wwPDB X-ray Structure Validation Summary Report (i)

Dec 17, 2023 – 04:03 pm GMT

PDB ID	:	4ATP
Title	:	Structure of GABA-transaminase A1R958 from Arthrobacter aurescens in complex with PLP
Authors	:	Bruce, H.; Tuan, A.N.; Mangas Sanchez, J.; Hart, S.; Turkenburg, J.P.; Grogan, G.
Deposited on	:	2012-05-09
Resolution	:	2.80 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 (i) 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 (i)) were used in the production of this report:

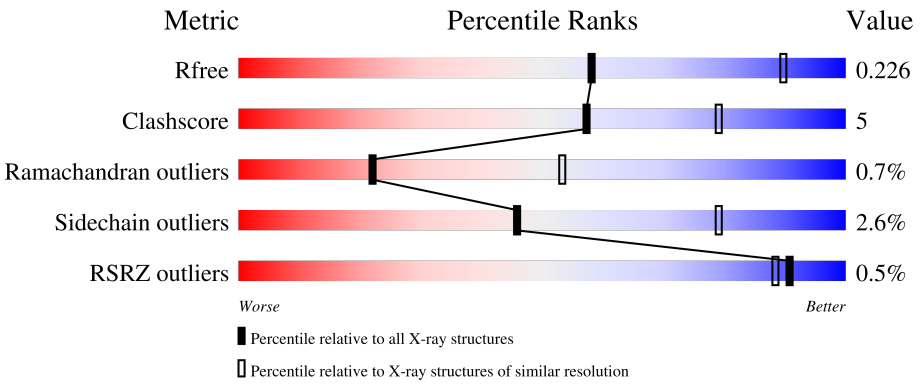
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 <=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	456	88% 7% • •
1	B	456	87% 8% • •
1	C	456	87% 9% • •
1	D	456	86% 9% • •
1	E	456	87% 8% • •

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Mol	Chain	Length	Quality of chain
1	F	456	86% 9%
1	G	456	.% 85% 10%
1	H	456	.% 86% 9%
1	I	456	87% 8%
1	J	456	.% 85% 9%
1	K	456	.% 86% 9%
1	L	456	.% 86% 9%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 39107 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 4-AMINOBUTYRATE TRANSAMINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	442	3242	2056	565	607	14	0	1	0
1	B	442	3217	2045	557	601	14	0	0	0
1	C	442	3225	2046	561	604	14	0	0	0
1	D	439	3205	2030	559	602	14	0	0	0
1	E	442	3226	2044	563	605	14	0	0	0
1	F	439	3206	2035	560	597	14	0	1	0
1	G	440	3130	1984	542	590	14	0	0	0
1	H	440	3161	2006	549	592	14	0	0	0
1	I	441	3190	2023	556	597	14	0	0	0
1	J	438	3152	2000	553	585	14	0	0	0
1	K	439	3130	1980	543	593	14	0	0	0
1	L	436	3097	1964	536	583	14	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	113	THR	ALA	SEE REMARK 999	UNP A1R958
B	113	THR	ALA	SEE REMARK 999	UNP A1R958
C	113	THR	ALA	SEE REMARK 999	UNP A1R958
D	113	THR	ALA	SEE REMARK 999	UNP A1R958
E	113	THR	ALA	SEE REMARK 999	UNP A1R958

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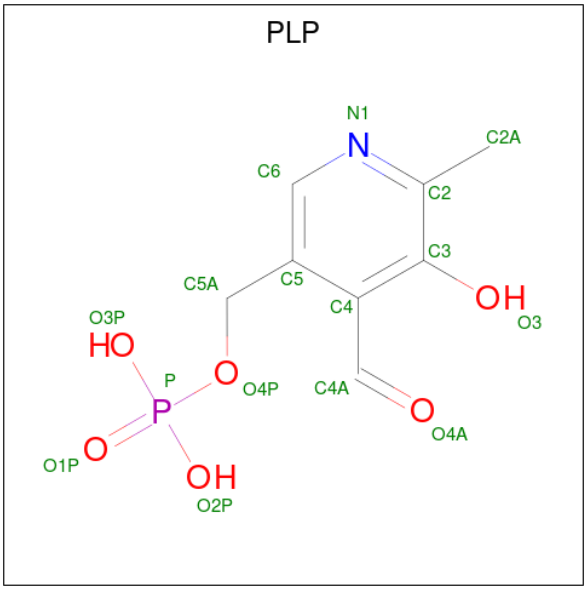
Chain	Residue	Modelled	Actual	Comment	Reference
F	113	THR	ALA	SEE REMARK 999	UNP A1R958
G	113	THR	ALA	SEE REMARK 999	UNP A1R958
H	113	THR	ALA	SEE REMARK 999	UNP A1R958
I	113	THR	ALA	SEE REMARK 999	UNP A1R958
J	113	THR	ALA	SEE REMARK 999	UNP A1R958
K	113	THR	ALA	SEE REMARK 999	UNP A1R958
L	113	THR	ALA	SEE REMARK 999	UNP A1R958

