



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:27 PM UTC

PDB ID : 7PGF / pdb\_00007pgf  
Title : Calcium-selective Sp1 channel pore domain only  
Authors : Lolicato, M.; Arrigoni, C.  
Deposited on : 2021-08-13  
Resolution : 3.50 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](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

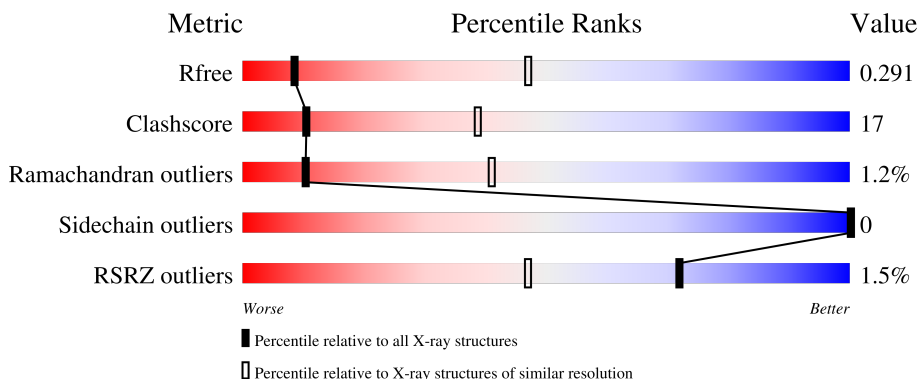
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	C	138	
1	D	138	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2031 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 Ion transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	130	1008	666	158	178	6	0	0	0
1	D	134	1023	674	157	186	6	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	176	ASP	GLU	engineered mutation	UNP A0A7Y7EFG5
C	177	ASP	SER	engineered mutation	UNP A0A7Y7EFG5
C	180	ASP	MET	engineered mutation	UNP A0A7Y7EFG5
D	176	ASP	GLU	engineered mutation	UNP A0A7Y7EFG5
D	177	ASP	SER	engineered mutation	UNP A0A7Y7EFG5
D	180	ASP	MET	engineered mutation	UNP A0A7Y7EFG5



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.68Å 133.68Å 130.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	14.93 – 3.50 14.93 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (14.93-3.50) 97.2 (14.93-3.50)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.61 (at 3.53Å)	Xtrriage
Refinement program	REFMAC 5.8.0, PHENIX 1.17.1_3660	Depositor
R, $R_{free}$	0.265 , 0.290 0.274 , 0.291	Depositor DCC
$R_{free}$ test set	420 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	134.6	Xtrriage
Anisotropy	0.220	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 108.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2031	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	153.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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	C	0.49	3/1032 (0.3%)	0.83	5/1408 (0.4%)
1	D	0.47	3/1048 (0.3%)	0.83	4/1433 (0.3%)
All	All	0.48	6/2080 (0.3%)	0.83	9/2841 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	3
1	D	0	2
All	All	0	5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	210	ASN	CG-ND2	-8.61	1.15	1.33
1	C	210	ASN	CG-ND2	-8.10	1.16	1.33
1	C	210	ASN	CG-OD1	-6.86	1.10	1.23
1	D	210	ASN	CG-OD1	-6.86	1.10	1.23
1	C	218	ASN	CG-OD1	-6.45	1.11	1.23
1	D	218	ASN	CG-OD1	-5.64	1.12	1.23

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	121	GLY	CA-C-N	10.18	140.02	121.70
1	D	121	GLY	C-N-CA	10.18	140.02	121.70
1	C	242	ARG	CB-CG-CD	8.58	131.04	111.30
1	C	121	GLY	CA-C-N	7.57	136.01	121.54
1	C	121	GLY	C-N-CA	7.57	136.01	121.54
1	C	242	ARG	CA-CB-CG	7.55	129.20	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	148	THR	OG1-CB-CG2	-6.19	96.92	109.30
1	D	158	TRP	CA-CB-CG	5.64	124.32	113.60
1	C	158	TRP	CA-CB-CG	5.53	124.10	113.60

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	121	GLY	Peptide
1	C	158	TRP	Peptide
1	C	218	ASN	Sidechain
1	D	158	TRP	Peptide
1	D	218	ASN	Sidechain

## 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	C	1008	0	992	36	1
1	D	1023	0	991	41	1
All	All	2031	0	1983	68	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 17.

