



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 05:25 pm BST

PDB ID : 6B1S
Title : Hydrogen Bonding Complementary, not size complementarity is key in the formation of the double helix
Authors : Singh, I.; Georgiadis, M.M.
Deposited on : 2017-09-18
Resolution : 2.00 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 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	:	2.11
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)	:	2.11

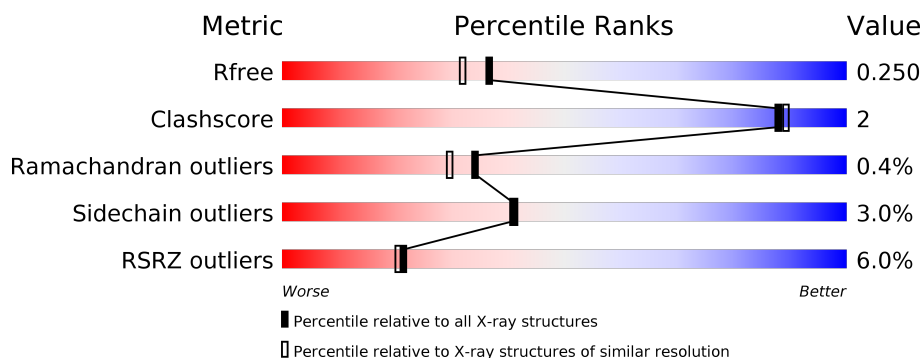
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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	A	259	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>5%</div> <div>5%</div> </div> </div>
1	B	259	<div> <div>5%</div> <div> <div></div> <div>89%</div> <div>6%</div> <div>5%</div> </div> </div>
2	E	16	<div> <div>38%</div> <div> <div></div> <div>75%</div> <div>25%</div> </div> </div>
2	F	16	<div> <div>19%</div> <div> <div></div> <div>56%</div> <div>44%</div> </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9147 atoms, of which 4291 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.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	245	Total	C	H	N	O	S	0	0	0
			3938	1261	1978	343	350	6			
1	B	246	Total	C	H	N	O	S	0	0	0
			3964	1272	1987	344	354	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	GLY	-	expression tag	UNP P03355
A	21	SER	-	expression tag	UNP P03355
A	22	HIS	-	expression tag	UNP P03355
A	23	MET	-	expression tag	UNP P03355
B	20	GLY	-	expression tag	UNP P03355
B	21	SER	-	expression tag	UNP P03355
B	22	HIS	-	expression tag	UNP P03355
B	23	MET	-	expression tag	UNP P03355

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*TP*TP*AP*TP*AP*(CGY)P*(CGY)P*TP*TP*TP*AP*TP*AP*AP*G)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	E	16	Total	C	H	N	O	P	0	0	0
			490	159	163	55	98	15			
2	F	16	Total	C	H	N	O	P	0	0	0
			490	159	163	55	98	15			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	147	Total	O	0	0
			147	147		

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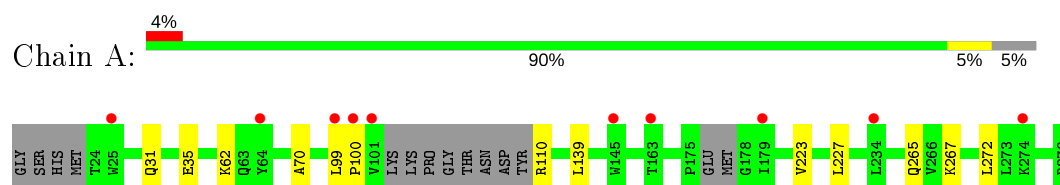
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	117	Total 117	O 117	0	0
3	E	1	Total 1	O 1	0	0

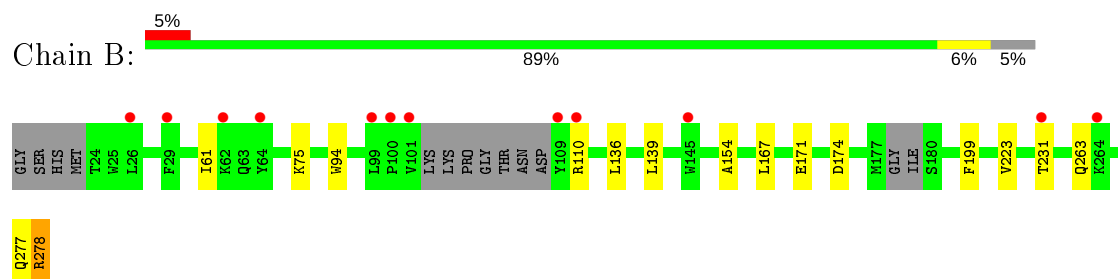
3 Residue-property plots [i](#)

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.

