



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 02:30 am BST

PDB ID : 3B94  
Title : Crystal structure of human GITRL  
Authors : Song, X.M.; Zhou, Z.C.  
Deposited on : 2007-11-02  
Resolution : 2.50 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](mailto: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.

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

MolProbity : 4.02b-467  
Xtrriage (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

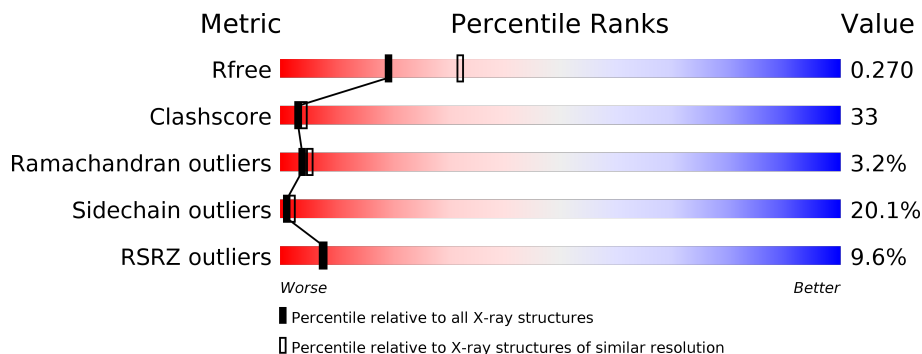
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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  $\geq 3$ , 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	133	<div style="display: flex; align-items: center;"> <div style="width: 13%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 33%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 36%; 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: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 23%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">13% 33% 36% 6% 23%</p>
1	B	133	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 36%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 29%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 12%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 15%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">5% 36% 29% 12% 8% 15%</p>
1	C	133	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 32%; 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: 15%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 25%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">3% 32% 24% 15% 25%</p>
1	D	133	<div style="display: flex; align-items: center;"> <div style="width: 10%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 44%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 29%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 11%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 16%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">10% 44% 29% 11% 16%</p>

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 3293 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 Tumor necrosis factor ligand superfamily member 18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	102	777	500	130	142	5	0	0	0
1	B	113	859	558	140	156	5	0	0	0
1	C	100	781	512	125	139	5	0	0	0
1	D	112	847	550	141	152	4	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	45	GLY	-	expression tag	UNP Q9UNG2
A	46	ALA	-	expression tag	UNP Q9UNG2
A	47	MET	-	expression tag	UNP Q9UNG2
A	48	ALA	-	expression tag	UNP Q9UNG2
A	49	SER	-	expression tag	UNP Q9UNG2
B	45	GLY	-	expression tag	UNP Q9UNG2
B	46	ALA	-	expression tag	UNP Q9UNG2
B	47	MET	-	expression tag	UNP Q9UNG2
B	48	ALA	-	expression tag	UNP Q9UNG2
B	49	SER	-	expression tag	UNP Q9UNG2
C	45	GLY	-	expression tag	UNP Q9UNG2
C	46	ALA	-	expression tag	UNP Q9UNG2
C	47	MET	-	expression tag	UNP Q9UNG2
C	48	ALA	-	expression tag	UNP Q9UNG2
C	49	SER	-	expression tag	UNP Q9UNG2
D	45	GLY	-	expression tag	UNP Q9UNG2
D	46	ALA	-	expression tag	UNP Q9UNG2
D	47	MET	-	expression tag	UNP Q9UNG2
D	48	ALA	-	expression tag	UNP Q9UNG2
D	49	SER	-	expression tag	UNP Q9UNG2

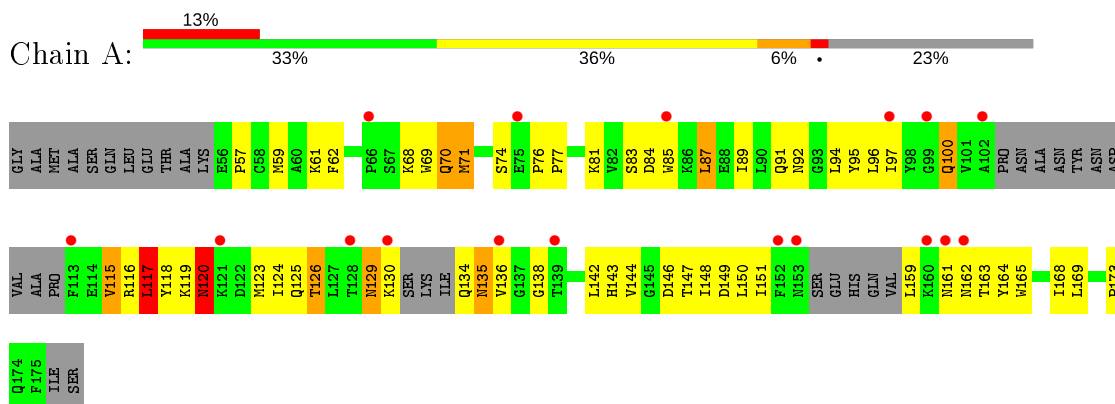
- Molecule 2 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
2	A	6	Total O 6 6	0	0
2	B	8	Total O 8 8	0	0
2	C	10	Total O 10 10	0	0
2	D	5	Total O 5 5	0	0

