



wwPDB X-ray Structure Validation Summary Report ⓘ

May 4, 2016 – 05:31 PM EDT

PDB ID : 5F9E
Title : Structure of Protein Kinase C theta with compound 10: 2,2-dimethyl-7-(2-oxidanylidene-3 {H}-imidazo[4,5-b]pyridin-1-yl)-1-(phenylmethyl)-3 {H}-quinazolin-4-one
Authors : Klein, M.
Deposited on : 2015-12-09
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027457
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

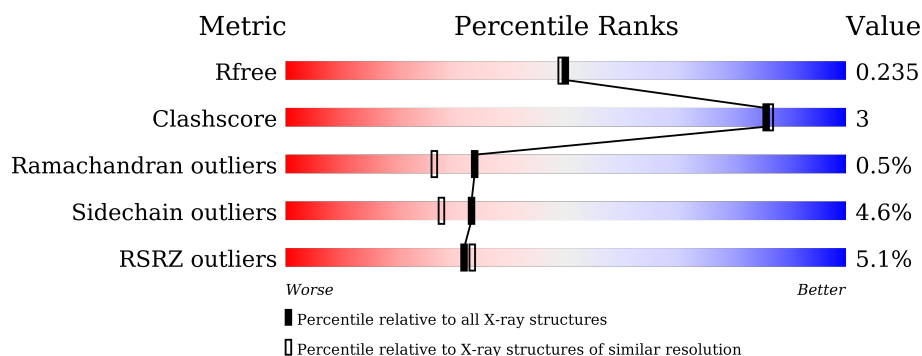
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	353	<div> <div>2%</div> <div>88%</div> <div>7% • 5%</div> </div>
1	B	353	<div> <div>7%</div> <div>74%</div> <div>8% • 17%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5508 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.

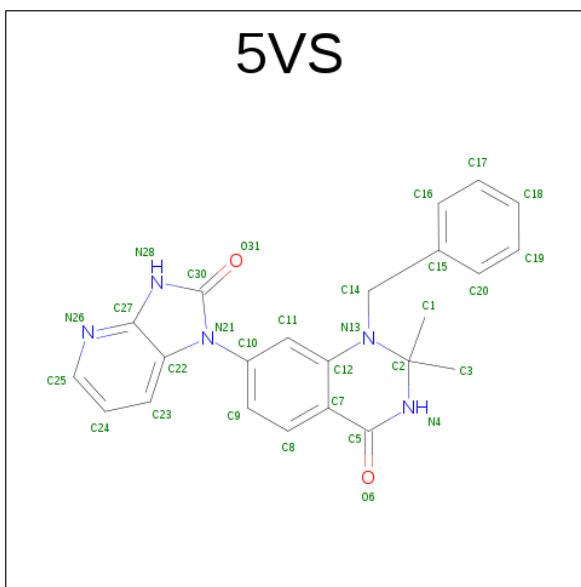
- Molecule 1 is a protein called Protein kinase C theta type.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	P	S	0	6	0
			2832	1831	474	503	2	22			
1	B	294	Total	C	N	O	P	S	0	1	0
			2452	1595	406	433	1	17			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	360	MET	-	initiating methionine	UNP Q04759
A	381	GLU	ILE	conflict	UNP Q04759
A	538	GLU	THR	conflict	UNP Q04759
A	707	HIS	-	expression tag	UNP Q04759
A	708	HIS	-	expression tag	UNP Q04759
A	709	HIS	-	expression tag	UNP Q04759
A	710	HIS	-	expression tag	UNP Q04759
A	711	HIS	-	expression tag	UNP Q04759
A	712	HIS	-	expression tag	UNP Q04759
B	360	MET	-	initiating methionine	UNP Q04759
B	381	GLU	ILE	conflict	UNP Q04759
B	538	GLU	THR	conflict	UNP Q04759
B	707	HIS	-	expression tag	UNP Q04759
B	708	HIS	-	expression tag	UNP Q04759
B	709	HIS	-	expression tag	UNP Q04759
B	710	HIS	-	expression tag	UNP Q04759
B	711	HIS	-	expression tag	UNP Q04759
B	712	HIS	-	expression tag	UNP Q04759

- Molecule 2 is 2,2-dimethyl-7-(2-oxidanylidene-3 {H}-imidazo[4,5-b]pyridin-1-yl)-1-(phenylmethyl)-3 {H}-quinazolin-4-one (three-letter code: 5VS) (formula: C₂₃H₂₁N₅O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			30	23	5	2		
2	B	1	Total	C	N	O	0	0
			30	23	5	2		

