



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 03:38 pm BST

PDB ID : 6CL1  
Title : Caspase-7 in complex with Ac-DW3-KE  
Authors : Solania, A.T.; Gonzalez-Paez, G.E.; Wolan, D.W.  
Deposited on : 2018-03-01  
Resolution : 2.65 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.

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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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

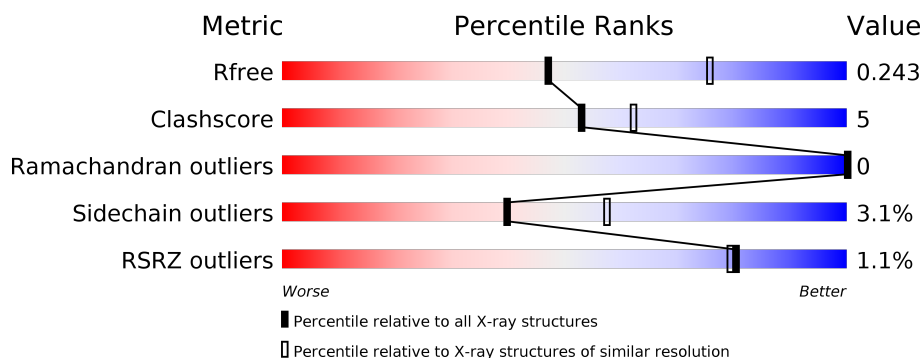
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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))
$R_{free}$	130704	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 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	198	<div> <div>61%</div> <div>10%</div> <div>29%</div> </div>
1	C	198	<div> <div>61%</div> <div>9%</div> <div>29%</div> </div>
2	B	113	<div> <div>2%</div> <div>71%</div> <div>10%</div> <div>19%</div> </div>
2	D	113	<div> <div>2%</div> <div>66%</div> <div>14%</div> <div>19%</div> </div>
3	E	8	<div> <div>13%</div> <div>25%</div> <div>13%</div> <div>63%</div> </div>
3	F	8	<div> <div>25%</div> <div>13%</div> <div>63%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3705 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 Caspase-7 subunit p20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	140	Total	C	N	O	S	0	0	0
			1073	673	182	207	11			
1	C	140	Total	C	N	O	S	0	0	0
			1091	686	186	208	11			

- Molecule 2 is a protein called Caspase-7 subunit p11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	91	Total	C	N	O	S	0	0	0
			734	474	121	135	4			
2	D	91	Total	C	N	O	S	0	0	0
			727	472	122	129	4			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	304	LEU	-	expression tag	UNP P55210
B	305	GLU	-	expression tag	UNP P55210
B	306	HIS	-	expression tag	UNP P55210
B	307	HIS	-	expression tag	UNP P55210
B	308	HIS	-	expression tag	UNP P55210
B	309	HIS	-	expression tag	UNP P55210
B	310	HIS	-	expression tag	UNP P55210
B	311	HIS	-	expression tag	UNP P55210
D	304	LEU	-	expression tag	UNP P55210
D	305	GLU	-	expression tag	UNP P55210
D	306	HIS	-	expression tag	UNP P55210
D	307	HIS	-	expression tag	UNP P55210
D	308	HIS	-	expression tag	UNP P55210
D	309	HIS	-	expression tag	UNP P55210
D	310	HIS	-	expression tag	UNP P55210
D	311	HIS	-	expression tag	UNP P55210

- Molecule 3 is a protein called ACE-1MH-ASP-B3L-PHE-1U8.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	3	Total	C	N	O	0	0	0
			29	21	3	5			
3	F	3	Total	C	N	O	0	0	0
			23	15	3	5			

