



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 10, 2024 – 10:53 AM EST

PDB ID : 2R0Q
Title : Crystal structure of a serine recombinase- DNA regulatory complex
Authors : Rice, P.A.; Mouw, K.W.
Deposited on : 2007-08-21
Resolution : 3.20 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 : 2.36
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) : 2.36

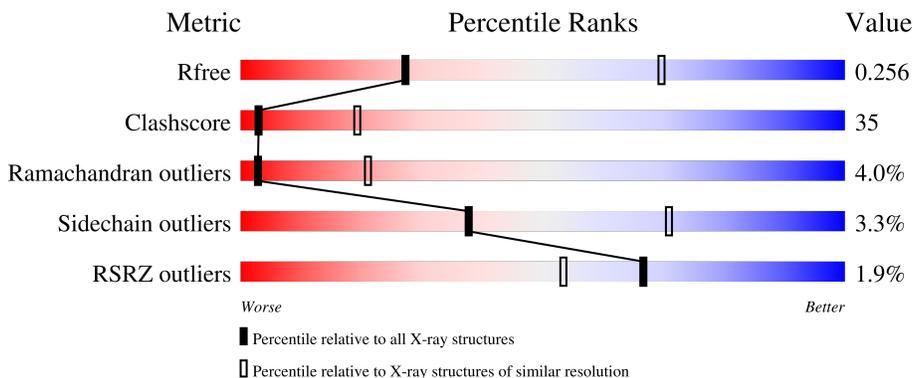
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	A	31	
1	G	31	
2	B	31	
2	H	31	
3	C	209	

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Mol	Chain	Length	Quality of chain
3	D	209	
3	E	209	
3	F	209	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8700 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 31-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	31	639	309	114	186	30	0	0	0
1	G	31	639	309	114	186	30	0	0	0

- Molecule 2 is a DNA chain called 31-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	31	626	304	110	182	30	0	0	0
2	H	31	626	304	110	182	30	0	0	0

- Molecule 3 is a protein called Putative transposon Tn552 DNA-invertase bin3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	193	1573	992	286	287	8	0	0	0
3	D	191	1507	950	271	278	8	0	0	0
3	E	193	1573	992	286	287	8	0	0	0
3	F	191	1507	950	271	278	8	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

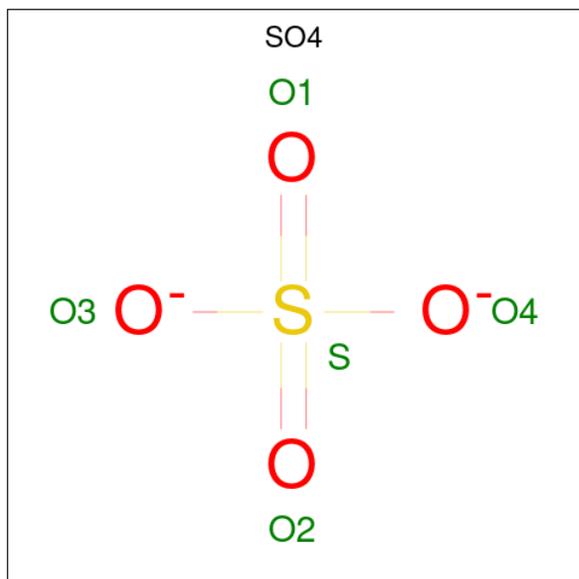
Chain	Residue	Modelled	Actual	Comment	Reference
C	203	SER	-	expression tag	UNP P20384
C	204	HIS	-	expression tag	UNP P20384
C	205	HIS	-	expression tag	UNP P20384
C	206	HIS	-	expression tag	UNP P20384
C	207	HIS	-	expression tag	UNP P20384

