



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 17, 2017 – 08:17 PM EST

PDB ID : 5VP1  
Title : Discovery of Clinical Candidate N-{(1S)-1-[3-Fluoro-4-(trifluoromethoxy)phenyl]-2-methoxyethyl}-7-methoxy-2-oxo-2,3-dihydropyrido[2,3-b]pyrazine-4(1H)-carboxamide (TAK-915), A Highly Potent, Selective, and Brain-Penetrating Phosphodiesterase 2A Inhibitor for the Treatment of Cognitive Disorders  
Authors : Hoffman, I.  
Deposited on : unknown  
Resolution : 1.86 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20030345

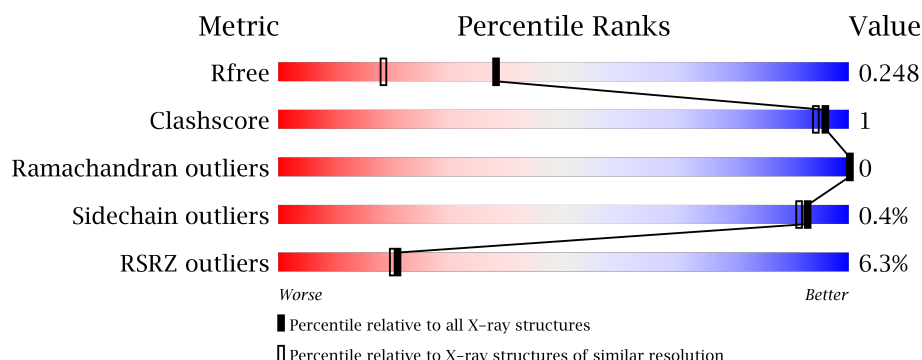
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.86 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))
$R_{free}$	100719	1923 (1.86-1.86)
Clashscore	112137	2083 (1.86-1.86)
Ramachandran outliers	110173	2060 (1.86-1.86)
Sidechain outliers	110143	2060 (1.86-1.86)
RSRZ outliers	101464	1932 (1.86-1.86)

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	345	<div> <div>7%</div> <div>94%</div> <div>5%</div> <div>• •</div> </div>
1	B	345	<div> <div>4%</div> <div>94%</div> <div>5%</div> <div>•</div> </div>
1	C	345	<div> <div>7%</div> <div>88%</div> <div>9%</div> <div>•</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
3	MG	A	1003	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8522 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 cGMP-dependent 3',5'-cyclic phosphodiesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	1	0
			2768	1763	474	506	25			
1	B	342	Total	C	N	O	S	0	1	0
			2793	1777	480	511	25			
1	C	313	Total	C	N	O	S	0	1	0
			2578	1644	445	464	25			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	575	GLY	-	expression tag	UNP O00408
A	576	HIS	-	expression tag	UNP O00408
A	577	ALA	-	expression tag	UNP O00408
B	575	GLY	-	expression tag	UNP O00408
B	576	HIS	-	expression tag	UNP O00408
B	577	ALA	-	expression tag	UNP O00408
C	575	GLY	-	expression tag	UNP O00408
C	576	HIS	-	expression tag	UNP O00408
C	577	ALA	-	expression tag	UNP O00408

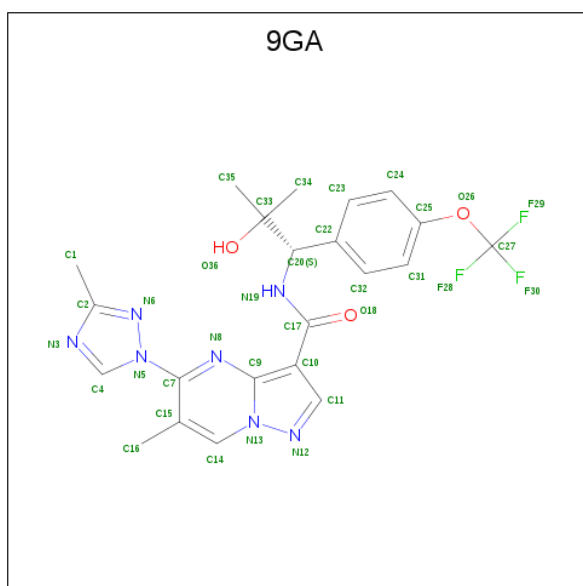
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	2	Total Mg 2 2	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is N-{(1S)-2-hydroxy-2-methyl-1-[4-(trifluoromethoxy)phenyl]propyl}-6-methyl-5-(3-methyl-1H-1,2,4-triazol-1-yl)pyrazolo[1,5-a]pyrimidine-3-carboxamide (three-letter code: 9GA) (formula: C<sub>22</sub>H<sub>22</sub>F<sub>3</sub>N<sub>7</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C F N O 35 22 3 7 3	0	0
4	B	1	Total C F N O 35 22 3 7 3	0	0
4	C	1	Total C F N O 35 22 3 7 3	0	0

