



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 10:27 PM UTC

PDB ID : 3LWS / pdb_00003lws
Title : Crystal structure of Putative aromatic amino acid beta-eliminating lyase/threonine aldolase. (YP_001813866.1) from Exiguobacterium sp. 255-15 at 2.00 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2010-02-24
Resolution : 2.00 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

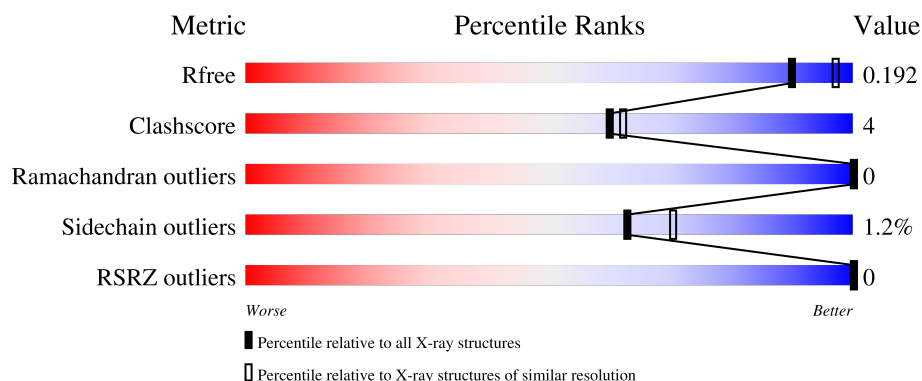
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	357	 92% 7% .
1	B	357	 86% 13% ..
1	C	357	 90% 9% .
1	D	357	 87% 11% ..
1	E	357	 86% 13% .

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Mol	Chain	Length	Quality of chain
1	F	357	 89% 11% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18270 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 Aromatic amino acid beta-eliminating lyase/threonine aldolase.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	355	Total	C	N	O	P	S	Se	0	6	0
			2817	1793	469	541	1	5	8			
1	B	354	Total	C	N	O	P	S	Se	0	2	0
			2803	1781	475	533	1	5	8			
1	C	356	Total	C	N	O	P	S	Se	0	7	0
			2821	1798	470	539	1	5	8			
1	D	354	Total	C	N	O	P	S	Se	0	5	0
			2807	1790	472	532	1	5	7			
1	E	354	Total	C	N	O	P	S	Se	0	7	0
			2825	1801	474	536	1	5	8			
1	F	357	Total	C	N	O	P	S	Se	0	11	0
			2858	1818	477	549	1	5	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP B1YFH3
B	0	GLY	-	expression tag	UNP B1YFH3
C	0	GLY	-	expression tag	UNP B1YFH3
D	0	GLY	-	expression tag	UNP B1YFH3
E	0	GLY	-	expression tag	UNP B1YFH3
F	0	GLY	-	expression tag	UNP B1YFH3

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	241	Total	O	0	4
			244	244		
2	B	197	Total	O	0	0
			197	197		
2	C	230	Total	O	0	4
			234	234		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	165	Total 166	O 166	0	1
2	E	234	Total 236	O 236	0	2
2	F	261	Total 262	O 262	0	2

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.

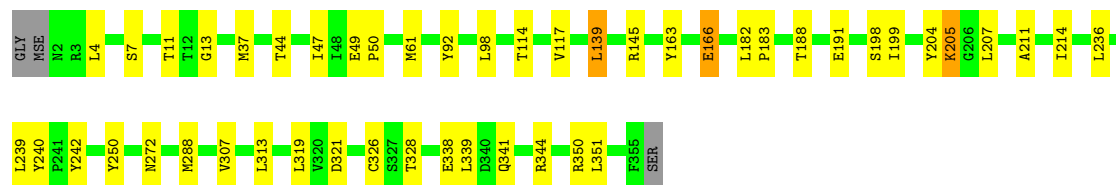
- Molecule 1: Aromatic amino acid beta-eliminating lyase/threonine aldolase

Chain A: 



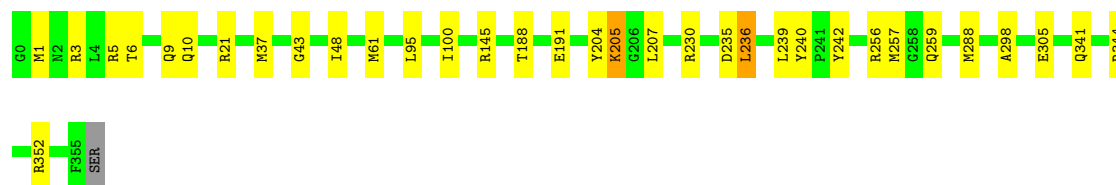
- Molecule 1: Aromatic amino acid beta-eliminating lyase/threonine aldolase

