



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2018 – 12:09 pm GMT

PDB ID : 5VQX  
Title : Crystal Structure of HIV-1 Reverse Transcriptase (Y181C) Variant in Complex with 2-chloro-N-(6-cyano-3-(2-(2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy)phenoxy)-4-methylnaphthalen-1-yl)-N-methylacetamide (JLJ686), a Non-nucleoside Inhibitor  
Authors : Chan, A.H.; Anderson, K.S.  
Deposited on : 2017-05-09  
Resolution : 2.40 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.

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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	:	1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix)	:	1.13
EDS	:	trunk31020
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk31020

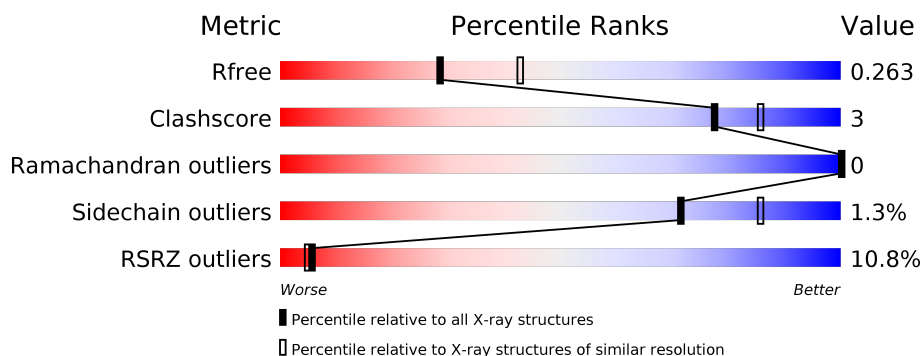
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	111664	3481 (2.40-2.40)
Clashscore	122126	3956 (2.40-2.40)
Ramachandran outliers	120053	3897 (2.40-2.40)
Sidechain outliers	120020	3898 (2.40-2.40)
RSRZ outliers	108989	3386 (2.40-2.40)

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	557	<div> <div>8%</div> <div>87%</div> <div>11%</div> <div>.</div> </div>
2	B	428	<div> <div>14%</div> <div>84%</div> <div>10%</div> <div>6%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7933 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	547	Total	C	N	O	S	0	0	0
			4413	2858	729	817	9			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P03366
A	0	VAL	-	expression tag	UNP P03366
A	172	ALA	LYS	engineered mutation	UNP P03366
A	173	ALA	LYS	engineered mutation	UNP P03366
A	181	CYS	TYR	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366

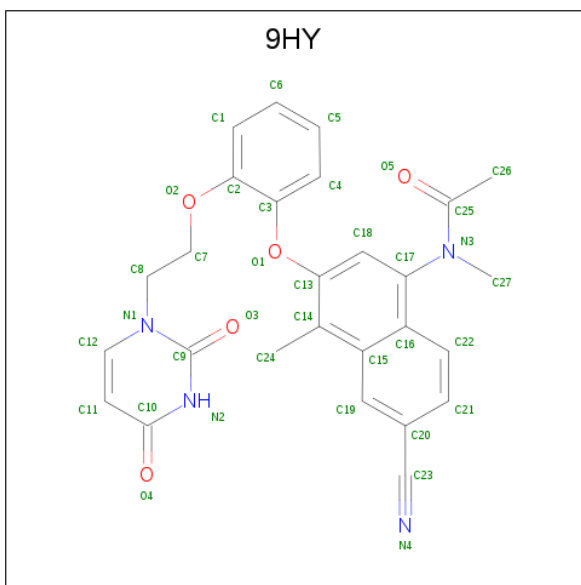
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	401	Total	C	N	O	S	0	0	0
			3323	2163	551	603	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 3 is N-(6-cyano-3-{2-[2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy]phenoxy}-4-methylnaphthalen-1-yl)-N-methylacetamide (three-letter code: 9HY) (formula: C<sub>27</sub>H<sub>24</sub>N<sub>4</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			36	27	4	5		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

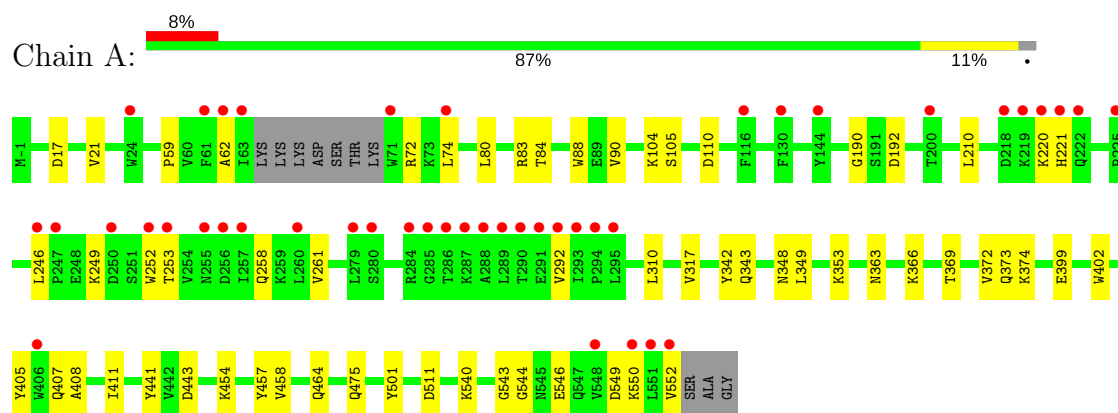
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	99	Total	O	0	0
			99	99		
5	B	52	Total	O	0	0
			52	52		

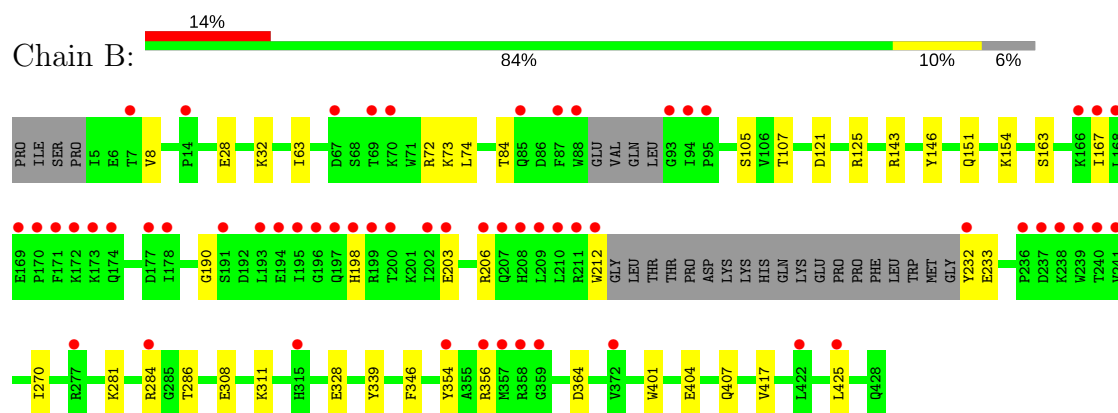
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Reverse transcriptase/ribonuclease H



#### • Molecule 2: p51 RT



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	162.30Å 73.53Å 108.67Å 90.00° 99.30° 90.00°	Depositor
Resolution (Å)	43.20 – 2.40 43.20 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (43.20-2.40) 94.8 (43.20-2.40)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.29 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, $R_{free}$	0.226 , 0.262 0.226 , 0.263	Depositor DCC
$R_{free}$ test set	2000 reflections (4.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.7	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 43.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7933	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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: 9HY, SO4

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	0.24	0/4529	0.42	0/6166
2	B	0.24	0/3417	0.42	0/4639
All	All	0.24	0/7946	0.42	0/10805

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 [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	4413	0	4425	32	0
2	B	3323	0	3352	22	0
3	A	36	0	0	0	0
4	A	10	0	0	0	0
5	A	99	0	0	0	0
5	B	52	0	0	0	0
All	All	7933	0	7777	50	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 (50) 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:544:GLY:HA2	2:B:286:THR:HG22	1.72	0.72
1:A:543:GLY:HA3	2:B:284:ARG:HA	1.78	0.65
1:A:253:THR:HG22	1:A:292:VAL:HG22	1.78	0.65
2:B:72:ARG:NH2	2:B:151:GLN:OE1	2.32	0.63
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.30	0.63
1:A:443:ASP:HB3	1:A:550:LYS:HD3	1.84	0.60
2:B:308:GLU:HA	2:B:311:LYS:HE2	1.84	0.59
1:A:372:VAL:HG11	1:A:411:ILE:HG13	1.88	0.55
2:B:203:GLU:HA	2:B:206:ARG:HG2	1.89	0.54
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.88	0.54
1:A:62:ALA:HA	1:A:72:ARG:O	2.07	0.54
1:A:110:ASP:HB2	1:A:221:HIS:NE2	2.23	0.53
1:A:353:LYS:O	1:A:374:LYS:NZ	2.40	0.52
1:A:88:TRP:CD1	2:B:143:ARG:HD2	2.46	0.52
1:A:105:SER:O	1:A:190:GLY:HA2	2.11	0.50
2:B:84:THR:HB	2:B:154:LYS:HE2	1.94	0.49
1:A:342:TYR:HB3	1:A:348:ASN:HA	1.96	0.47
1:A:249:LYS:HB2	1:A:252:TRP:CE2	2.50	0.47
1:A:258:GLN:HA	1:A:261:VAL:HG12	1.97	0.47
1:A:369:THR:O	1:A:373:GLN:HG2	2.14	0.47
1:A:246:LEU:HD11	1:A:310:LEU:HD12	1.97	0.46
2:B:28:GLU:HG2	2:B:32:LYS:HD2	1.96	0.46
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.15	0.46
2:B:167:ILE:HG12	2:B:212:TRP:CE3	2.50	0.46
2:B:105:SER:O	2:B:190:GLY:HA2	2.15	0.45
2:B:354:TYR:CE1	2:B:356:ARG:HB3	2.52	0.45
1:A:454:LYS:HZ2	1:A:552:VAL:HB	1.82	0.44
2:B:328:GLU:O	2:B:339:TYR:HA	2.18	0.44
2:B:281:LYS:HG2	2:B:284:ARG:NH1	2.32	0.44
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.53	0.44
2:B:270:ILE:HG12	2:B:346:PHE:HB3	1.99	0.43
1:A:343:GLN:HG3	1:A:349:LEU:HD11	2.00	0.43
1:A:363:ASN:ND2	1:A:366:LYS:HE3	2.33	0.42
2:B:425:LEU:HD23	2:B:425:LEU:HA	1.91	0.42
1:A:441:TYR:O	1:A:457:TYR:HA	2.20	0.42
2:B:401:TRP:HE3	2:B:404:GLU:HG3	1.85	0.42
1:A:369:THR:HA	1:A:411:ILE:HD11	2.01	0.42
1:A:540:LYS:HA	1:A:540:LYS:HD3	1.90	0.42
1:A:80:LEU:O	1:A:84:THR:OG1	2.30	0.42
2:B:163:SER:O	2:B:167:ILE:HG13	2.19	0.41
1:A:408:ALA:HB1	2:B:364:ASP:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:LYS:HB2	1:A:192:ASP:HA	2.01	0.41
1:A:17:ASP:O	1:A:83:ARG:HD3	2.22	0.41
2:B:107:THR:OG1	2:B:198:HIS:NE2	2.42	0.41
2:B:121:ASP:O	2:B:125:ARG:HG3	2.22	0.40
1:A:458:VAL:HG12	1:A:464:GLN:HG2	2.04	0.40
1:A:399:GLU:HA	1:A:402:TRP:CD1	2.56	0.40
2:B:63:ILE:HD12	2:B:407:GLN:HA	2.03	0.40
1:A:317:VAL:HG23	1:A:349:LEU:HD23	2.04	0.40
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.57	0.40

There are no symmetry-related clashes.

## 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	543/557 (98%)	534 (98%)	9 (2%)	0	100	100
2	B	395/428 (92%)	386 (98%)	9 (2%)	0	100	100
All	All	938/985 (95%)	920 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	480/495 (97%)	474 (99%)	6 (1%)	71	86
2	B	365/390 (94%)	360 (99%)	5 (1%)	69	84
All	All	845/885 (96%)	834 (99%)	11 (1%)	71	86

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

Mol	Chain	Res	Type
1	A	74	LEU
1	A	90	VAL
1	A	210	LEU
1	A	220	LYS
1	A	546	GLU
1	A	549	ASP
2	B	8	VAL
2	B	74	LEU
2	B	232	TYR
2	B	233	GLU
2	B	417	VAL

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

### 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 ⓘ

3 ligands 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	9HY	A	601	1	34,39,39	1.14	3 (8%)	41,55,55	2.42	5 (12%)
4	SO4	A	602	-	4,4,4	0.15	0	6,6,6	0.07	0
4	SO4	A	603	-	4,4,4	0.14	0	6,6,6	0.07	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	9HY	A	601	1	-	0/20/20/20	0/4/4/4
4	SO4	A	602	-	-	0/0/0/0	0/0/0/0
4	SO4	A	603	-	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	9HY	C8-N1	-2.24	1.44	1.48
3	A	601	9HY	C22-C21	2.09	1.41	1.36
3	A	601	9HY	C10-N2	3.60	1.39	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	9HY	C11-C10-N2	-3.52	115.00	123.17
3	A	601	9HY	C18-C13-C14	-2.09	119.86	122.39
3	A	601	9HY	C8-N1-C12	2.25	122.32	118.18
3	A	601	9HY	C16-C17-N3	3.83	122.62	119.00
3	A	601	9HY	C10-N2-C9	13.55	125.80	114.14

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

### 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, 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	547/557 (98%)	0.54	44 (8%)	12 11	31, 53, 96, 137	0
2	B	401/428 (93%)	0.84	58 (14%)	2 2	31, 52, 107, 124	0
All	All	948/985 (96%)	0.67	102 (10%)	6 5	31, 53, 101, 137	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	289	LEU	9.9
2	B	241	VAL	8.5
1	A	290	THR	7.7
1	A	287	LYS	7.2
2	B	358	ARG	7.1
1	A	288	ALA	6.5
1	A	219	LYS	6.4
2	B	357	MET	6.0
1	A	286	THR	5.9
1	A	552	VAL	5.7
2	B	200	THR	5.6
2	B	207	GLN	5.5
1	A	221	HIS	5.5
2	B	359	GLY	5.4
2	B	240	THR	5.3
2	B	94	ILE	5.3
2	B	238	LYS	5.3
2	B	88	TRP	5.1
1	A	548	VAL	5.0
1	A	116	PHE	5.0
1	A	285	GLY	4.9
1	A	295	LEU	4.8
1	A	292	VAL	4.8
2	B	196	GLY	4.7

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Mol	Chain	Res	Type	RSRZ
2	B	212	TRP	4.7
1	A	24	TRP	4.6
2	B	209	LEU	4.6
2	B	67	ASP	4.5
2	B	195	ILE	4.5
2	B	168	LEU	4.4
2	B	356	ARG	4.3
2	B	237	ASP	4.1
2	B	69	THR	4.0
2	B	85	GLN	4.0
2	B	202	ILE	3.9
2	B	166	LYS	3.9
2	B	206	ARG	3.9
1	A	255	ASN	3.9
1	A	256	ASP	3.8
2	B	87	PHE	3.7
2	B	95	PRO	3.7
2	B	232	TYR	3.6
2	B	284	ARG	3.5
1	A	220	LYS	3.5
1	A	257	ILE	3.5
1	A	247	PRO	3.5
1	A	280	SER	3.4
2	B	210	LEU	3.4
1	A	252	TRP	3.3
1	A	63	ILE	3.3
1	A	551	LEU	3.3
2	B	7	THR	3.2
2	B	70	LYS	3.2
1	A	222	GLN	3.2
1	A	291	GLU	3.2
2	B	193	LEU	3.2
1	A	218	ASP	3.1
1	A	225	PRO	3.0
2	B	173	LYS	3.0
2	B	198	HIS	3.0
1	A	200	THR	3.0
2	B	211	ARG	3.0
2	B	178	ILE	2.9
2	B	197	GLN	2.9
1	A	62	ALA	2.8
2	B	174	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	191	SER	2.7
2	B	239	TRP	2.7
1	A	293	ILE	2.6
2	B	169	GLU	2.6
1	A	71	TRP	2.6
2	B	14	PRO	2.6
2	B	170	PRO	2.6
2	B	199	ARG	2.6
1	A	550	LYS	2.5
2	B	203	GLU	2.4
2	B	93	GLY	2.4
2	B	277	ARG	2.4
1	A	294	PRO	2.4
1	A	284	ARG	2.3
2	B	354	TYR	2.3
1	A	74	LEU	2.3
1	A	246	LEU	2.3
2	B	425	LEU	2.3
2	B	177	ASP	2.3
1	A	406	TRP	2.3
1	A	250	ASP	2.3
1	A	253	THR	2.3
2	B	172	LYS	2.3
1	A	130	PHE	2.3
1	A	61	PHE	2.2
2	B	171	PHE	2.2
1	A	144	TYR	2.2
2	B	208	HIS	2.2
2	B	236	PRO	2.2
1	A	279	LEU	2.1
2	B	194	GLU	2.1
2	B	372	VAL	2.1
2	B	315	HIS	2.1
2	B	422	LEU	2.1
2	B	167	ILE	2.1
1	A	260	LEU	2.0

## 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 [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. 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	SO4	A	603	5/5	0.90	0.26	84,95,103,111	0
3	9HY	A	601	36/36	0.95	0.17	38,44,56,58	0
4	SO4	A	602	5/5	0.97	0.10	67,75,79,83	0

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

There are no such residues in this entry.