



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:55 PM UTC

PDB ID : 3WKV / pdb_00003wkv
Title : Voltage-gated proton channel: VSOP/Hv1 chimeric channel
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Deposited on : 2013-10-31
Resolution : 3.45 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

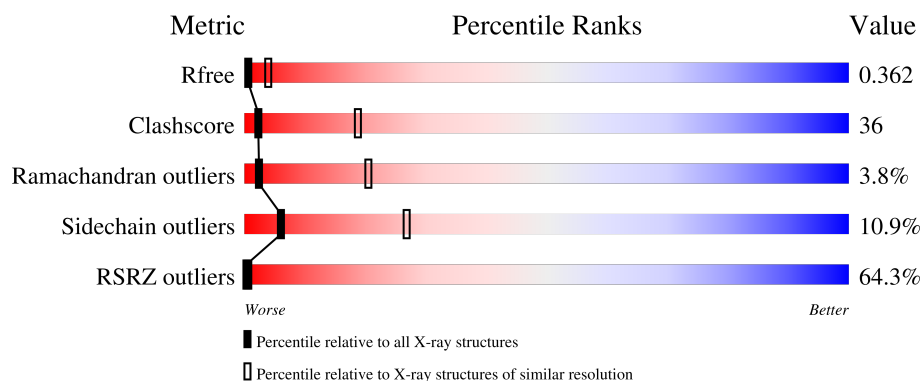
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 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	1070 (3.50-3.42)
Clashscore	190562	1128 (3.50-3.42)
Ramachandran outliers	187476	1101 (3.50-3.42)
Sidechain outliers	187428	1102 (3.50-3.42)
RSRZ outliers	180081	1070 (3.50-3.42)

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	196	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1085 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.

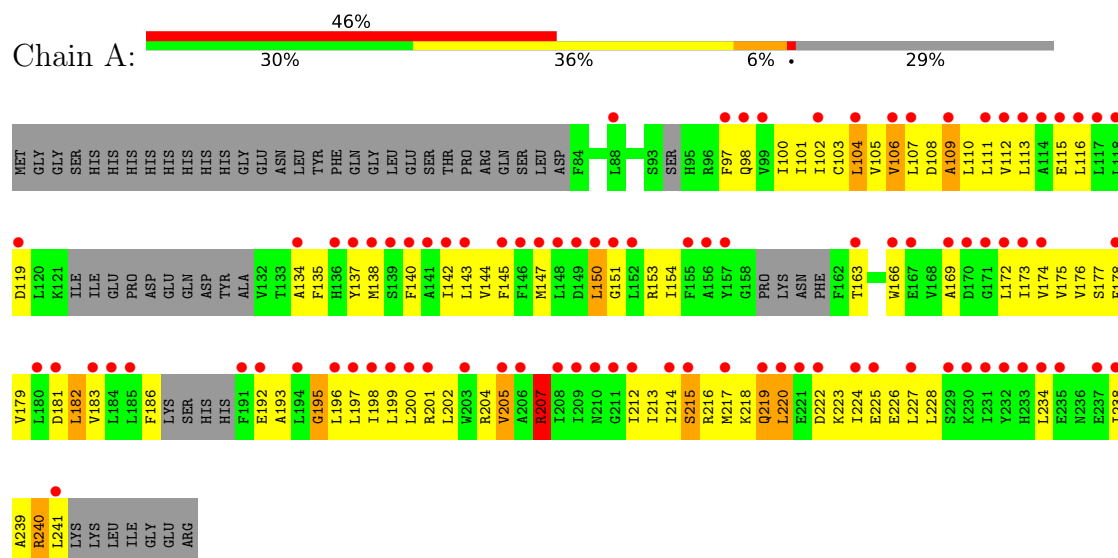
- Molecule 1 is a protein called Ion channel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	140	Total	C	N	O	S	0	0	0
			1085	726	177	178	4			

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: Ion channel



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	86.54Å 86.54Å 89.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.33 – 3.45 28.33 – 3.45	Depositor EDS
% Data completeness (in resolution range)	98.9 (28.33-3.45) 99.1 (28.33-3.45)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.341 , 0.357 0.341 , 0.362	Depositor DCC
R_{free} test set	232 reflections (4.57%)	wwPDB-VP
Wilson B-factor (Å ²)	166.0	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 242.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.095 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	1085	wwPDB-VP
Average B, all atoms (Å ²)	196.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.70% 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](#)

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	0.65	0/1099	1.04	2/1489 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	135	PHE	N-CA-C	-5.91	104.84	111.28
1	A	207	ARG	N-CA-C	-5.20	105.15	112.12

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	1085	0	1114	79	0
All	All	1085	0	1114	79	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 36.

