



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 23, 2024 – 11:02 PM EDT

PDB ID : 1ZX4
Title : Structure of ParB bound to DNA
Authors : Schumacher, M.A.; Funnell, B.E.
Deposited on : 2005-06-06
Resolution : 2.98 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

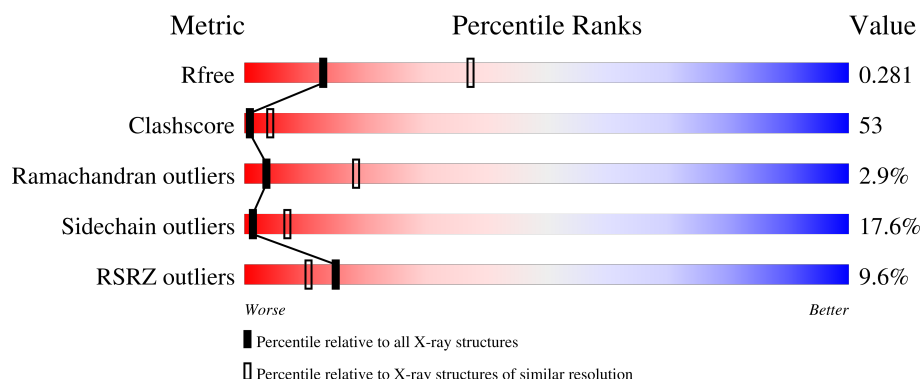
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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}	164625	3360 (3.00-2.96)
Clashscore	180529	3751 (3.00-2.96)
Ramachandran outliers	177936	3628 (3.00-2.96)
Sidechain outliers	177891	3631 (3.00-2.96)
RSRZ outliers	164620	3372 (3.00-2.96)

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	T	25	<div> <div>4%</div> <div>28%</div> <div>72%</div> </div>
2	S	25	<div> <div>28%</div> <div>68%</div> <div>.</div> </div>
3	A	192	<div> <div>12%</div> <div>25%</div> <div>54%</div> <div>15%</div> <div>6%</div> </div>
3	B	192	<div> <div>7%</div> <div>26%</div> <div>54%</div> <div>11%</div> <div>8%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3894 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 parS-small DNA centromere site.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	25	Total	C	N	O	P	0	0	0
			512	244	98	146	24			

- Molecule 2 is a DNA chain called parS-small DNA centromere site.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S	25	Total	C	N	O	P	0	0	0
			507	243	90	150	24			

- Molecule 3 is a protein called Plasmid Partition par B protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	A	180	Total	C	N	O	S	Se	0	0	0
			1437	899	254	277	1	6			
3	B	176	Total	C	N	O	S	Se	0	0	0
			1405	881	247	270	1	6			

There are 14 discrepancies between the modelled and reference sequences:

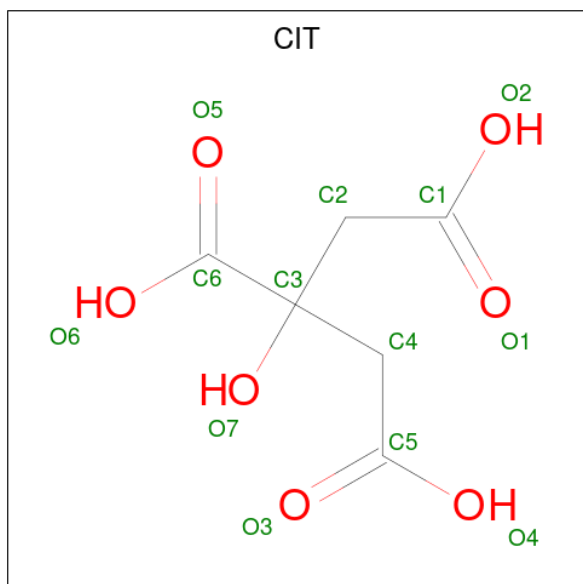
Chain	Residue	Modelled	Actual	Comment	Reference
A	159	MSE	MET	modified residue	UNP Q38420
A	161	MSE	MET	modified residue	UNP Q38420
A	166	MSE	MET	modified residue	UNP Q38420
A	220	MSE	MET	modified residue	UNP Q38420
A	245	ASN	ASP	conflict	UNP Q38420
A	247	MSE	MET	modified residue	UNP Q38420
A	318	MSE	MET	modified residue	UNP Q38420
B	159	MSE	MET	modified residue	UNP Q38420
B	161	MSE	MET	modified residue	UNP Q38420
B	166	MSE	MET	modified residue	UNP Q38420
B	220	MSE	MET	modified residue	UNP Q38420
B	245	ASN	ASP	conflict	UNP Q38420

