



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 28, 2024 – 08:45 AM EDT

PDB ID : 3CZ6  
Title : Crystal Structure of the Rap1 C-terminus  
Authors : Feeser, E.A.; Wolberger, C.  
Deposited on : 2008-04-28  
Resolution : 1.85 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	:	4.02b-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

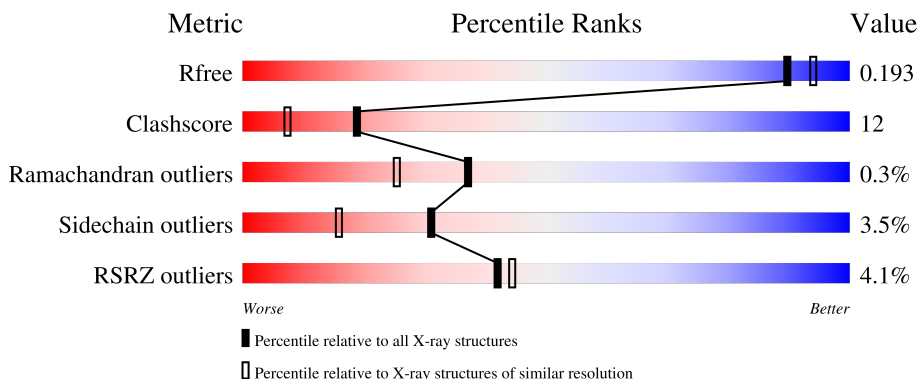
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 1.85 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	3097 (1.86-1.86)
Clashscore	180529	3359 (1.86-1.86)
Ramachandran outliers	177936	3335 (1.86-1.86)
Sidechain outliers	177891	3335 (1.86-1.86)
RSRZ outliers	164620	3097 (1.86-1.86)

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	168	
1	B	168	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2814 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 DNA-binding protein RAP1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	151	Total	C	N	O	S	Se	0	0	0
			1237	785	208	237	2	5			
1	B	151	Total	C	N	O	S	Se	0	0	0
			1227	779	204	237	2	5			

There are 24 discrepancies between the modelled and reference sequences:

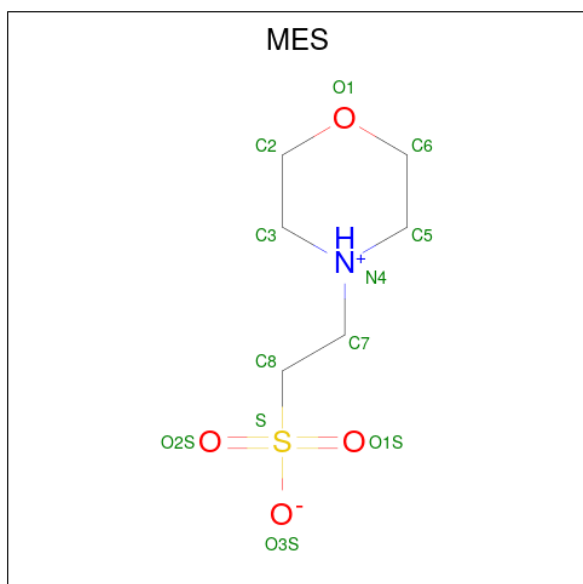
Chain	Residue	Modelled	Actual	Comment	Reference
A	671	GLY	-	expression tag	UNP P11938
A	828	VAL	-	expression tag	UNP P11938
A	829	PRO	-	expression tag	UNP P11938
A	830	ARG	-	expression tag	UNP P11938
A	831	GLY	-	expression tag	UNP P11938
A	832	SER	-	expression tag	UNP P11938
A	833	HIS	-	expression tag	UNP P11938
A	834	HIS	-	expression tag	UNP P11938
A	835	HIS	-	expression tag	UNP P11938
A	836	HIS	-	expression tag	UNP P11938
A	837	HIS	-	expression tag	UNP P11938
A	838	HIS	-	expression tag	UNP P11938
B	671	GLY	-	expression tag	UNP P11938
B	828	VAL	-	expression tag	UNP P11938
B	829	PRO	-	expression tag	UNP P11938
B	830	ARG	-	expression tag	UNP P11938
B	831	GLY	-	expression tag	UNP P11938
B	832	SER	-	expression tag	UNP P11938
B	833	HIS	-	expression tag	UNP P11938
B	834	HIS	-	expression tag	UNP P11938
B	835	HIS	-	expression tag	UNP P11938
B	836	HIS	-	expression tag	UNP P11938
B	837	HIS	-	expression tag	UNP P11938
B	838	HIS	-	expression tag	UNP P11938

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:  $C_6H_{14}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula:  $C_6H_{13}NO_4S$ ).



