



# Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 08:54 am BST

PDB ID : 5W4S  
Title : Solution structure of C2 domain from protein kinase C alpha in ternary complex with calcium and V5-pHM peptide  
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Deposited on : 2017-06-12

This is a Full wwPDB NMR 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/NMRValidationReportHelp>

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:

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : 2.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

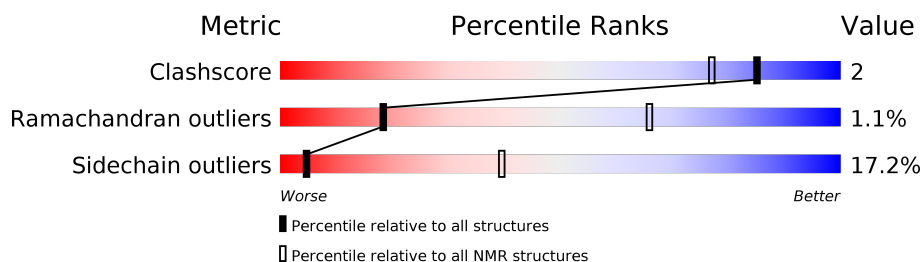
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 1%.

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)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	139	 80% 19% .
2	B	12	 25% 8% 67%

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:156-A:293, B:653-B:656 (142)	0.25	2

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 6, 8, 11, 12, 13, 14, 16, 18, 20
2	4, 5, 7, 19
3	9, 15
Single-model clusters	10; 17

### 3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2446 atoms, of which 1209 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein kinase C alpha type.

Mol	Chain	Residues	Atoms						Trace
1	A	139	Total	C	H	N	O	S	0
			2286	725	1143	197	217	4	

- Molecule 2 is a protein called V5-pHM peptide.

Mol	Chain	Residues	Atoms						Trace
2	B	12	Total	C	H	N	O	P	1
			158	55	66	12	24	1	

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

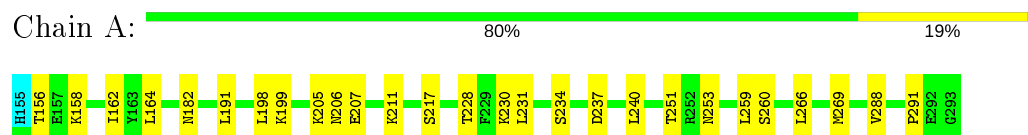
Mol	Chain	Residues	Atoms	
3	A	2	Total	Ca
			2	2