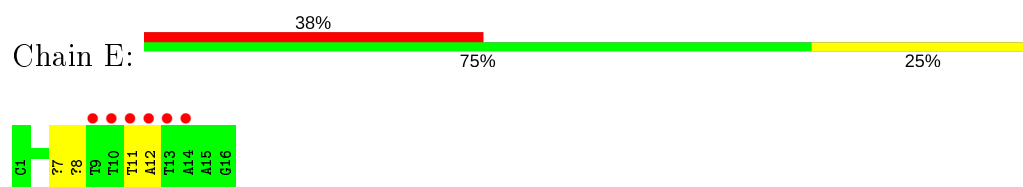
- Molecule 1: Reverse transcriptase



- Molecule 1: Reverse transcriptase



- Molecule 2: DNA (5'-D(*CP*TP*TP*AP*TP*AP*(CGY)P*(CGY)P*TP*TP*TP*AP*TP*AP*AP*G)-3')



- Molecule 2: DNA (5'-D(*CP*TP*TP*AP*TP*AP*(CGY)P*(CGY)P*TP*TP*TP*AP*TP*AP*AP*G)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	53.12Å 95.80Å 144.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.74 – 2.00 35.68 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (14.74-2.00) 99.9 (35.68-2.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.217 , 0.251 0.217 , 0.250	Depositor DCC
R_{free} test set	2468 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	27.8	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9147	wwPDB-VP
Average B, all atoms (Å ²)	42.0	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 19.98 % 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 9.6163e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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: CGY

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	0/2012	0.47	0/2741
1	B	0.25	0/2030	0.46	0/2765
2	E	0.52	0/315	1.03	0/482
2	F	0.59	0/315	1.06	0/482
All	All	0.31	0/4672	0.59	0/6470

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	1960	1978	1977	4	0
1	B	1977	1987	1987	5	0
2	E	327	163	163	3	0
2	F	327	163	163	6	0
3	A	147	0	0	1	0
3	B	117	0	0	1	0
3	E	1	0	0	0	0
All	All	4856	4291	4290	18	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 2.

The worst 5 of 18 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:31:GLN:NE2	3:A:302:HOH:O	2.26	0.68
2:F:8:CGY:N4	2:F:8:CGY:ON2	2.27	0.67
2:E:7:CGY:N4	2:E:7:CGY:ON2	2.26	0.65
2:E:8:CGY:ON2	2:E:8:CGY:N4	2.29	0.61
2:F:7:CGY:N4	2:F:7:CGY:ON2	2.34	0.58

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	239/259 (92%)	233 (98%)	5 (2%)	1 (0%)	34	30
1	B	240/259 (93%)	235 (98%)	4 (2%)	1 (0%)	34	30
All	All	479/518 (92%)	468 (98%)	9 (2%)	2 (0%)	34	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	VAL
1	B	223	VAL

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	215/227 (95%)	209 (97%)	6 (3%)	43	44
1	B	217/227 (96%)	210 (97%)	7 (3%)	39	38
All	All	432/454 (95%)	419 (97%)	13 (3%)	41	41

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	267	LYS
1	B	61	ILE
1	B	231	THR
1	A	227	LEU
1	B	139	LEU

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 ⓘ

4 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	CGY	F	8	2	19,23,24	1.22	3 (15%)	22,33,36	2.83	6 (27%)
2	CGY	F	7	2	19,23,24	1.25	3 (15%)	22,33,36	2.58	6 (27%)
2	CGY	E	7	2	19,23,24	1.26	3 (15%)	22,33,36	2.66	4 (18%)
2	CGY	E	8	2	19,23,24	1.22	3 (15%)	22,33,36	2.46	3 (13%)

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	CGY	F	8	2	-	2/7/25/26	0/2/2/2
2	CGY	F	7	2	-	2/7/25/26	0/2/2/2
2	CGY	E	7	2	-	0/7/25/26	0/2/2/2
2	CGY	E	8	2	-	0/7/25/26	0/2/2/2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	7	CGY	C2-N1	-2.86	1.27	1.34
2	E	7	CGY	C2-N1	-2.85	1.27	1.34
2	E	8	CGY	C2-N1	-2.85	1.27	1.34
2	F	8	CGY	C2-N1	-2.83	1.27	1.34
2	E	7	CGY	C4-N4	-2.80	1.27	1.34

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	7	CGY	ON2-N5-C5	7.46	120.59	106.67
2	E	8	CGY	ON2-N5-C5	7.22	120.13	106.67
2	F	8	CGY	ON2-N5-C5	7.21	120.11	106.67
2	E	7	CGY	ON1-N5-C5	7.20	120.10	106.67
2	E	7	CGY	ON2-N5-C5	7.17	120.05	106.67

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	8	CGY	C3'-C4'-C5'-O5'
2	F	7	CGY	O4'-C4'-C5'-O5'
2	F	7	CGY	C3'-C4'-C5'-O5'
2	F	8	CGY	O4'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	8	CGY	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	7	CGY	1	0
2	E	7	CGY	1	0
2	E	8	CGY	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	A	245/259 (94%)	0.61	10 (4%) 37 36	16, 31, 60, 84	0
1	B	246/259 (94%)	0.51	12 (4%) 29 28	18, 34, 62, 87	0
2	E	14/16 (87%)	1.43	6 (42%) 0 0	35, 56, 74, 83	0
2	F	14/16 (87%)	1.34	3 (21%) 0 0	37, 57, 77, 81	0
All	All	519/550 (94%)	0.61	31 (5%) 21 20	16, 34, 65, 87	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	LEU	5.3
1	A	100	PRO	4.2
1	B	231	THR	3.6
2	E	13	DT	3.5
1	B	26	LEU	3.4

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	CGY	E	8	22/23	0.77	0.23	62,68,74,76	0
2	CGY	F	7	22/23	0.78	0.29	57,72,82,90	0
2	CGY	F	8	22/23	0.79	0.27	58,69,83,86	0
2	CGY	E	7	22/23	0.80	0.26	52,65,74,75	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.