



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:47 AM UTC

PDB ID : 7MHR / pdb_00007mhr
Title : KcsA E71V closed gate with K+
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Deposited on : 2021-04-15
Resolution : 2.77 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

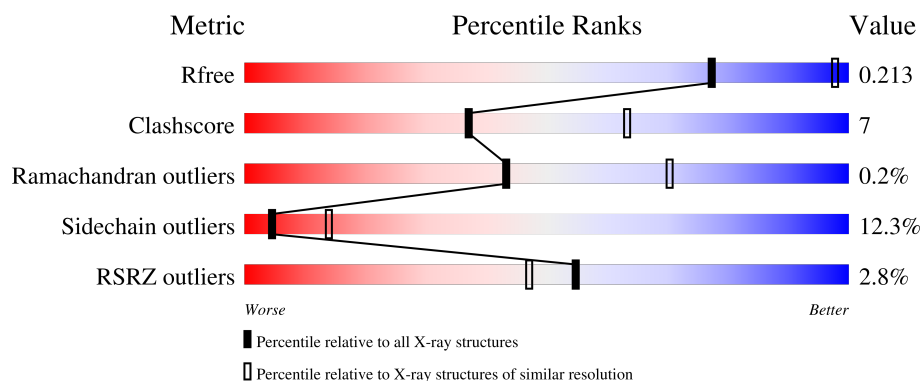
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.77 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	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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	219	5% 68% 29% .
2	B	212	% 71% 25% .
3	C	124	2% 69% 13% . 17%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4240 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 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1605	1020	267	312	6			

- Molecule 2 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	0	0
			1646	1022	282	337	5			

- Molecule 3 is a protein called pH-gated potassium channel KcsA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	103	Total	C	N	O	S	0	0	0
			763	501	130	130	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	MET	-	initiating methionine	UNP P0A334
C	2	ALA	-	expression tag	UNP P0A334
C	71	VAL	GLU	engineered mutation	UNP P0A334
C	90	CYS	LEU	engineered mutation	UNP P0A334

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	3	Total	K	0	0
			3	3		

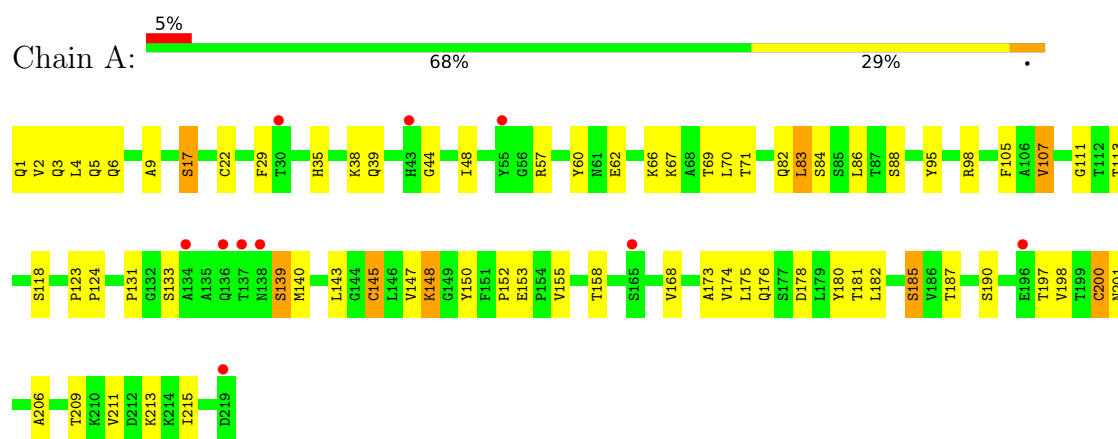
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	58	Total 58	O 58	0	0
5	B	88	Total 88	O 88	0	0
5	C	77	Total 77	O 77	0	0

