



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 11:45 PM UTC

PDB ID : 8PNR / pdb_00008pnr
Title : Structure of human KCTD15 BTB domain mutant G88D crystal form 1
Authors : Cruz Walma, D.A.; Cros, J.; Bradshaw, W.; Richardson, W.; Chen, Z.; Chalk, R.; Wilkie, A.; Bullock, A.N.
Deposited on : 2023-06-30
Resolution : 2.25 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 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

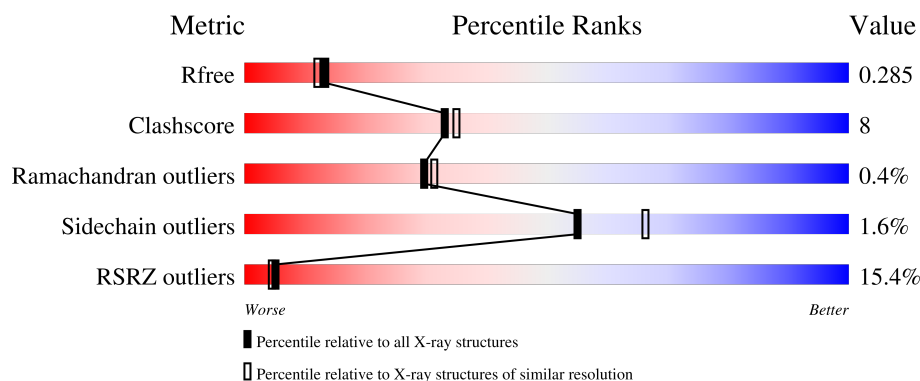
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	116	20% 61% 19% 18%
1	B	116	9% 68% 19% 11%
1	C	116	24% 70% 19% 11%
1	D	116	9% 78% 7% 13%
1	E	116	8% 78% 9% 12%

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Mol	Chain	Length	Quality of chain
1	F	116	
1	G	116	
1	H	116	
1	I	116	
1	J	116	
1	K	116	
1	L	116	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9546 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 KCTD15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	103	Total	C	N	O	S	0	0	0
			808	525	131	150	2			
1	A	95	Total	C	N	O	S	0	0	0
			713	461	116	134	2			
1	J	101	Total	C	N	O	S	0	1	0
			832	538	138	154	2			
1	I	102	Total	C	N	O	S	0	0	0
			828	531	137	158	2			
1	B	103	Total	C	N	O	S	0	0	0
			833	535	143	153	2			
1	E	102	Total	C	N	O	S	0	0	0
			834	534	136	162	2			
1	G	98	Total	C	N	O	S	0	0	0
			792	513	129	148	2			
1	H	100	Total	C	N	O	S	0	0	0
			803	517	135	149	2			
1	K	96	Total	C	N	O	S	0	0	0
			747	487	119	139	2			
1	L	95	Total	C	N	O	S	0	0	0
			739	481	118	138	2			
1	D	101	Total	C	N	O	S	0	0	0
			820	528	135	155	2			
1	F	96	Total	C	N	O	S	0	0	0
			708	464	109	133	2			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	SER	-	expression tag	UNP Q96SI1
C	2	MET	LEU	conflict	UNP Q96SI1
C	39	ASP	GLY	conflict	UNP Q96SI1
A	1	SER	-	expression tag	UNP Q96SI1
A	2	MET	LEU	conflict	UNP Q96SI1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	39	ASP	GLY	conflict	UNP Q96SI1
J	1	SER	-	expression tag	UNP Q96SI1
J	2	MET	LEU	conflict	UNP Q96SI1
J	39	ASP	GLY	conflict	UNP Q96SI1
I	1	SER	-	expression tag	UNP Q96SI1
I	2	MET	LEU	conflict	UNP Q96SI1
I	39	ASP	GLY	conflict	UNP Q96SI1
B	1	SER	-	expression tag	UNP Q96SI1
B	2	MET	LEU	conflict	UNP Q96SI1
B	39	ASP	GLY	conflict	UNP Q96SI1
E	1	SER	-	expression tag	UNP Q96SI1
E	2	MET	LEU	conflict	UNP Q96SI1
E	39	ASP	GLY	conflict	UNP Q96SI1
G	1	SER	-	expression tag	UNP Q96SI1
G	2	MET	LEU	conflict	UNP Q96SI1
G	39	ASP	GLY	conflict	UNP Q96SI1
H	1	SER	-	expression tag	UNP Q96SI1
H	2	MET	LEU	conflict	UNP Q96SI1
H	39	ASP	GLY	conflict	UNP Q96SI1
K	1	SER	-	expression tag	UNP Q96SI1
K	2	MET	LEU	conflict	UNP Q96SI1
K	39	ASP	GLY	conflict	UNP Q96SI1
L	1	SER	-	expression tag	UNP Q96SI1
L	2	MET	LEU	conflict	UNP Q96SI1
L	39	ASP	GLY	conflict	UNP Q96SI1
D	1	SER	-	expression tag	UNP Q96SI1
D	2	MET	LEU	conflict	UNP Q96SI1
D	39	ASP	GLY	conflict	UNP Q96SI1
F	1	SER	-	expression tag	UNP Q96SI1
F	2	MET	LEU	conflict	UNP Q96SI1
F	39	ASP	GLY	conflict	UNP Q96SI1

