



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:59 PM GMT

PDB ID : 1DJU
Title : CRYSTAL STRUCTURE OF AROMATIC AMINOTRANSFERASE FROM
PYROCOCUS HORIKOSHII OT3
Authors : Matsui, I.; Matsui, E.; Sakai, Y.; Kikuchi, H.; Kawarabayashi, H.
Deposited on : 1999-12-06
Resolution : 2.10 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

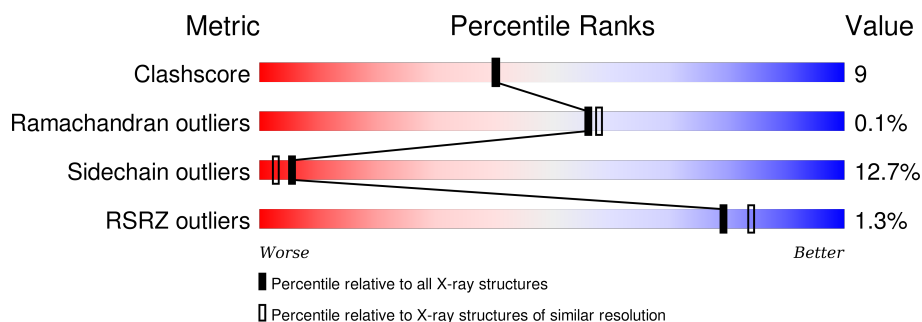
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	388	<div> <div>2%</div> <div>68%</div> <div>23%</div> <div>5%</div> <div>• •</div> </div>
1	B	388	<div> <div>2%</div> <div>63%</div> <div>25%</div> <div>7%</div> <div>• •</div> </div>

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.

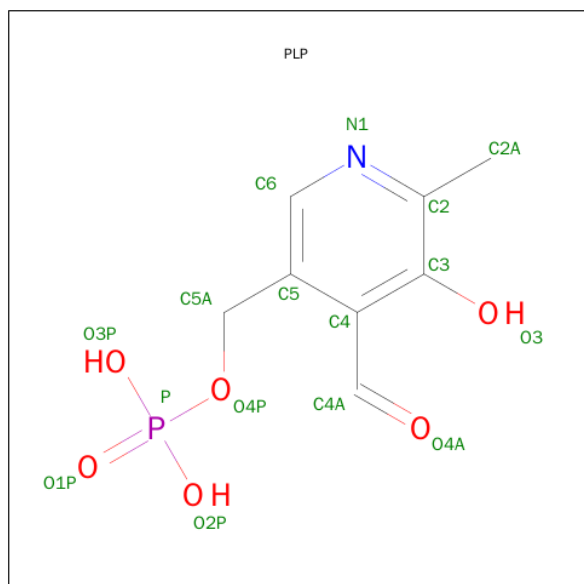
- Molecule 1 is a protein called AROMATIC AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	375	Total 2983	C 1918	N 498	O 554	S 13	0	0	0
1	B	373	Total 2969	C 1909	N 495	O 552	S 13	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	377	GLU	ASP	CONFLICT	UNP O59096
B	377	GLU	ASP	CONFLICT	UNP O59096

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $\text{C}_8\text{H}_{10}\text{NO}_6\text{P}$).



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

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

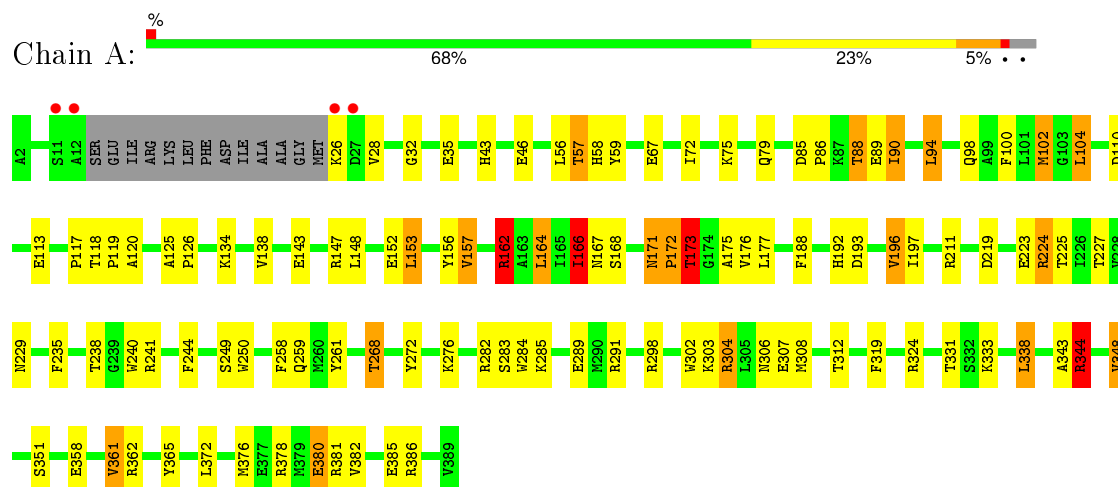
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	107	Total	O	0	0
			107	107		
3	B	93	Total	O	0	0
			93	93		

