



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:26 AM UTC

PDB ID : 6HPG / pdb\_00006hpg  
Title : Arabidopsis OM64 TPR domain  
Authors : Schwenkert, S.  
Deposited on : 2018-09-20  
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](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

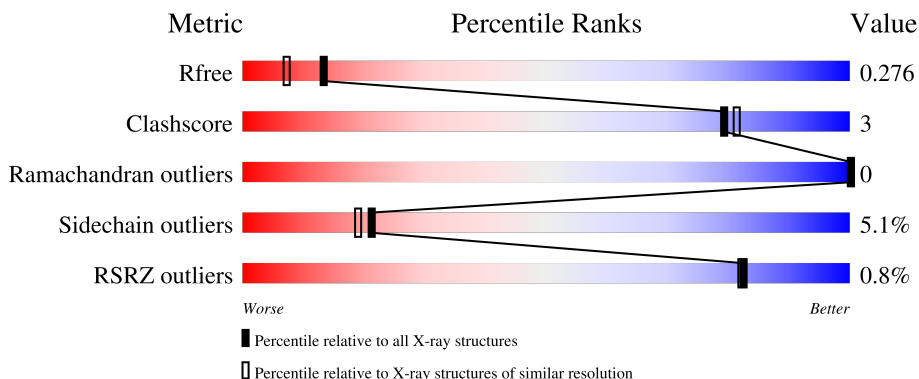
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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  $\geq 3$ , 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	121	
1	B	121	
1	C	121	
1	D	121	
1	E	121	

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Mol	Chain	Length	Quality of chain
1	F	121	 91% 6%
2	a	8	 88% 12%
2	b	8	 88% 12%
2	c	8	 75% 12% 12%
2	d	8	 88% 12%
2	e	8	 75% 12% 12%
2	f	8	 62% 25% 12%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6613 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 Outer envelope protein 64, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	121	Total 965	C 604	N 179	O 175	S 7	0	0	0
1	B	117	Total 926	C 580	N 169	O 170	S 7	0	0	0
1	C	117	Total 926	C 580	N 169	O 170	S 7	0	0	0
1	D	121	Total 970	C 608	N 179	O 175	S 8	0	1	0
1	E	117	Total 937	C 587	N 171	O 172	S 7	0	2	0
1	F	117	Total 926	C 580	N 169	O 170	S 7	0	0	0

- Molecule 2 is a protein called Heat shock protein 90-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	a	8	Total 61	C 35	N 9	O 16	S 1	0	0	0
2	b	8	Total 61	C 35	N 9	O 16	S 1	0	0	0
2	c	7	Total 57	C 33	N 8	O 15	S 1	0	0	0
2	d	8	Total 61	C 35	N 9	O 16	S 1	0	0	0
2	e	7	Total 57	C 33	N 8	O 15	S 1	0	0	0
2	f	7	Total 57	C 33	N 8	O 15	S 1	0	0	0

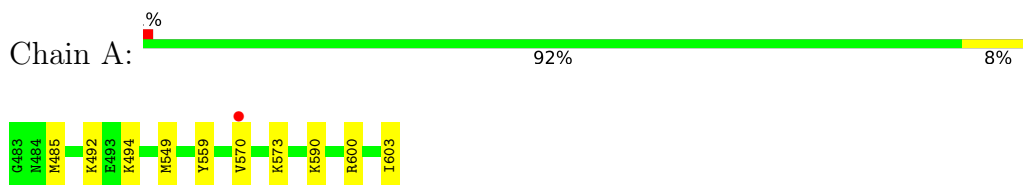
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	107	Total O 107 107	0	0
3	B	87	Total O 87 87	0	0
3	C	100	Total O 100 100	0	0
3	D	92	Total O 92 92	0	0
3	E	78	Total O 78 78	0	0
3	F	79	Total O 79 79	0	0
3	a	12	Total O 12 12	0	0
3	b	12	Total O 12 12	0	0
3	c	12	Total O 12 12	0	0
3	d	12	Total O 12 12	0	0
3	e	10	Total O 10 10	0	0
3	f	8	Total O 8 8	0	0

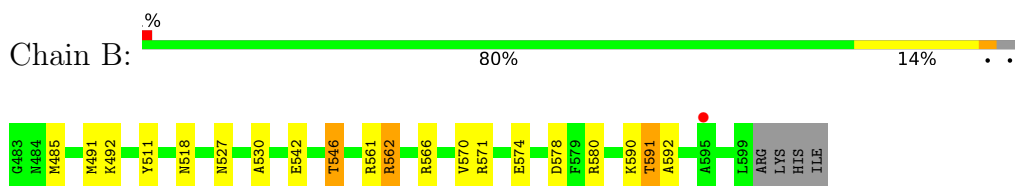
### 3 Residue-property plots [i](#)

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.