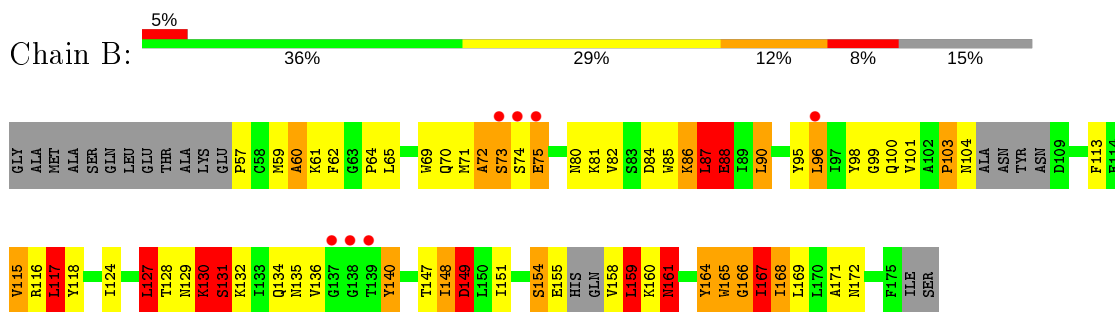
### 3 Residue-property plots [i](#)

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.

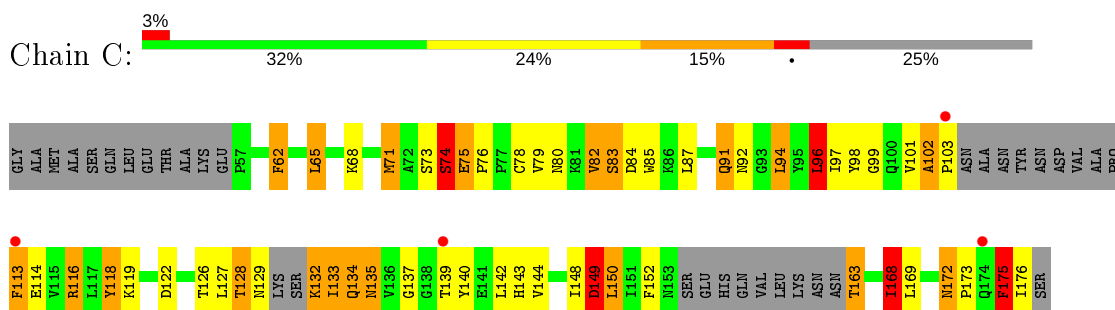
- Molecule 1: Tumor necrosis factor ligand superfamily member 18



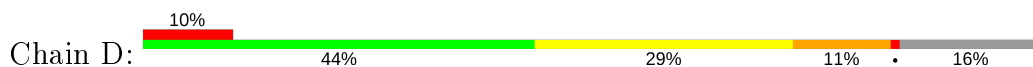
- Molecule 1: Tumor necrosis factor ligand superfamily member 18

