



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 10:33 AM UTC

PDB ID : 3WWI / pdb_00003wwi
Title : Crystal structure of the G136F mutant of the first R-stereoselective -
transaminase identified from *Arthrobacter* sp. KNK168 (FERM-BP-5228)
Authors : Guan, L.J.; Ohtsuka, J.; Miyakawa, T.; Zhi, Y.; Ito, N.; Yasohara, Y.;
Tanokura, M.
Deposited on : 2014-06-18
Resolution : 2.27 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

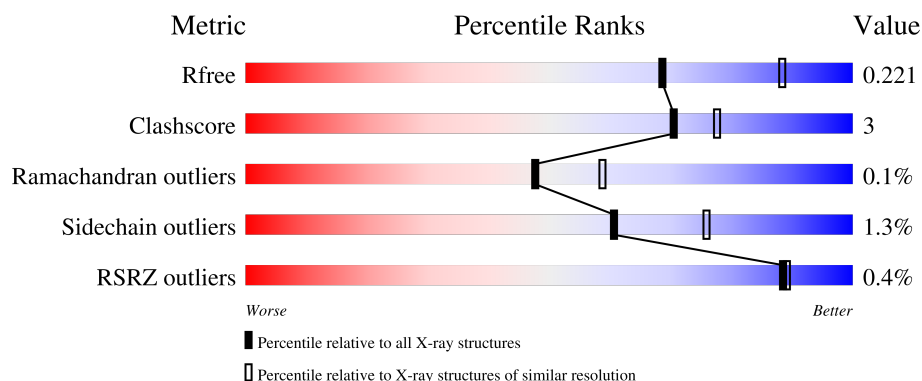
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	330	93% 5% •
1	B	330	92% 6% •
1	C	330	91% 6% ••
1	D	330	92% 5% •
1	E	330	91% 5% ••

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Mol	Chain	Length	Quality of chain
1	F	330	89% 8% .
1	G	330	91% 7% .
1	H	330	92% 5% .
1	I	330	92% 5% .
1	J	330	89% 8% .
1	K	330	89% 8% .
1	L	330	2% 82% 15% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 32328 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 (R)-amine transaminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	B	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	C	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	D	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	E	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	F	322	Total	C	N	O	S	0	0	0
			2521	1606	427	484	4			
1	G	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	H	322	Total	C	N	O	S	0	0	0
			2521	1606	427	484	4			
1	I	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	J	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	K	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			
1	L	322	Total	C	N	O	S	0	0	0
			2525	1609	428	484	4			

There are 12 discrepancies between the modelled and reference sequences:

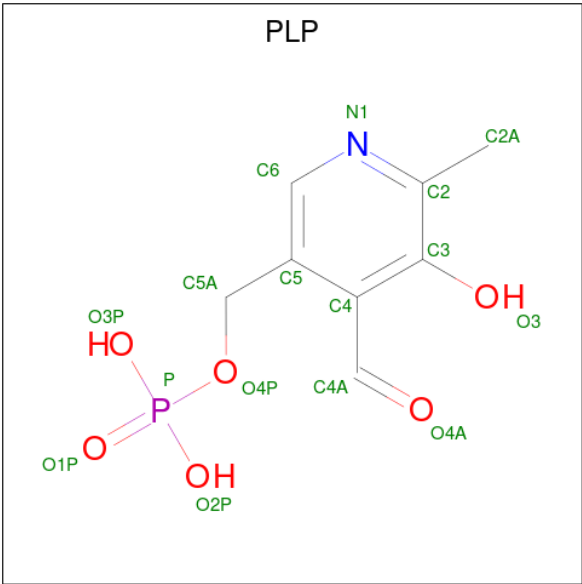
Chain	Residue	Modelled	Actual	Comment	Reference
A	136	PHE	GLY	engineered mutation	UNP F7J696
B	136	PHE	GLY	engineered mutation	UNP F7J696
C	136	PHE	GLY	engineered mutation	UNP F7J696
D	136	PHE	GLY	engineered mutation	UNP F7J696
E	136	PHE	GLY	engineered mutation	UNP F7J696

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Chain	Residue	Modelled	Actual	Comment	Reference
F	136	PHE	GLY	engineered mutation	UNP F7J696
G	136	PHE	GLY	engineered mutation	UNP F7J696
H	136	PHE	GLY	engineered mutation	UNP F7J696
I	136	PHE	GLY	engineered mutation	UNP F7J696
J	136	PHE	GLY	engineered mutation	UNP F7J696
K	136	PHE	GLY	engineered mutation	UNP F7J696
L	136	PHE	GLY	engineered mutation	UNP F7J696

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: C₈H₁₀NO₆P).