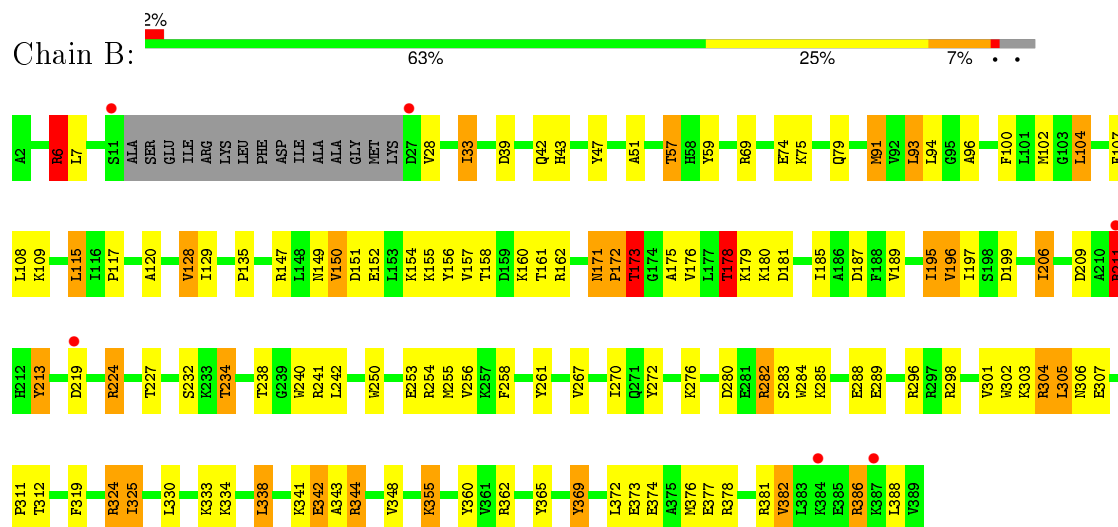
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: AROMATIC AMINOTRANSFERASE



• Molecule 1: AROMATIC AMINOTRANSFERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.01Å 124.87Å 128.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.10 28.03 – 2.02	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.10) 84.2 (28.03-2.02)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.34 (at 2.03Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.185 , 0.254 0.199 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 78.4	EDS
Estimated twinning fraction	0.021 for -h,l,k	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 57422 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6182	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.89	1/3043 (0.0%)	1.60	45/4105 (1.1%)
1	B	0.92	2/3029 (0.1%)	1.62	54/4087 (1.3%)
All	All	0.90	3/6072 (0.0%)	1.61	99/8192 (1.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	176	VAL	CA-CB	5.98	1.67	1.54
1	B	224	ARG	NE-CZ	5.75	1.40	1.33
1	A	289	GLU	CB-CG	5.08	1.61	1.52

