



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 02:20 PM GMT

PDB ID : 1V1H  
Title : ADENOVIRUS FIBRE SHAFT SEQUENCE N-TERMINALLY FUSED TO  
THE BACTERIOPHAGE T4 FIBRITIN FOLDON TRIMERISATION MO-  
TIF WITH A SHORT LINKER  
Authors : Papanikolopoulou, K.; Teixeira, S.; Belrhali, H.; Forsyth, V.T.; Mitraki, A.;  
Van Raaij, M.J.  
Deposited on : 2004-04-16  
Resolution : 1.90 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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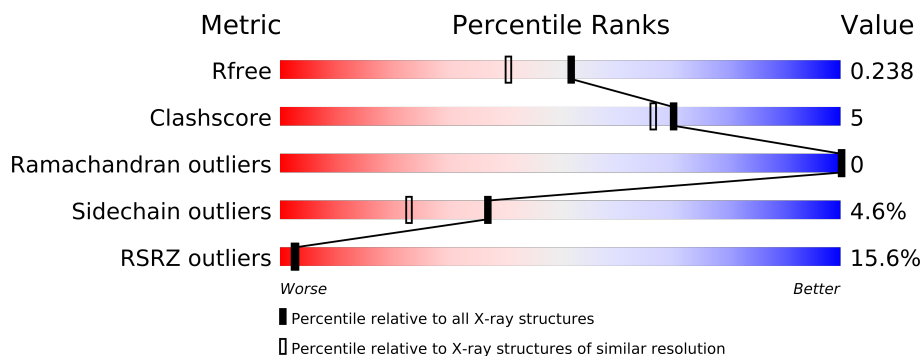
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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))
$R_{free}$	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	103	
1	B	103	
1	C	103	
1	D	103	
1	E	103	
1	F	103	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5033 atoms, of which 0 are hydrogen and 0 are deuterium.

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 FIBRITIN, FIBER PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	103	Total	C	N	O	S	0	2	0
			766	481	126	158	1			
1	B	101	Total	C	N	O	S	0	1	0
			755	474	124	156	1			
1	C	101	Total	C	N	O	S	0	3	0
			761	480	125	155	1			
1	D	101	Total	C	N	O	S	0	1	0
			754	475	124	154	1			
1	E	103	Total	C	N	O	S	0	4	0
			778	489	128	160	1			
1	F	101	Total	C	N	O	S	0	7	0
			777	491	126	159	1			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	478	LEU	PHE	CONFLICT	UNP P10104
B	478	LEU	PHE	CONFLICT	UNP P10104
C	478	LEU	PHE	CONFLICT	UNP P10104
D	478	LEU	PHE	CONFLICT	UNP P10104
E	478	LEU	PHE	CONFLICT	UNP P10104
F	478	LEU	PHE	CONFLICT	UNP P10104

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	77	Total	O	0	0
			77	77		
2	B	72	Total	O	0	0
			72	72		
2	C	73	Total	O	0	0
			73	73		

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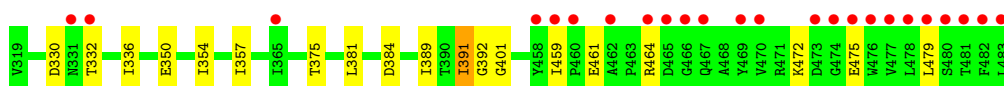
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	71	Total 71	O 71	0	0
2	E	74	Total 74	O 74	0	0
2	F	75	Total 75	O 75	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

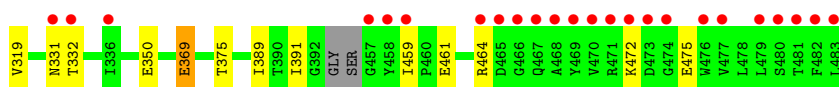
- Molecule 1: FIBRITIN, FIBER PROTEIN

Chain A: 



