



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:37 PM UTC

PDB ID : 1CZE / pdb_00001cze
Title : ASPARTATE AMINOTRANSFERASE MUTANT ATB17/139S/142N WITH SUCCINIC ACID
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Deposited on : 1999-09-02
Resolution : 2.40 Å(reported)

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

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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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

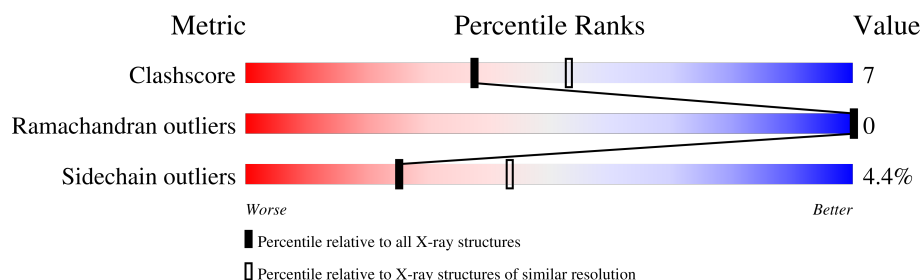
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	396	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SIN	A	414	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3198 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 ASPARTATE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	396	3072	1937	536	586	13	0	0	0

There are 15 discrepancies between the modelled and reference sequences:

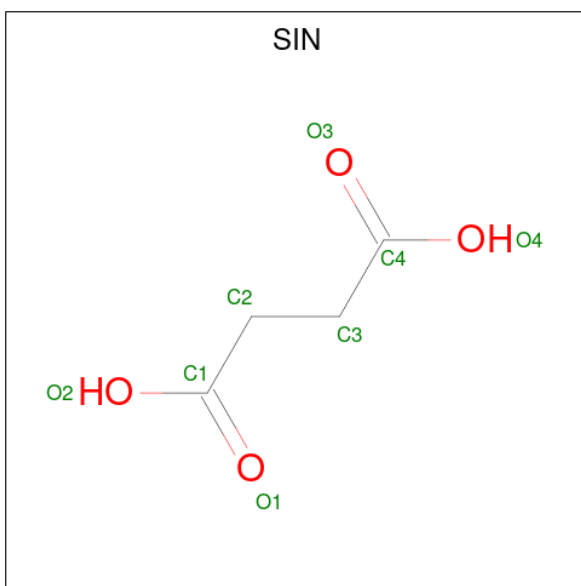
Chain	Residue	Modelled	Actual	Comment	Reference
A	11	THR	ALA	engineered mutation	UNP P00509
A	24	LEU	PHE	engineered mutation	UNP P00509
A	34	ASP	ASN	engineered mutation	UNP P00509
A	37	MET	ILE	engineered mutation	UNP P00509
A	41	ASN	LYS	engineered mutation	UNP P00509
A	126	ARG	LYS	engineered mutation	UNP P00509
A	269	THR	ALA	engineered mutation	UNP P00509
A	293	VAL	ALA	engineered mutation	UNP P00509
A	297	SER	ASN	engineered mutation	UNP P00509
A	311	GLY	SER	engineered mutation	UNP P00509
A	353	THR	ILE	engineered mutation	UNP P00509
A	361	PHE	SER	engineered mutation	UNP P00509
A	363	GLY	SER	engineered mutation	UNP P00509
A	387	LEU	VAL	engineered mutation	UNP P00509
A	397	LEU	MET	engineered mutation	UNP P00509

- 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		

- Molecule 3 is SUCCINIC ACID (CCD ID: SIN) (formula: $C_4H_6O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	4	4		

- Molecule 4 is water.