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	15	8	1	5	1	0	0
2	B	1	15	8	1	5	1	0	0
2	C	1	15	8	1	5	1	0	0
2	D	1	15	8	1	5	1	0	0
2	E	1	15	8	1	5	1	0	0
2	F	1	15	8	1	5	1	0	0
2	G	1	15	8	1	5	1	0	0
2	H	1	15	8	1	5	1	0	0

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

- Molecule 3 is water.

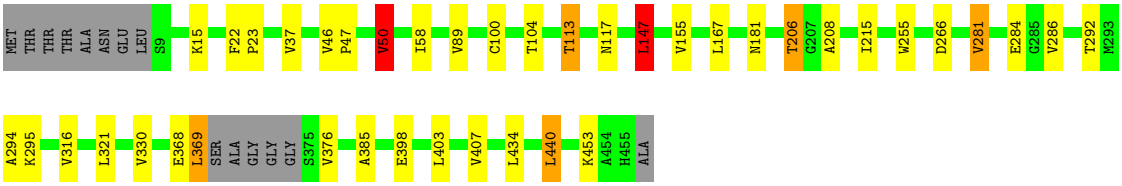
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	120	120	120	0	0
3	B	105	105	105	0	0
3	C	95	95	95	0	0
3	D	63	63	63	0	0
3	E	110	110	110	0	0
3	F	85	85	85	0	0
3	G	38	38	38	0	0
3	H	28	28	28	0	0
3	I	32	32	32	0	0
3	J	24	24	24	0	0
3	K	25	25	25	0	0
3	L	21	21	21	0	0

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.

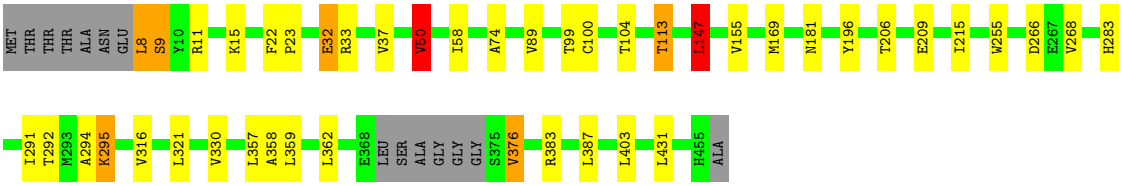
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain A:



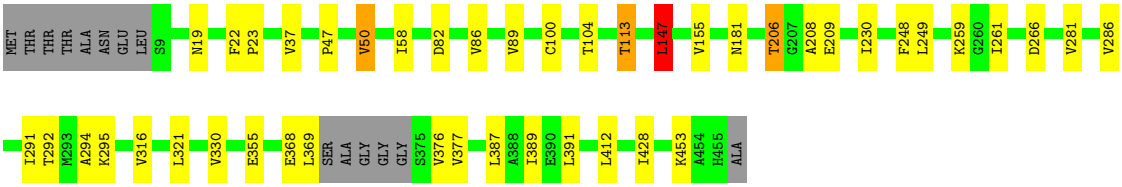
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain B:



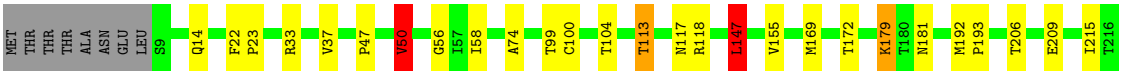
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain C:



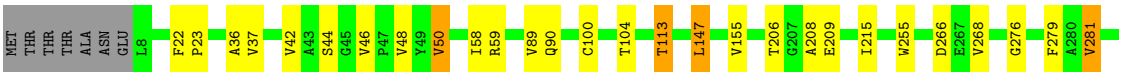
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain D:



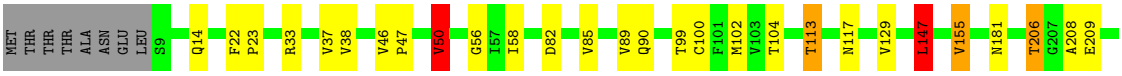
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

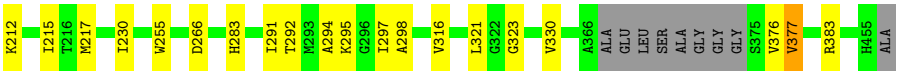
Chain E:



• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

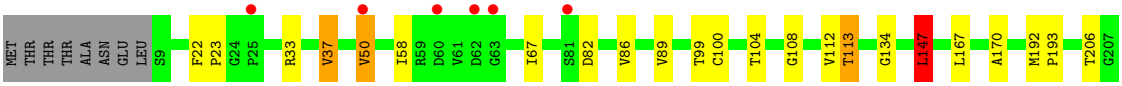
Chain F:

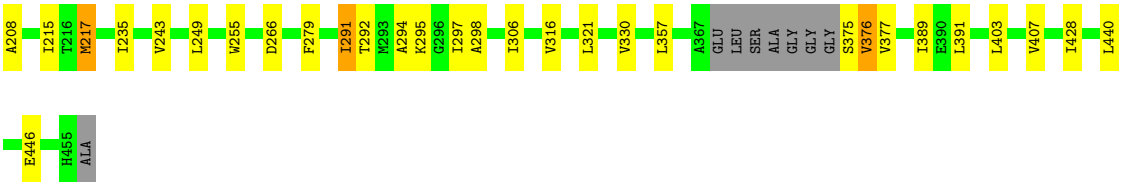




• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

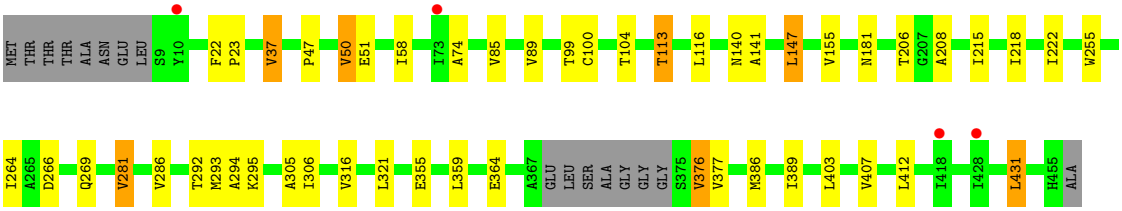
Chain G:





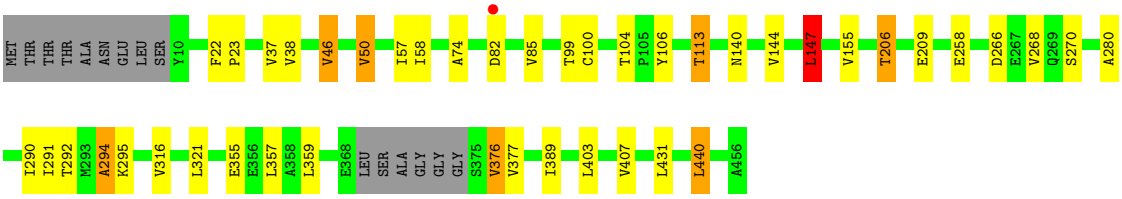
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain H:



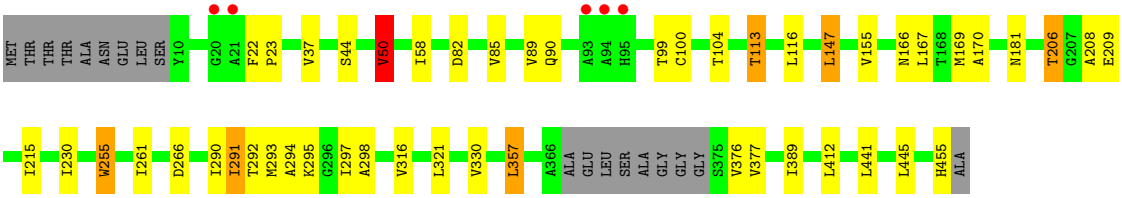
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain I:



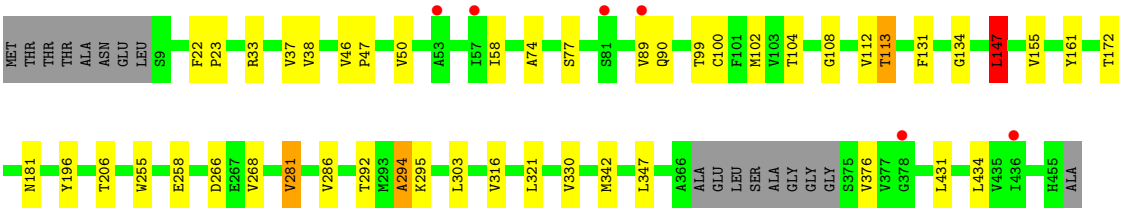
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain J:



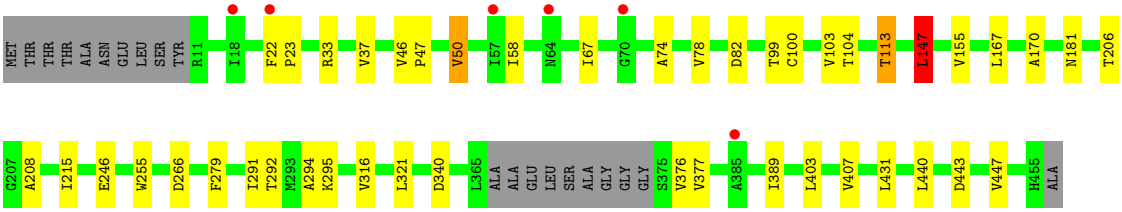
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain K:



• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	175.70Å 290.99Å 104.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.84 – 2.80 89.84 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (89.84-2.80) 100.0 (89.84-2.80)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.71 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.6.0119	Depositor
R, R_{free}	0.193 , 0.229 0.193 , 0.226	Depositor DCC
R_{free} test set	6667 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	34.7	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 33.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	39107	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.64	0/3305	0.73	2/4492 (0.0%)
1	B	0.68	0/3275	0.77	4/4452 (0.1%)
1	C	0.65	0/3283	0.75	3/4462 (0.1%)
1	D	0.64	0/3264	0.73	3/4439 (0.1%)
1	E	0.63	0/3285	0.75	0/4468
1	F	0.64	0/3268	0.74	3/4445 (0.1%)
1	G	0.60	1/3188 (0.0%)	0.73	3/4351 (0.1%)
1	H	0.58	0/3220	0.72	1/4387 (0.0%)
1	I	0.57	0/3249	0.71	2/4425 (0.0%)
1	J	0.57	1/3211 (0.0%)	0.69	1/4376 (0.0%)
1	K	0.58	0/3188	0.71	1/4349 (0.0%)
1	L	0.56	0/3155	0.72	3/4306 (0.1%)
All	All	0.61	2/38891 (0.0%)	0.73	26/52952 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	446	GLU	CG-CD	5.76	1.60	1.51
1	J	255	TRP	CD2-CE2	5.27	1.47	1.41

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	340	ASP	CB-CG-OD1	11.89	129.00	118.30
1	L	340	ASP	CB-CG-OD2	-8.97	110.23	118.30
1	C	147	LEU	CA-CB-CG	6.61	130.50	115.30
1	H	431	LEU	CB-CG-CD1	-6.50	99.95	111.00
1	G	217	MET	CG-SD-CE	-6.29	90.14	100.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	3242	0	3239	30	0
1	B	3217	0	3214	32	0
1	C	3225	0	3218	32	0
1	D	3205	0	3188	38	0
1	E	3226	0	3218	43	0
1	F	3206	0	3191	46	0
1	G	3130	0	3047	44	0
1	H	3161	0	3114	42	0
1	I	3190	0	3157	42	0
1	J	3152	0	3117	44	0
1	K	3130	0	3036	39	0
1	L	3097	0	3017	38	0
2	A	15	0	7	0	0
2	B	15	0	6	0	0
2	C	15	0	6	0	0
2	D	15	0	6	0	0
2	E	15	0	6	0	0
2	F	15	0	6	0	0
2	G	15	0	6	2	0
2	H	15	0	6	0	0
2	I	15	0	6	3	0
2	J	15	0	6	0	0
2	K	15	0	6	1	0
2	L	15	0	6	0	0
3	A	120	0	0	3	0
3	B	105	0	0	1	0
3	C	95	0	0	2	0
3	D	63	0	0	3	0
3	E	110	0	0	1	0
3	F	85	0	0	2	0
3	G	38	0	0	3	0
3	H	28	0	0	2	0
3	I	32	0	0	0	0
3	J	24	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	25	0	0	0	0
3	L	21	0	0	3	0
All	All	39107	0	37829	372	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 5.

The worst 5 of 372 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:E:281:VAL:HG22	1:E:286:VAL:HG22	1.34	1.09
1:C:248:PHE:C	1:C:249:LEU:CA	2.33	0.96
1:F:14:GLN:HE22	1:F:56:GLY:H	1.12	0.96
1:D:14:GLN:HE22	1:D:56:GLY:H	1.12	0.96
1:E:281:VAL:CG2	1:E:286:VAL:HG22	1.98	0.93

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	439/456 (96%)	417 (95%)	19 (4%)	3 (1%)	22	53
1	B	438/456 (96%)	417 (95%)	18 (4%)	3 (1%)	22	53
1	C	436/456 (96%)	415 (95%)	18 (4%)	3 (1%)	22	53
1	D	435/456 (95%)	414 (95%)	18 (4%)	3 (1%)	22	53
1	E	438/456 (96%)	417 (95%)	17 (4%)	4 (1%)	17	46
1	F	436/456 (96%)	415 (95%)	18 (4%)	3 (1%)	22	53
1	G	436/456 (96%)	413 (95%)	20 (5%)	3 (1%)	22	53
1	H	436/456 (96%)	414 (95%)	19 (4%)	3 (1%)	22	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	437/456 (96%)	414 (95%)	20 (5%)	3 (1%)	22	53
1	J	434/456 (95%)	412 (95%)	19 (4%)	3 (1%)	22	53
1	K	435/456 (95%)	413 (95%)	19 (4%)	3 (1%)	22	53
1	L	432/456 (95%)	411 (95%)	18 (4%)	3 (1%)	22	53
All	All	5232/5472 (96%)	4972 (95%)	223 (4%)	37 (1%)	22	53

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	367	ALA
1	A	295	LYS
1	B	294	ALA
1	B	295	LYS
1	C	294	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	321/336 (96%)	310 (97%)	11 (3%)	37	71
1	B	314/336 (94%)	302 (96%)	12 (4%)	33	67
1	C	316/336 (94%)	309 (98%)	7 (2%)	52	83
1	D	315/336 (94%)	308 (98%)	7 (2%)	52	83
1	E	318/336 (95%)	309 (97%)	9 (3%)	43	77
1	F	312/336 (93%)	305 (98%)	7 (2%)	52	83
1	G	297/336 (88%)	290 (98%)	7 (2%)	49	81
1	H	304/336 (90%)	297 (98%)	7 (2%)	50	82
1	I	309/336 (92%)	301 (97%)	8 (3%)	46	79
1	J	305/336 (91%)	296 (97%)	9 (3%)	41	75
1	K	297/336 (88%)	290 (98%)	7 (2%)	49	81
1	L	295/336 (88%)	290 (98%)	5 (2%)	60	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3703/4032 (92%)	3607 (97%)	96 (3%)	46 79

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	291	ILE
1	I	155	VAL
1	G	376	VAL
1	H	281	VAL
1	J	50	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	14	GLN
1	D	90	GLN
1	F	14	GLN
1	F	283	HIS
1	K	181	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 monosaccharides 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	H	500	1	15,15,16	3.80	4 (26%)	20,22,23	1.99	8 (40%)
2	PLP	C	500	1	15,15,16	2.84	3 (20%)	20,22,23	1.99	6 (30%)
2	PLP	D	500	1	15,15,16	3.76	4 (26%)	20,22,23	1.98	6 (30%)
2	PLP	B	500	1	15,15,16	3.31	4 (26%)	20,22,23	2.34	8 (40%)
2	PLP	I	500	1	15,15,16	2.80	3 (20%)	20,22,23	3.76	8 (40%)
2	PLP	K	500	1	15,15,16	3.50	3 (20%)	20,22,23	2.19	6 (30%)
2	PLP	J	500	1	15,15,16	3.46	4 (26%)	20,22,23	1.88	7 (35%)
2	PLP	G	500	1	15,15,16	3.09	4 (26%)	20,22,23	2.08	9 (45%)
2	PLP	L	500	1	15,15,16	2.87	3 (20%)	20,22,23	1.54	4 (20%)
2	PLP	A	500	1	15,15,16	2.97	3 (20%)	20,22,23	1.67	3 (15%)
2	PLP	F	500	1	15,15,16	2.91	3 (20%)	20,22,23	2.19	6 (30%)
2	PLP	E	500	1	15,15,16	3.51	3 (20%)	20,22,23	1.90	7 (35%)

