



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 09:04 PM UTC

PDB ID : 4BW5 / pdb_00004bw5
Title : Crystal structure of human two pore domain potassium ion channel TREK2 (K2P10.1)
Authors : Pike, A.C.W.; Dong, Y.Y.; Dong, L.; Quigley, A.; Shrestha, L.; Mukhopadhyay, S.; Strain-Damerell, C.; Goubin, S.; Grieben, M.; Shintre, C.A.; Mackenzie, A.; Vollmar, M.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Burgess-Brown, N.; Carpenter, E.P.
Deposited on : 2013-06-30
Resolution : 3.20 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
Mogul	:	2022.3.0, CSD as543be (2022)
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)

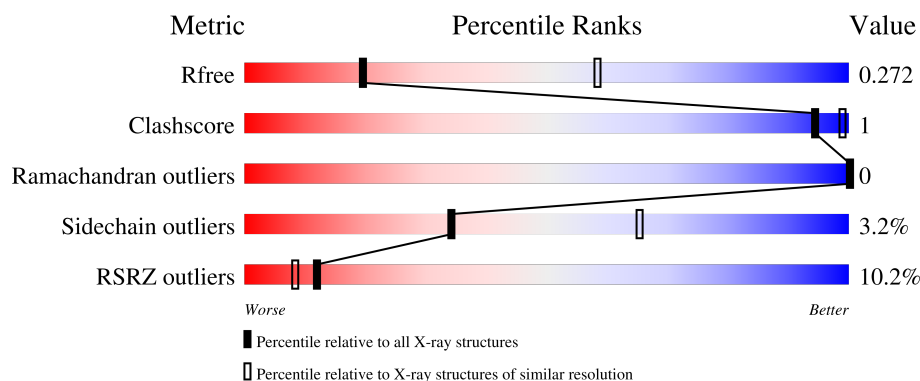
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	282	7% 83% 5% 12%
1	B	282	5% 84% 6% 10%
1	C	282	11% 79% . 17%
1	D	282	13% 83% 5% 11%

Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7235 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 POTASSIUM CHANNEL SUBFAMILY K MEMBER 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	0	0
			1824	1215	283	322	4			
1	B	254	Total	C	N	O	S	0	0	0
			1862	1245	285	328	4			
1	C	233	Total	C	N	O	S	0	0	0
			1690	1128	257	301	4			
1	D	250	Total	C	N	O	S	0	0	0
			1827	1215	284	324	4			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	MET	-	expression tag	UNP P57789
A	341	ALA	-	expression tag	UNP P57789
A	342	GLU	-	expression tag	UNP P57789
A	343	ASN	-	expression tag	UNP P57789
A	344	LEU	-	expression tag	UNP P57789
A	345	TYR	-	expression tag	UNP P57789
A	346	PHE	-	expression tag	UNP P57789
A	347	GLN	-	expression tag	UNP P57789
B	66	MET	-	expression tag	UNP P57789
B	341	ALA	-	expression tag	UNP P57789
B	342	GLU	-	expression tag	UNP P57789
B	343	ASN	-	expression tag	UNP P57789
B	344	LEU	-	expression tag	UNP P57789
B	345	TYR	-	expression tag	UNP P57789
B	346	PHE	-	expression tag	UNP P57789
B	347	GLN	-	expression tag	UNP P57789
C	66	MET	-	expression tag	UNP P57789
C	341	ALA	-	expression tag	UNP P57789
C	342	GLU	-	expression tag	UNP P57789
C	343	ASN	-	expression tag	UNP P57789
C	344	LEU	-	expression tag	UNP P57789

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Chain	Residue	Modelled	Actual	Comment	Reference
C	345	TYR	-	expression tag	UNP P57789
C	346	PHE	-	expression tag	UNP P57789
C	347	GLN	-	expression tag	UNP P57789
D	66	MET	-	expression tag	UNP P57789
D	341	ALA	-	expression tag	UNP P57789
D	342	GLU	-	expression tag	UNP P57789
D	343	ASN	-	expression tag	UNP P57789
D	344	LEU	-	expression tag	UNP P57789
D	345	TYR	-	expression tag	UNP P57789
D	346	PHE	-	expression tag	UNP P57789
D	347	GLN	-	expression tag	UNP P57789

