



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 4, 2026 – 10:19 PM UTC

PDB ID : 9ZVU / pdb_00009zvu
Title : The ubiquitin-associated domain of human thirty-eight negative kinase-1 rigidly fused to a double trigger variant of the 1TEL crystallization chaperone, alternate crystal form
Authors : Averett, B.J.; Averett, J.C.; Wilson, E.W.; Bradford, M.J.; Anderson, E.; Anderson, A.; Doukov, T.; Moody, J.D.
Deposited on : 2025-12-30
Resolution : 1.96 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

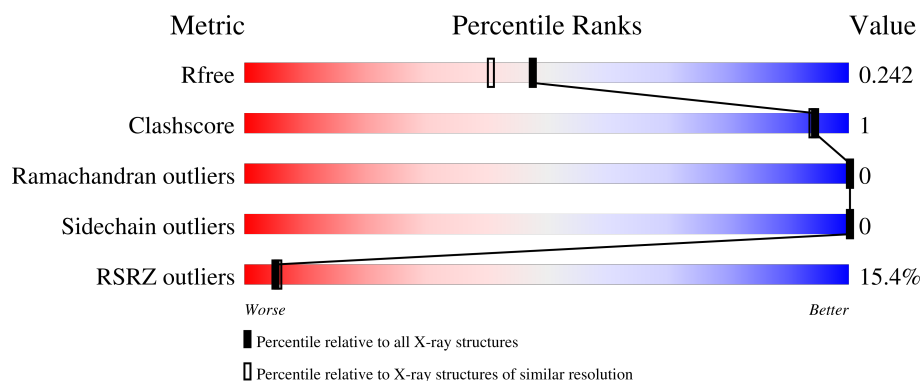
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	165	
1	B	165	

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
2	TLA	A	202	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4656 atoms, of which 2149 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 factor ETV6,Non-receptor tyrosine-protein kinase TNK1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	153	Total	C	H	N	O	S	0	1	0
			2227	738	1066	206	215	2			
1	B	153	Total	C	H	N	O	S	0	0	0
			2234	737	1073	211	211	2			

There are 36 discrepancies between the modelled and reference sequences:

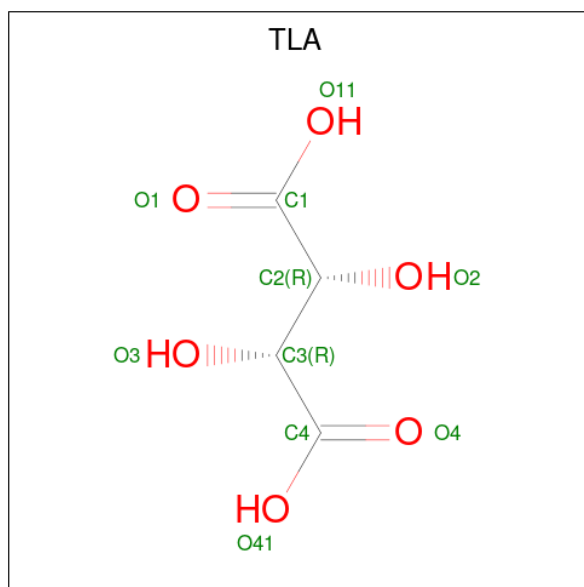
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P41212
A	2	GLY	-	expression tag	UNP P41212
A	3	HIS	-	expression tag	UNP P41212
A	4	HIS	-	expression tag	UNP P41212
A	5	HIS	-	expression tag	UNP P41212
A	6	HIS	-	expression tag	UNP P41212
A	7	HIS	-	expression tag	UNP P41212
A	8	HIS	-	expression tag	UNP P41212
A	9	HIS	-	expression tag	UNP P41212
A	10	HIS	-	expression tag	UNP P41212
A	11	HIS	-	expression tag	UNP P41212
A	12	HIS	-	expression tag	UNP P41212
A	46	SER	ARG	engineered mutation	UNP P41212
A	62	GLU	LEU	engineered mutation	UNP P41212
A	78	GLU	VAL	engineered mutation	UNP P41212
A	90	VAL	LEU	engineered mutation	UNP Q13470
A	109	ALA	CYS	engineered mutation	UNP Q13470
A	143	ALA	CYS	engineered mutation	UNP Q13470
B	1	MET	-	initiating methionine	UNP P41212
B	2	GLY	-	expression tag	UNP P41212
B	3	HIS	-	expression tag	UNP P41212
B	4	HIS	-	expression tag	UNP P41212
B	5	HIS	-	expression tag	UNP P41212
B	6	HIS	-	expression tag	UNP P41212