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	3	Total O 3 3	0	0
2	J	17	Total O 17 17	0	0
2	I	14	Total O 14 14	0	0
2	B	3	Total O 3 3	0	0

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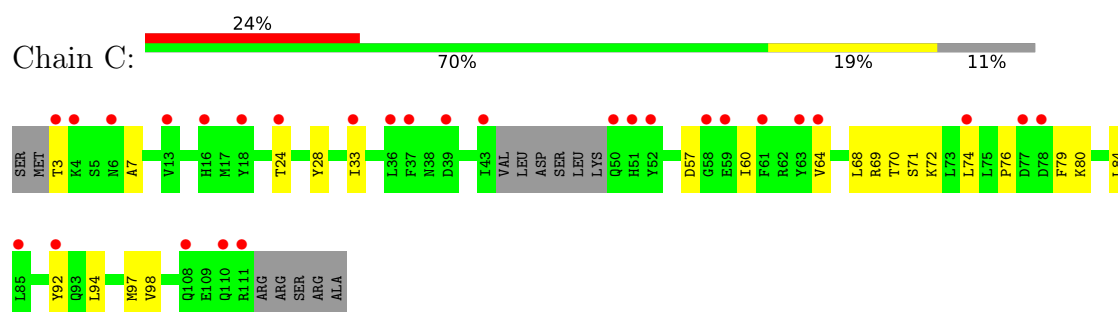
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	13	Total 13	O 13	0	0
2	G	9	Total 9	O 9	0	0
2	H	8	Total 8	O 8	0	0
2	K	3	Total 3	O 3	0	0
2	L	8	Total 8	O 8	0	0
2	D	9	Total 9	O 9	0	0
2	F	2	Total 2	O 2	0	0

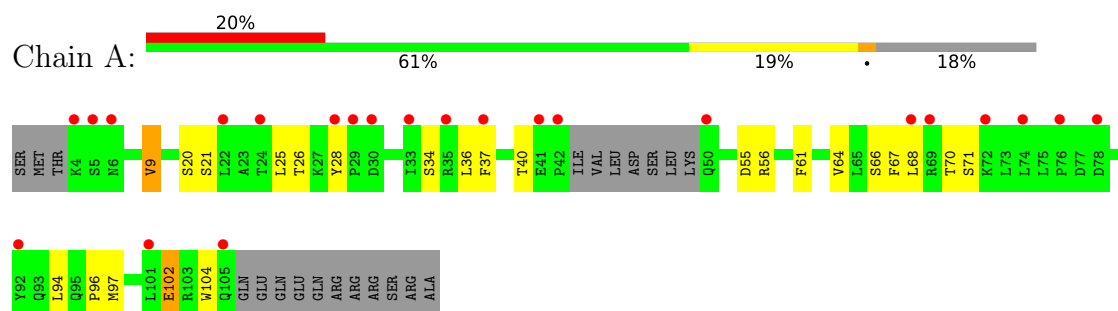
3 Residue-property plots [i](#)

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.

