



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:46 AM UTC

PDB ID : 1WTP / pdb\_00001wtp  
Title : Hyperthermophile chromosomal protein SAC7D single mutant M29F in complex with DNA GCGA(UBr)CGC  
Authors : Chen, C.-Y.; Ko, T.-P.; Lin, T.-W.; Chou, C.-C.; Chen, C.-J.; Wang, A.H.-J.  
Deposited on : 2004-11-29  
Resolution : 1.90 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](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.

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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

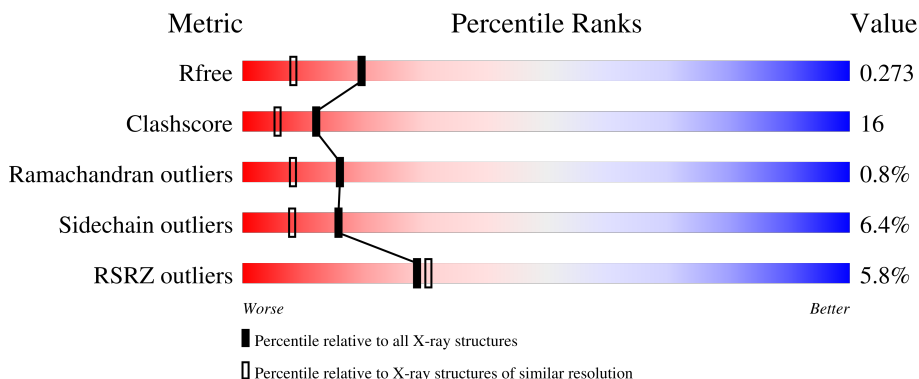
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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.



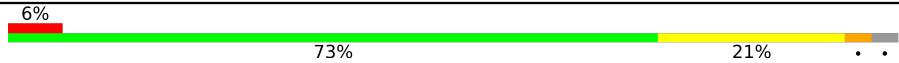
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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  $\leq 5\%$ . 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	C	8	
1	D	8	
1	E	8	
1	F	8	
2	A	66	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	B	66	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into segments: a small red segment at the beginning labeled '6%', a large green segment labeled '73%', and a yellow segment at the end labeled '21%'. There are two small black dots at the far right end of the bar.</p>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1827 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 5'-D(\*GP\*CP\*GP\*AP\*(BRU)P\*CP\*GP\*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	Br	C	N	O				P
1	C	8	Total 161	Br 1	C 76	N 31	O 46	P 7	0	0	0
1	D	8	Total 161	Br 1	C 76	N 31	O 46	P 7	0	0	0
1	E	8	Total 161	Br 1	C 76	N 31	O 46	P 7	0	0	0
1	F	8	Total 161	Br 1	C 76	N 31	O 46	P 7	0	0	0

- Molecule 2 is a protein called DNA-binding proteins 7a/7b/7d.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	63	Total 509	C 323	N 89	O 96	S 1	0	0	0
2	B	64	Total 518	C 329	N 91	O 97	S 1	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	PHE	MET	engineered mutation	UNP P13123
B	29	PHE	MET	engineered mutation	UNP P13123

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	22	Total 22	O 22	0	0
3	D	19	Total 19	O 19	0	0
3	E	17	Total 17	O 17	0	0

*Continued on next page...*

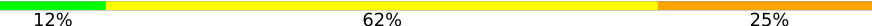
*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
3	F	6	Total O 6 6	0	0
3	A	63	Total O 63 63	0	0
3	B	29	Total O 29 29	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 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.

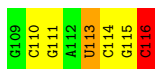
- Molecule 1: 5'-D(\*GP\*CP\*GP\*AP\*(BRU)P\*CP\*GP\*C)-3'

Chain C: 



- Molecule 1: 5'-D(\*GP\*CP\*GP\*AP\*(BRU)P\*CP\*GP\*C)-3'

Chain D: 



- Molecule 1: 5'-D(\*GP\*CP\*GP\*AP\*(BRU)P\*CP\*GP\*C)-3'

Chain E: 



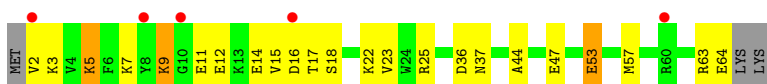
- Molecule 1: 5'-D(\*GP\*CP\*GP\*AP\*(BRU)P\*CP\*GP\*C)-3'

Chain F: 



- Molecule 2: DNA-binding proteins 7a/7b/7d

Chain A: 



- Molecule 2: DNA-binding proteins 7a/7b/7d

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	38.22Å 47.89Å 52.49Å 90.00° 102.67° 90.00°	Depositor
Resolution (Å)	40.00 – 1.90 40.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.2 (40.00-1.90) 96.2 (40.00-1.90)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.90 (at 1.88Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.222 , 0.287 0.210 , 0.273	Depositor DCC
$R_{free}$ test set	1503 reflections (10.13%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.2	Xtrriage
Anisotropy	0.328	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 41.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	1827	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.28% 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: BRU

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	C	0.68	0/157	1.06	2/238 (0.8%)
1	D	0.61	0/157	0.99	1/238 (0.4%)
1	E	0.45	0/157	0.88	0/238
1	F	0.44	0/157	0.87	0/238
2	A	0.97	2/516 (0.4%)	1.14	2/685 (0.3%)
2	B	0.81	0/525	1.07	1/696 (0.1%)
All	All	0.78	2/1669 (0.1%)	1.05	6/2333 (0.3%)