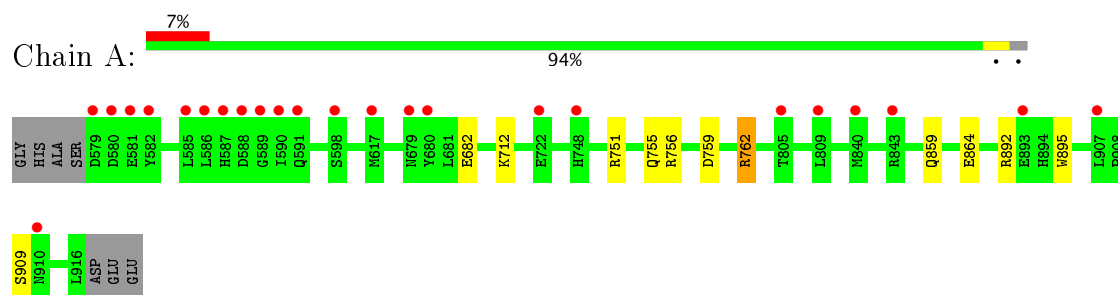
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	107	Total O 107 107	0	0
5	B	87	Total O 87 87	0	0
5	C	77	Total O 77 77	0	0

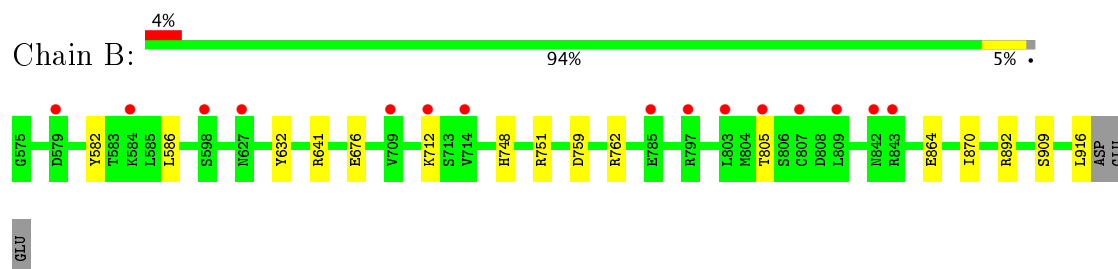
### 3 Residue-property plots [i](#)

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.

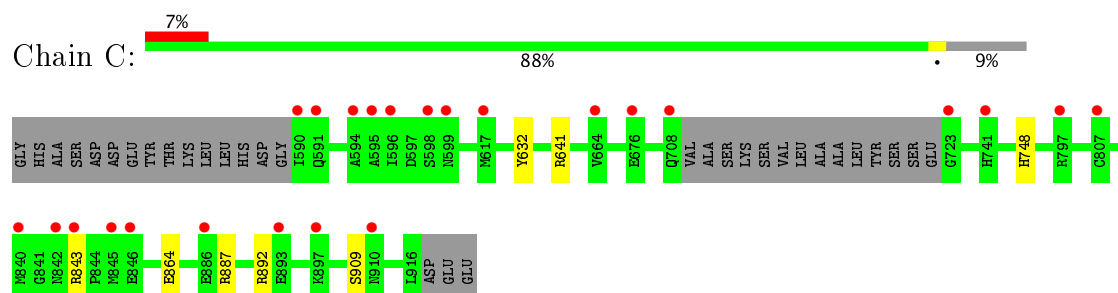
- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase



- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase



- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	165.13Å 72.71Å 90.06Å 90.00° 109.15° 90.00°	Depositor
Resolution (Å)	30.00 – 1.86 30.00 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.6 (30.00-1.86) 98.6 (30.00-1.85)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.35 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.225 , 0.243 0.230 , 0.248	Depositor DCC
$R_{free}$ test set	4051 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.7	Xtriage
Anisotropy	0.524	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 34.7	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	0.95	EDS
Total number of atoms	8522	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.37 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.8661e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, 9GA

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	0.41	0/2840	0.63	1/3832 (0.0%)
1	B	0.49	1/2866 (0.0%)	0.65	2/3867 (0.1%)
1	C	0.42	0/2646	0.64	2/3567 (0.1%)
All	All	0.44	1/8352 (0.0%)	0.64	5/11266 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	916	LEU	C-O	13.95	1.49	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	641	ARG	NE-CZ-NH1	6.45	123.52	120.30
1	B	641	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	A	762	ARG	NE-CZ-NH2	-5.19	117.71	120.30
1	C	641	ARG	NE-CZ-NH2	-5.07	117.76	120.30
1	B	641	ARG	NE-CZ-NH2	-5.04	117.78	120.30

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	2768	0	2710	9	0
1	B	2793	0	2730	13	1
1	C	2578	0	2527	3	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	35	0	0	0	0
4	B	35	0	0	1	0
4	C	35	0	0	0	0
5	A	107	0	0	0	0
5	B	87	0	0	0	0
5	C	77	0	0	0	0
All	All	8522	0	7967	21	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 1.

