



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 15, 2023 – 06:27 PM EDT

PDB ID : 1T03
Title : HIV-1 reverse transcriptase crosslinked to tenofovir terminated template-primer (complex P)
Authors : Tuske, S.; Sarafianos, S.G.; Ding, J.; Arnold, E.
Deposited on : 2004-04-07
Resolution : 3.10 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

<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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

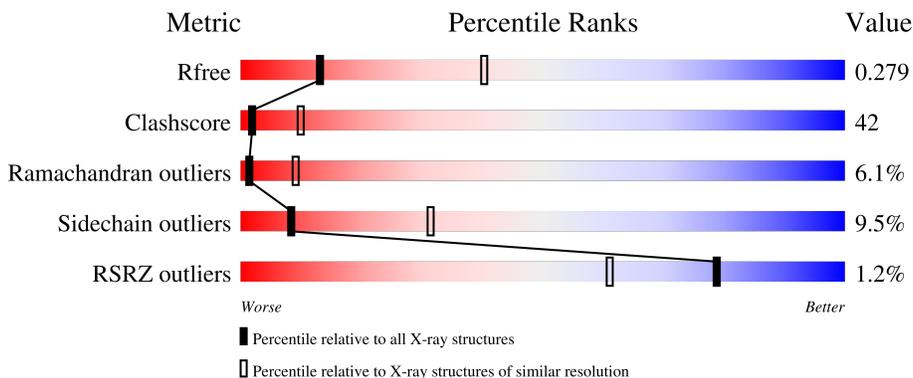
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



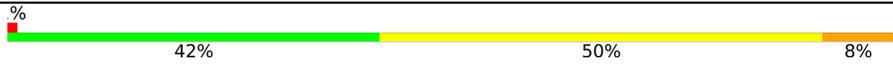
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 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	T	27	 4% 33% 44% 7% 15%
2	P	21	 24% 52% 19% 5%
3	A	558	 2% 41% 51% 8%
4	B	437	 36% 51% 10% 3% 2%
5	L	211	 39% 53% 7%

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Mol	Chain	Length	Quality of chain
6	H	225	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '42%', a yellow segment in the middle labeled '50%', and a red segment on the right labeled '8%'. A small red square is positioned at the beginning of the bar, followed by a '%' symbol.</p>

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 12252 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 DNA chain called Synthetic oligonucleotide template.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	T	23	473	223	95	133	22	0	0	0

- Molecule 2 is a DNA chain called Synthetic oligonucleotide primer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	P	20	434	209	80	125	20	0	2	0

- Molecule 3 is a protein called POL polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	558	4482	2901	741	832	8	15	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	258	CYS	GLN	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 4 is a protein called POL polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	B	429	3534	2304	586	637	7	4	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	engineered mutation	UNP P03366
B	430	GLY	-	cloning artifact	UNP P03366

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Chain	Residue	Modelled	Actual	Comment	Reference
B	431	GLY	-	cloning artifact	UNP P03366
B	432	HIS	-	expression tag	UNP P03366
B	433	HIS	-	expression tag	UNP P03366
B	434	HIS	-	expression tag	UNP P03366
B	435	HIS	-	expression tag	UNP P03366
B	436	HIS	-	expression tag	UNP P03366
B	437	HIS	-	expression tag	UNP P03366

- Molecule 5 is a protein called monoclonal antibody light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	L	211	1643	1025	270	342	6	0	0	0

- Molecule 6 is a protein called monoclonal antibody heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	H	225	1685	1060	276	340	9	0	0	0

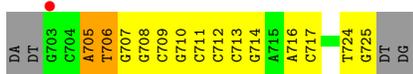
- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
7	A	1	1	1	0	0

3 Residue-property plots

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.

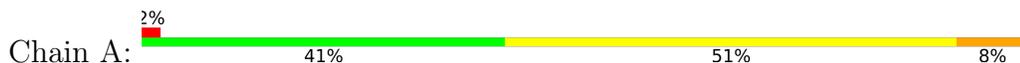
- Molecule 1: Synthetic oligonucleotide template



- Molecule 2: Synthetic oligonucleotide primer

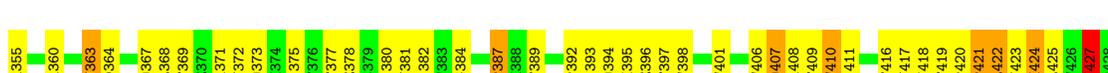
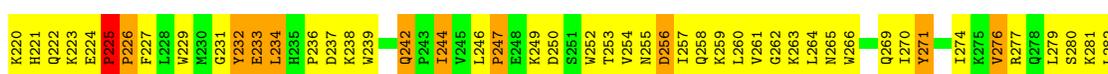
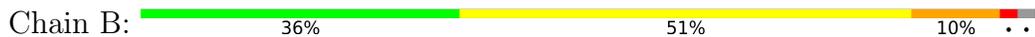