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	7	HIS	-	expression tag	UNP P41212
B	8	HIS	-	expression tag	UNP P41212
B	9	HIS	-	expression tag	UNP P41212
B	10	HIS	-	expression tag	UNP P41212
B	11	HIS	-	expression tag	UNP P41212
B	12	HIS	-	expression tag	UNP P41212
B	46	SER	ARG	engineered mutation	UNP P41212
B	62	GLU	LEU	engineered mutation	UNP P41212
B	78	GLU	VAL	engineered mutation	UNP P41212
B	90	VAL	LEU	engineered mutation	UNP Q13470
B	109	ALA	CYS	engineered mutation	UNP Q13470
B	143	ALA	CYS	engineered mutation	UNP Q13470

- Molecule 2 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C H O 7 2 2 3	0	0
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C H O 7 2 2 3	0	0
2	B	1	Total C H O 7 2 2 3	0	0

Continued on next page...

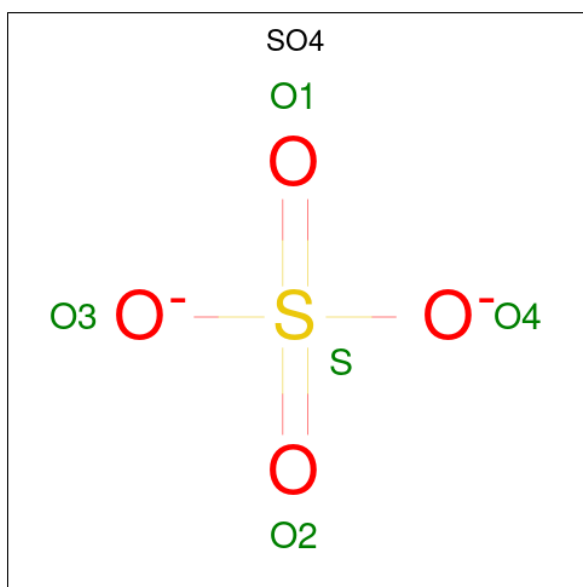
Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

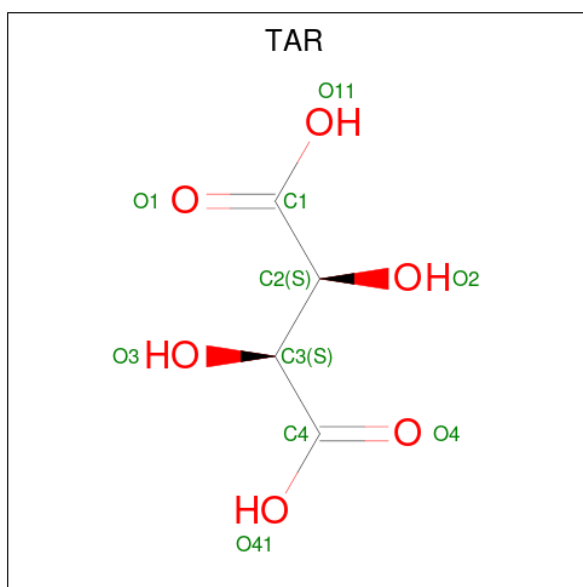
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Na	0	0
			4	4		
3	B	4	Total	Na	0	0
			4	4		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is D(-)-TARTARIC ACID (CCD ID: TAR) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			14	4	4	6		

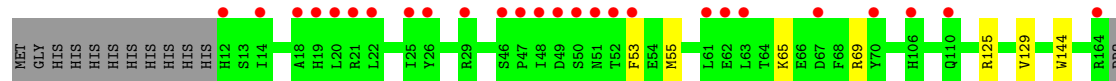
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	67	Total	O	0	0
			67	67		
6	B	54	Total	O	0	0
			54	54		

