

# wwPDB X-ray Structure Validation Summary Report (i)

Sep 3, 2023 – 02:31 PM EDT

PDB ID : 3SG3

Title : Crystal Structure of GCaMP3-D380Y

Authors : Schreiter, E.R.; Akerboom, J.; Looger, L.L.

Deposited on : 2011-06-14

Resolution : 2.10 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.35

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

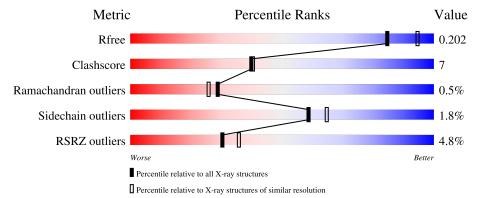
Validation Pipeline (wwPDB-VP) : 2.35

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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		
			4%		
1	A	449	71%	16%	12%



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3470 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-1 chimera.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	395	Total 3187	C 2005	N 533	O 635	S 14	0	7	0

There are 67 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q6LDG3
A	1	ARG	-	expression tag	UNP Q6LDG3
A	2	GLY	-	expression tag	UNP Q6LDG3
A	3	SER		expression tag	UNP Q6LDG3
A	4	HIS	-	expression tag	UNP Q6LDG3
A	5	HIS	-	expression tag	UNP Q6LDG3
A	6	HIS	-	expression tag	UNP Q6LDG3
A	7	HIS	-	expression tag	UNP Q6LDG3
A	8	HIS	-	expression tag	UNP Q6LDG3
A	9	HIS	-	expression tag	UNP Q6LDG3
A	10	GLY	-	expression tag	UNP Q6LDG3
A	11	MET	-	expression tag	UNP Q6LDG3
A	12	ALA	-	expression tag	UNP Q6LDG3
A	13	SER	-	expression tag	UNP Q6LDG3
A	14	MET	-	expression tag	UNP Q6LDG3
A	15	THR	-	expression tag	UNP Q6LDG3
A	16	GLY	-	expression tag	UNP Q6LDG3
A	17	GLY	-	expression tag	UNP Q6LDG3
A	18	GLN	-	expression tag	UNP Q6LDG3
A	19	GLN	-	expression tag	UNP Q6LDG3
A	20	MET	-	expression tag	UNP Q6LDG3
A	21	GLY	-	expression tag	UNP Q6LDG3
A	22	ARG	-	expression tag	UNP Q6LDG3
A	23	ASP	-	expression tag	UNP Q6LDG3
A	24	LEU	-	expression tag	UNP Q6LDG3
A	25	TYR	-	expression tag	UNP Q6LDG3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	26	ASP	-	expression tag	UNP Q6LDG3
A	27	ASP	-	expression tag	UNP Q6LDG3
A	28	ASP	-	expression tag	UNP Q6LDG3
A	29	ASP	-	expression tag	UNP Q6LDG3
A	30	LYS	-	expression tag	UNP Q6LDG3
A	31	ASP	-	expression tag	UNP Q6LDG3
A	32	LEU	-	expression tag	UNP Q6LDG3
A	33	ALA	-	expression tag	UNP Q6LDG3
A	34	THR	-	expression tag	UNP Q6LDG3
A	35	MET	-	expression tag	UNP Q6LDG3
A	36	VAL	_	expression tag	UNP Q6LDG3
A	37	ASP	-	expression tag	UNP Q6LDG3
A	38	SER	-	expression tag	UNP Q6LDG3
A	39	SER	_	expression tag	UNP Q6LDG3
A	44	ASN	GLN	engineered mutation	UNP Q6LDG3
A	59	LEU	-	linker	UNP Q6LDG3
A	60	GLU	-	linker	UNP Q6LDG3
A	65	LYS	MET	engineered mutation	UNP P42212
A	75	ALA	VAL	engineered mutation	UNP P42212
A	87	GLY	SER	engineered mutation	UNP P42212
A	92	TYR	ASP	engineered mutation	UNP P42212
A	115	VAL	THR	engineered mutation	UNP P42212
A	118	LYS	ALA	engineered mutation	UNP P42212
A	143	LEU	HIS	engineered mutation	UNP P42212
A	151	GLY	-	linker	UNP P42212
A	152	GLY	-	linker	UNP P42212
A	153	THR	-	linker	UNP P42212
A	154	GLY	-	linker	UNP P42212
A	155	GLY	-	linker	UNP P42212
A	156	SER	-	linker	UNP P42212
A	157	MET	-	linker	UNP P42212
A	158	VAL	-	linker	UNP P42212
A	221	LEU	PHE	engineered mutation	UNP P42212
A	?	-	SER	deletion	UNP P42212
A	?	-	TYR	deletion	UNP P42212
A	223	CRO	GLY	chromophore	UNP P42212
A	250	ILE	VAL	engineered mutation	UNP P42212
A	302	THR	-	linker	UNP P42212
A	303	ARG	-	linker	UNP P42212
A	362	ASP	ASN	engineered mutation	UNP P0DP29
A	380	TYR	ASP	engineered mutation	UNP P0DP29

 $\bullet$  Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).



