



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4OR9 / pdb_00004or9
Title : Crystal structure of human calcineurin
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Deposited on : 2014-02-11
Resolution : 2.23 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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	:	4-5-2 with Phenix2.0
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

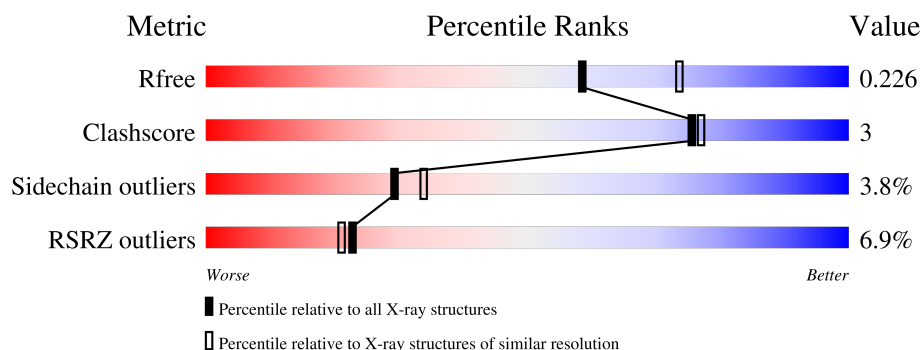
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

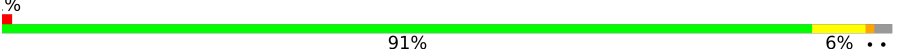
The reported resolution of this entry is 2.23 Å.

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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	544	
2	B	170	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4855 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 Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	5	0
			3274	2105	551	597	21			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P16298
A	-18	GLY	-	expression tag	UNP P16298
A	-17	SER	-	expression tag	UNP P16298
A	-16	SER	-	expression tag	UNP P16298
A	-15	HIS	-	expression tag	UNP P16298
A	-14	HIS	-	expression tag	UNP P16298
A	-13	HIS	-	expression tag	UNP P16298
A	-12	HIS	-	expression tag	UNP P16298
A	-11	HIS	-	expression tag	UNP P16298
A	-10	HIS	-	expression tag	UNP P16298
A	-9	SER	-	expression tag	UNP P16298
A	-8	SER	-	expression tag	UNP P16298
A	-7	GLY	-	expression tag	UNP P16298
A	-6	LEU	-	expression tag	UNP P16298
A	-5	VAL	-	expression tag	UNP P16298
A	-4	PRO	-	expression tag	UNP P16298
A	-3	ARG	-	expression tag	UNP P16298
A	-2	GLY	-	expression tag	UNP P16298
A	-1	SER	-	expression tag	UNP P16298
A	0	HIS	-	expression tag	UNP P16298

- Molecule 2 is a protein called Calcineurin subunit B type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	166	Total	C	N	O	S	0	0	0
			1324	836	219	261	8			

- Molecule 3 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Fe	0	0
			1	1		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	4	Total	Ca	0	0
			4	4		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	197	Total	O	0	0
			197	197		
6	B	54	Total	O	0	0
			54	54		

4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	110.87Å 110.87Å 282.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.78 – 2.23 47.78 – 2.23	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.78-2.23) 99.8 (47.78-2.23)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.95 (at 2.22Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.183 , 0.215 (Not available) , 0.226	Depositor DCC
R_{free} test set	2586 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	40.8	Xtriage
Anisotropy	0.623	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4855	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, ZN, FE

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	0.48	0/3373	0.81	5/4577 (0.1%)
2	B	0.45	0/1343	0.75	0/1797
All	All	0.47	0/4716	0.79	5/6374 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	492	MET	CA-C-N	7.74	125.31	119.66
1	A	492	MET	C-N-CA	7.74	125.31	119.66
1	A	234	GLY	CA-C-N	6.53	125.76	118.97
1	A	234	GLY	C-N-CA	6.53	125.76	118.97
1	A	19	PRO	O-C-N	5.08	123.64	121.31

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	3274	0	3192	23	0
2	B	1324	0	1304	7	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	4	0	0	0	0
6	A	197	0	0	3	0
6	B	54	0	0	1	0
All	All	4855	0	4496	27	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 3.

