



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 09:04 PM GMT

PDB ID : 3VWS
Title : Dengue serotype 3 RNA-dependent RNA polymerase bound to NITD-107
Authors : Noble, C.G.; Lescar, J.
Deposited on : 2012-08-31
Resolution : 2.10 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

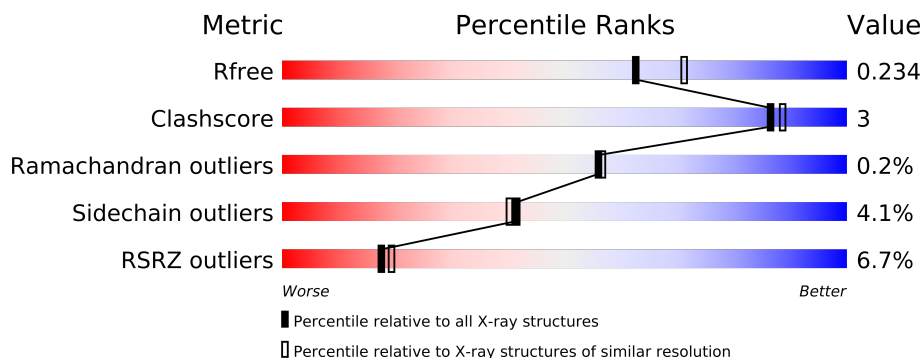
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.10 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}	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	635	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	PEG	A	1005	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5342 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Non-structural protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	592	4853	3066	870	884	33	0	5	0

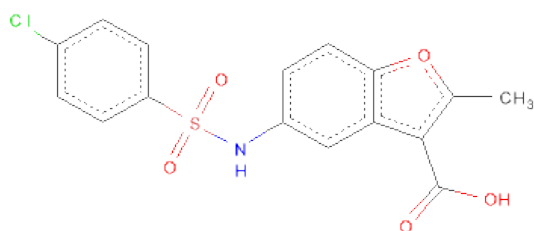
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	266	GLY	-	EXPRESSION TAG	UNP Q6DLV0
A	267	SER	-	EXPRESSION TAG	UNP Q6DLV0
A	268	HIS	-	EXPRESSION TAG	UNP Q6DLV0
A	269	MET	-	EXPRESSION TAG	UNP Q6DLV0
A	270	LEU	-	EXPRESSION TAG	UNP Q6DLV0
A	271	ASP	-	EXPRESSION TAG	UNP Q6DLV0
A	374	GLU	GLY	SEE REMARK 999	UNP Q6DLV0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is 5-[[[(4-CHLOROPHENYL)SULFONYL]AMINO}-2-METHYL-1-BENZOFURAN-3-CARBOXYLICACID (three-letter code: VWS) (formula: C₁₆H₁₂ClNO₅S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	S	0	0
			24	16	1	1	5	1		
3	A	1	Total	C	Cl	N	O	S	0	0
			24	16	1	1	5	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is water.

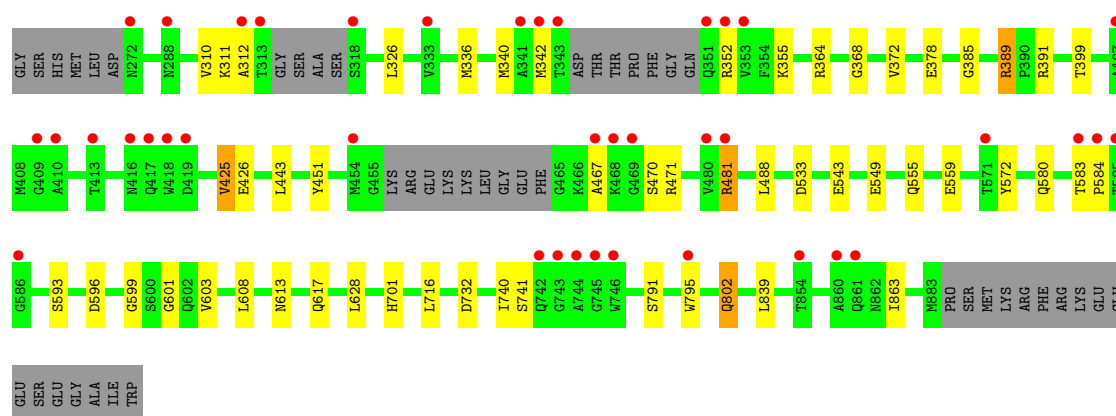
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	432	Total 432	O 432	0	0

3 Residue-property plots

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: Non-structural protein 5

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	161.46Å 177.73Å 57.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.88 – 2.10 29.88 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.88-2.10) 99.7 (29.88-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.10Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.181 , 0.224 0.190 , 0.234	Depositor DCC
R_{free} test set	2482 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.169	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 49017 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5342	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PEG, VWS