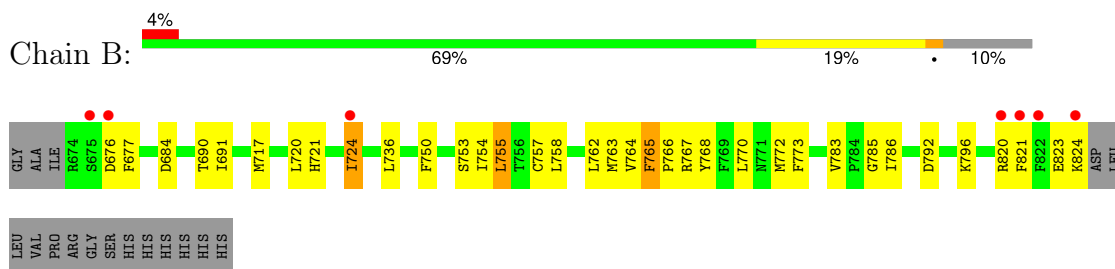
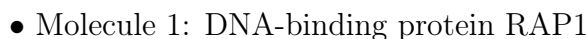
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	130	Total	O	0	0
			130	130		
4	B	172	Total	O	0	0
			172	172		

i

- Molecule 1: DNA-binding protein RAP1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.01Å 47.98Å 72.56Å 90.00° 94.23° 90.00°	Depositor
Resolution (Å)	50.00 – 1.85 50.00 – 1.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-1.85) 99.5 (50.00-1.85)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.29 (at 1.85Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.175 , 0.199 0.182 , 0.193	Depositor DCC
$R_{free}$ test set	1426 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.9	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 53.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2814	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.39% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, MES

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	0.32	0/1263	0.54	0/1696
1	B	0.35	0/1253	0.57	0/1685
All	All	0.33	0/2516	0.56	0/3381

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	A	1237	0	1193	25	0
1	B	1227	0	1171	31	0
2	A	16	0	28	1	0
2	B	8	0	14	2	0
3	B	24	0	25	0	0
4	A	130	0	0	1	0
4	B	172	0	0	1	0
All	All	2814	0	2431	58	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 12.



The worst 5 of 58 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:A:697:ILE:HD11	1:A:778:ASN:HB2	1.31	1.12
1:A:686:ILE:HD12	1:A:774:LYS:HD3	1.44	0.95
1:A:729:GLU:HG2	1:A:730:PRO:HD2	1.51	0.92
2:B:4002:MPD:HM3	2:B:4002:MPD:O4	1.73	0.88
1:B:753:SER:HB3	2:B:4002:MPD:H12	1.56	0.88

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	149/168 (89%)	147 (99%)	1 (1%)	1 (1%)	19	8
1	B	149/168 (89%)	147 (99%)	2 (1%)	0	100	100
All	All	298/336 (89%)	294 (99%)	3 (1%)	1 (0%)	37	25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	730	PRO

### 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	142/151 (94%)	138 (97%)	4 (3%)	38	24
1	B	140/151 (93%)	134 (96%)	6 (4%)	25	10
All	All	282/302 (93%)	272 (96%)	10 (4%)	31	16

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	757	CYS
1	B	765	PHE
1	B	821	PHE
1	A	821	PHE
1	B	676	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	778	ASN
1	A	802	GLN
1	B	800	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](#)

5 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
3	MES	B	3440	-	12,12,12	1.94	4 (33%)	15,16,16	2.44	5 (33%)
2	MPD	B	4002	-	7,7,7	1.39	1 (14%)	9,10,10	4.26	6 (66%)
3	MES	B	3441	-	12,12,12	1.22	1 (8%)	15,16,16	0.93	1 (6%)
2	MPD	A	4001	-	7,7,7	0.56	0	9,10,10	0.57	0
2	MPD	A	4003	-	7,7,7	1.14	1 (14%)	9,10,10	4.22	5 (55%)

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
3	MES	B	3440	-	-	0/6/14/14	0/1/1/1
2	MPD	B	4002	-	-	1/5/5/5	-
3	MES	B	3441	-	-	0/6/14/14	0/1/1/1
2	MPD	A	4001	-	-	0/5/5/5	-
2	MPD	A	4003	-	-	0/5/5/5	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	3440	MES	C3-N4	3.59	1.56	1.46
3	B	3440	MES	C7-N4	-3.41	1.39	1.47
3	B	3440	MES	C5-N4	3.34	1.55	1.46
3	B	3441	MES	C8-S	3.29	1.82	1.77
2	B	4002	MPD	C3-C2	2.95	1.62	1.54

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4002	MPD	O2-C2-C3	-7.86	79.86	109.27
2	A	4003	MPD	O2-C2-C3	-7.23	82.23	109.27
2	A	4003	MPD	CM-C2-C3	-6.41	82.53	110.20
2	B	4002	MPD	C1-C2-C3	-6.14	83.72	110.20
2	B	4002	MPD	O2-C2-C1	5.56	125.32	107.99

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	4002	MPD	O2-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	4002	MPD	2	0
2	A	4003	MPD	1	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, 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	146/168 (86%)	-0.03	5 (3%)	48	51	11, 19, 53, 69	0
1	B	146/168 (86%)	-0.16	7 (4%)	36	39	9, 16, 37, 61	0
All	All	292/336 (86%)	-0.09	12 (4%)	42	44	9, 17, 48, 69	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	676	ASP	4.4
1	B	822	PHE	4.3
1	B	821	PHE	3.5
1	A	728	TYR	2.9
1	A	821	PHE	2.8

### 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, 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( $\text{\AA}^2$ )	Q<0.9
2	MPD	B	4002	8/8	0.68	0.21	35,37,41,44	0
2	MPD	A	4003	8/8	0.73	0.18	41,42,43,44	0
2	MPD	A	4001	8/8	0.86	0.12	23,26,29,30	0
3	MES	B	3441	12/12	0.97	0.07	12,16,19,19	0
3	MES	B	3440	12/12	0.98	0.06	9,13,16,16	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.