All (21) 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:755:GLN:OE1	1:B:712:LYS:NZ	2.10	0.84
1:B:805:THR:CG2	1:B:870:ILE:HD13	2.27	0.64
1:B:805:THR:HG22	1:B:870:ILE:HD13	1.85	0.59
1:A:712:LYS:HE3	1:B:751:ARG:HG2	1.89	0.54
1:B:805:THR:HG23	4:B:1003:9GA:F30	1.99	0.53
1:A:864:GLU:HG3	1:A:892:ARG:HD2	1.93	0.51
1:C:864:GLU:CG	1:C:892:ARG:HD2	2.41	0.51
1:B:805:THR:CG2	1:B:870:ILE:CD1	2.89	0.50
1:B:864:GLU:CG	1:B:892:ARG:HD2	2.42	0.50
1:C:864:GLU:HG3	1:C:892:ARG:HD2	1.93	0.50
1:A:755:GLN:HB2	1:B:712:LYS:HD3	1.94	0.50
1:B:864:GLU:HG3	1:B:892:ARG:HD2	1.93	0.50
1:A:864:GLU:CG	1:A:892:ARG:HD2	2.41	0.49
1:A:751:ARG:HG2	1:B:712:LYS:HD2	1.97	0.47
1:B:632:TYR:O	1:B:748:HIS:NE2	2.41	0.46
1:B:759:ASP:OD1	1:B:762:ARG:NH2	2.49	0.45
1:A:759:ASP:OD1	1:A:762:ARG:NH2	2.50	0.43
1:C:632:TYR:O	1:C:748:HIS:NE2	2.41	0.42
1:B:582:TYR:O	1:B:586:LEU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:859:GLN:HG2	1:A:895:TRP:CE2	2.56	0.41
1:A:682:GLU:OE1	1:A:756:ARG:NH2	2.55	0.40

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)
1:B:676:GLU:OE2	1:C:843:ARG:NH1[3_555]	2.12	0.08

## 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	337/345 (98%)	335 (99%)	2 (1%)	0	100	100
1	B	341/345 (99%)	340 (100%)	1 (0%)	0	100	100
1	C	310/345 (90%)	308 (99%)	2 (1%)	0	100	100
All	All	988/1035 (96%)	983 (100%)	5 (0%)	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	306/310 (99%)	305 (100%)	1 (0%)	94	93
1	B	308/310 (99%)	307 (100%)	1 (0%)	94	93
1	C	285/310 (92%)	283 (99%)	2 (1%)	87	83
All	All	899/930 (97%)	895 (100%)	4 (0%)	93	91

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	909	SER
1	B	909	SER
1	C	887	ARG
1	C	909	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	591	GLN
1	A	708	GLN
1	A	875	GLN
1	B	576	HIS
1	B	591	GLN
1	B	708	GLN
1	B	875	GLN
1	C	591	GLN
1	C	708	GLN
1	C	794	GLN
1	C	875	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 10 ligands modelled in this entry, 7 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
4	9GA	A	1004	-	28,38,38	1.05	1 (3%)	34,58,58	2.34	6 (17%)
4	9GA	B	1003	-	28,38,38	1.18	1 (3%)	34,58,58	2.34	8 (23%)
4	9GA	C	1003	-	28,38,38	1.16	2 (7%)	34,58,58	2.31	6 (17%)

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	9GA	A	1004	-	-	0/21/27/27	0/4/4/4
4	9GA	B	1003	-	-	0/21/27/27	0/4/4/4
4	9GA	C	1003	-	-	0/21/27/27	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1003	9GA	C10-C17	-2.76	1.45	1.50
4	A	1004	9GA	C4-N3	-2.74	1.30	1.35
4	C	1003	9GA	C10-C17	-2.49	1.46	1.50
4	C	1003	9GA	C4-N3	-2.34	1.30	1.35

