



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 06:13 PM UTC

PDB ID : 2FB9 / pdb\_00002fb9  
Title : Crystal structure of the Apo form of D-alanine: D-alanine ligase (Ddl) from *Thermus caldophilus*: a basis for the substrate-induced conformational changes  
Authors : Lee, J.H.; Na, Y.; Eom, S.H.  
Deposited on : 2005-12-08  
Resolution : 1.90 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

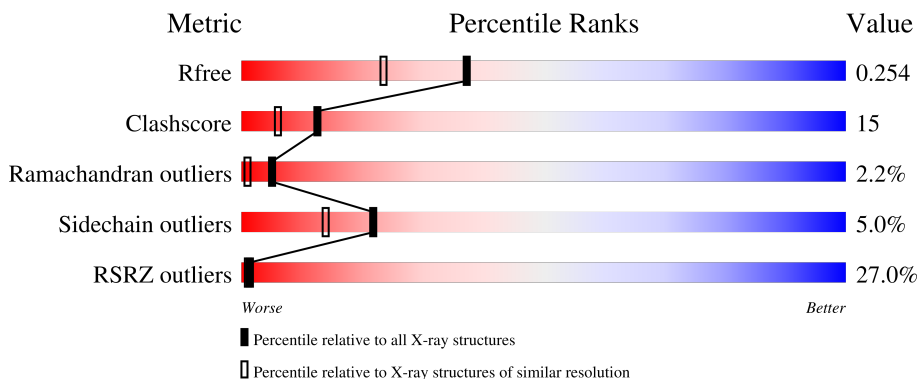
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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  $\geq 3$ , 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	322	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2596 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 D-alanine:D-alanine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	322	2481	1612	409	454	6	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	cloning artifact	UNP Q3T920
A	2	GLU	-	cloning artifact	UNP Q3T920
A	3	PHE	-	cloning artifact	UNP Q3T920

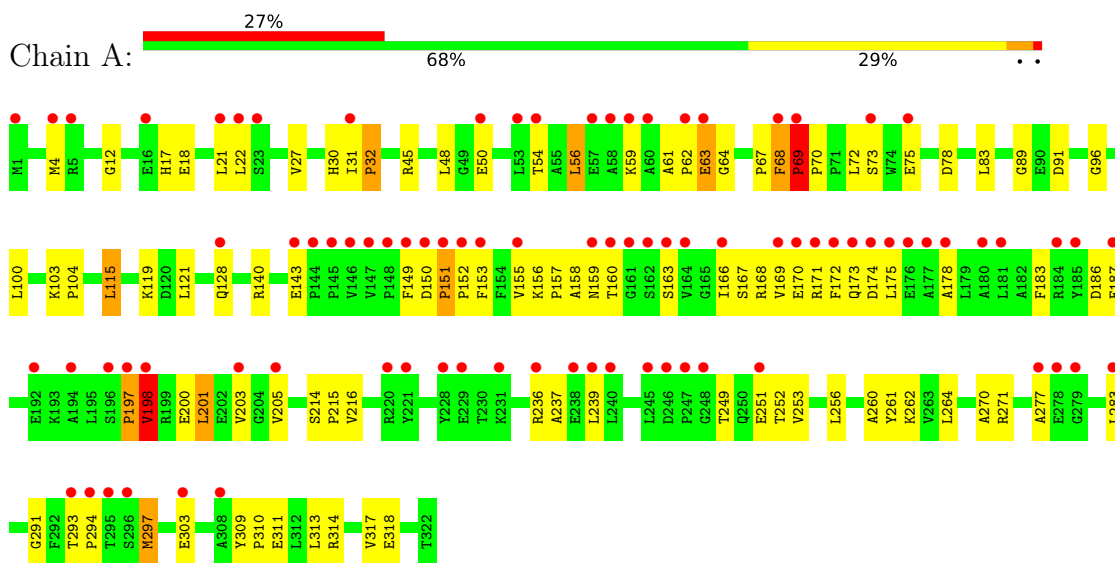
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	115	Total	O	0	0
			115	115		

