



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 8FVM / pdb_00008fvm
Title : PCSK9 in complex with an inhibitor
Authors : Xu, M.; Chopra, R.
Deposited on : 2023-01-19
Resolution : 2.85 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

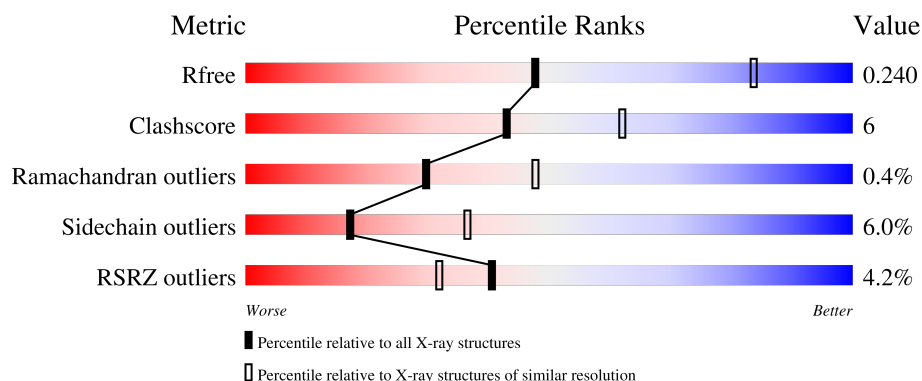
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	180053	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	152	
2	B	540	
3	C	10	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4378 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 Proprotein convertase subtilisin/kexin type 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	92	Total	C	N	O	S	0	1	0
			748	479	136	131	2			

- Molecule 2 is a protein called Proprotein convertase subtilisin/kexin type 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	476	Total	C	N	O	S	0	0	0
			3539	2183	654	671	31			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	474	ILE	VAL	variant	UNP Q8NBP7
B	670	GLU	GLY	variant	UNP Q8NBP7

- Molecule 3 is a protein called DGN-DVA-YC3-GLU-PRO-THR-THR-PHE-MAA-A1BC0 inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	10	Total	C	N	O	S	0	0	0
			90	62	12	14	2			

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.47Å 70.73Å 148.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.20 – 2.85 48.20 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.20-2.85) 99.7 (48.20-2.85)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1	Depositor
R, R_{free}	0.198 , 0.238 0.202 , 0.240	Depositor DCC
R_{free} test set	779 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	50.8	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4378	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: A1BC0, DGN, DVA, CA, MAA, YC3

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	0.76	0/768	1.02	1/1037 (0.1%)
2	B	0.73	0/3600	1.09	7/4883 (0.1%)
3	C	0.98	0/41	1.80	2/55 (3.6%)
All	All	0.74	0/4409	1.08	10/5975 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	203	THR	N-CA-C	9.51	124.69	112.89
1	A	84	GLU	N-CA-C	7.58	119.54	111.28
2	B	673	THR	N-CA-C	7.29	120.29	108.41
2	B	596	ILE	N-CA-C	6.33	117.81	108.45
3	C	4	GLU	CB-CA-C	6.03	121.56	110.10
2	B	154	ILE	CA-C-N	5.86	125.87	119.90
2	B	154	ILE	C-N-CA	5.86	125.87	119.90
3	C	6	THR	N-CA-C	-5.32	106.29	112.89
2	B	336	VAL	N-CA-C	5.26	115.44	107.75
2	B	304	LEU	N-CA-C	-5.08	105.92	111.82

There are no chirality outliers.

There are no planarity outliers.

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	748	0	763	4	0
2	B	3539	0	3453	48	1
3	C	90	0	58	7	0
4	B	1	0	0	0	0
All	All	4378	0	4274	54	1

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 6.