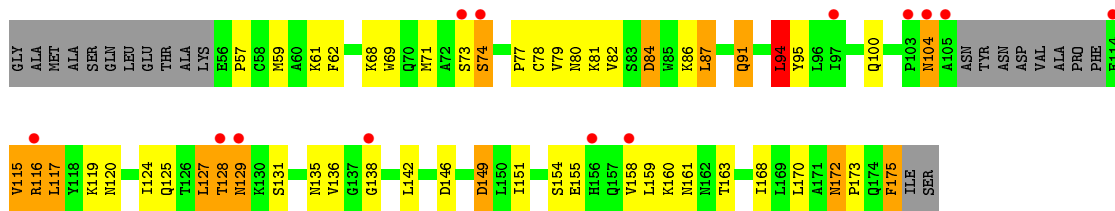


- Molecule 1: Tumor necrosis factor ligand superfamily member 18



- Molecule 1: Tumor necrosis factor ligand superfamily member 18





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	141.94Å 141.94Å 47.21Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.50 30.95 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.8 (30.00-2.50) 95.8 (30.95-2.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.08 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.217 , 0.276 0.212 , 0.270	Depositor DCC
$R_{free}$ test set	1067 reflections (5.81%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.1	Xtrriage
Anisotropy	0.210	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 57.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.037 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3293	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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	1.14	1/793 (0.1%)	1.10	2/1078 (0.2%)
1	B	1.82	16/880 (1.8%)	1.65	15/1199 (1.3%)
1	C	1.58	11/800 (1.4%)	1.44	8/1087 (0.7%)
1	D	1.54	5/868 (0.6%)	1.42	13/1187 (1.1%)
All	All	1.55	33/3341 (1.0%)	1.42	38/4551 (0.8%)

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	A	0	1
1	B	0	5
1	C	0	1
All	All	0	7

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	60	ALA	C-O	11.11	1.44	1.23
1	B	166	GLY	C-O	10.82	1.41	1.23
1	B	165	TRP	C-O	9.36	1.41	1.23
1	D	78	CYS	CB-SG	8.90	1.97	1.82
1	B	72	ALA	CA-CB	-8.32	1.34	1.52
1	B	164	TYR	CA-CB	7.92	1.71	1.53
1	B	88	GLU	CG-CD	-7.68	1.40	1.51
1	C	140	TYR	CZ-OH	7.41	1.50	1.37
1	D	95	TYR	CD1-CE1	7.19	1.50	1.39
1	B	165	TRP	CA-C	-6.51	1.36	1.52
1	C	152	PHE	CE2-CZ	6.50	1.49	1.37
1	D	172	ASN	CB-CG	-6.49	1.36	1.51
1	D	175	PHE	CD2-CE2	6.43	1.52	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	79	VAL	CB-CG2	6.23	1.66	1.52
1	B	159	LEU	N-CA	-6.18	1.33	1.46
1	C	98	TYR	CD1-CE1	6.11	1.48	1.39
1	B	167	ILE	CA-C	-6.10	1.37	1.52
1	C	118	TYR	CZ-OH	6.02	1.48	1.37
1	B	149	ASP	CB-CG	-5.77	1.39	1.51
1	C	82	VAL	CB-CG1	5.76	1.65	1.52
1	C	119	LYS	CD-CE	5.67	1.65	1.51
1	A	164	TYR	CD1-CE1	5.63	1.47	1.39
1	C	116	ARG	CB-CG	-5.45	1.37	1.52
1	B	140	TYR	CD1-CE1	5.44	1.47	1.39
1	C	140	TYR	CD2-CE2	5.43	1.47	1.39
1	C	119	LYS	CE-NZ	5.43	1.62	1.49
1	B	135	ASN	CB-CG	5.29	1.63	1.51
1	B	88	GLU	CB-CG	5.26	1.62	1.52
1	B	148	ILE	CB-CG2	5.22	1.69	1.52
1	C	80	ASN	CB-CG	5.15	1.62	1.51
1	B	140	TYR	CE2-CZ	5.13	1.45	1.38
1	C	140	TYR	CE1-CZ	5.09	1.45	1.38
1	B	81	LYS	CD-CE	5.03	1.63	1.51