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	C	0	2
1	D	0	2
1	E	0	3
1	F	0	3
All	All	0	10

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	44	ALA	CA-CB	6.33	1.64	1.53
2	A	57	MET	SD-CE	-5.70	1.65	1.79

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	116	DC	C5'-C4'-O4'	-6.98	98.93	109.40

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	108	DC	C4'-C3'-O3'	-6.95	99.57	110.00
2	A	36	ASP	N-CA-C	-6.88	98.85	108.54
2	B	50	ALA	N-CA-C	6.51	119.07	109.50
1	C	108	DC	C2'-C3'-O3'	-6.04	102.44	111.50

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	103	DG	Sidechain
1	C	106	DC	Sidechain
1	D	114	DC	Sidechain
1	D	116	DC	Sidechain
1	E	102	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	C	161	0	88	4	0
1	D	161	0	88	9	0
1	E	161	0	88	7	0
1	F	161	0	88	5	0
2	A	509	0	524	18	0
2	B	518	0	537	14	0
3	A	63	0	0	3	0
3	B	29	0	0	0	0
3	C	22	0	0	0	0
3	D	19	0	0	0	0
3	E	17	0	0	1	0
3	F	6	0	0	0	0
All	All	1827	0	1413	48	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 16.

The worst 5 of 48 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:E:101:DG:H2''	1:E:102:DC:H5'	1.29	1.13
1:C:107:DG:H2''	1:C:108:DC:H5''	1.53	0.89
2:A:3:LYS:HG2	2:A:14:GLU:HG2	1.64	0.78
1:D:115:DG:H2''	1:D:116:DC:C5'	2.15	0.76
1:C:105:BRU:OP1	2:A:22:LYS:HE3	1.93	0.68

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
2	A	61/66 (92%)	57 (93%)	3 (5%)	1 (2%)	7 2
2	B	62/66 (94%)	60 (97%)	2 (3%)	0	100 100
All	All	123/132 (93%)	117 (95%)	5 (4%)	1 (1%)	16 8

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	37	ASN

### 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
2	A	54/57 (95%)	49 (91%)	5 (9%)	8 3

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	55/57 (96%)	53 (96%)	2 (4%)	31	23
All	All	109/114 (96%)	102 (94%)	7 (6%)	16	8

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	53	GLU
2	A	64	GLU
2	B	15	VAL
2	B	14	GLU
2	A	18	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	37	ASN
2	B	37	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](#)

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
1	BRU	D	113	1	18,21,22	1.90	1 (5%)	25,30,33	0.84	1 (4%)
1	BRU	E	105	1	18,21,22	2.23	1 (5%)	25,30,33	0.78	1 (4%)
1	BRU	F	113	1	18,21,22	2.28	1 (5%)	25,30,33	0.90	0
1	BRU	C	105	1	18,21,22	1.33	1 (5%)	25,30,33	1.16	2 (8%)

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
1	BRU	D	113	1	-	2/7/21/22	0/2/2/2
1	BRU	E	105	1	-	0/7/21/22	0/2/2/2
1	BRU	F	113	1	-	0/7/21/22	0/2/2/2
1	BRU	C	105	1	-	0/7/21/22	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	105	BRU	BR-C5	-9.37	1.66	1.88
1	F	113	BRU	BR-C5	-9.22	1.67	1.88
1	D	113	BRU	BR-C5	-7.54	1.71	1.88
1	C	105	BRU	BR-C5	-4.45	1.78	1.88

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	105	BRU	BR-C5-C4	3.35	121.88	118.02
1	C	105	BRU	C6-C5-C4	-3.33	117.29	120.67
1	E	105	BRU	BR-C5-C4	2.00	120.33	118.02
1	D	113	BRU	BR-C5-C4	2.00	120.32	118.02

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	113	BRU	C3'-C4'-C5'-O5'
1	D	113	BRU	O4'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	113	BRU	1	0
1	F	113	BRU	2	0
1	C	105	BRU	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides 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, 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	C	7/8 (87%)	-0.35	0	100	100	21, 28, 30, 34	0
1	D	7/8 (87%)	-0.15	0	100	100	21, 27, 34, 34	0
1	E	7/8 (87%)	-0.14	0	100	100	28, 34, 40, 40	0
1	F	7/8 (87%)	-0.00	0	100	100	33, 35, 37, 43	0
2	A	63/66 (95%)	0.50	5 (7%)	18	20	16, 29, 52, 56	0
2	B	64/66 (96%)	0.51	4 (6%)	26	27	21, 35, 51, 58	0
All	All	155/164 (94%)	0.39	9 (5%)	29	30	16, 33, 52, 58	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	2	VAL	3.8
2	A	8	TYR	3.1
2	B	9	LYS	3.0
2	A	10	GLY	3.0
2	B	64	GLU	2.6

### 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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
1	BRU	E	105	20/21	0.93	0.10	26,32,37,49	0
1	BRU	F	113	20/21	0.95	0.09	27,36,43,43	0
1	BRU	C	105	20/21	0.96	0.07	18,24,28,38	0
1	BRU	D	113	20/21	0.96	0.08	21,26,35,37	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.