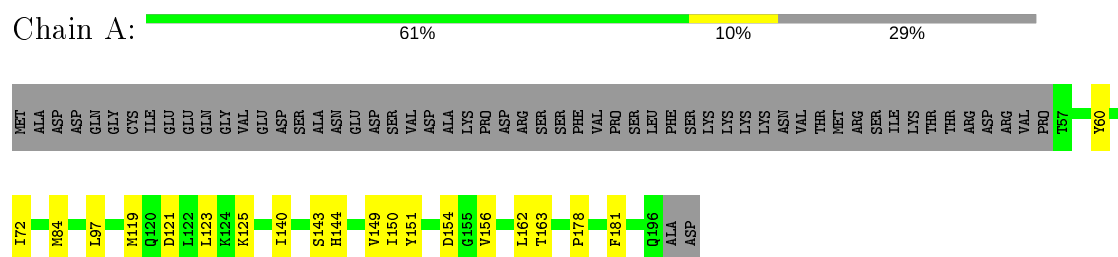
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	3	Total	O	0	0
			3	3		
4	C	12	Total	O	0	0
			12	12		
4	D	5	Total	O	0	0
			5	5		

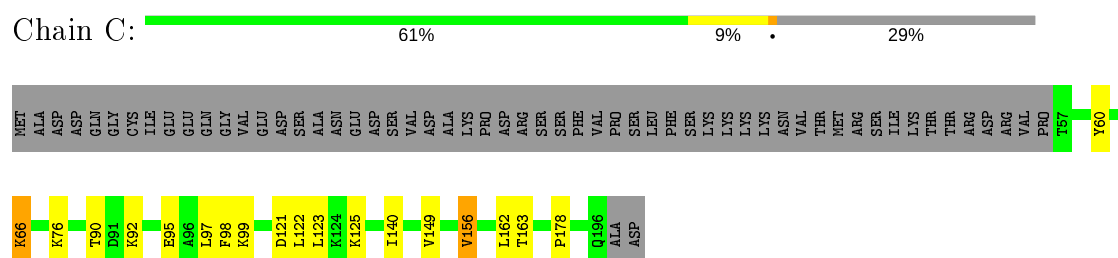
### 3 Residue-property plots

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

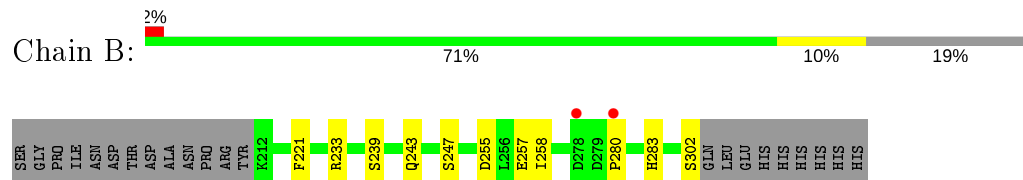
- Molecule 1: Caspase-7 subunit p20



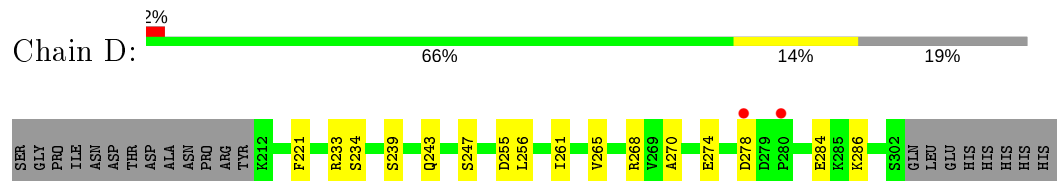
- Molecule 1: Caspase-7 subunit p20



- Molecule 2: Caspase-7 subunit p11



- Molecule 2: Caspase-7 subunit p11



- Molecule 3: ACE-1MH-ASP-B3L-PHE-1U8



ALA	CYS	GLU	1MH	ASP	X404	F405	F406
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● Molecule 3: ACE-1MH-ASP-B3L-PHE-1U8



ALA	CYS	GLU	1MH	ASP	X404	F405	F406
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.37Å 88.37Å 186.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.24 – 2.65 48.24 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.24-2.65) 99.5 (48.24-2.65)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.15	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 2.65Å)	Xtriage
Refinement program	PHENIX (dev_2747: ???)	Depositor
R, $R_{free}$	0.197 , 0.243 0.200 , 0.243	Depositor DCC
$R_{free}$ test set	1190 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.2	Xtriage
Anisotropy	0.619	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 32.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3705	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: B3L, 1U8