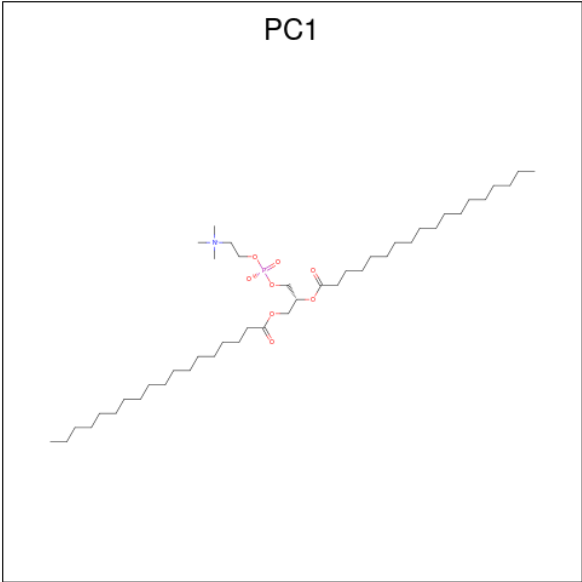
- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total K 4 4	0	0
2	C	4	Total K 4 4	0	0

- Molecule 3 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Cd 2 2	0	0

- Molecule 4 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).

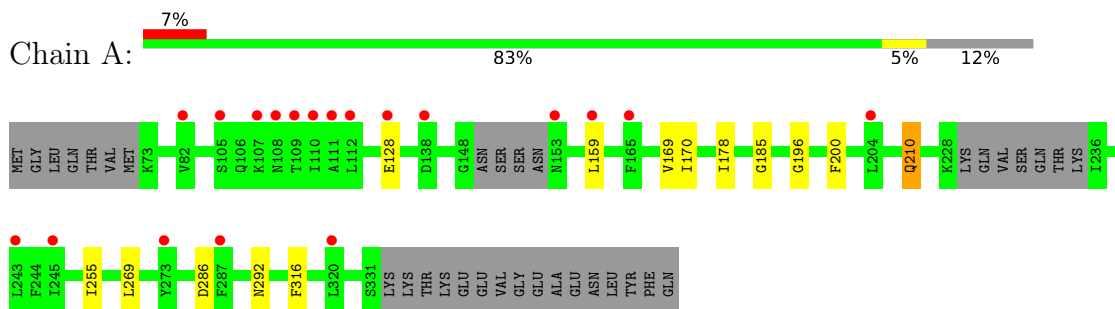


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	C	0	0
			11	11		
4	B	1	Total	C	0	0
			11	11		

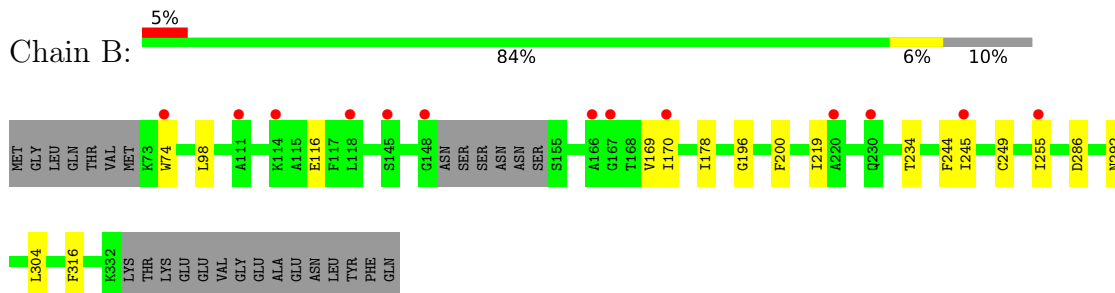
3 Residue-property plots [i](#)

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.

