HE2	1.87	0.56
1:B:98:ALA:HB2	1:B:118:PHE:CD2	2.41	0.56
1:A:114:SER:H	1:A:117:GLN:HE21	1.53	0.56
1:A:39:ARG:HD2	1:A:39:ARG:N	2.20	0.56
1:A:90:ASN:CG	1:A:355:ILE:HD11	2.27	0.55
1:B:39:ARG:HG2	1:B:168:PHE:CB	2.35	0.55
1:A:37:ASP:C	1:A:38:LEU:HG	2.27	0.55
1:B:135:PRO:HG2	1:B:138:THR:HG21	1.88	0.55
1:A:228:LEU:O	1:A:237:GLU:CG	2.55	0.55
1:A:83:ARG:HG3	1:A:83:ARG:NH1	2.22	0.55
1:A:257:PRO:HA	1:A:286:GLY:O	2.07	0.55
1:A:114:SER:OG	1:A:117:GLN:HG3	2.07	0.55
1:B:257:PRO:HD3	1:B:288:ILE:HD12	1.89	0.54
1:B:45:LYS:N	1:B:45:LYS:HD3	2.21	0.54
1:A:153:ASP:O	1:A:154:ASN:HB2	2.07	0.54
1:B:93:ARG:N	1:B:94:PRO:HD3	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:THR:O	1:A:140:GLY:N	2.36	0.54
1:A:331:PRO:HG2	1:A:332:VAL:H	1.72	0.54
1:A:312:GLY:O	1:A:322:VAL:HG13	2.08	0.54
1:A:90:ASN:OD1	1:A:355:ILE:HD11	2.08	0.54
1:A:247:ILE:O	1:A:296:PHE:HB3	2.07	0.54
1:A:243:ASN:O	1:A:301:ALA:HA	2.08	0.53
1:A:247:ILE:HD12	1:A:247:ILE:N	2.23	0.53
1:B:274:LEU:O	1:B:279:LEU:HB2	2.08	0.53
1:A:39:ARG:HG2	1:B:64:GLU:OE1	2.08	0.53
1:B:144:LEU:HD23	1:B:169:CYS:HB3	1.89	0.53
1:A:83:ARG:HB2	1:A:133:LEU:HD22	1.91	0.53
1:A:235:THR:HG23	1:A:288:ILE:H	1.74	0.53
1:A:228:LEU:O	1:A:235:THR:O	2.27	0.53
1:B:279:LEU:HD13	1:B:335:ARG:CZ	2.39	0.53
1:A:93:ARG:N	1:A:94:PRO:HD3	2.24	0.52
1:B:174:PRO:HD3	3:B:387:HOH:O	2.08	0.52
1:A:228:LEU:O	1:A:229:ASP:HB3	2.08	0.52
1:A:44:TRP:CZ2	1:A:47:GLY:HA2	2.45	0.51
1:B:133:LEU:HD23	1:B:134:PRO:HD2	1.93	0.51
1:B:300:GLY:CA	1:B:311:ILE:HG12	2.41	0.51
1:A:94:PRO:CB	1:A:119:ILE:HD12	2.39	0.51
1:A:289:ARG:HB3	1:A:289:ARG:NH1	2.26	0.51
1:B:131:HIS:H	1:B:131:HIS:CD2	2.28	0.50
1:B:146:PRO:HB3	1:B:167:VAL:HG22	1.93	0.50
1:B:81:ALA:HA	1:B:90:ASN:O	2.11	0.50
1:A:354:TRP:N	1:A:354:TRP:CD1	2.77	0.50
1:B:43:HIS:H	1:B:50:ASP:CB	2.23	0.50
1:A:232:THR:O	1:A:232:THR:HG23	2.12	0.49
1:A:279:LEU:O	1:A:281:LEU:HG	2.12	0.49
1:B:120:ASP:OD1	1:B:124:GLN:NE2	2.45	0.49
1:A:35:ARG:HG3	1:A:39:ARG:HH21	1.76	0.49
1:B:238:GLU:OE2	2:B:372:PLP:N1	2.45	0.49
1:B:106:ARG:NE	1:B:112:GLU:OE2	2.45	0.49
1:B:290:ILE:HG13	1:B:316:HIS:CE1	2.46	0.49
1:A:90:ASN:ND2	1:A:355:ILE:HG13	2.28	0.49
1:B:186:ILE:HG13	1:B:315:GLN:HB3	1.94	0.49
1:B:158:ARG:HB3	1:B:158:ARG:NH1	2.25	0.48
1:B:79:LEU:N	1:B:79:LEU:HD23	2.28	0.48
1:B:89:ILE:HB	1:B:358:VAL:HB	1.94	0.48
1:A:106:ARG:HH22	1:A:107:ARG:HD3	1.77	0.48