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

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Protein kinase C alpha type



- Molecule 2: V5-pHM peptide

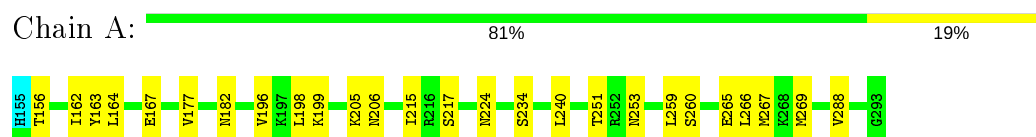


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

- Molecule 1: Protein kinase C alpha type

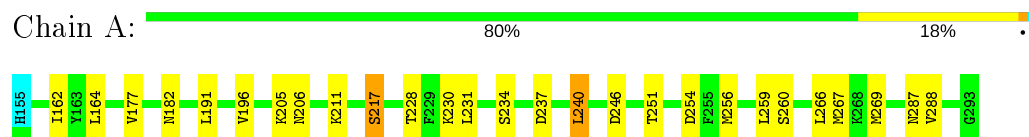


- Molecule 2: V5-pHM peptide



### 4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Protein kinase C alpha type

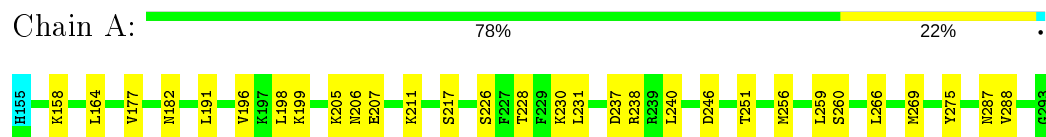


- Molecule 2: V5-pHM peptide



### 4.2.3 Score per residue for model 3

- Molecule 1: Protein kinase C alpha type

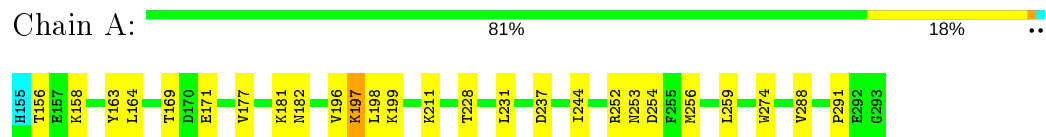


- Molecule 2: V5-pHM peptide



### 4.2.4 Score per residue for model 4

- Molecule 1: Protein kinase C alpha type

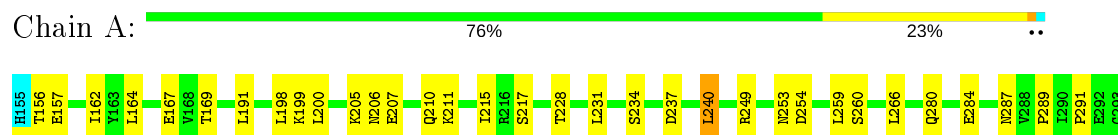


- Molecule 2: V5-pHM peptide



### 4.2.5 Score per residue for model 5

- Molecule 1: Protein kinase C alpha type

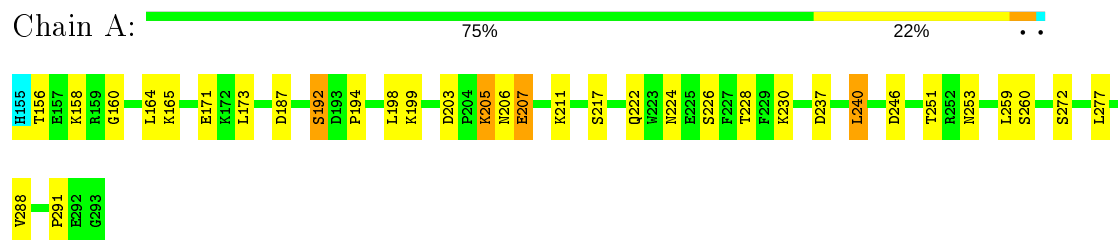


- Molecule 2: V5-pHM peptide



### 4.2.6 Score per residue for model 6

- Molecule 1: Protein kinase C alpha type

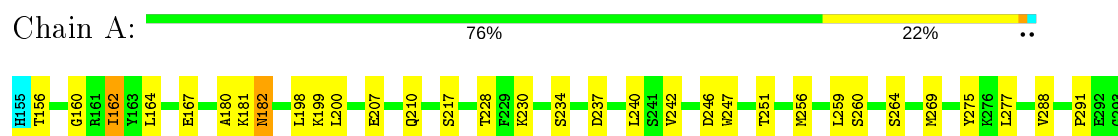


- Molecule 2: V5-pHM peptide



### 4.2.7 Score per residue for model 7

- Molecule 1: Protein kinase C alpha type



- Molecule 2: V5-pHM peptide





#### 4.2.8 Score per residue for model 8

- Molecule 1: Protein kinase C alpha type

Chain A: 78% 21% ..



- Molecule 2: V5-PHM peptide

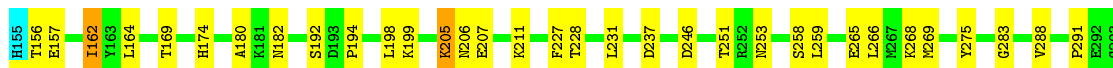
Chain B: 33% 67%



#### 4.2.9 Score per residue for model 9

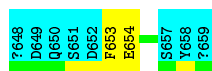
- Molecule 1: Protein kinase C alpha type

Chain A: 76% 22% ..



- Molecule 2: V5-PHM peptide

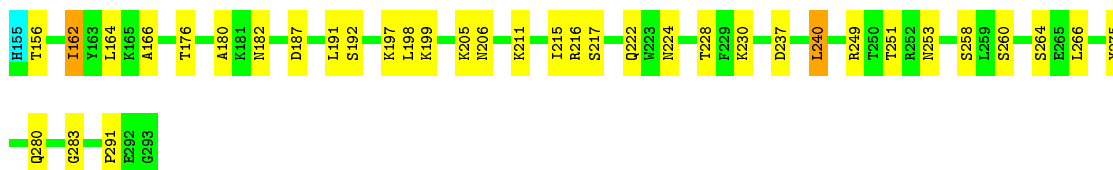
Chain B: 17% 17% 67%



#### 4.2.10 Score per residue for model 10

- Molecule 1: Protein kinase C alpha type

Chain A: 73% 24% ..



