



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:58 PM GMT

PDB ID : 4QKX  
Title : Structure of beta2 adrenoceptor bound to a covalent agonist and an engineered nanobody  
Authors : Weichert, D.; Kruse, A.C.; Manglik, A.; Hiller, C.; Zhang, C.; Huebner, H.; Kobilka, B.K.; Gmeiner, P.  
Deposited on : 2014-06-10  
Resolution : 3.30 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
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:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

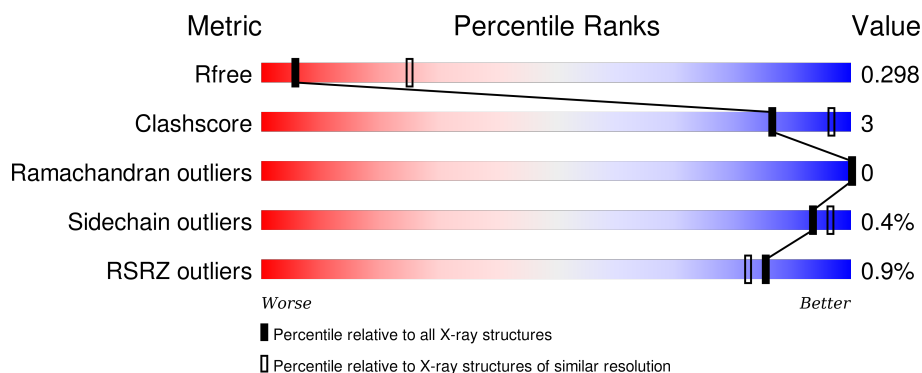
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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. 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	469	<div> <div></div> <div>90%</div> <div>6%</div> <div>.</div> </div>
2	B	120	<div> <div></div> <div>91%</div> <div>9%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	35V	A	1403	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4462 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 Beta-2 adrenergic receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	454	Total	C	N	O	S	0	0	0
			3549	2313	584	630	22			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	852	ASP	-	EXPRESSION TAG	UNP D9IEF7
A	853	TYR	-	EXPRESSION TAG	UNP D9IEF7
A	854	LYS	-	EXPRESSION TAG	UNP D9IEF7
A	855	ASP	-	EXPRESSION TAG	UNP D9IEF7
A	856	ASP	-	EXPRESSION TAG	UNP D9IEF7
A	857	ASP	-	EXPRESSION TAG	UNP D9IEF7
A	858	ASP	-	EXPRESSION TAG	UNP D9IEF7
A	859	ALA	-	EXPRESSION TAG	UNP D9IEF7
A	860	GLU	-	EXPRESSION TAG	UNP D9IEF7
A	861	ASN	-	EXPRESSION TAG	UNP D9IEF7
A	862	LEU	-	EXPRESSION TAG	UNP D9IEF7
A	863	TYR	-	EXPRESSION TAG	UNP D9IEF7
A	864	PHE	-	EXPRESSION TAG	UNP D9IEF7
A	865	GLN	-	EXPRESSION TAG	UNP D9IEF7
A	866	GLY	-	EXPRESSION TAG	UNP D9IEF7
A	919	THR	CYS	ENGINEERED MUTATION	UNP D9IEF7
A	962	ALA	CYS	ENGINEERED MUTATION	UNP D9IEF7
A	1027	ALA	-	LINKER	UNP D9IEF7
A	1028	ALA	-	LINKER	UNP D9IEF7
A	1093	CYS	HIS	ENGINEERED MUTATION	UNP P07550
A	1096	THR	MET	ENGINEERED MUTATION	UNP P07550
A	1098	THR	MET	ENGINEERED MUTATION	UNP P07550
A	1187	GLU	ASN	ENGINEERED MUTATION	UNP P07550
A	?	-	LYS	DELETION	UNP P07550
A	?	-	SER	DELETION	UNP P07550
A	?	-	GLU	DELETION	UNP P07550
A	?	-	GLY	DELETION	UNP P07550

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	DELETION	UNP P07550
A	?	-	PHE	DELETION	UNP P07550
A	?	-	HIS	DELETION	UNP P07550
A	?	-	VAL	DELETION	UNP P07550
A	?	-	GLN	DELETION	UNP P07550
A	?	-	ASN	DELETION	UNP P07550
A	?	-	LEU	DELETION	UNP P07550
A	?	-	SER	DELETION	UNP P07550
A	?	-	GLN	DELETION	UNP P07550
A	?	-	VAL	DELETION	UNP P07550
A	?	-	GLU	DELETION	UNP P07550
A	?	-	GLN	DELETION	UNP P07550
A	?	-	ASP	DELETION	UNP P07550
A	?	-	GLY	DELETION	UNP P07550
A	?	-	ARG	DELETION	UNP P07550
A	?	-	THR	DELETION	UNP P07550
A	?	-	GLY	DELETION	UNP P07550
A	?	-	HIS	DELETION	UNP P07550
A	?	-	GLY	DELETION	UNP P07550
A	?	-	LEU	DELETION	UNP P07550
A	?	-	ARG	DELETION	UNP P07550
A	?	-	ARG	DELETION	UNP P07550
A	?	-	SER	DELETION	UNP P07550
A	?	-	SER	DELETION	UNP P07550
A	1265	ALA	CYS	ENGINEERED MUTATION	UNP P07550