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Chain	Residue	Modelled	Actual	Comment	Reference
B	247	MSE	MET	modified residue	UNP Q38420
B	318	MSE	MET	modified residue	UNP Q38420

- Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 13 6 7	0	0
4	A	1	Total C O 13 6 7	0	0

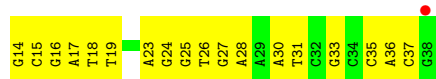
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	3	Total O 3 3	0	0
5	B	4	Total O 4 4	0	0

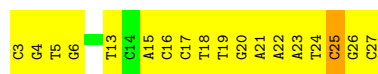
3 Residue-property plots

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.

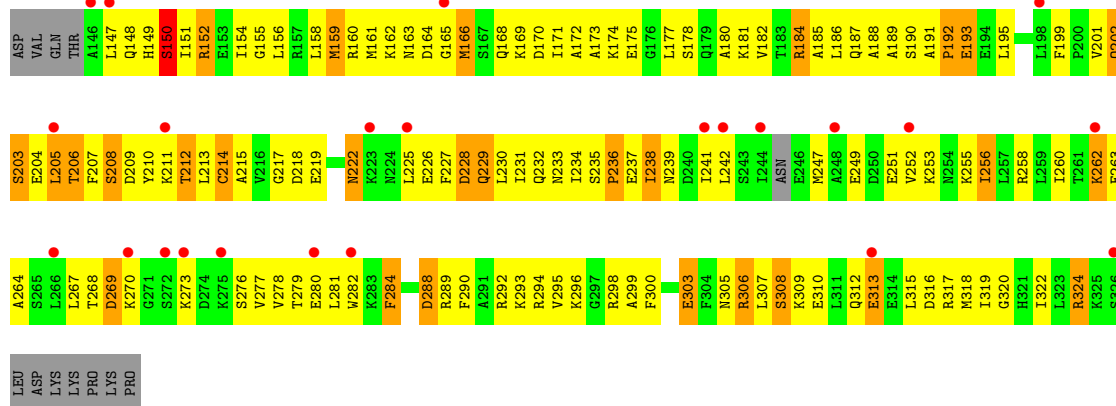
- Molecule 1: parS-small DNA centromere site



- Molecule 2: parS-small DNA centromere site



- Molecule 3: Plasmid Partition par B protein



- Molecule 3: Plasmid Partition par B protein



D209	Y210	K211	T212	L213	G214	A215	V216	G217	D218	E219	M220	G221	E222	K223	N224	L225	E226	F227	D228	Q229	L230	I231	Q232	N233	I234	S235	P236	E237	I238	N239	D240	I241	L242	S243	I244	N245	E246	N247	A248	E249	D250	E251	V252	K253	N254	K255	I256	L257	F258	L259		K262	E263	A264	S265	L266	L267		K270
K271	SER	LYS	ASP	K276	S276	V277	V278	T279	E280	L281	W282	K283	F284	E286	D286	K287	D288	R289		R292	K293	R294	V295	K296		A299	F300	S301	Y302	F303	F304	N305	R306	L307		L311	Q312	E313	E314	L315	D316	R317	K318	I319	G320	H321	I322	L323	R324	K325	S326	L327		L328	LYS	LYS	PRO	LYS	PRO

4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	154.60Å 154.60Å 132.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.61 – 2.98 50.61 – 2.98	Depositor EDS
% Data completeness (in resolution range)	94.4 (50.61-2.98) 90.8 (50.61-2.98)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.93 (at 2.96Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.248 , 0.296 0.234 , 0.281	Depositor DCC
R_{free} test set	2158 reflections (12.11%)	wwPDB-VP
Wilson B-factor (Å ²)	72.7	Xtriage
Anisotropy	0.490	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 139.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3894	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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: CIT