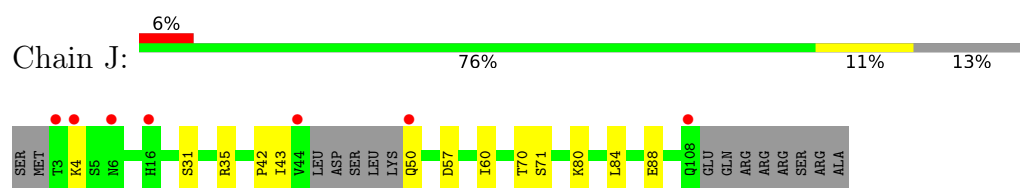
- Molecule 1: BTB/POZ domain-containing protein KCTD15



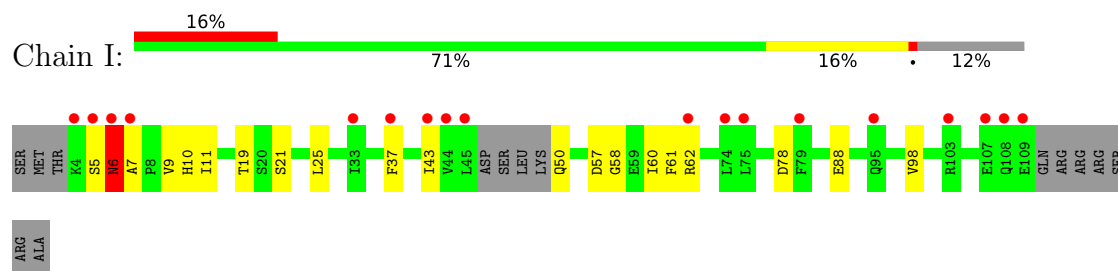
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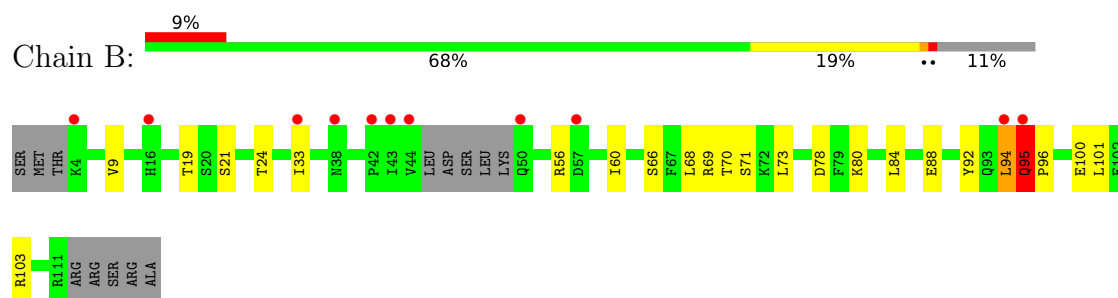
- Molecule 1: BTB/POZ domain-containing protein KCTD15



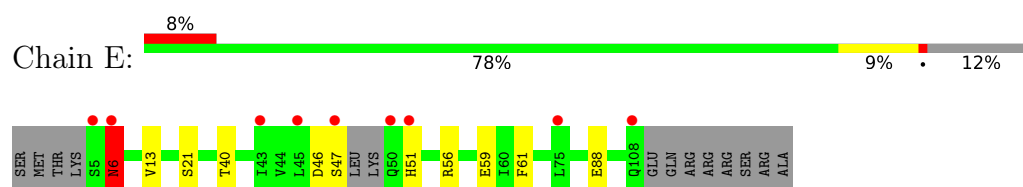
- Molecule 1: BTB/POZ domain-containing protein KCTD15