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

### • Molecule 3 is water.

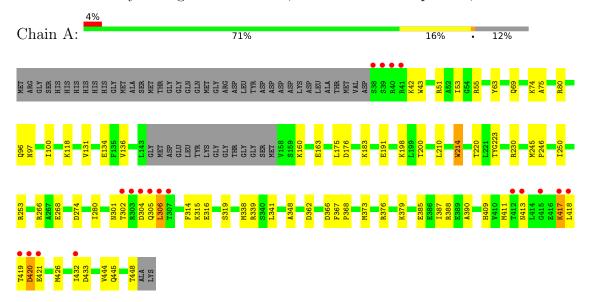
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	279	Total O 279 279	0	0



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





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	120.44Å 120.44Å 98.00Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.80 - 2.10	Depositor
rtesolution (A)	19.80 - 2.10	EDS
% Data completeness	99.8 (19.80-2.10)	Depositor
(in resolution range)	100.0 (19.80-2.10)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$< I/\sigma(I) > 1$	2.97 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.6.0111	Depositor
P. P.	0.165 , 0.199	Depositor
$R, R_{free}$	0.172 , $0.202$	DCC
$R_{free}$ test set	2177 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.0	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.39, 54.2	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3470	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: CRO, CA

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).

Mal	Chain	Bo	nd lengths	Bond angles		
MIOI	$ig  \operatorname{Mol} ig  \operatorname{Chain} ig _{\mathbb{R}}$		# Z  > 5	RMSZ	# Z >5	
1	A	1.33	$15/3241 \ (0.5\%)$	1.07	$14/4366 \ (0.3\%)$	

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$\operatorname{Ideal}( ext{\AA})$
1	A	319	SER	CB-OG	10.68	1.56	1.42
1	A	348	ALA	CA-CB	8.17	1.69	1.52
1	A	191	GLU	CG-CD	6.46	1.61	1.51
1	A	385	GLU	CG-CD	6.22	1.61	1.51
1	A	390	ALA	CA-CB	5.96	1.65	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
1	A	376	ARG	NE-CZ-NH1	-8.46	116.07	120.30
1	A	362	ASP	CB-CG-OD1	7.53	125.08	118.30
1	A	266	ARG	NE-CZ-NH2	-6.33	117.14	120.30
1	A	339	ARG	NE-CZ-NH2	-6.21	117.19	120.30
1	A	253	ARG	NE-CZ-NH1	6.16	123.38	120.30

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	3187	0	3103	46	0
2	A	4	0	0	0	0
3	A	279	0	0	4	0
All	All	3470	0	3103	46	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 7.

The worst 5 of 46 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:A:250:ILE:CD1	1:A:268[B]:GLU:HG2	2.17	0.75
1:A:175[A]:LEU:HD23	1:A:176:ASP:N	2.03	0.74
1:A:96[A]:GLN:HG2	3:A:701:HOH:O	1.88	0.72
1:A:409:HIS:CE1	1:A:413:ASN:ND2	2.58	0.72
1:A:96[A]:GLN:CG	3:A:701:HOH:O	2.38	0.71

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	395/449 (88%)	380 (96%)	13 (3%)	2 (0%)	29 26

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	305	GLN
1	A	420	ASP



#### 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	Analysed Rotameric		Percentiles	
1	A	348/382 (91%)	342 (98%)	6 (2%)	60 67	

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\operatorname{Res}$	Type
1	A	316	GLU
1	A	417	LYS
1	A	448	THR
1	A	301	ASN
1	A	160	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	44	ASN
1	A	343	GLN
1	A	409	HIS
1	A	413	ASN
1	A	445	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)

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		
WIOI	туре	Chain	rtes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	CRO	A	223	1	23,23,24	4.32	4 (17%)	30,32,34	1.59	6 (20%)

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.

$\mathbf{Mol}$	Type	Chain	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
1	CRO	A	223	1	-	0/12/31/32	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
1	A	223	CRO	CB2-CA2	18.52	1.50	1.35
1	A	223	CRO	CA2-C2	-6.08	1.42	1.48
1	A	223	CRO	O2-C2	4.67	1.32	1.23
1	A	223	CRO	C2-N3	-3.35	1.32	1.39

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

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	223	CRO	C2-N3-C1	3.96	109.97	107.97
1	A	223	CRO	CA2-N2-C1	-3.57	103.14	105.77
1	A	223	CRO	C2-CA2-N2	3.27	111.22	108.93
1	A	223	CRO	CB2-CA2-N2	-3.20	124.38	128.83
1	A	223	CRO	O3-C3-CA3	-2.24	119.64	126.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 5.5 Carbohydrates (i)

There are no monosaccharides 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 (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,  $95^{th}$  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>	# RSRZ > 2		$OWAB(A^2)$	Q<0.9
1	A	394/449 (87%)	-0.21	19 (4%)	30 36	15, 26, 74, 111	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	305	GLN	7.5
1	A	417	LYS	6.1
1	A	303	ARG	4.9
1	A	304	ASP	4.0
1	A	306	LEU	3.9

## 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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	CRO	A	223	22/23	0.98	0.07	14,18,20,21	0

### 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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	CA	A	454	1/1	0.97	0.03	45,45,45,45	0
2	CA	A	453	1/1	0.98	0.04	41,41,41,41	0
2	CA	A	451	1/1	1.00	0.05	17,17,17,17	0
2	CA	A	452	1/1	1.00	0.06	20,20,20,20	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