All (79) 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:109:ALA:HA	1:A:201:ARG:HH21	1.27	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:GLY:HA2	1:A:198:ILE:HD12	1.70	0.74
1:A:217:MET:HA	1:A:220:LEU:HD23	1.69	0.74
1:A:201:ARG:HB3	1:A:204:ARG:HH21	1.52	0.74
1:A:105:VAL:HG22	1:A:204:ARG:NH1	2.06	0.71
1:A:215:SER:OG	1:A:216:ARG:N	2.24	0.69
1:A:101:ILE:O	1:A:105:VAL:HG23	1.95	0.67
1:A:197:LEU:HA	1:A:200:LEU:HD12	1.78	0.65
1:A:198:ILE:HA	1:A:201:ARG:NH1	2.11	0.65
1:A:214:ILE:HA	1:A:217:MET:HG2	1.79	0.65
1:A:179:VAL:O	1:A:182:LEU:HG	1.97	0.64
1:A:98:GLN:O	1:A:102:ILE:HG13	1.99	0.63
1:A:97:PHE:HA	1:A:100:ILE:HD12	1.79	0.63
1:A:201:ARG:HB3	1:A:204:ARG:NH2	2.14	0.63
1:A:142:ILE:O	1:A:145:PHE:HB2	2.00	0.62
1:A:163:THR:OG1	1:A:166:TRP:NE1	2.33	0.61
1:A:178:PHE:HZ	1:A:204:ARG:HB2	1.64	0.61
1:A:196:LEU:O	1:A:199:LEU:HG	2.01	0.59
1:A:199:LEU:HA	1:A:202:LEU:HD12	1.83	0.59
1:A:101:ILE:HA	1:A:104:LEU:HG	1.84	0.59
1:A:193:ALA:O	1:A:196:LEU:HB2	2.02	0.59
1:A:109:ALA:HA	1:A:201:ARG:NH2	2.10	0.58
1:A:216:ARG:O	1:A:220:LEU:N	2.21	0.57
1:A:105:VAL:HG22	1:A:204:ARG:HH11	1.69	0.56
1:A:198:ILE:HA	1:A:201:ARG:HH12	1.69	0.56
1:A:195:GLY:CA	1:A:198:ILE:HD12	2.34	0.56
1:A:205:VAL:C	1:A:207:ARG:H	2.13	0.55
1:A:172:LEU:O	1:A:176:VAL:HG13	2.06	0.55
1:A:175:VAL:O	1:A:179:VAL:HG13	2.07	0.55
1:A:183:VAL:O	1:A:186:PHE:HD2	1.91	0.54
1:A:213:ILE:HB	1:A:217:MET:HE2	1.90	0.54
1:A:178:PHE:HA	1:A:181:ASP:HB2	1.90	0.53
1:A:216:ARG:O	1:A:220:LEU:HB3	2.08	0.53
1:A:108:ASP:OD1	1:A:109:ALA:N	2.41	0.53
1:A:108:ASP:HA	1:A:111:LEU:HB2	1.90	0.52
1:A:113:LEU:O	1:A:116:LEU:HG	2.08	0.52
1:A:178:PHE:CZ	1:A:204:ARG:HB2	2.43	0.52
1:A:97:PHE:O	1:A:101:ILE:HG23	2.10	0.52
1:A:109:ALA:CA	1:A:201:ARG:HH21	2.10	0.52
1:A:201:ARG:O	1:A:204:ARG:HB3	2.10	0.52
1:A:169:ALA:O	1:A:173:ILE:HG13	2.10	0.51
1:A:176:VAL:HA	1:A:179:VAL:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:ILE:O	1:A:177:SER:OG	2.25	0.51
1:A:140:PHE:O	1:A:144:VAL:HG23	2.10	0.51
1:A:112:VAL:O	1:A:115:GLU:HB3	2.11	0.51
1:A:138:MET:HE3	1:A:142:ILE:HD11	1.91	0.51
1:A:150:LEU:HG	1:A:151:GLY:N	2.26	0.51
1:A:218:LYS:NZ	1:A:222:ASP:OD1	2.39	0.50
1:A:105:VAL:HG13	1:A:204:ARG:CZ	2.41	0.49
1:A:225:GLU:C	1:A:227:LEU:H	2.20	0.49
1:A:116:LEU:HA	1:A:119:ASP:HB2	1.94	0.49
1:A:143:LEU:O	1:A:147:MET:HG2	2.13	0.48
1:A:154:ILE:HD13	1:A:154:ILE:HA	1.75	0.47
1:A:102:ILE:O	1:A:106:VAL:HG13	2.15	0.46
1:A:153:ARG:HD3	1:A:153:ARG:HA	1.65	0.46
1:A:110:LEU:HA	1:A:113:LEU:HG	1.98	0.46
1:A:174:VAL:O	1:A:177:SER:HB2	2.16	0.45
1:A:107:LEU:HA	1:A:110:LEU:HG	1.98	0.45
1:A:204:ARG:HD2	1:A:205:VAL:N	2.31	0.45
1:A:214:ILE:O	1:A:217:MET:HB2	2.17	0.45
1:A:239:ALA:HA	1:A:241:LEU:N	2.33	0.44
1:A:215:SER:O	1:A:216:ARG:C	2.60	0.43
1:A:220:LEU:HA	1:A:223:LYS:HE2	2.01	0.43
1:A:103:CYS:O	1:A:106:VAL:HG22	2.18	0.43
1:A:113:LEU:HA	1:A:116:LEU:HD21	2.00	0.43
1:A:199:LEU:HA	1:A:202:LEU:CG	2.49	0.43
1:A:199:LEU:HA	1:A:202:LEU:HB2	2.00	0.43
1:A:205:VAL:O	1:A:207:ARG:N	2.53	0.42
1:A:239:ALA:HA	1:A:240:ARG:C	2.45	0.42
1:A:112:VAL:CG2	1:A:143:LEU:HD11	2.49	0.42
1:A:207:ARG:HD2	1:A:207:ARG:HA	1.65	0.42
1:A:199:LEU:HA	1:A:202:LEU:CD1	2.48	0.42
1:A:134:ALA:O	1:A:137:TYR:HB3	2.19	0.41
1:A:197:LEU:O	1:A:200:LEU:HB2	2.20	0.41
1:A:234:LEU:O	1:A:238:ILE:HG13	2.20	0.41
1:A:105:VAL:CG2	1:A:204:ARG:HD3	2.50	0.41
1:A:176:VAL:O	1:A:179:VAL:HG22	2.21	0.41
1:A:240:ARG:HD3	1:A:240:ARG:HA	1.59	0.41
1:A:219:GLN:HG2	1:A:220:LEU:N	2.31	0.41