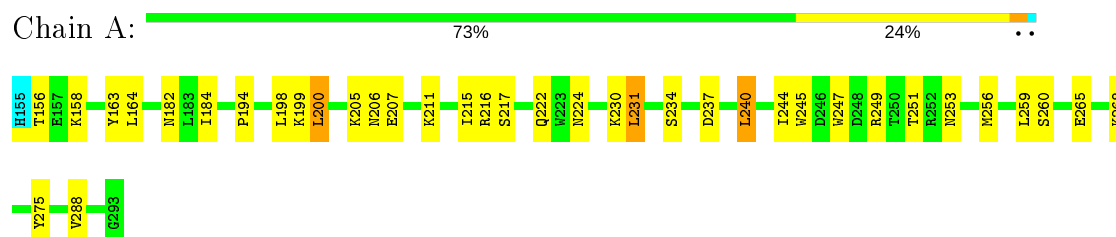


- Molecule 2: V5-pHM peptide



#### 4.2.11 Score per residue for model 11

- Molecule 1: Protein kinase C alpha type

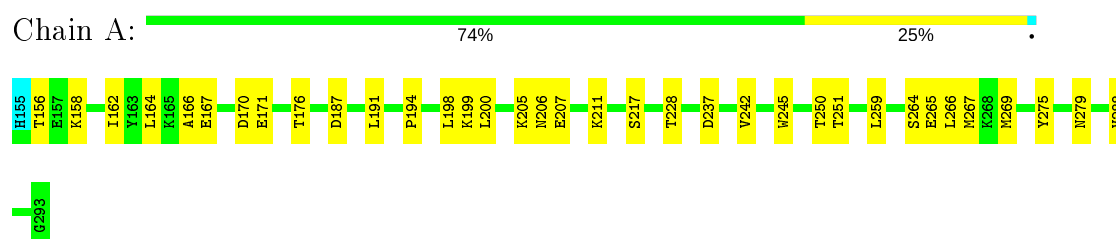


- Molecule 2: V5-pHM peptide



#### 4.2.12 Score per residue for model 12

- Molecule 1: Protein kinase C alpha type

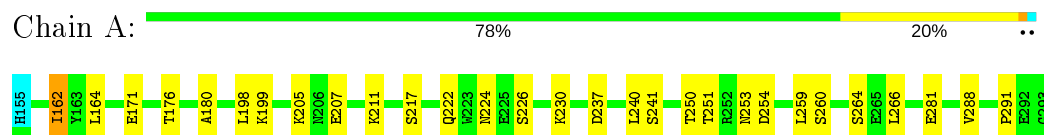


- Molecule 2: V5-pHM peptide



### 4.2.13 Score per residue for model 13

- Molecule 1: Protein kinase C alpha type

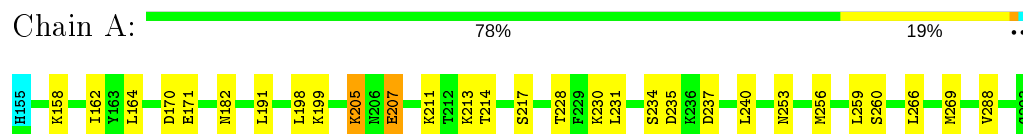


- Molecule 2: V5-pHM peptide



### 4.2.14 Score per residue for model 14

- Molecule 1: Protein kinase C alpha type

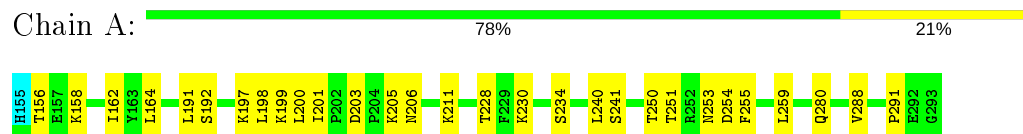


- Molecule 2: V5-pHM peptide



### 4.2.15 Score per residue for model 15

- Molecule 1: Protein kinase C alpha type

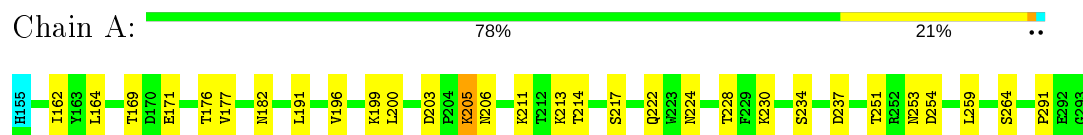