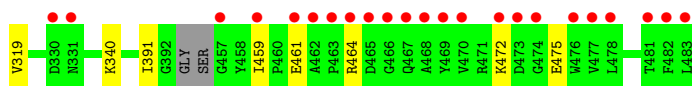
- Molecule 1: FIBRITIN, FIBER PROTEIN

Chain B: 



- Molecule 1: FIBRITIN, FIBER PROTEIN

Chain C: 



- Molecule 1: FIBRITIN, FIBER PROTEIN

Chain D: 



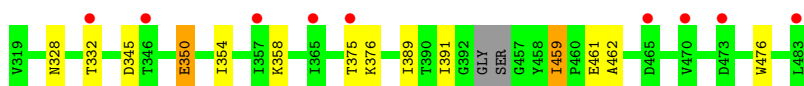
- Molecule 1: FIBRITIN, FIBER PROTEIN

Chain E: 



- Molecule 1: FIBRITIN, FIBER PROTEIN

Chain F: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.77 Å 183.33 Å 58.97 Å 90.00° 129.29° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 19.98 – 1.90	Depositor EDS
% Data completeness (in resolution range)	89.0 (20.00-1.90) 88.9 (19.98-1.90)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.85 (at 1.90 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.182 , 0.240 0.185 , 0.238	Depositor DCC
$R_{free}$ test set	1625 reflections (3.79%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.3	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 47.8	EDS
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 44490 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5033	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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	0.75	0/786	0.87	2/1061 (0.2%)
1	B	0.72	0/770	0.84	0/1038
1	C	0.75	0/784	0.84	0/1056
1	D	0.75	0/769	0.85	1/1037 (0.1%)
1	E	0.73	0/806	0.84	2/1087 (0.2%)
1	F	0.71	0/816	0.81	0/1100
All	All	0.73	0/4731	0.84	5/6379 (0.1%)

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	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	345	ASP	CB-CG-OD2	5.46	123.21	118.30
1	A	384	ASP	CB-CG-OD2	5.44	123.20	118.30
1	D	330	ASP	CB-CG-OD2	5.25	123.03	118.30
1	E	465	ASP	CB-CG-OD2	5.06	122.85	118.30
1	A	330	ASP	CB-CG-OD2	5.06	122.85	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	391	ILE	Peptide
1	D	391	ILE	Peptide