All (27) 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:86:THR:HG22	1:A:226:ARG:HH11	1.41	0.84
1:A:164[A]:HIS:HD2	1:A:492:MET:HE2	1.54	0.73
1:A:358:VAL:HB	2:B:115:LEU:HD21	1.77	0.67
1:A:275:CYS:SG	6:A:821:HOH:O	2.53	0.65
2:B:115:LEU:HD23	2:B:128:LEU:HD11	1.83	0.60
1:A:121:ARG:NH2	6:A:849:HOH:O	2.33	0.60
1:A:86:THR:HG22	1:A:226:ARG:NH1	2.16	0.59
1:A:385:GLU:HA	2:B:24:LYS:HD2	1.87	0.55
1:A:256:HIS:HD2	6:A:852:HOH:O	1.92	0.53
1:A:40:SER:N	1:A:69:ILE:HD11	2.23	0.52
1:A:39:THR:C	1:A:69:ILE:HD11	2.34	0.52
1:A:302:LYS:HD2	1:A:307:GLY:O	2.10	0.52
1:A:86:THR:HB	1:A:226:ARG:HD3	1.90	0.52
1:A:421:VAL:HG12	1:A:422:LEU:H	1.78	0.48
1:A:419:PHE:HB3	2:B:118:MET:O	2.13	0.48
1:A:357:ASP:OD2	1:A:359:PHE:HB2	2.15	0.47
1:A:270:ASN:CG	1:A:272:PRO:HD2	2.42	0.45
1:A:212:SER:HB2	1:A:238:ASP:HB2	1.99	0.44
1:A:241:TRP:CZ2	1:A:492:MET:HE3	2.53	0.44
1:A:77:GLY:HA3	1:A:143:TRP:CD1	2.53	0.43
2:B:84:LYS:NZ	6:B:324:HOH:O	2.52	0.43
1:A:32:PHE:HA	1:A:33:PRO:HD3	1.93	0.42
2:B:160:ASP:HA	2:B:162:HIS:CE1	2.55	0.42
1:A:129:VAL:O	1:A:130:ASP:HB2	2.19	0.41
2:B:47:GLU:CD	2:B:47:GLU:H	2.27	0.41
1:A:312:ILE:HD13	1:A:338:MET:HE1	2.01	0.41
1:A:164[A]:HIS:NE2	1:A:493:PRO:O	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

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	
1	A	363/470 (77%)	348 (96%)	15 (4%)	27	30
2	B	148/151 (98%)	143 (97%)	5 (3%)	32	38
All	All	511/621 (82%)	491 (96%)	20 (4%)	29	33

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	ARG
1	A	86	THR
1	A	91	GLU
1	A	165	LEU
1	A	167[A]	GLU
1	A	167[B]	GLU
1	A	251	GLU
1	A	288	ARG
1	A	383	ASP
1	A	386	LEU
1	A	417	ARG
1	A	418	VAL
1	A	421	VAL
1	A	422	LEU
1	A	485	LEU
2	B	9	GLU
2	B	36	SER
2	B	37	LEU
2	B	47	GLU
2	B	166	VAL

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	344	ASN
2	B	55	GLN
2	B	121	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	399/544 (73%)	0.15	38 (9%) 14 12	22, 45, 108, 166	5 (1%)
2	B	166/170 (97%)	0.10	1 (0%) 85 87	35, 54, 79, 111	0
All	All	565/714 (79%)	0.14	39 (6%) 23 21	22, 47, 97, 166	5 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	418	VAL	12.0
1	A	416	ALA	9.4
1	A	422	LEU	6.9
1	A	15	PRO	6.6
2	B	4	ALA	5.7
1	A	387	MET	5.1
1	A	385	GLU	4.9
1	A	386	LEU	4.8
1	A	485	LEU	4.7
1	A	421	VAL	4.6
1	A	488	ILE	4.5
1	A	491	ARG	4.1
1	A	495	ARG	3.8
1	A	419	PHE	3.8
1	A	423	ARG	3.8
1	A	417	ARG	3.6
1	A	383	ASP	3.6
1	A	492	MET	3.5
1	A	494	PRO	3.5
1	A	484	GLY	3.2
1	A	490	GLU	2.8
1	A	478	SER	2.6
1	A	35	THR	2.6
1	A	482	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	17	PRO	2.5
1	A	21	PRO	2.5
1	A	305	THR	2.5
1	A	22	GLY	2.5
1	A	479	PHE	2.4
1	A	16	PRO	2.4
1	A	420	SER	2.4
1	A	486	ASP	2.3
1	A	487	ARG	2.2
1	A	254	GLN	2.2
1	A	252	LYS	2.1
1	A	83	ARG	2.1
1	A	489	ASN	2.1
1	A	384	ASP	2.0
1	A	483	LYS	2.0

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](#)

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($\text{\AA}^2$)	Q<0.9
3	FE	A	601	1/1	0.86	0.23	248,248,248,248	0
4	ZN	A	602	1/1	0.86	0.22	290,290,290,290	0
5	CA	B	202	1/1	0.89	0.22	111,111,111,111	0
5	CA	B	204	1/1	0.92	0.15	65,65,65,65	0
5	CA	B	201	1/1	0.96	0.18	79,79,79,79	0
5	CA	B	203	1/1	0.97	0.12	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.