



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 06:24 PM UTC

PDB ID : 6JVB / pdb\_00006jvb  
Title : Crystal Structure of Human CRMP2 1-532, AGE-modified  
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Deposited on : 2019-04-16  
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](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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

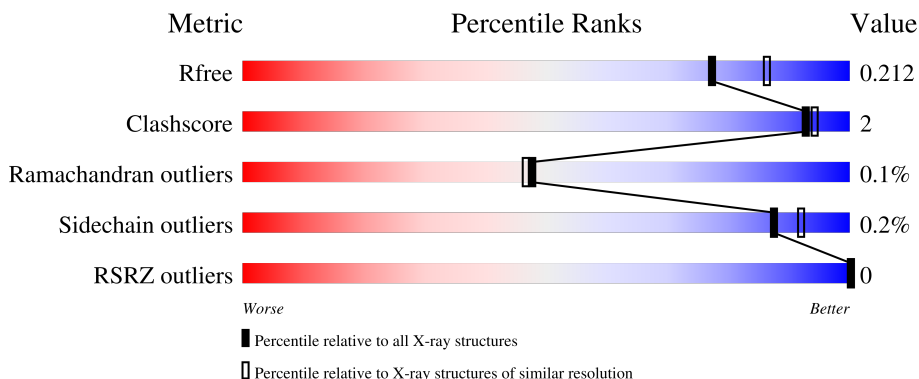
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


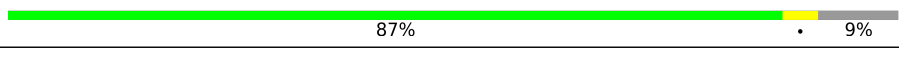
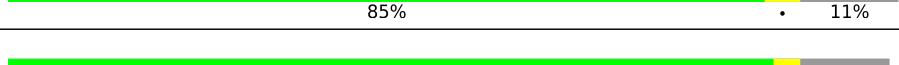

The reported resolution of this entry is 2.00 Å.

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))
$R_{free}$	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 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	A	540	 85% 11%
1	B	540	 87% 9%
1	C	540	 85% 11%
1	D	540	 86% 10%

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 15561 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 Dihydropyrimidinase-related protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	482	3688	2320	633	717	18	0	0	0
1	B	491	3751	2363	642	727	19	0	0	0
1	C	482	3687	2321	633	715	18	0	0	0
1	D	485	3707	2335	635	719	18	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP Q16555
A	-6	HIS	-	expression tag	UNP Q16555
A	-5	HIS	-	expression tag	UNP Q16555
A	-4	HIS	-	expression tag	UNP Q16555
A	-3	HIS	-	expression tag	UNP Q16555
A	-2	HIS	-	expression tag	UNP Q16555
A	-1	HIS	-	expression tag	UNP Q16555
A	0	HIS	-	expression tag	UNP Q16555
B	-7	MET	-	initiating methionine	UNP Q16555
B	-6	HIS	-	expression tag	UNP Q16555
B	-5	HIS	-	expression tag	UNP Q16555
B	-4	HIS	-	expression tag	UNP Q16555
B	-3	HIS	-	expression tag	UNP Q16555
B	-2	HIS	-	expression tag	UNP Q16555
B	-1	HIS	-	expression tag	UNP Q16555
B	0	HIS	-	expression tag	UNP Q16555
C	-7	MET	-	initiating methionine	UNP Q16555
C	-6	HIS	-	expression tag	UNP Q16555
C	-5	HIS	-	expression tag	UNP Q16555
C	-4	HIS	-	expression tag	UNP Q16555
C	-3	HIS	-	expression tag	UNP Q16555

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	UNP Q16555
C	-1	HIS	-	expression tag	UNP Q16555
C	0	HIS	-	expression tag	UNP Q16555
D	-7	MET	-	initiating methionine	UNP Q16555
D	-6	HIS	-	expression tag	UNP Q16555
D	-5	HIS	-	expression tag	UNP Q16555
D	-4	HIS	-	expression tag	UNP Q16555
D	-3	HIS	-	expression tag	UNP Q16555
D	-2	HIS	-	expression tag	UNP Q16555
D	-1	HIS	-	expression tag	UNP Q16555
D	0	HIS	-	expression tag	UNP Q16555

- Molecule 2 is water.

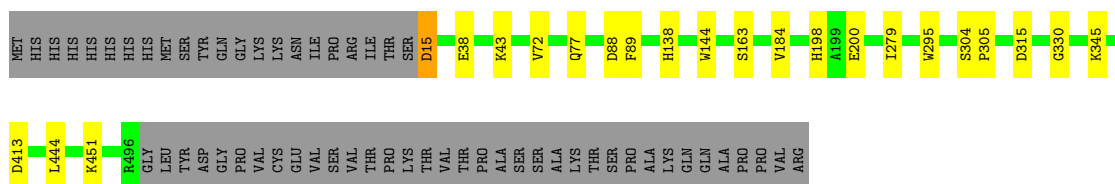
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	211	Total 211	O 211	0	0
2	B	191	Total 191	O 191	0	0
2	C	197	Total 197	O 197	0	0
2	D	129	Total 129	O 129	0	0