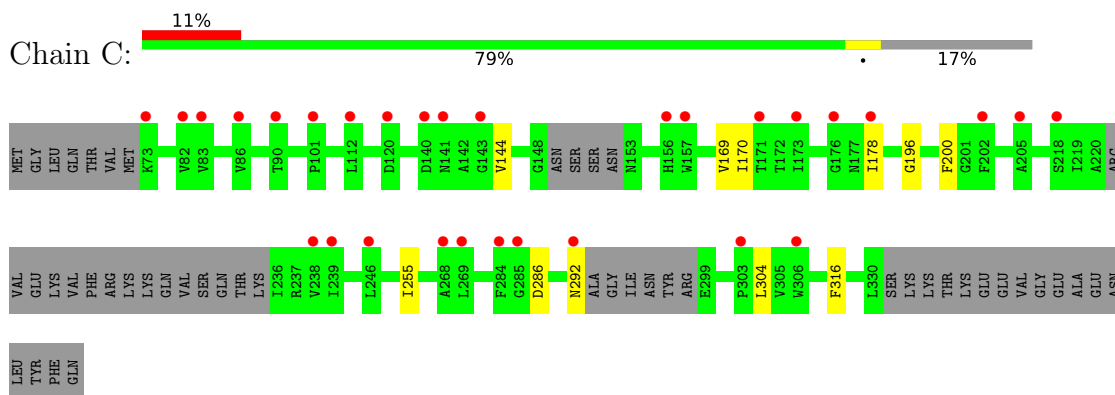
- Molecule 1: POTASSIUM CHANNEL SUBFAMILY K MEMBER 10



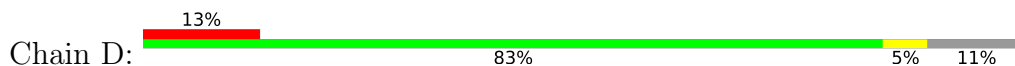
- Molecule 1: POTASSIUM CHANNEL SUBFAMILY K MEMBER 10

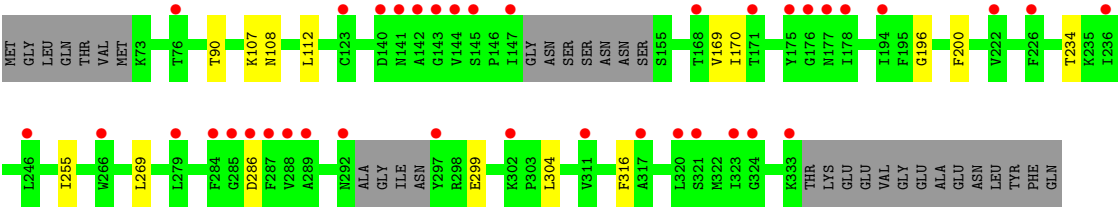


- Molecule 1: POTASSIUM CHANNEL SUBFAMILY K MEMBER 10



- Molecule 1: POTASSIUM CHANNEL SUBFAMILY K MEMBER 10





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.83Å 96.96Å 103.70Å 90.00° 92.58° 90.00°	Depositor
Resolution (Å)	39.57 – 3.20 39.57 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (39.57-3.20) 99.2 (39.57-3.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 3.18Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.237 , 0.254 0.252 , 0.272	Depositor DCC
R_{free} test set	1458 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	130.1	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 96.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.038 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7235	wwPDB-VP
Average B, all atoms (Å ²)	155.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PC1, K, CD

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	0.84	1/1871 (0.1%)	1.45	3/2563 (0.1%)
1	B	0.83	1/1908 (0.1%)	1.48	3/2613 (0.1%)
1	C	0.83	1/1734 (0.1%)	1.45	3/2377 (0.1%)
1	D	0.83	1/1872 (0.1%)	1.48	5/2565 (0.2%)
All	All	0.83	4/7385 (0.1%)	1.46	14/10118 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	255	ILE	CA-CB	6.13	1.57	1.54
1	C	255	ILE	CA-CB	5.37	1.56	1.54
1	B	255	ILE	CA-CB	5.33	1.56	1.54
1	D	255	ILE	CA-CB	5.13	1.56	1.54

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	286	ASP	CA-CB-CG	5.89	118.49	112.60
1	C	286	ASP	CA-CB-CG	5.76	118.36	112.60
1	D	286	ASP	CA-CB-CG	5.75	118.35	112.60
1	A	286	ASP	CA-CB-CG	5.73	118.33	112.60
1	A	169	VAL	CA-C-N	5.35	127.79	120.46
1	A	169	VAL	C-N-CA	5.35	127.79	120.46
1	D	169	VAL	CA-C-N	5.33	127.76	120.46
1	D	169	VAL	C-N-CA	5.33	127.76	120.46
1	B	169	VAL	CA-C-N	5.28	127.70	120.46
1	B	169	VAL	C-N-CA	5.28	127.70	120.46
1	C	169	VAL	CA-C-N	5.28	127.69	120.46
1	C	169	VAL	C-N-CA	5.28	127.69	120.46
1	D	90	THR	CA-C-N	5.09	125.59	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	90	THR	C-N-CA	5.09	125.59	119.94

There are no chirality outliers.