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	0.50	0/4988	0.66	0/6748

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4853	0	4758	25	0
2	A	2	0	0	0	0
3	A	48	0	22	2	0
4	A	7	0	10	0	0
5	A	432	0	0	3	0
All	All	5342	0	4790	25	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (25) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:802:GLN:H	1:A:802:GLN:HE21	1.32	0.78
1:A:399:THR:HG23	1:A:425:VAL:HG13	1.80	0.62
1:A:385:GLY:HA3	1:A:555:GLN:HE22	1.66	0.59
1:A:572:TYR:OH	1:A:603:VAL:O	2.19	0.58
1:A:716:LEU:HD21	1:A:839:LEU:HD23	1.88	0.55
1:A:368:GLY:O	1:A:372:VAL:HG23	2.09	0.53
1:A:378:GLU:HG2	5:A:1437:HOH:O	2.12	0.50
1:A:481:ARG:HG3	1:A:603:VAL:HG23	1.95	0.49
1:A:311:LYS:HG2	1:A:312:ALA:H	1.79	0.48
1:A:795:TRP:HZ3	3:A:1003:VWS:H5	1.62	0.47
1:A:467:ALA:H	1:A:580:GLN:NE2	2.12	0.47
1:A:701:HIS:HE1	5:A:1243:HOH:O	1.97	0.46
1:A:583:THR:HB	1:A:584:PRO:HD2	1.98	0.45
1:A:389:ARG:NH2	5:A:1528:HOH:O	2.49	0.45
1:A:336:MET:HB3	1:A:732:ASP:HB3	1.99	0.45
1:A:613:ASN:O	1:A:617:GLN:HG2	2.19	0.43
1:A:340:MET:HB3	1:A:740:ILE:HD11	2.00	0.43
1:A:543:GLU:CG	1:A:596:ASP:HB3	2.49	0.43
1:A:467:ALA:H	1:A:580:GLN:HE22	1.67	0.42
1:A:549:GLU:HB3	1:A:608:LEU:HD22	2.01	0.42
1:A:372:VAL:HG11	1:A:628:LEU:HD11	2.03	0.41
1:A:451:TYR:OH	1:A:599:GLY:HA2	2.21	0.41
1:A:399:THR:HG23	1:A:425:VAL:CG1	2.50	0.40
1:A:543:GLU:HG3	1:A:596:ASP:HB3	2.03	0.40
1:A:601:GLY:HA2	3:A:1003:VWS:H12	2.03	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	589/635 (93%)	576 (98%)	12 (2%)	1 (0%)	56 57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	791	SER

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	519/552 (94%)	498 (96%)	21 (4%)	42 41

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	310	VAL
1	A	326	LEU
1	A	342	MET
1	A	352	ARG
1	A	355	LYS
1	A	364	ARG
1	A	389	ARG
1	A	391	ARG
1	A	425	VAL
1	A	426	GLU
1	A	443	LEU
1	A	470	SER
1	A	471	ARG
1	A	481	ARG
1	A	488	LEU
1	A	533	ASP
1	A	559	GLU
1	A	593	SER
1	A	741	SER
1	A	802	GLN
1	A	863	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	339	GLN

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Mol	Chain	Res	Type
1	A	416	ASN
1	A	548	ASN
1	A	555	GLN
1	A	580	GLN
1	A	682	ASN
1	A	693	GLN
1	A	704	GLN
1	A	760	GLN
1	A	768	HIS
1	A	802	GLN
1	A	835	ASN
1	A	869	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\# Z > 2$
3	VWS	A	1003	-	25,26,26	2.75	12 (48%)	35,39,39	5.23	15 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	VWS	A	1004	-	25,26,26	2.68	14 (56%)	35,39,39	4.86	16 (45%)
4	PEG	A	1005	-	6,6,6	0.60	0	5,5,5	0.65	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
3	VWS	A	1003	-	-	0/13/15/15	0/1/3/3
3	VWS	A	1004	-	-	0/13/15/15	0/1/3/3
4	PEG	A	1005	-	-	0/4/4/4	0/0/0/0

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1003	VWS	C1-S1	-9.58	1.62	1.76
3	A	1004	VWS	O1-S1	6.16	1.50	1.43
3	A	1004	VWS	C1-S1	-5.83	1.67	1.76
3	A	1004	VWS	C2-C1	4.09	1.45	1.38
3	A	1003	VWS	C2-C1	4.04	1.45	1.38
3	A	1004	VWS	C13-C15	3.75	1.54	1.50
3	A	1003	VWS	C12-N1	-3.46	1.37	1.42
3	A	1004	VWS	C6-C5	3.31	1.44	1.38
3	A	1004	VWS	C8-C7	3.08	1.43	1.36
3	A	1003	VWS	C8-C7	2.90	1.42	1.36
3	A	1003	VWS	C16-C14	2.87	1.52	1.48
3	A	1003	VWS	C11-C12	2.78	1.44	1.37
3	A	1004	VWS	C11-C12	2.76	1.44	1.37
3	A	1004	VWS	C7-C12	2.72	1.43	1.39
3	A	1004	VWS	C5-CL1	2.66	1.80	1.74
3	A	1004	VWS	C8-C9	2.54	1.43	1.38
3	A	1003	VWS	C6-C5	2.46	1.42	1.38
3	A	1003	VWS	O2-S1	2.40	1.46	1.43
3	A	1003	VWS	C13-C15	2.31	1.52	1.50
3	A	1003	VWS	C7-C12	2.29	1.43	1.39
3	A	1004	VWS	C12-N1	-2.24	1.39	1.42
3	A	1003	VWS	C8-C9	2.23	1.43	1.38
3	A	1004	VWS	C3-C1	2.20	1.42	1.38
3	A	1004	VWS	C6-C2	2.20	1.43	1.38
3	A	1004	VWS	O2-S1	2.01	1.45	1.43
3	A	1003	VWS	C6-C2	2.00	1.42	1.38

