



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 05:38 PM GMT

PDB ID : 4DFY  
Title : Crystal structure of R194A mutant of cAMP-dependent protein kinase with unphosphorylated activation loop  
Authors : Steichen, J.M.; Kuchinskas, M.; Yang, J.; Taylor, S.S.  
Deposited on : 2012-01-24  
Resolution : 3.00 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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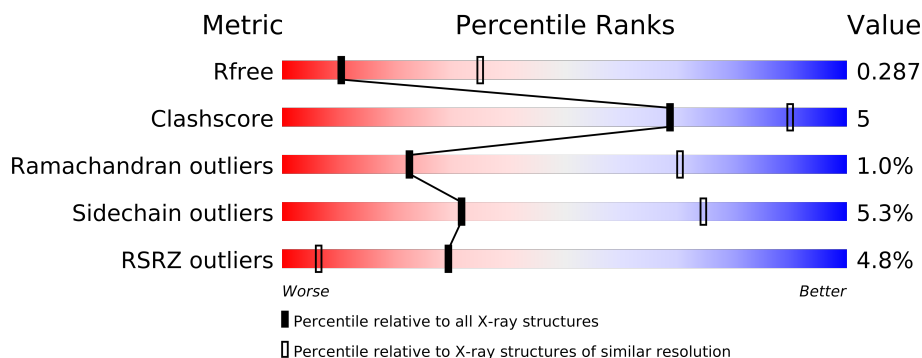
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.00 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))
$R_{free}$	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (3.00-3.00)

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 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	371	
1	E	371	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4991 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 cAMP-dependent protein kinase catalytic subunit alpha.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	P	S	0	0	0
			2484	1609	411	456	1	7			
1	E	313	Total	C	N	O	P	S	0	0	0
			2500	1624	416	452	1	7			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	EXPRESSION TAG	UNP P05132
A	-19	GLY	-	EXPRESSION TAG	UNP P05132
A	-18	SER	-	EXPRESSION TAG	UNP P05132
A	-17	SER	-	EXPRESSION TAG	UNP P05132
A	-16	HIS	-	EXPRESSION TAG	UNP P05132
A	-15	HIS	-	EXPRESSION TAG	UNP P05132
A	-14	HIS	-	EXPRESSION TAG	UNP P05132
A	-13	HIS	-	EXPRESSION TAG	UNP P05132
A	-12	HIS	-	EXPRESSION TAG	UNP P05132
A	-11	HIS	-	EXPRESSION TAG	UNP P05132
A	-10	SER	-	EXPRESSION TAG	UNP P05132
A	-9	SER	-	EXPRESSION TAG	UNP P05132
A	-8	GLY	-	EXPRESSION TAG	UNP P05132
A	-7	LEU	-	EXPRESSION TAG	UNP P05132
A	-6	VAL	-	EXPRESSION TAG	UNP P05132
A	-5	PRO	-	EXPRESSION TAG	UNP P05132
A	-4	ARG	-	EXPRESSION TAG	UNP P05132
A	-3	GLY	-	EXPRESSION TAG	UNP P05132
A	-2	SER	-	EXPRESSION TAG	UNP P05132
A	-1	HIS	-	EXPRESSION TAG	UNP P05132
A	194	ALA	ARG	ENGINEERED MUTATION	UNP P05132
E	-20	MET	-	EXPRESSION TAG	UNP P05132
E	-19	GLY	-	EXPRESSION TAG	UNP P05132
E	-18	SER	-	EXPRESSION TAG	UNP P05132
E	-17	SER	-	EXPRESSION TAG	UNP P05132

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-16	HIS	-	EXPRESSION TAG	UNP P05132
E	-15	HIS	-	EXPRESSION TAG	UNP P05132
E	-14	HIS	-	EXPRESSION TAG	UNP P05132
E	-13	HIS	-	EXPRESSION TAG	UNP P05132
E	-12	HIS	-	EXPRESSION TAG	UNP P05132
E	-11	HIS	-	EXPRESSION TAG	UNP P05132
E	-10	SER	-	EXPRESSION TAG	UNP P05132
E	-9	SER	-	EXPRESSION TAG	UNP P05132
E	-8	GLY	-	EXPRESSION TAG	UNP P05132
E	-7	LEU	-	EXPRESSION TAG	UNP P05132
E	-6	VAL	-	EXPRESSION TAG	UNP P05132
E	-5	PRO	-	EXPRESSION TAG	UNP P05132
E	-4	ARG	-	EXPRESSION TAG	UNP P05132
E	-3	GLY	-	EXPRESSION TAG	UNP P05132
E	-2	SER	-	EXPRESSION TAG	UNP P05132
E	-1	HIS	-	EXPRESSION TAG	UNP P05132
E	194	ALA	ARG	ENGINEERED MUTATION	UNP P05132

- Molecule 2 is water.

