



wwPDB X-ray Structure Validation Summary Report ⓘ

May 23, 2020 – 05:37 pm BST

PDB ID : 3DRX
Title : X-ray crystal structure of human KCTD5 protein crystallized in high-salt buffer
Authors : Tereshko, V.; Dementieva, I.; Goldstein, S.A.N.
Deposited on : 2008-07-11
Resolution : 3.11 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

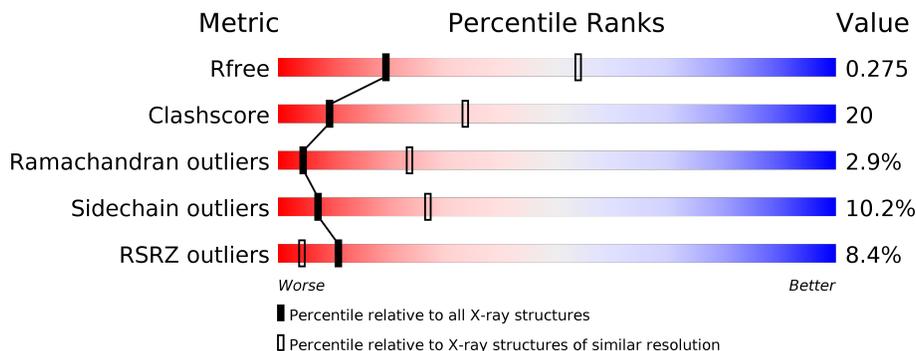
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.11 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	1292 (3.14-3.10)
Clashscore	141614	1389 (3.14-3.10)
Ramachandran outliers	138981	1337 (3.14-3.10)
Sidechain outliers	138945	1337 (3.14-3.10)
RSRZ outliers	127900	1260 (3.14-3.10)

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	202	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 47%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 26%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 20%; height: 10px; background-color: grey;"></div> </div>
1	B	202	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 54%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 25%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 15%; height: 10px; background-color: grey;"></div> </div>
1	C	202	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 52%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 26%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 12%; height: 10px; background-color: grey;"></div> </div>
1	D	202	<div style="display: flex; align-items: center;"> <div style="width: 13%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 62%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 22%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 12%; height: 10px; background-color: grey;"></div> </div>
1	E	202	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 53%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 24%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 16%; height: 10px; background-color: grey;"></div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6907 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 BTB/POZ domain-containing protein KCTD5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	161	1306	831	223	246	6	0	0	0
1	B	172	1385	874	236	269	6	0	0	0
1	C	177	1430	902	243	279	6	0	0	0
1	D	177	1427	901	243	277	6	0	0	0
1	E	169	1359	860	232	261	6	0	0	0

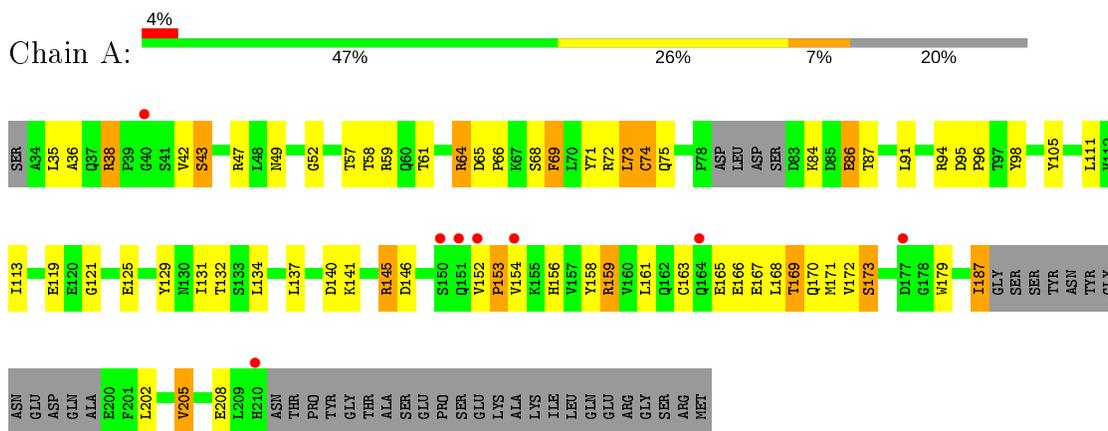
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	SER	-	EXPRESSION TAG	UNP Q9NXV2
B	33	SER	-	EXPRESSION TAG	UNP Q9NXV2
C	33	SER	-	EXPRESSION TAG	UNP Q9NXV2
D	33	SER	-	EXPRESSION TAG	UNP Q9NXV2
E	33	SER	-	EXPRESSION TAG	UNP Q9NXV2

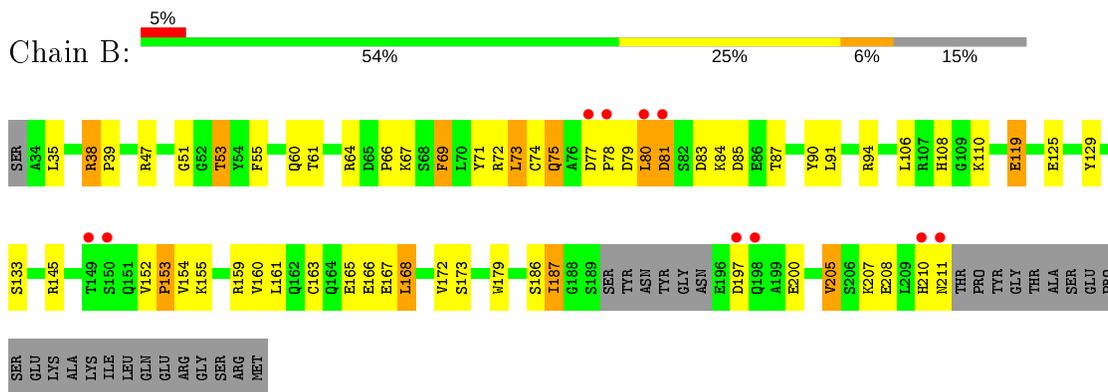
3 Residue-property plots [i](#)

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.

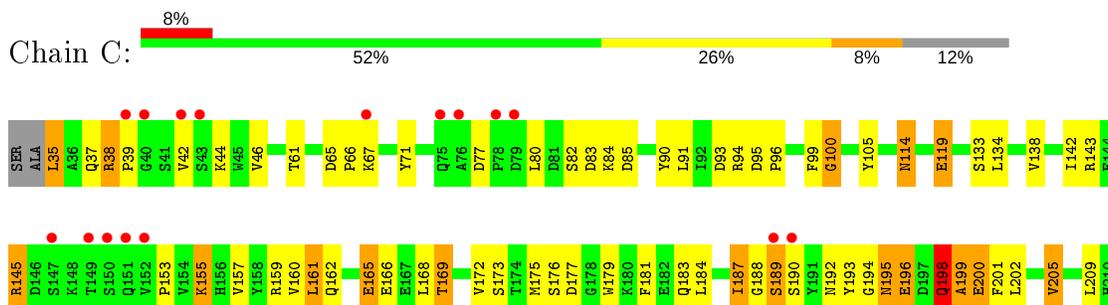
- Molecule 1: BTB/POZ domain-containing protein KCTD5



- Molecule 1: BTB/POZ domain-containing protein KCTD5



- Molecule 1: BTB/POZ domain-containing protein KCTD5



R211
THR
PRO
TYR
GLY
THR
ALA
SER
GLU
PRO
SER
GLU
LYS
ALA
LYS
ILE
LEU
GLN
GLU
ARG
GLY
SER
ARG
MET

- Molecule 1: BTB/POZ domain-containing protein KCTD5

Chain D: 13% 62% 22% 12%

SER
A34
L35
A36
Q37
R38
P39
G40
S41
V42
S43
L62
G63
R64
D65
P66
Y71
R72
L73
C74
Q75
A76
D77
P78
D79
L80
D85
E86
Y90
L91
D95
P96
T97
Y98
G109
K110
E119
E120
G121
R143
E144
R145
D146
S147
K148
T149
S150
Q151
Y152
P153
H156

V157
Y158
R159
V160
L161
Q162
C163
Q164
E165
E166
E167
L168
T169
Q170
M171
V172
S173
T174
M175
S176
W179
K180
L187
G188
S189
G194
N195
E196
ASP
Q198
A199
L202
V205
E208
N211
THR
PRO
TYR
GLY
THR
ALA
SER
GLU
PRO
SER
GLU
LYS
ALA
LYS
ILE
LEU
GLU

ARG
GLY
SER
ARG
MET

- Molecule 1: BTB/POZ domain-containing protein KCTD5

Chain E: 5% 53% 24% 7% 16%

S33
A34
L35
R38
P39
G40
S41
V42
S43
K44
W45
L48
Y54
F55
L56
R59
K67
S68
F69
L70
Y71
C74
D77
P78
D79
S82
D83
K84
D85
E86
T87
G88
L91
D95
P96
T97
Y98
I113
L117
A118
E119
E120
G121
Y129
L134
I135