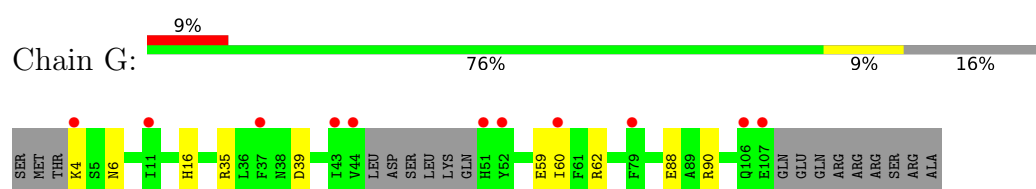
- Molecule 1: BTB/POZ domain-containing protein KCTD15



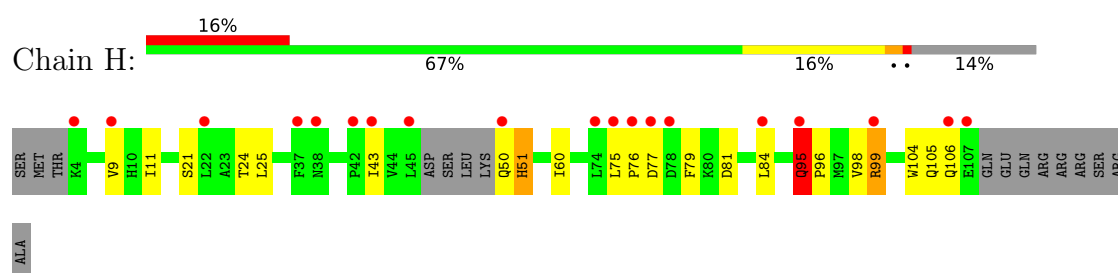
- Molecule 1: BTB/POZ domain-containing protein KCTD15



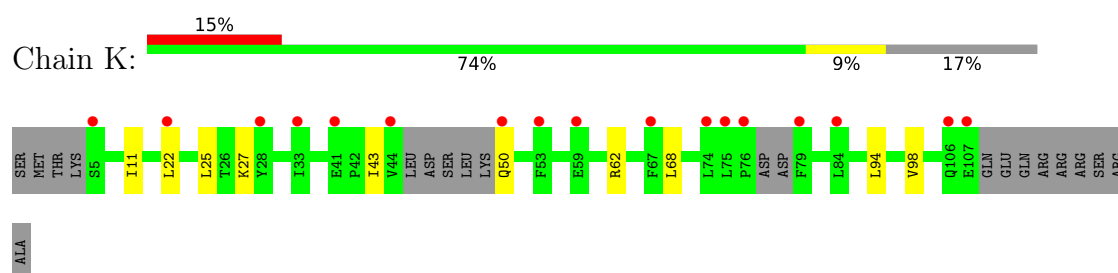
- Molecule 1: BTB/POZ domain-containing protein KCTD15



- Molecule 1: BTB/POZ domain-containing protein KCTD15



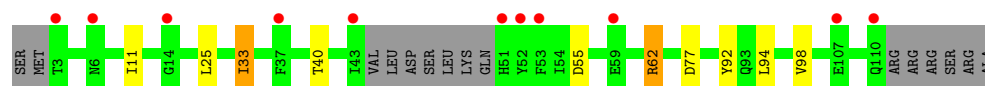
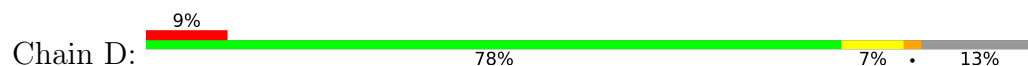
- Molecule 1: BTB/POZ domain-containing protein KCTD15