1:A:298:GLU:OE1	1:A:331:PRO:HD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:LEU:HD22	1:B:310:PRO:CG	2.43	0.48
1:A:101:MET:HE3	1:A:113:LEU:HD12	1.96	0.48
1:A:55:THR:HG22	1:A:56:GLU:H	1.77	0.48
1:B:26:TRP:HE3	1:B:29:LEU:HD12	1.78	0.48
1:A:176:PHE:C	1:A:178:GLY:H	2.17	0.48
1:A:180:LEU:HB2	1:A:329:PRO:HG2	1.96	0.47
1:A:355:ILE:HG23	1:A:355:ILE:O	2.14	0.47
1:A:215:TYR:HE2	1:A:219:LYS:HZ1	1.60	0.47
1:B:351:PRO:HG2	1:B:354:TRP:CG	2.49	0.47
1:B:263:LEU:HD13	1:B:264:PRO:N	2.30	0.47
1:A:93:ARG:NH1	1:A:270:SER:OG	2.42	0.47
1:A:153:ASP:HB3	1:B:33:TYR:CD2	2.50	0.47
1:B:135:PRO:HG2	1:B:138:THR:HG23	1.96	0.47
1:B:244:PHE:O	1:B:256:THR:HG23	2.15	0.47
1:A:226:ILE:HG12	1:A:239:ALA:HA	1.97	0.46
1:B:180:LEU:HD23	1:B:180:LEU:HA	1.79	0.46
1:A:256:THR:CG2	1:A:257:PRO:HD2	2.45	0.46
1:B:253:LYS:HE2	1:B:284:GLU:HB2	1.98	0.46
1:A:44:TRP:HB2	1:A:49:TRP:CZ3	2.51	0.46
1:B:102:ARG:NH2	1:B:115:ASP:OD1	2.36	0.45
1:A:33:TYR:C	1:A:34:ILE:HG13	2.35	0.45
1:A:219:LYS:C	1:A:221:ASP:H	2.20	0.45
1:B:301:ALA:O	1:B:308:ILE:HA	2.16	0.45
1:B:256:THR:HG23	1:B:257:PRO:HD2	1.99	0.45
1:A:265:SER:HB3	1:A:268:LYS:HB2	1.99	0.44
1:B:214:GLY:O	1:B:218:LYS:HG3	2.17	0.44
1:B:229:ASP:HA	1:B:230:PRO:HD3	1.86	0.44
1:A:28:THR:O	1:A:29:LEU:C	2.56	0.44
1:A:270:SER:O	1:A:274:LEU:HD13	2.17	0.44
1:A:279:LEU:O	1:A:281:LEU:N	2.50	0.44
1:A:79:LEU:N	1:A:79:LEU:HD23	2.33	0.44
1:A:118:PHE:HD2	1:A:119:ILE:HD13	1.83	0.43
1:A:39:ARG:HE	1:A:58:ASN:CB	2.31	0.43
1:A:62:LEU:N	1:A:62:LEU:HD12	2.33	0.43
1:B:234:THR:O	1:B:290:ILE:HD13	2.18	0.43
1:A:191:ASP:OD2	1:B:195:PRO:HG2	2.18	0.43
1:A:232:THR:O	1:A:234:THR:N	2.52	0.43
1:A:62:LEU:H	1:A:62:LEU:HD12	1.83	0.43
1:B:228:LEU:HD21	1:B:290:ILE:HG21	2.00	0.43
1:B:68:ALA:HB2	1:B:149:ILE:HB	2.00	0.43
1:B:192:ARG:CB	1:B:192:ARG:HH11	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:ASN:CG	1:B:155:ILE:N	2.72	0.43
1:B:247:ILE:CG2	1:B:251:GLY:HA2	2.48	0.43
1:A:31:PHE:CD1	1:A:172:VAL:HG11	2.54	0.43
1:B:334:ARG:HH11	1:B:334:ARG:HB2	1.83	0.43
1:B:243:ASN:O	1:B:301:ALA:HA	2.19	0.43
1:A:188:SER:HB2	1:A:225:VAL:HG21	1.99	0.43
1:A:289:ARG:NH1	1:A:291:ASP:HB2	2.34	0.43
1:A:55:THR:CG2	1:A:56:GLU:N	2.82	0.43
1:A:277:HIS:C	1:A:278:ARG:HG2	2.39	0.43
1:B:43:HIS:H	1:B:50:ASP:HB2	1.82	0.43
1:A:114:SER:H	1:A:117:GLN:NE2	2.17	0.43
1:A:328:GLU:HA	1:A:329:PRO:HD3	1.82	0.43