- Molecule 2: V5-pHM peptide



### 4.2.16 Score per residue for model 16

- Molecule 1: Protein kinase C alpha type

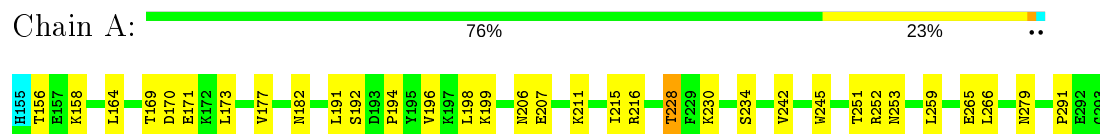


- Molecule 2: V5-pHM peptide



### 4.2.17 Score per residue for model 17

- Molecule 1: Protein kinase C alpha type

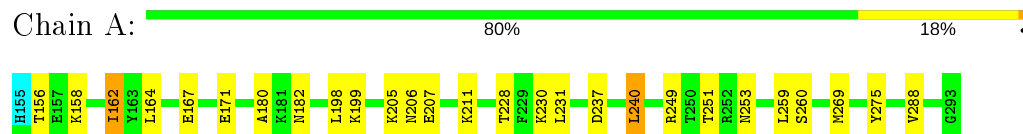


- Molecule 2: V5-pHM peptide



### 4.2.18 Score per residue for model 18

- Molecule 1: Protein kinase C alpha type

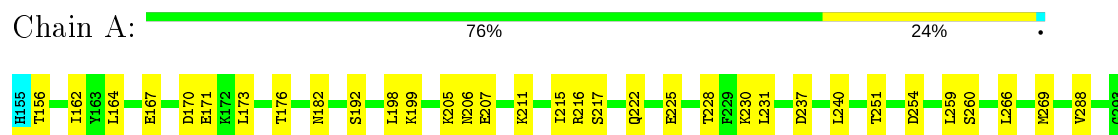


- Molecule 2: V5-pHM peptide



### 4.2.19 Score per residue for model 19

- Molecule 1: Protein kinase C alpha type

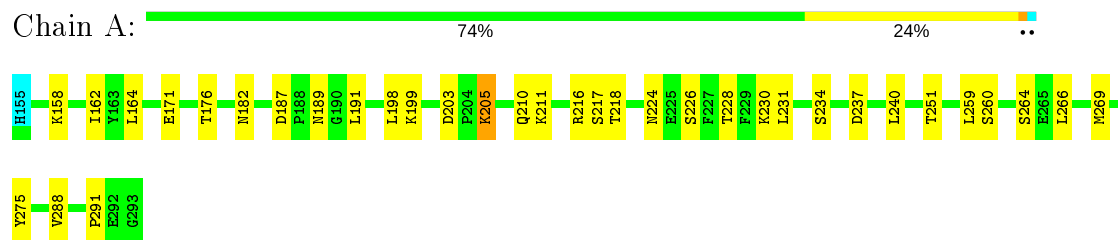


- Molecule 2: V5-pHM peptide



### 4.2.20 Score per residue for model 20

- Molecule 1: Protein kinase C alpha type



- Molecule 2: V5-pHM peptide



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing*.

