



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 06:46 PM UTC

PDB ID : 3EK7 / pdb_00003ek7
Title : Calcium-saturated GCaMP2 dimer
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Deposited on : 2008-09-18
Resolution : 1.85 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	FAILED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

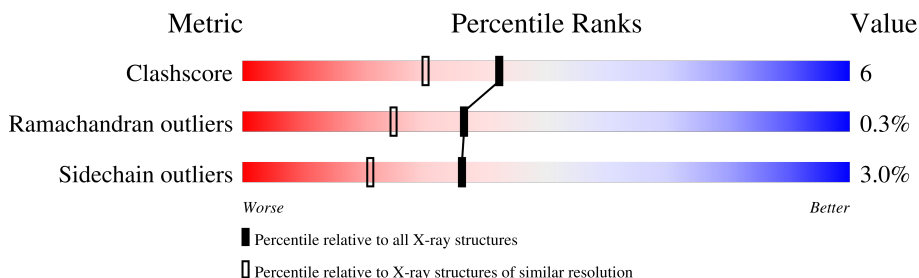
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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))
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (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 ≥ 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 $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	449	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3333 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 Myosin light chain kinase, Green fluorescent protein, Calmodulin chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	4	0
			3131	1966	526	623	16			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	76	ALA	VAL	see remark 999	UNP P42212
A	88	GLY	SER	see remark 999	UNP P42212
A	93	TYR	ASP	see remark 999	UNP P42212
A	119	LYS	ALA	see remark 999	UNP P42212
A	144	LEU	HIS	see remark 999	UNP P42212
A	152	GLY	-	linker	UNP P42212
A	153	GLY	-	linker	UNP P42212
A	154	THR	-	linker	UNP P42212
A	155	GLY	-	linker	UNP P42212
A	156	GLY	-	linker	UNP P42212
A	157	SER	-	linker	UNP P42212
A	158	MET	-	linker	UNP P42212
A	159	VAL	-	linker	UNP P42212
A	222	LEU	PHE	see remark 999	UNP P42212
A	224	CRO	SER	chromophore	UNP P42212
A	?	-	TYR	chromophore	UNP P42212
A	?	-	GLY	chromophore	UNP P42212
A	251	ILE	VAL	see remark 999	UNP P42212
A	303	THR	-	linker	UNP P42212
A	304	ARG	-	linker	UNP P42212

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

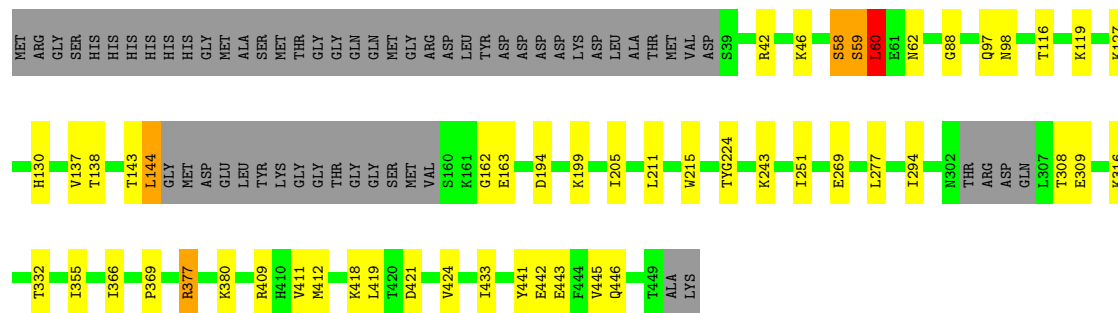
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Ca	0	0
			4	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	198	Total 198	O 198	0	0

Note EDS failed to run properly.

- Molecule 1: Myosin light chain kinase, Green fluorescent protein, Calmodulin chimera



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	126.13Å 47.31Å 68.94Å 90.00° 100.48° 90.00°	Depositor
Resolution (Å)	20.67 – 1.85	Depositor
% Data completeness (in resolution range)	98.5 (20.67-1.85)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.26 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.189 , 0.241	Depositor
Wilson B-factor (Å ²)	21.6	Xtriage
Anisotropy	0.329	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3333	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.56% 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: CA, CRO

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	1.05	4/3165 (0.1%)	0.99	3/4259 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	366	ILE	CA-CB	6.58	1.61	1.54
1	A	62	ASN	CG-OD1	6.07	1.35	1.23
1	A	446	GLN	CD-OE1	5.69	1.34	1.23
1	A	97	GLN	CD-OE1	5.08	1.33	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	LEU	N-CA-C	-7.38	96.02	108.26
1	A	88	GLY	N-CA-C	-6.05	105.87	112.04
1	A	58	SER	N-CA-C	5.05	117.68	111.82

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	3131	0	3034	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	4	0	0	0	0
3	A	198	0	0	4	1
All	All	3333	0	3034	39	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 6.