1:A:95:ASP:OD2	1:A:96:GLN:NE2	2.46	0.43
1:B:231:ALA:O	1:B:232:THR:HG23	2.19	0.42
1:A:179:GLY:O	1:A:181:THR:N	2.52	0.42
1:B:279:LEU:HD13	1:B:335:ARG:NH2	2.34	0.42
1:B:220:ARG:O	1:B:221:ASP:HB2	2.18	0.42
1:B:289:ARG:HG2	1:B:289:ARG:H	1.61	0.42
1:B:246:ALA:C	1:B:247:ILE:HD12	2.40	0.42
1:B:321:HIS:HE1	3:B:376:HOH:O	2.01	0.42
1:A:210:SER:O	1:A:213:PRO:HG2	2.20	0.42
1:B:194:ALA:HB1	1:B:195:PRO:HD2	2.01	0.42
1:A:212:LEU:N	1:A:213:PRO:HD2	2.34	0.42
1:A:57:ASP:O	1:A:59:GLN:N	2.53	0.42
1:A:89:ILE:HG23	1:A:133:LEU:HD11	2.01	0.42
1:B:101:MET:HE3	1:B:113:LEU:HD12	2.01	0.42
1:B:232:THR:OG1	1:B:232:THR:O	2.30	0.42
1:A:225:VAL:HG22	1:A:226:ILE:N	2.34	0.42
1:A:229:ASP:HA	1:A:237:GLU:HG3	2.02	0.42
1:B:227:TYR:O	1:B:237:GLU:HB2	2.20	0.42
1:B:289:ARG:HG2	1:B:292:GLU:CD	2.39	0.42
1:A:350:ALA:HA	1:A:351:PRO:HD3	1.94	0.42
1:B:277:HIS:O	1:B:278:ARG:CB	2.58	0.42
1:B:80:LYS:HD3	1:B:141:SER:OG	2.20	0.41
1:A:229:ASP:HA	1:A:230:PRO:HD3	1.95	0.41
1:B:192:ARG:NH1	1:B:206:ASN:O	2.54	0.41
1:A:37:ASP:O	1:A:38:LEU:HG	2.20	0.41
1:B:149:ILE:H	1:B:149:ILE:HD13	1.85	0.41
1:B:158:ARG:CB	1:B:158:ARG:NH1	2.84	0.41
1:B:180:LEU:HD22	1:B:310:PRO:HG3	2.02	0.41
1:B:43:HIS:O	1:B:50:ASP:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:ALA:O	1:A:230:PRO:HG3	2.20	0.41
1:A:247:ILE:CD1	1:A:247:ILE:N	2.83	0.41
1:A:250:ASP:OD2	1:A:252:GLN:HB2	2.20	0.41
1:A:289:ARG:HH11	1:A:289:ARG:CB	2.34	0.41
1:A:144:LEU:O	1:A:146:PRO:HD3	2.20	0.41
1:B:247:ILE:HB	1:B:298:GLU:HG3	2.03	0.41
1:A:91:LEU:HG	1:A:94:PRO:CG	2.43	0.41
1:B:98:ALA:HB2	1:B:118:PHE:CG	2.56	0.41
1:B:149:ILE:N	1:B:149:ILE:HD13	2.36	0.41
1:B:96:GLN:HB3	1:B:266:ILE:CD1	2.40	0.41
1:A:257:PRO:HD3	1:A:288:ILE:HD12	2.03	0.41
1:B:213:PRO:HB2	1:B:225:VAL:HG21	2.03	0.41
1:A:39:ARG:HE	1:A:58:ASN:HB3	1.84	0.41
1:A:301:ALA:O	1:A:308:ILE:HA	2.20	0.40
1:B:252:GLN:O	1:B:282:GLU:HG2	2.21	0.40
1:A:155:ILE:HD11	1:B:32:SER:C	2.42	0.40
1:A:224:ASP:CG	1:A:225:VAL:H	2.25	0.40
1:B:45:LYS:O	1:B:45:LYS:HE3	2.20	0.40
1:B:44:TRP:CH2	1:B:47:GLY:HA2	2.54	0.40
1:B:183:THR:OG1	1:B:223:ALA:HB2	2.21	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	333/358 (93%)	287 (86%)	34 (10%)	12 (4%)	<b>3</b> <b>4</b>
1	B	335/358 (94%)	312 (93%)	20 (6%)	3 (1%)	<b>17</b> <b>31</b>
All	All	668/716 (93%)	599 (90%)	54 (8%)	15 (2%)	<b>6</b> <b>10</b>