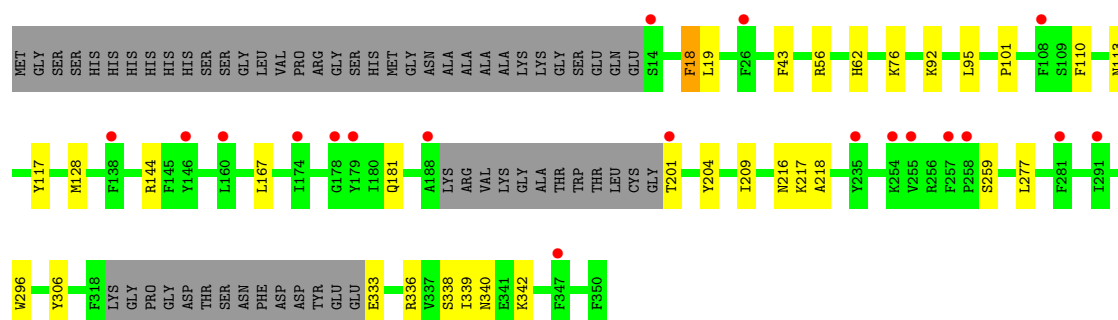
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total O 5 5	0	0
2	E	2	Total O 2 2	0	0

### 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.

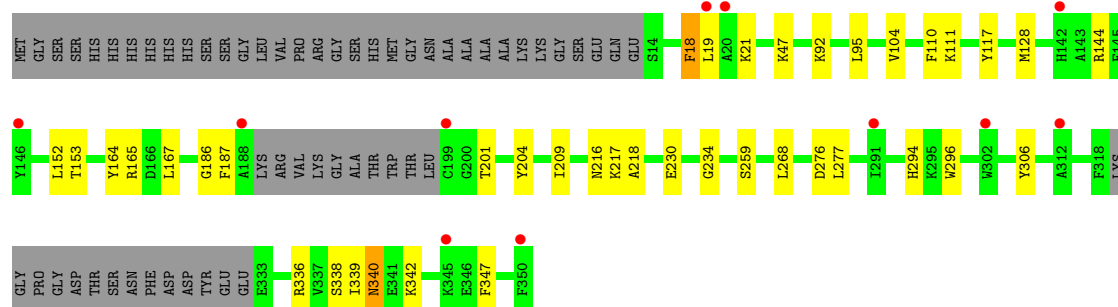
- Molecule 1: cAMP-dependent protein kinase catalytic subunit alpha

Chain A: 



- Molecule 1: cAMP-dependent protein kinase catalytic subunit alpha

Chain E: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.75Å 95.75Å 173.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.52 – 3.00 46.16 – 3.00	Depositor EDS
% Data completeness (in resolution range)	93.5 (47.52-3.00) 93.5 (46.16-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.50 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.252 , 0.286 0.247 , 0.287	Depositor DCC
$R_{free}$ test set	915 reflections (5.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	98.4	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 67.7	EDS
Estimated twinning fraction	0.007 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Outliers	0 of 17901 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4991	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SEP

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	0/2531	0.68	0/3424
1	E	0.65	1/2550 (0.0%)	0.68	0/3448
All	All	0.63	1/5081 (0.0%)	0.68	0/6872

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	164	TYR	CE1-CZ	7.30	1.48	1.38

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	2484	0	0	11	0
1	E	2500	0	0	13	0
2	A	5	0	0	0	0
2	E	2	0	0	0	0
All	All	4991	0	0	24	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 (24) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:186:GLY:O	1:E:187:PHE:CD1	2.38	0.76
1:E:18:PHE:C	1:E:18:PHE:CD2	2.59	0.76
1:A:18:PHE:CD2	1:A:18:PHE:C	2.61	0.73
1:E:167:LEU:CD2	1:E:204:TYR:CD1	2.89	0.55
1:E:18:PHE:CZ	1:E:306:TYR:OH	2.67	0.48
1:E:230:GLU:O	1:E:234:GLY:N	2.48	0.46
1:A:144:ARG:NH1	1:A:296:TRP:O	2.49	0.46
1:A:76:LYS:NZ	1:A:113:ASN:O	2.49	0.45
1:A:101:PRO:O	1:A:181:GLN:NE2	2.51	0.44
1:E:110:PHE:CE1	1:E:117:TYR:CD2	3.06	0.44
1:A:110:PHE:CE1	1:A:117:TYR:CD2	3.06	0.43
1:E:216:ASN:O	1:E:218:ALA:N	2.51	0.43
1:A:216:ASN:O	1:A:218:ALA:N	2.52	0.43
1:A:43:PHE:CE1	1:A:62:HIS:CD2	3.07	0.42
1:A:167:LEU:CD2	1:A:204:TYR:CD1	3.03	0.42
1:E:144:ARG:NH1	1:E:296:TRP:O	2.52	0.42
1:A:306:TYR:CD2	1:A:306:TYR:C	2.93	0.42
1:A:18:PHE:CZ	1:A:306:TYR:OH	2.74	0.41
1:E:152:LEU:O	1:E:153:THR:C	2.59	0.41
1:E:268:LEU:CB	1:E:294:HIS:CE1	3.04	0.41
1:E:338:SEP:O2P	1:E:340:ASN:ND2	2.54	0.41
1:A:338:SEP:O3P	1:A:339:ILE:N	2.54	0.41
1:E:338:SEP:O3P	1:E:339:ILE:N	2.55	0.40
1:E:111:LYS:NZ	1:E:347:PHE:O	2.55	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	304/371 (82%)	285 (94%)	17 (6%)	2 (1%)	30 78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	306/371 (82%)	282 (92%)	20 (6%)	4 (1%)	18	62
All	All	610/742 (82%)	567 (93%)	37 (6%)	6 (1%)	22	70