All (39) 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:409:ARG:HG3	1:A:424:VAL:HG21	1.51	0.89
1:A:194:ASP:OD2	3:A:611:HOH:O	1.95	0.84
1:A:143:THR:HG23	1:A:144:LEU:HD12	1.62	0.81
1:A:163:GLU:HG3	3:A:527:HOH:O	1.88	0.73
1:A:412:MET:HE1	1:A:419:LEU:HD11	1.71	0.71
1:A:409:ARG:HD3	1:A:421:ASP:OD2	1.95	0.67
1:A:116[A]:THR:HG22	1:A:137:VAL:HG22	1.78	0.65
1:A:412:MET:CE	1:A:419:LEU:HD11	2.30	0.61
1:A:130:HIS:HB3	1:A:205:ILE:HD13	1.82	0.60
1:A:59[B]:SER:C	1:A:60:LEU:HD12	2.28	0.58
1:A:418:LYS:O	1:A:419:LEU:HD23	2.07	0.55
1:A:58:SER:O	1:A:60:LEU:CD1	2.55	0.55
1:A:251:ILE:HD12	1:A:269:GLU:HG2	1.87	0.55
1:A:59[A]:SER:C	1:A:60:LEU:HD12	2.31	0.54
1:A:377:ARG:O	1:A:377:ARG:CG	2.55	0.54
1:A:138:THR:HG21	1:A:369:PRO:HG2	1.90	0.53
1:A:60:LEU:HD12	1:A:60:LEU:N	2.23	0.53
1:A:251:ILE:CD1	1:A:269:GLU:HG2	2.39	0.52
1:A:433:ILE:HD12	1:A:443:GLU:HG2	1.93	0.51
1:A:294:ILE:N	1:A:294:ILE:HD12	2.26	0.50
1:A:442:GLU:H	1:A:442:GLU:CD	2.20	0.50
1:A:130:HIS:CB	1:A:205:ILE:HD13	2.41	0.49
1:A:143:THR:O	1:A:144:LEU:HB2	2.11	0.49
1:A:60:LEU:CD1	1:A:60:LEU:N	2.77	0.48
1:A:211:LEU:HD22	1:A:215:TRP:CE2	2.49	0.47
1:A:441:TYR:CZ	1:A:445:VAL:HG21	2.49	0.47
1:A:441:TYR:CZ	1:A:445:VAL:CG2	3.00	0.45
1:A:130:HIS:HB3	1:A:205:ILE:CD1	2.47	0.45
1:A:163:GLU:CG	3:A:527:HOH:O	2.57	0.44
1:A:377:ARG:O	1:A:377:ARG:HG3	2.17	0.44
1:A:332:THR:CG2	1:A:355:ILE:HD12	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:LEU:C	1:A:277:LEU:HD13	2.44	0.43
1:A:162:GLY:HA3	1:A:243:LYS:O	2.19	0.42
1:A:411:VAL:HG23	3:A:580:HOH:O	2.19	0.42
1:A:58:SER:C	1:A:60:LEU:HD12	2.44	0.42
1:A:138:THR:CG2	1:A:369:PRO:HG2	2.49	0.41
1:A:442:GLU:CD	1:A:442:GLU:N	2.79	0.41
1:A:98:ASN:HA	1:A:251:ILE:O	2.22	0.40
1:A:199:LYS:HD2	1:A:316:LYS:NZ	2.35	0.40

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:627:HOH:O	3:A:643:HOH:O[1_545]	1.76	0.44

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	385/449 (86%)	380 (99%)	4 (1%)	1 (0%)	36	25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	377	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	340/382 (89%)	329 (97%)	11 (3%)	34	19

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	ARG
1	A	46	LYS
1	A	59[A]	SER
1	A	59[B]	SER
1	A	60	LEU
1	A	119	LYS
1	A	127	LYS
1	A	144	LEU
1	A	308	THR
1	A	309	GLU
1	A	380	LYS

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

Mol	Chain	Res	Type
1	A	77	ASN
1	A	279	ASN
1	A	293	ASN
1	A	345	ASN
1	A	438	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	CRO	A	224	1	22,23,24	3.28	5 (22%)	30,32,34	2.61	8 (26%)

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	CRO	A	224	1	-	1/12/31/32	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	224	CRO	CB2-CA2	12.65	1.47	1.35
1	A	224	CRO	CA2-C2	-5.44	1.42	1.48
1	A	224	CRO	C1-N2	4.01	1.38	1.32
1	A	224	CRO	C2-N3	-3.76	1.31	1.40
1	A	224	CRO	O2-C2	2.83	1.28	1.23

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	224	CRO	O2-C2-CA2	-9.33	125.06	131.02
1	A	224	CRO	CA2-C2-N3	6.39	108.87	103.50
1	A	224	CRO	C2-N3-C1	-3.62	106.39	108.07
1	A	224	CRO	C1-CA1-N1	-3.18	104.09	109.78
1	A	224	CRO	CA2-N2-C1	-2.92	103.52	105.80
1	A	224	CRO	CE1-CD1-CG2	-2.84	117.55	121.22
1	A	224	CRO	OG1-CB1-CA1	2.38	114.07	109.00
1	A	224	CRO	CD2-CG2-CD1	2.10	120.77	117.65

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	224	CRO	N3-C1-CA1-CB1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 [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

6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.