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	159	LEU	CB-CG-CD1	-17.64	81.01	111.00
1	D	87	LEU	CB-CG-CD1	-10.48	93.17	111.00
1	D	172	ASN	CB-CA-C	-8.54	93.31	110.40
1	C	65	LEU	CA-CB-CG	7.88	133.43	115.30
1	D	59	MET	CG-SD-CE	7.86	112.77	100.20
1	B	165	TRP	N-CA-CB	7.54	124.16	110.60
1	D	61	LYS	CD-CE-NZ	-7.52	94.41	111.70
1	B	127	LEU	CA-CB-CG	7.25	131.97	115.30
1	D	149	ASP	CB-CG-OD1	-7.18	111.84	118.30
1	C	62	PHE	C-N-CA	-7.17	107.25	122.30
1	B	168	ILE	CB-CA-C	-7.12	97.37	111.60
1	C	134	GLN	N-CA-C	6.91	129.65	111.00
1	A	138	GLY	N-CA-C	-6.83	96.02	113.10
1	C	168	ILE	CB-CA-C	-6.81	97.99	111.60
1	B	165	TRP	O-C-N	-6.67	111.86	123.20
1	B	164	TYR	CB-CA-C	-6.60	97.20	110.40
1	C	149	ASP	CB-CG-OD1	-6.39	112.55	118.30
1	B	96	LEU	CA-CB-CG	6.33	129.86	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	127	LEU	CB-CG-CD1	-6.25	100.38	111.00
1	B	117	LEU	CB-CG-CD1	6.24	121.61	111.00
1	B	87	LEU	CB-CG-CD2	-6.07	100.68	111.00
1	B	167	ILE	CG1-CB-CG2	-6.02	98.16	111.40
1	D	138	GLY	N-CA-C	-5.99	98.12	113.10
1	B	116	ARG	CB-CG-CD	-5.90	96.25	111.60
1	B	87	LEU	CA-CB-CG	5.90	128.86	115.30
1	D	149	ASP	CB-CG-OD2	5.88	123.59	118.30
1	C	150	LEU	CB-CG-CD2	5.76	120.79	111.00
1	D	117	LEU	CA-CB-CG	5.63	128.25	115.30
1	D	128	THR	N-CA-C	-5.52	96.11	111.00
1	D	84	ASP	CB-CG-OD1	5.47	123.22	118.30
1	C	122	ASP	CB-CG-OD1	-5.40	113.44	118.30
1	D	161	ASN	CB-CA-C	-5.34	99.71	110.40
1	A	117	LEU	CA-CB-CG	5.31	127.51	115.30
1	C	96	LEU	CA-CB-CG	5.20	127.27	115.30
1	B	161	ASN	CB-CA-C	5.18	120.76	110.40
1	D	94	LEU	CA-CB-CG	5.15	127.15	115.30
1	B	130	LYS	N-CA-C	-5.11	97.20	111.00
1	B	90	LEU	CB-CG-CD2	5.08	119.64	111.00

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	LEU	Peptide
1	B	118	TYR	Peptide
1	B	130	LYS	Peptide
1	B	131	SER	Peptide
1	B	161	ASN	Peptide
1	B	167	ILE	Mainchain
1	C	175	PHE	Peptide

## 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	777	0	736	58	0
1	B	859	0	818	64	0
1	C	781	0	754	69	0
1	D	847	0	809	34	0
2	A	6	0	0	1	0
2	B	8	0	0	4	0
2	C	10	0	0	3	0
2	D	5	0	0	0	0
All	All	3293	0	3117	213	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 33.