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	0.49	0/1090	0.62	0/1468
1	C	0.67	0/1108	0.67	0/1487
2	B	0.44	0/756	0.58	0/1026
2	D	0.45	0/749	0.59	0/1016
3	E	1.04	0/11	0.36	0/13
3	F	0.75	0/4	0.98	0/4
All	All	0.54	0/3718	0.62	0/5014

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
3	E	0	1
3	F	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	404	B3L	Peptide
3	F	404	B3L	Mainchain



## 5.2 Too-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 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	1073	0	1019	15	0
1	C	1091	0	1068	12	0
2	B	734	0	695	5	0
2	D	727	0	696	10	0
3	E	29	0	26	0	0
3	F	23	0	19	0	0
4	A	8	0	0	0	0
4	B	3	0	0	0	0
4	C	12	0	0	0	0
4	D	5	0	0	0	0
All	All	3705	0	3523	39	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 5.

All (39) 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:C:121:ASP:O	1:C:125:LYS:HG2	1.90	0.71
2:D:233:ARG:HA	2:D:239:SER:HA	1.77	0.66
1:C:149:VAL:CG1	1:C:156:VAL:HG22	2.25	0.66
1:A:84:MET:HG2	1:A:144:HIS:CD2	2.33	0.64
1:C:97:LEU:HD13	1:C:140:ILE:HG21	1.81	0.63
1:C:95:GLU:HG3	1:C:99:LYS:HE3	1.81	0.62
1:C:149:VAL:HG13	1:C:156:VAL:HG22	1.83	0.61
1:A:163:THR:HG21	2:B:221:PHE:HE2	1.65	0.61
2:D:239:SER:O	2:D:243:GLN:HG2	2.01	0.60
1:C:163:THR:HG21	2:D:221:PHE:HE2	1.67	0.59
2:D:270:ALA:O	2:D:286:LYS:NZ	2.36	0.59
2:B:239:SER:O	2:B:243:GLN:HG2	2.04	0.57
1:A:84:MET:HG2	1:A:144:HIS:CG	2.41	0.55
2:B:233:ARG:HA	2:B:239:SER:HA	1.88	0.54
1:C:149:VAL:CG1	1:C:156:VAL:CG2	2.90	0.50
2:D:247:SER:OG	2:D:268:ARG:NH1	2.47	0.48
2:D:274:GLU:HG3	2:D:286:LYS:HD3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:SER:HB3	1:A:150:ILE:HD11	1.96	0.47
1:A:97:LEU:HD13	1:A:140:ILE:HG21	1.97	0.46
1:A:163:THR:HG22	1:A:181:PHE:CE2	2.51	0.46
1:A:149:VAL:HG13	1:A:156:VAL:HB	1.97	0.46
1:C:123:LEU:HD12	1:C:162:LEU:HB3	1.98	0.45
1:C:66:LYS:HE2	1:C:66:LYS:HB2	1.40	0.45
1:A:121:ASP:O	1:A:125:LYS:HG2	2.16	0.45
1:A:123:LEU:HD22	1:A:162:LEU:HB3	1.99	0.45
1:C:163:THR:HG21	2:D:221:PHE:CE2	2.49	0.45
2:D:274:GLU:HG2	2:D:284:GLU:HA	1.99	0.44
1:A:60:TYR:CD1	1:A:178:PRO:HD3	2.53	0.44
1:A:72:ILE:HG12	1:A:140:ILE:HD12	2.00	0.43
1:A:119:MET:HB2	1:A:119:MET:HE3	1.94	0.43
1:A:149:VAL:CG1	1:A:156:VAL:HB	2.49	0.43
2:B:257:GLU:OE2	2:B:258:ILE:HG22	2.19	0.43
1:C:60:TYR:CD1	1:C:178:PRO:HD3	2.55	0.42
1:A:97:LEU:HD23	1:A:97:LEU:HA	1.83	0.42
2:D:256:LEU:HA	2:D:256:LEU:HD23	1.73	0.42
1:C:76:LYS:HD2	1:C:90:THR:HG22	2.01	0.42
1:A:84:MET:HE1	1:A:151:TYR:CZ	2.55	0.41
2:B:280:PRO:HA	2:B:283:HIS:HB2	2.02	0.41
2:D:261:ILE:O	2:D:265:VAL:HG23	2.22	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	138/198 (70%)	134 (97%)	4 (3%)	0	100	100
1	C	138/198 (70%)	134 (97%)	4 (3%)	0	100	100
2	B	89/113 (79%)	87 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	89/113 (79%)	88 (99%)	1 (1%)	0	100	100
3	E	1/8 (12%)	0	1 (100%)	0	100	100
3	F	1/8 (12%)	1 (100%)	0	0	100	100
All	All	456/638 (72%)	444 (97%)	12 (3%)	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	113/172 (66%)	112 (99%)	1 (1%)	78	87
1	C	118/172 (69%)	113 (96%)	5 (4%)	30	45
2	B	80/103 (78%)	77 (96%)	3 (4%)	33	49
2	D	78/103 (76%)	75 (96%)	3 (4%)	33	49
3	E	1/4 (25%)	1 (100%)	0	100	100
All	All	390/554 (70%)	378 (97%)	12 (3%)	40	57