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	130/196 (66%)	109 (84%)	16 (12%)	5 (4%)	2	20

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	VAL
1	A	226	GLU
1	A	109	ALA
1	A	215	SER
1	A	195	GLY

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	110/176 (62%)	98 (89%)	12 (11%)	6	27

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	LEU
1	A	106	VAL
1	A	150	LEU
1	A	182	LEU
1	A	192	GLU
1	A	207	ARG

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Mol	Chain	Res	Type
1	A	212	ILE
1	A	219	GLN
1	A	220	LEU
1	A	224	ILE
1	A	228	LEU
1	A	240	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

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	140/196 (71%)	3.08	90 (64%) 0 0	71, 199, 293, 380	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	LEU	11.3
1	A	235	GLU	9.5
1	A	241	LEU	8.9
1	A	237	GLU	8.3
1	A	233	HIS	8.0
1	A	149	ASP	7.8
1	A	98	GLN	7.5
1	A	171	GLY	7.2
1	A	184	LEU	7.2
1	A	238	ILE	6.9
1	A	147	MET	6.8
1	A	197	LEU	6.6
1	A	229	SER	6.3
1	A	180	LEU	6.2
1	A	225	GLU	6.0
1	A	200	LEU	5.9
1	A	194	LEU	5.7
1	A	140	PHE	5.6
1	A	214	ILE	5.6
1	A	196	LEU	5.5
1	A	114	ALA	5.2
1	A	205	VAL	4.8
1	A	107	LEU	4.7
1	A	111	LEU	4.7
1	A	211	GLY	4.7
1	A	137	TYR	4.7
1	A	201	ARG	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	116	LEU	4.6
1	A	183	VAL	4.6
1	A	212	ILE	4.4
1	A	115	GLU	4.4
1	A	198	ILE	4.4
1	A	203	TRP	4.3
1	A	112	VAL	4.3
1	A	224	ILE	4.3
1	A	163	THR	4.2
1	A	88	LEU	4.0
1	A	143	LEU	4.0
1	A	230	LYS	4.0
1	A	219	GLN	4.0
1	A	145	PHE	4.0
1	A	170	ASP	3.9
1	A	220	LEU	3.9
1	A	221	GLU	3.9
1	A	173	ILE	3.9
1	A	142	ILE	3.9
1	A	119	ASP	3.8
1	A	117	LEU	3.8
1	A	150	LEU	3.7
1	A	134	ALA	3.7
1	A	113	LEU	3.7
1	A	104	LEU	3.6
1	A	181	ASP	3.6
1	A	109	ALA	3.3
1	A	138	MET	3.3
1	A	106	VAL	3.3
1	A	231	ILE	3.3
1	A	215	SER	3.2
1	A	152	LEU	3.2
1	A	192	GLU	3.1
1	A	169	ALA	3.1
1	A	210	ASN	3.1
1	A	139	SER	3.1
1	A	136	HIS	3.0
1	A	209	ILE	3.0
1	A	217	MET	3.0
1	A	172	LEU	2.9
1	A	99	VAL	2.9
1	A	185	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	157	TYR	2.6
1	A	178	PHE	2.6
1	A	97	PHE	2.6
1	A	174	VAL	2.6
1	A	191	PHE	2.6
1	A	151	GLY	2.5
1	A	118	LEU	2.5
1	A	227	LEU	2.4
1	A	206	ALA	2.4
1	A	146	PHE	2.3
1	A	155	PHE	2.3
1	A	199	LEU	2.3
1	A	166	TRP	2.2
1	A	141	ALA	2.2
1	A	167	GLU	2.2
1	A	102	ILE	2.2
1	A	208	ILE	2.2
1	A	222	ASP	2.1
1	A	148	LEU	2.1
1	A	232	TYR	2.1
1	A	156	ALA	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.