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	766	0	754	12	0
1	B	755	0	739	8	0
1	C	761	0	754	7	0
1	D	754	0	744	7	0
1	E	778	0	766	8	0
1	F	777	0	768	13	0
2	A	77	0	0	2	0
2	B	72	0	0	1	0
2	C	73	0	0	2	0
2	D	71	0	0	0	0
2	E	74	0	0	1	0
2	F	75	0	0	1	0
All	All	5033	0	4525	42	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (42) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:340[B]:LYS:NZ	2:C:2018:HOH:O	1.81	1.12
1:C:340[A]:LYS:NZ	2:C:2019:HOH:O	1.97	0.90
1:D:459:ILE:HD13	1:F:476:TRP:HZ2	1.49	0.78
1:B:461:GLU:HA	1:C:459:ILE:HD11	1.67	0.77
1:D:319:VAL:HG21	1:D:334:ILE:HD11	1.69	0.74
1:B:331:ASN:O	1:B:332:THR:HB	1.94	0.68
1:B:350:GLU:HG3	2:B:2037:HOH:O	1.95	0.67
1:A:392:GLY:HA3	2:A:2062:HOH:O	1.97	0.64
1:A:350:GLU:HG2	1:A:354:ILE:HD12	1.80	0.63
1:D:375:THR:HG21	1:D:389:ILE:HD11	1.82	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:375:THR:HG21	1:A:389:ILE:HD11	1.86	0.58
1:A:459:ILE:HD11	1:C:461:GLU:HA	1.88	0.56
1:D:466:GLY:HA2	1:E:473:ASP:OD2	2.06	0.56
1:D:459:ILE:HD13	1:F:476:TRP:CZ2	2.37	0.54
1:B:375:THR:HG21	1:B:389:ILE:HD11	1.91	0.53
1:A:391:ILE:HG22	1:C:391:ILE:HD11	1.89	0.53
1:D:381:LEU:HD12	1:F:391[A]:ILE:HG13	1.90	0.52
1:E:402:SER:HB2	1:E:458:TYR:CD2	2.44	0.52
1:B:461:GLU:HA	1:C:459:ILE:CD1	2.38	0.51
1:A:479:LEU:HB3	2:A:2074:HOH:O	2.11	0.51
1:F:328[B]:ASN:ND2	2:F:2007:HOH:O	2.45	0.49
1:E:389:ILE:HD12	1:F:375[B]:THR:CG2	2.43	0.48
1:F:345:ASP:HB2	1:F:358:LYS:HD2	1.96	0.47
1:A:391:ILE:CG2	1:C:391:ILE:HD11	2.46	0.45
1:A:381:LEU:HA	1:A:381:LEU:HD23	1.78	0.45
1:A:350:GLU:CG	1:A:354:ILE:HD12	2.47	0.45
1:F:350:GLU:H	1:F:350:GLU:HG2	1.65	0.44
1:E:459:ILE:HG13	1:F:459:ILE:HD11	2.00	0.43
1:F:461[A]:GLU:HG3	1:F:462:ALA:O	2.18	0.43
2:E:2067:HOH:O	1:F:376:LYS:HE2	2.18	0.43
1:A:461:GLU:HA	1:B:459:ILE:HD11	2.01	0.42
1:E:462:ALA:HA	1:E:476:TRP:CD1	2.54	0.42
1:E:389:ILE:HD12	1:F:375[B]:THR:HG22	2.01	0.42
1:F:350:GLU:HB2	1:F:354:ILE:HB	2.02	0.42
1:D:462:ALA:HA	1:D:476:TRP:CD1	2.55	0.41
1:F:375[A]:THR:HG21	1:F:389:ILE:HD11	2.02	0.41
1:A:392:GLY:HA3	1:A:401:GLY:HA3	1.61	0.41
1:A:336:ILE:HG21	1:A:357:ILE:HD12	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	103/103 (100%)	99 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	98/103 (95%)	94 (96%)	4 (4%)	0	100	100
1	C	100/103 (97%)	97 (97%)	3 (3%)	0	100	100
1	D	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
1	E	105/103 (102%)	101 (96%)	4 (4%)	0	100	100
1	F	104/103 (101%)	98 (94%)	6 (6%)	0	100	100
All	All	608/618 (98%)	584 (96%)	24 (4%)	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	83/81 (102%)	79 (95%)	4 (5%)	35	21
1	B	81/81 (100%)	74 (91%)	7 (9%)	15	6
1	C	83/81 (102%)	79 (95%)	4 (5%)	35	21
1	D	81/81 (100%)	78 (96%)	3 (4%)	45	32
1	E	85/81 (105%)	82 (96%)	3 (4%)	48	34
1	F	87/81 (107%)	84 (97%)	3 (3%)	49	36
All	All	500/486 (103%)	476 (95%)	24 (5%)	37	21

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	332	THR
1	A	464	ARG
1	A	472	LYS
1	A	475	GLU
1	B	319	VAL
1	B	369[A]	GLU
1	B	369[B]	GLU
1	B	391	ILE
1	B	464	ARG

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Mol	Chain	Res	Type
1	B	472	LYS
1	B	475	GLU
1	C	319	VAL
1	C	464	ARG
1	C	472	LYS
1	C	475	GLU
1	D	319	VAL
1	D	472	LYS
1	D	475	GLU
1	E	369[A]	GLU
1	E	369[B]	GLU
1	E	464	ARG
1	F	332	THR
1	F	350	GLU
1	F	459	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	331	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

