



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2022 – 07:08 pm BST

PDB ID : 7P6F  
Title : 1.93 Å resolution X-ray crystal structure of the transcriptional regulator SrnR from *Streptomyces griseus*  
Authors : Mazzei, L.; Ciurli, S.  
Deposited on : 2021-07-16  
Resolution : 1.93 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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : **FAILED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.28.1

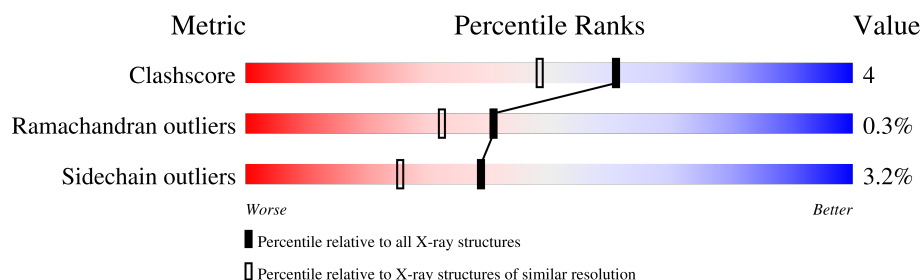
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.93 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))
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)

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  $\geq 3$ , 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  $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	AAA	117	77% 11% 12%
1	BBB	117	71% 13% 14%
1	CCC	117	77% 11% 12%
1	DDD	117	76% 7% 17%

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
2	ACT	BBB	401	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3558 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 Transcriptional regulator SrnR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	103	Total	C	N	O	S	0	3	0
			816	507	156	151	2			
1	BBB	101	Total	C	N	O	S	0	5	0
			807	498	158	149	2			
1	CCC	103	Total	C	N	O	S	0	5	0
			835	517	164	152	2			
1	DDD	97	Total	C	N	O	S	0	0	0
			734	456	139	137	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-2	GLY	-	expression tag	UNP Q8L1Y3
AAA	-1	SER	-	expression tag	UNP Q8L1Y3
AAA	0	HIS	-	expression tag	UNP Q8L1Y3
BBB	-2	GLY	-	expression tag	UNP Q8L1Y3
BBB	-1	SER	-	expression tag	UNP Q8L1Y3
BBB	0	HIS	-	expression tag	UNP Q8L1Y3
CCC	-2	GLY	-	expression tag	UNP Q8L1Y3
CCC	-1	SER	-	expression tag	UNP Q8L1Y3
CCC	0	HIS	-	expression tag	UNP Q8L1Y3
DDD	-2	GLY	-	expression tag	UNP Q8L1Y3
DDD	-1	SER	-	expression tag	UNP Q8L1Y3
DDD	0	HIS	-	expression tag	UNP Q8L1Y3

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	AAA	1	Total C O 4 2 2	0	0
2	AAA	1	Total C O 4 2 2	0	0
2	BBB	1	Total C O 4 2 2	0	0
2	CCC	1	Total C O 4 2 2	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	1	Total Na 1 1	0	0
3	BBB	1	Total Na 1 1	0	0
3	DDD	1	Total Na 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	93	Total O 93 93	0	0
4	BBB	91	Total O 91 91	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	CCC	104	Total 104	O 104	0	0
4	DDD	59	Total 59	O 59	0	0

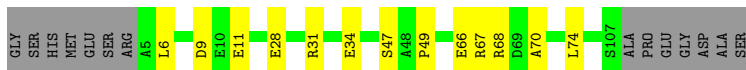
### 3 Residue-property plots [i](#)

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. 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. 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.


Note EDS failed to run properly.

- Molecule 1: Transcriptional regulator SrnR

Chain AAA: 




- Molecule 1: Transcriptional regulator SrnR

Chain BBB: 




- Molecule 1: Transcriptional regulator SrnR

Chain CCC: 



- Molecule 1: Transcriptional regulator SrnR

Chain DDD: 



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.36Å 113.36Å 124.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	51.67 – 1.93	Depositor
% Data completeness (in resolution range)	100.0 (51.67-1.93)	Depositor
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.19 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.178 , 0.217	Depositor
Wilson B-factor (Å <sup>2</sup> )	30.7	Xtriage
Anisotropy	0.167	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3558	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.37% 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: NA, ACT

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	AAA	0.91	0/827	0.96	1/1116 (0.1%)
1	BBB	0.87	1/816 (0.1%)	1.02	2/1099 (0.2%)
1	CCC	1.03	2/846 (0.2%)	1.02	2/1140 (0.2%)
1	DDD	0.82	0/743	0.97	0/1003
All	All	0.91	3/3232 (0.1%)	0.99	5/4358 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CCC	11[A]	GLU	CD-OE2	9.11	1.35	1.25
1	CCC	11[B]	GLU	CD-OE2	9.11	1.35	1.25
1	BBB	80	GLU	CD-OE1	6.61	1.32	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	16[A]	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	BBB	16[B]	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	CCC	81	ARG	CG-CD-NE	-8.09	94.81	111.80
1	CCC	67	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	AAA	66	GLU	CB-CA-C	-5.02	100.35	110.40

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	AAA	816	0	831	10	0
1	BBB	807	0	830	10	0
1	CCC	835	0	854	8	0
1	DDD	734	0	753	4	0
2	AAA	8	0	6	0	0
2	BBB	4	0	3	3	0
2	CCC	4	0	3	0	0
3	AAA	1	0	0	0	0
3	BBB	1	0	0	0	0
3	DDD	1	0	0	0	0
4	AAA	93	0	0	3	0
4	BBB	91	0	0	0	0
4	CCC	104	0	0	0	0
4	DDD	59	0	0	0	0
All	All	3558	0	3280	29	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 4.