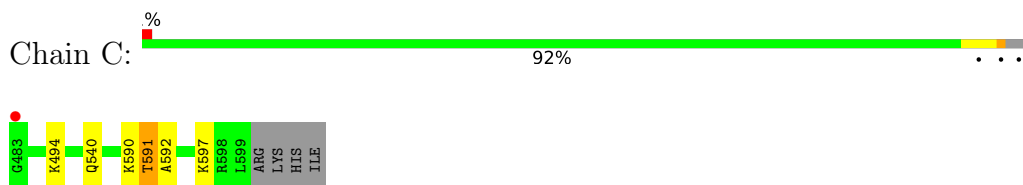
- Molecule 1: Outer envelope protein 64, mitochondrial



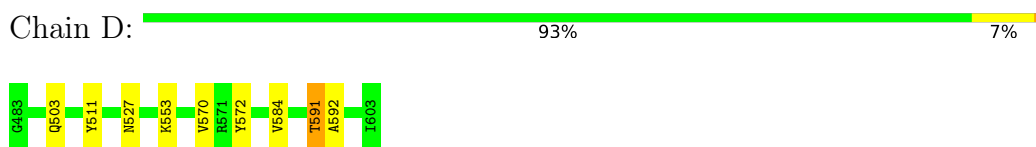
- Molecule 1: Outer envelope protein 64, mitochondrial



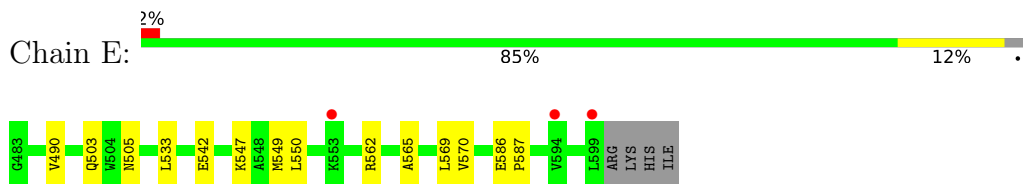
- Molecule 1: Outer envelope protein 64, mitochondrial



- Molecule 1: Outer envelope protein 64, mitochondrial



- Molecule 1: Outer envelope protein 64, mitochondrial




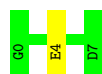
- Molecule 1: Outer envelope protein 64, mitochondrial

Chain F:  91% 6%




• Molecule 2: Heat shock protein 90-4

Chain a:  88% 12%




• Molecule 2: Heat shock protein 90-4

Chain b:  88% 12%




• Molecule 2: Heat shock protein 90-4

Chain c:  75% 12% 12%



• Molecule 2: Heat shock protein 90-4

Chain d:  88% 12%



• Molecule 2: Heat shock protein 90-4

Chain e:  75% 12% 12%



• Molecule 2: Heat shock protein 90-4

Chain f:  62% 25% 12%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	29.39Å 61.13Å 106.56Å 87.57° 87.99° 78.26°	Depositor
Resolution (Å)	29.91 – 2.00 29.91 – 2.00	Depositor EDS
% Data completeness (in resolution range)	92.7 (29.91-2.00) 92.7 (29.91-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.82 (at 2.00Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.182 , 0.265 0.196 , 0.276	Depositor DCC
$R_{free}$ test set	2395 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.9	Xtrriage
Anisotropy	0.157	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.010 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6613	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.56 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.3617e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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	0.95	0/979	1.04	0/1308
1	B	1.51	1/939 (0.1%)	1.05	1/1257 (0.1%)
1	C	1.58	2/939 (0.2%)	1.16	1/1257 (0.1%)
1	D	1.44	1/987 (0.1%)	1.01	3/1318 (0.2%)
1	E	0.89	0/956	1.02	2/1280 (0.2%)
1	F	0.87	0/939	1.02	0/1257
2	a	0.92	0/60	0.86	0/76
2	b	0.87	0/60	0.95	0/76
2	c	0.80	0/56	1.24	0/71
2	d	0.88	0/60	0.90	0/76
2	e	0.93	0/56	0.91	0/71
2	f	0.78	0/56	0.88	0/71
All	All	1.22	4/6087 (0.1%)	1.05	7/8118 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	591	THR	C-N	39.28	1.87	1.33
1	B	591	THR	C-N	34.91	1.79	1.33
1	D	591	THR	C-N	33.84	1.83	1.33
1	C	540	GLN	C-O	-5.16	1.18	1.24

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	591	THR	O-C-N	-19.72	95.25	122.46
1	D	591	THR	CA-C-N	-6.81	109.11	120.68
1	D	591	THR	C-N-CA	-6.81	109.11	120.68
1	B	591	THR	O-C-N	-5.38	116.53	122.07
1	E	586	GLU	CA-C-N	5.21	125.26	119.32

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	965	0	978	5	0
1	B	926	0	933	14	0
1	C	926	0	933	2	0
1	D	970	0	986	6	0
1	E	937	0	948	6	0
1	F	926	0	934	1	0
2	a	61	0	57	0	0
2	b	61	0	57	1	0
2	c	57	0	54	0	0
2	d	61	0	57	0	0
2	e	57	0	54	0	0
2	f	57	0	54	0	0
3	A	107	0	0	2	0
3	B	87	0	0	1	1
3	C	100	0	0	0	0
3	D	92	0	0	0	0
3	E	78	0	0	1	0
3	F	79	0	0	0	1
3	a	12	0	0	0	0
3	b	12	0	0	1	0
3	c	12	0	0	0	0
3	d	12	0	0	0	0
3	e	10	0	0	0	0
3	f	8	0	0	0	0
All	All	6613	0	6045	33	1

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 3.

