



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 19, 2026 – 01:49 AM UTC

PDB ID : 5WMH / pdb_00005wmh
Title : Arabidopsis thaliana prephenate aminotransferase
Authors : Holland, C.K.; Jez, J.M.
Deposited on : 2017-07-28
Resolution : 3.00 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

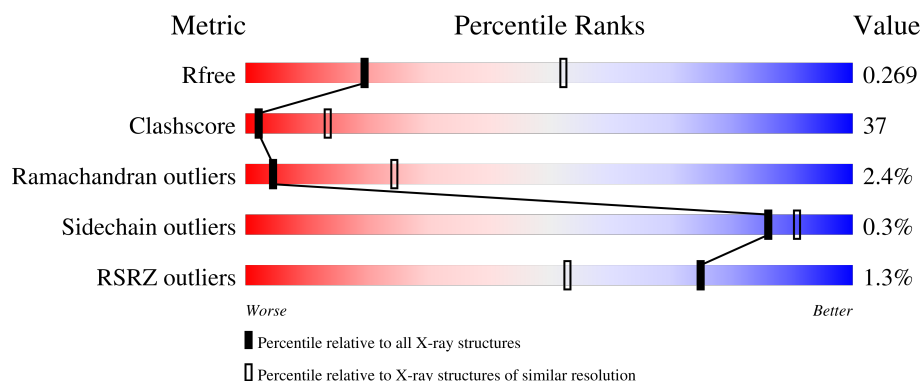
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	475	% 58% 24% • 16%
1	B	475	% 58% 24% • 16%
1	C	475	% 57% 26% •• 16%
1	D	475	 53% 28% • 16%
1	E	475	2% 34% 47% • 16%

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Mol	Chain	Length	Quality of chain
1	F	475	2% 23% 52% 7% • 16%

2 Entry composition [i](#)

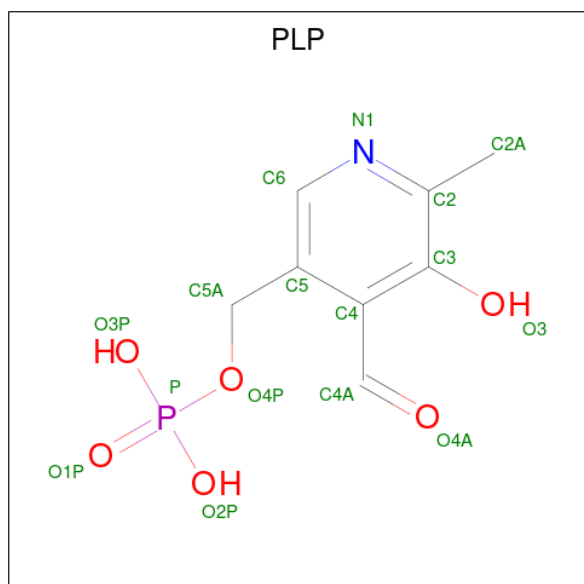
There are 3 unique types of molecules in this entry. The entry contains 18299 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	1	0
			3034	1941	507	576	10			
1	B	399	Total	C	N	O	S	0	0	0
			3027	1936	505	576	10			
1	C	401	Total	C	N	O	S	0	0	0
			3038	1940	507	580	11			
1	D	400	Total	C	N	O	S	0	0	0
			3035	1941	506	577	11			
1	E	399	Total	C	N	O	S	0	0	0
			3027	1936	505	576	10			
1	F	397	Total	C	N	O	S	0	0	0
			3007	1921	501	574	11			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: 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		
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		

