



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 10:54 pm BST

PDB ID : 3UKT
Title : Structure of the C-linker/CNBHD of zELK channels in P1 21 1 space group
Authors : Brelidze, T.I.
Deposited on : 2011-11-09
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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

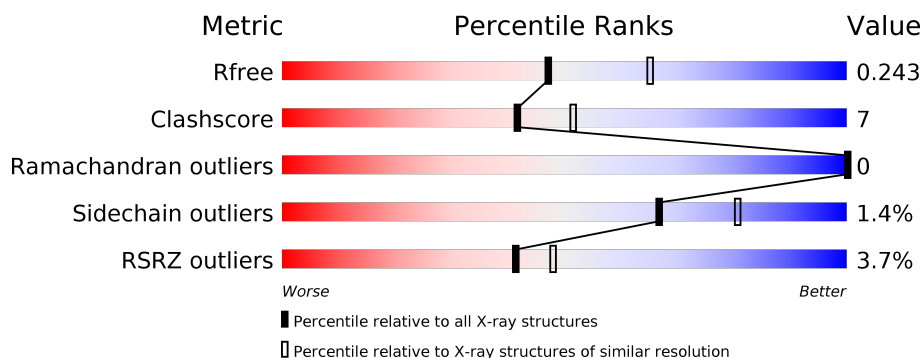
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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 on 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	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 13%, green 78%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> % 78% 13% 8% </div> </div>
1	B	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 2%, yellow 14%, green 79%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 2% 79% 14% 7% </div> </div>
1	C	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 11%, green 81%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> % 81% 11% 8% </div> </div>
1	D	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 9%, orange 9%, yellow 17%, green 66%, grey 17%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 9% 66% 17% 17% </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5973 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 Novel protein similar to vertebrate potassium voltage-gated channel, subfamily H (Eag-related) family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	198	Total	C	N	O	S	0	0	0
			1507	965	253	281	8			
1	A	196	Total	C	N	O	S	0	0	0
			1506	965	257	276	8			
1	C	196	Total	C	N	O	S	0	0	0
			1471	945	243	276	7			
1	D	177	Total	C	N	O	S	0	0	0
			1277	819	214	236	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	539	GLY	-	EXPRESSION TAG	UNP A8WHX9
B	540	ALA	-	EXPRESSION TAG	UNP A8WHX9
B	541	MET	-	EXPRESSION TAG	UNP A8WHX9
B	542	ASP	-	EXPRESSION TAG	UNP A8WHX9
A	539	GLY	-	EXPRESSION TAG	UNP A8WHX9
A	540	ALA	-	EXPRESSION TAG	UNP A8WHX9
A	541	MET	-	EXPRESSION TAG	UNP A8WHX9
A	542	ASP	-	EXPRESSION TAG	UNP A8WHX9
C	539	GLY	-	EXPRESSION TAG	UNP A8WHX9
C	540	ALA	-	EXPRESSION TAG	UNP A8WHX9
C	541	MET	-	EXPRESSION TAG	UNP A8WHX9
C	542	ASP	-	EXPRESSION TAG	UNP A8WHX9
D	539	GLY	-	EXPRESSION TAG	UNP A8WHX9
D	540	ALA	-	EXPRESSION TAG	UNP A8WHX9
D	541	MET	-	EXPRESSION TAG	UNP A8WHX9
D	542	ASP	-	EXPRESSION TAG	UNP A8WHX9

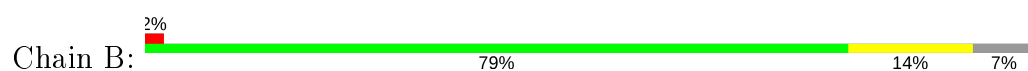
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	66	Total 66	O 66	0	0
2	A	66	Total 66	O 66	0	0
2	C	49	Total 49	O 49	0	0
2	D	31	Total 31	O 31	0	0

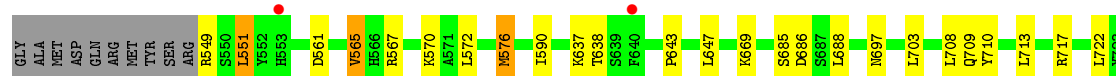
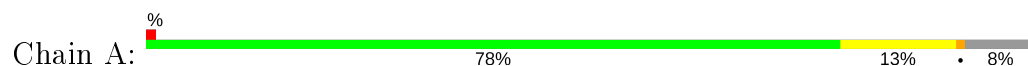
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

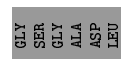
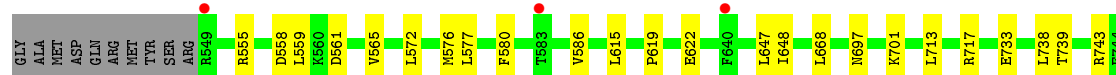
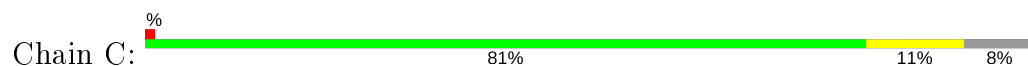
- Molecule 1: Novel protein similar to vertebrate potassium voltage-gated channel, subfamily H (Eag-related) family



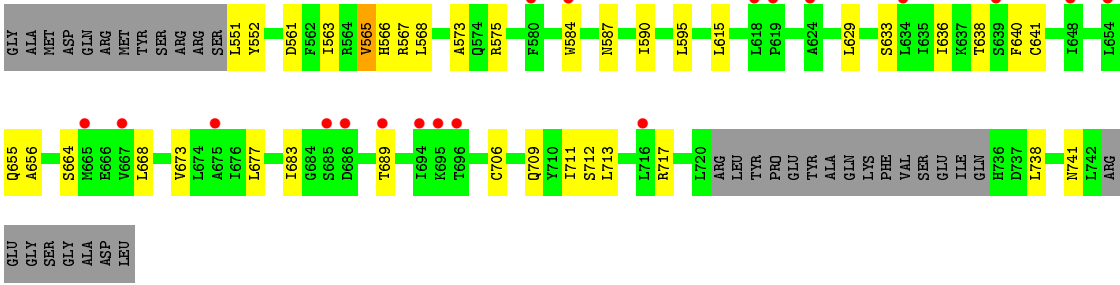
- Molecule 1: Novel protein similar to vertebrate potassium voltage-gated channel, subfamily H (Eag-related) family



- Molecule 1: Novel protein similar to vertebrate potassium voltage-gated channel, subfamily H (Eag-related) family



- Molecule 1: Novel protein similar to vertebrate potassium voltage-gated channel, subfamily H (Eag-related) family



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.66 Å 107.81 Å 77.58 Å 90.00° 97.38° 90.00°	Depositor
Resolution (Å)	44.15 – 2.30 76.94 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.0 (44.15-2.30) 93.0 (76.94-2.30)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 2.29 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.205 , 0.258 0.193 , 0.243	Depositor DCC
R_{free} test set	1877 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	50.1	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5973	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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	0.44	0/1530	0.58	1/2071 (0.0%)
1	B	0.46	0/1531	0.58	0/2075
1	C	0.41	0/1495	0.54	0/2033
1	D	0.34	0/1296	0.50	0/1765
All	All	0.42	0/5852	0.55	1/7944 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	576	MET	CG-SD-CE	-6.12	90.41	100.20

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	1506	0	1504	25	0
1	B	1507	0	1476	18	0
1	C	1471	0	1424	17	0
1	D	1277	0	1194	25	0
2	A	66	0	0	2	0
2	B	66	0	0	1	0
2	C	49	0	0	1	0
2	D	31	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5973	0	5598	80	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 (80) 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:587:ASN:HD21	1:D:655:GLN:H	1.15	0.94
1:A:570:LYS:HZ3	1:C:733:GLU:HG3	1.37	0.90
1:A:570:LYS:NZ	1:C:733:GLU:HG3	1.87	0.89
1:C:739:THR:OG1	2:C:22:HOH:O	2.06	0.74
1:A:717:ARG:HD2	2:A:176:HOH:O	1.87	0.73
1:C:555:ARG:HB3	1:C:580:PHE:HZ	1.57	0.68
1:B:661:CYS:O	1:B:679:LYS:HG3	1.94	0.66
1:D:590:ILE:O	2:D:138:HOH:O	2.14	0.66
1:D:668:LEU:HD23	1:D:673:VAL:HA	1.77	0.65
1:B:561:ASP:HB3	1:A:549:ARG:NH2	2.13	0.64
1:B:595:LEU:HB2	2:B:43:HOH:O	1.99	0.62
1:B:731:VAL:O	1:B:734:ILE:HG22	2.00	0.62
1:D:587:ASN:ND2	1:D:655:GLN:H	1.95	0.61
1:D:713:LEU:O	1:D:717:ARG:HG3	2.00	0.60
1:C:555:ARG:HB3	1:C:580:PHE:CZ	2.36	0.60
1:A:669:LYS:HE2	1:A:697:ASN:O	2.03	0.58
1:C:559:LEU:HD23	1:C:577:LEU:HD23	1.84	0.58
1:A:572:LEU:HG	1:A:576:MET:SD	2.43	0.58
1:D:633:SER:HA	1:D:636:ILE:HD12	1.87	0.56
1:D:615:LEU:HD23	1:D:615:LEU:C	2.26	0.56
1:B:713:LEU:O	1:B:717:ARG:HG3	2.06	0.55
1:C:647:LEU:HG	1:C:648:ILE:HG13	1.89	0.55
1:A:567:ARG:O	2:A:60:HOH:O	2.18	0.54
1:C:668:LEU:HD12	1:C:701:LYS:HD3	1.90	0.54
1:A:561:ASP:O	1:A:565:VAL:HG13	2.08	0.53
1:A:570:LYS:HZ1	1:C:733:GLU:HG3	1.71	0.53
1:B:641:CYS:HB2	1:B:706:CYS:HB2	1.89	0.53
1:A:713:LEU:O	1:A:717:ARG:HG3	2.08	0.53
1:A:740:TYR:HE2	1:A:742:LEU:HD23	1.74	0.53
1:D:656:ALA:HB2	1:D:712:SER:HA	1.90	0.53
1:C:586:VAL:HB	1:C:647:LEU:HD12	1.92	0.52
1:D:638:THR:HG22	1:D:709:GLN:HG2	1.92	0.52
1:D:551:LEU:N	2:D:85:HOH:O	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:697:ASN:HB3	1:A:744:GLU:HA	1.93	0.51
1:D:677:LEU:HD13	1:D:683:ILE:HD11	1.93	0.51
1:A:647:LEU:HD13	1:A:708:LEU:HD13	1.94	0.50
1:C:713:LEU:O	1:C:717:ARG:HG3	2.12	0.50
1:D:668:LEU:HD21	1:D:673:VAL:HG22	1.94	0.50
1:B:732:SER:O	1:B:733:GLU:HG2	2.11	0.49
1:D:551:LEU:N	2:D:88:HOH:O	2.46	0.49
1:C:615:LEU:O	1:C:615:LEU:HD23	2.14	0.48
1:A:647:LEU:HD13	1:A:708:LEU:CD1	2.44	0.47
1:A:729:LYS:O	1:A:733:GLU:HG2	2.14	0.47
1:B:685:SER:OG	1:B:743:ARG:HB2	2.14	0.47
1:B:561:ASP:O	1:B:565:VAL:HG13	2.14	0.47
1:A:722:LEU:C	1:A:724:PRO:HD3	2.36	0.46
1:B:734:ILE:O	1:B:738:LEU:HB2	2.15	0.46
1:D:552:TYR:HD1	1:D:584:TRP:CD1	2.34	0.46
1:A:688:LEU:O	1:A:717:ARG:NE	2.48	0.46
1:A:572:LEU:O	1:A:576:MET:SD	2.74	0.45
1:D:575:ARG:NH2	2:D:71:HOH:O	2.35	0.45
1:D:563:ILE:HG23	1:D:568:LEU:HB2	1.99	0.45
1:A:643:PRO:HB3	1:A:703:LEU:O	2.17	0.45
1:D:563:ILE:HG21	1:D:573:ALA:HB2	1.99	0.45
1:C:561:ASP:O	1:C:565:VAL:HG13	2.17	0.44
1:A:637:LYS:HB2	1:A:710:TYR:CZ	2.53	0.44
1:B:637:LYS:HB2	1:B:710:TYR:CZ	2.52	0.43
1:D:590:ILE:N	2:D:138:HOH:O	2.50	0.43
1:A:688:LEU:HD22	1:A:713:LEU:HD22	2.00	0.43
1:A:551:LEU:HD11	1:A:590:ILE:HA	2.00	0.43
1:C:558:ASP:HB3	1:D:595:LEU:HD11	2.01	0.42
1:D:640:PHE:HA	1:D:706:CYS:O	2.19	0.42
1:B:664:SER:HA	1:B:677:LEU:O	2.19	0.42
1:D:738:LEU:HD23	1:D:741:ASN:HB2	2.02	0.42
1:C:572:LEU:O	1:C:576:MET:HG3	2.19	0.42
1:D:656:ALA:HB1	1:D:711:ILE:O	2.20	0.42
1:B:647:LEU:HD11	1:B:658:TYR:CD1	2.55	0.42
1:C:697:ASN:ND2	1:C:743:ARG:O	2.52	0.41
1:D:561:ASP:O	1:D:565:VAL:HB	2.20	0.41
1:D:566:HIS:O	1:D:567:ARG:C	2.59	0.41
1:D:689:THR:O	1:D:717:ARG:HD3	2.19	0.41
1:A:703:LEU:HD23	1:A:703:LEU:HA	1.86	0.41
1:C:619:PRO:O	1:C:622:GLU:HB2	2.20	0.41
1:B:571:ALA:O	1:B:575:ARG:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:653:ALA:HA	1:B:694:ILE:O	2.20	0.41
1:A:638:THR:HG22	1:A:709:GLN:HG2	2.01	0.41
1:A:685:SER:OG	1:A:686:ASP:N	2.54	0.40
1:B:729:LYS:O	1:B:733:GLU:HG3	2.21	0.40
1:B:638:THR:HG22	1:B:709:GLN:HG2	2.03	0.40
1:B:722:LEU:HA	1:B:722:LEU:HD23	1.79	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	194/212 (92%)	187 (96%)	7 (4%)	0	100	100
1	B	196/212 (92%)	187 (95%)	9 (5%)	0	100	100
1	C	194/212 (92%)	189 (97%)	5 (3%)	0	100	100
1	D	173/212 (82%)	161 (93%)	12 (7%)	0	100	100
All	All	757/848 (89%)	724 (96%)	33 (4%)	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	158/186 (85%)	156 (99%)	2 (1%)	69	82
1	B	155/186 (83%)	154 (99%)	1 (1%)	86	94
1	C	150/186 (81%)	149 (99%)	1 (1%)	84	92
1	D	122/186 (66%)	118 (97%)	4 (3%)	38	53
All	All	585/744 (79%)	577 (99%)	8 (1%)	67	81

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	565	VAL
1	A	551	LEU
1	A	565	VAL
1	C	738	LEU
1	D	565	VAL
1	D	629	LEU
1	D	641	CYS
1	D	664	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	553	HIS
1	D	587	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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, 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	196/212 (92%)	0.25	2 (1%) 82 86	29, 48, 80, 126	0
1	B	198/212 (93%)	0.29	4 (2%) 65 71	27, 47, 82, 116	0
1	C	196/212 (92%)	0.20	3 (1%) 73 79	31, 52, 82, 114	0
1	D	177/212 (83%)	0.63	19 (10%) 6 8	42, 73, 125, 186	0
All	All	767/848 (90%)	0.34	28 (3%) 41 48	27, 53, 95, 186	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	694	ILE	4.6
1	D	624	ALA	3.8
1	B	694	ILE	3.1
1	D	696	THR	3.1
1	D	580	PHE	3.0
1	A	640	PHE	3.0
1	D	695	LYS	2.9
1	A	553	HIS	2.9
1	B	640	PHE	2.8
1	D	619	PRO	2.8
1	D	584	TRP	2.8
1	B	690	LYS	2.7
1	D	675	ALA	2.6
1	D	648	ILE	2.5
1	D	654	LEU	2.5
1	C	549	ARG	2.4
1	D	634	LEU	2.4
1	D	618	LEU	2.2
1	D	665	MET	2.2
1	B	734	ILE	2.2
1	D	685	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	686	ASP	2.2
1	C	640	PHE	2.1
1	D	639	SER	2.1
1	D	716	LEU	2.0
1	C	583	THR	2.0
1	D	667	VAL	2.0
1	D	689	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 carbohydrates 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.