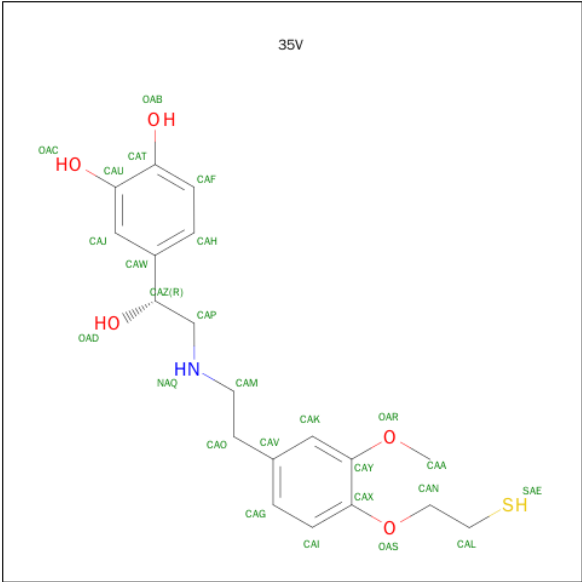
- Molecule 2 is a protein called R9 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	120	Total	C	N	O	S	0	0	0
			885	555	153	173	4			

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Na	2	0
			2	2		

- Molecule 4 is 4-[(1R)-1-HYDROXY-2-({2-[3-METHOXY-4-(2-SULFANYLETHOXY)PH ENYL]ETHYL}AMINO)ETHYL]BENZENE-1,2-DIOL (three-letter code: 35V) (formula: C<sub>19</sub>H<sub>25</sub>NO<sub>5</sub>S).

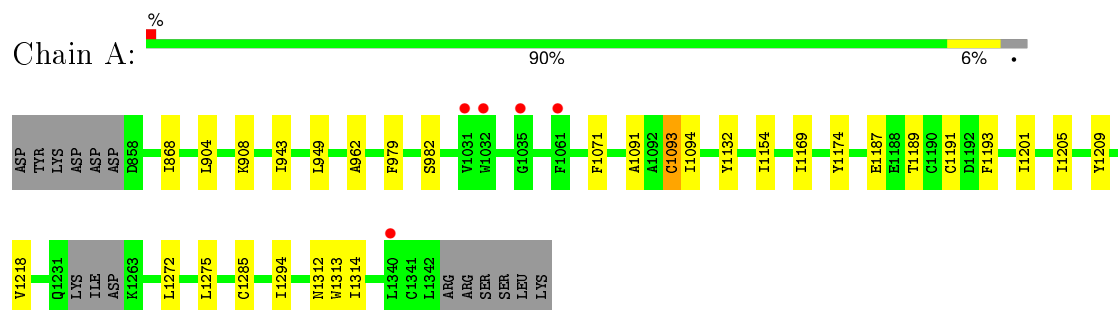


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			26	19	1	5	1		

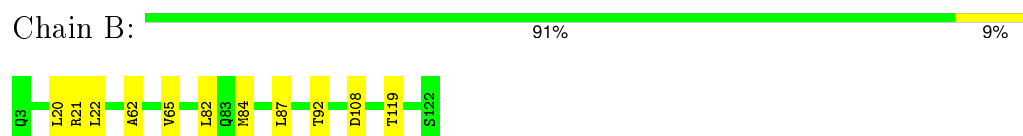
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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: Beta-2 adrenergic receptor



- Molecule 2: R9 protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.56Å 67.21Å 301.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.26 – 3.30 33.26 – 3.30	Depositor EDS
% Data completeness (in resolution range)	78.5 (33.26-3.30) 68.2 (33.26-3.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 3.32Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1241)	Depositor
R, $R_{free}$	0.236 , 0.280 0.252 , 0.298	Depositor DCC
$R_{free}$ test set	1462 reflections (12.24%)	DCC
Wilson B-factor (Å <sup>2</sup> )	55.8	Xtriage
Anisotropy	0.356	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 43.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	1 of 12024 reflections (0.008%)	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	4462	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA, 35V

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	0.21	0/3629	0.36	0/4945
2	B	0.20	0/902	0.36	0/1228
All	All	0.21	0/4531	0.36	0/6173

There are no bond length outliers.