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	233	HIS
1	B	233	HIS
1	A	27	SER
1	A	29	LEU
1	A	139	GLY
1	A	180	LEU
1	A	280	GLY
1	A	355	ILE
1	A	308	ILE
1	B	308	ILE
1	A	58	ASN
1	A	178	GLY
1	B	155	ILE
1	A	229	ASP
1	A	230	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	270/289 (93%)	255 (94%)	15 (6%)	21	40
1	B	271/289 (94%)	257 (95%)	14 (5%)	23	44
All	All	541/578 (94%)	512 (95%)	29 (5%)	22	42

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ILE
1	A	37	ASP
1	A	39	ARG
1	A	58	ASN
1	A	62	LEU
1	A	67	THR
1	A	79	LEU
1	A	133	LEU
1	A	170	VAL

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Mol	Chain	Res	Type
1	A	220	ARG
1	A	243	ASN
1	A	290	ILE
1	A	320	PHE
1	A	340	LEU
1	A	355	ILE
1	B	39	ARG
1	B	45	LYS
1	B	62	LEU
1	B	133	LEU
1	B	149	ILE
1	B	181	THR
1	B	192	ARG
1	B	211	LEU
1	B	221	ASP
1	B	232	THR
1	B	235	THR
1	B	243	ASN
1	B	279	LEU
1	B	290	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	ASN
1	A	117	GLN
1	A	154	ASN
1	A	233	HIS
1	A	249	GLN
1	A	344	GLN
1	B	97	ASN
1	B	117	GLN
1	B	131	HIS
1	B	315	GLN
1	B	316	HIS
1	B	344	GLN

### 5.3.3 RNA ⓘ

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](#)

2 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	371	-	15,15,16	2.28	6 (40%)	20,22,23	1.77	6 (30%)
2	PLP	B	372	-	15,15,16	2.57	6 (40%)	20,22,23	1.74	5 (25%)

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	371	-	-	0/6/6/8	0/1/1/1
2	PLP	B	372	-	-	0/6/6/8	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	372	PLP	C5-C4	7.06	1.48	1.40
2	A	371	PLP	C5-C4	6.16	1.47	1.40
2	B	372	PLP	C4A-C4	3.72	1.59	1.51
2	A	371	PLP	C4A-C4	3.49	1.58	1.51
2	A	371	PLP	C6-N1	2.63	1.40	1.34
2	B	372	PLP	C3-C4	2.59	1.45	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	372	PLP	C6-N1	2.47	1.39	1.34
2	A	371	PLP	C3-C4	2.46	1.45	1.40
2	A	371	PLP	C2-N1	2.35	1.38	1.33
2	B	372	PLP	C3-C2	2.28	1.43	1.40
2	B	372	PLP	C2-N1	2.25	1.38	1.33
2	A	371	PLP	C2A-C2	2.11	1.54	1.50

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	372	PLP	C4A-C4-C5	3.37	124.41	120.94
2	A	371	PLP	C4A-C4-C5	3.20	124.23	120.94
2	A	371	PLP	C5A-C5-C6	-2.87	114.65	119.37
2	B	372	PLP	C5A-C5-C6	-2.86	114.67	119.37
2	B	372	PLP	O4P-C5A-C5	2.69	114.48	109.35
2	B	372	PLP	C6-N1-C2	2.50	123.79	119.17
2	A	371	PLP	O4P-C5A-C5	2.46	114.05	109.35
2	A	371	PLP	C6-N1-C2	2.41	123.64	119.17
2	A	371	PLP	O2P-P-O4P	-2.33	100.52	106.73
2	A	371	PLP	C5-C6-N1	-2.21	120.13	123.82
2	B	372	PLP	C5-C6-N1	-2.15	120.23	123.82

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
2	B	372	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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	335/358 (93%)	0.37	20 (5%) 21 22	20, 46, 78, 130	0
1	B	337/358 (94%)	0.14	13 (3%) 39 42	17, 33, 68, 157	0
All	All	672/716 (93%)	0.26	33 (4%) 29 31	17, 39, 75, 157	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	178	GLY	5.7
1	B	179	GLY	5.0
1	B	175	TYR	4.3
1	B	176	PHE	4.1
1	A	240	GLY	3.6
1	B	318	ASP	3.3
1	A	167	VAL	3.2
1	B	307	VAL	3.2
1	A	28	THR	3.1
1	B	300	GLY	3.1
1	B	28	THR	3.1
1	A	318	ASP	3.1
1	A	228	LEU	3.0
1	A	178	GLY	3.0
1	A	81	ALA	2.8
1	A	299	ALA	2.6
1	B	299	ALA	2.6
1	B	177	LYS	2.6
1	A	307	VAL	2.4
1	A	144	LEU	2.4
1	A	358	VAL	2.3
1	B	22	ALA	2.3
1	A	177	LYS	2.2
1	A	218	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	244	PHE	2.2
1	A	51	ALA	2.2
1	A	220	ARG	2.1
1	B	239	ALA	2.1
1	A	181	THR	2.1
1	A	300	GLY	2.1
1	B	174	PRO	2.1
1	A	57	ASP	2.1
1	A	176	PHE	2.0

## 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 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, 95<sup>th</sup> 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	PLP	B	372	15/16	0.93	0.17	18,27,34,46	0
2	PLP	A	371	15/16	0.94	0.13	18,25,33,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.