



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 7, 2024 – 08:18 PM EDT

PDB ID : 8FVP  
Title : PCSK9 in complex with an inhibitor  
Authors : Xu, M.; Chopra, R.  
Deposited on : 2023-01-19  
Resolution : 2.60 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.

The types of validation reports are described at

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

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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 : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 1.20.1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

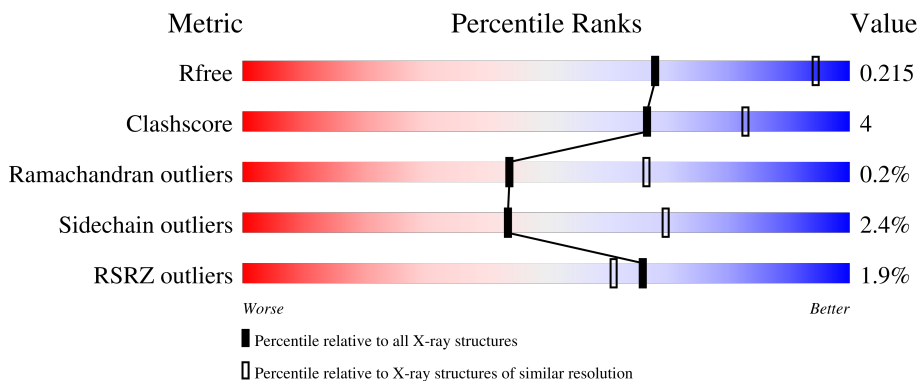
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	164625	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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  $\geq 3$ , 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	152	
2	B	540	
3	L	9	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4424 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
			Total	C	N	O	S			
1	A	92	740	474	133	131	2	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	477	3537	2185	651	670	31	0	0	0

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 PPI-YD5-NLE-7T2-SER-7T2-DPP-GLY-NH2 inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	Cl	N	O			
3	L	9	64	43	2	9	10	0	0	1

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	24	Total	O	0	0
			24	24		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	B	57	Total	O	0	0
			57	57		
5	L	1	Total	O	0	0
			1	1		

### 3 Residue-property plots i

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Proprotein convertase subtilisin/kexin type 9

Chain A: 

MET  
GLY  
THR  
VAL  
SER  
SER  
ARG  
ARG  
SER  
TRP  
TRP  
PRO  
LEU  
PRO  
LEU  
LEU  
LEU  
LEU  
LEU  
LEU  
LEU  
LEU  
GLY  
PRO  
ALA  
GLY  
ALA  
ARG  
ALA  
ALA  
GLN  
GLU  
ASP  
GLU  
ASP  
GLY  
ASP  
TYR  
GLU  
GLU  
VAL  
LEU  
LEU  
ALA  
LEU  
ARG  
SER  
GLU  
GLU  
ASP  
GLY  
LEU  
ALA  
GLU  
ALA  
PRO  
GLU  
HIS  
GLY  
THR

T81  
R96  
Q101  
M126  
L130  
L133  
Q152

- Molecule 2: Proprotein convertase subtilisin/kexin type 9

Chain B: 

S153  
R166  
Y166  
R167  
ALA  
ASP  
GLU  
TYR  
GLN  
PRO  
PRO  
ASP  
G176  
G177  
S178  
L179  
Y183  
L184  
L185  
D186  
I189  
R194  
V200  
M201  
D212  
GLY  
THR  
ARG  
PHE  
HIS  
ARG  
GLN  
R220  
L230  
G244  
M247  
R248  
L265  
L271  
Q278  
P279  
V280  
L286  
E332  
D343

G344  
P345  
L348  
L351  
C375  
S376  
T377  
S383  
L408  
V423  
L424  
V435  
P446  
S447  
T448  
H449  
GLY  
ALA  
G452  
V461  
S465  
G466  
P467  
T468  
R469  
A473  
F515  
L529  
A532  
H537  
A542  
GLU  
ALA  
SER  
MET  
G547  
T548  
R549  
V550  
H553  
GLN  
GLN  
GLY

H557  
L571  
GLY  
THR  
HIS  
LYS  
PRO  
PRO  
VAL  
LEU  
LEU  
PRO  
ARG  
ARG  
GLY  
GLN  
P585  
V589  
I596  
G605  
L606  
E612  
P616  
ALA  
PRO  
Q619  
T623  
L638  
P639  
GLY  
THR  
S642  
L645  
R659  
ASP  
VAL  
SER  
THR  
THR  
GLY  
SER  
THR  
SER  
GLU  
GLU  
V671  
V672  
T673  
V675

S681  
ARG  
HIS  
LEU  
ALA  
GLN  
ALA  
SER  
GLN  
GLU  
LEU  
GLN

- Molecule 3: PPI-YD5-NLE-7T2-SER-7T2-DPP-GLY-NH2 inhibitor

Chain L: 

PPI3  
YD52  
S5  
F6  
NH29

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.03Å 70.41Å 150.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.96 – 2.60 46.96 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.96-2.60) 99.9 (46.96-2.60)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.78 (at 2.61Å)	Xtrriage
Refinement program	PHENIX 1	Depositor
R, $R_{free}$	0.178 , 0.215 0.182 , 0.215	Depositor DCC
$R_{free}$ test set	1059 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.3	Xtrriage
Anisotropy	0.423	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 34.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4424	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NLE, 7T2, DPP, NH2, CA, YD5, PPI

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	0.56	0/757	0.67	0/1023
2	B	0.56	1/3599 (0.0%)	0.73	3/4882 (0.1%)
3	L	0.76	0/8	1.29	0/7
All	All	0.56	1/4364 (0.0%)	0.72	3/5912 (0.1%)

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
2	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	423	VAL	CB-CG1	-6.92	1.38	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	179	LEU	CA-CB-CG	5.46	127.86	115.30
2	B	348	LEU	CA-CB-CG	-5.14	103.47	115.30
2	B	265	LEU	CA-CB-CG	5.09	127.01	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	244	GLY	Peptide

## 5.2 Too-close contacts [i](#)

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	740	0	750	2	0
2	B	3537	0	3451	28	1
3	L	64	0	27	3	0
4	B	1	0	0	0	0
5	A	24	0	0	0	0
5	B	57	0	0	1	0
5	L	1	0	0	0	0
All	All	4424	0	4228	31	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 4.

All (31) 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:638:LEU:HD23	2:B:639:PRO:HD2	1.57	0.86
2:B:185:LEU:HD11	2:B:271:ILE:HD11	1.75	0.68
2:B:446:PRO:HB2	2:B:448:THR:HG22	1.81	0.62
2:B:550:VAL:N	2:B:596:ILE:HD11	2.16	0.61
2:B:469:ARG:HD2	2:B:515:PHE:CD2	2.37	0.59
2:B:638:LEU:HD12	2:B:673:THR:HG21	1.89	0.54
2:B:351:LEU:HD13	3:L:2:YD5:C41	2.38	0.53
2:B:435:VAL:HG12	2:B:461:TRP:CZ2	2.43	0.53
2:B:467:PRO:O	2:B:469:ARG:NH1	2.44	0.51
1:A:126:MET:HB2	1:A:130:LEU:HD12	1.93	0.50
2:B:383:SER:O	3:L:5:SER:HA	2.14	0.47
2:B:345:PRO:HD3	2:B:424:ILE:HG23	1.96	0.47
2:B:343:ASP:HB3	2:B:423:VAL:HG12	1.96	0.47
2:B:194:ARG:HG3	2:B:377:THR:HG22	1.98	0.45
2:B:529:LEU:HG	2:B:532:ALA:HB2	1.98	0.45
2:B:200:VAL:HG22	2:B:247:MET:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:469:ARG:HD2	2:B:515:PHE:CG	2.51	0.45
2:B:184:LEU:HD13	2:B:286:LEU:HD23	1.99	0.44
2:B:348:LEU:HD12	2:B:348:LEU:HA	1.81	0.44
2:B:606:LEU:HD12	2:B:606:LEU:HA	1.80	0.44
2:B:186:ASP:OD2	2:B:230:LEU:HD12	2.17	0.43
2:B:332:GLU:O	2:B:408:LEU:HD21	2.18	0.43
3:L:5:SER:N	3:L:6:7T2:CM	2.80	0.43
2:B:605:GLY:O	2:B:681:SER:HA	2.18	0.43
2:B:549:ARG:HG2	2:B:589:VAL:HG22	2.00	0.43
2:B:212:ASP:HA	5:B:851:HOH:O	2.18	0.43
1:A:101:GLN:HB3	1:A:133:LEU:HD21	2.01	0.42
2:B:465:SER:HB3	2:B:473:ALA:HB2	2.01	0.42
2:B:189:ILE:CD1	2:B:200:VAL:HG11	2.51	0.41
2:B:612:GLU:HG2	2:B:675:VAL:HG22	2.01	0.41
2:B:183:TYR:CZ	2:B:248:ARG:HD2	2.56	0.41

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]	2.18	0.02

## 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	90/152 (59%)	89 (99%)	1 (1%)	0	100	100
2	B	457/540 (85%)	448 (98%)	8 (2%)	1 (0%)	44	66
3	L	2/9 (22%)	2 (100%)	0	0	100	100
All	All	549/701 (78%)	539 (98%)	9 (2%)	1 (0%)	44	66

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	280	VAL

### 5.3.2 Protein sidechains [i](#)

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	79/127 (62%)	78 (99%)	1 (1%)	65 84
2	B	381/431 (88%)	371 (97%)	10 (3%)	41 67
3	L	1/1 (100%)	1 (100%)	0	100 100
All	All	461/559 (82%)	450 (98%)	11 (2%)	44 70

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	ARG
2	B	201	MET
2	B	278	GLN
2	B	375	CYS
2	B	537	HIS
2	B	571	LEU
2	B	623	THR
2	B	638	LEU
2	B	645	LEU
2	B	659	ARG
2	B	672	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

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	DPP	L	7	3	4,5,6	0.66	0	1,5,7	0.48	0
3	YD5	L	2	3	6,8,10	1.09	0	6,8,12	1.87	1 (16%)
3	7T2	L	4	3	12,13,14	1.20	0	15,16,18	0.93	0
3	NLE	L	3	3	6,7,8	0.76	0	2,7,9	0.25	0
3	7T2	L	6	3	12,13,14	1.21	0	15,16,18	1.08	1 (6%)

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	DPP	L	7	3	-	0/2/4/6	-
3	YD5	L	2	3	-	2/5/7/10	-
3	7T2	L	4	3	-	0/5/8/10	0/1/1/1
3	NLE	L	3	3	-	3/5/6/8	-
3	7T2	L	6	3	-	0/5/8/10	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	2	YD5	C41-CA-N	3.90	115.92	108.80
3	L	6	7T2	CB-CA-N	2.69	114.44	110.48

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L	2	YD5	C4-C32-C33-N
3	L	3	NLE	N-CA-CB-CG
3	L	3	NLE	C-CA-CB-CG
3	L	3	NLE	CE-CD-CG-CB
3	L	2	YD5	C32-C33-N-CA

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	2	YD5	1	0
3	L	6	7T2	1	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 [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, 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	92/152 (60%)	-0.94	0 <b>100</b> <b>100</b>	4, 11, 29, 45	0
2	B	477/540 (88%)	-0.64	11 (2%) 61 55	2, 13, 47, 74	0
3	L	2/9 (22%)	0.66	0 <b>100</b> <b>100</b>	9, 9, 9, 24	0
All	All	571/701 (81%)	-0.68	11 (1%) 66 61	2, 13, 45, 74	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	177	GLY	5.9
2	B	616	PRO	3.6
2	B	449	HIS	3.6
2	B	571	LEU	3.2
2	B	585	PRO	3.1
2	B	515	PHE	3.1
2	B	671	ALA	2.9
2	B	542	ALA	2.8
2	B	469	ARG	2.7
2	B	220	ALA	2.7
2	B	642	SER	2.1

### 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, 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	7T2	L	6	13/14	0.80	0.12	6,7,11,24	0
3	DPP	L	7	6/7	0.85	0.11	8,11,19,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	7T2	L	4	13/14	0.90	0.09	5,7,20,35	0
3	YD5	L	2	9/11	0.93	0.07	8,10,13,15	0
3	NLE	L	3	8/9	0.95	0.08	7,10,11,11	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 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( $\text{\AA}^2$ )	Q<0.9
4	CA	B	701	1/1	0.89	0.08	46,46,46,46	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.