All (68) 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:VAL:HG21	1:D:195:LEU:HD22	1.49	0.91
1:D:175:LEU:O	1:D:177:ASP:N	2.18	0.76
1:D:176:ASP:O	1:D:178:TRP:N	2.21	0.72
1:C:249:ARG:O	1:C:253:LEU:HD23	1.90	0.72
1:D:187:MET:HE1	1:D:194:TRP:HD1	1.59	0.68
1:D:148:THR:HG22	1:D:152:ALA:HB2	1.75	0.68
1:C:187:MET:HE1	1:C:194:TRP:HD1	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:176:ASP:N	1:C:176:ASP:OD1	2.29	0.64
1:C:233:ASP:HA	1:C:236:ARG:HB2	1.83	0.61
1:D:169:LEU:HD13	1:D:200:PHE:HE2	1.65	0.61
1:D:123:ILE:O	1:D:127:PRO:HD2	2.01	0.61
1:D:179:SER:HA	1:D:182:ILE:HG22	1.84	0.59
1:C:169:LEU:HD13	1:C:200:PHE:HE2	1.67	0.59
1:D:233:ASP:HA	1:D:236:ARG:HB2	1.83	0.59
1:C:123:ILE:O	1:C:127:PRO:HD2	2.02	0.58
1:C:151:PHE:HE2	1:C:196:PHE:HD2	1.51	0.57
1:D:171:GLN:HG3	1:D:176:ASP:OD2	2.06	0.55
1:D:151:PHE:HE2	1:D:196:PHE:HD2	1.53	0.55
1:D:187:MET:HE1	1:D:194:TRP:CD1	2.42	0.55
1:C:221:GLN:HE22	1:D:221:GLN:NE2	2.05	0.54
1:C:151:PHE:HE2	1:C:196:PHE:CD2	2.25	0.53
1:D:151:PHE:HE2	1:D:196:PHE:CD2	2.27	0.53
1:D:144:ALA:O	1:D:148:THR:OG1	2.22	0.53
1:C:202:MET:HE2	1:D:199:PRO:HB3	1.91	0.53
1:C:187:MET:HE1	1:C:194:TRP:CD1	2.44	0.52
1:D:169:LEU:HD13	1:D:200:PHE:CE2	2.45	0.51
1:C:169:LEU:HD13	1:C:200:PHE:CE2	2.46	0.50
1:D:157:ASP:O	1:D:164:LEU:HD21	2.12	0.50
1:D:179:SER:O	1:D:182:ILE:HG22	2.13	0.49
1:C:142:ILE:O	1:C:146:ILE:HD12	2.13	0.49
1:C:157:ASP:O	1:C:164:LEU:HD21	2.13	0.48
1:C:217:VAL:HG11	1:D:214:GLY:C	2.38	0.48
1:C:135:LEU:O	1:C:139:ILE:HG22	2.13	0.48
1:D:142:ILE:O	1:D:146:ILE:HD12	2.14	0.48
1:C:217:VAL:HG13	1:D:215:LEU:HD23	1.95	0.47
1:D:135:LEU:O	1:D:139:ILE:HG22	2.13	0.47
1:C:145:VAL:O	1:C:149:LYS:N	2.41	0.47
1:D:199:PRO:O	1:D:203:ILE:HG12	2.15	0.47
1:C:199:PRO:O	1:C:203:ILE:HG12	2.16	0.46
1:D:136:MET:O	1:D:140:PHE:HB2	2.16	0.46
1:C:242:ARG:HG3	1:D:243:LEU:HB3	1.98	0.46
1:C:194:TRP:CZ3	1:D:194:TRP:HH2	2.34	0.46
1:D:126:LEU:HB3	1:D:127:PRO:HD3	1.98	0.46
1:C:136:MET:O	1:C:140:PHE:HB2	2.16	0.46
1:C:184:ARG:HD2	1:C:184:ARG:HA	1.66	0.46
1:C:150:LEU:HD11	1:C:151:PHE:CE2	2.51	0.45
1:C:126:LEU:HB3	1:C:127:PRO:HD3	1.97	0.45
1:C:182:ILE:HG23	1:C:183:VAL:HG23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:244:GLU:O	1:D:248:GLN:HB2	2.17	0.44
1:D:228:ASP:HA	1:D:231:ARG:HH11	1.83	0.44
1:C:182:ILE:HG23	1:C:183:VAL:N	2.33	0.43
1:D:138:ILE:O	1:D:142:ILE:HG13	2.18	0.43
1:C:228:ASP:HA	1:C:231:ARG:HH11	1.83	0.42
1:D:182:ILE:HG23	1:D:183:VAL:HG23	2.01	0.42
1:C:194:TRP:CH2	1:D:194:TRP:HH2	2.37	0.42
1:C:138:ILE:O	1:C:142:ILE:HG13	2.20	0.42
1:C:158:TRP:O	1:C:159:PHE:HD1	2.02	0.42
1:D:150:LEU:HD11	1:D:151:PHE:CE2	2.55	0.41
1:D:208:VAL:O	1:D:212:LEU:HG	2.20	0.41
1:C:209:VAL:O	1:C:213:VAL:HG23	2.19	0.41
1:C:221:GLN:OE1	1:D:218:ASN:ND2	2.53	0.41
1:D:209:VAL:O	1:D:213:VAL:HG23	2.20	0.41
1:D:176:ASP:C	1:D:178:TRP:H	2.23	0.41
1:C:247:ASP:OD1	1:C:251:ASN:OD1	2.37	0.41
1:D:169:LEU:O	1:D:173:MET:HG2	2.20	0.41
1:C:208:VAL:O	1:C:212:LEU:HG	2.20	0.41
1:D:161:ASP:OD1	1:D:161:ASP:C	2.64	0.41
1:D:158:TRP:O	1:D:159:PHE:HD1	2.03	0.41

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)
1:C:249:ARG:NH2	1:D:153:ALA:O[7_455]	2.19	0.01

## 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	C	126/138 (91%)	116 (92%)	9 (7%)	1 (1%)	16 49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	132/138 (96%)	122 (92%)	8 (6%)	2 (2%)	8	37
All	All	258/276 (94%)	238 (92%)	17 (7%)	3 (1%)	10	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	176	ASP
1	C	122	PHE
1	D	177	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	Rotameric	Outliers	Percentiles	
1	C	103/115 (90%)	103 (100%)	0	100	100
1	D	104/115 (90%)	104 (100%)	0	100	100
All	All	207/230 (90%)	207 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	D	210	ASN
1	D	218	ASN
1	D	221	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](#)

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	C	130/138 (94%)	-0.25	2 (1%) 72 47	99, 149, 218, 263	0
1	D	134/138 (97%)	-0.07	2 (1%) 72 47	97, 148, 224, 281	0
All	All	264/276 (95%)	-0.16	4 (1%) 72 47	97, 149, 222, 281	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	160	GLY	3.0
1	C	160	GLY	2.3
1	D	248	GLN	2.3
1	C	124	THR	2.2

### 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.