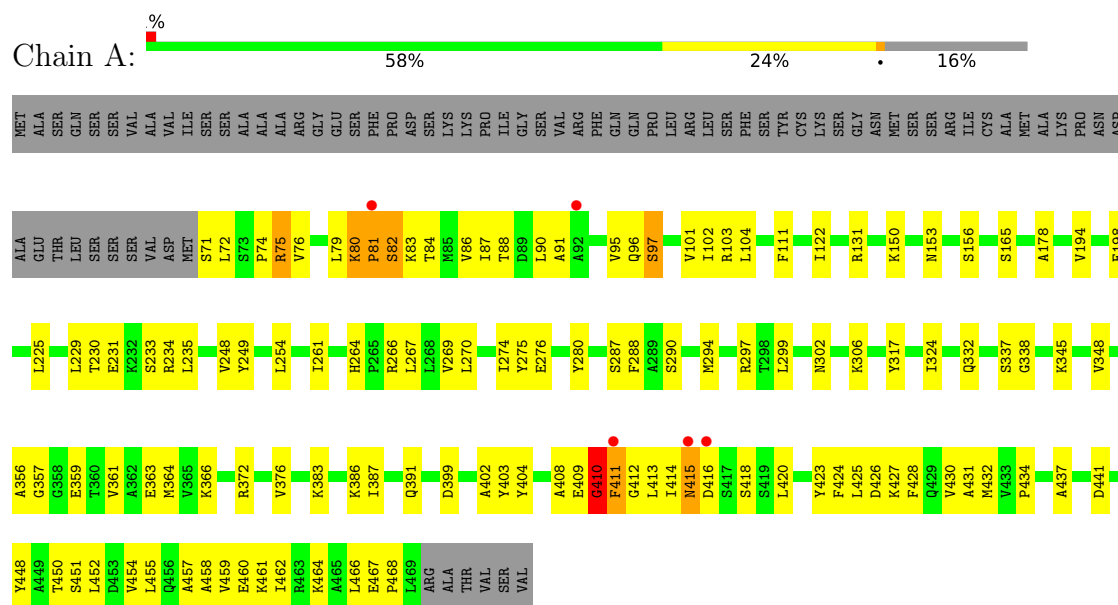
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		
3	B	14	Total	O	0	0
			14	14		
3	C	8	Total	O	0	0
			8	8		
3	D	11	Total	O	0	0
			11	11		
3	E	1	Total	O	0	0
			1	1		
3	F	3	Total	O	0	0
			3	3		

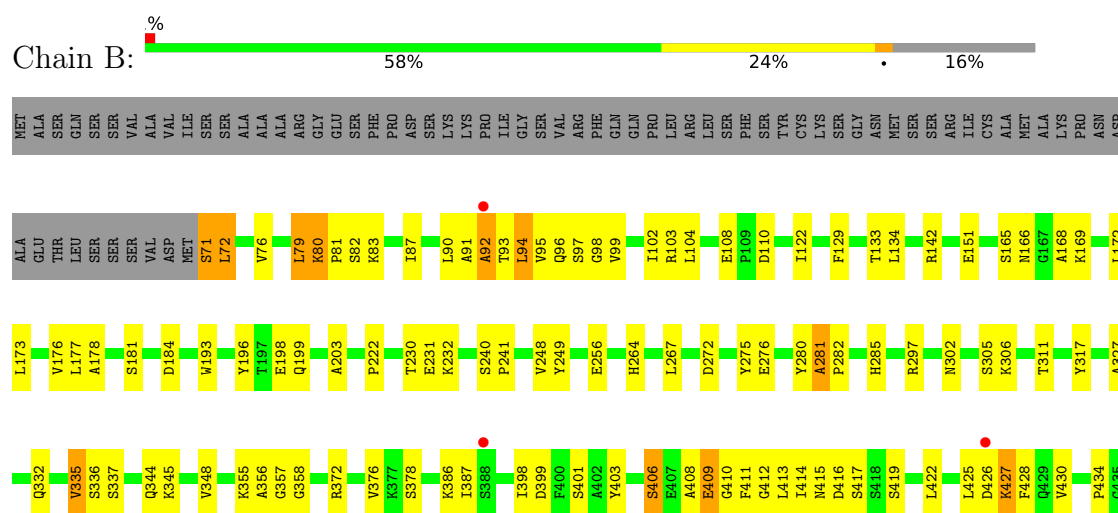
3 Residue-property plots

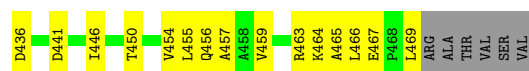
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase

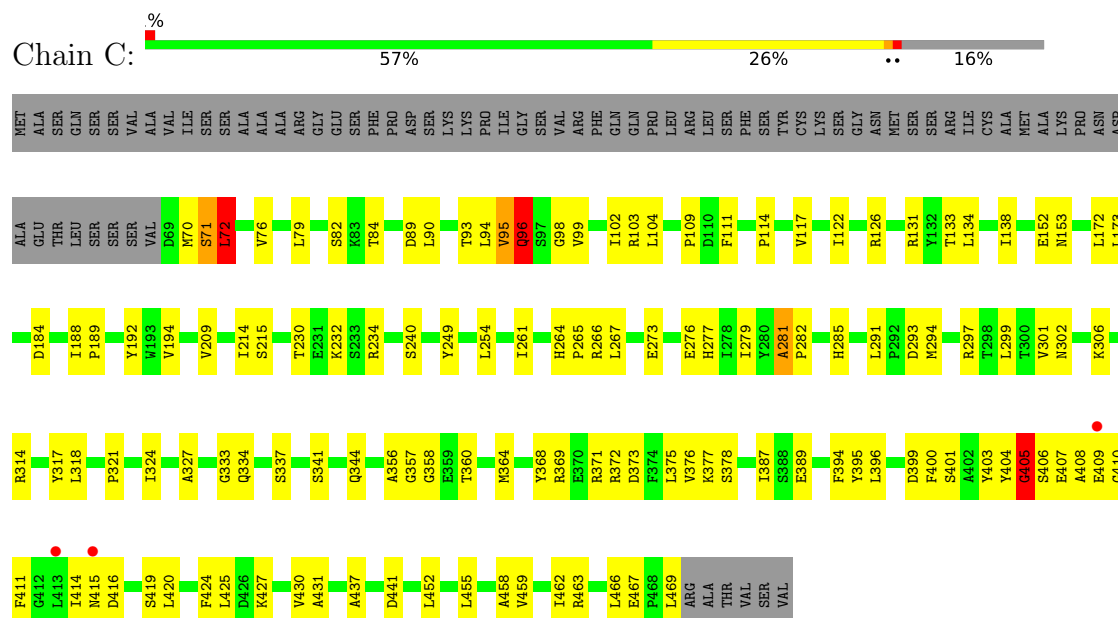


- Molecule 1: Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase

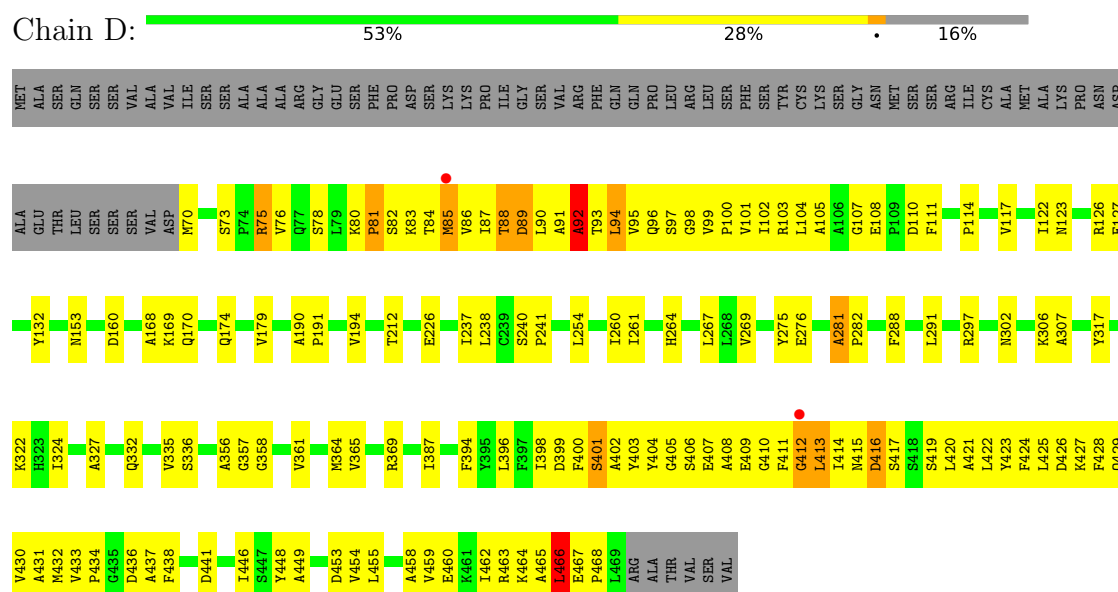




- Molecule 1: Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase

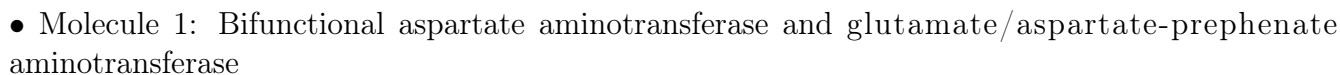


- Molecule 1: Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase



- Molecule 1: Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase





MET	ALA	GLU	THR	GLN	SER	SER	VAL	ALA	MET	MET	GLY	ASN	MET	SER	ARG	CYS	ALA	MET	LYS	PRO	ASN	VAL	GLY	SER	CYS	THR	SER	PHE	ASP	SER	LYS	LYS	PRO	ILE	GLY	GLN	ARG	PHE	VAL	SER	GLY	DRO	L90	D89	L79	L78	L77	L76	L75	L74	L73	L72	L71	L70	L69	L68	L67	L66	L65	L64	L63	L62	L61	L60	L59	L58	L57	L56	L55	L54	L53	L52	L51	L50	L49	L48	L47	L46	L45	L44	L43	L42	L41	L40	L39	L38	L37	L36	L35	L34	L33	L32	L31	L30	L29	L28	L27	L26	L25	L24	L23	L22	L21	L20	L19	L18	L17	L16	L15	L14	L13	L12	L11	L10	L09	L08	L07	L06	L05	L04	L03	L02	L01	L00	L99	L98	L97	L96	L95	L94	L93	L92	L91	L90	L89	L88	L87	L86	L85	L84	L83	L82	L81	L80	L79	L78	L77	L76	L75	L74	L73	L72	L71	L70	L69	L68	L67	L66	L65	L64	L63	L62	L61	L60	L59	L58	L57	L56	L55	L54	L53	L52	L51	L50	L49	L48	L47	L46	L45	L44	L43	L42	L41	L40	L39	L38	L37	L36	L35	L34	L33	L32	L31	L30	L29	L28	L27	L26	L25	L24	L23	L22	L21	L20	L19	L18	L17	L16	L15	L14	L13	L12	L11	L10	L09	L08	L07	L06	L05	L04	L03	L02	L01	L00	L99	L98	L97	L96	L95	L94	L93	L92	L91	L90	L89	L88	L87	L86	L85	L84	L83	L82	L81	L80	L79	L78	L77	L76	L75	L74	L73	L72	L71	L70	L69	L68	L67	L66	L65	L64	L63	L62	L61	L60	