There are no bond angle outliers.

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	3549	0	3510	16	0
2	B	885	0	820	6	0
3	A	2	0	0	0	0
4	A	26	0	22	4	0
All	All	4462	0	4352	24	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.

All (24) 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:1193:PHE:HB2	4:A:1403:35V:H20	1.65	0.78
2:B:92:THR:HG23	2:B:119:THR:HA	1.84	0.59
1:A:943:ILE:HG23	1:A:949:LEU:HB3	1.87	0.57
2:B:22:LEU:HD12	2:B:82:LEU:HD23	1.88	0.55
1:A:1093:CYS:SG	1:A:1094:ILE:N	2.84	0.50
1:A:904:LEU:HG	1:A:908:LYS:HE2	1.94	0.49
1:A:1201:ILE:HA	1:A:1294:ILE:HD11	1.95	0.48
2:B:84:MET:HB3	2:B:87:LEU:HD21	1.96	0.48
4:A:1403:35V:H23	4:A:1403:35V:H21	1.61	0.47
1:A:1205:ILE:HA	1:A:1209:TYR:HB2	1.97	0.47
2:B:108:ASP:N	2:B:108:ASP:OD1	2.47	0.46
1:A:1169:ILE:HA	1:A:1174:TYR:CD1	2.51	0.46
1:A:1187:GLU:HG3	1:A:1189:THR:H	1.81	0.45
1:A:1071:PHE:HD1	1:A:1154:ILE:HD11	1.82	0.44
1:A:1272:LEU:HD12	1:A:1275:LEU:HD11	1.99	0.44
1:A:1285:CYS:HA	1:A:1314:ILE:HG22	2.00	0.44
1:A:868:ILE:HD13	1:A:962:ALA:O	2.18	0.44
2:B:62:ALA:HB3	2:B:65:VAL:HG22	2.02	0.42
1:A:979:PHE:HB3	1:A:982:SER:HB2	2.01	0.42
1:A:1191:CYS:O	4:A:1403:35V:H23	2.20	0.42
4:A:1403:35V:H13	4:A:1403:35V:H16	1.59	0.41
1:A:1091:ALA:HB2	1:A:1313:TRP:CH2	2.56	0.41
2:B:20:LEU:HD23	2:B:21:ARG:N	2.36	0.40
1:A:1132:TYR:HB2	1:A:1218:VAL:HG13	2.02	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	450/469 (96%)	430 (96%)	20 (4%)	0	100	100
2	B	118/120 (98%)	112 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	568/589 (96%)	542 (95%)	26 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	370/405 (91%)	368 (100%)	2 (0%)	92	95
2	B	86/94 (92%)	86 (100%)	0	100	100
All	All	456/499 (91%)	454 (100%)	2 (0%)	93	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1093	CYS
1	A	1312	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	934	GLN
1	A	997	ASN
1	A	1142	GLN
1	A	1224	GLN
1	A	1301	ASN
1	A	1337	GLN
2	B	41	GLN
2	B	78	ASN
2	B	114	GLN
2	B	117	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z  > 2$
4	35V	A	1403	1	27,27,27	1.83	2 (7%)	33,35,35	1.66	6 (18%)

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
4	35V	A	1403	1	-	0/17/17/17	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1403	35V	CAW-CAZ	-8.32	1.39	1.52
4	A	1403	35V	CAO-CAV	-4.00	1.40	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1403	35V	CAA-OAR-CAY	-3.37	112.43	117.54
4	A	1403	35V	CAN-OAS-CAX	-2.90	110.52	117.64
4	A	1403	35V	CAM-CAO-CAV	-2.61	107.42	112.83
4	A	1403	35V	CAO-CAV-CAK	-2.23	116.83	120.56
4	A	1403	35V	CAH-CAF-CAT	-2.21	118.22	120.49
4	A	1403	35V	CAP-NAQ-CAM	5.96	127.37	113.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1403	35V	4	0

## 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	454/469 (96%)	-0.16	5 (1%) 82 78	68, 93, 149, 194	0
2	B	120/120 (100%)	-0.25	0 100 100	77, 105, 138, 161	0
All	All	574/589 (97%)	-0.18	5 (0%) 85 82	68, 96, 148, 194	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1340	LEU	3.9
1	A	1031	VAL	3.8
1	A	1032	TRP	2.3
1	A	1035	GLY	2.3
1	A	1061	PHE	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	35V	A	1403	26/26	0.89	0.29	3.18	80,104,134,198	0
3	NA	A	1401	1/1	-	-	-	83,83,83,83	1
3	NA	A	1402	1/1	-	-	-	82,82,82,82	1

## 6.5 Other polymers ⓘ

There are no such residues in this entry.