### 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: D-alanine:D-alanine ligase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.22Å 132.74Å 59.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.90 30.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-1.90) 98.8 (30.00-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.06 (at 1.88Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.228 , 0.268 (Not available) , 0.254	Depositor DCC
$R_{free}$ test set	1814 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.2	Xtrriage
Anisotropy	0.420	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 38.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2596	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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	0.40	0/2547	0.94	9/3472 (0.3%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	69	PRO	CA-C-N	6.41	124.27	119.66
1	A	69	PRO	C-N-CA	6.41	124.27	119.66
1	A	30	HIS	N-CA-C	6.14	121.05	113.50
1	A	159	ASN	N-CA-C	5.89	120.04	112.26
1	A	158	ALA	N-CA-C	5.75	117.63	111.36
1	A	151	PRO	N-CA-C	5.30	117.17	110.70
1	A	91	ASP	N-CA-C	5.23	119.29	113.02
1	A	149	PHE	N-CA-C	5.12	115.81	108.74
1	A	271	ARG	N-CA-C	-5.08	100.23	108.52

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	2481	0	2494	76	0
2	A	115	0	0	2	0
All	All	2596	0	2494	76	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 15.

All (76) 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:155:VAL:HG21	1:A:178:ALA:HB1	1.26	1.09
1:A:239:LEU:HD13	1:A:297:MET:HG2	1.48	0.96
1:A:293:THR:HB	1:A:294:PRO:HD2	1.59	0.83
1:A:252:THR:O	1:A:256:LEU:HD13	1.84	0.78
1:A:197:PRO:O	1:A:198:VAL:HG12	1.84	0.77
1:A:68:PHE:O	1:A:70:PRO:N	2.24	0.70
1:A:68:PHE:O	1:A:70:PRO:HD3	1.92	0.69
1:A:78:ASP:O	1:A:104:PRO:HG2	1.93	0.69
1:A:203:VAL:HG21	1:A:253:VAL:HG12	1.75	0.68
1:A:205:VAL:HG11	1:A:261:TYR:CD1	2.29	0.67
1:A:157:PRO:HG2	1:A:160:THR:OG1	1.96	0.65
1:A:68:PHE:O	1:A:70:PRO:CD	2.44	0.65
1:A:17:HIS:CE1	1:A:61:ALA:H	2.17	0.61
1:A:260:ALA:O	1:A:264:LEU:HD23	2.00	0.61
1:A:171:ARG:HH21	1:A:172:PHE:HD1	1.49	0.61
1:A:4:MET:HG2	1:A:78:ASP:OD1	2.02	0.60
1:A:201:LEU:N	1:A:201:LEU:HD22	2.17	0.60
1:A:163:SER:HA	1:A:166:ILE:HD12	1.84	0.59
1:A:4:MET:HE1	1:A:317:VAL:HG11	1.85	0.59
1:A:151:PRO:HG2	1:A:152:PRO:HD3	1.83	0.58
1:A:151:PRO:HB3	1:A:171:ARG:NH2	2.18	0.58
1:A:96:GLY:O	1:A:100:LEU:HD23	2.04	0.57