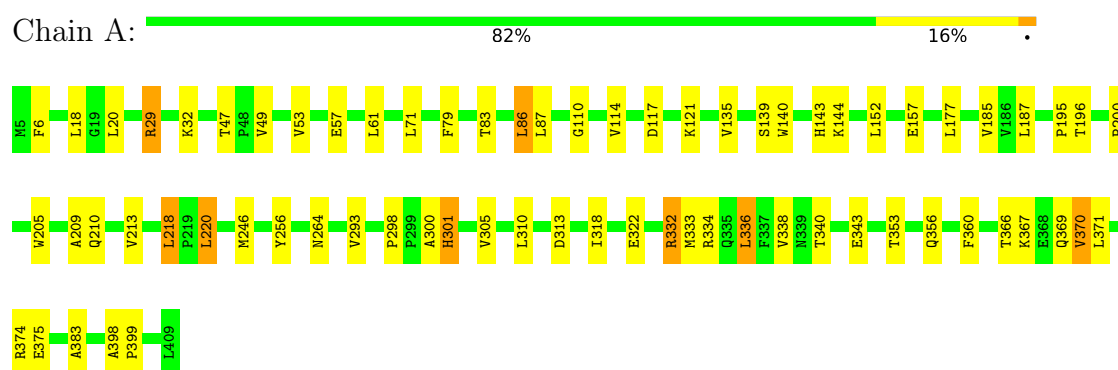
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	103	Total 103	O 103	0	0

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. 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. 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.

Note EDS was not executed.

- Molecule 1: ASPARTATE AMINOTRANSFERASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	156.64 Å 85.06 Å 78.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.40	Depositor
% Data completeness (in resolution range)	90.7 (10.00-2.40)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.189 , 0.244	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3198	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SIN, 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	0.51	0/3133	0.97	12/4246 (0.3%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	360	PHE	N-CA-C	7.83	122.27	110.14
1	A	196	THR	N-CA-C	6.61	119.31	111.71
1	A	300	ALA	N-CA-C	6.50	118.16	111.14
1	A	313	ASP	N-CA-C	6.22	118.87	111.71
1	A	29	ARG	CA-C-N	6.15	125.37	118.97
1	A	29	ARG	C-N-CA	6.15	125.37	118.97
1	A	298	PRO	N-CA-C	5.71	117.67	110.70
1	A	47	THR	CA-C-N	5.54	125.52	120.03
1	A	47	THR	C-N-CA	5.54	125.52	120.03
1	A	71	LEU	N-CA-C	5.40	119.87	113.28
1	A	264	ASN	N-CA-C	5.28	119.59	113.20
1	A	301	HIS	N-CA-C	5.28	120.02	111.37

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	3072	0	3014	43	0
2	A	15	0	6	0	0
3	A	8	0	4	2	0
4	A	103	0	0	1	0
All	All	3198	0	3024	43	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 7.