All (99) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	298	ARG	NE-CZ-NH2	-12.57	114.02	120.30
1	A	298	ARG	NE-CZ-NH1	12.42	126.51	120.30
1	B	224	ARG	CA-CB-CG	11.71	139.17	113.40
1	A	282	ARG	NE-CZ-NH1	10.95	125.78	120.30
1	A	102	MET	CG-SD-CE	-10.85	82.84	100.20
1	B	224	ARG	NE-CZ-NH1	10.56	125.58	120.30
1	B	304	ARG	NE-CZ-NH2	-9.84	115.38	120.30
1	A	284	TRP	CD1-CG-CD2	9.54	113.93	106.30
1	B	381	ARG	NE-CZ-NH1	9.02	124.81	120.30
1	A	324	ARG	NE-CZ-NH1	8.76	124.68	120.30
1	B	298	ARG	NE-CZ-NH1	8.70	124.65	120.30
1	A	291	ARG	NE-CZ-NH1	8.65	124.62	120.30
1	A	291	ARG	NE-CZ-NH2	-8.48	116.06	120.30
1	A	250	TRP	CD1-CG-CD2	8.24	112.89	106.30
1	B	69	ARG	NE-CZ-NH2	-8.14	116.23	120.30
1	B	324	ARG	NE-CZ-NH1	8.01	124.31	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	173	THR	N-CA-CB	-7.93	95.22	110.30
1	B	147	ARG	NE-CZ-NH2	-7.92	116.34	120.30
1	A	284	TRP	CE2-CD2-CG	-7.85	101.02	107.30
1	B	325	ILE	CA-CB-CG1	-7.77	96.23	111.00
1	B	102	MET	CG-SD-CE	-7.76	87.79	100.20
1	A	304	ARG	NE-CZ-NH2	-7.68	116.46	120.30
1	B	250	TRP	CD1-CG-CD2	7.63	112.40	106.30
1	B	250	TRP	CE2-CD2-CG	-7.61	101.21	107.30
1	A	302	TRP	CD1-CG-CD2	7.57	112.35	106.30
1	B	57	THR	N-CA-CB	-7.52	96.01	110.30
1	A	143	GLU	CA-CB-CG	7.44	129.77	113.40
1	A	241	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	A	250	TRP	CE2-CD2-CG	-7.31	101.45	107.30
1	B	302	TRP	CD1-CG-CD2	7.17	112.04	106.30
1	A	240	TRP	CD1-CG-CD2	7.17	112.04	106.30
1	B	284	TRP	CD1-CG-CD2	7.17	112.03	106.30
1	B	240	TRP	CE2-CD2-CG	-7.13	101.59	107.30
1	B	240	TRP	CD1-CG-CD2	7.12	112.00	106.30
1	B	69	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	B	254	ARG	NE-CZ-NH2	-7.03	116.78	120.30
1	B	284	TRP	CE2-CD2-CG	-7.02	101.68	107.30
1	B	199	ASP	CB-CG-OD2	6.98	124.58	118.30
1	A	298	ARG	CB-CG-CD	-6.97	93.47	111.60
1	B	344	ARG	NE-CZ-NH1	6.94	123.77	120.30
1	B	211	ARG	NE-CZ-NH2	-6.92	116.84	120.30
1	B	173	THR	N-CA-CB	-6.89	97.21	110.30
1	A	110	ASP	N-CA-C	6.88	129.58	111.00
1	B	302	TRP	CE2-CD2-CG	-6.84	101.83	107.30
1	A	240	TRP	CE2-CD2-CG	-6.75	101.90	107.30
1	A	59	TYR	CB-CG-CD2	-6.74	116.96	121.00
1	B	241	ARG	NE-CZ-NH2	-6.71	116.95	120.30
1	A	302	TRP	CE2-CD2-CG	-6.61	102.01	107.30
1	A	344	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	B	213	TYR	CB-CG-CD2	-6.53	117.08	121.00
1	B	224	ARG	CB-CG-CD	6.49	128.46	111.60
1	A	282	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	B	304	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	B	369	TYR	CB-CG-CD2	-6.42	117.15	121.00
1	A	284	TRP	CG-CD1-NE1	-6.36	103.75	110.10
1	A	361	VAL	CG1-CB-CG2	6.31	121.00	110.90
1	B	149	ASN	N-CA-CB	-6.30	99.26	110.60
1	A	386	ARG	NE-CZ-NH1	6.28	123.44	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	196	VAL	CB-CA-C	-6.16	99.70	111.40
1	B	298	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	B	6	ARG	NE-CZ-NH1	6.13	123.37	120.30
1	A	361	VAL	CA-CB-CG2	-6.09	101.76	110.90
1	A	224	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	B	224	ARG	NH1-CZ-NH2	-6.03	112.77	119.40
1	A	162	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	B	59	TYR	CB-CG-CD2	-5.99	117.41	121.00
1	B	180	LYS	CA-CB-CG	-5.95	100.32	113.40
1	B	261	TYR	CB-CG-CD2	-5.89	117.46	121.00
1	A	261	TYR	CB-CG-CD1	-5.83	117.50	121.00
1	A	110	ASP	CA-C-N	5.83	127.86	116.20
1	B	386	ARG	CB-CG-CD	5.76	126.56	111.60
1	A	147	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	A	333	LYS	CA-CB-CG	5.67	125.86	113.40
1	A	88	THR	N-CA-CB	-5.65	99.56	110.30
1	A	235	PHE	CA-C-N	5.59	129.50	117.20
1	B	196	VAL	CB-CA-C	-5.57	100.82	111.40
1	B	241	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	A	235	PHE	O-C-N	-5.54	113.83	122.70
1	B	150	VAL	CG1-CB-CG2	-5.52	102.07	110.90
1	B	199	ASP	CB-CG-OD1	-5.44	113.40	118.30
1	A	304	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	B	240	TRP	CG-CD2-CE3	5.40	138.76	133.90
1	B	209	ASP	CB-CG-OD2	5.34	123.10	118.30
1	B	298	ARG	CB-CG-CD	-5.32	97.78	111.60
1	A	338	LEU	CA-CB-CG	5.29	127.48	115.30
1	A	57	THR	N-CA-CB	-5.29	100.25	110.30
1	B	178	THR	N-CA-CB	-5.24	100.34	110.30
1	B	93	LEU	CA-CB-CG	5.23	127.33	115.30
1	B	325	ILE	CA-CB-CG2	5.16	121.21	110.90
1	A	211	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	B	360	TYR	CB-CG-CD2	-5.13	117.92	121.00
1	B	39	ASP	CB-CG-OD1	5.11	122.90	118.30
1	B	147	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	B	282	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	A	331	THR	CA-CB-CG2	5.06	119.48	112.40
1	B	355	LYS	CA-CB-CG	-5.05	102.30	113.40
1	B	381	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	A	166	ILE	CA-CB-CG1	-5.01	101.47	111.00
1	A	157	VAL	CB-CA-C	-5.01	101.88	111.40