1:A:4:MET:HE1	1:A:317:VAL:CG1	2.34	0.57
1:A:68:PHE:CG	1:A:69:PRO:N	2.73	0.56
1:A:173:GLN:HG3	1:A:174:ASP:OD1	2.05	0.56
1:A:150:ASP:HB2	1:A:152:PRO:HD2	1.90	0.53
1:A:155:VAL:CG2	1:A:167:SER:HB2	2.40	0.52
1:A:68:PHE:CD1	1:A:68:PHE:C	2.87	0.50
1:A:27:VAL:O	1:A:31:ILE:HG22	2.11	0.50
1:A:314:ARG:NH1	1:A:318:GLU:OE2	2.44	0.50
1:A:236:ARG:HG2	1:A:237:ALA:N	2.26	0.50
1:A:262:LYS:C	1:A:262:LYS:HD3	2.38	0.49
1:A:156:LYS:CB	1:A:166:ILE:HG12	2.42	0.49
1:A:73:SER:O	1:A:75:GLU:N	2.37	0.48
1:A:115:LEU:HD13	1:A:264:LEU:CD1	2.43	0.48
1:A:17:HIS:HE1	1:A:61:ALA:H	1.58	0.48
1:A:115:LEU:HD13	1:A:264:LEU:HD12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:PHE:O	1:A:69:PRO:C	2.57	0.47
1:A:251:GLU:H	1:A:251:GLU:CD	2.22	0.47
1:A:205:VAL:HG11	1:A:261:TYR:CE1	2.50	0.47
1:A:140:ARG:O	1:A:143:GLU:HB3	2.14	0.47
1:A:45:ARG:HB2	1:A:64:GLY:HA3	1.96	0.46
1:A:151:PRO:N	1:A:152:PRO:HD2	2.30	0.46
1:A:18:GLU:OE2	1:A:59:LYS:HE3	2.15	0.46
1:A:203:VAL:HG22	1:A:216:VAL:HG22	1.96	0.46
1:A:249:THR:O	1:A:253:VAL:HG23	2.16	0.46
1:A:314:ARG:O	1:A:318:GLU:HG3	2.16	0.46
1:A:175:LEU:C	1:A:175:LEU:HD13	2.41	0.46
1:A:68:PHE:CD2	1:A:69:PRO:HD3	2.51	0.46
1:A:163:SER:HA	1:A:166:ILE:CD1	2.44	0.46
1:A:205:VAL:CG1	1:A:261:TYR:CE1	2.99	0.45
1:A:156:LYS:HB3	1:A:166:ILE:HG12	1.99	0.45
1:A:198:VAL:HG23	1:A:277:ALA:HB2	1.98	0.45
1:A:21:LEU:HD22	1:A:56:LEU:HD12	1.98	0.44
1:A:168:ARG:NH1	1:A:170:GLU:OE2	2.49	0.44
1:A:183:PHE:HA	1:A:186:ASP:O	2.17	0.44
1:A:309:TYR:N	1:A:310:PRO:HD2	2.33	0.44
1:A:239:LEU:CD1	1:A:297:MET:HG2	2.34	0.43
1:A:48:LEU:HD22	1:A:72:LEU:HD13	1.99	0.43
1:A:119:LYS:HE2	1:A:156:LYS:HD3	2.00	0.43
1:A:153:PHE:CE1	1:A:169:VAL:HB	2.54	0.43
1:A:311:GLU:OE1	1:A:314:ARG:NH2	2.51	0.42
1:A:62:PRO:HD2	1:A:63:GLU:OE1	2.18	0.42
1:A:50:GLU:O	1:A:54:THR:HG23	2.20	0.42
1:A:214:SER:HB2	1:A:215:PRO:HD2	2.01	0.42
1:A:200:GLU:C	1:A:201:LEU:HD22	2.44	0.42
1:A:291:GLY:HA2	2:A:340:HOH:O	2.19	0.42
1:A:314:ARG:NH1	1:A:318:GLU:CD	2.78	0.42
1:A:293:THR:HB	1:A:294:PRO:CD	2.40	0.42
1:A:169:VAL:HG13	1:A:174:ASP:HB2	2.01	0.41
1:A:187:GLU:HG2	2:A:436:HOH:O	2.19	0.41
1:A:12:GLY:O	1:A:17:HIS:HD2	2.03	0.41
1:A:205:VAL:HG12	1:A:270:ALA:O	2.20	0.41
1:A:67:PRO:O	1:A:68:PHE:C	2.64	0.41
1:A:32:PRO:HG2	1:A:314:ARG:HB2	2.03	0.40
1:A:45:ARG:HH11	1:A:45:ARG:HG3	1.86	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	320/322 (99%)	301 (94%)	12 (4%)	7 (2%)	5 1