L59	L58	L57	L56	L55	L54	L53	L52	L51	L50	L49	L48	L47	L46	L45	L44	L43	L42	L41	L40	L39	L38	L37	L36	L35	L34	L33	L32	L31	L30	L29	L28	L27	L26	L25	L24	L23	L22	L21	L20	L19	L18	L17	L16	L15	L14	L13	L12	L11	L10	L09	L08	L07	L06	L05	L04	L03	L02	L01	L00	L99	L98	L97	L96	L95	L94	L93	L92	L91	L90	L89	L88	L87	L86	L85	L84	L83	L82	L81	L80	L79	L78
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L462	
A465	
L466	
E467	
P468	
L469	
ARG	
ALA	
THR	
VAL	
SER	
VAL	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.34Å 111.58Å 141.78Å 90.00° 90.37° 90.00°	Depositor
Resolution (Å)	33.27 – 3.00 33.27 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (33.27-3.00) 99.6 (33.27-3.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.14 (at 3.00Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575)	Depositor
R, R_{free}	0.210 , 0.270 0.211 , 0.269	Depositor DCC
R_{free} test set	4326 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	64.5	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	18299	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.85% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.66	1/3096 (0.0%)	0.92	6/4203 (0.1%)
1	B	0.67	0/3085	1.13	12/4187 (0.3%)
1	C	0.65	0/3096	0.95	7/4201 (0.2%)
1	D	0.69	1/3093 (0.0%)	0.96	8/4197 (0.2%)
1	E	0.61	0/3085	0.95	7/4187 (0.2%)
1	F	0.89	12/3063 (0.4%)	1.63	69/4155 (1.7%)
All	All	0.70	14/18518 (0.1%)	1.12	109/25130 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	1
1	C	0	2
1	D	0	2
1	E	0	2
1	F	0	10
All	All	0	20

