



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 12, 2020 – 09:03 PM BST

PDB ID : 2ZP9
Title : The Nature of the TRAP:Anti-TRAP complex
Authors : Watanabe, M.; Heddle, J.G.; Unzai, S.; Akashi, S.; Park, S.Y.; Tame, J.R.H.
Deposited on : 2008-07-08
Resolution : 3.20 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.14.4.dev1
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) : 2.14.4.dev1

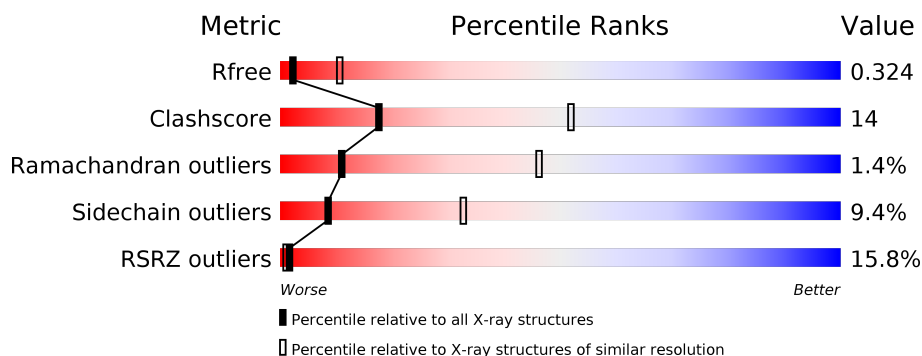
1 Overall quality at a glance

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}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (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 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	81	<div> <div>2%</div> <div> <div>51%</div> <div>26%</div> <div>•</div> <div>22%</div> </div> </div>
1	B	81	<div> <div>%</div> <div> <div>51%</div> <div>26%</div> <div>•</div> <div>21%</div> </div> </div>
1	F	81	<div> <div>15%</div> <div> <div>60%</div> <div>17%</div> <div>•</div> <div>22%</div> </div> </div>
1	G	81	<div> <div>9%</div> <div> <div>51%</div> <div>26%</div> <div>•</div> <div>22%</div> </div> </div>
1	K	81	<div> <div>7%</div> <div> <div>38%</div> <div>38%</div> <div>•</div> <div>22%</div> </div> </div>
1	L	81	<div> <div>16%</div> <div> <div>58%</div> <div>19%</div> <div>•</div> <div>22%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	C	53	
2	D	53	
2	E	53	
2	H	53	
2	I	53	
2	J	53	
2	M	53	
2	N	53	
2	O	53	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TRP	F	100	-	-	X	-
3	TRP	G	100	-	-	X	-
3	TRP	K	100	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5728 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 Transcription attenuation protein mtrB.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	63	Total	C	N	O	0	0	0
			491	309	91	91			
1	B	64	Total	C	N	O	0	0	0
			499	315	92	92			
1	F	63	Total	C	N	O	0	0	0
			491	309	91	91			
1	G	63	Total	C	N	O	0	0	0
			491	309	91	91			
1	K	63	Total	C	N	O	0	0	0
			491	309	91	91			
1	L	63	Total	C	N	O	0	0	0
			491	309	91	91			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ALA	-	LINKER	UNP Q9X6J6
A	78	ALA	-	LINKER	UNP Q9X6J6
A	79	ALA	-	LINKER	UNP Q9X6J6
A	80	ALA	-	LINKER	UNP Q9X6J6
A	81	ALA	-	LINKER	UNP Q9X6J6
A	82	ALA	-	LINKER	UNP Q9X6J6
A	83	ALA	-	LINKER	UNP Q9X6J6
B	77	ALA	-	LINKER	UNP Q9X6J6
B	78	ALA	-	LINKER	UNP Q9X6J6
B	79	ALA	-	LINKER	UNP Q9X6J6
B	80	ALA	-	LINKER	UNP Q9X6J6
B	81	ALA	-	LINKER	UNP Q9X6J6
B	82	ALA	-	LINKER	UNP Q9X6J6
B	83	ALA	-	LINKER	UNP Q9X6J6
F	77	ALA	-	LINKER	UNP Q9X6J6
F	78	ALA	-	LINKER	UNP Q9X6J6
F	79	ALA	-	LINKER	UNP Q9X6J6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	80	ALA	-	LINKER	UNP Q9X6J6
F	81	ALA	-	LINKER	UNP Q9X6J6
F	82	ALA	-	LINKER	UNP Q9X6J6
F	83	ALA	-	LINKER	UNP Q9X6J6
G	77	ALA	-	LINKER	UNP Q9X6J6
G	78	ALA	-	LINKER	UNP Q9X6J6
G	79	ALA	-	LINKER	UNP Q9X6J6
G	80	ALA	-	LINKER	UNP Q9X6J6
G	81	ALA	-	LINKER	UNP Q9X6J6
G	82	ALA	-	LINKER	UNP Q9X6J6
G	83	ALA	-	LINKER	UNP Q9X6J6
K	77	ALA	-	LINKER	UNP Q9X6J6
K	78	ALA	-	LINKER	UNP Q9X6J6
K	79	ALA	-	LINKER	UNP Q9X6J6
K	80	ALA	-	LINKER	UNP Q9X6J6
K	81	ALA	-	LINKER	UNP Q9X6J6
K	82	ALA	-	LINKER	UNP Q9X6J6
K	83	ALA	-	LINKER	UNP Q9X6J6
L	77	ALA	-	LINKER	UNP Q9X6J6
L	78	ALA	-	LINKER	UNP Q9X6J6
L	79	ALA	-	LINKER	UNP Q9X6J6
L	80	ALA	-	LINKER	UNP Q9X6J6
L	81	ALA	-	LINKER	UNP Q9X6J6
L	82	ALA	-	LINKER	UNP Q9X6J6
L	83	ALA	-	LINKER	UNP Q9X6J6

