



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 12:26 PM GMT

PDB ID : 3CVE  
Title : Crystal Structure of the carboxy terminus of Homer1  
Authors : Hayashi, M.K.; Stearns, M.H.; Giannini, V.; Xu, R.-M.; Sala, C.; Hayashi, Y.  
Deposited on : 2008-04-18  
Resolution : 1.75 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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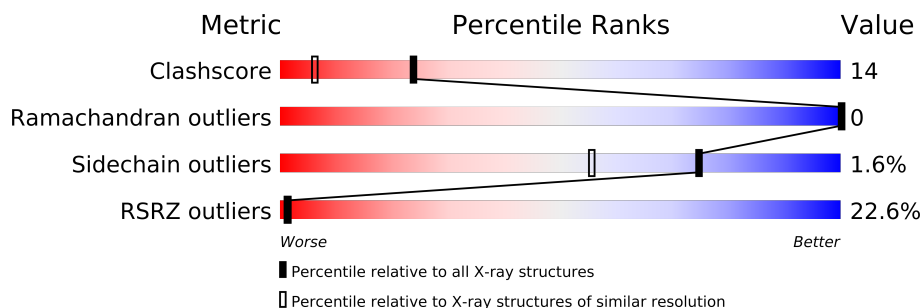
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.75 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	79885	1304 (1.76-1.76)
Ramachandran outliers	78287	1288 (1.76-1.76)
Sidechain outliers	78261	1288 (1.76-1.76)
RSRZ outliers	66119	1135 (1.76-1.76)

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	72	
1	B	72	
1	C	72	
1	D	72	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2417 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 Homer protein homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	68	Total	C	N	O	Se	0	0	0
			561	346	99	114	2			
1	B	66	Total	C	N	O	Se	0	0	0
			543	336	94	111	2			
1	C	66	Total	C	N	O	Se	0	0	0
			543	336	94	111	2			
1	D	61	Total	C	N	O	Se	0	0	0
			501	311	86	103	1			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	283	GLY	-	EXPRESSION TAG	UNP Q9Z214
A	284	SER	-	EXPRESSION TAG	UNP Q9Z214
A	285	HIS	-	EXPRESSION TAG	UNP Q9Z214
A	286	ASN	-	EXPRESSION TAG	UNP Q9Z214
A	287	SER	-	EXPRESSION TAG	UNP Q9Z214
A	288	HIS	-	EXPRESSION TAG	UNP Q9Z214
A	289	MSE	-	EXPRESSION TAG	UNP Q9Z214
A	308	MSE	LEU	ENGINEERED	UNP Q9Z214
B	283	GLY	-	EXPRESSION TAG	UNP Q9Z214
B	284	SER	-	EXPRESSION TAG	UNP Q9Z214
B	285	HIS	-	EXPRESSION TAG	UNP Q9Z214
B	286	ASN	-	EXPRESSION TAG	UNP Q9Z214
B	287	SER	-	EXPRESSION TAG	UNP Q9Z214
B	288	HIS	-	EXPRESSION TAG	UNP Q9Z214
B	289	MSE	-	EXPRESSION TAG	UNP Q9Z214
B	308	MSE	LEU	ENGINEERED	UNP Q9Z214
B	283	GLY	-	EXPRESSION TAG	UNP Q9Z214
B	284	SER	-	EXPRESSION TAG	UNP Q9Z214
C	283	GLY	-	EXPRESSION TAG	UNP Q9Z214
C	284	SER	-	EXPRESSION TAG	UNP Q9Z214
C	285	HIS	-	EXPRESSION TAG	UNP Q9Z214

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Chain	Residue	Modelled	Actual	Comment	Reference
C	286	ASN	-	EXPRESSION TAG	UNP Q9Z214
C	287	SER	-	EXPRESSION TAG	UNP Q9Z214
C	288	HIS	-	EXPRESSION TAG	UNP Q9Z214
C	289	MSE	-	EXPRESSION TAG	UNP Q9Z214
C	308	MSE	LEU	ENGINEERED	UNP Q9Z214
D	285	HIS	-	EXPRESSION TAG	UNP Q9Z214
D	286	ASN	-	EXPRESSION TAG	UNP Q9Z214
D	287	SER	-	EXPRESSION TAG	UNP Q9Z214
D	288	HIS	-	EXPRESSION TAG	UNP Q9Z214
D	289	MSE	-	EXPRESSION TAG	UNP Q9Z214
D	308	MSE	LEU	ENGINEERED	UNP Q9Z214