All (213) 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:C:96:LEU:HB3	1:C:168:ILE:CD1	1.76	1.13
1:C:96:LEU:HG	1:C:168:ILE:HD11	1.35	1.09
1:C:132:LYS:HB2	1:C:133:ILE:HD12	1.25	1.08
1:B:134:GLN:HB2	2:B:21:HOH:O	1.63	0.99
1:C:132:LYS:CB	1:C:133:ILE:HD12	1.93	0.97
1:B:103:PRO:HG2	1:B:132:LYS:O	1.69	0.92
1:C:96:LEU:HB3	1:C:168:ILE:HD12	1.47	0.92
1:A:57:PRO:HG3	1:A:168:ILE:HD11	1.56	0.86
1:A:59:MET:HE3	1:B:171:ALA:HB1	1.58	0.85
1:D:116:ARG:HG3	1:D:116:ARG:HH11	1.42	0.85
1:B:88:GLU:HG2	1:B:147:THR:HG22	1.59	0.84
1:A:59:MET:CE	1:B:171:ALA:HB1	2.09	0.82
1:C:113:PHE:HE1	1:C:128:THR:HA	1.43	0.81
1:B:70:GLN:HG2	2:B:24:HOH:O	1.79	0.81
1:C:113:PHE:C	1:C:113:PHE:HD1	1.83	0.81
1:B:86:LYS:HG2	1:B:149:ASP:HB3	1.62	0.80
1:C:132:LYS:HB2	1:C:133:ILE:CD1	2.10	0.80
1:C:113:PHE:CE1	1:C:128:THR:HA	2.18	0.78
1:B:113:PHE:CD1	1:B:129:ASN:CB	2.66	0.78
1:B:103:PRO:CG	1:B:132:LYS:O	2.32	0.78
1:C:75:GLU:CB	1:C:76:PRO:HD3	2.14	0.78
1:A:69:TRP:CD1	1:A:81:LYS:HB2	2.18	0.77
1:C:75:GLU:CB	1:C:76:PRO:CD	2.62	0.77
1:C:96:LEU:CG	1:C:168:ILE:HD11	2.14	0.77
1:A:62:PHE:HB2	1:A:69:TRP:CZ3	2.19	0.76
1:D:115:VAL:O	1:D:151:ILE:O	2.03	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:LYS:O	1:A:70:GLN:NE2	2.19	0.76
1:C:113:PHE:C	1:C:113:PHE:CD1	2.58	0.75
1:A:87:LEU:CD2	1:A:165:TRP:HH2	1.99	0.75
1:C:134:GLN:HE21	1:C:135:ASN:HD22	1.32	0.75
1:C:92:ASN:ND2	1:C:144:VAL:H	1.85	0.75
1:C:133:ILE:HG22	1:C:133:ILE:O	1.85	0.74
1:C:96:LEU:HB3	1:C:168:ILE:HD11	1.70	0.73
1:A:87:LEU:HD22	1:A:165:TRP:CH2	2.24	0.73
1:A:92:ASN:OD1	1:A:143:HIS:HA	1.89	0.72
1:D:115:VAL:HG13	1:D:127:LEU:HB2	1.71	0.72
1:D:104:ASN:HB3	1:D:159:LEU:CD2	2.20	0.71
1:D:175:PHE:N	1:D:175:PHE:CD2	2.56	0.71
1:C:96:LEU:CB	1:C:168:ILE:CD1	2.64	0.71
1:C:101:VAL:O	1:C:163:THR:HG23	1.92	0.70
1:D:116:ARG:CG	1:D:116:ARG:HH11	2.04	0.70
1:D:104:ASN:HB3	1:D:159:LEU:HD21	1.74	0.70
1:C:132:LYS:N	2:C:5:HOH:O	2.24	0.70
1:C:84:ASP:O	1:C:85:TRP:HB2	1.92	0.69
1:D:86:LYS:HD2	1:D:149:ASP:OD1	1.93	0.69
1:C:128:THR:O	1:C:129:ASN:C	2.30	0.69
1:A:87:LEU:CD2	1:A:165:TRP:CH2	2.76	0.68
1:B:64:PRO:HB2	1:B:161:ASN:OD1	1.93	0.67
1:B:117:LEU:HD13	1:B:124:ILE:HD11	1.77	0.66
1:A:62:PHE:HB2	1:A:69:TRP:CE3	2.31	0.65
1:B:88:GLU:CG	1:B:147:THR:HG22	2.27	0.65
1:C:149:ASP:OD1	1:C:149:ASP:N	2.29	0.65
1:B:101:VAL:O	1:B:103:PRO:HD3	1.97	0.65
1:A:119:LYS:HA	1:A:148:ILE:HD13	1.78	0.65
1:B:103:PRO:O	1:B:104:ASN:HB3	1.98	0.63
1:A:150:LEU:HD22	1:A:165:TRP:CD1	2.34	0.63
1:B:65:LEU:H	1:B:161:ASN:HD21	1.47	0.63
1:C:176:ILE:N	2:C:17:HOH:O	2.33	0.61
1:C:62:PHE:O	1:C:68:LYS:O	2.18	0.61
1:B:103:PRO:HG2	1:B:132:LYS:C	2.20	0.61
1:D:104:ASN:CB	1:D:159:LEU:HD21	2.31	0.60
1:C:82:VAL:O	1:C:83:SER:HB3	1.99	0.60
1:A:125:GLN:HG2	1:A:126:THR:N	2.16	0.60
1:C:92:ASN:ND2	1:C:143:HIS:HA	2.17	0.60
1:B:155:GLU:O	1:B:158:VAL:CB	2.50	0.59
1:A:129:ASN:HD22	1:A:130:LYS:N	2.01	0.59
1:B:72:ALA:HB2	1:C:175:PHE:HE1	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:LEU:CB	1:C:168:ILE:HD11	2.30	0.59
1:D:57:PRO:HG2	1:D:168:ILE:HD11	1.84	0.58
1:B:87:LEU:CD1	1:B:87:LEU:C	2.72	0.58
1:D:116:ARG:HA	1:D:125:GLN:O	2.03	0.58
1:A:125:GLN:HG2	1:A:126:THR:H	1.69	0.58
1:B:128:THR:O	1:B:129:ASN:CB	2.52	0.58
1:C:101:VAL:O	1:C:102:ALA:CB	2.52	0.57
1:B:72:ALA:HB2	1:C:175:PHE:CE1	2.39	0.57
1:C:92:ASN:HD22	1:C:143:HIS:HA	1.69	0.57
1:D:68:LYS:HE3	1:D:84:ASP:OD1	2.04	0.57
1:C:135:ASN:H	1:C:135:ASN:HD22	1.52	0.57
1:C:172:ASN:HD22	1:C:172:ASN:N	2.02	0.56
1:A:135:ASN:OD1	1:B:140:TYR:CE2	2.59	0.56
1:B:103:PRO:O	1:B:159:LEU:HA	2.05	0.56
1:A:126:THR:H	1:C:133:ILE:HG21	1.69	0.56
1:B:57:PRO:O	1:B:73:SER:HB2	2.06	0.56
1:A:95:TYR:CD1	1:A:142:LEU:HD12	2.41	0.56
1:C:175:PHE:C	2:C:17:HOH:O	2.44	0.56
1:D:173:PRO:HB2	1:D:175:PHE:CZ	2.40	0.56
1:C:127:LEU:O	1:C:128:THR:CG2	2.55	0.55
1:B:101:VAL:HG13	1:B:159:LEU:CD1	2.36	0.55
1:C:135:ASN:ND2	1:C:135:ASN:O	2.39	0.55
1:A:117:LEU:HD13	1:A:124:ILE:HD11	1.88	0.55
1:D:173:PRO:HB2	1:D:175:PHE:CE2	2.42	0.55
1:B:99:GLY:HA3	1:B:165:TRP:HA	1.88	0.55
1:D:80:ASN:O	1:D:87:LEU:HD12	2.08	0.54
1:A:95:TYR:CE2	1:A:169:LEU:HB2	2.42	0.54
1:B:84:ASP:O	1:B:85:TRP:HB2	2.07	0.54
1:A:57:PRO:CG	1:A:168:ILE:HD11	2.33	0.53
1:A:59:MET:HE1	1:B:171:ALA:HB1	1.86	0.53
1:B:65:LEU:H	1:B:161:ASN:ND2	2.06	0.53
1:D:158:VAL:HG22	1:D:159:LEU:C	2.28	0.52
1:C:99:GLY:O	1:C:135:ASN:HB2	2.09	0.52
1:D:94:LEU:HD13	1:D:170:LEU:HD12	1.90	0.52
1:C:127:LEU:C	1:C:128:THR:HG23	2.30	0.52
1:B:70:GLN:NE2	2:B:24:HOH:O	2.31	0.51
1:B:87:LEU:C	1:B:87:LEU:HD12	2.31	0.51
1:C:134:GLN:HE21	1:C:135:ASN:ND2	2.03	0.51
1:B:59:MET:SD	1:C:173:PRO:HG3	2.51	0.51
1:B:82:VAL:HB	1:B:86:LYS:HB3	1.91	0.51
1:D:116:ARG:CG	1:D:116:ARG:NH1	2.67	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:LYS:C	1:C:133:ILE:HG13	2.31	0.51
1:A:85:TRP:CH2	1:A:163:THR:HG22	2.46	0.50
1:A:129:ASN:HB3	1:A:134:GLN:HE22	1.76	0.50
1:C:134:GLN:NE2	1:C:135:ASN:ND2	2.59	0.50
1:C:142:LEU:HD13	1:C:148:ILE:HD11	1.94	0.50
1:D:125:GLN:HE22	1:D:136:VAL:HA	1.76	0.50
1:A:120:ASN:HD22	1:A:146:ASP:HA	1.77	0.50
1:C:94:LEU:CD2	1:C:139:THR:HG22	2.40	0.50
1:C:94:LEU:HD21	1:C:139:THR:HG22	1.93	0.50
1:C:172:ASN:HD22	1:C:172:ASN:H	1.60	0.50
1:B:101:VAL:HG13	1:B:159:LEU:HD12	1.93	0.50
1:A:59:MET:HE1	1:B:171:ALA:CB	2.42	0.49
1:B:101:VAL:CG1	1:B:159:LEU:HD12	2.43	0.49
1:D:74:SER:O	1:D:77:PRO:HB3	2.13	0.49
1:A:62:PHE:CZ	1:A:84:ASP:HA	2.48	0.49
1:B:104:ASN:HB3	1:B:159:LEU:HA	1.95	0.49
1:A:61:LYS:HG2	1:A:62:PHE:N	2.27	0.49
1:D:119:LYS:HB2	1:D:124:ILE:HD13	1.94	0.48
1:A:120:ASN:HA	1:A:147:THR:OG1	2.13	0.48
1:B:159:LEU:HD23	1:B:159:LEU:O	2.13	0.48
1:B:62:PHE:O	1:B:164:TYR:HB2	2.13	0.48
1:B:115:VAL:HA	1:B:151:ILE:O	2.13	0.48
1:C:118:TYR:O	1:C:148:ILE:HA	2.13	0.48
1:A:129:ASN:C	1:A:129:ASN:HD22	2.16	0.48
1:A:84:ASP:HB3	1:A:85:TRP:CD1	2.49	0.48
1:D:115:VAL:O	1:D:116:ARG:HB2	2.14	0.48
1:B:74:SER:O	1:B:75:GLU:O	2.31	0.47
1:D:158:VAL:HG22	1:D:160:LYS:N	2.28	0.47
1:A:96:LEU:HD12	1:A:97:ILE:N	2.29	0.47
1:A:125:GLN:HE22	1:A:136:VAL:HA	1.79	0.47
1:A:150:LEU:CD2	1:A:165:TRP:CD1	2.98	0.47
1:A:68:LYS:HB2	1:A:68:LYS:HE2	1.57	0.47
1:C:113:PHE:HE1	1:C:128:THR:CA	2.21	0.47
1:B:113:PHE:HD1	1:B:129:ASN:CB	2.23	0.47
1:C:127:LEU:O	1:C:128:THR:HG23	2.15	0.47
1:D:158:VAL:CG2	1:D:159:LEU:N	2.78	0.47
1:C:84:ASP:O	1:C:85:TRP:CB	2.63	0.46
1:A:62:PHE:HE2	1:A:85:TRP:CE2	2.33	0.46
1:B:159:LEU:HD23	1:B:159:LEU:C	2.35	0.46
1:B:60:ALA:O	1:B:166:GLY:CA	2.64	0.46
1:B:80:ASN:HB2	1:B:90:LEU:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:HIS:O	1:A:144:VAL:C	2.53	0.46
1:B:95:TYR:CZ	1:B:169:LEU:HD13	2.51	0.46
1:C:97:ILE:O	1:C:137:GLY:HA3	2.16	0.46
1:A:143:HIS:N	1:A:146:ASP:OD2	2.45	0.46
1:A:83:SER:O	1:A:84:ASP:C	2.54	0.45
1:A:89:ILE:O	1:A:144:VAL:HA	2.17	0.45
1:A:59:MET:CE	1:B:171:ALA:CB	2.88	0.45
1:B:80:ASN:HD21	1:D:91:GLN:HE21	1.63	0.45
1:A:118:TYR:HB2	1:A:149:ASP:HB3	1.99	0.45
1:B:154:SER:OG	1:B:155:GLU:N	2.50	0.45
1:C:74:SER:O	1:C:75:GLU:C	2.55	0.45
1:D:62:PHE:HB2	1:D:69:TRP:CE2	2.51	0.44
1:B:98:TYR:HA	1:B:136:VAL:O	2.17	0.44
1:A:126:THR:HG22	1:C:133:ILE:HG12	2.00	0.44
1:B:148:ILE:O	1:B:149:ASP:HB3	2.17	0.44
1:C:135:ASN:ND2	1:C:135:ASN:C	2.71	0.44
1:D:104:ASN:HB3	1:D:159:LEU:HD23	1.99	0.44
1:A:85:TRP:HH2	1:A:163:THR:HG22	1.81	0.44
1:B:101:VAL:HG21	1:B:115:VAL:HG21	2.00	0.44
1:B:64:PRO:CB	1:B:161:ASN:OD1	2.62	0.44
1:B:70:GLN:CG	2:B:24:HOH:O	2.51	0.44
1:B:74:SER:O	1:B:75:GLU:C	2.56	0.44
1:A:116:ARG:HB3	1:A:123:MET:HG2	1.99	0.44
1:B:103:PRO:O	1:B:158:VAL:O	2.35	0.44
1:C:133:ILE:O	1:C:134:GLN:CD	2.56	0.44
1:C:92:ASN:HD22	1:C:144:VAL:H	1.63	0.44
1:A:116:ARG:HB2	1:A:118:TYR:CE1	2.54	0.43
1:C:134:GLN:NE2	1:C:135:ASN:HD22	2.05	0.43