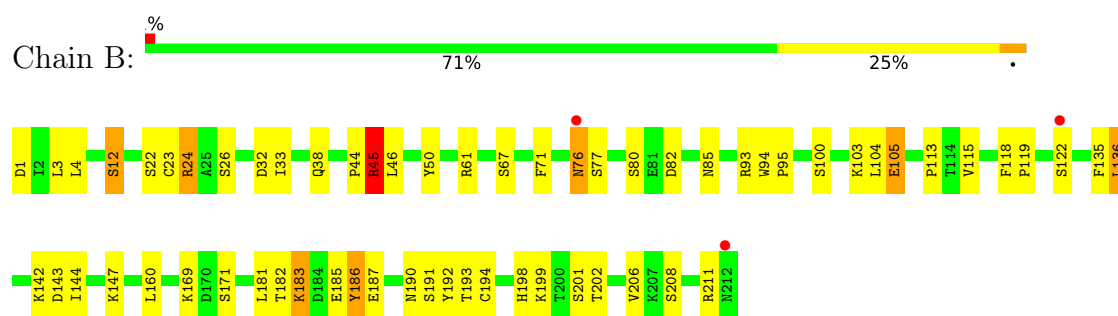
3 Residue-property plots [i](#)

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.

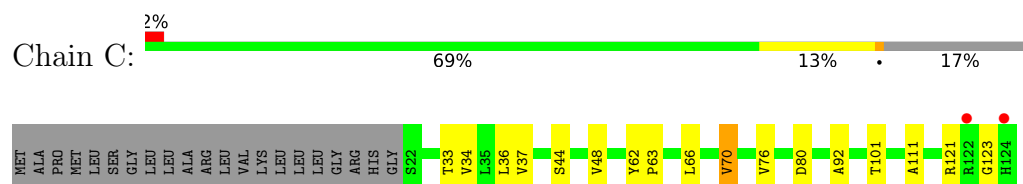
- Molecule 1: Fab heavy chain



- Molecule 2: Fab light chain



- Molecule 3: pH-gated potassium channel KcsA



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	155.83Å 155.83Å 76.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.01 – 2.77 50.01 – 2.77	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.01-2.77) 99.9 (50.01-2.77)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.168 , 0.203 0.175 , 0.213	Depositor DCC
R_{free} test set	1186 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	52.2	Xtriage
Anisotropy	0.544	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 73.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.020 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4240	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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:
K

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	1.29	4/1649 (0.2%)	1.59	15/2261 (0.7%)
2	B	1.27	2/1683 (0.1%)	1.60	12/2283 (0.5%)
3	C	1.39	3/782 (0.4%)	1.65	7/1075 (0.7%)
All	All	1.30	9/4114 (0.2%)	1.61	34/5619 (0.6%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	46	LEU	C-O	-6.42	1.16	1.23
1	A	35	HIS	CE1-NE2	6.23	1.38	1.32
3	C	76	VAL	C-O	6.05	1.30	1.24
2	B	32	ASP	C-O	5.99	1.30	1.23
3	C	101	THR	C-O	-5.73	1.17	1.24
3	C	92	ALA	C-O	5.56	1.30	1.24
1	A	107	VAL	C-O	-5.36	1.18	1.24
1	A	44	GLY	C-O	5.30	1.28	1.23
1	A	153	GLU	CD-OE1	5.19	1.35	1.25

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	ASP	CA-CB-CG	7.34	119.94	112.60
2	B	45	ARG	CB-CA-C	6.74	120.46	110.62
1	A	69	THR	CA-CB-OG1	-6.53	99.81	109.60
3	C	123	GLY	N-CA-C	-6.46	105.40	115.67
3	C	80	ASP	N-CA-C	-6.29	104.52	111.82
3	C	80	ASP	CA-CB-CG	6.21	118.81	112.60
1	A	22	CYS	CA-C-O	-6.19	112.74	119.98
2	B	105	GLU	CB-CA-C	6.19	119.00	110.34
2	B	1	ASP	CB-CA-C	6.14	121.76	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	GLN	CB-CA-C	5.83	120.50	110.77
2	B	24	ARG	CB-CG-CD	5.76	124.54	111.30
3	C	70	VAL	N-CA-CB	5.75	117.28	110.55
3	C	111	ALA	N-CA-C	-5.67	105.18	111.36
1	A	178	ASP	CB-CA-C	5.58	120.04	111.39
1	A	173	ALA	CA-C-O	-5.54	115.67	121.55
2	B	50	TYR	CB-CA-C	5.54	119.60	111.73
1	A	139	SER	N-CA-C	-5.45	106.47	113.23
2	B	198	HIS	CA-C-N	5.44	129.81	120.72
2	B	198	HIS	C-N-CA	5.44	129.81	120.72
3	C	36	LEU	CA-C-O	-5.41	115.14	120.82
3	C	48	VAL	N-CA-C	-5.38	105.48	110.53
1	A	29	PHE	CA-C-N	5.31	127.83	120.29
1	A	29	PHE	C-N-CA	5.31	127.83	120.29
1	A	131	PRO	CA-C-N	5.29	125.13	120.10
1	A	131	PRO	C-N-CA	5.29	125.13	120.10
1	A	105	PHE	CA-C-N	5.18	127.18	120.44
1	A	105	PHE	C-N-CA	5.18	127.18	120.44
1	A	83	LEU	CA-C-O	-5.17	115.16	120.54
2	B	186	TYR	N-CA-C	-5.10	105.80	111.36
1	A	168	VAL	CA-C-N	5.07	130.28	122.93
1	A	168	VAL	C-N-CA	5.07	130.28	122.93
2	B	76	ASN	CA-C-O	-5.01	115.22	120.58
2	B	23	CYS	CA-C-O	-5.01	114.93	120.24
2	B	44	PRO	CB-CA-C	5.01	117.58	111.12

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	1605	0	1532	30	0
2	B	1646	0	1572	25	0
3	C	763	0	773	3	0
4	C	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	58	0	0	3	0
5	B	88	0	0	3	0
5	C	77	0	0	0	0
All	All	4240	0	3877	55	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 7.

All (55) 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:1:GLN:CA	1:A:1:GLN:OE1	2.16	0.93
1:A:145:CYS:HG	1:A:200:CYS:HG	1.01	0.91
1:A:38:LYS:HB2	1:A:48:ILE:HD11	1.69	0.75
2:B:115:VAL:HG13	2:B:136:LEU:HD13	1.70	0.74
1:A:39:GLN:HE22	2:B:38:GLN:HE22	1.42	0.68
2:B:136:LEU:HD22	2:B:136:LEU:N	2.09	0.67
1:A:145:CYS:CB	1:A:200:CYS:HG	2.08	0.66
1:A:140:MET:HE3	1:A:187:THR:HG22	1.82	0.61
1:A:182:LEU:C	1:A:182:LEU:HD12	2.27	0.60
2:B:61:ARG:NH1	2:B:82:ASP:OD1	2.35	0.60
2:B:80:SER:HG	2:B:171:SER:HG	1.50	0.59
2:B:115:VAL:HG13	2:B:136:LEU:CD1	2.35	0.56
3:C:44:SER:OG	3:C:66:LEU:HA	2.06	0.56
1:A:174:VAL:HG21	2:B:160:LEU:HD13	1.86	0.56
1:A:6:GLN:HE22	1:A:95:TYR:HA	1.70	0.56
1:A:67:LYS:NZ	5:A:302:HOH:O	2.40	0.53
1:A:175:LEU:HD13	1:A:180:TYR:CZ	2.44	0.52
2:B:33:ILE:HG21	2:B:71:PHE:CD2	2.45	0.52
1:A:3:GLN:HB2	1:A:107:VAL:HG21	1.92	0.51
1:A:6:GLN:NE2	1:A:111:GLY:HA2	2.26	0.51
1:A:83:LEU:HB3	1:A:86:LEU:HD21	1.94	0.50
1:A:3:GLN:OE1	1:A:98:ARG:NH1	2.45	0.50
2:B:12:SER:HA	2:B:105:GLU:O	2.12	0.49
1:A:17:SER:HB2	1:A:84:SER:HA	1.95	0.48
2:B:61:ARG:NH1	2:B:82:ASP:OD2	2.47	0.48
2:B:61:ARG:NH1	2:B:82:ASP:CG	2.72	0.48
2:B:3:LEU:HB3	2:B:26:SER:HB3	1.95	0.47
2:B:136:LEU:HD22	2:B:136:LEU:H	1.79	0.47
2:B:183:LYS:O	2:B:187:GLU:HG2	2.14	0.47
1:A:60:TYR:CE2	1:A:70:LEU:HG	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:LEU:HB3	1:A:215:ILE:HG21	1.96	0.47
2:B:136:LEU:N	2:B:136:LEU:CD2	2.77	0.46
2:B:45:ARG:HD3	5:B:305:HOH:O	2.15	0.45
1:A:143:LEU:HD12	1:A:198:VAL:HG11	1.99	0.43
1:A:148:LYS:HB3	1:A:181:THR:HG23	2.00	0.43
2:B:113:PRO:HG3	2:B:144:ILE:HD11	2.00	0.43
1:A:150:TYR:CE1	1:A:155:VAL:HG13	2.54	0.42
3:C:62:TYR:N	3:C:63:PRO:CD	2.82	0.42
1:A:185:SER:HB2	2:B:135:PHE:CE2	2.55	0.42
1:A:9:ALA:HA	1:A:113:THR:O	2.20	0.41
1:A:123:PRO:HB3	1:A:209:THR:HG21	2.02	0.41
1:A:152:PRO:HD2	1:A:206:ALA:HB3	2.02	0.41
2:B:104:LEU:HG	2:B:105:GLU:N	2.35	0.41
2:B:201:SER:HB3	5:B:301:HOH:O	2.21	0.41
2:B:94:TRP:HA	2:B:95:PRO:HA	1.89	0.41
1:A:175:LEU:HD13	1:A:180:TYR:CE2	2.55	0.41
2:B:118:PHE:HA	2:B:119:PRO:HD3	1.97	0.41
1:A:155:VAL:CG2	1:A:182:LEU:HD21	2.51	0.40
3:C:33:THR:O	3:C:37:VAL:HG23	2.21	0.40
1:A:124:PRO:HB2	1:A:147:VAL:HG13	2.04	0.40
1:A:197:THR:HG22	5:A:333:HOH:O	2.21	0.40
2:B:93:ARG:NE	5:B:303:HOH:O	2.41	0.40
2:B:186:TYR:HA	2:B:192:TYR:OH	2.21	0.40
2:B:187:GLU:O	2:B:211:ARG:NH2	2.55	0.40
1:A:3:GLN:HG3	5:A:346:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	217/219 (99%)	209 (96%)	8 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	210/212 (99%)	197 (94%)	12 (6%)	1 (0%)	24	52
3	C	101/124 (82%)	98 (97%)	3 (3%)	0	100	100
All	All	528/555 (95%)	504 (96%)	23 (4%)	1 (0%)	43	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	77	SER

5.3.2 Protein sidechains ⓘ

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	170/185 (92%)	148 (87%)	22 (13%)	4	13
2	B	189/190 (100%)	161 (85%)	28 (15%)	3	9
3	C	72/91 (79%)	69 (96%)	3 (4%)	26	58
All	All	431/466 (92%)	378 (88%)	53 (12%)	4	14

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	VAL
1	A	4	LEU
1	A	5	GLN
1	A	17	SER
1	A	57	ARG
1	A	62	GLU
1	A	66	LYS
1	A	71	THR
1	A	88	SER
1	A	118	SER
1	A	133	SER
1	A	139	SER
1	A	145	CYS

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Mol	Chain	Res	Type
1	A	148	LYS
1	A	158	THR
1	A	176	GLN
1	A	185	SER
1	A	190	SER
1	A	200	CYS
1	A	201	ASN
1	A	211	VAL
1	A	213	LYS
2	B	4	LEU
2	B	12	SER
2	B	22	SER
2	B	24	ARG
2	B	45	ARG
2	B	67	SER
2	B	76	ASN
2	B	85	ASN
2	B	100	SER
2	B	103	LYS
2	B	122	SER
2	B	136	LEU
2	B	142	LYS
2	B	143	ASP
2	B	147	LYS
2	B	169	LYS
2	B	181	LEU
2	B	182	THR
2	B	183	LYS
2	B	185	GLU
2	B	190	ASN
2	B	191	SER
2	B	193	THR
2	B	194	CYS
2	B	199	LYS
2	B	202	THR
2	B	206	VAL
2	B	208	SER
3	C	34	VAL
3	C	70	VAL
3	C	121	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	6	GLN
1	A	43	HIS
1	A	176	GLN
2	B	38	GLN
2	B	92	ASN
2	B	124	GLN
2	B	137	ASN
2	B	138	ASN
2	B	166	GLN
2	B	189	HIS
3	C	25	HIS