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	103/103 (100%)	1.22	24 (23%) 1 1	14, 28, 85, 90	0
1	B	101/103 (98%)	0.92	24 (23%) 1 1	14, 28, 85, 90	0
1	C	101/103 (98%)	0.99	23 (22%) 1 1	13, 28, 85, 90	0
1	D	101/103 (98%)	0.46	7 (6%) 17 16	15, 29, 59, 68	0
1	E	103/103 (100%)	0.46	8 (7%) 13 13	16, 29, 60, 68	0
1	F	101/103 (98%)	0.46	9 (8%) 10 9	17, 30, 60, 68	0
All	All	610/618 (98%)	0.76	95 (15%) 3 2	13, 29, 82, 90	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	479	LEU	7.4
1	A	466	GLY	7.3
1	A	470	VAL	7.2
1	A	467	GLN	7.2
1	C	463	PRO	6.6
1	B	464	ARG	6.4
1	C	470	VAL	6.4
1	A	473	ASP	6.0
1	A	483	LEU	6.0
1	A	465	ASP	5.9
1	B	483	LEU	5.8
1	C	481	THR	5.8
1	C	483	LEU	5.8
1	B	470	VAL	5.7
1	A	478	LEU	5.7
1	B	473	ASP	5.5
1	A	481	THR	5.4
1	A	474	GLY	5.3
1	A	469	TYR	5.2

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Mol	Chain	Res	Type	RSRZ
1	A	477	VAL	5.2
1	C	467	GLN	5.2
1	C	477	VAL	5.1
1	B	469	TYR	5.0
1	B	466	GLY	4.8
1	B	482	PHE	4.7
1	C	462	ALA	4.5
1	B	481	THR	4.5
1	B	459	ILE	4.4
1	E	331	ASN	4.4
1	A	482	PHE	4.2
1	C	465	ASP	4.2
1	C	459	ILE	4.2
1	C	469	TYR	4.2
1	D	483	LEU	4.1
1	B	472	LYS	4.1
1	B	331	ASN	3.9
1	E	483	LEU	3.9
1	B	457	GLY	3.8
1	B	476	TRP	3.8
1	C	468	ALA	3.7
1	A	459	ILE	3.7
1	C	473	ASP	3.7
1	A	480	SER	3.7
1	A	464	ARG	3.6
1	A	331	ASN	3.5
1	D	470	VAL	3.4
1	B	458	TYR	3.4
1	E	332	THR	3.4
1	E	466	GLY	3.4
1	C	464	ARG	3.4
1	A	332	THR	3.3
1	A	476	TRP	3.3
1	B	465	ASP	3.2
1	B	477	VAL	3.1
1	E	473	ASP	3.1
1	B	479	LEU	3.1
1	B	474	GLY	3.1
1	A	460	PRO	3.1
1	C	461	GLU	3.1
1	F	483	LEU	3.0
1	C	466	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	476	TRP	3.0
1	C	331	ASN	2.9
1	D	457	GLY	2.8
1	E	464	ARG	2.8
1	B	480	SER	2.8
1	C	474	GLY	2.7
1	B	471	ARG	2.7
1	C	478	LEU	2.6
1	E	467	GLN	2.6
1	F	465	ASP	2.6
1	C	457	GLY	2.6
1	A	462	ALA	2.6
1	C	330	ASP	2.6
1	F	357	ILE	2.5
1	A	475	GLU	2.5
1	F	470	VAL	2.4
1	B	467	GLN	2.4
1	F	375[A]	THR	2.4
1	A	458	TYR	2.3
1	D	375	THR	2.3
1	F	473	ASP	2.3
1	E	481	THR	2.3
1	F	332	THR	2.2
1	B	468	ALA	2.2
1	A	365[A]	ILE	2.2
1	D	475	GLU	2.2
1	F	365[A]	ILE	2.2
1	C	472	LYS	2.1
1	B	336	ILE	2.0
1	D	336	ILE	2.0
1	D	365	ILE	2.0
1	B	332	THR	2.0
1	F	346	THR	2.0
1	C	482	PHE	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.