All (29) 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:AAA:31[B]:ARG:CZ	1:CCC:31:ARG:HH12	1.87	0.88
1:BBB:16[A]:ARG:HD3	2:BBB:401:ACT:O	1.80	0.82
1:CCC:100:LEU:O	1:CCC:101[A]:ARG:HD3	1.87	0.74
4:AAA:308:HOH:O	2:BBB:401:ACT:H1	1.93	0.67
1:CCC:101[B]:ARG:HD3	1:CCC:103:THR:HG22	1.79	0.62
1:AAA:31[B]:ARG:CZ	1:CCC:31:ARG:NH1	2.62	0.60
1:BBB:69:ASP:O	1:BBB:72:ARG:HG2	2.06	0.56
1:AAA:11[B]:GLU:CD	4:AAA:303:HOH:O	2.45	0.54
1:AAA:31[B]:ARG:NH1	4:AAA:302:HOH:O	2.43	0.51
1:CCC:48:ALA:HB3	1:CCC:49:PRO:HD3	1.93	0.51
1:BBB:66:GLU:HG3	1:BBB:73:ILE:CG2	2.40	0.51
1:DDD:47:SER:HB2	1:DDD:49:PRO:HD2	1.93	0.49
1:BBB:31[B]:ARG:HD3	1:BBB:77:LEU:CD2	2.43	0.49
1:AAA:31[B]:ARG:NH2	1:CCC:31:ARG:HH12	2.13	0.46
1:BBB:16[A]:ARG:CD	2:BBB:401:ACT:O	2.59	0.46
1:AAA:28:GLU:HB3	1:AAA:31[B]:ARG:NH2	2.31	0.45
1:DDD:48:ALA:N	1:DDD:49:PRO:CD	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:68:ARG:HB2	1:AAA:68:ARG:HH11	1.83	0.43
1:BBB:83:ALA:O	1:BBB:87:GLY:HA3	2.19	0.43
1:AAA:6:LEU:O	1:AAA:9:ASP:HB2	2.19	0.43
1:DDD:48:ALA:N	1:DDD:49:PRO:HD2	2.34	0.42
1:BBB:46:ILE:HD11	1:BBB:51:ILE:CD1	2.50	0.42
1:AAA:47:SER:CB	1:AAA:49:PRO:HD2	2.49	0.42
1:DDD:101:ARG:HD3	1:DDD:101:ARG:HA	1.81	0.42
1:BBB:47[B]:SER:HB2	1:BBB:49:PRO:HD2	2.01	0.42
1:BBB:103:THR:HB	1:CCC:39:GLU:OE1	2.20	0.42
1:CCC:5:ALA:HB1	1:CCC:9:ASP:HB2	2.02	0.41
1:AAA:34:GLU:HG2	1:AAA:74:LEU:HB3	2.03	0.41
1:BBB:48:ALA:N	1:BBB:49:PRO:CD	2.84	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	AAA	104/117 (89%)	101 (97%)	2 (2%)	1 (1%)	15	6
1	BBB	104/117 (89%)	100 (96%)	4 (4%)	0	100	100
1	CCC	106/117 (91%)	101 (95%)	5 (5%)	0	100	100
1	DDD	95/117 (81%)	92 (97%)	3 (3%)	0	100	100
All	All	409/468 (87%)	394 (96%)	14 (3%)	1 (0%)	41	39

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	70	ALA

### 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	AAA	83/90 (92%)	82 (99%)	1 (1%)	71	64
1	BBB	83/90 (92%)	79 (95%)	4 (5%)	25	10
1	CCC	85/90 (94%)	84 (99%)	1 (1%)	71	64
1	DDD	75/90 (83%)	71 (95%)	4 (5%)	22	9
All	All	326/360 (91%)	316 (97%)	10 (3%)	39	26

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	67	ARG
1	BBB	4	ARG
1	BBB	6	LEU
1	BBB	72	ARG
1	BBB	103	THR
1	CCC	6	LEU
1	DDD	67	ARG
1	DDD	68	ARG
1	DDD	90	LEU
1	DDD	103	THR

Sometimes 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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	$\# Z  > 2$
2	ACT	AAA	201	-	1,3,3	5.13	1 (100%)	0,3,3	-	-
2	ACT	BBB	401	-	1,3,3	2.15	1 (100%)	0,3,3	-	-
2	ACT	CCC	201	-	1,3,3	5.49	1 (100%)	0,3,3	-	-
2	ACT	AAA	203	-	1,3,3	4.21	1 (100%)	0,3,3	-	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	CCC	201	ACT	CH3-C	5.49	1.55	1.48
2	AAA	201	ACT	CH3-C	5.13	1.55	1.48
2	AAA	203	ACT	CH3-C	4.21	1.54	1.48
2	BBB	401	ACT	CH3-C	2.15	1.51	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BBB	401	ACT	3	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

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

### 6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

### 6.4 Ligands

EDS failed to run properly - this section is therefore empty.

### 6.5 Other polymers

EDS failed to run properly - this section is therefore empty.