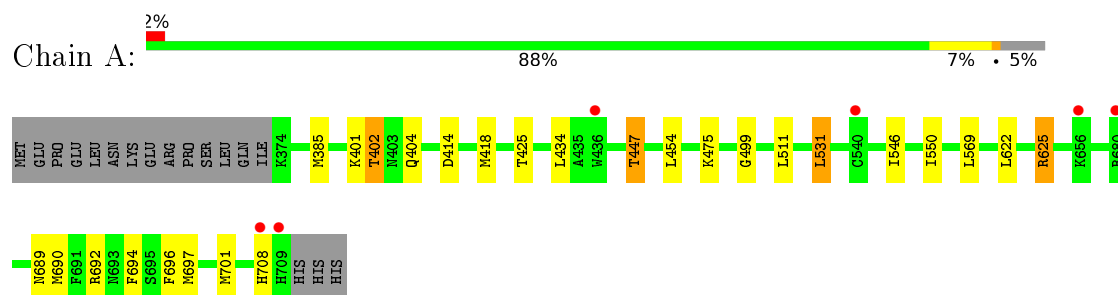
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	126	Total	O	0	0
			126	126		
3	B	38	Total	O	0	0
			38	38		

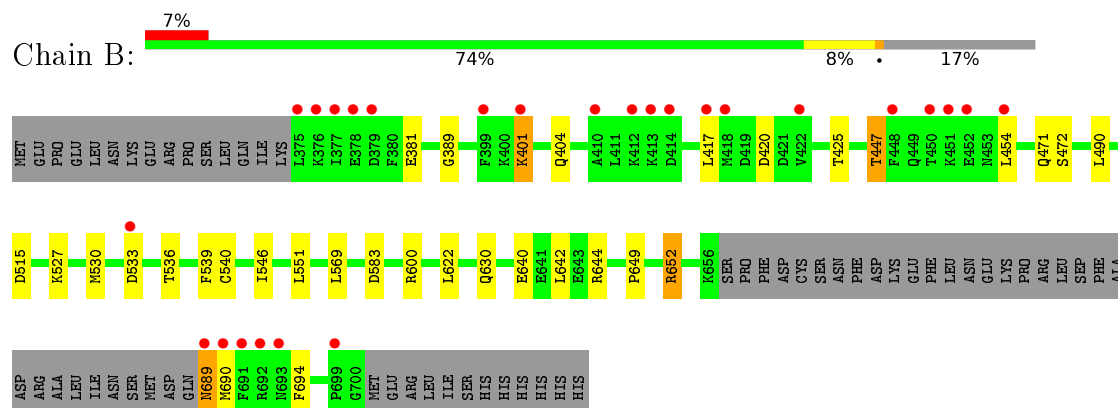
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: Protein kinase C theta type



- Molecule 1: Protein kinase C theta type



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.60 Å 76.79 Å 149.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.80 – 2.00 41.76 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.3 (41.80-2.00) 97.4 (41.76-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.00 Å)	Xtriage
Refinement program	REFMAC 5.7.0025	Depositor
R, R_{free}	0.197 , 0.233 0.203 , 0.235	Depositor DCC
R_{free} test set	2929 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	40.1	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5508	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 5VS, 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	0.54	0/2903	0.71	0/3898
1	B	0.45	1/2509 (0.0%)	0.65	3/3371 (0.1%)
All	All	0.50	1/5412 (0.0%)	0.69	3/7269 (0.0%)

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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	540	CYS	CB-SG	-5.84	1.72	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	583	ASP	CB-CG-OD1	5.97	123.67	118.30
1	B	540	CYS	N-CA-CB	-5.58	100.55	110.60
1	B	652	ARG	NE-CZ-NH2	-5.20	117.70	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	539	PHE	Peptide

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	2832	0	2797	19	0
1	B	2452	0	2422	11	0
2	A	30	0	0	0	0
2	B	30	0	0	0	0
3	A	126	0	0	3	0
3	B	38	0	0	1	0
All	All	5508	0	5219	30	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 3.