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	H	500	1	-	0/6/6/8	0/1/1/1
2	PLP	C	500	1	-	0/6/6/8	0/1/1/1
2	PLP	D	500	1	-	0/6/6/8	0/1/1/1
2	PLP	B	500	1	-	0/6/6/8	0/1/1/1
2	PLP	I	500	1	-	3/6/6/8	0/1/1/1
2	PLP	K	500	1	-	2/6/6/8	0/1/1/1
2	PLP	J	500	1	-	0/6/6/8	0/1/1/1
2	PLP	G	500	1	-	2/6/6/8	0/1/1/1
2	PLP	L	500	1	-	2/6/6/8	0/1/1/1
2	PLP	A	500	1	-	0/6/6/8	0/1/1/1
2	PLP	F	500	1	-	3/6/6/8	0/1/1/1
2	PLP	E	500	1	-	5/6/6/8	0/1/1/1

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	500	PLP	C3-C2	10.85	1.51	1.40
2	D	500	PLP	C3-C2	10.25	1.51	1.40
2	E	500	PLP	C3-C2	10.10	1.51	1.40
2	J	500	PLP	C5-C4	9.94	1.51	1.40
2	K	500	PLP	C5-C4	9.63	1.51	1.40

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	I	500	PLP	C4A-C4-C5	12.69	134.01	120.94
2	I	500	PLP	C3-C4-C5	-6.21	112.03	118.74
2	F	500	PLP	C3-C4-C5	-5.71	112.58	118.74
2	A	500	PLP	C3-C4-C5	-5.04	113.29	118.74
2	D	500	PLP	C6-C5-C4	4.95	122.06	118.16

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	500	PLP	C4-C5-C5A-O4P
2	E	500	PLP	C6-C5-C5A-O4P
2	E	500	PLP	C5A-O4P-P-O1P
2	E	500	PLP	C5A-O4P-P-O2P
2	E	500	PLP	C5A-O4P-P-O3P

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	500	PLP	3	0
2	K	500	PLP	1	0
2	G	500	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	442/456 (96%)	-0.58	0	100	100	9, 17, 35, 59	0
1	B	442/456 (96%)	-0.55	0	100	100	7, 16, 28, 47	0
1	C	442/456 (96%)	-0.51	0	100	100	9, 17, 32, 48	0
1	D	439/456 (96%)	-0.47	0	100	100	9, 20, 35, 64	0
1	E	442/456 (96%)	-0.55	0	100	100	10, 19, 33, 50	0
1	F	439/456 (96%)	-0.51	0	100	100	10, 20, 35, 56	0
1	G	440/456 (96%)	-0.13	6 (1%)	75	70	15, 36, 54, 65	0
1	H	440/456 (96%)	-0.09	4 (0%)	84	80	16, 36, 57, 69	0
1	I	441/456 (96%)	-0.26	1 (0%)	95	94	14, 31, 51, 72	0
1	J	438/456 (96%)	-0.21	5 (1%)	80	75	14, 33, 50, 67	0
1	K	439/456 (96%)	-0.04	6 (1%)	75	70	20, 39, 63, 87	0
1	L	436/456 (95%)	0.02	6 (1%)	75	70	20, 41, 62, 72	0
All	All	5280/5472 (96%)	-0.32	28 (0%)	91	88	7, 26, 53, 87	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	53	ALA	3.2
1	J	93	ALA	3.2
1	J	20	GLY	3.1
1	G	25	PRO	3.1
1	K	81	SER	3.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides 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(Å^2)	Q<0.9
2	PLP	G	500	15/16	0.95	0.20	25,27,37,39	0
2	PLP	I	500	15/16	0.96	0.22	30,34,36,39	0
2	PLP	J	500	15/16	0.96	0.13	22,24,27,28	0
2	PLP	K	500	15/16	0.96	0.20	35,40,44,48	0
2	PLP	L	500	15/16	0.96	0.15	33,36,38,44	0
2	PLP	D	500	15/16	0.97	0.16	15,16,17,18	0
2	PLP	E	500	15/16	0.97	0.16	12,13,14,15	0
2	PLP	C	500	15/16	0.97	0.15	16,17,19,21	0
2	PLP	H	500	15/16	0.97	0.18	22,25,30,33	0
2	PLP	B	500	15/16	0.98	0.16	11,13,14,15	0
2	PLP	A	500	15/16	0.98	0.15	15,16,19,20	0
2	PLP	F	500	15/16	0.98	0.14	13,14,15,16	0

6.5 Other polymers (i)

There are no such residues in this entry.