Of the 400 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
ARIA	structure calculation	
CNS	refinement	
HADDOCK	structure calculation	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	59
Number of shifts mapped to atoms	59
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	1%

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality ⓘ

### 6.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CA, NH2, ACE, SEP

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1133	1133	1132	5±2
2	B	35	27	27	0±0
All	All	23400	23200	23180	102

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 2.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:177:VAL:HG21	1:A:196:VAL:HG21	0.65	1.67	17	7
1:A:258:SER:O	1:A:283:GLY:HA3	0.57	2.00	10	2
1:A:266:LEU:HA	1:A:269:MET:O	0.56	1.99	20	8
1:A:191:LEU:HD21	1:A:217:SER:HA	0.53	1.79	12	5
1:A:215:ILE:HG22	1:A:216:ARG:H	0.53	1.62	11	4
1:A:222:GLN:HG2	1:A:224:ASN:OD1	0.53	2.04	13	5
1:A:203:ASP:OD2	1:A:205:LYS:HD2	0.51	2.04	6	2
1:A:240:LEU:O	1:A:260:SER:HA	0.51	2.04	10	13
1:A:166:ALA:HB1	1:A:266:LEU:HD21	0.50	1.83	12	2
1:A:162:ILE:HG12	1:A:180:ALA:HB2	0.50	1.84	7	5
1:A:191:LEU:HG	1:A:192:SER:N	0.49	2.21	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:187:ASP:HB2	1:A:191:LEU:O	0.49	2.08	20	3
1:A:160:GLY:O	1:A:277:LEU:HG	0.49	2.07	7	2
1:A:275:TYR:OH	1:A:287:ASN:HA	0.48	2.09	3	1
1:A:203:ASP:OD2	1:A:205:LYS:HG3	0.47	2.08	15	2
1:A:192:SER:O	1:A:194:PRO:HD3	0.46	2.11	6	2
1:A:173:LEU:O	1:A:228:THR:HA	0.46	2.11	6	3
1:A:173:LEU:HD11	1:A:266:LEU:HD23	0.45	1.87	19	1
1:A:191:LEU:HG	1:A:192:SER:H	0.45	1.72	10	2
1:A:238:ARG:HA	1:A:238:ARG:NE	0.44	2.28	3	1
1:A:215:ILE:HG22	1:A:216:ARG:N	0.44	2.27	19	2
1:A:269:MET:HG3	1:A:269:MET:O	0.44	2.13	9	1
1:A:181:LYS:HE2	1:A:274:TRP:CH2	0.43	2.48	4	1
1:A:244:ILE:O	1:A:256:MET:HB2	0.43	2.14	11	2
1:A:246:ASP:HB3	1:A:254:ASP:HB2	0.43	1.89	2	1
1:A:194:PRO:HA	1:A:245:TRP:O	0.43	2.14	17	3
1:A:200:LEU:HB3	1:A:231:LEU:HD23	0.43	1.90	11	1
1:A:255:PHE:CZ	1:A:280:GLN:HG3	0.43	2.49	15	1
1:A:252:ARG:O	1:A:252:ARG:HD2	0.43	2.14	17	1
1:A:287:ASN:O	1:A:289:PRO:HD3	0.42	2.13	5	1
1:A:165:LYS:HG3	1:A:272:SER:OG	0.42	2.14	6	1
1:A:176:THR:HA	1:A:225:GLU:O	0.42	2.15	19	1
1:A:205:LYS:HD3	1:A:207:GLU:CG	0.42	2.45	14	3
1:A:174:HIS:HA	1:A:227:PHE:O	0.42	2.15	9	1
1:A:260:SER:OG	1:A:284:GLU:HA	0.42	2.15	5	1
1:A:265:GLU:O	1:A:268:LYS:HG3	0.41	2.15	11	1
1:A:216:ARG:O	1:A:218:THR:HG22	0.41	2.15	20	1
1:A:247:TRP:CE2	2:B:656:PHE:HB2	0.41	2.50	11	1
1:A:247:TRP:CH2	2:B:654:GLU:HA	0.41	2.51	7	1
1:A:181:LYS:O	1:A:182:ASN:HB2	0.41	2.16	7	1
1:A:265:GLU:OE1	1:A:268:LYS:HE2	0.40	2.16	9	1
2:B:653:PHE:HB3	2:B:654:GLU:OE1	0.40	2.16	5	1
1:A:213:LYS:HG3	1:A:214:THR:N	0.40	2.32	16	1
1:A:280:GLN:O	1:A:284:GLU:HG2	0.40	2.16	5	1
1:A:197:LYS:HE3	2:B:653:PHE:CE1	0.40	2.51	15	1