### 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.

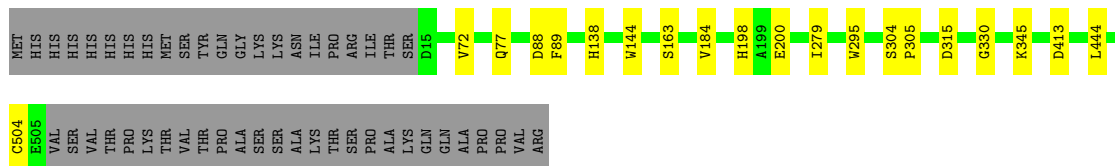
- Molecule 1: Dihydropyrimidinase-related protein 2

Chain A: 85% 11%



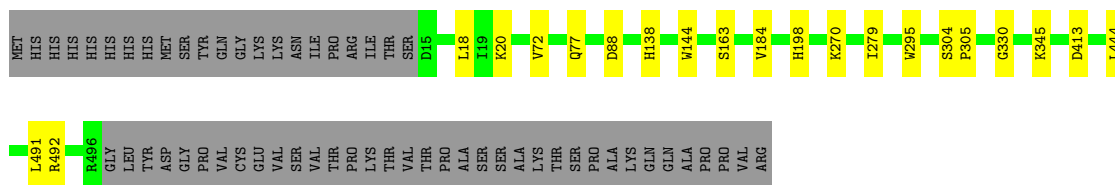
- Molecule 1: Dihydropyrimidinase-related protein 2

Chain B: 87% 9%



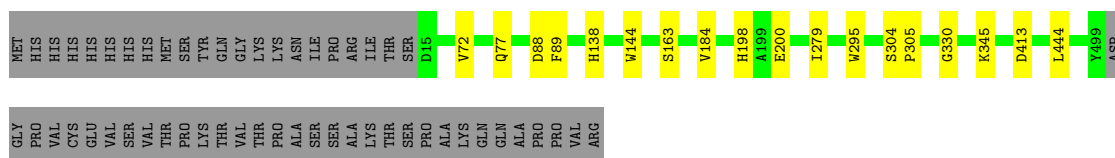
- Molecule 1: Dihydropyrimidinase-related protein 2

Chain C: 85% 11%



- Molecule 1: Dihydropyrimidinase-related protein 2

Chain D: 86% 10%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.21Å 147.33Å 95.23Å 90.00° 103.91° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.00) 99.9 (50.00-2.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.58 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.183 , 0.204 0.192 , 0.212	Depositor DCC
$R_{free}$ test set	8768 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.0	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 22.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.279 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	15561	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.69% 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](#)

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	0.75	0/3764	0.86	0/5111
1	B	0.76	0/3829	0.86	0/5201
1	C	0.76	0/3763	0.88	1/5110 (0.0%)
1	D	0.75	0/3784	0.86	0/5140
All	All	0.75	0/15140	0.87	1/20562 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	491	LEU	N-CA-C	8.60	121.51	111.02

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	3688	0	3604	14	0
1	B	3751	0	3671	11	0
1	C	3687	0	3609	10	0
1	D	3707	0	3621	10	0
2	A	211	0	0	2	0
2	B	191	0	0	1	0
2	C	197	0	0	1	0
2	D	129	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	15561	0	14505	45	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 45 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:C:198:HIS:HD2	2:C:716:HOH:O	1.73	0.71
1:D:77:GLN:HE21	1:D:89:PHE:H	1.39	0.70
1:B:138:HIS:HD2	1:B:163:SER:OG	1.76	0.68
1:B:77:GLN:HE21	1:B:89:PHE:H	1.39	0.68
1:A:77:GLN:HE21	1:A:89:PHE:H	1.42	0.67

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	480/540 (89%)	467 (97%)	13 (3%)	0	100	100
1	B	489/540 (91%)	475 (97%)	14 (3%)	0	100	100
1	C	480/540 (89%)	465 (97%)	14 (3%)	1 (0%)	43	42
1	D	483/540 (89%)	469 (97%)	14 (3%)	0	100	100
All	All	1932/2160 (89%)	1876 (97%)	55 (3%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	492	ARG

### 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	397/455 (87%)	396 (100%)	1 (0%)	86	91
1	B	404/455 (89%)	403 (100%)	1 (0%)	87	92
1	C	397/455 (87%)	396 (100%)	1 (0%)	86	91
1	D	398/455 (88%)	398 (100%)	0	100	100
All	All	1596/1820 (88%)	1593 (100%)	3 (0%)	87	92

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ASP
1	B	504	CYS
1	C	270	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	247	ASN
1	C	138	HIS
1	D	196	GLN
1	C	122	GLN
1	C	198	HIS

### 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](#)

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	A	482/540 (89%)	-1.41	0 100 100	16, 23, 45, 76	0
1	B	491/540 (90%)	-1.38	0 100 100	16, 24, 46, 74	0
1	C	482/540 (89%)	-1.40	0 100 100	16, 23, 47, 71	0
1	D	485/540 (89%)	-1.36	0 100 100	17, 25, 49, 76	0
All	All	1940/2160 (89%)	-1.39	0 100 100	16, 24, 47, 76	0

There are no RSRZ outliers to report.

### 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 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.