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Chain	Residue	Modelled	Actual	Comment	Reference
C	208	HIS	-	expression tag	UNP P20384
C	209	HIS	-	expression tag	UNP P20384
D	203	SER	-	expression tag	UNP P20384
D	204	HIS	-	expression tag	UNP P20384
D	205	HIS	-	expression tag	UNP P20384
D	206	HIS	-	expression tag	UNP P20384
D	207	HIS	-	expression tag	UNP P20384
D	208	HIS	-	expression tag	UNP P20384
D	209	HIS	-	expression tag	UNP P20384
E	203	SER	-	expression tag	UNP P20384
E	204	HIS	-	expression tag	UNP P20384
E	205	HIS	-	expression tag	UNP P20384
E	206	HIS	-	expression tag	UNP P20384
E	207	HIS	-	expression tag	UNP P20384
E	208	HIS	-	expression tag	UNP P20384
E	209	HIS	-	expression tag	UNP P20384
F	203	SER	-	expression tag	UNP P20384
F	204	HIS	-	expression tag	UNP P20384
F	205	HIS	-	expression tag	UNP P20384
F	206	HIS	-	expression tag	UNP P20384
F	207	HIS	-	expression tag	UNP P20384
F	208	HIS	-	expression tag	UNP P20384
F	209	HIS	-	expression tag	UNP P20384

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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 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.

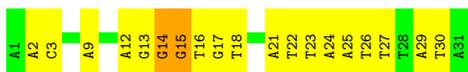
- Molecule 1: 31-MER

Chain A: 



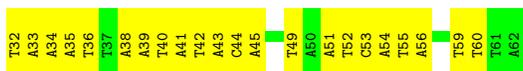
- Molecule 1: 31-MER

Chain G: 



- Molecule 2: 31-MER

Chain B: 



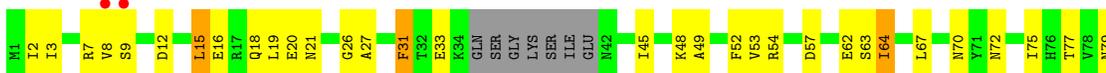
- Molecule 2: 31-MER

Chain H: 



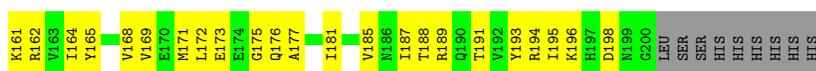
- Molecule 3: Putative transposon Tn552 DNA-invertase bin3

Chain C: 

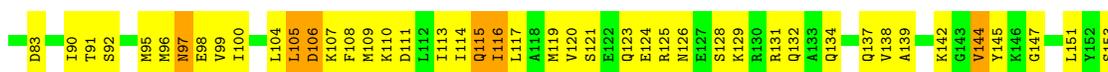




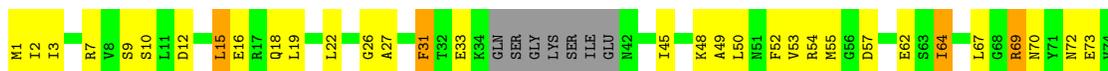
• Molecule 3: Putative transposon Tn552 DNA-invertase bin3



• Molecule 3: Putative transposon Tn552 DNA-invertase bin3



• Molecule 3: Putative transposon Tn552 DNA-invertase bin3



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	132.50Å 132.50Å 315.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.20 45.66 – 3.20	Depositor EDS
% Data completeness (in resolution range)	93.6 (50.00-3.20) 93.6 (45.66-3.20)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 3.19Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.267 , 0.291 0.246 , 0.256	Depositor DCC
R_{free} test set	2512 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	92.9	Xtrriage
Anisotropy	0.239	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 22.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.057 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8700	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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: 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	0.55	0/717	0.84	0/1107
1	G	0.52	0/717	0.85	0/1107
2	B	0.61	0/701	0.86	0/1078
2	H	0.64	0/701	0.86	0/1078
3	C	0.59	0/1592	0.83	3/2133 (0.1%)
3	D	0.58	0/1524	0.67	0/2048
3	E	0.59	0/1592	0.82	3/2133 (0.1%)
3	F	0.56	0/1524	0.67	0/2048
All	All	0.58	0/9068	0.79	6/12732 (0.0%)

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
1	A	0	2
1	G	0	2
2	H	0	1
3	E	0	1
All	All	0	6