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	GLU
1	A	68	PHE
1	A	89	GLY
1	A	198	VAL
1	A	69	PRO
1	A	32	PRO
1	A	197	PRO

### 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	259/259 (100%)	246 (95%)	13 (5%)	22 14

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LEU
1	A	56	LEU
1	A	83	LEU
1	A	103	LYS

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Mol	Chain	Res	Type
1	A	115	LEU
1	A	121	LEU
1	A	128	GLN
1	A	198	VAL
1	A	201	LEU
1	A	283	LEU
1	A	297	MET
1	A	303	GLU
1	A	313	LEU

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

Mol	Chain	Res	Type
1	A	17	HIS
1	A	42	GLN
1	A	128	GLN
1	A	159	ASN
1	A	284	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](#)

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	322/322 (100%)	1.47	87 (27%) <b>1</b> <b>1</b>	23, 35, 59, 72	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	151	PRO	9.8
1	A	247	PRO	8.6
1	A	173	GLN	7.1
1	A	150	ASP	6.9
1	A	68	PHE	6.8
1	A	295	THR	6.5
1	A	294	PRO	6.1
1	A	146	VAL	5.8
1	A	246	ASP	5.8
1	A	162	SER	5.5
1	A	172	PHE	5.4
1	A	198	VAL	5.3
1	A	63	GLU	5.3
1	A	197	PRO	5.1
1	A	149	PHE	4.9
1	A	171	ARG	4.9
1	A	69	PRO	4.8
1	A	251	GLU	4.6
1	A	164	VAL	4.6
1	A	152	PRO	4.6
1	A	221	TYR	4.5
1	A	248	GLY	4.5
1	A	62	PRO	4.2
1	A	59	LYS	4.1
1	A	75	GLU	4.1
1	A	144	PRO	4.0
1	A	159	ASN	4.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	176	GLU	4.0
1	A	293	THR	3.9
1	A	163	SER	3.9
1	A	54	THR	3.8
1	A	147	VAL	3.8
1	A	73	SER	3.7
1	A	236	ARG	3.7
1	A	174	ASP	3.7
1	A	169	VAL	3.7
1	A	22	LEU	3.5
1	A	180	ALA	3.5
1	A	161	GLY	3.4
1	A	175	LEU	3.4
1	A	194	ALA	3.4
1	A	60	ALA	3.2
1	A	145	PRO	3.2
1	A	57	GLU	3.1
1	A	278	GLU	3.1
1	A	177	ALA	3.1
1	A	5	ARG	3.0
1	A	229	GLU	3.0
1	A	184	ARG	3.0
1	A	155	VAL	2.9
1	A	31	ILE	2.9
1	A	245	LEU	2.8
1	A	23	SER	2.8
1	A	303	GLU	2.8
1	A	296	SER	2.7
1	A	178	ALA	2.7
1	A	170	GLU	2.7
1	A	148	PRO	2.6
1	A	160	THR	2.6
1	A	279	GLY	2.6
1	A	143	GLU	2.6
1	A	153	PHE	2.5
1	A	166	ILE	2.5
1	A	308	ALA	2.5
1	A	239	LEU	2.5
1	A	128	GLN	2.5
1	A	240	LEU	2.4
1	A	53	LEU	2.3
1	A	181	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	220	ARG	2.3
1	A	187	GLU	2.3
1	A	228	TYR	2.3
1	A	277	ALA	2.3
1	A	4	MET	2.3
1	A	238	GLU	2.2
1	A	231	LYS	2.2
1	A	185	TYR	2.2
1	A	50	GLU	2.2
1	A	58	ALA	2.2
1	A	16	GLU	2.2
1	A	1	MET	2.1
1	A	192	GLU	2.1
1	A	283	LEU	2.1
1	A	205	VAL	2.1
1	A	21	LEU	2.1
1	A	196	SER	2.0
1	A	203	VAL	2.0

## 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 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.