There are no planarity outliers.

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	1824	0	1739	5	0
1	B	1862	0	1808	7	0
1	C	1690	0	1584	4	0
1	D	1827	0	1741	5	0
2	A	4	0	0	0	0
2	C	4	0	0	0	0
3	A	2	0	0	0	0
4	A	11	0	18	0	0
4	B	11	0	18	0	0
All	All	7235	0	6908	18	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 1.

All (18) 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:D:170:ILE:HD12	1:D:196:GLY:HA3	1.80	0.63
1:A:170:ILE:HD12	1:A:196:GLY:HA3	1.79	0.63
1:C:170:ILE:HD12	1:C:196:GLY:HA3	1.80	0.62
1:B:170:ILE:HD12	1:B:196:GLY:HA3	1.81	0.62
1:C:170:ILE:CG2	1:C:200:PHE:HB2	2.38	0.54
1:B:170:ILE:CG2	1:B:200:PHE:HB2	2.38	0.53
1:A:170:ILE:CG2	1:A:200:PHE:HB2	2.40	0.51
1:C:144:VAL:HG11	1:D:107:LYS:HA	1.93	0.51
1:D:170:ILE:CG2	1:D:200:PHE:HB2	2.41	0.50
1:C:170:ILE:HG22	1:C:200:PHE:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:170:ILE:HG22	1:B:200:PHE:HB2	1.95	0.48
1:D:170:ILE:HG22	1:D:200:PHE:HB2	1.97	0.47
1:A:210:GLN:HG2	1:B:74:TRP:CE3	2.51	0.46
1:A:170:ILE:HG22	1:A:200:PHE:HB2	1.96	0.46
1:D:108:ASN:O	1:D:112:LEU:HG	2.18	0.42
1:B:219:ILE:HD11	1:B:244:PHE:HB2	2.00	0.42
1:A:185:GLY:HA2	1:B:98:LEU:HD13	2.01	0.41
1:B:245:ILE:O	1:B:249:CYS:HB2	2.21	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	242/282 (86%)	235 (97%)	7 (3%)	0	100	100
1	B	250/282 (89%)	244 (98%)	6 (2%)	0	100	100
1	C	225/282 (80%)	220 (98%)	5 (2%)	0	100	100
1	D	244/282 (86%)	238 (98%)	6 (2%)	0	100	100
All	All	961/1128 (85%)	937 (98%)	24 (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	175/233 (75%)	168 (96%)	7 (4%)	28	61
1	B	182/233 (78%)	176 (97%)	6 (3%)	33	65
1	C	160/233 (69%)	156 (98%)	4 (2%)	42	69
1	D	175/233 (75%)	170 (97%)	5 (3%)	37	67
All	All	692/932 (74%)	670 (97%)	22 (3%)	34	65

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	GLU
1	A	159	LEU
1	A	178	ILE
1	A	210	GLN
1	A	269	LEU
1	A	292	ASN
1	A	316	PHE
1	B	116	GLU
1	B	178	ILE
1	B	234	THR
1	B	292	ASN
1	B	304	LEU
1	B	316	PHE
1	C	178	ILE
1	C	292	ASN
1	C	304	LEU
1	C	316	PHE
1	D	234	THR
1	D	269	LEU
1	D	299	GLU
1	D	304	LEU
1	D	316	PHE

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	156	HIS
1	D	108	ASN
1	D	156	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 10 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
4	PC1	A	800	-	10,10,53	0.16	0	9,9,61	0.08	0
4	PC1	B	800	-	10,10,53	0.20	0	9,9,61	0.09	0

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.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PC1	A	800	-	-	0/8/8/57	-
4	PC1	B	800	-	-	0/8/8/57	-