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	ASP
2	B	247	SER
2	B	255	ASP
2	B	302	SER
1	C	66	LYS
1	C	92	LYS
1	C	98	PHE
1	C	122	LEU
1	C	156	VAL
2	D	234	SER
2	D	255	ASP
2	D	278	ASP

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 molecules in this entry.

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

4 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	$\# Z  > 2$
3	1U8	E	406	1,3	4,8,20	0.76	0	2,10,27	0.80	0
3	B3L	F	404	3	8,8,9	1.00	0	7,9,11	1.15	1 (14%)
3	B3L	E	404	3	8,8,9	1.37	1 (12%)	7,9,11	1.18	1 (14%)
3	1U8	F	406	1,3	4,8,20	0.80	0	2,10,27	0.65	0

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
3	1U8	E	406	1,3	-	2/5/8/17	-
3	B3L	F	404	3	-	3/7/7/8	-
3	B3L	E	404	3	-	3/7/7/8	-
3	1U8	F	406	1,3	-	2/5/8/17	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	404	B3L	CA-C	2.74	1.56	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	404	B3L	O-C-CA	-2.62	117.79	125.43
3	E	404	B3L	CB-CA-C	2.60	116.08	112.25

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	404	B3L	N-CB-CG-CD
3	E	406	1U8	N-CA-CB-CG
3	E	404	B3L	CA-CB-CG-CD
3	F	404	B3L	C-CA-CB-N
3	F	406	1U8	C-CA-CB-CG
3	F	406	1U8	N-CA-CB-CG
3	E	404	B3L	CE2-CD-CG-CB
3	F	404	B3L	O-C-CA-CB
3	E	406	1U8	C-CA-CB-CG
3	F	404	B3L	CE1-CD-CG-CB

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates 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 ⓘ

### 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	140/198 (70%)	-0.44	0 100 100	34, 50, 67, 71	0
1	C	140/198 (70%)	-0.46	0 100 100	30, 39, 61, 71	0
2	B	91/113 (80%)	-0.19	2 (2%) 62 57	31, 45, 86, 103	0
2	D	91/113 (80%)	-0.38	2 (2%) 62 57	29, 44, 83, 95	0
3	E	1/8 (12%)	2.30	1 (100%) 0 0	83, 83, 83, 83	0
3	F	1/8 (12%)	-0.63	0 100 100	53, 53, 53, 53	0
All	All	464/638 (72%)	-0.38	5 (1%) 80 79	29, 44, 70, 103	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	280	PRO	4.7
2	B	278	ASP	3.5
3	E	405	PHE	2.3
2	B	280	PRO	2.2
2	D	278	ASP	2.1

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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	B3L	E	404	9/10	0.57	0.37	74,78,82,87	0
3	B3L	F	404	9/10	0.90	0.30	58,63,68,70	0
3	1U8	E	406	9/20	0.94	0.16	51,59,65,66	0
3	1U8	F	406	9/20	0.97	0.12	41,43,52,52	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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.