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	2983	0	3024	50	0
1	B	2969	0	3006	56	0
2	A	15	0	6	0	0
2	B	15	0	6	1	0
3	A	107	0	0	4	0
3	B	93	0	0	3	0
All	All	6182	0	6042	105	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 9.

All (105) 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:173:THR:HG22	1:B:175:ALA:H	1.47	0.79
1:B:91:MET:HE1	1:B:255:MET:HB2	1.65	0.79
1:B:171:ASN:HD21	1:B:362:ARG:HH11	1.30	0.78
1:A:98:GLN:HE22	1:A:259:GLN:HE22	1.34	0.76
1:B:211:ARG:HD3	1:B:213:TYR:HE1	1.51	0.75
1:A:88:THR:HG22	1:A:89:GLU:HG3	1.69	0.72
1:A:348:VAL:HG13	1:A:362:ARG:HB3	1.72	0.71
1:B:158:THR:HG22	1:B:160:LYS:H	1.56	0.71
1:B:178:THR:HG22	1:B:181:ASP:H	1.57	0.68
1:B:91:MET:HE1	1:B:255:MET:CB	2.25	0.67
1:A:171:ASN:HD21	1:A:362:ARG:HH11	1.40	0.67
1:A:28:VAL:HA	1:A:344:ARG:HB3	1.78	0.65
1:B:104:LEU:HD13	1:B:197:ILE:HD11	1.76	0.65
1:B:211:ARG:HD3	1:B:213:TYR:CE1	2.30	0.63
1:B:150:VAL:HG12	1:B:154:LYS:HE2	1.83	0.59
1:A:168:SER:HB3	3:A:434:HOH:O	2.02	0.59
1:B:43:HIS:HE1	1:B:283:SER:OG	1.85	0.59
1:B:151:ASP:O	1:B:155:LYS:HD3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:ARG:HH22	1:A:380:GLU:HG3	1.69	0.57
1:A:193:ASP:HA	1:A:224:ARG:NH2	2.20	0.57
1:B:107:PHE:CZ	1:B:195:ILE:HG12	2.41	0.56
1:A:35:GLU:HB2	1:A:238:THR:HG21	1.87	0.56
1:B:280:ASP:OD2	1:B:282:ARG:HD3	2.06	0.55
1:A:173:THR:HG22	1:A:175:ALA:H	1.73	0.54
1:B:51:ALA:HB2	1:B:272:TYR:CD2	2.41	0.54
1:B:179:LYS:HB2	1:B:213:TYR:CE1	2.42	0.54
1:A:171:ASN:HD22	1:A:172:PRO:HA	1.73	0.54
1:B:117:PRO:O	1:B:120:ALA:HB2	2.08	0.53
1:A:58:HIS:O	1:A:268:THR:HG21	2.08	0.53
1:B:171:ASN:HD21	1:B:362:ARG:NH1	2.03	0.52
1:B:6:ARG:HD3	1:B:129:ILE:O	2.11	0.51
1:B:234:THR:HG22	3:B:468:HOH:O	2.11	0.51
1:A:303:LYS:O	1:A:307:GLU:HB2	2.11	0.51
1:A:117:PRO:O	1:A:120:ALA:HB2	2.10	0.50
1:A:372:LEU:O	1:A:376:MET:HG2	2.11	0.50
1:A:88:THR:HG23	1:A:249:SER:HB3	1.94	0.50
1:B:378:ARG:O	1:B:382:VAL:HG12	2.12	0.49
1:A:113:GLU:HA	1:A:134:LYS:O	2.13	0.49
1:B:369:TYR:O	1:B:373:GLU:HG3	2.13	0.49
1:B:386:ARG:HG3	1:B:388:LEU:HG	1.95	0.48
1:B:303:LYS:O	1:B:307:GLU:HG2	2.13	0.48
1:A:118:THR:HG22	1:A:138:VAL:O	2.12	0.48
1:A:98:GLN:HB3	1:A:102:MET:HE3	1.95	0.48
1:B:173:THR:HG21	3:B:473:HOH:O	2.13	0.47
1:B:33:ILE:H	1:B:33:ILE:HD13	1.79	0.47
1:A:164:LEU:HD13	1:A:166:ILE:HD13	1.95	0.47
1:A:229:ASN:HB3	1:A:244:PHE:CE2	2.49	0.47
1:B:206:ILE:H	1:B:206:ILE:HD13	1.80	0.47
1:B:100:PHE:O	1:B:104:LEU:HB2	2.15	0.47
1:A:118:THR:HG21	3:A:447:HOH:O	2.15	0.47
1:B:311:PRO:HG2	1:B:324:ARG:NH1	2.29	0.47
1:A:32:GLY:HA2	3:A:436:HOH:O	2.15	0.47
1:A:167:ASN:ND2	1:A:171:ASN:H	2.14	0.46
1:B:343:ALA:O	1:B:378:ARG:HD3	2.15	0.46
1:A:162:ARG:HD3	3:A:487:HOH:O	2.15	0.46
1:A:100:PHE:O	1:A:104:LEU:HB2	2.15	0.46
1:B:152:GLU:O	1:B:156:TYR:HD1	1.97	0.46
1:A:171:ASN:HD21	1:A:362:ARG:NH1	2.10	0.46
1:B:211:ARG:HD2	1:B:211:ARG:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:ASP:O	1:B:185:ILE:HG23	2.16	0.45
1:B:301:VAL:HG11	1:B:372:LEU:HD22	1.97	0.45
1:A:94:LEU:HD22	1:B:94:LEU:HD22	1.99	0.45
1:B:234:THR:HG21	3:B:428:HOH:O	2.16	0.45
1:A:118:THR:HA	1:A:119:PRO:C	2.37	0.45
1:A:348:VAL:CG1	1:A:362:ARG:HB3	2.44	0.45
1:A:381:ARG:HH21	1:A:385:GLU:HG2	1.82	0.45
1:A:188:PHE:O	1:A:192:HIS:HD2	2.00	0.44
1:A:85:ASP:OD1	1:A:88:THR:HB	2.17	0.44
1:B:343:ALA:HB2	1:B:382:VAL:HG11	1.99	0.44
1:B:232:SER:HB3	1:B:238:THR:HG22	2.00	0.44
1:B:28:VAL:HA	1:B:344:ARG:O	2.18	0.43
1:B:305:LEU:HD13	1:B:376:MET:SD	2.58	0.43
1:B:338:LEU:O	1:B:342:GLU:HB2	2.18	0.43
1:A:28:VAL:HA	1:A:344:ARG:O	2.18	0.43
1:A:43:HIS:HE1	1:A:283:SER:OG	2.01	0.43
1:B:171:ASN:HD22	1:B:172:PRO:HA	1.83	0.43
1:A:306:ASN:HD21	1:A:312:THR:H	1.65	0.43
1:B:96:ALA:HB3	2:B:400:PLP:H5A1	2.00	0.43
1:A:193:ASP:HA	1:A:224:ARG:HH21	1.83	0.43
1:B:75:LYS:HZ3	1:B:79:GLN:HE21	1.67	0.43
1:A:272:TYR:CZ	1:A:276:LYS:HE2	2.54	0.43
1:B:242:LEU:HD22	1:B:270:ILE:HG22	2.01	0.43
1:A:72:ILE:HG21	1:A:90:ILE:HD13	2.01	0.43
1:B:306:ASN:HD21	1:B:312:THR:H	1.66	0.43
1:A:343:ALA:O	1:A:378:ARG:HD3	2.19	0.43
1:A:319:PHE:HA	1:A:365:TYR:CZ	2.54	0.42
1:B:319:PHE:HA	1:B:365:TYR:CZ	2.55	0.42
1:A:85:ASP:HA	1:A:86:PRO:HD2	1.91	0.42
1:B:296:ARG:HD2	1:B:296:ARG:HH11	1.75	0.42
1:A:75:LYS:HZ3	1:A:79:GLN:HE21	1.66	0.41
1:A:171:ASN:HD22	1:A:172:PRO:CA	2.34	0.41
1:B:115:LEU:HD22	1:B:161:THR:HG21	2.02	0.41
1:A:125:ALA:HB3	1:A:126:PRO:HD3	2.02	0.41
1:B:171:ASN:ND2	1:B:362:ARG:HH11	2.09	0.41
1:A:75:LYS:NZ	1:A:79:GLN:HE21	2.19	0.41
1:A:152:GLU:O	1:A:156:TYR:HD1	2.04	0.41
1:B:185:ILE:O	1:B:189:VAL:HG23	2.21	0.41
1:A:148:LEU:HD11	1:A:153:LEU:HD13	2.01	0.41
1:B:47:TYR:CD2	1:B:276:LYS:HD3	2.56	0.41
1:B:33:ILE:H	1:B:33:ILE:CD1	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:355:LYS:HA	1:B:355:LYS:HD3	1.66	0.40
1:A:104:LEU:HD13	1:A:197:ILE:HD11	2.02	0.40
1:A:308:MET:HB3	1:A:380:GLU:HG2	2.03	0.40
1:B:128:VAL:HG22	1:B:135:PRO:HD3	2.04	0.40
1:B:285:LYS:HB2	1:B:285:LYS:HE3	1.97	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	371/388 (96%)	358 (96%)	13 (4%)	0	100	100
1	B	369/388 (95%)	356 (96%)	12 (3%)	1 (0%)	46	45
All	All	740/776 (95%)	714 (96%)	25 (3%)	1 (0%)	56	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	219	ASP

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	316/326 (97%)	282 (89%)	34 (11%)	8	4
1	B	315/326 (97%)	269 (85%)	46 (15%)	4	2
All	All	631/652 (97%)	551 (87%)	80 (13%)	5	3

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LYS
1	A	46	GLU
1	A	56	LEU
1	A	57	THR
1	A	67	GLU
1	A	90	ILE
1	A	94	LEU
1	A	104	LEU
1	A	153	LEU
1	A	157	VAL
1	A	162	ARG
1	A	164	LEU
1	A	166	ILE
1	A	171	ASN
1	A	172	PRO
1	A	173	THR
1	A	176	VAL
1	A	177	LEU
1	A	196	VAL
1	A	219	ASP
1	A	223	GLU
1	A	225	THR
1	A	227	THR
1	A	258	PHE
1	A	268	THR
1	A	285	LYS
1	A	338	LEU
1	A	344	ARG
1	A	348	VAL
1	A	351	SER
1	A	358	GLU
1	A	361	VAL

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Mol	Chain	Res	Type
1	A	380	GLU
1	A	382	VAL
1	B	6	ARG
1	B	7	LEU
1	B	33	ILE
1	B	42	GLN
1	B	57	THR
1	B	74	GLU
1	B	91	MET
1	B	93	LEU
1	B	104	LEU
1	B	108	LEU
1	B	109	LYS
1	B	115	LEU
1	B	128	VAL
1	B	157	VAL
1	B	162	ARG
1	B	171	ASN
1	B	172	PRO
1	B	173	THR
1	B	178	THR
1	B	187	ASP
1	B	195	ILE
1	B	196	VAL
1	B	206	ILE
1	B	211	ARG
1	B	224	ARG
1	B	227	THR
1	B	234	THR
1	B	253	GLU
1	B	256	VAL
1	B	258	PHE
1	B	267	VAL
1	B	288	GLU
1	B	289	GLU
1	B	304	ARG
1	B	305	LEU
1	B	325	ILE
1	B	330	LEU
1	B	333	LYS
1	B	334	LYS
1	B	338	LEU

