Full wwPDB X-ray Structure Validation Report (i)

Oct 18, 2023 – 04:17 AM EDT

PDB ID	:	2E4F
Title	:	Crystal Structure of the Cytoplasmic Domain of G-Protein-Gated Inward Rectifier Potassium Channel Kir3.2
Authors	:	Inanobe, A.; Kurachi, Y.
Deposited on	:	2006-12-06
Resolution	:	2.30 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 (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:

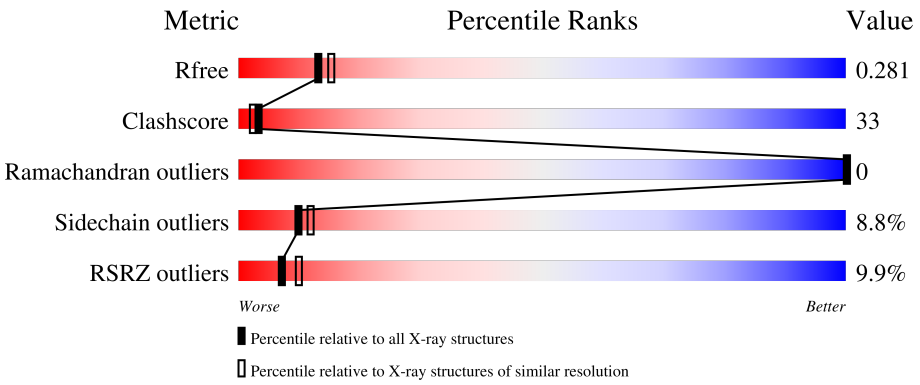
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	208	9% 52% 35% 5% 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1594 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 G protein-activated inward rectifier potassium channel 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	191	1485	946	253	279	7	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	GLY	-	cloning artifact	UNP P48542
A	50	SER	-	cloning artifact	UNP P48542
A	51	HIS	-	cloning artifact	UNP P48542
A	52	MET	-	cloning artifact	UNP P48542
A	260	THR	SER	SEE REMARK 999	UNP P48542
A	313	MET	ILE	SEE REMARK 999	UNP P48542
A	344	LEU	MET	SEE REMARK 999	UNP P48542

- Molecule 2 is water.

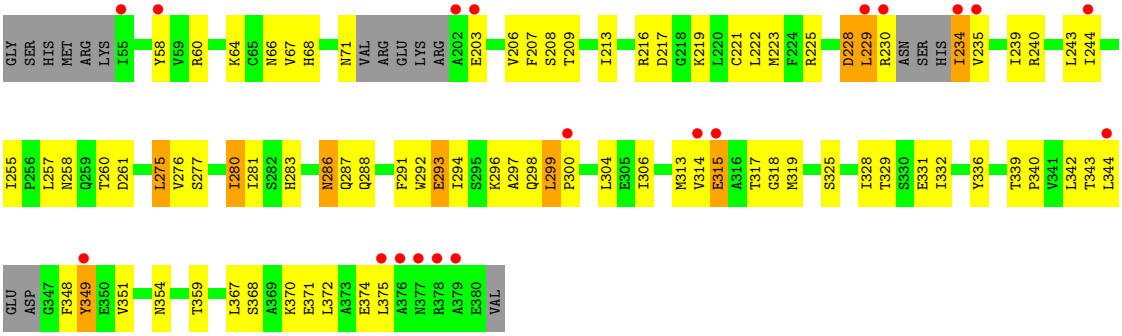
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	109	109	109	0	0

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: G protein-activated inward rectifier potassium channel 2

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α, β, γ	77.17Å 77.17Å 87.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.30 46.27 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.1 (10.00-2.30) 96.4 (46.27-2.30)	Depositor EDS
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.94 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.244 , 0.279 0.245 , 0.281	Depositor DCC
R_{free} test set	1262 reflections (10.33%)	wwPDB-VP
Wilson B-factor (Å^2)	39.0	Xtriage
Anisotropy	0.169	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 60.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	1594	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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 (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	0.42	0/1511	0.68	0/2044

There are no bond length outliers.

There are no bond angle outliers.

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	1485	0	1460	97	0
2	A	109	0	0	12	0
All	All	1594	0	1460	97	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 33.