- Molecule 1: Transcription factor ETV6,Non-receptor tyrosine-protein kinase TNK1



- Molecule 1: Transcription factor ETV6,Non-receptor tyrosine-protein kinase TNK1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	38.21Å 79.37Å 119.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.59 – 1.96 59.59 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.9 (59.59-1.96) 94.6 (59.59-1.96)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 1.97Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.211 , 0.247 0.207 , 0.242	Depositor DCC
R_{free} test set	1297 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 69.5	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	4656	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.96% 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: TLA, SO4, TAR, NA

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	0.18	0/1191	0.30	0/1621
1	B	0.15	0/1189	0.28	0/1617
All	All	0.17	0/2380	0.29	0/3238

There are no bond length outliers.

There are no bond angle outliers.

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	1161	1066	1061	2	0
1	B	1161	1073	1058	4	0
2	A	18	4	1	0	0
2	B	13	2	0	0	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
4	A	5	0	0	0	0
4	B	10	0	0	0	0
5	B	10	4	4	0	0
6	A	67	0	0	0	0
6	B	54	0	0	0	0
All	All	2507	2149	2124	6	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 1.

All (6) 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:48:ILE:HD13	1:A:79:LEU:HD11	1.88	0.56
1:A:46:SER:O	1:A:48:ILE:HG13	2.10	0.51
1:B:129:VAL:HG21	1:B:144:TRP:CE3	2.51	0.46
1:B:65:LYS:O	1:B:69:ARG:HG3	2.20	0.41
1:B:53:PHE:O	1:B:55:MET:N	2.54	0.40
1:B:125:ARG:O	1:B:129:VAL:HG23	2.21	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	152/165 (92%)	151 (99%)	1 (1%)	0	100	100
1	B	151/165 (92%)	149 (99%)	2 (1%)	0	100	100
All	All	303/330 (92%)	300 (99%)	3 (1%)	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	108/145 (74%)	108 (100%)	0	100	100
1	B	109/145 (75%)	109 (100%)	0	100	100
All	All	217/290 (75%)	217 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	91	GLN
1	A	131	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 8 are monoatomic - leaving 11 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	$\# Z > 2$
2	TLA	A	203	-	3,3,9	1.23	0	3,3,12	1.40	0
2	TLA	A	204	-	4,4,9	1.28	0	4,4,12	2.39	2 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	TLA	A	201	-	3,3,9	1.20	0	3,3,12	1.40	0
4	SO4	B	209	-	4,4,4	0.22	0	6,6,6	0.12	0
2	TLA	A	202	-	4,4,9	1.30	0	4,4,12	2.24	2 (50%)
4	SO4	A	209	-	4,4,4	0.25	0	6,6,6	0.08	0
5	TAR	B	204	-	9,9,9	1.38	2 (22%)	12,12,12	1.66	2 (16%)
2	TLA	B	201	-	4,4,9	1.28	0	4,4,12	2.53	2 (50%)
4	SO4	B	210	-	4,4,4	0.24	0	6,6,6	0.08	0
2	TLA	B	202	-	3,3,9	1.22	0	3,3,12	1.37	0
2	TLA	B	203	-	3,3,9	1.24	0	3,3,12	1.33	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
5	TAR	B	204	-	-	4/12/12/12	-
2	TLA	A	202	-	-	2/2/2/12	-
2	TLA	A	204	-	-	0/2/2/12	-
2	TLA	B	201	-	-	0/2/2/12	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	204	TAR	O1-C1	3.07	1.31	1.22
5	B	204	TAR	O11-C1	-2.77	1.21	1.30

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	201	TLA	O41-C4-C3	3.65	118.53	111.90
2	A	204	TLA	O11-C1-C2	3.27	117.85	111.90
5	B	204	TAR	O11-C1-C2	3.26	122.37	113.31
2	B	201	TLA	O4-C4-C3	-3.17	114.31	123.48
5	B	204	TAR	O1-C1-C2	-3.15	113.23	121.62
2	A	204	TLA	O1-C1-C2	-2.94	114.96	123.48
2	A	202	TLA	O41-C4-C3	2.90	117.18	111.90
2	A	202	TLA	O4-C4-C3	-2.79	115.41	123.48