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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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 [i](#)

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	219/219 (100%)	0.08	10 (4%) 37 31	39, 72, 103, 135	0
2	B	212/212 (100%)	-0.13	3 (1%) 73 67	30, 67, 107, 123	0
3	C	103/124 (83%)	-0.33	2 (1%) 66 59	28, 41, 72, 90	0
All	All	534/555 (96%)	-0.08	15 (2%) 55 47	28, 64, 104, 135	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	ASN	3.9
1	A	137	THR	3.7
1	A	55	TYR	3.3
2	B	212	ASN	3.3
1	A	30	THR	2.8
1	A	165	SER	2.6
1	A	136	GLN	2.4
3	C	124	HIS	2.3
1	A	196	GLU	2.3
1	A	43	HIS	2.2
2	B	76	ASN	2.2
2	B	122	SER	2.2
1	A	219	ASP	2.2
1	A	134	ALA	2.1
3	C	122	ARG	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](#)

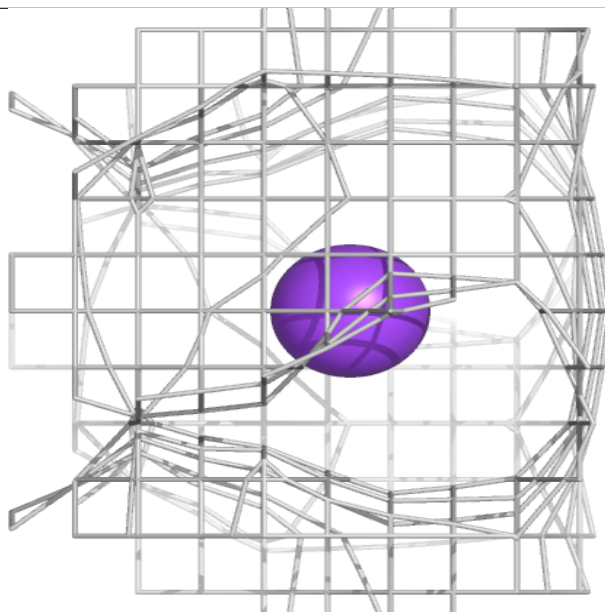
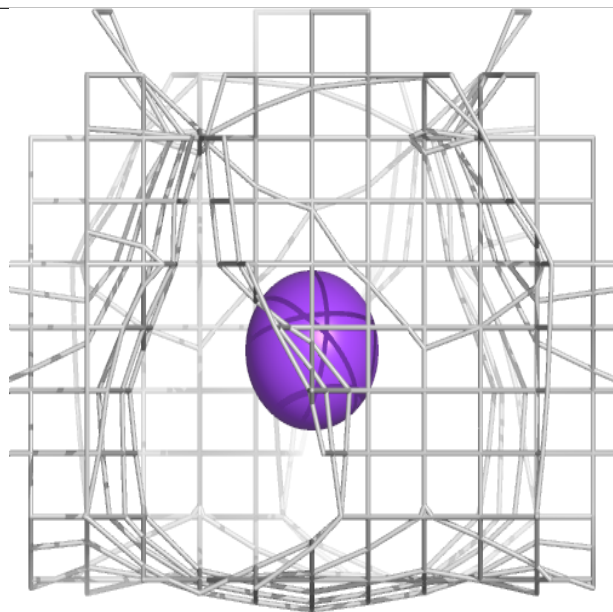
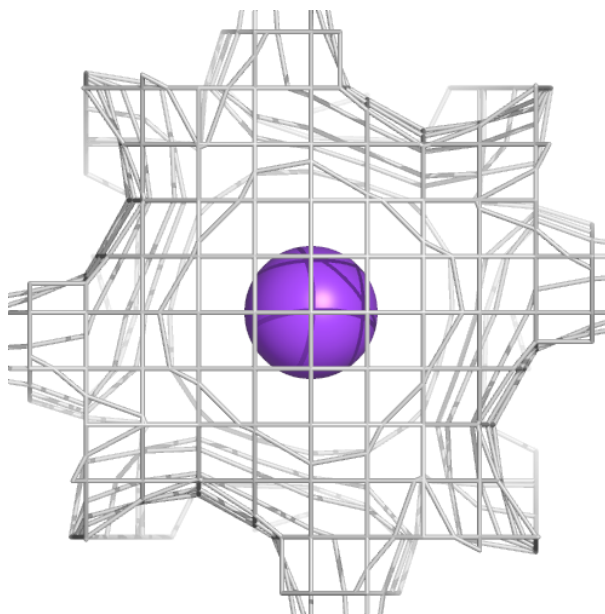
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	K	C	201	1/1	1.00	0.01	35,35,35,35	1
4	K	C	202	1/1	1.00	0.07	47,47,47,47	1
4	K	C	203	1/1	1.00	0.02	31,31,31,31	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