All (97) 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:234:ILE:HG21	1:A:275:LEU:H	1.19	1.01
1:A:293:GLU:HG2	1:A:370:LYS:HD3	1.50	0.91
1:A:255:ILE:HG21	1:A:258:ASN:HB2	1.53	0.90
1:A:291:PHE:O	1:A:294:ILE:HG22	1.73	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ILE:CG2	1:A:275:LEU:H	1.85	0.89
1:A:234:ILE:HG12	1:A:234:ILE:O	1.73	0.86
1:A:297:ALA:O	1:A:300:PRO:HD2	1.76	0.85
1:A:228:ASP:HB3	1:A:230:ARG:H	1.42	0.84
1:A:234:ILE:HG21	1:A:275:LEU:N	1.94	0.80
1:A:315:GLU:HA	1:A:315:GLU:OE1	1.82	0.78
1:A:293:GLU:CG	1:A:370:LYS:HD3	2.15	0.77
1:A:292:TRP:HH2	2:A:420:HOH:O	1.70	0.75
1:A:223:MET:SD	1:A:280:ILE:HD11	2.28	0.73
1:A:222:LEU:HD21	1:A:306:ILE:HD13	1.69	0.72
1:A:255:ILE:CG2	1:A:258:ASN:HB2	2.22	0.69
1:A:58:TYR:HE2	1:A:276:VAL:HG11	1.57	0.69
1:A:343:THR:HG22	2:A:422:HOH:O	1.95	0.66
1:A:313:MET:HA	1:A:319:MET:O	1.94	0.66
1:A:299:LEU:HD21	1:A:332:ILE:HD11	1.77	0.65
1:A:304:LEU:HD11	2:A:459:HOH:O	1.97	0.64
1:A:209:THR:HG21	2:A:458:HOH:O	1.97	0.64
1:A:280:ILE:HG21	2:A:462:HOH:O	1.96	0.64
1:A:336:TYR:HD2	1:A:359:THR:HG1	1.43	0.64
1:A:276:VAL:HG13	1:A:277:SER:H	1.63	0.63
1:A:255:ILE:HG23	2:A:444:HOH:O	1.98	0.63
1:A:342:LEU:CD2	1:A:351:VAL:HG22	2.29	0.62
1:A:243:LEU:HB3	1:A:260:THR:OG1	1.98	0.62
1:A:342:LEU:HD21	1:A:351:VAL:HG22	1.82	0.61
1:A:207:PHE:CD1	1:A:325:SER:HB2	2.36	0.60
1:A:206:VAL:HG13	2:A:470:HOH:O	2.00	0.60
1:A:244:ILE:HG23	1:A:257:LEU:HG	1.85	0.59
1:A:286:ASN:HD22	1:A:286:ASN:C	2.06	0.59
1:A:208:SER:HB3	1:A:225:ARG:HB3	1.85	0.59
1:A:315:GLU:OE1	1:A:315:GLU:CA	2.51	0.58
1:A:240:ARG:HG3	2:A:443:HOH:O	2.04	0.57
1:A:276:VAL:HG13	1:A:277:SER:N	2.19	0.57
1:A:304:LEU:HD21	2:A:459:HOH:O	2.05	0.57
1:A:280:ILE:HG22	2:A:430:HOH:O	2.04	0.56
1:A:228:ASP:C	1:A:230:ARG:H	2.08	0.56
1:A:58:TYR:CE2	1:A:276:VAL:HG11	2.37	0.56
1:A:314:VAL:HG12	1:A:315:GLU:N	2.21	0.55
1:A:203:GLU:HG2	1:A:229:LEU:CD2	2.37	0.55
1:A:243:LEU:HD21	1:A:304:LEU:HD22	1.88	0.54
1:A:203:GLU:HG2	1:A:229:LEU:HD21	1.90	0.54
1:A:370:LYS:O	1:A:374:GLU:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:ASN:ND2	1:A:288:GLN:H	2.07	0.53
1:A:293:GLU:CD	1:A:298:GLN:HE22	2.11	0.53
1:A:58:TYR:OH	1:A:276:VAL:HG13	2.09	0.53
1:A:339:THR:HG23	1:A:340:PRO:HD2	1.92	0.52
1:A:339:THR:HG22	1:A:340:PRO:O	2.10	0.52
1:A:228:ASP:HB3	1:A:230:ARG:N	2.18	0.52
1:A:328:ILE:CG1	1:A:331:GLU:HG3	2.40	0.51
1:A:317:THR:HB	1:A:319:MET:HG2	1.93	0.51
1:A:371:GLU:O	1:A:375:LEU:HG	2.10	0.51
1:A:332:ILE:HG13	1:A:332:ILE:O	2.11	0.50
1:A:71:ASN:OD1	1:A:230:ARG:NH2	2.43	0.50
1:A:297:ALA:C	1:A:300:PRO:HD2	2.31	0.50
1:A:328:ILE:HG12	1:A:331:GLU:CD	2.33	0.49
1:A:317:THR:CB	1:A:319:MET:HG2	2.42	0.49
1:A:344:LEU:HD12	1:A:348:PHE:O	2.12	0.49
1:A:317:THR:OG1	1:A:319:MET:HG2	2.12	0.49
1:A:328:ILE:HG13	1:A:331:GLU:HG3	1.93	0.48
1:A:314:VAL:O	1:A:318:GLY:HA2	2.13	0.48
1:A:336:TYR:HD2	1:A:359:THR:OG1	1.97	0.48
1:A:372:LEU:C	1:A:372:LEU:HD23	2.34	0.48
1:A:313:MET:HB3	1:A:318:GLY:O	2.14	0.47
1:A:344:LEU:HA	1:A:348:PHE:O	2.14	0.47
1:A:58:TYR:OH	1:A:277:SER:HB3	2.14	0.47
1:A:296:LYS:O	1:A:300:PRO:HD3	2.15	0.47
1:A:222:LEU:HB3	1:A:283:HIS:HB3	1.97	0.47
1:A:344:LEU:HD22	1:A:349:TYR:CE2	2.50	0.47
1:A:206:VAL:CG1	2:A:470:HOH:O	2.63	0.46
1:A:304:LEU:C	1:A:304:LEU:HD12	2.36	0.46
1:A:291:PHE:CZ	1:A:306:ILE:HD11	2.51	0.46
1:A:368:SER:OG	1:A:371:GLU:HG3	2.16	0.46
1:A:58:TYR:HH	1:A:67:VAL:HG21	1.82	0.45
1:A:216:ARG:NH2	1:A:280:ILE:HD13	2.32	0.45
1:A:213:ILE:HA	1:A:221:CYS:O	2.17	0.45
1:A:314:VAL:HG12	1:A:315:GLU:H	1.82	0.45
1:A:243:LEU:C	1:A:243:LEU:HD13	2.38	0.44
1:A:217:ASP:O	1:A:219:LYS:HE2	2.17	0.44
1:A:228:ASP:C	1:A:230:ARG:N	2.66	0.44
1:A:234:ILE:O	1:A:234:ILE:CG1	2.48	0.44
1:A:255:ILE:HG21	1:A:258:ASN:CB	2.38	0.44
1:A:287:GLN:HA	1:A:292:TRP:CD2	2.53	0.43
1:A:244:ILE:HG23	1:A:257:LEU:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:PHE:HE1	1:A:304:LEU:HD21	1.82	0.43
1:A:294:ILE:HD11	1:A:299:LEU:HG	2.00	0.42
1:A:239:ILE:HD13	1:A:281:ILE:HG13	2.02	0.42
1:A:64:LYS:CD	2:A:486:HOH:O	2.68	0.41
1:A:294:ILE:O	1:A:294:ILE:HG23	2.20	0.41
1:A:60:ARG:HG2	1:A:66:ASN:HD21	1.86	0.41
1:A:58:TYR:OH	1:A:67:VAL:HG21	2.21	0.41
1:A:344:LEU:HD22	1:A:349:TYR:HE2	1.86	0.41
1:A:372:LEU:HD23	1:A:372:LEU:O	2.21	0.40
1:A:235:VAL:HB	1:A:313:MET:HB2	2.02	0.40
1:A:354:ASN:OD1	1:A:354:ASN:C	2.60	0.40