## 6.3 Torsion angles ⓘ

### 6.3.1 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 PDB entries followed by that with respect to all NMR

entries. 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	137/139 (99%)	123±2 (90±1%)	12±2 (9±1%)	1±1 (1±1%)	20	68
2	B	4/12 (33%)	2±1 (45±22%)	2±1 (50±25%)	0±0 (5±10%)	4	25
All	All	2820/3020 (93%)	2505 (89%)	283 (10%)	32 (1%)	18	66

All 5 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	253	ASN	14
1	A	291	PRO	11
2	B	655	GLY	4
1	A	249	ARG	2
1	A	215	ILE	1

### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	128/129 (99%)	106±3 (83±2%)	22±3 (17±2%)	5	40
2	B	3/8 (38%)	2±1 (75±23%)	1±1 (25±23%)	2	25
All	All	2620/2740 (96%)	2169 (83%)	451 (17%)	5	39

All 63 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	164	LEU	20
1	A	259	LEU	19
1	A	199	LYS	19
1	A	198	LEU	18
1	A	211	LYS	18
1	A	251	THR	17
1	A	237	ASP	16
1	A	205	LYS	16

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Mol	Chain	Res	Type	Models (Total)
1	A	228	THR	16
1	A	288	VAL	16
1	A	162	ILE	15
1	A	230	LYS	15
1	A	206	ASN	15
1	A	182	ASN	15
1	A	156	THR	14
2	B	653	PHE	11
1	A	207	GLU	11
1	A	234	SER	11
1	A	231	LEU	11
1	A	158	LYS	11
1	A	171	GLU	10
1	A	217	SER	10
1	A	240	LEU	8
1	A	275	TYR	7
1	A	200	LEU	7
1	A	167	GLU	6
1	A	264	SER	6
1	A	254	ASP	6
1	A	176	THR	6
1	A	169	THR	5
1	A	170	ASP	5
1	A	163	TYR	4
1	A	246	ASP	4
1	A	226	SER	4
2	B	654	GLU	4
1	A	256	MET	4
1	A	191	LEU	4
1	A	267	MET	4
1	A	250	THR	3
1	A	266	LEU	3
1	A	269	MET	3
1	A	210	GLN	3
1	A	265	GLU	3
1	A	192	SER	3
1	A	242	VAL	3
1	A	157	GLU	2
1	A	279	ASN	2
1	A	224	ASN	2
1	A	241	SER	2
1	A	280	GLN	1

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Mol	Chain	Res	Type	Models (Total)
1	A	184	ILE	1
1	A	201	ILE	1
1	A	189	ASN	1
1	A	214	THR	1
1	A	235	ASP	1
1	A	252	ARG	1
1	A	213	LYS	1
1	A	197	LYS	1
1	A	281	GLU	1
1	A	287	ASN	1
1	A	222	GLN	1
1	A	215	ILE	1
1	A	187	ASP	1

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	SEP	B	657	2	8,9,10	1.50±0.01	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	SEP	B	657	2	8,12,14	2.03±0.08	0±0 (0±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
2	SEP	B	657	2	-	0±0,5,8,10	-

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 1% for the well-defined parts and 3% for the entire structure.

### 7.1 Chemical shift list 1

File name: input\_cs.cif

Chemical shift list name: *pSer10\_deposit\_star3\_v2.txt*

#### 7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	59
Number of shifts mapped to atoms	59
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

#### 7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

#### 7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 1%, i.e. 24 atoms were assigned a chemical shift out of a possible 1844. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	8/690 (1%)	8/274 (3%)	0/284 (0%)	0/132 (0%)
Sidechain	8/1004 (1%)	8/595 (1%)	0/359 (0%)	0/50 (0%)
Aromatic	8/150 (5%)	8/78 (10%)	0/66 (0%)	0/6 (0%)
Overall	24/1844 (1%)	24/947 (3%)	0/709 (0%)	0/188 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 3%, i.e. 52 atoms were assigned a chemical shift out of a possible 1917. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	18/720 (2%)	18/286 (6%)	0/296 (0%)	0/138 (0%)
Sidechain	22/1031 (2%)	22/611 (4%)	0/369 (0%)	0/51 (0%)
Aromatic	12/166 (7%)	12/86 (14%)	0/72 (0%)	0/8 (0%)
Overall	52/1917 (3%)	52/983 (5%)	0/737 (0%)	0/197 (0%)

#### 7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain B:

