Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2024 – 01:17 AM EDT

PDB ID	:	6ERY
Title	:	The crystal structure of mouse chloride intracellular channel protein 6
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Deposited on	:	2017-10-19
Resolution	:	1.79 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:

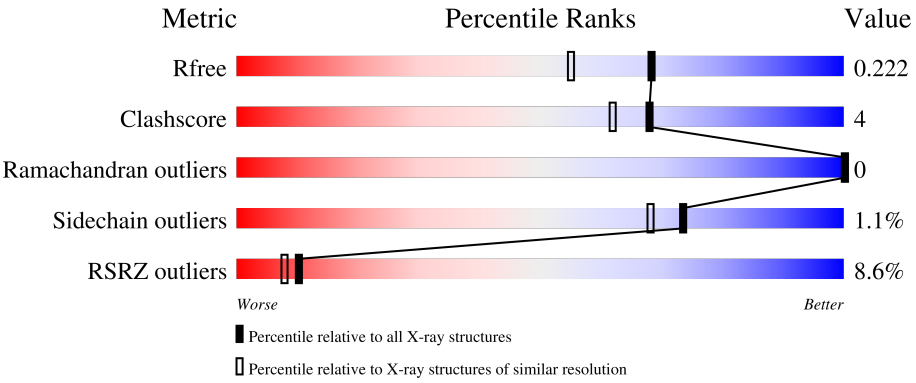
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.79 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}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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
1	A	238	9% 90% 8% .
1	B	238	8% 88% 8% .

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3871 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.

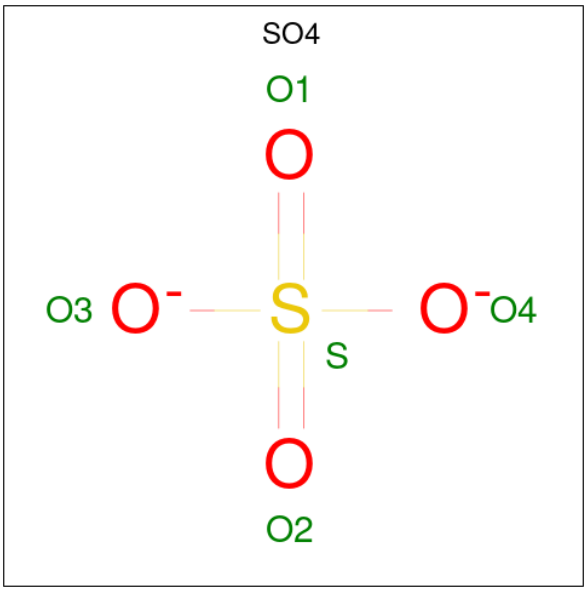
- Molecule 1 is a protein called Chloride intracellular channel protein 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	230	Total	C	N	O	S	0	0	0
			1754	1124	285	338	7			
1	A	234	Total	C	N	O	S	0	1	0
			1794	1154	292	342	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	359	GLY	-	expression tag	UNP Q8BHB9
B	360	ALA	-	expression tag	UNP Q8BHB9
B	361	MET	-	expression tag	UNP Q8BHB9
B	362	GLY	-	expression tag	UNP Q8BHB9
A	359	GLY	-	expression tag	UNP Q8BHB9
A	360	ALA	-	expression tag	UNP Q8BHB9
A	361	MET	-	expression tag	UNP Q8BHB9
A	362	GLY	-	expression tag	UNP Q8BHB9

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0

- Molecule 3 is water.

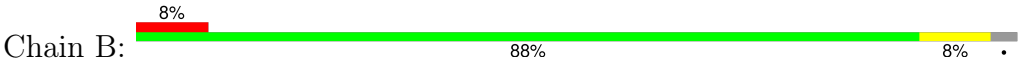
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	143	Total O 143 143	0	0
3	A	165	Total O 165 165	0	0

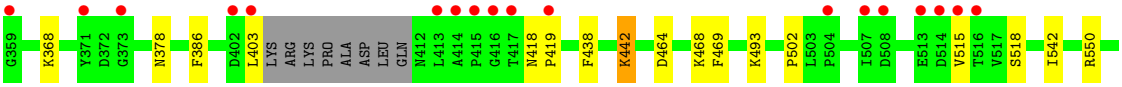
3 Residue-property plots (i)

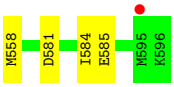
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Chloride intracellular channel protein 6

Chain B:

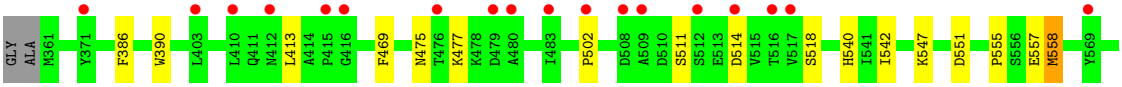


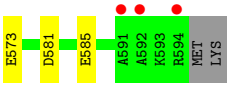




• Molecule 1: Chloride intracellular channel protein 6

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	42.62Å 68.99Å 80.98Å 90.00° 95.14° 90.00°	Depositor
Resolution (Å)	40.33 – 1.79 42.45 – 1.80	Depositor EDS
% Data completeness (in resolution range)	86.0 (40.33-1.79) 86.1 (42.45-1.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.00 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.181 , 0.220 0.184 , 0.222	Depositor DCC
R_{free} test set	1884 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	28.7	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 46.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3871	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.39	0/1839	0.57	1/2504 (0.0%)
1	B	0.39	0/1794	0.55	0/2441
All	All	0.39	0/3633	0.56	1/4945 (0.0%)

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	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	558	MET	CG-SD-CE	6.41	110.45	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	418	ASN	Peptide

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	1794	0	1694	13	0
1	B	1754	0	1639	13	0
2	A	5	0	0	0	0
2	B	10	0	0	0	0
3	A	165	0	0	4	1
3	B	143	0	0	5	0
All	All	3871	0	3333	26	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 4.

All (26) 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:557:GLU:OE1	3:A:701:HOH:O	1.93	0.87
1:B:515:VAL:O	3:B:702:HOH:O	2.10	0.69
1:A:511:SER:O	3:A:702:HOH:O	2.13	0.66
1:B:493:LYS:HA	1:B:558:MET:HE2	1.79	0.63
1:B:469:PHE:CG	1:B:542:ILE:HG12	2.42	0.54
1:A:390:TRP:CD1	1:A:573:GLU:HG3	2.45	0.52
1:B:378:ASN:HD22	1:B:584:ILE:HG12	1.74	0.52
1:B:550:ARG:NH2	3:B:701:HOH:O	1.96	0.52
1:A:502:PRO:HA	1:A:518:SER:HB2	1.92	0.52
1:B:438:PHE:CZ	1:B:442:LYS:HG3	2.45	0.52
1:A:547:LYS:NZ	1:A:551:ASP:OD2	2.41	0.52
1:A:555:PRO:HD2	1:A:558:MET:HE3	1.91	0.52
1:A:555:PRO:HD2	1:A:558:MET:CE	2.41	0.51
1:B:502:PRO:HA	1:B:518:SER:HB2	1.93	0.51
1:A:581:ASP:O	1:A:585:GLU:HG3	2.13	0.47
1:A:469:PHE:CG	1:A:542:ILE:HG12	2.51	0.46
3:B:704:HOH:O	1:A:540:HIS:HE1	2.00	0.44
1:B:493:LYS:CA	1:B:558:MET:HE2	2.47	0.44
1:B:464:ASP:O	1:B:468:LYS:HG2	2.18	0.43
1:A:413:LEU:HA	3:A:717:HOH:O	2.18	0.43
1:A:514:ASP:HB2	3:A:702:HOH:O	2.17	0.43
1:B:368:LYS:CG	1:B:419:PRO:HG2	2.49	0.43
1:B:550:ARG:NE	3:B:701:HOH:O	2.52	0.42
1:B:378:ASN:ND2	3:B:711:HOH:O	2.53	0.42
1:A:475:ASN:ND2	1:A:477:LYS:H	2.19	0.41
1:B:581:ASP:O	1:B:585:GLU:HG3	2.21	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:785:HOH:O	3:A:823:HOH:O[2_556]	1.40	0.80

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	233/238 (98%)	230 (99%)	3 (1%)	0	100	100
1	B	226/238 (95%)	222 (98%)	4 (2%)	0	100	100
All	All	459/476 (96%)	452 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	182/208 (88%)	181 (100%)	1 (0%)	88	87
1	B	178/208 (86%)	175 (98%)	3 (2%)	60	51
All	All	360/416 (86%)	356 (99%)	4 (1%)	73	68

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	386	PHE
1	B	403	LEU
1	B	442	LYS
1	A	386	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	378	ASN
1	B	383	GLN
1	B	576	ASN
1	A	475	ASN
1	A	540	HIS
1	A	576	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

3 ligands are 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	$\#\|Z\|>2$
2	SO4	B	601	-	4,4,4	0.24	0	6,6,6	0.16	0
2	SO4	A	601	-	4,4,4	0.26	0	6,6,6	0.10	0
2	SO4	B	602	-	4,4,4	0.25	0	6,6,6	0.11	0

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, 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>2			OWAB(Å^2)	Q<0.9
1	A	234/238 (98%)	0.53	21 (8%)	9	7	20, 36, 70, 88	0
1	B	230/238 (96%)	0.55	19 (8%)	11	8	20, 36, 68, 97	0
All	All	464/476 (97%)	0.54	40 (8%)	10	8	20, 36, 70, 97	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	415	PRO	12.0
1	A	592	ALA	6.7
1	A	415	PRO	6.6
1	B	403	LEU	5.5
1	A	591	ALA	5.4
1	B	371	TYR	4.9
1	B	416	GLY	4.4
1	B	417	THR	4.4
1	B	419	PRO	4.3
1	B	413	LEU	4.2
1	A	476	THR	4.2
1	A	594	ARG	4.1
1	A	509	ALA	3.8
1	B	402	ASP	3.7
1	B	414	ALA	3.7
1	A	483	ILE	3.5
1	B	515	VAL	3.4
1	B	516	THR	3.2
1	A	416	GLY	3.2
1	B	514	ASP	3.1
1	A	517	VAL	3.0
1	A	410	LEU	2.8
1	A	480	ALA	2.7
1	A	371	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	502	PRO	2.7
1	B	595	MET	2.6
1	A	403	LEU	2.6
1	A	514	ASP	2.5
1	A	512	SER	2.4
1	B	373	GLY	2.4
1	A	569	TYR	2.4
1	A	508	ASP	2.3
1	B	507	ILE	2.3
1	B	359	GLY	2.3
1	A	412	ASN	2.3
1	B	508	ASP	2.2
1	B	504	PRO	2.2
1	A	479	ASP	2.1
1	B	513	GLU	2.1
1	A	516	THR	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 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	B-factors(Å^2)	Q<0.9
2	SO4	A	601	5/5	0.68	0.38	154,155,157,159	0
2	SO4	B	602	5/5	0.70	0.25	114,114,117,122	0
2	SO4	B	601	5/5	0.82	0.34	125,126,128,129	0

6.5 Other polymers (i)

There are no such residues in this entry.