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	183/208 (88%)	172 (94%)	11 (6%)	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	160/185 (86%)	146 (91%)	14 (9%)	10 12

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	HIS
1	A	228	ASP
1	A	229	LEU
1	A	234	ILE
1	A	261	ASP
1	A	275	LEU
1	A	280	ILE
1	A	286	ASN
1	A	293	GLU
1	A	299	LEU
1	A	315	GLU
1	A	329	THR
1	A	349	TYR
1	A	367	LEU

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

Mol	Chain	Res	Type
1	A	258	ASN
1	A	286	ASN
1	A	298	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 monosaccharides 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, 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	191/208 (91%)	0.44	19 (9%) 7 10	22, 41, 79, 93	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	ILE	5.5
1	A	378	ARG	4.2
1	A	235	VAL	4.1
1	A	230	ARG	3.9
1	A	376	ALA	3.9
1	A	300	PRO	3.7
1	A	349	TYR	3.6
1	A	377	ASN	3.3
1	A	379	ALA	3.3
1	A	315	GLU	3.2
1	A	58	TYR	3.1
1	A	344	LEU	2.7
1	A	55	ILE	2.7
1	A	202	ALA	2.4
1	A	229	LEU	2.4
1	A	203	GLU	2.3
1	A	244	ILE	2.2
1	A	375	LEU	2.1
1	A	314	VAL	2.1

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.