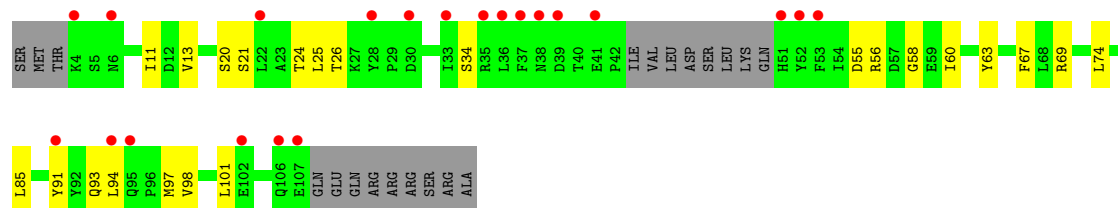
- Molecule 1: BTB/POZ domain-containing protein KCTD15



- Molecule 1: BTB/POZ domain-containing protein KCTD15



- Molecule 1: BTB/POZ domain-containing protein KCTD15



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	151.08Å 151.08Å 155.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.75 – 2.25 46.75 – 2.25	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.75-2.25) 99.9 (46.75-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 2.24Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.246 , 0.285 0.247 , 0.285	Depositor DCC
R_{free} test set	4178 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	65.8	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for -h,l,k 0.007 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9546	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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

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	0.33	0/734	0.67	2/1004 (0.2%)
1	B	0.42	0/854	0.83	4/1156 (0.3%)
1	C	0.32	0/829	0.59	0/1128
1	D	0.38	0/841	0.55	0/1141
1	E	0.49	0/855	0.71	2/1161 (0.2%)
1	F	0.31	0/728	0.60	0/996
1	G	0.40	0/813	0.62	0/1105
1	H	0.47	0/824	1.04	6/1119 (0.5%)
1	I	0.55	1/849 (0.1%)	0.77	2/1154 (0.2%)
1	J	0.39	0/854	0.61	3/1159 (0.3%)
1	K	0.37	0/767	0.55	0/1046
1	L	0.40	0/758	0.61	0/1036
All	All	0.41	1/9706 (0.0%)	0.69	19/13205 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	E	0	1
1	I	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	5	SER	CA-C	6.97	1.62	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	99	ARG	CG-CD-NE	16.27	147.80	112.00
1	H	99	ARG	CB-CG-CD	-14.26	78.51	111.30
1	B	95	GLN	CA-CB-CG	-13.04	88.01	114.10
1	B	94	LEU	CA-C-N	-10.24	96.82	121.80
1	B	94	LEU	C-N-CA	-10.24	96.82	121.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	95	GLN	Sidechain
1	E	6	ASN	Peptide
1	I	6	ASN	Peptide

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	713	0	595	17	0
1	B	833	0	772	13	0
1	C	808	0	734	21	0
1	D	820	0	759	8	0
1	E	834	0	770	6	0
1	F	708	0	600	20	0
1	G	792	0	735	7	0
1	H	803	0	736	15	0
1	I	828	0	759	14	0
1	J	832	0	785	10	0
1	K	747	0	670	9	0
1	L	739	0	675	14	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	9	0	0	0	0
2	E	13	0	0	0	0
2	F	2	0	0	0	0
2	G	9	0	0	0	0
2	H	8	0	0	1	0
2	I	14	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	17	0	0	0	0
2	K	3	0	0	0	0
2	L	8	0	0	0	0
All	All	9546	0	8590	140	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 8.