- Molecule 2 is a protein called Tryptophan RNA-binding attenuator protein-inhibitory protein.

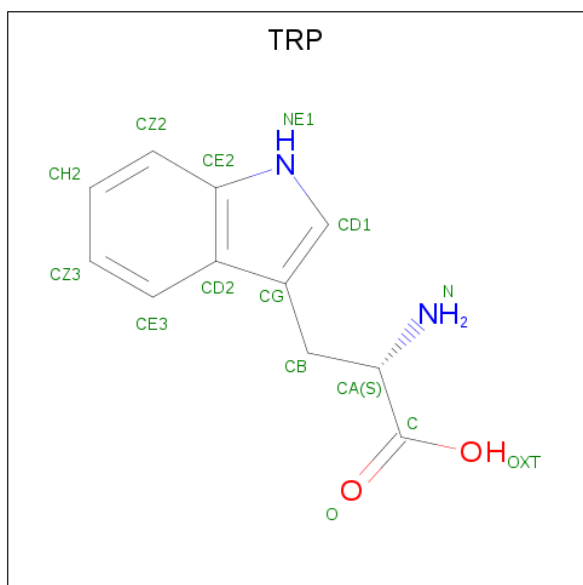
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	46	Total	C	N	O	S	0	0	0
			338	212	57	64	5			
2	D	45	Total	C	N	O	S	8	0	0
			334	210	56	63	5			
2	E	49	Total	C	N	O	S	0	0	0
			356	223	60	68	5			
2	H	42	Total	C	N	O	S	25	0	0
			310	197	49	59	5			
2	I	39	Total	C	N	O	S	0	0	0
			290	182	47	57	4			
2	J	41	Total	C	N	O	S	17	0	0
			301	192	48	56	5			
2	M	42	Total	C	N	O	S	25	0	0
			310	197	49	59	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	17	Total	C	N	O		0	0	0
			139	91	23	25				
2	O	41	Total	C	N	O	S	17	0	0
			301	192	48	56	5			

- Molecule 3 is TRYPTOPHAN (three-letter code: TRP) (formula: $C_{11}H_{12}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			15	11	2	2		
3	B	1	Total	C	N	O	0	0
			15	11	2	2		
3	F	1	Total	C	N	O	0	0
			15	11	2	2		
3	G	1	Total	C	N	O	0	0
			15	11	2	2		
3	K	1	Total	C	N	O	0	0
			15	11	2	2		
3	L	1	Total	C	N	O	0	0
			15	11	2	2		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	J	1	Total	Zn	0	0
			1	1		

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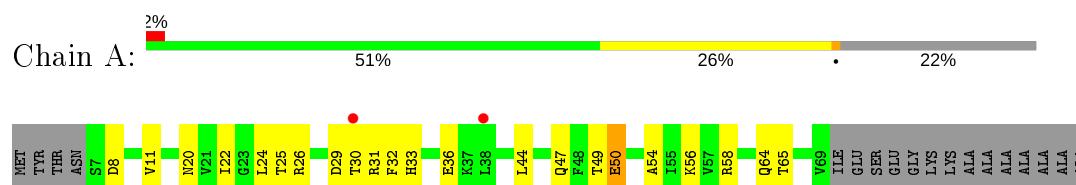
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	1	Total 1	Zn 1	0	0
4	D	1	Total 1	Zn 1	0	0
4	C	1	Total 1	Zn 1	0	0
4	E	1	Total 1	Zn 1	0	0

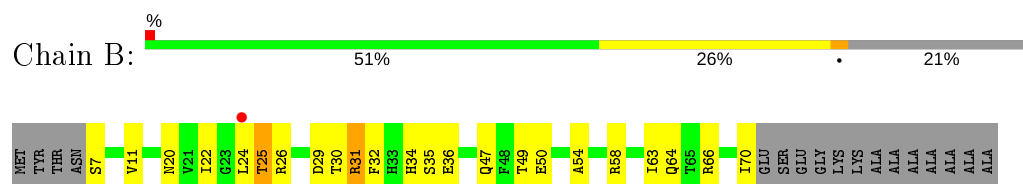
3 Residue-property plots [i](#)

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.

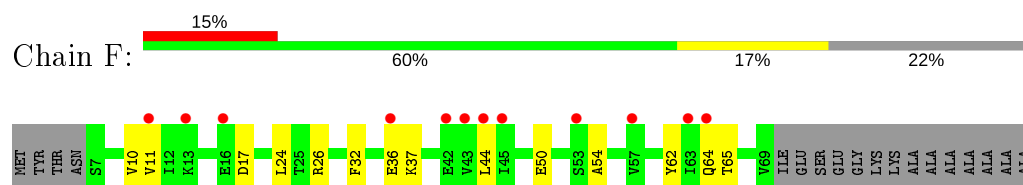
- Molecule 1: Transcription attenuation protein mtrB



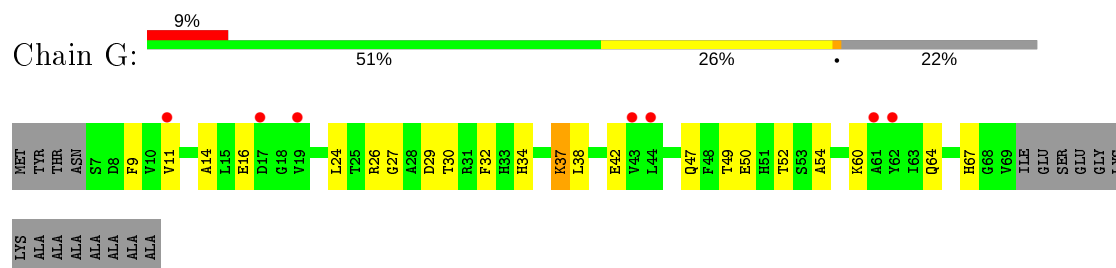
- Molecule 1: Transcription attenuation protein mtrB



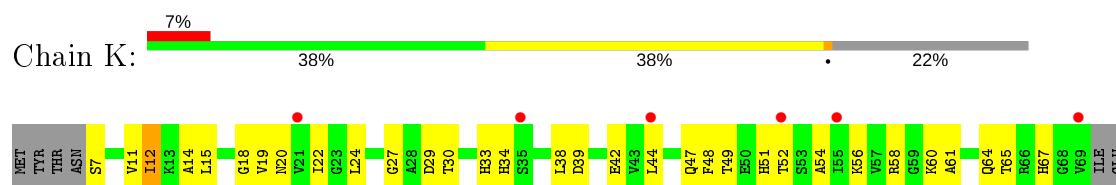
- Molecule 1: Transcription attenuation protein mtrB

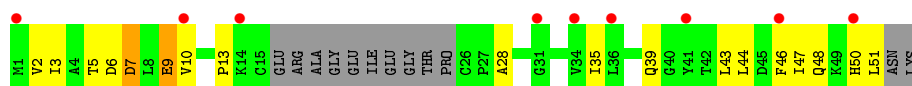


- Molecule 1: Transcription attenuation protein mtrB

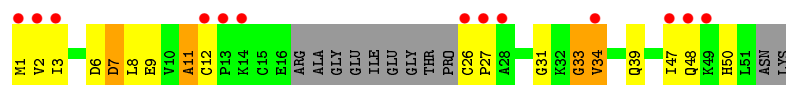


- Molecule 1: Transcription attenuation protein mtrB

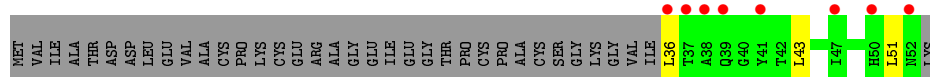




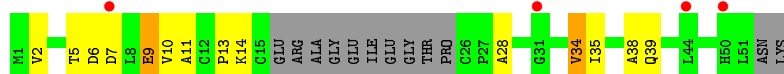
- Molecule 2: Tryptophan RNA-binding attenuator protein-inhibitory protein



- Molecule 2: Tryptophan RNA-binding attenuator protein-inhibitory protein



- Molecule 2: Tryptophan RNA-binding attenuator protein-inhibitory protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 6	Depositor
Cell constants a, b, c, α , β , γ	197.13 Å 197.13 Å 56.66 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.20 37.25 – 3.20	Depositor EDS
% Data completeness (in resolution range)	91.0 (20.00-3.20) 90.8 (37.25-3.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.93 (at 3.18 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.303 , 0.325 0.302 , 0.324	Depositor DCC
R_{free} test set	989 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	93.3	Xtriage
Anisotropy	0.501	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 91.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.439 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	5728	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	0.46	0/498	0.62	0/669
1	B	0.53	0/506	0.67	0/680
1	F	0.38	0/498	0.55	0/669
1	G	0.42	0/498	0.58	0/669
1	K	0.39	0/498	0.57	0/669
1	L	0.37	0/498	0.55	0/669
2	C	0.38	0/341	0.59	0/459
2	D	1.41	3/337 (0.9%)	2.27	4/454 (0.9%)
2	E	0.44	0/360	0.60	0/486
2	H	0.91	3/313 (1.0%)	3.48	8/422 (1.9%)
2	I	0.41	0/293	0.57	0/395
2	J	1.48	2/304 (0.7%)	1.08	3/410 (0.7%)
2	M	0.75	3/313 (1.0%)	3.26	5/422 (1.2%)
2	N	0.42	0/141	0.50	0/190
2	O	1.77	2/304 (0.7%)	1.66	5/410 (1.2%)
All	All	0.78	13/5702 (0.2%)	1.42	25/7673 (0.3%)

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
2	D	0	1
2	H	0	2
2	J	0	2
2	M	0	3
2	O	0	1
All	All	0	9

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	7	ASP	C-N	-27.86	0.69	1.34
2	J	7	ASP	C-N	-22.03	0.83	1.34
2	D	34	VAL	C-N	17.88	1.75	1.34
2	D	35	ILE	C-N	-14.52	1.00	1.34
2	J	9	GLU	C-N	-11.23	1.08	1.34

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	9	GLU	O-C-N	-64.52	19.48	122.70
2	H	9	GLU	O-C-N	-61.24	24.71	122.70
2	D	34	VAL	O-C-N	-36.43	64.41	122.70
2	H	33	GLY	O-C-N	-26.49	80.32	122.70
2	D	34	VAL	CA-C-N	24.14	170.30	117.20

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	35	ILE	Mainchain
2	H	33	GLY	Mainchain,Peptide
2	J	7	ASP	Mainchain
2	J	9	GLU	Mainchain
2	M	11	ALA	Mainchain

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	491	0	497	18	1
1	B	499	0	508	15	0
1	F	491	0	497	8	0
1	G	491	0	497	21	0
1	K	491	0	497	22	0
1	L	491	0	497	13	0
2	C	338	0	343	12	0
2	D	334	0	337	15	0
2	E	356	0	358	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	310	0	316	12	0
2	I	290	0	285	12	0
2	J	301	0	306	14	0
2	M	310	0	317	10	0
2	N	139	0	140	2	0
2	O	301	0	310	8	0
3	A	15	0	9	5	0
3	B	15	0	9	2	1
3	F	15	0	9	6	0
3	G	15	0	9	10	0
3	K	15	0	9	2	0
3	L	15	0	9	1	0
4	C	1	0	0	1	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	I	1	0	0	1	0
4	J	1	0	0	0	0
All	All	5728	0	5759	151	1

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 14.

The worst 5 of 151 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:G:27:GLY:H	3:G:100:TRP:HB2	1.18	1.09
2:I:15:CYS:HG	4:I:54:ZN:ZN	0.84	0.90
2:C:12:CYS:HG	4:C:54:ZN:ZN	0.64	0.89
3:G:100:TRP:HA	1:K:49:THR:CB	2.09	0.83
3:G:100:TRP:HA	1:K:49:THR:OG1	1.79	0.81

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:THR:OG1	3:B:100:TRP:OXT[6_555]	2.15	0.05

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	61/81 (75%)	60 (98%)	1 (2%)	0	100	100
1	B	62/81 (76%)	61 (98%)	1 (2%)	0	100	100
1	F	61/81 (75%)	58 (95%)	3 (5%)	0	100	100
1	G	61/81 (75%)	60 (98%)	1 (2%)	0	100	100
1	K	61/81 (75%)	59 (97%)	1 (2%)	1 (2%)	9	43
1	L	61/81 (75%)	60 (98%)	1 (2%)	0	100	100
2	C	42/53 (79%)	38 (90%)	3 (7%)	1 (2%)	6	34
2	D	41/53 (77%)	33 (80%)	6 (15%)	2 (5%)	2	17
2	E	45/53 (85%)	40 (89%)	4 (9%)	1 (2%)	6	35
2	H	38/53 (72%)	34 (90%)	3 (8%)	1 (3%)	5	31
2	I	35/53 (66%)	33 (94%)	1 (3%)	1 (3%)	4	28
2	J	37/53 (70%)	34 (92%)	1 (3%)	2 (5%)	2	14
2	M	38/53 (72%)	34 (90%)	3 (8%)	1 (3%)	5	31
2	N	15/53 (28%)	15 (100%)	0	0	100	100
2	O	37/53 (70%)	36 (97%)	1 (3%)	0	100	100
All	All	695/963 (72%)	655 (94%)	30 (4%)	10 (1%)	11	46

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	16	GLU
2	E	16	GLU
2	H	34	VAL
2	I	35	ILE
2	M	34	VAL

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	52/62 (84%)	47 (90%)	5 (10%)	8	32
1	B	53/62 (86%)	49 (92%)	4 (8%)	13	45
1	F	52/62 (84%)	50 (96%)	2 (4%)	33	67
1	G	52/62 (84%)	48 (92%)	4 (8%)	13	44
1	K	52/62 (84%)	46 (88%)	6 (12%)	5	24
1	L	52/62 (84%)	50 (96%)	2 (4%)	33	67
2	C	37/43 (86%)	32 (86%)	5 (14%)	4	18
2	D	37/43 (86%)	30 (81%)	7 (19%)	1	8
2	E	39/43 (91%)	35 (90%)	4 (10%)	7	29
2	H	35/43 (81%)	31 (89%)	4 (11%)	5	24
2	I	33/43 (77%)	28 (85%)	5 (15%)	3	13
2	J	34/43 (79%)	31 (91%)	3 (9%)	10	36
2	M	35/43 (81%)	33 (94%)	2 (6%)	20	56
2	N	15/43 (35%)	14 (93%)	1 (7%)	16	50
2	O	34/43 (79%)	31 (91%)	3 (9%)	10	36
All	All	612/759 (81%)	555 (91%)	57 (9%)	8	33

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	17	ASP
2	H	2	VAL
2	M	48	GLN
1	F	37	LYS
1	G	30	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	48	GLN
2	J	39	GLN
1	L	67	HIS
1	G	47	GLN
2	M	39	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 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	$\# Z > 2$
3	TRP	F	100	-	12,16,16	0.75	0	12,22,22	0.88	0
3	TRP	A	100	-	12,16,16	0.84	0	12,22,22	0.89	0
3	TRP	B	100	-	12,16,16	0.96	0	12,22,22	0.99	0
3	TRP	K	100	-	12,16,16	0.65	0	12,22,22	0.85	0
3	TRP	L	100	-	12,16,16	0.67	0	12,22,22	0.87	0
3	TRP	G	100	-	12,16,16	0.68	0	12,22,22	0.89	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
3	TRP	F	100	-	-	1/3/8/8	0/2/2/2
3	TRP	A	100	-	-	0/3/8/8	0/2/2/2
3	TRP	B	100	-	-	1/3/8/8	0/2/2/2
3	TRP	K	100	-	-	2/3/8/8	0/2/2/2
3	TRP	L	100	-	-	1/3/8/8	0/2/2/2
3	TRP	G	100	-	-	1/3/8/8	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	K	100	TRP	N-CA-CB-CG
3	K	100	TRP	C-CA-CB-CG
3	G	100	TRP	N-CA-CB-CG
3	B	100	TRP	N-CA-CB-CG
3	F	100	TRP	CA-CB-CG-CD1

There are no ring outliers.

6 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	100	TRP	6	0
3	A	100	TRP	5	0
3	B	100	TRP	2	1
3	K	100	TRP	2	0
3	L	100	TRP	1	0
3	G	100	TRP	10	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	H	2
2	O	2
2	J	2
2	D	2
2	M	2

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	34:VAL	C	35:ILE	N	1.75
1	M	11:ALA	C	12:CYS	N	1.18
1	M	33:GLY	C	34:VAL	N	1.18
1	H	11:ALA	C	12:CYS	N	1.15
1	H	31:GLY	C	32:LYS	N	1.11

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	63/81 (77%)	0.78	2 (3%) 47 31	83, 86, 88, 90	0
1	B	64/81 (79%)	0.67	1 (1%) 72 59	81, 86, 88, 90	0
1	F	63/81 (77%)	1.06	12 (19%) 1 1	84, 86, 89, 95	0
1	G	63/81 (77%)	0.95	7 (11%) 5 3	84, 86, 89, 97	0
1	K	63/81 (77%)	0.77	6 (9%) 8 4	83, 86, 89, 96	0
1	L	63/81 (77%)	1.29	13 (20%) 1 1	84, 86, 89, 97	0
2	C	46/53 (86%)	0.93	6 (13%) 3 2	85, 86, 87, 90	3 (6%)
2	D	44/53 (83%)	1.31	8 (18%) 1 1	82, 86, 86, 87	11 (25%)
2	E	49/53 (92%)	0.79	2 (4%) 37 24	77, 86, 86, 88	7 (14%)
2	H	38/53 (71%)	1.68	10 (26%) 0 0	85, 86, 86, 86	2 (5%)
2	I	39/53 (73%)	2.02	14 (35%) 0 0	85, 86, 86, 87	8 (20%)
2	J	39/53 (73%)	1.02	9 (23%) 0 0	86, 86, 87, 88	3 (7%)
2	M	38/53 (71%)	2.41	13 (34%) 0 0	85, 86, 87, 88	2 (5%)
2	N	17/53 (32%)	2.17	8 (47%) 0 0	85, 86, 86, 87	1 (5%)
2	O	39/53 (73%)	0.91	4 (10%) 6 4	85, 86, 87, 88	3 (7%)
All	All	728/963 (75%)	1.15	115 (15%) 2 1	77, 86, 88, 97	40 (5%)

The worst 5 of 115 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	52	ASN	11.9
2	M	1	MET	11.7
2	H	1	MET	8.8
2	M	12	CYS	8.7
2	M	28	ALA	7.0

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 monosaccharides 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(\AA^2)	Q<0.9
3	TRP	K	100	15/15	0.76	0.46	122,122,122,122	0
4	ZN	C	54	1/1	0.84	0.17	133,133,133,133	0
3	TRP	F	100	15/15	0.85	0.45	92,92,93,93	0
3	TRP	L	100	15/15	0.86	0.41	111,111,112,112	0
3	TRP	B	100	15/15	0.87	0.34	66,68,69,70	0
4	ZN	I	54	1/1	0.87	0.23	140,140,140,140	0
3	TRP	G	100	15/15	0.89	0.20	93,93,93,93	0
4	ZN	J	54	1/1	0.94	0.23	118,118,118,118	0
3	TRP	A	100	15/15	0.95	0.29	56,57,58,58	0
4	ZN	D	54	1/1	0.97	0.25	123,123,123,123	0
4	ZN	E	54	1/1	0.99	0.29	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.