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	131	ARG	NE-CZ-NH1	-14.21	113.19	120.30
3	C	131	ARG	NE-CZ-NH2	-13.94	113.33	120.30
3	C	131	ARG	NE-CZ-NH1	13.07	126.84	120.30
3	E	131	ARG	NE-CZ-NH2	12.38	126.49	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	131	ARG	CD-NE-CZ	6.90	133.27	123.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	14	DG	Sidechain
1	A	17	DG	Sidechain
1	G	14	DG	Sidechain
1	G	15	DG	Sidechain
2	H	46	DC	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	A	639	0	356	38	0
1	G	639	0	356	41	0
2	B	626	0	354	38	0
2	H	626	0	354	38	0
3	C	1573	0	1639	118	0
3	D	1507	0	1522	100	0
3	E	1573	0	1639	122	0
3	F	1507	0	1522	106	0
4	D	5	0	0	0	0
4	F	5	0	0	0	0
All	All	8700	0	7742	568	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 35.

The worst 5 of 568 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)
2:H:54:DA:H2''	2:H:55:DT:H5'	1.28	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:54:DA:H2''	2:B:55:DT:H5'	1.29	1.11
1:A:16:DT:H2''	1:A:17:DG:H5''	1.33	1.10
3:D:97:ASN:HA	3:D:100:ILE:HD11	1.25	1.09
1:G:16:DT:H2''	1:G:17:DG:H5''	1.37	1.06

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	
3	C	189/209 (90%)	143 (76%)	36 (19%)	10 (5%)	2	15
3	D	185/209 (88%)	144 (78%)	36 (20%)	5 (3%)	5	30
3	E	189/209 (90%)	145 (77%)	34 (18%)	10 (5%)	2	15
3	F	185/209 (88%)	140 (76%)	40 (22%)	5 (3%)	5	30
All	All	748/836 (90%)	572 (76%)	146 (20%)	30 (4%)	3	21

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	128	SER
3	E	128	SER
3	C	115	GLN
3	C	116	ILE
3	C	197	HIS

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	C	174/189 (92%)	171 (98%)	3 (2%)	60	83
3	D	160/189 (85%)	152 (95%)	8 (5%)	24	60
3	E	174/189 (92%)	169 (97%)	5 (3%)	42	74
3	F	160/189 (85%)	154 (96%)	6 (4%)	33	67
All	All	668/756 (88%)	646 (97%)	22 (3%)	38	71

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	97	ASN
3	F	69	ARG
3	F	31	PHE
3	F	95	MET
3	D	95	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	79	ASN
3	E	137	GLN
3	F	176	GLN
3	F	51	ASN
3	F	97	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](#)

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](#)

2 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	$\# Z > 2$
4	SO4	D	210	-	4,4,4	0.33	0	6,6,6	0.20	0
4	SO4	F	210	-	4,4,4	0.31	0	6,6,6	0.16	0

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	A	31/31 (100%)	-0.80	0 100 100	43, 85, 109, 117	0
1	G	31/31 (100%)	-0.81	0 100 100	44, 85, 109, 117	0
2	B	31/31 (100%)	-0.81	0 100 100	52, 77, 102, 104	0
2	H	31/31 (100%)	-0.74	0 100 100	51, 77, 103, 105	0
3	C	193/209 (92%)	-0.16	2 (1%) 82 72	46, 74, 113, 132	0
3	D	191/209 (91%)	-0.02	7 (3%) 41 26	46, 74, 149, 172	0
3	E	193/209 (92%)	-0.20	1 (0%) 91 86	44, 73, 114, 132	0
3	F	191/209 (91%)	-0.01	7 (3%) 41 26	47, 75, 149, 172	0
All	All	892/960 (92%)	-0.20	17 (1%) 66 53	43, 75, 129, 172	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	137	GLN	4.9
3	F	134	GLN	3.7
3	F	143	GLY	3.6
3	D	136	ILE	3.6
3	F	138	VAL	3.6

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 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
4	SO4	F	210	5/5	0.90	0.17	127,128,128,128	0
4	SO4	D	210	5/5	0.93	0.16	99,99,100,100	0

6.5 Other polymers [i](#)

There are no such residues in this entry.