The worst 5 of 140 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:6:ASN:HA	1:E:21:SER:HB2	1.49	0.93
1:F:56:ARG:HD2	1:F:91:TYR:CD2	2.16	0.80
1:C:33:ILE:HD12	1:C:68:LEU:HD11	1.65	0.77
1:F:56:ARG:HD2	1:F:91:TYR:HD2	1.47	0.77
1:B:33:ILE:HD12	1:B:68:LEU:HD11	1.66	0.75

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	91/116 (78%)	86 (94%)	5 (6%)	0	100	100
1	B	99/116 (85%)	93 (94%)	6 (6%)	0	100	100
1	C	99/116 (85%)	94 (95%)	5 (5%)	0	100	100
1	D	97/116 (84%)	95 (98%)	2 (2%)	0	100	100
1	E	98/116 (84%)	95 (97%)	3 (3%)	0	100	100
1	F	92/116 (79%)	85 (92%)	7 (8%)	0	100	100
1	G	94/116 (81%)	90 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	96/116 (83%)	90 (94%)	3 (3%)	3 (3%)	3	1
1	I	98/116 (84%)	89 (91%)	9 (9%)	0	100	100
1	J	98/116 (84%)	94 (96%)	4 (4%)	0	100	100
1	K	90/116 (78%)	88 (98%)	2 (2%)	0	100	100
1	L	91/116 (78%)	84 (92%)	5 (6%)	2 (2%)	5	2
All	All	1143/1392 (82%)	1083 (95%)	55 (5%)	5 (0%)	30	31

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	95	GLN
1	L	71	SER
1	H	105	GLN
1	L	79	PHE
1	H	76	PRO

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	65/109 (60%)	64 (98%)	1 (2%)	57	68
1	B	85/109 (78%)	83 (98%)	2 (2%)	43	54
1	C	80/109 (73%)	80 (100%)	0	100	100
1	D	86/109 (79%)	83 (96%)	3 (4%)	32	39
1	E	90/109 (83%)	88 (98%)	2 (2%)	45	56
1	F	64/109 (59%)	63 (98%)	1 (2%)	55	66
1	G	83/109 (76%)	83 (100%)	0	100	100
1	H	82/109 (75%)	81 (99%)	1 (1%)	63	74
1	I	87/109 (80%)	86 (99%)	1 (1%)	65	75
1	J	89/109 (82%)	88 (99%)	1 (1%)	65	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	75/109 (69%)	75 (100%)	0	100	100
1	L	75/109 (69%)	72 (96%)	3 (4%)	28	34
All	All	961/1308 (74%)	946 (98%)	15 (2%)	55	66

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	51	HIS
1	D	62	ARG
1	L	5	SER
1	F	74	LEU
1	D	33	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	38	ASN
1	J	93	GLN
1	I	95	GLN
1	E	16	HIS
1	D	16	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](#)

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	95/116 (81%)	1.54	23 (24%) 2 1	84, 99, 117, 133	0
1	B	103/116 (88%)	0.99	11 (10%) 11 10	61, 80, 103, 123	0
1	C	103/116 (88%)	1.43	28 (27%) 1 1	72, 87, 108, 116	0
1	D	101/116 (87%)	0.76	11 (10%) 10 10	56, 69, 97, 120	0
1	E	102/116 (87%)	0.71	9 (8%) 15 14	55, 65, 96, 115	0
1	F	96/116 (82%)	1.47	21 (21%) 2 2	76, 93, 125, 166	0
1	G	98/116 (84%)	0.83	11 (11%) 10 9	56, 72, 111, 125	0
1	H	100/116 (86%)	1.05	19 (19%) 3 3	51, 67, 110, 132	0
1	I	102/116 (87%)	1.10	18 (17%) 4 3	57, 76, 118, 147	0
1	J	101/116 (87%)	0.75	7 (6%) 23 21	35, 72, 99, 115	1 (0%)
1	K	96/116 (82%)	1.21	17 (17%) 4 3	66, 83, 103, 125	0
1	L	95/116 (81%)	0.94	9 (9%) 14 13	58, 74, 98, 113	0
All	All	1192/1392 (85%)	1.06	184 (15%) 5 4	35, 79, 112, 166	1 (0%)

The worst 5 of 184 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	44	VAL	6.0
1	C	43	ILE	5.8
1	A	105	GLN	5.8
1	L	44	VAL	5.6
1	K	107	GLU	5.5

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.