The worst 5 of 30 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:A:625[B]:ARG:HG2	1:A:625[B]:ARG:HH21	1.35	0.92
1:A:625[B]:ARG:NH2	1:A:625[B]:ARG:HG2	1.87	0.87
1:A:625[B]:ARG:HH21	1:A:625[B]:ARG:CG	1.89	0.86
1:A:418[B]:MET:HE1	3:A:1130:HOH:O	1.80	0.81
1:A:385:MET:HE3	3:A:1157:HOH:O	1.79	0.81

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	338/353 (96%)	330 (98%)	6 (2%)	2 (1%)	30 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	290/353 (82%)	277 (96%)	12 (4%)	1 (0%)	46	41
All	All	628/706 (89%)	607 (97%)	18 (3%)	3 (0%)	34	26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	689	ASN
1	A	402	THR
1	B	401	LYS

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	309/320 (97%)	297 (96%)	12 (4%)	39	35
1	B	265/320 (83%)	250 (94%)	15 (6%)	25	19
All	All	574/640 (90%)	547 (95%)	27 (5%)	33	27

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	381	GLU
1	B	417	LEU
1	B	630	GLN
1	B	401	LYS
1	A	511	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	404	GLN
1	A	684	ASN
1	A	693	ASN

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Mol	Chain	Res	Type
1	B	404	GLN
1	B	689	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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	676	1	7,9,10	0.86	0	8,12,14	5.71	1 (12%)
1	SEP	A	695	1	7,9,10	1.00	0	8,12,14	1.87	5 (62%)
1	SEP	B	695	1	7,9,10	0.70	0	8,12,14	1.51	2 (25%)

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	676	1	-	0/5/8/10	0/0/0/0
1	SEP	A	695	1	-	0/5/8/10	0/0/0/0
1	SEP	B	695	1	-	0/5/8/10	0/0/0/0

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	695	SEP	OG-P-O1P	-2.39	101.07	107.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	695	SEP	O3P-P-OG	-2.32	99.94	106.72
1	A	695	SEP	OG-CB-CA	-2.25	106.30	108.26
1	A	695	SEP	O2P-P-OG	-2.05	100.73	106.72
1	A	695	SEP	O2P-P-O1P	2.07	117.38	110.63

There are no chirality outliers.

There are no torsion outliers.

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](#)

2 ligands 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	$\# Z > 2$
2	5VS	A	1001	-	32,34,34	1.39	3 (9%)	39,51,51	3.06	11 (28%)
2	5VS	B	1001	-	32,34,34	1.21	3 (9%)	39,51,51	2.90	11 (28%)

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	5VS	A	1001	-	-	0/8/27/27	0/5/5/5
2	5VS	B	1001	-	-	0/8/27/27	0/5/5/5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	5VS	C10-N21	-3.85	1.40	1.46
2	B	1001	5VS	C10-N21	-3.35	1.41	1.46
2	B	1001	5VS	C27-N26	-2.41	1.33	1.37
2	A	1001	5VS	C3-C2	2.29	1.56	1.52
2	B	1001	5VS	C27-N28	2.72	1.39	1.35

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	5VS	O6-C5-N4	-9.33	115.71	121.85
2	B	1001	5VS	C1-C2-C3	-7.19	104.85	111.68
2	B	1001	5VS	O6-C5-N4	-4.64	118.80	121.85
2	A	1001	5VS	C1-C2-N4	-3.31	102.37	109.83
2	B	1001	5VS	C12-C7-C5	-3.24	117.50	120.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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 ²)	Q<0.9
1	A	334/353 (94%)	0.17	6 (1%) 71 72	29, 43, 72, 101	0
1	B	293/353 (83%)	0.49	26 (8%) 12 13	38, 60, 102, 119	0
All	All	627/706 (88%)	0.32	32 (5%) 32 33	29, 51, 90, 119	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	451	LYS	6.2
1	B	690	MET	5.8
1	B	692	ARG	5.4
1	B	375	LEU	5.4
1	B	454	LEU	5.2

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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, 95th 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	LLDF	B-factors(Å ²)	Q<0.9
1	SEP	A	676	10/11	0.95	0.09	-	57,60,64,65	0
1	SEP	B	695	10/11	0.86	0.17	-	89,94,100,101	0
1	SEP	A	695	10/11	0.96	0.10	-	40,45,53,54	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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, 95th 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	LLDF	B-factors(\AA^2)	Q<0.9
2	5VS	A	1001	30/30	0.97	0.14	-0.01	35,38,43,47	0
2	5VS	B	1001	30/30	0.97	0.11	-0.59	46,49,52,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.