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		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	E	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	F	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	G	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	H	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	I	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	J	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	K	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	L	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

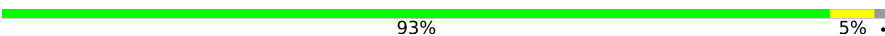
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	182	Total	O	0	0
			182	182		
3	B	187	Total	O	0	0
			187	187		
3	C	185	Total	O	0	0
			185	185		
3	D	211	Total	O	0	0
			211	211		
3	E	101	Total	O	0	0
			101	101		
3	F	197	Total	O	0	0
			197	197		
3	G	139	Total	O	0	0
			139	139		
3	H	229	Total	O	0	0
			229	229		
3	I	176	Total	O	0	0
			176	176		
3	J	82	Total	O	0	0
			82	82		
3	K	115	Total	O	0	0
			115	115		
3	L	52	Total	O	0	0
			52	52		

3 Residue-property plots [i](#)

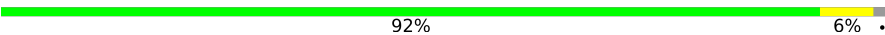
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: (R)-amine transaminase

Chain A:  93% 5% .



- Molecule 1: (R)-amine transaminase

Chain B:  92% 6% .

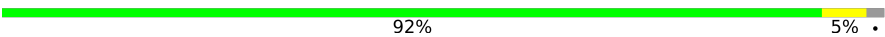


- Molecule 1: (R)-amine transaminase

Chain C:  91% 6% ..

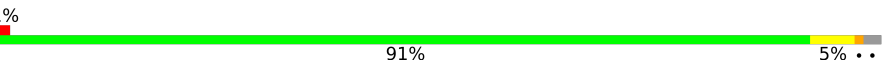


- Molecule 1: (R)-amine transaminase

Chain D:  92% 5% .



- Molecule 1: (R)-amine transaminase

Chain E:  91% 5% ..



- Molecule 1: (R)-amine transaminase

L326		MET
	G	ALA
Y330		PHE
	SER	SER
	ALA	ALA
	ASP	ASP
	THR	THR
	SER	SER
	E9	E9
		H40
		G43
		A44
		R52
		V65
		S132
		T133
		T134
		P135
		F136
		D139
		I140
		T141
		V152
		P153
		R162
		K188
		A198
		T202
		E208
		G222
		F225
		R236
		S237
		P238
		A265
		S299
		R313
		E316
		S321

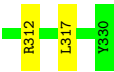
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|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| MET | ALA | PHE | SER | ALA | ASP | THR | SER | E9 | I10 | R52 | G59 | S63 | Y67 | E92 | V113 | T116 | E117 | L118 | T134 | R138 | H143 | I157 | R162 | K188 | Q191 | V199 | T202 | G222 | F225 | L279 | A284 | V293 |
|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|

- | MET |
|------|
| ALA |
| PHE |
| SER |
| ALA |
| ASP |
| THR |
| SER |
| E9 |
| D15 |
| P30 |
| G37 |
| P48 |
| D81 |
| E92 |
| K106 |
| R139 |
| T141 |
| I157 |
| V158 |
| V175 |
| K188 |
| A198 |
| T202 |
| R240 |
| I263 |
| L279 |
| V330 |

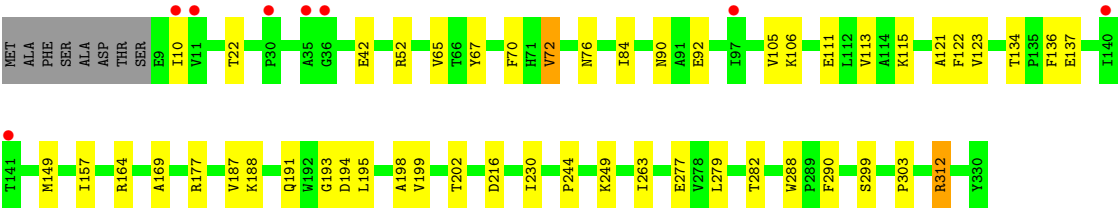
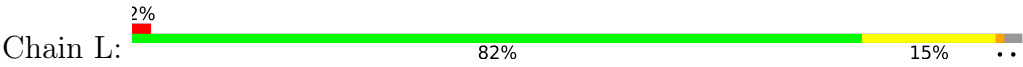
- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| NET | ALA | PHE | SER | ALA | ASP | THR | SER | E9 | Y67 | N90 | F122 | E137 | R138 | V152 | P153 | K188 | V199 | T202 | V229 | R240 | E277 | V278 | L279 | D300 | G301 | V302 | P303 | G304 | V330 |
|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|

- | MET | |
|------|----|
| ALA | |
| PHE | |
| SER | |
| ASP | |
| THR | |
| SER | E9 |
| R52 | |
| Q58 | |
| V65 | |
| T66 | |
| Y67 | |
| D82 | |
| E92 | |
| F122 | |
| G130 | |
| P135 | |
| I140 | |
| V152 | |
| P153 | |
| K188 | |
| G193 | |
| D194 | |
| L195 | |
| V199 | |
| T202 | |
| E208 | |
| A220 | |
| S223 | |
| I230 | |
| V235 | |
| R236 | |
| R240 | |
| T246 | |
| I263 | |
| D276 | |
| L279 | |
| P289 | |
| T307 | |
| Y330 | |

- | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|------|
| MET | ALA | PHE | SER | ALA | ASP | THR | SER | E9 | T16 | I21 | E42 | S49 | R52 | L61 | V65 | I127 | E137 | V147 | R164 | K188 | L195 | V199 | T202 | L219 | S223 | V227 | V228 | V229 | L230 | R236 | S237 | P238 | A265 | E277 | V278 | L279 | D292 |
|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|------|



- Molecule 1: (R)-amine transaminase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.96Å 134.28Å 196.04Å 90.00° 100.34° 90.00°	Depositor
Resolution (Å)	40.00 – 2.27 40.00 – 2.27	Depositor EDS
% Data completeness (in resolution range)	98.8 (40.00-2.27) 99.1 (40.00-2.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.171 , 0.218 0.178 , 0.221	Depositor DCC
R_{free} test set	9595 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	36.0	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.005 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	32328	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.47 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.2659e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.93	0/2588	0.91	1/3534 (0.0%)
1	B	0.93	1/2588 (0.0%)	0.90	1/3534 (0.0%)
1	C	0.89	0/2588	0.90	0/3534
1	D	0.94	0/2588	0.92	3/3534 (0.1%)
1	E	0.77	0/2588	0.88	0/3534
1	F	0.86	0/2584	0.90	0/3530
1	G	0.79	0/2588	0.88	0/3534
1	H	0.97	1/2584 (0.0%)	0.94	2/3530 (0.1%)
1	I	0.88	0/2588	0.90	2/3534 (0.1%)
1	J	0.79	1/2588 (0.0%)	0.87	1/3534 (0.0%)
1	K	0.77	0/2588	0.87	1/3534 (0.0%)
1	L	0.73	0/2588	0.87	2/3534 (0.1%)
All	All	0.86	3/31048 (0.0%)	0.90	13/42400 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	220	ALA	CA-C	6.47	1.55	1.52
1	H	92	GLU	C-O	-5.59	1.17	1.24
1	B	46	VAL	C-O	-5.35	1.20	1.24

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	64	ASP	N-CA-C	-5.69	101.68	109.71
1	I	122	PHE	N-CA-C	-5.49	99.95	108.90
1	H	263	ILE	N-CA-C	5.40	117.86	108.90
1	D	97	ILE	CA-C-N	-5.29	114.94	120.38
1	D	97	ILE	C-N-CA	-5.29	114.94	120.38

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	2525	0	2464	12	0
1	B	2525	0	2464	15	0
1	C	2525	0	2464	21	0
1	D	2525	0	2464	17	0
1	E	2525	0	2464	15	0
1	F	2521	0	2453	17	0
1	G	2525	0	2464	17	0
1	H	2521	0	2453	9	0
1	I	2525	0	2464	12	0
1	J	2525	0	2464	20	0
1	K	2525	0	2464	23	0
1	L	2525	0	2464	30	0
2	A	15	0	6	2	0
2	B	15	0	7	4	0
2	C	15	0	6	2	0
2	D	15	0	6	4	0
2	E	15	0	6	2	0
2	F	15	0	7	2	0
2	G	15	0	6	2	0
2	H	15	0	6	3	0
2	I	15	0	6	2	0
2	J	15	0	6	3	0
2	K	15	0	6	2	0
2	L	15	0	6	2	0
3	A	182	0	0	1	0
3	B	187	0	0	1	0
3	C	185	0	0	4	0
3	D	211	0	0	1	0
3	E	101	0	0	0	0
3	F	197	0	0	2	0
3	G	139	0	0	3	0
3	H	229	0	0	1	0
3	I	176	0	0	1	0
3	J	82	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	115	0	0	2	0
3	L	52	0	0	1	0
All	All	32328	0	29620	191	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.

The worst 5 of 191 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:D:188:LYS:HZ3	2:D:401:PLP:C4A	1.38	1.33
1:B:188:LYS:HZ1	2:B:401:PLP:C4A	1.44	1.30
1:H:188:LYS:HZ1	2:H:401:PLP:C4A	1.54	1.20
1:A:188:LYS:HZ1	2:A:401:PLP:C4A	1.63	1.08
1:F:188:LYS:HZ1	2:F:401:PLP:C4A	1.58	1.03

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	320/330 (97%)	308 (96%)	12 (4%)	0	100	100
1	B	320/330 (97%)	310 (97%)	10 (3%)	0	100	100
1	C	320/330 (97%)	311 (97%)	9 (3%)	0	100	100
1	D	320/330 (97%)	311 (97%)	9 (3%)	0	100	100
1	E	320/330 (97%)	314 (98%)	6 (2%)	0	100	100
1	F	320/330 (97%)	316 (99%)	3 (1%)	1 (0%)	36	44
1	G	320/330 (97%)	309 (97%)	11 (3%)	0	100	100
1	H	320/330 (97%)	309 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	320/330 (97%)	307 (96%)	13 (4%)	0	100	100
1	J	320/330 (97%)	307 (96%)	13 (4%)	0	100	100
1	K	320/330 (97%)	311 (97%)	9 (3%)	0	100	100
1	L	320/330 (97%)	308 (96%)	10 (3%)	2 (1%)	21	25
All	All	3840/3960 (97%)	3721 (97%)	116 (3%)	3 (0%)	48	59

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	299	SER
1	F	299	SER
1	L	244	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	273/279 (98%)	273 (100%)	0	100	100
1	B	273/279 (98%)	271 (99%)	2 (1%)	76	86
1	C	273/279 (98%)	271 (99%)	2 (1%)	76	86
1	D	273/279 (98%)	270 (99%)	3 (1%)	65	79
1	E	273/279 (98%)	268 (98%)	5 (2%)	51	68
1	F	272/279 (98%)	268 (98%)	4 (2%)	57	72
1	G	273/279 (98%)	271 (99%)	2 (1%)	76	86
1	H	272/279 (98%)	268 (98%)	4 (2%)	57	72
1	I	273/279 (98%)	270 (99%)	3 (1%)	65	79
1	J	273/279 (98%)	269 (98%)	4 (2%)	57	72
1	K	273/279 (98%)	269 (98%)	4 (2%)	57	72
1	L	273/279 (98%)	265 (97%)	8 (3%)	37	52
All	All	3274/3348 (98%)	3233 (99%)	41 (1%)	61	76

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	122	PHE
1	L	65	VAL
1	K	49	SER
1	K	317	LEU
1	L	92	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	62	HIS
1	I	260	HIS
1	L	143	HIS
1	H	226	ASN
1	I	74	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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	E	401	1	15,15,16	2.78	4 (26%)	21,22,23	1.75	5 (23%)
2	PLP	B	401	1	15,15,16	2.61	3 (20%)	21,22,23	1.52	4 (19%)
2	PLP	C	401	1	15,15,16	2.30	4 (26%)	21,22,23	1.46	3 (14%)
2	PLP	D	401	1	15,15,16	2.62	3 (20%)	21,22,23	1.58	6 (28%)
2	PLP	K	401	1	15,15,16	2.70	4 (26%)	21,22,23	1.47	3 (14%)
2	PLP	J	401	1	15,15,16	2.75	3 (20%)	21,22,23	1.73	3 (14%)
2	PLP	G	401	1	15,15,16	2.56	3 (20%)	21,22,23	1.20	2 (9%)
2	PLP	F	401	1	15,15,16	2.21	4 (26%)	21,22,23	1.60	5 (23%)
2	PLP	H	401	1	15,15,16	1.69	4 (26%)	21,22,23	1.64	7 (33%)
2	PLP	A	401	1	15,15,16	2.21	4 (26%)	21,22,23	1.57	5 (23%)
2	PLP	L	401	1	15,15,16	2.49	3 (20%)	21,22,23	1.56	4 (19%)
2	PLP	I	401	1	15,15,16	2.44	3 (20%)	21,22,23	1.55	6 (28%)

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	E	401	1	-	0/6/6/8	0/1/1/1
2	PLP	B	401	1	-	0/6/6/8	0/1/1/1
2	PLP	C	401	1	-	0/6/6/8	0/1/1/1
2	PLP	D	401	1	-	0/6/6/8	0/1/1/1
2	PLP	K	401	1	-	0/6/6/8	0/1/1/1
2	PLP	J	401	1	-	0/6/6/8	0/1/1/1
2	PLP	G	401	1	-	0/6/6/8	0/1/1/1
2	PLP	F	401	1	-	0/6/6/8	0/1/1/1
2	PLP	H	401	1	-	0/6/6/8	0/1/1/1
2	PLP	A	401	1	-	0/6/6/8	0/1/1/1
2	PLP	L	401	1	-	0/6/6/8	0/1/1/1
2	PLP	I	401	1	-	0/6/6/8	0/1/1/1

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	401	PLP	C5-C4	8.13	1.49	1.40
2	I	401	PLP	C5-C4	7.08	1.48	1.40
2	D	401	PLP	C5-C4	7.00	1.48	1.40
2	E	401	PLP	C3-C2	6.81	1.48	1.41
2	E	401	PLP	C5-C4	6.52	1.47	1.40

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	401	PLP	C4A-C4-C5	3.94	125.00	120.94
2	L	401	PLP	O3P-P-O2P	3.52	121.02	107.80
2	E	401	PLP	O2P-P-O4P	-3.29	98.08	106.67
2	E	401	PLP	O3P-P-O2P	3.12	119.48	107.80
2	K	401	PLP	O2P-P-O4P	-3.08	98.63	106.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	401	PLP	2	0
2	B	401	PLP	4	0
2	C	401	PLP	2	0
2	D	401	PLP	4	0
2	K	401	PLP	2	0
2	J	401	PLP	3	0
2	G	401	PLP	2	0
2	F	401	PLP	2	0
2	H	401	PLP	3	0
2	A	401	PLP	2	0
2	L	401	PLP	2	0
2	I	401	PLP	2	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	322/330 (97%)	-0.49	1 (0%) 90 90	24, 34, 52, 105	0
1	B	322/330 (97%)	-0.46	1 (0%) 90 90	26, 34, 57, 94	0
1	C	322/330 (97%)	-0.48	1 (0%) 90 90	26, 36, 57, 90	0
1	D	322/330 (97%)	-0.53	0 100 100	25, 34, 55, 88	0
1	E	322/330 (97%)	0.01	3 (0%) 81 82	35, 53, 78, 115	0
1	F	322/330 (97%)	-0.48	0 100 100	26, 35, 55, 95	0
1	G	322/330 (97%)	-0.34	1 (0%) 90 90	31, 44, 69, 103	0
1	H	322/330 (97%)	-0.61	1 (0%) 90 90	24, 31, 48, 105	0
1	I	322/330 (97%)	-0.47	0 100 100	23, 38, 58, 93	0
1	J	322/330 (97%)	0.20	1 (0%) 90 90	33, 52, 75, 96	0
1	K	322/330 (97%)	-0.22	0 100 100	29, 48, 74, 105	0
1	L	322/330 (97%)	0.41	8 (2%) 58 60	40, 68, 91, 114	0
All	All	3864/3960 (97%)	-0.29	17 (0%) 88 89	23, 40, 75, 115	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	140	ILE	4.1
1	L	140	ILE	4.0
1	E	10	ILE	3.5
1	B	140	ILE	3.0
1	L	35	ALA	2.8

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	PLP	L	401	15/16	0.91	0.10	49,62,66,71	0
2	PLP	J	401	15/16	0.95	0.09	37,52,56,60	0
2	PLP	K	401	15/16	0.96	0.07	33,40,47,48	0
2	PLP	I	401	15/16	0.96	0.08	25,37,46,48	0
2	PLP	E	401	15/16	0.97	0.06	35,44,50,51	0
2	PLP	F	401	15/16	0.98	0.05	22,28,34,36	0
2	PLP	G	401	15/16	0.98	0.07	28,39,47,48	0
2	PLP	H	401	15/16	0.98	0.05	20,28,34,36	0
2	PLP	B	401	15/16	0.98	0.05	25,29,36,37	0
2	PLP	C	401	15/16	0.98	0.06	26,32,37,43	0
2	PLP	D	401	15/16	0.98	0.05	22,28,37,42	0
2	PLP	A	401	15/16	0.98	0.05	26,29,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.