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	202	TLA	O3-C3-C4-O4
2	A	202	TLA	O3-C3-C4-O41
5	B	204	TAR	C1-C2-C3-O3
5	B	204	TAR	O2-C2-C3-O3
5	B	204	TAR	O2-C2-C3-C4
5	B	204	TAR	C1-C2-C3-C4

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 [i](#)

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	153/165 (92%)	0.85	21 (13%) 6 7	18, 41, 78, 108	2 (1%)
1	B	153/165 (92%)	0.83	26 (16%) 4 4	24, 49, 80, 120	0
All	All	306/330 (92%)	0.84	47 (15%) 5 5	18, 44, 80, 120	2 (0%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	20	LEU	5.7
1	B	20	LEU	4.6
1	A	56	ASN	4.5
1	A	21	ARG	4.3
1	B	51	ASN	4.3
1	A	137	SER	4.1
1	B	19	HIS	4.0
1	A	47	PRO	4.0
1	A	25	ILE	3.7
1	B	14	ILE	3.7
1	A	22	LEU	3.6
1	B	49	ASP	3.5
1	A	19	HIS	3.4
1	A	48	ILE	3.3
1	A	49	ASP	3.3
1	B	63	LEU	3.1
1	A	51	ASN	3.1
1	A	14	ILE	3.0
1	B	70	TYR	3.0
1	B	25	ILE	3.0
1	B	50	SER	3.0
1	B	18	ALA	2.9
1	A	16	LEU	2.9
1	A	18	ALA	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	164	ARG	2.9
1	A	41	ASN	2.8
1	B	53	PHE	2.8
1	A	62	GLU	2.8
1	B	22	LEU	2.8
1	A	15	ARG	2.7
1	B	61	LEU	2.6
1	A	13	SER	2.6
1	A	52	THR	2.6
1	A	134	HIS	2.5
1	B	48	ILE	2.3
1	B	67	ASP	2.2
1	B	26	TYR	2.2
1	A	30	ASP	2.2
1	B	46	SER	2.2
1	B	106	HIS	2.1
1	B	110	GLN	2.1
1	B	29	ARG	2.1
1	B	62	GLU	2.1
1	B	21	ARG	2.1
1	B	47	PRO	2.1
1	B	52	THR	2.1
1	B	12	HIS	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.

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	TLA	B	203	4/10	0.44	0.24	57,65,67,73	0
2	TLA	B	202	4/10	0.67	0.27	59,61,63,68	0
5	TAR	B	204	10/10	0.69	0.16	63,81,99,99	0
2	TLA	A	203	4/10	0.73	0.23	53,58,63,66	0
4	SO4	A	209	5/5	0.74	0.20	38,42,44,61	5
3	NA	A	205	1/1	0.75	0.25	74,74,74,74	0
3	NA	B	206	1/1	0.75	0.24	74,74,74,74	0
2	TLA	A	201	4/10	0.77	0.18	57,58,60,61	0
3	NA	A	207	1/1	0.78	0.14	64,64,64,64	0
4	SO4	B	210	5/5	0.79	0.13	68,82,85,98	0
3	NA	B	207	1/1	0.80	0.29	72,72,72,72	0
2	TLA	A	204	5/10	0.85	0.15	66,68,81,85	0
2	TLA	B	201	5/10	0.88	0.12	42,48,53,58	0
3	NA	A	206	1/1	0.89	0.10	48,48,48,48	0
2	TLA	A	202	5/10	0.90	0.12	37,45,53,60	0
3	NA	A	208	1/1	0.91	0.33	75,75,75,75	0
3	NA	B	208	1/1	0.93	0.21	66,66,66,66	0
3	NA	B	205	1/1	0.93	0.10	49,49,49,49	0
4	SO4	B	209	5/5	0.97	0.07	42,46,48,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.