All (54) 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)
2:B:199:ARG:NH1	2:B:243:LYS:O	2.21	0.73
2:B:523:ILE:HD13	2:B:648:TYR:HB3	1.73	0.69
2:B:554:GLN:HG3	2:B:557:HIS:CG	2.29	0.68
2:B:469:ARG:CZ	2:B:469:ARG:H	2.08	0.67
2:B:615:ILE:HD11	2:B:619:GLN:HG2	1.80	0.63
2:B:539:ALA:HB2	2:B:550:VAL:HG13	1.81	0.62
2:B:468:THR:HG22	2:B:471:ALA:HB2	1.82	0.62
2:B:550:VAL:HG22	2:B:596:ILE:HG23	1.82	0.62
1:A:98:LEU:HB2	1:A:137:LEU:HD11	1.82	0.62
2:B:201:MET:HE3	2:B:248:ARG:HD3	1.82	0.61
2:B:476:ARG:HG2	2:B:508:VAL:HG22	1.84	0.60
2:B:480:ASP:OD2	2:B:480:ASP:N	2.36	0.59
2:B:541:PRO:HA	2:B:548:THR:HG21	1.86	0.57
2:B:464:HIS:CE1	2:B:491:ARG:HH12	2.23	0.57
2:B:584:GLN:HB2	2:B:587:GLN:HB3	1.86	0.57
2:B:203:THR:O	2:B:204:ASP:HB2	2.05	0.56
3:C:4:GLU:C	3:C:6:THR:H	2.12	0.55
2:B:553:HIS:ND1	2:B:554:GLN:OE1	2.39	0.55
2:B:549:ARG:HG2	2:B:589:VAL:HG12	1.89	0.54
2:B:156:TRP:CZ3	2:B:341:ALA:HA	2.43	0.54
2:B:158:LEU:O	2:B:162:THR:HG23	2.09	0.53
2:B:464:HIS:HE1	2:B:491:ARG:HH12	1.57	0.52
2:B:196:ILE:O	2:B:199:ARG:HG2	2.11	0.50
2:B:345:PRO:HD3	2:B:424:ILE:HG23	1.94	0.49
2:B:418:PHE:CD2	2:B:445:PRO:HB3	2.47	0.49
2:B:433:GLN:OE1	2:B:436:LEU:HD12	2.13	0.49
2:B:206:GLU:OE2	2:B:251:ARG:NH2	2.38	0.48
2:B:468:THR:OG1	2:B:469:ARG:NH2	2.48	0.47
2:B:346:VAL:HG11	3:C:3:YC3:C17	2.45	0.46
3:C:4:GLU:C	3:C:6:THR:N	2.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:490:SER:HB3	2:B:520:VAL:HG12	1.97	0.46
2:B:483:LEU:HD23	2:B:507:LEU:HB3	1.98	0.46
2:B:553:HIS:CD2	2:B:553:HIS:H	2.32	0.46
2:B:432:ASP:OD2	2:B:491:ARG:NE	2.49	0.45
2:B:469:ARG:HD3	2:B:515:PHE:HD1	1.81	0.45
2:B:410:GLU:HA	2:B:528:LEU:HD11	1.98	0.45
2:B:607:GLU:O	2:B:679:CYS:HA	2.16	0.45
2:B:436:LEU:HD21	2:B:521:TYR:CE1	2.52	0.45
2:B:332:GLU:O	2:B:408:LEU:HD21	2.17	0.45
3:C:10:A1BC0:CB	3:C:10:A1BC0:C2	2.95	0.45
1:A:152:GLN:C	3:C:7:THR:HG23	2.42	0.44
1:A:146:ASP:OD2	2:B:262:SER:OG	2.34	0.44
2:B:317:ASN:HB2	3:C:9:MAA:HM1	2.00	0.44
2:B:199:ARG:HH12	2:B:244:GLY:HA2	1.82	0.44
2:B:539:ALA:CB	2:B:550:VAL:HG13	2.47	0.44
1:A:152:GLN:OE1	2:B:316:GLY:HA2	2.18	0.43
2:B:554:GLN:HG3	2:B:557:HIS:ND1	2.32	0.43
2:B:496:ARG:HG3	2:B:514:ALA:HB2	2.01	0.43
3:C:8:PHE:HA	3:C:9:MAA:HA	1.64	0.42
2:B:181:GLU:OE1	2:B:248:ARG:NE	2.52	0.42
2:B:302:GLN:O	2:B:306:ARG:HG2	2.21	0.41
2:B:194:ARG:HA	2:B:194:ARG:HD3	1.94	0.41
2:B:292:GLY:O	2:B:293:TYR:C	2.65	0.40
2:B:154:ILE:HD12	2:B:154:ILE:HG23	1.81	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:165:ARG:NH1	2:B:612:GLU:OE2[4_555]	2.09	0.11

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	91/152 (60%)	89 (98%)	2 (2%)	0	100	100
2	B	458/540 (85%)	443 (97%)	13 (3%)	2 (0%)	30	48
3	C	5/10 (50%)	4 (80%)	1 (20%)	0	100	100
All	All	554/702 (79%)	536 (97%)	16 (3%)	2 (0%)	30	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	280	VAL
2	B	568	VAL

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	80/127 (63%)	75 (94%)	5 (6%)	16	34
2	B	381/431 (88%)	360 (94%)	21 (6%)	19	41
3	C	5/5 (100%)	3 (60%)	2 (40%)	0	0
All	All	466/563 (83%)	438 (94%)	28 (6%)	17	36

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	ASP
1	A	83	LYS
1	A	90	GLN
1	A	97	ARG
1	A	132	GLU
2	B	165	ARG
2	B	277	VAL
2	B	283	LEU
2	B	462	SER

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Mol	Chain	Res	Type
2	B	468	THR
2	B	469	ARG
2	B	480	ASP
2	B	499	ARG
2	B	508	VAL
2	B	531	GLN
2	B	548	THR
2	B	550	VAL
2	B	555	GLN
2	B	569	GLU
2	B	584	GLN
2	B	592	ARG
2	B	596	ILE
2	B	615	ILE
2	B	620	GLU
2	B	645	LEU
2	B	673	THR
3	C	4	GLU
3	C	6	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	190	GLN
2	B	278	GLN
2	B	417	HIS
2	B	464	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

5 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	A1BC0	C	10	3	8,8,8	0.90	1 (12%)	9,10,10	1.88	2 (22%)
3	YC3	C	3	3	18,20,21	0.66	0	20,26,28	0.83	1 (5%)
3	DVA	C	2	3	4,6,7	0.76	0	6,7,9	1.11	1 (16%)
3	DGN	C	1	3	7,8,9	0.78	0	4,9,11	0.57	0
3	MAA	C	9	3	4,5,6	0.76	0	2,5,7	2.38	1 (50%)

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	A1BC0	C	10	3	-	6/10/10/10	-
3	YC3	C	3	3	-	0/10/12/14	0/2/2/2
3	DVA	C	2	3	-	2/5/6/8	-
3	DGN	C	1	3	-	3/6/7/9	-
3	MAA	C	9	3	-	0/2/4/6	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	10	A1BC0	CB-CA	2.23	1.55	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	10	A1BC0	CA-C-N1	3.57	122.56	118.53
3	C	9	MAA	CB-CA-N	3.17	117.58	110.20
3	C	10	A1BC0	CA-CB-SG	-3.06	107.86	114.40
3	C	2	DVA	O-C-CA	-2.15	119.23	124.77
3	C	3	YC3	C17-C16-C21	2.13	120.93	118.93

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	DVA	C-CA-CB-CG2

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Mol	Chain	Res	Type	Atoms
3	C	10	A1BC0	N1-C-CA-N
3	C	10	A1BC0	C-CA-CB-SG
3	C	10	A1BC0	N-CA-CB-SG
3	C	10	A1BC0	O-C-CA-CB
3	C	10	A1BC0	N1-C-CA-CB
3	C	10	A1BC0	O-C-CA-N
3	C	2	DVA	C-CA-CB-CG1
3	C	1	DGN	NE2-CD-CG-CB
3	C	1	DGN	C-CA-CB-CG
3	C	1	DGN	OE1-CD-CG-CB

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	10	A1BC0	1	0
3	C	3	YC3	1	0
3	C	9	MAA	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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.

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 ⓘ

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, 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	92/152 (60%)	-0.20	0 100 100	28, 38, 58, 68	1 (1%)
2	B	476/540 (88%)	0.22	24 (5%) 34 27	26, 48, 81, 109	0
3	C	5/10 (50%)	0.39	0 100 100	40, 50, 54, 55	0
All	All	573/702 (81%)	0.16	24 (4%) 40 32	26, 46, 80, 109	1 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	591	HIS	3.5
2	B	570	ASP	3.3
2	B	531	GLN	3.3
2	B	542	ALA	3.2
2	B	244	GLY	3.2
2	B	619	GLN	3.1
2	B	556	GLY	3.0
2	B	220	ALA	3.0
2	B	671	ALA	3.0
2	B	491	ARG	2.7
2	B	672	VAL	2.6
2	B	615	ILE	2.6
2	B	557	HIS	2.6
2	B	178	SER	2.4
2	B	642	SER	2.4
2	B	639	PRO	2.4
2	B	153	SER	2.3
2	B	167	ARG	2.3
2	B	447	SER	2.2
2	B	659	ARG	2.2
2	B	643	HIS	2.2
2	B	553	HIS	2.1
2	B	568	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	584	GLN	2.0

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. 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	B-factors(Å ²)	Q<0.9
3	DGN	C	1	9/10	0.86	0.13	49,56,64,65	0
3	DVA	C	2	7/8	0.91	0.11	43,52,53,57	0
3	MAA	C	9	6/7	0.93	0.10	36,46,47,48	0
3	YC3	C	3	19/20	0.95	0.09	33,43,53,61	0
3	A1BC0	C	10	9/9	0.96	0.09	48,52,57,58	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
4	CA	B	701	1/1	0.86	0.07	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.