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1003	9GA	C34-C33-C35	-3.02	106.04	110.53
4	B	1003	9GA	C34-C33-C35	-2.92	106.18	110.53
4	B	1003	9GA	C32-C22-C20	-2.00	117.62	120.81
4	A	1004	9GA	C1-C2-N3	2.19	125.97	120.49
4	B	1003	9GA	C23-C22-C32	2.25	121.13	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1003	9GA	C1-C2-N3	2.28	126.20	120.49
4	C	1003	9GA	C1-C2-N3	2.33	126.31	120.49
4	B	1003	9GA	C20-N19-C17	2.44	125.38	121.17
4	C	1003	9GA	C22-C20-N19	2.46	115.78	112.73
4	A	1004	9GA	C22-C20-N19	2.61	115.97	112.73
4	A	1004	9GA	C16-C15-C7	2.89	124.76	120.99
4	B	1003	9GA	C22-C20-N19	3.63	117.24	112.73
4	C	1003	9GA	C20-N19-C17	3.98	128.06	121.17
4	A	1004	9GA	C20-N19-C17	4.05	128.18	121.17
4	B	1003	9GA	C15-C7-N5	5.66	124.02	118.27
4	C	1003	9GA	C15-C7-N5	5.94	124.31	118.27
4	A	1004	9GA	C15-C7-N5	6.73	125.11	118.27
4	A	1004	9GA	C11-N12-N13	9.12	110.20	103.70
4	B	1003	9GA	C11-N12-N13	9.30	110.33	103.70
4	C	1003	9GA	C11-N12-N13	9.34	110.36	103.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1003	9GA	1	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 ⓘ

### 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	338/345 (97%)	0.53	24 (7%) 17 16	19, 34, 66, 89	0
1	B	342/345 (99%)	0.39	15 (4%) 35 34	20, 35, 52, 70	0
1	C	313/345 (90%)	0.55	24 (7%) 14 14	22, 37, 62, 77	0
All	All	993/1035 (95%)	0.49	63 (6%) 21 20	19, 35, 61, 89	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	589	GLY	8.3
1	A	586	LEU	7.9
1	B	843	ARG	6.2
1	A	580	ASP	5.2
1	C	840	MET	5.1
1	A	843	ARG	4.9
1	A	591	GLN	4.6
1	A	582	TYR	4.3
1	C	595	ALA	4.2
1	C	594	ALA	4.1
1	C	591	GLN	4.1
1	A	598	SER	3.9
1	A	588	ASP	3.9
1	C	845	MET	3.8
1	C	842	ASN	3.7
1	C	843	ARG	3.6
1	B	709	VAL	3.6
1	A	910	ASN	3.5
1	C	664	VAL	3.5
1	C	617	MET	3.4
1	A	579	ASP	3.4
1	B	598	SER	3.3
1	C	897	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	723	GLY	3.3
1	A	680	TYR	3.0
1	B	809	LEU	2.9
1	C	676	GLU	2.8
1	A	587	HIS	2.8
1	B	714	VAL	2.8
1	A	748	HIS	2.8
1	B	712	LYS	2.6
1	C	893	GLU	2.6
1	B	785	GLU	2.6
1	A	617	MET	2.6
1	C	886	GLU	2.5
1	C	741	HIS	2.5
1	C	598	SER	2.5
1	A	722	GLU	2.5
1	A	840	MET	2.5
1	C	910	ASN	2.5
1	A	581	GLU	2.4
1	A	893	GLU	2.4
1	B	842	ASN	2.4
1	C	708	GLN	2.4
1	C	596	ILE	2.4
1	B	579	ASP	2.4
1	B	797	ARG	2.4
1	A	805	THR	2.4
1	A	907	LEU	2.3
1	A	585	LEU	2.3
1	B	584	LYS	2.3
1	B	805	THR	2.3
1	C	590	ILE	2.3
1	B	803	LEU	2.2
1	B	807	CYS	2.2
1	C	599	ASN	2.2
1	A	590	ILE	2.2
1	C	797	ARG	2.1
1	C	807	CYS	2.1
1	C	846	GLU	2.1
1	A	809	LEU	2.1
1	B	627	ASN	2.1
1	A	679	ASN	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
3	MG	A	1003	1/1	0.71	0.17	2.00	49,49,49,49	0
4	9GA	A	1004	35/35	0.94	0.14	0.01	22,25,31,33	0
4	9GA	C	1003	35/35	0.95	0.15	-0.15	22,26,31,31	0
4	9GA	B	1003	35/35	0.94	0.12	-0.22	22,25,30,31	0
3	MG	A	1002	1/1	0.97	0.12	-0.46	22,22,22,22	0
3	MG	C	1002	1/1	0.95	0.06	-1.62	21,21,21,21	0
3	MG	B	1002	1/1	0.98	0.10	-1.66	22,22,22,22	0
2	ZN	C	1001	1/1	1.00	0.09	-1.78	24,24,24,24	0
2	ZN	A	1001	1/1	1.00	0.09	-2.40	23,23,23,23	0
2	ZN	B	1001	1/1	1.00	0.09	-6.94	25,25,25,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.