R143
R144
R145
T149
S150
Q151
P153
V154
K155
H156
R159
V160
L161
E165
E166
E167
L168
T169
Q170
M171
Y172
S173
T174
M175
S176
D177
G178
W179
K180
F181
E182
V185
S186
I187
G188
SER
SER
TYR
ASN
TYR
GLY
ASN
GLU
ASP
GLN
A199
E200
F201
L202
C203
V204
V205
S206

R211
THR
PRO
TYR
GLY
THR
ALA
SER
GLU
PRO
SER
GLU
LYS
ALA
LYS
ILE
LEU
GLN
GLU
ARG
GLY
SER
ARG
MET

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.86Å 128.58Å 152.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.11 19.94 – 3.11	Depositor EDS
% Data completeness (in resolution range)	98.9 (20.00-3.11) 99.0 (19.94-3.11)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 3.09Å)	Xtrriage
Refinement program	REFMAC 5.4.0073	Depositor
R, R_{free}	0.227 , 0.275 0.225 , 0.275	Depositor DCC
R_{free} test set	1321 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	62.6	Xtrriage
Anisotropy	0.023	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 68.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6907	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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	0.39	0/1329	0.52	0/1793
1	B	0.44	0/1409	0.53	0/1903
1	C	0.45	0/1457	0.61	1/1970 (0.1%)
1	D	0.42	0/1453	0.53	0/1963
1	E	0.43	0/1383	0.56	0/1868
All	All	0.42	0/7031	0.55	1/9497 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	143	ARG	NE-CZ-NH2	5.36	122.98	120.30

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	1306	0	1309	62	0
1	B	1385	0	1371	46	0
1	C	1430	0	1405	67	0
1	D	1427	0	1405	46	0
1	E	1359	0	1353	65	0
All	All	6907	0	6843	274	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 20.

The worst 5 of 274 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:E:152:VAL:CG1	1:E:153:PRO:HD2	1.77	1.13
1:E:38:ARG:HG2	1:E:38:ARG:HH11	1.09	1.07
1:E:152:VAL:HG12	1:E:153:PRO:HD2	1.37	1.03
1:E:165:GLU:O	1:E:168:LEU:HB2	1.69	0.92
1:A:72:ARG:HG3	1:A:73:LEU:HD13	1.49	0.91

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	155/202 (77%)	128 (83%)	22 (14%)	5 (3%)	4	21
1	B	168/202 (83%)	152 (90%)	12 (7%)	4 (2%)	6	26
1	C	175/202 (87%)	146 (83%)	23 (13%)	6 (3%)	3	19
1	D	173/202 (86%)	148 (86%)	20 (12%)	5 (3%)	4	23
1	E	165/202 (82%)	144 (87%)	17 (10%)	4 (2%)	6	26
All	All	836/1010 (83%)	718 (86%)	94 (11%)	24 (3%)	4	23

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	SER
1	A	74	CYS
1	A	153	PRO
1	B	81	ASP
1	C	198	GLN

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	147/181 (81%)	129 (88%)	18 (12%)	5	20
1	B	156/181 (86%)	134 (86%)	22 (14%)	3	15
1	C	161/181 (89%)	141 (88%)	20 (12%)	4	19
1	D	160/181 (88%)	154 (96%)	6 (4%)	33	65
1	E	153/181 (84%)	140 (92%)	13 (8%)	10	36
All	All	777/905 (86%)	698 (90%)	79 (10%)	7	27

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	166	GLU
1	C	46	VAL
1	E	119	GLU
1	B	168	LEU
1	C	35	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	164	GLN
1	E	151	GLN
1	D	156	HIS
1	C	75	GLN
1	C	195	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 carbohydrates 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	161/202 (79%)	0.12	8 (4%) 28 13	53, 66, 82, 85	2 (1%)
1	B	172/202 (85%)	0.14	10 (5%) 23 10	52, 65, 85, 96	1 (0%)
1	C	177/202 (87%)	0.23	17 (9%) 8 3	52, 66, 83, 85	0
1	D	177/202 (87%)	0.58	27 (15%) 2 1	53, 68, 84, 106	0
1	E	169/202 (83%)	0.09	10 (5%) 22 10	42, 64, 79, 84	0
All	All	856/1010 (84%)	0.24	72 (8%) 11 4	42, 66, 83, 106	3 (0%)

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	36	ALA	8.8
1	D	78	PRO	5.8
1	D	35	LEU	5.8
1	D	41	SER	4.9
1	D	79	ASP	4.8

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

There are no such residues in this entry.