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	259	SER
1	E	217	LYS
1	E	259	SER
1	E	276	ASP
1	A	217	LYS
1	E	165	ARG

### 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	255/321 (79%)	242 (95%)	13 (5%)	33	76
1	E	256/321 (80%)	242 (94%)	14 (6%)	30	73
All	All	511/642 (80%)	484 (95%)	27 (5%)	32	74

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	PHE
1	A	19	LEU
1	A	56	ARG
1	A	92	LYS
1	A	95	LEU
1	A	128	MET
1	A	201	THR
1	A	209	ILE
1	A	277	LEU
1	A	333	GLU
1	A	336	ARG
1	A	340	ASN

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Mol	Chain	Res	Type
1	A	342	LYS
1	E	18	PHE
1	E	19	LEU
1	E	21	LYS
1	E	47	LYS
1	E	92	LYS
1	E	95	LEU
1	E	104	VAL
1	E	128	MET
1	E	201	THR
1	E	209	ILE
1	E	277	LEU
1	E	336	ARG
1	E	340	ASN
1	E	342	LYS

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 ⓘ

2 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	$\# Z  > 2$
1	SEP	A	338	1	9,9,10	6.05	3 (33%)	10,12,14	1.44	2 (20%)
1	SEP	E	338	1	9,9,10	6.06	3 (33%)	10,12,14	1.68	3 (30%)

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
1	SEP	A	338	1	-	0/6/8/10	0/0/0/0
1	SEP	E	338	1	-	0/6/8/10	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	338	SEP	O-C	17.55	1.23	1.11
1	A	338	SEP	O-C	17.50	1.23	1.11
1	A	338	SEP	P-O1P	2.86	1.60	1.51
1	E	338	SEP	P-O1P	2.82	1.60	1.51
1	E	338	SEP	CA-C	2.75	1.53	1.48
1	A	338	SEP	CA-C	2.63	1.53	1.48

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	338	SEP	OG-CB-CA	3.56	113.73	108.69
1	E	338	SEP	OG-P-O1P	2.50	114.04	106.71
1	E	338	SEP	P-OG-CB	-2.37	111.33	118.19
1	A	338	SEP	OG-P-O1P	2.36	113.63	106.71
1	A	338	SEP	P-OG-CB	-2.17	111.92	118.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	311/371 (83%)	0.36	19 (6%)	21 5	68, 106, 165, 234	4 (1%)
1	E	313/371 (84%)	0.28	11 (3%)	42 8	60, 99, 149, 186	3 (0%)
All	All	624/742 (84%)	0.32	30 (4%)	29 6	60, 103, 153, 234	7 (1%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	199	CYS	11.0
1	E	19	LEU	4.6
1	A	14	SER	4.5
1	A	174	ILE	4.0
1	A	255	VAL	4.0
1	E	350	PHE	3.9
1	E	188	ALA	3.2
1	A	146	TYR	3.1
1	A	138	PHE	2.9
1	A	257	PHE	2.7
1	A	188	ALA	2.6
1	E	312	ALA	2.6
1	A	178	GLY	2.5
1	A	201	THR	2.5
1	A	254	LYS	2.5
1	A	108	PHE	2.4
1	E	345	LYS	2.4
1	A	291	ILE	2.3
1	E	291	ILE	2.3
1	A	235	TYR	2.3
1	A	26	PHE	2.3
1	E	142	HIS	2.3
1	E	20	ALA	2.3
1	A	179	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	347	PHE	2.2
1	A	160	LEU	2.2
1	E	302	TRP	2.2
1	A	258	PRO	2.2
1	E	146	TYR	2.1
1	A	281	PHE	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	SEP	A	338	10/11	0.17	-0.19	92,94,96,97	0
1	SEP	E	338	10/11	0.12	-0.67	116,120,125,127	0

## 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.