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1003	VWS	O2-S1-O1	-23.64	87.75	119.55
3	A	1004	VWS	O2-S1-O1	-18.69	94.41	119.55
3	A	1004	VWS	C1-S1-N1	10.55	119.31	106.81
3	A	1003	VWS	O1-S1-C1	9.84	120.59	107.98
3	A	1004	VWS	O2-S1-N1	-8.27	85.54	106.72
3	A	1004	VWS	O1-S1-N1	7.86	126.83	106.72
3	A	1004	VWS	O2-S1-C1	-7.41	98.49	107.98
3	A	1003	VWS	O1-S1-N1	6.81	124.15	106.72
3	A	1003	VWS	C1-S1-N1	6.30	114.28	106.81
3	A	1003	VWS	O2-S1-C1	-5.94	100.37	107.98
3	A	1004	VWS	C2-C1-S1	5.81	126.51	119.78
3	A	1003	VWS	C2-C1-S1	5.77	126.46	119.78
3	A	1003	VWS	O2-S1-N1	-5.62	92.32	106.72
3	A	1004	VWS	O5-C15-C13	5.37	122.39	114.46
3	A	1003	VWS	C13-C10-C9	-5.12	103.81	107.44
3	A	1004	VWS	C13-C10-C9	-4.79	104.04	107.44
3	A	1003	VWS	C3-C1-S1	-4.33	114.76	119.78
3	A	1004	VWS	C4-C3-C1	4.32	124.43	119.50
3	A	1004	VWS	O1-S1-C1	4.12	113.26	107.98
3	A	1004	VWS	O4-C15-C13	-3.93	117.65	122.34
3	A	1003	VWS	C4-C5-CL1	-3.63	113.36	119.34
3	A	1003	VWS	C6-C5-CL1	3.14	124.51	119.34
3	A	1003	VWS	C16-C14-C13	3.07	136.25	128.69
3	A	1004	VWS	C16-C14-C13	2.80	135.58	128.69
3	A	1003	VWS	C12-N1-S1	2.74	131.76	123.51
3	A	1004	VWS	C3-C1-S1	-2.69	116.65	119.78
3	A	1003	VWS	O5-C15-C13	2.61	118.31	114.46
3	A	1004	VWS	C2-C1-C3	-2.25	116.83	120.39
3	A	1004	VWS	C6-C5-CL1	2.20	122.96	119.34
3	A	1003	VWS	C4-C3-C1	2.17	121.98	119.50
3	A	1004	VWS	C14-C13-C10	-2.08	108.05	109.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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	592/635 (93%)	0.13	40 (6%) 17 19	23, 42, 85, 124	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	418	TRP	7.9
1	A	343	THR	7.5
1	A	353	VAL	6.9
1	A	351	GLN	6.9
1	A	410	ALA	5.5
1	A	743	GLY	4.5
1	A	318	SER	4.4
1	A	312	ALA	4.2
1	A	342	MET	3.8
1	A	313	THR	3.7
1	A	745	GLY	3.5
1	A	746	TRP	3.4
1	A	854	THR	3.4
1	A	469	GLY	3.4
1	A	417	GLN	3.3
1	A	480	VAL	3.2
1	A	585	THR	3.2
1	A	454	MET	3.0
1	A	272	ASN	3.0
1	A	409	GLY	3.0
1	A	583	THR	2.9
1	A	416	ASN	2.9
1	A	419	ASP	2.7
1	A	341	ALA	2.7
1	A	586	GLY	2.7
1	A	407	ALA	2.6
1	A	467	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	333	VAL	2.6
1	A	468	LYS	2.6
1	A	352	ARG	2.5
1	A	413	THR	2.4
1	A	571	THR	2.3
1	A	288	ASN	2.3
1	A	795	TRP	2.3
1	A	861	GLN	2.2
1	A	481	ARG	2.2
1	A	584	PRO	2.2
1	A	742	GLN	2.2
1	A	744	ALA	2.2
1	A	860	ALA	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	PEG	A	1005	7/7	0.09	3.54	47,48,54,56	0
3	VWS	A	1004	24/24	0.17	0.42	61,87,90,91	0
3	VWS	A	1003	24/24	0.17	0.19	63,74,87,88	0
2	ZN	A	1002	1/1	0.09	-1.43	39,39,39,39	0
2	ZN	A	1001	1/1	0.03	-3.94	49,49,49,49	0

6.5 Other polymers ⓘ

There are no such residues in this entry.