Chain B: 



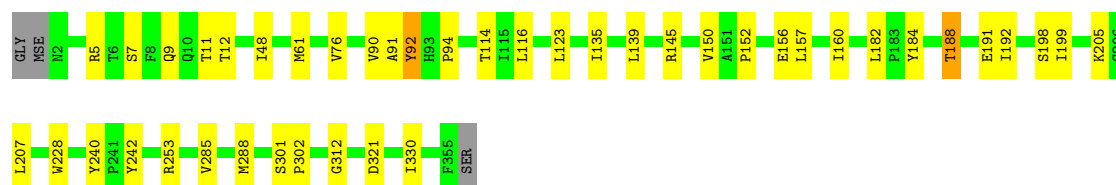
- Molecule 1: Aromatic amino acid beta-eliminating lyase/threonine aldolase

Chain C: 



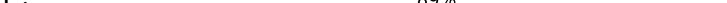
- Molecule 1: Aromatic amino acid beta-eliminating lyase/threonine aldolase

Chain D: 



- Molecule 1: Aromatic amino acid beta-eliminating lyase/threonine aldolase

[illegible]

- Chain F:  89% 11%

[illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	142.15Å 142.15Å 102.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.53 – 2.00 46.53 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.53-2.00) 99.9 (46.53-2.00)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0102, PHENIX	Depositor
R, R_{free}	0.144 , 0.190 0.147 , 0.192	Depositor DCC
R_{free} test set	7789 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 23.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.044 for -h,-k,l 0.467 for h,-h-k,-l 0.045 for -k,-h,-l	Xtriage
Reported twinning fraction	0.537 for H, K, L 0.463 for K, H, -L	Depositor
Outliers	0 of 156754 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18270	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LLP

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	0.91	0/2864	0.95	0/3867
1	B	0.87	0/2838	0.98	2/3829 (0.1%)
1	C	0.95	1/2870 (0.0%)	0.96	2/3872 (0.1%)
1	D	0.90	0/2851	0.95	3/3850 (0.1%)
1	E	0.86	0/2875	0.94	3/3882 (0.1%)
1	F	0.86	0/2919	0.93	2/3937 (0.1%)
All	All	0.89	1/17217 (0.0%)	0.95	12/23237 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	100	ILE	CA-CB	5.51	1.61	1.54

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	240	TYR	CA-C-N	-5.63	113.09	119.28
1	B	240	TYR	C-N-CA	-5.63	113.09	119.28
1	E	100	ILE	N-CA-C	5.58	119.11	113.47
1	F	145	ARG	CG-CD-NE	-5.54	99.81	112.00
1	D	48	ILE	N-CA-C	5.33	115.54	110.53

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	2817	0	2735	16	0
1	B	2803	0	2725	28	0
1	C	2821	0	2747	23	0
1	D	2807	0	2741	27	0
1	E	2825	0	2766	26	0
1	F	2858	0	2792	24	0
2	A	244	0	0	1	0
2	B	197	0	0	3	0
2	C	234	0	0	7	0
2	D	166	0	0	1	0
2	E	236	0	0	1	0
2	F	262	0	0	2	0
All	All	18270	0	16506	142	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 4.

The worst 5 of 142 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:188[A]:THR:HG21	2:F:752:HOH:O	1.75	0.86
1:E:37[B]:MSE:HA	1:E:37[B]:MSE:HE2	1.56	0.86
1:C:188[A]:THR:HG21	2:C:713:HOH:O	1.76	0.84
1:D:188[A]:THR:HG21	2:D:385:HOH:O	1.83	0.79
1:A:5:ARG:O	1:A:9:GLN:HG2	1.93	0.68