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 [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	248/282 (87%)	0.37	19 (7%)	19 13	90, 153, 220, 258	0
1	B	254/282 (90%)	0.25	13 (5%)	33 21	88, 140, 192, 203	0
1	C	233/282 (82%)	0.60	30 (12%)	7 6	102, 170, 219, 237	0
1	D	250/282 (88%)	0.77	38 (15%)	5 4	103, 164, 210, 236	0
All	All	985/1128 (87%)	0.49	100 (10%)	12 8	88, 154, 213, 258	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	177	ASN	12.2
1	D	285	GLY	10.5
1	D	176	GLY	9.4
1	D	288	VAL	7.8
1	D	287	PHE	7.0
1	A	111	ALA	7.0
1	A	108	ASN	6.8
1	D	321	SER	6.6
1	D	145	SER	6.3
1	D	140	ASP	6.2
1	C	171	THR	5.7
1	A	109	THR	5.3
1	D	286	ASP	5.2
1	C	239	ILE	5.0
1	D	142	ALA	5.0
1	D	175	TYR	4.8
1	B	145	SER	4.8
1	C	141	ASN	4.8
1	C	82	VAL	4.7
1	D	292	ASN	4.5
1	C	112	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
1	D	246	LEU	4.3
1	B	118	LEU	4.3
1	C	269	LEU	4.2
1	D	289	ALA	4.1
1	B	220	ALA	4.1
1	C	83	VAL	4.0
1	B	111	ALA	4.0
1	C	238	VAL	3.8
1	C	140	ASP	3.8
1	D	317	ALA	3.7
1	D	171	THR	3.7
1	B	245	ILE	3.7
1	D	143	GLY	3.5
1	D	147	ILE	3.4
1	A	165	PHE	3.2
1	D	320	LEU	3.2
1	D	324	GLY	3.1
1	B	170	ILE	3.1
1	A	107	LYS	3.1
1	B	114	LYS	3.0
1	C	173	ILE	3.0
1	D	144	VAL	3.0
1	A	105	SER	3.0
1	D	297	TYR	3.0
1	A	159	LEU	2.9
1	C	86	VAL	2.9
1	D	226	PHE	2.9
1	A	320	LEU	2.9
1	A	110	ILE	2.9
1	B	148	GLY	2.8
1	C	202	PHE	2.8
1	C	178	ILE	2.8
1	C	156	HIS	2.8
1	B	166	ALA	2.8
1	A	82	VAL	2.8
1	A	153	ASN	2.7
1	C	303	PRO	2.7
1	D	178	ILE	2.7
1	C	120	ASP	2.7
1	D	266	TRP	2.6
1	C	306	TRP	2.6
1	A	287	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	167	GLY	2.6
1	A	243	LEU	2.6
1	B	255	ILE	2.5
1	A	138	ASP	2.5
1	D	311	VAL	2.5
1	D	76	THR	2.4
1	D	194	ILE	2.4
1	C	292	ASN	2.4
1	A	245	ILE	2.4
1	C	268	ALA	2.4
1	C	285	GLY	2.3
1	C	284	PHE	2.3
1	D	123	CYS	2.3
1	B	230	GLN	2.3
1	D	333	LYS	2.3
1	C	218	SER	2.3
1	A	112	LEU	2.3
1	D	323	ILE	2.2
1	C	205	ALA	2.2
1	D	222	VAL	2.2
1	C	143	GLY	2.2
1	D	168	THR	2.2
1	C	73	LYS	2.2
1	C	90	THR	2.2
1	C	246	LEU	2.2
1	D	302	LYS	2.2
1	C	157	TRP	2.1
1	D	284	PHE	2.1
1	A	128	GLU	2.1
1	D	141	ASN	2.1
1	D	236	ILE	2.1
1	C	101	PRO	2.1
1	A	273	TYR	2.1
1	A	204	LEU	2.0
1	D	279	LEU	2.0
1	B	74	TRP	2.0
1	C	176	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

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, 95th 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	K	C	600	1/1	0.79	0.21	167,167,167,167	0
4	PC1	B	800	11/54	0.87	0.33	139,141,144,144	0
4	PC1	A	800	11/54	0.88	0.26	137,138,142,142	0
2	K	A	600	1/1	0.97	0.13	119,119,119,119	0
2	K	C	603	1/1	0.97	0.09	113,113,113,113	0
2	K	A	603	1/1	0.98	0.09	109,109,109,109	0
3	CD	A	702	1/1	0.99	0.06	126,126,126,126	0
2	K	C	602	1/1	0.99	0.11	103,103,103,103	0
2	K	C	601	1/1	0.99	0.10	117,117,117,117	0
2	K	A	602	1/1	1.00	0.09	93,93,93,93	0
2	K	A	601	1/1	1.00	0.07	97,97,97,97	0
3	CD	A	701	1/1	1.00	0.03	125,125,125,125	0

6.5 Other polymers [i](#)

There are no such residues in this entry.