The worst 5 of 33 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:B:591:THR:C	1:B:592:ALA:N	1.79	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:591:THR:C	1:D:592:ALA:N	1.83	1.33
1:C:591:THR:C	1:C:592:ALA:N	1.87	1.32
1:B:546:THR:HG22	1:B:562:ARG:HE	1.55	0.70
1:D:591:THR:C	1:D:592:ALA:CA	2.67	0.68

All (1) 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)
3:B:702:HOH:O	3:F:724:HOH:O[1_645]	1.79	0.41

## 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	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
1	B	115/121 (95%)	110 (96%)	5 (4%)	0	100	100
1	C	115/121 (95%)	113 (98%)	2 (2%)	0	100	100
1	D	120/121 (99%)	117 (98%)	3 (2%)	0	100	100
1	E	117/121 (97%)	114 (97%)	3 (3%)	0	100	100
1	F	115/121 (95%)	112 (97%)	3 (3%)	0	100	100
2	a	6/8 (75%)	5 (83%)	1 (17%)	0	100	100
2	b	6/8 (75%)	6 (100%)	0	0	100	100
2	c	5/8 (62%)	5 (100%)	0	0	100	100
2	d	6/8 (75%)	6 (100%)	0	0	100	100
2	e	5/8 (62%)	5 (100%)	0	0	100	100
2	f	5/8 (62%)	5 (100%)	0	0	100	100
All	All	734/774 (95%)	714 (97%)	20 (3%)	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	96/96 (100%)	92 (96%)	4 (4%)	26	25
1	B	92/96 (96%)	86 (94%)	6 (6%)	15	12
1	C	92/96 (96%)	89 (97%)	3 (3%)	33	34
1	D	97/96 (101%)	95 (98%)	2 (2%)	47	52
1	E	94/96 (98%)	89 (95%)	5 (5%)	20	18
1	F	92/96 (96%)	87 (95%)	5 (5%)	20	17
2	a	7/7 (100%)	6 (86%)	1 (14%)	3	2
2	b	7/7 (100%)	6 (86%)	1 (14%)	3	2
2	c	7/7 (100%)	6 (86%)	1 (14%)	3	2
2	d	7/7 (100%)	6 (86%)	1 (14%)	3	2
2	e	7/7 (100%)	6 (86%)	1 (14%)	3	2
2	f	7/7 (100%)	5 (71%)	2 (29%)	0	0
All	All	605/618 (98%)	573 (95%)	32 (5%)	21	18

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	d	4	GLU
2	e	4	GLU
1	C	597	LYS
1	C	590	LYS
2	f	3	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	540	GLN

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Mol	Chain	Res	Type
1	F	484	ASN
1	F	539	GLN
1	F	503	GLN
1	C	503	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](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1
1	D	1
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	591:THR	C	592:ALA	N	1.87

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	591:THR	C	592:ALA	N	1.83
1	B	591:THR	C	592:ALA	N	1.79

## 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, 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	121/121 (100%)	-0.07	1 (0%) 82 82	14, 24, 44, 68	0
1	B	117/121 (96%)	0.24	1 (0%) 81 80	20, 27, 48, 55	0
1	C	117/121 (96%)	0.04	1 (0%) 81 80	17, 25, 48, 65	0
1	D	121/121 (100%)	0.03	0 100 100	15, 26, 47, 65	1 (0%)
1	E	117/121 (96%)	0.05	3 (2%) 57 56	13, 27, 58, 89	2 (1%)
1	F	117/121 (96%)	0.16	0 100 100	17, 30, 53, 61	0
2	a	8/8 (100%)	0.15	0 100 100	22, 32, 37, 49	0
2	b	8/8 (100%)	0.39	0 100 100	26, 35, 47, 59	0
2	c	7/8 (87%)	0.66	0 100 100	28, 40, 53, 54	0
2	d	8/8 (100%)	0.55	0 100 100	28, 40, 52, 54	0
2	e	7/8 (87%)	0.28	0 100 100	31, 34, 42, 50	0
2	f	7/8 (87%)	0.61	0 100 100	30, 44, 55, 60	0
All	All	755/774 (97%)	0.10	6 (0%) 82 82	13, 27, 53, 89	3 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	570	VAL	2.8
1	E	599	LEU	2.5
1	E	553	LYS	2.3
1	C	483	GLY	2.1
1	E	594	VAL	2.1

### 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.