- Molecule 3: POL polyprotein

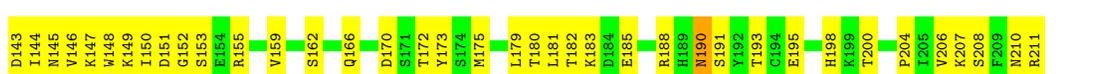




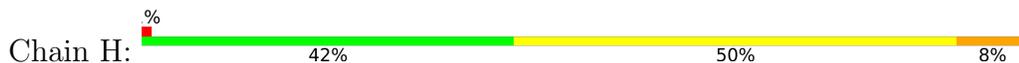
• Molecule 4: POL polyprotein

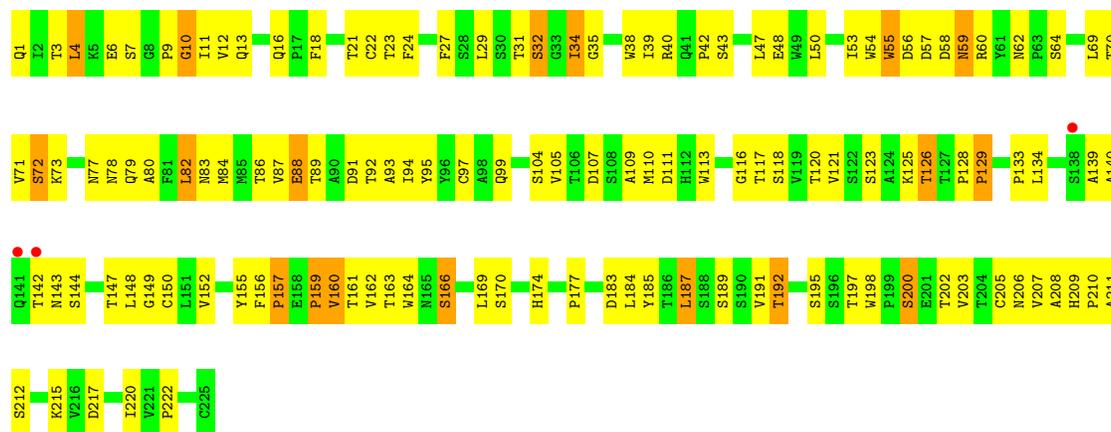


• Molecule 5: monoclonal antibody light chain



• Molecule 6: monoclonal antibody heavy chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, α , β , γ	166.78Å 166.78Å 221.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.10 32.57 – 3.10	Depositor EDS
% Data completeness (in resolution range)	93.9 (20.00-3.10) 95.0 (32.57-3.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 3.12Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.256 , 0.295 0.237 , 0.279	Depositor DCC
R_{free} test set	2454 reflections (4.04%)	wwPDB-VP
Wilson B-factor (Å ²)	70.1	Xtrriage
Anisotropy	0.010	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.057 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	12252	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.92% 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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MRG, TFO, MG

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	T	0.73	2/532 (0.4%)	1.04	4/820 (0.5%)
2	P	0.90	2/420 (0.5%)	1.01	3/640 (0.5%)
3	A	0.45	1/4600 (0.0%)	0.65	0/6259
4	B	0.52	1/3639 (0.0%)	0.74	3/4949 (0.1%)
5	L	0.43	0/1681	0.71	1/2283 (0.0%)
6	H	0.48	0/1729	0.77	0/2372
All	All	0.51	6/12601 (0.0%)	0.74	11/17323 (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
4	B	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	248	GLU	CD-OE2	7.06	1.33	1.25
2	P	821[A]	DC	C2'-C1'	6.65	1.58	1.52
2	P	821[B]	DC	C2'-C1'	6.65	1.58	1.52
1	T	705	DA	C3'-C2'	-6.58	1.44	1.52
4	B	212	TRP	CB-CG	-5.57	1.40	1.50

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	706	DT	O5'-P-OP1	8.87	121.34	110.70
1	T	705	DA	OP1-P-O3'	-8.69	86.08	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	705	DA	N9-C1'-C2'	-7.34	98.66	112.60
2	P	821[A]	DC	N1-C1'-C2'	-7.32	98.69	112.60
2	P	821[B]	DC	N1-C1'-C2'	-7.32	98.69	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B	188	TYR	Sidechain

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	T	473	0	257	32	0
2	P	434	0	248	23	0
3	A	4482	0	4485	398	0
4	B	3534	0	3568	318	1
5	L	1643	0	1565	160	0
6	H	1685	0	1640	119	0
7	A	1	0	0	0	0
All	All	12252	0	11763	1008	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 42.