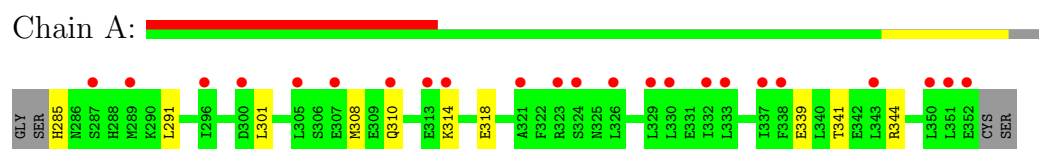
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	77	Total O 77 77	0	0
2	B	69	Total O 69 69	0	0
2	C	57	Total O 57 57	0	0
2	D	66	Total O 66 66	0	0

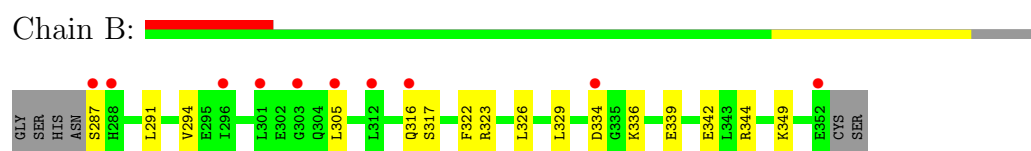
### 3 Residue-property plots

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.

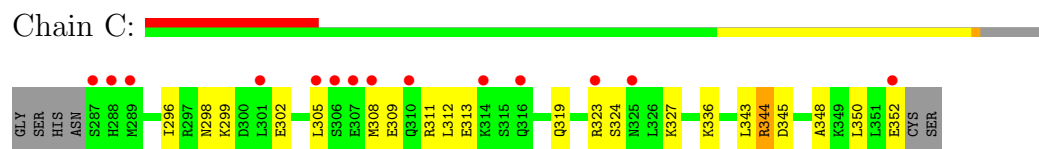
- Molecule 1: Homer protein homolog 1



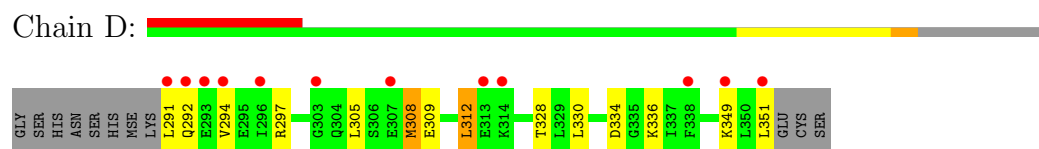
- Molecule 1: Homer protein homolog 1



- Molecule 1: Homer protein homolog 1



- Molecule 1: Homer protein homolog 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	39.01Å 62.51Å 57.53Å 90.00° 102.14° 90.00°	Depositor
Resolution (Å)	7.97 – 1.75 7.97 – 1.75	Depositor EDS
% Data completeness (in resolution range)	98.7 (7.97-1.75) 98.7 (7.97-1.75)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.21 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.216 , 0.289 (Not available) , (Not available)	Depositor DCC
$R_{free}$ test set	NotAvailable	DCC
Wilson B-factor (Å <sup>2</sup> )	25.9	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.62 , 83.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 26692 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	2417	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.16% 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	0.59	0/562	0.65	0/745
1	B	0.63	0/543	0.70	0/719
1	C	0.56	0/543	0.65	0/719
1	D	0.61	0/501	0.72	0/666
All	All	0.60	0/2149	0.68	0/2849

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	561	0	565	15	0
1	B	543	0	552	23	0
1	C	543	0	552	26	0
1	D	501	0	512	32	0
2	A	77	0	0	3	0
2	B	69	0	0	8	0
2	C	57	0	0	2	0
2	D	66	0	0	5	0
All	All	2417	0	2181	62	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 14.