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	372	ARG	NE-CZ	11.30	1.45	1.33
1	F	369	ARG	CA-C	10.58	1.67	1.52
1	F	369	ARG	C-N	10.33	1.46	1.33
1	F	372	ARG	CD-NE	9.01	1.58	1.46
1	F	370	GLU	N-CA	8.80	1.56	1.46

The worst 5 of 109 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	166	ASN	CB-CG-ND2	-26.92	76.02	116.40
1	B	166	ASN	CB-CG-OD1	25.86	172.53	120.80
1	B	166	ASN	OD1-CG-ND2	-20.64	101.96	122.60
1	F	372	ARG	NE-CZ-NH1	16.88	138.38	121.50
1	F	369	ARG	CA-C-N	16.00	141.77	120.65

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	280	TYR	Peptide
1	A	410	GLY	Peptide
1	A	71	SER	Peptide
1	B	280	TYR	Peptide
1	C	96	GLN	Sidechain

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	3034	0	3097	123	1
1	B	3027	0	3090	135	0
1	C	3038	0	3087	132	0
1	D	3035	0	3099	168	1
1	E	3027	0	3090	306	0
1	F	3007	0	3048	553	0
2	A	15	0	7	2	0
2	B	15	0	7	1	0
2	C	15	0	7	2	0
2	D	15	0	7	3	0
2	E	15	0	7	1	0
2	F	15	0	7	4	0
3	A	4	0	0	0	0
3	B	14	0	0	2	1
3	C	8	0	0	0	0
3	D	11	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	1	0	0	0	0
3	F	3	0	0	1	0
All	All	18299	0	18553	1365	2

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 37.

The worst 5 of 1365 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:F:143:GLU:N	1:F:147:ARG:HH12	1.13	1.45
1:B:102:ILE:HD12	1:B:103:ARG:N	1.37	1.34
1:F:143:GLU:CA	1:F:147:ARG:CZ	2.05	1.33
1:F:143:GLU:N	1:F:147:ARG:NH1	1.74	1.33
1:C:96:GLN:HE21	1:C:96:GLN:CA	1.34	1.29

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:ASN:ND2	1:D:416:ASP:OD1[2_555]	2.00	0.20
3:B:812:HOH:O	3:D:809:HOH:O[1_665]	2.03	0.17

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	398/475 (84%)	378 (95%)	13 (3%)	7 (2%)	6	31
1	B	397/475 (84%)	374 (94%)	13 (3%)	10 (2%)	4	23
1	C	399/475 (84%)	378 (95%)	17 (4%)	4 (1%)	12	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	398/475 (84%)	371 (93%)	18 (4%)	9 (2%)	5	25
1	E	397/475 (84%)	368 (93%)	21 (5%)	8 (2%)	6	28
1	F	393/475 (83%)	353 (90%)	22 (6%)	18 (5%)	2	11
All	All	2382/2850 (84%)	2222 (93%)	104 (4%)	56 (2%)	4	24

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	80	LYS
1	A	81	PRO
1	A	97	SER
1	B	72	LEU
1	B	281	ALA

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	327/390 (84%)	327 (100%)	0	100	100
1	B	326/390 (84%)	326 (100%)	0	100	100
1	C	326/390 (84%)	326 (100%)	0	100	100
1	D	327/390 (84%)	326 (100%)	1 (0%)	86	91
1	E	326/390 (84%)	323 (99%)	3 (1%)	70	85
1	F	322/390 (83%)	321 (100%)	1 (0%)	86	91
All	All	1954/2340 (84%)	1949 (100%)	5 (0%)	86	91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	466	LEU
1	E	253	LEU
1	E	255	GLU