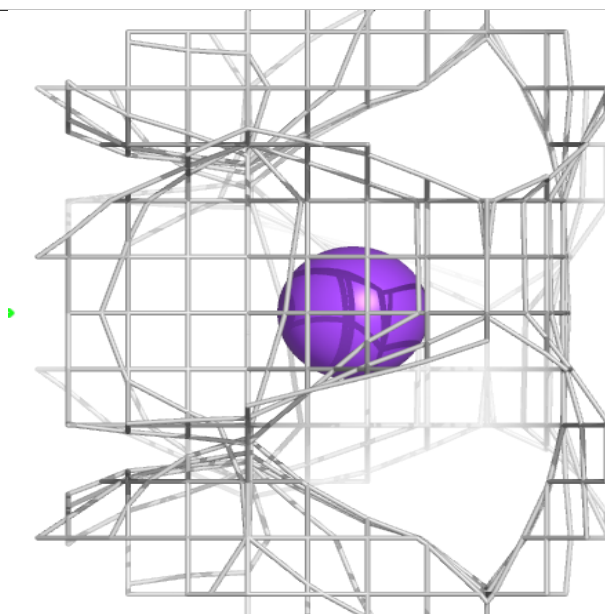
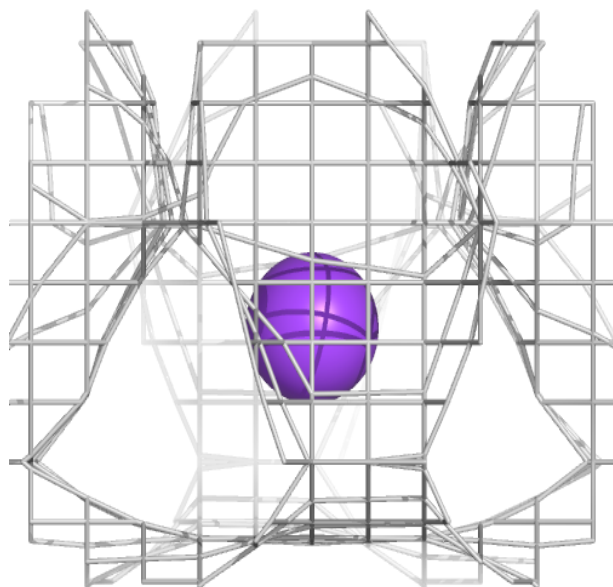
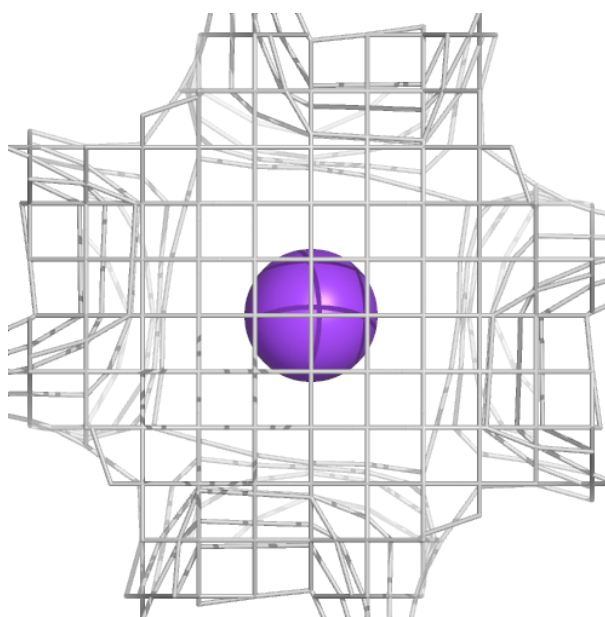
Electron density around K C 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



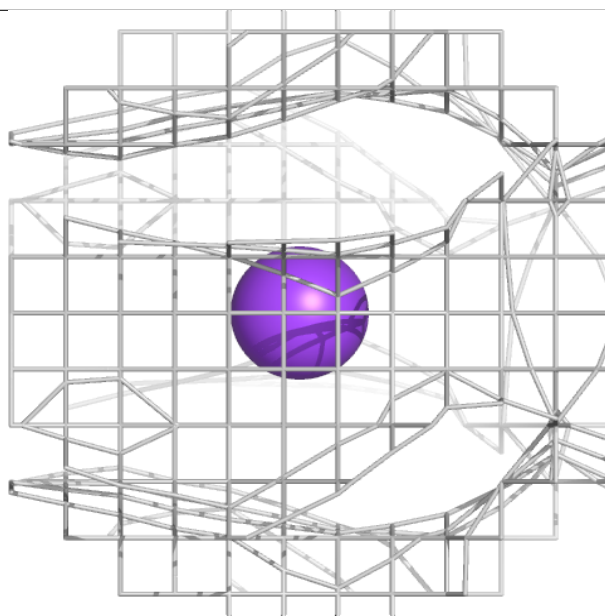
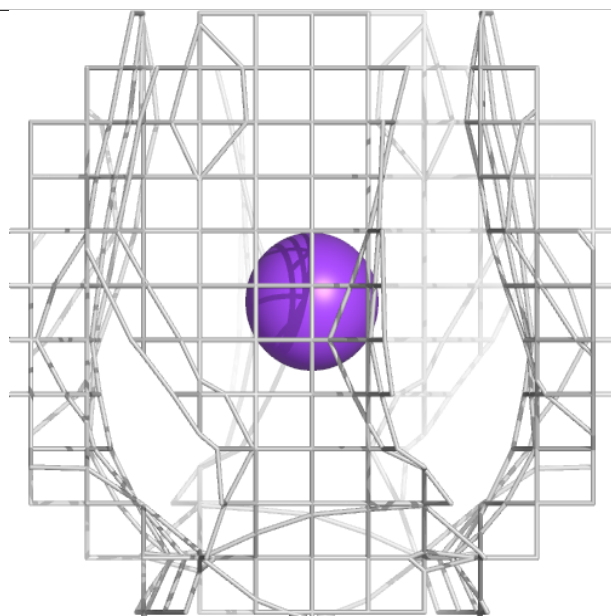
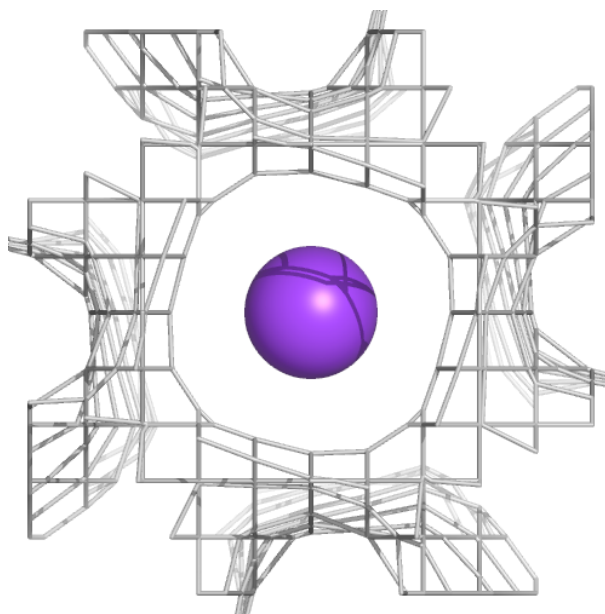
Electron density around K C 202:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around K C 203:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.