The worst 5 of 1008 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)
3:A:501:TYR:CE1	3:A:505:ILE:HD11	1.86	1.10
3:A:50:ILE:HD11	3:A:145:GLN:HB2	1.10	1.09
3:A:344:GLU:HG3	3:A:345:PRO:HD2	1.36	1.07
3:A:138:GLU:HG2	3:A:139:THR:H	1.10	1.06
5:L:61:ARG:HB2	5:L:76:SER:HB3	1.36	1.06

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:2:ILE:O	4:B:2:ILE:O[6_565]	1.67	0.53

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	
3	A	556/558 (100%)	431 (78%)	92 (16%)	33 (6%)	1	10
4	B	427/437 (98%)	324 (76%)	75 (18%)	28 (7%)	1	7
5	L	209/211 (99%)	165 (79%)	34 (16%)	10 (5%)	2	14
6	H	223/225 (99%)	185 (83%)	23 (10%)	15 (7%)	1	7
All	All	1415/1431 (99%)	1105 (78%)	224 (16%)	86 (6%)	1	9

5 of 86 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	67	ASP
3	A	138	GLU
3	A	273	GLY
3	A	466	VAL
3	A	474	ASN

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	
3	A	485/498 (97%)	444 (92%)	41 (8%)	10	37
4	B	388/397 (98%)	343 (88%)	45 (12%)	5	22
5	L	190/190 (100%)	178 (94%)	12 (6%)	18	48
6	H	196/196 (100%)	174 (89%)	22 (11%)	6	24
All	All	1259/1281 (98%)	1139 (90%)	120 (10%)	8	31

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	220	LYS
6	H	123	SER
4	B	324	ASP
6	H	111	ASP
6	H	200	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
4	B	363	ASN
5	L	138	ASN
4	B	373	GLN
5	L	77	ASN
5	L	210	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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
2	TFO	P	822[B]	2	13,19,20	1.15	2 (15%)	7,26,29	1.05	1 (14%)
2	MRG	P	817	2,1	18,24,29	1.15	2 (11%)	19,35,42	0.91	2 (10%)
2	TFO	P	822[A]	2	13,19,20	3.79	6 (46%)	7,26,29	2.12	2 (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	TFO	P	822[B]	2	-	0/5/9/10	0/2/2/2
2	MRG	P	817	2,1	-	0/3/21/27	0/3/3/3
2	TFO	P	822[A]	2	-	2/5/9/10	0/2/2/2

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	822[A]	TFO	C6'-N9	-8.28	1.39	1.48
2	P	822[A]	TFO	O9'-C9'	7.59	1.52	1.42
2	P	822[A]	TFO	C8'-C7'	5.65	1.73	1.51
2	P	822[A]	TFO	C4-N3	-3.83	1.30	1.35
2	P	817	MRG	C5-C6	-2.83	1.41	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	822[A]	TFO	C5-C6-N6	4.32	126.91	120.35
2	P	817	MRG	O3'-C3'-C2'	-2.77	101.00	110.90
2	P	822[A]	TFO	N3-C2-N1	-2.06	125.45	128.68
2	P	822[B]	TFO	C5-C6-N6	2.04	123.46	120.35
2	P	817	MRG	O6-C6-C5	2.03	128.34	124.37

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	P	822[A]	TFO	N9-C6'-C7'-O9'
2	P	822[A]	TFO	N9-C6'-C7'-C8'

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	822[B]	TFO	5	0
2	P	817	MRG	3	0
2	P	822[A]	TFO	2	0

5.5 Carbohydrates [i](#)

There are no monosaccharides 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, 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	T	23/27 (85%)	0.11	1 (4%) 35 17	53, 99, 132, 135	0
2	P	18/21 (85%)	0.08	0 100 100	61, 87, 109, 121	0
3	A	556/558 (99%)	-0.26	12 (2%) 62 41	16, 69, 117, 131	1 (0%)
4	B	429/437 (98%)	-0.41	2 (0%) 91 81	15, 48, 112, 128	1 (0%)
5	L	211/211 (100%)	-0.33	0 100 100	26, 60, 105, 116	0
6	H	225/225 (100%)	-0.44	3 (1%) 77 59	16, 48, 92, 129	0
All	All	1462/1479 (98%)	-0.33	18 (1%) 79 61	15, 58, 113, 135	2 (0%)

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	B	315	HIS	4.2
6	H	141	GLN	3.7
3	A	222	GLN	3.5
3	A	258	CYS	3.1
6	H	138	SER	2.7

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
2	TFO	P	822[A]	18/19	0.80	0.42	85,98,98,98	18
2	TFO	P	822[B]	18/19	0.80	0.42	86,98,98,98	18
2	MRG	P	817	22/27	0.94	0.15	97,109,112,115	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, 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
7	MG	A	559	1/1	0.98	0.26	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.