All (62) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:344:ARG:HD2	1:D:334:ASP:OD1	1.23	1.28
1:B:344:ARG:CD	1:D:334:ASP:OD1	1.94	1.16
1:C:308:MSE:HE2	1:D:309:GLU:HA	1.45	0.98
1:D:328:THR:HB	2:D:248:HOH:O	1.68	0.92
1:B:294:VAL:HG23	2:B:267:HOH:O	1.70	0.90
1:C:308:MSE:CE	1:D:309:GLU:HA	2.07	0.85
1:C:348:ALA:O	1:C:352:GLU:HG2	1.77	0.85
1:C:308:MSE:CE	1:D:312:LEU:HD23	2.12	0.79
1:C:308:MSE:SE	1:D:312:LEU:HD23	2.38	0.73
1:B:342:GLU:HG2	2:B:86:HOH:O	1.88	0.73
1:A:310:GLN:HG3	2:A:142:HOH:O	1.90	0.70
1:A:339:GLU:HB3	1:D:336:LYS:CE	2.21	0.70
1:C:308:MSE:HE3	1:D:312:LEU:HD23	1.70	0.70
1:B:316:GLN:HG3	2:B:196:HOH:O	1.92	0.69
1:C:312:LEU:HD22	1:D:308:MSE:HE1	1.77	0.67
1:B:344:ARG:HD3	1:D:334:ASP:OD1	1.95	0.65
1:B:334:ASP:HB2	2:B:51:HOH:O	1.97	0.63
1:B:344:ARG:HD2	1:D:334:ASP:CG	2.15	0.63
1:A:291:LEU:HD12	1:B:294:VAL:HG21	1.81	0.62
1:D:291:LEU:N	2:D:261:HOH:O	2.32	0.62
1:C:324:SER:HA	1:C:327:LYS:HD2	1.80	0.62
1:D:292:GLN:HB2	2:D:234:HOH:O	2.00	0.61
1:B:323:ARG:NH2	1:D:351:LEU:O	2.32	0.59
1:C:308:MSE:HE2	1:D:309:GLU:CA	2.29	0.58
1:A:314:LYS:HE3	1:A:318:GLU:OE2	2.03	0.58
1:C:305:LEU:O	1:C:309:GLU:HG3	2.05	0.57
1:C:298:ASN:ND2	1:D:294:VAL:HG22	2.18	0.57
1:A:339:GLU:CB	1:D:336:LYS:CE	2.83	0.56
1:C:299:LYS:HE2	2:C:185:HOH:O	2.06	0.56
1:A:285:HIS:N	2:A:226:HOH:O	2.39	0.55
1:C:296:ILE:HA	1:C:299:LYS:HE3	1.88	0.55
1:B:336:LYS:NZ	2:B:265:HOH:O	2.40	0.55
1:A:339:GLU:HB3	1:D:336:LYS:HE3	1.88	0.55
1:A:339:GLU:CB	1:D:336:LYS:HE3	2.38	0.54
1:A:341:THR:HG23	1:A:344:ARG:NH2	2.23	0.54
1:C:344:ARG:HD3	1:C:345:ASP:OD1	2.09	0.53
1:C:309:GLU:O	1:C:313:GLU:HG3	2.09	0.53
1:B:349:LYS:HE3	2:B:161:HOH:O	2.08	0.53
1:B:287:SER:N	2:B:14:HOH:O	2.43	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:291:LEU:CD1	1:B:294:VAL:HG21	2.41	0.50
1:C:308:MSE:SE	1:D:312:LEU:CD2	3.08	0.50
1:A:308:MSE:HE1	1:B:305:LEU:HD11	1.94	0.50
1:B:291:LEU:HD12	2:B:267:HOH:O	2.11	0.49
1:A:339:GLU:HB3	1:D:336:LYS:HE2	1.93	0.49
1:C:311:ARG:HD2	1:D:312:LEU:HD21	1.94	0.48
1:B:339:GLU:HB3	1:C:336:LYS:NZ	2.29	0.48
1:A:339:GLU:CB	1:D:336:LYS:HE2	2.44	0.48
1:C:308:MSE:HE3	1:D:312:LEU:CD2	2.40	0.47
1:C:336:LYS:NZ	2:C:181:HOH:O	2.48	0.46
1:B:344:ARG:HG2	1:D:330:LEU:CD1	2.45	0.46
1:B:326:LEU:HD23	1:D:351:LEU:HD21	1.98	0.46
1:B:322:PHE:CE1	1:C:350:LEU:HG	2.51	0.46
1:B:329:LEU:HD22	1:C:343:LEU:HD12	1.97	0.45
1:C:302:GLU:CD	1:D:297:ARG:NH2	2.69	0.45
1:D:305:LEU:O	1:D:309:GLU:HG3	2.16	0.45
1:B:339:GLU:HB3	1:C:336:LYS:HZ3	1.83	0.44
1:C:319:GLN:HG3	1:C:323:ARG:CZ	2.48	0.43
1:D:336:LYS:HD3	2:D:27:HOH:O	2.19	0.42
1:A:314:LYS:HB2	2:A:188:HOH:O	2.20	0.42
1:A:301:LEU:CD2	1:B:305:LEU:HD22	2.50	0.41
1:C:312:LEU:HD22	1:D:308:MSE:CE	2.47	0.40
1:D:349:LYS:HG3	2:D:209:HOH:O	2.21	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	66/72 (92%)	66 (100%)	0	0	100	100
1	B	64/72 (89%)	64 (100%)	0	0	100	100
1	C	64/72 (89%)	64 (100%)	0	0	100	100
1	D	59/72 (82%)	59 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	253/288 (88%)	253 (100%)	0	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	64/65 (98%)	64 (100%)	0	100	100
1	B	62/65 (95%)	61 (98%)	1 (2%)	75	55
1	C	62/65 (95%)	61 (98%)	1 (2%)	75	55
1	D	57/65 (88%)	55 (96%)	2 (4%)	48	19
All	All	245/260 (94%)	241 (98%)	4 (2%)	75	55