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Mol	Chain	Res	Type
1	B	341	LYS
1	B	342	GLU
1	B	348	VAL
1	B	374	GLU
1	B	377	GLU
1	B	382	VAL

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

Mol	Chain	Res	Type
1	A	43	HIS
1	A	62	ASN
1	A	79	GLN
1	A	98	GLN
1	A	167	ASN
1	A	171	ASN
1	A	192	HIS
1	A	204	HIS
1	A	306	ASN
1	B	43	HIS
1	B	58	HIS
1	B	79	GLN
1	B	167	ASN
1	B	171	ASN
1	B	306	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 carbohydrates in this entry.

5.6 Ligand geometry

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	400	1	15,15,16	1.97	3 (20%)	21,22,23	3.16	11 (52%)
2	PLP	B	400	1	15,15,16	1.81	2 (13%)	21,22,23	2.52	9 (42%)

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	400	1	-	0/6/6/8	0/1/1/1
2	PLP	B	400	1	-	0/6/6/8	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	400	PLP	C4A-C4	-4.90	1.41	1.51
2	A	400	PLP	C4A-C4	-4.60	1.42	1.51
2	A	400	PLP	P-O4P	-3.20	1.49	1.60
2	B	400	PLP	P-O4P	-2.48	1.51	1.60
2	A	400	PLP	C3-C2	-2.05	1.39	1.40

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	400	PLP	C3-C4-C5	-5.80	112.45	118.78
2	B	400	PLP	C5A-C5-C6	-3.82	112.06	119.28
2	B	400	PLP	C5-C6-N1	-3.81	117.25	123.86
2	B	400	PLP	C3-C4-C5	-3.43	115.04	118.78
2	A	400	PLP	C5A-C5-C6	-3.29	113.06	119.28
2	A	400	PLP	C5-C6-N1	-2.78	119.04	123.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	400	PLP	O4P-P-O1P	-2.68	100.33	107.14
2	A	400	PLP	O3-C3-C2	-2.33	113.61	117.66
2	B	400	PLP	C4A-C4-C5	2.45	123.44	120.88
2	A	400	PLP	O2P-P-O4P	2.53	113.85	106.56
2	B	400	PLP	C6-N1-C2	2.64	124.67	119.28
2	B	400	PLP	C2A-C2-C3	2.71	124.30	121.04
2	B	400	PLP	O2P-P-O4P	2.83	114.72	106.56
2	A	400	PLP	O3P-P-O4P	2.84	114.75	106.56
2	B	400	PLP	O4P-C5A-C5	3.66	115.05	108.99
2	A	400	PLP	O4P-C5A-C5	4.67	116.72	108.99
2	A	400	PLP	C2A-C2-C3	4.84	126.88	121.04
2	A	400	PLP	C4A-C4-C5	5.54	126.65	120.88
2	A	400	PLP	C6-C5-C4	5.98	123.22	118.15
2	B	400	PLP	C6-C5-C4	6.09	123.31	118.15

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	400	PLP	1	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	375/388 (96%)	-0.13	4 (1%) 82 86	13, 23, 40, 71	0
1	B	373/388 (96%)	-0.10	6 (1%) 74 79	14, 23, 39, 61	0
All	All	748/776 (96%)	-0.12	10 (1%) 79 84	13, 23, 40, 71	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	11	SER	4.2
1	A	27	ASP	3.9
1	A	26	LYS	3.3
1	B	11	SER	3.1
1	B	219	ASP	3.0
1	B	387	LYS	3.0
1	A	12	ALA	2.8
1	B	211	ARG	2.6
1	B	384	LYS	2.4
1	B	27	ASP	2.3

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(\AA^2)	Q<0.9
2	PLP	A	400	15/16	0.96	0.14	0.81	16,22,26,26	0
2	PLP	B	400	15/16	0.97	0.10	-0.51	15,18,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.