All (43) 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:A:210:GLN:HG2	1:A:246:MET:HE1	1.64	0.79
1:A:370:VAL:HG21	1:A:383:ALA:HA	1.70	0.73
1:A:83:THR:HG22	1:A:256:TYR:OH	1.95	0.67
1:A:185:VAL:HG22	1:A:218:LEU:HD12	1.76	0.67
1:A:79:PHE:O	1:A:83:THR:HG23	1.94	0.66
1:A:398:ALA:HB3	1:A:399:PRO:HD3	1.77	0.66
1:A:371:LEU:O	1:A:375:GLU:HB2	1.97	0.65
1:A:200:PRO:HG2	1:A:205:TRP:CE2	2.34	0.62
1:A:144:LYS:H	1:A:144:LYS:HE2	1.67	0.59
1:A:57:GLU:OE2	1:A:301:HIS:HE1	1.85	0.59
1:A:29:ARG:O	1:A:32:LYS:HG3	2.05	0.57
1:A:301:HIS:HD2	4:A:511:HOH:O	1.87	0.57
1:A:117:ASP:O	1:A:121:LYS:HG2	2.07	0.53
1:A:366:THR:H	1:A:369:GLN:HE21	1.56	0.53
1:A:139:SER:HB3	1:A:144:LYS:HZ2	1.74	0.52
1:A:334:ARG:O	1:A:338:VAL:HG23	2.10	0.51
1:A:187:LEU:HD23	1:A:220:LEU:HG	1.95	0.48
1:A:53:VAL:HG13	1:A:305:VAL:HG11	1.96	0.48
1:A:143:HIS:HB2	1:A:144:LYS:HZ3	1.81	0.45
1:A:340:THR:HA	1:A:343:GLU:HG2	1.98	0.45
1:A:140:TRP:HE1	3:A:414:SIN:H32	1.81	0.45
1:A:318:ILE:O	1:A:322:GLU:HG3	2.16	0.45
1:A:140:TRP:NE1	3:A:414:SIN:H32	2.32	0.44
1:A:293:VAL:O	1:A:293:VAL:HG22	2.16	0.44
1:A:110:GLY:O	1:A:114:VAL:HG23	2.17	0.44
1:A:209:ALA:O	1:A:213:VAL:HG13	2.18	0.44
1:A:135:VAL:O	1:A:157:GLU:HA	2.18	0.43
1:A:83:THR:O	1:A:87:LEU:HG	2.19	0.43
1:A:139:SER:HB3	1:A:144:LYS:NZ	2.33	0.43
1:A:332:ARG:HH12	1:A:336:LEU:CB	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:LEU:HD23	1:A:86:LEU:HA	1.91	0.43
1:A:143:HIS:HB2	1:A:144:LYS:NZ	2.34	0.43
1:A:185:VAL:HG22	1:A:218:LEU:CD1	2.49	0.41
1:A:353:THR:HA	1:A:356:GLN:NE2	2.35	0.41
1:A:366:THR:O	1:A:370:VAL:HG13	2.21	0.41
1:A:367:LYS:O	1:A:371:LEU:HG	2.21	0.41
1:A:177:LEU:HD23	1:A:177:LEU:HA	1.95	0.41
1:A:332:ARG:HH12	1:A:336:LEU:HG	1.86	0.41
1:A:333:MET:HA	1:A:333:MET:HE2	2.03	0.41
1:A:332:ARG:NH1	1:A:336:LEU:HB2	2.36	0.41
1:A:332:ARG:HH12	1:A:336:LEU:HB2	1.85	0.41
1:A:210:GLN:O	1:A:213:VAL:HG22	2.21	0.41
1:A:6:PHE:CD1	1:A:6:PHE:N	2.88	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	394/396 (100%)	377 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	321/321 (100%)	307 (96%)	14 (4%)	25	43

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	LEU
1	A	20	LEU
1	A	49	VAL
1	A	61	LEU
1	A	86	LEU
1	A	152	LEU
1	A	195	PRO
1	A	218	LEU
1	A	220	LEU
1	A	310	LEU
1	A	332	ARG
1	A	336	LEU
1	A	370	VAL
1	A	374	ARG

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

Mol	Chain	Res	Type
1	A	63	ASN
1	A	84	GLN
1	A	96	ASN
1	A	148	ASN
1	A	165	ASN
1	A	166	HIS
1	A	206	GLN
1	A	286	GLN
1	A	301	HIS
1	A	321	GLN
1	A	328	GLN
1	A	335	GLN
1	A	356	GLN
1	A	357	ASN
1	A	369	GLN

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](#)

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	413	1	15,15,16	2.39	3 (20%)	21,22,23	1.44	4 (19%)
3	SIN	A	414	-	7,7,7	1.76	2 (28%)	8,8,8	1.69	1 (12%)

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	413	1	-	2/6/6/8	0/1/1/1
3	SIN	A	414	-	-	5/5/5/5	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	413	PLP	C4A-C4	-6.66	1.38	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	413	PLP	C3-C2	-4.55	1.36	1.41
3	A	414	SIN	O4-C4	-2.90	1.21	1.30
3	A	414	SIN	O2-C1	-2.57	1.22	1.30
2	A	413	PLP	C5-C4	-2.43	1.37	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	413	PLP	O4P-C5A-C5	4.02	116.89	109.36
3	A	414	SIN	C2-C3-C4	3.11	121.91	113.67
2	A	413	PLP	C6-C5-C4	2.50	120.15	118.10
2	A	413	PLP	C5-C6-N1	-2.48	119.80	123.83
2	A	413	PLP	C4A-C4-C5	-2.14	118.74	120.94

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	413	PLP	C4-C5-C5A-O4P
3	A	414	SIN	C1-C2-C3-C4
2	A	413	PLP	C6-C5-C5A-O4P
3	A	414	SIN	O2-C1-C2-C3
3	A	414	SIN	C2-C3-C4-O4
3	A	414	SIN	O1-C1-C2-C3
3	A	414	SIN	C2-C3-C4-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	414	SIN	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.