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Mol	Chain	Res	Type
1	E	413	LEU
1	F	397	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	166	ASN
1	F	264	HIS
1	F	391	GLN
1	F	302	ASN
1	C	135	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](#)

6 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	B	701	-	15,15,16	1.31	1 (6%)	21,22,23	1.48	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PLP	D	701	-	15,15,16	1.72	1 (6%)	21,22,23	1.42	4 (19%)
2	PLP	A	701	-	15,15,16	1.48	2 (13%)	21,22,23	1.74	8 (38%)
2	PLP	F	701	-	15,15,16	1.22	1 (6%)	21,22,23	1.21	2 (9%)
2	PLP	E	701	-	15,15,16	1.01	0	21,22,23	0.94	0
2	PLP	C	701	-	15,15,16	1.62	2 (13%)	21,22,23	1.32	3 (14%)

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	B	701	-	-	5/6/6/8	0/1/1/1
2	PLP	D	701	-	-	5/6/6/8	0/1/1/1
2	PLP	A	701	-	-	3/6/6/8	0/1/1/1
2	PLP	F	701	-	-	3/6/6/8	0/1/1/1
2	PLP	E	701	-	-	3/6/6/8	0/1/1/1
2	PLP	C	701	-	-	3/6/6/8	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	701	PLP	C3-C2	-4.58	1.36	1.41
2	A	701	PLP	C3-C2	-3.71	1.37	1.41
2	C	701	PLP	C3-C2	-3.18	1.37	1.41
2	B	701	PLP	C2A-C2	2.51	1.54	1.50
2	F	701	PLP	C3-C2	-2.29	1.38	1.41

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	PLP	C4A-C4-C5	-3.62	117.21	120.94
2	D	701	PLP	O4P-C5A-C5	3.48	115.89	109.36
2	B	701	PLP	O3P-P-O4P	3.34	115.36	106.67
2	C	701	PLP	C5-C6-N1	-2.67	119.49	123.83
2	B	701	PLP	C6-N1-C2	2.55	123.82	119.20

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	PLP	C5A-O4P-P-O2P
2	A	701	PLP	C5A-O4P-P-O3P
2	B	701	PLP	C4-C5-C5A-O4P
2	B	701	PLP	C6-C5-C5A-O4P
2	B	701	PLP	C5A-O4P-P-O3P

There are no ring outliers.

6 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	PLP	1	0
2	D	701	PLP	3	0
2	A	701	PLP	2	0
2	F	701	PLP	4	0
2	E	701	PLP	1	0
2	C	701	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	399/475 (84%)	-0.34	5 (1%) 75 53	30, 50, 99, 172	1 (0%)
1	B	399/475 (84%)	-0.40	3 (0%) 82 64	37, 47, 98, 162	0
1	C	401/475 (84%)	-0.33	3 (0%) 84 66	38, 53, 96, 185	0
1	D	400/475 (84%)	-0.26	2 (0%) 87 72	37, 49, 107, 195	0
1	E	399/475 (84%)	0.23	9 (2%) 61 38	57, 88, 133, 173	0
1	F	397/475 (83%)	0.42	10 (2%) 58 35	60, 107, 167, 235	0
All	All	2395/2850 (84%)	-0.11	32 (1%) 75 53	30, 63, 134, 235	1 (0%)

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	254	LEU	5.0
1	E	253	LEU	3.6
1	F	368	TYR	3.6
1	E	365	VAL	3.0
1	E	89	ASP	2.9

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(Å ²)	Q<0.9
2	PLP	F	701	15/16	0.90	0.15	97,115,123,125	0
2	PLP	E	701	15/16	0.92	0.12	80,86,96,101	0
2	PLP	C	701	15/16	0.94	0.11	41,48,59,65	0
2	PLP	D	701	15/16	0.94	0.09	39,40,66,69	0
2	PLP	A	701	15/16	0.95	0.10	37,50,56,62	0
2	PLP	B	701	15/16	0.96	0.07	38,47,56,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.