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	317	SER
1	C	344	ARG
1	D	308	MSE
1	D	312	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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	68/72 (94%)	1.69	23 (33%) 1 1	17, 29, 35, 44	0
1	B	66/72 (91%)	1.15	10 (15%) 3 4	17, 28, 36, 45	0
1	C	66/72 (91%)	1.27	14 (21%) 1 2	18, 27, 37, 38	0
1	D	61/72 (84%)	1.23	12 (19%) 2 2	5, 19, 27, 31	0
All	All	261/288 (90%)	1.34	59 (22%) 1 1	5, 26, 36, 45	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	287	SER	5.0
1	D	292	GLN	4.8
1	B	296	ILE	4.2
1	D	313	GLU	4.0
1	C	323	ARG	3.9
1	A	338	PHE	3.8
1	D	294	VAL	3.5
1	C	306	SER	3.5
1	D	296	ILE	3.4
1	D	314	LYS	3.2
1	D	291	LEU	3.2
1	A	289	MSE	3.2
1	A	352	GLU	3.1
1	B	352	GLU	3.1
1	B	301	LEU	3.1
1	A	330	LEU	3.1
1	A	333	LEU	3.1
1	D	293	GLU	3.0
1	A	313	GLU	3.0
1	C	288	HIS	2.9
1	C	307	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	305	LEU	2.9
1	A	332	ILE	2.8
1	C	308	MSE	2.8
1	D	307	GLU	2.8
1	A	337	ILE	2.8
1	A	321	ALA	2.8
1	B	288	HIS	2.8
1	A	310	GLN	2.8
1	A	314	LYS	2.8
1	A	351	LEU	2.7
1	B	305	LEU	2.7
1	B	303	GLY	2.7
1	C	352	GLU	2.7
1	D	349	LYS	2.7
1	B	316	GLN	2.6
1	A	300	ASP	2.6
1	C	325	ASN	2.6
1	A	329	LEU	2.6
1	A	296	ILE	2.6
1	A	307	GLU	2.5
1	A	350	LEU	2.5
1	C	305	LEU	2.5
1	C	289	MSE	2.5
1	A	343	LEU	2.4
1	D	303	GLY	2.4
1	C	301	LEU	2.3
1	A	324	SER	2.3
1	B	334	ASP	2.3
1	D	351	LEU	2.2
1	C	316	GLN	2.2
1	A	287	SER	2.2
1	A	323	ARG	2.1
1	C	314	LYS	2.1
1	B	287	SER	2.1
1	B	312	LEU	2.1
1	D	338	PHE	2.1
1	A	326	LEU	2.1
1	C	310	GLN	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.