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	T	0.85	0/575	0.91	0/886
2	S	0.87	0/567	1.01	0/873
3	A	0.54	0/1445	0.79	1/1919 (0.1%)
3	B	0.57	0/1412	0.87	2/1876 (0.1%)
All	All	0.66	0/3999	0.88	3/5554 (0.1%)

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
2	S	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	160	ARG	NE-CZ-NH2	-11.17	114.72	120.30
3	B	160	ARG	NE-CZ-NH1	6.24	123.42	120.30
3	A	184	ARG	NE-CZ-NH1	5.05	122.83	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	S	13	DT	Sidechain
2	S	25	DC	Sidechain

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	T	512	0	282	33	0
2	S	507	0	284	37	0
3	A	1437	0	1472	179	1
3	B	1405	0	1444	160	0
4	A	26	0	10	3	0
5	A	3	0	0	1	0
5	B	4	0	0	0	0
All	All	3894	0	3492	384	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 53.

The worst 5 of 384 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:T:25:DG:H2''	1:T:26:DT:C5'	1.78	1.13
3:A:278:VAL:HG12	3:A:294:ARG:HB2	1.38	1.05
1:T:25:DG:C2'	1:T:26:DT:H5'	1.91	1.00
3:A:238:ILE:HD11	3:A:256:ILE:HG13	1.41	1.00
3:B:224:ASN:H	3:B:224:ASN:ND2	1.57	0.98

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)
3:A:160:ARG:NH2	3:A:193:GLU:OE2[7_555]	2.15	0.05

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	
3	A	176/192 (92%)	149 (85%)	23 (13%)	4 (2%)	5	23
3	B	172/192 (90%)	136 (79%)	30 (17%)	6 (4%)	3	14
All	All	348/384 (91%)	285 (82%)	53 (15%)	10 (3%)	3	18

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	150	SER
3	A	308	SER
3	B	219	GLU
3	B	222	ASN
3	B	218	ASP

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	
3	A	158/164 (96%)	132 (84%)	26 (16%)	2	8
3	B	154/164 (94%)	125 (81%)	29 (19%)	1	6
All	All	312/328 (95%)	257 (82%)	55 (18%)	1	7

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	157	ARG
3	B	222	ASN
3	B	327	LEU
3	B	293	LYS
3	B	164	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	222	ASN
3	B	202	GLN
3	B	224	ASN
3	B	233	ASN
3	B	312	GLN

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 oligosaccharides 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	CIT	A	1585	-	12,12,12	1.60	3 (25%)	17,17,17	1.44	1 (5%)
4	CIT	A	1586	-	12,12,12	1.19	1 (8%)	17,17,17	1.29	1 (5%)

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	CIT	A	1585	-	-	0/16/16/16	-
4	CIT	A	1586	-	-	0/16/16/16	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1585	CIT	C3-C6	3.63	1.57	1.53
4	A	1586	CIT	C4-C3	2.24	1.56	1.54
4	A	1585	CIT	C4-C3	2.24	1.56	1.54
4	A	1585	CIT	C2-C3	2.11	1.56	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1585	CIT	O6-C6-C3	4.12	121.05	113.14
4	A	1586	CIT	O6-C6-C3	3.59	120.03	113.14

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
4	A	1585	CIT	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 [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	T	25/25 (100%)	-0.29	1 (4%) 43 29	45, 64, 84, 91	0
2	S	25/25 (100%)	-0.35	0 100 100	47, 62, 82, 90	0
3	A	174/192 (90%)	0.68	23 (13%) 8 6	48, 100, 145, 157	0
3	B	170/192 (88%)	0.61	14 (8%) 19 13	51, 89, 128, 149	0
All	All	394/434 (90%)	0.52	38 (9%) 15 10	45, 89, 142, 157	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	328	ASP	6.1
3	B	271	GLY	6.0
3	A	266	LEU	3.9
3	B	223	LYS	3.5
3	A	275	LYS	3.4

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(\AA^2)	Q<0.9
4	CIT	A	1585	13/13	0.54	0.15	153,166,170,172	0
4	CIT	A	1586	13/13	0.78	0.13	164,172,173,176	0

6.5 Other polymers [i](#)

There are no such residues in this entry.