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	358/357 (100%)	352 (98%)	6 (2%)	0	100	100
1	B	353/357 (99%)	342 (97%)	11 (3%)	0	100	100
1	C	360/357 (101%)	354 (98%)	6 (2%)	0	100	100
1	D	356/357 (100%)	351 (99%)	5 (1%)	0	100	100
1	E	358/357 (100%)	352 (98%)	6 (2%)	0	100	100
1	F	365/357 (102%)	360 (99%)	5 (1%)	0	100	100
All	All	2150/2142 (100%)	2111 (98%)	39 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	289/278 (104%)	287 (99%)	2 (1%)	76	82
1	B	286/278 (103%)	280 (98%)	6 (2%)	47	52
1	C	288/278 (104%)	286 (99%)	2 (1%)	76	82
1	D	287/278 (103%)	282 (98%)	5 (2%)	53	60
1	E	291/278 (105%)	289 (99%)	2 (1%)	76	82
1	F	296/278 (106%)	292 (99%)	4 (1%)	59	66
All	All	1737/1668 (104%)	1716 (99%)	21 (1%)	63	70

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	321	ASP
1	F	92	TYR
1	F	327	SER
1	F	200	TYR
1	E	188	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	223	GLN
1	E	41	GLN
1	B	2	ASN
1	A	266	GLN
1	D	341	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues 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$
1	LLP	E	205	1	23,24,25	1.73	6 (26%)	25,32,34	1.97	5 (20%)
1	LLP	C	205	1	23,24,25	1.85	4 (17%)	25,32,34	2.08	4 (16%)
1	LLP	F	205	1	23,24,25	1.81	4 (17%)	25,32,34	2.38	8 (32%)
1	LLP	D	205	1	23,24,25	1.84	5 (21%)	25,32,34	2.02	6 (24%)
1	LLP	B	205	1	23,24,25	1.55	3 (13%)	25,32,34	2.32	4 (16%)
1	LLP	A	205	1	23,24,25	1.65	4 (17%)	25,32,34	2.15	5 (20%)

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
1	LLP	E	205	1	-	7/16/17/19	0/1/1/1
1	LLP	C	205	1	-	6/16/17/19	0/1/1/1
1	LLP	F	205	1	-	9/16/17/19	0/1/1/1
1	LLP	D	205	1	-	6/16/17/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	LLP	B	205	1	-	7/16/17/19	0/1/1/1
1	LLP	A	205	1	-	6/16/17/19	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	205	LLP	O3-C3	-6.21	1.22	1.36
1	D	205	LLP	O3-C3	-5.93	1.23	1.36
1	F	205	LLP	O3-C3	-5.71	1.23	1.36
1	A	205	LLP	O3-C3	-4.91	1.25	1.36
1	B	205	LLP	O3-C3	-4.90	1.25	1.36

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	205	LLP	OP4-C5'-C5	8.13	124.59	109.36
1	C	205	LLP	OP4-C5'-C5	8.08	124.50	109.36
1	B	205	LLP	OP4-C5'-C5	8.07	124.48	109.36
1	D	205	LLP	OP4-C5'-C5	7.40	123.23	109.36
1	E	205	LLP	OP4-C5'-C5	7.16	122.78	109.36

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	205	LLP	C4-C4'-NZ-CE
1	A	205	LLP	O-C-CA-CB
1	B	205	LLP	C4-C4'-NZ-CE
1	B	205	LLP	O-C-CA-CB
1	B	205	LLP	CG-CD-CE-NZ

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	205	LLP	1	0
1	F	205	LLP	2	0
1	B	205	LLP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	346/357 (96%)	-1.67	0 100 100	13, 22, 33, 49	6 (1%)
1	B	346/357 (96%)	-1.67	0 100 100	12, 23, 35, 46	1 (0%)
1	C	347/357 (97%)	-1.65	0 100 100	13, 22, 34, 48	7 (2%)
1	D	346/357 (96%)	-1.63	0 100 100	12, 23, 36, 48	5 (1%)
1	E	346/357 (96%)	-1.66	0 100 100	11, 23, 35, 49	6 (1%)
1	F	348/357 (97%)	-1.68	0 100 100	12, 22, 34, 46	11 (3%)
All	All	2079/2142 (97%)	-1.66	0 100 100	11, 22, 35, 49	36 (1%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LLP	E	205	24/25	0.99	0.03	17,22,31,33	0
1	LLP	F	205	24/25	0.99	0.03	16,22,31,32	0
1	LLP	C	205	24/25	1.00	0.02	17,22,30,32	0
1	LLP	D	205	24/25	1.00	0.03	17,22,30,32	0
1	LLP	A	205	24/25	1.00	0.03	17,22,30,32	0
1	LLP	B	205	24/25	1.00	0.02	17,22,31,33	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.