1:D:120:ASN:HD21	1:D:146:ASP:HA	1.83	0.43
1:A:125:GLN:CG	1:A:126:THR:N	2.80	0.43
1:C:132:LYS:HB3	1:C:133:ILE:HD12	1.92	0.43
1:D:87:LEU:HA	1:D:87:LEU:HD12	1.75	0.43
1:A:71:MET:HG3	2:A:18:HOH:O	2.19	0.43
1:B:69:TRP:CZ2	1:B:87:LEU:HB3	2.53	0.43
1:B:127:LEU:HG	1:B:134:GLN:HG3	1.99	0.43
1:C:102:ALA:HA	1:C:103:PRO:HD2	1.54	0.43
1:B:86:LYS:HG2	1:B:149:ASP:CB	2.40	0.42
1:C:73:SER:C	1:C:74:SER:OG	2.57	0.42
1:B:84:ASP:O	1:B:85:TRP:CB	2.67	0.42
1:C:134:GLN:HE21	1:C:135:ASN:H	1.66	0.42
1:A:125:GLN:CG	1:A:126:THR:H	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:LYS:HB2	1:A:124:ILE:HD13	2.02	0.42
1:A:76:PRO:HA	1:A:77:PRO:HD3	1.90	0.42
1:D:158:VAL:HG22	1:D:159:LEU:N	2.34	0.42
1:B:172:ASN:N	1:B:172:ASN:OD1	2.52	0.42
1:C:113:PHE:CD1	1:C:114:GLU:N	2.87	0.42
1:C:127:LEU:C	1:C:128:THR:CG2	2.88	0.42
1:B:167:ILE:CG1	1:B:168:ILE:N	2.83	0.41
1:D:104:ASN:C	1:D:104:ASN:HD22	2.23	0.41
1:A:85:TRP:CE3	1:A:150:LEU:HD23	2.55	0.41
1:A:92:ASN:OD1	1:A:143:HIS:CA	2.62	0.41
1:B:127:LEU:CD1	1:B:134:GLN:HG3	2.50	0.41
1:A:115:VAL:HG22	1:A:151:ILE:O	2.21	0.41
1:C:78:CYS:HA	1:C:91:GLN:HG2	2.03	0.41
1:C:92:ASN:HD21	1:C:144:VAL:H	1.66	0.41
1:B:60:ALA:O	1:B:167:ILE:N	2.44	0.41
1:C:73:SER:O	1:C:74:SER:CB	2.68	0.41
1:D:142:LEU:HA	1:D:142:LEU:HD23	1.86	0.40
1:A:91:GLN:CG	1:A:92:ASN:N	2.85	0.40
1:C:91:GLN:HB2	1:C:91:GLN:HE21	1.71	0.40
1:A:100:GLN:O	1:A:163:THR:HA	2.21	0.40
1:D:129:ASN:C	1:D:131:SER:H	2.23	0.40
1:D:158:VAL:CG2	1:D:163:THR:OG1	2.69	0.40
1:A:144:VAL:HG23	1:A:144:VAL:H	1.61	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	94/133 (71%)	82 (87%)	10 (11%)	2 (2%)	<b>7</b>   <b>11</b>
1	B	107/133 (80%)	91 (85%)	14 (13%)	2 (2%)	<b>8</b>   <b>13</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	92/133 (69%)	77 (84%)	7 (8%)	8 (9%)	1	0
1	D	108/133 (81%)	98 (91%)	9 (8%)	1 (1%)	17	31
All	All	401/532 (75%)	348 (87%)	40 (10%)	13 (3%)	4	5

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	131	SER
1	C	71	MET
1	C	102	ALA
1	C	128	THR
1	A	173	PRO
1	C	75	GLU
1	C	83	SER
1	D	155	GLU
1	A	120	ASN
1	C	175	PHE
1	C	74	SER
1	B	75	GLU
1	C	133	ILE

### 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	80/116 (69%)	66 (82%)	14 (18%)	2	3
1	B	89/116 (77%)	71 (80%)	18 (20%)	1	2
1	C	82/116 (71%)	63 (77%)	19 (23%)	1	1
1	D	87/116 (75%)	70 (80%)	17 (20%)	1	2
All	All	338/464 (73%)	270 (80%)	68 (20%)	1	2

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	71	MET
1	A	74	SER
1	A	87	LEU
1	A	94	LEU
1	A	100	GLN
1	A	115	VAL
1	A	117	LEU
1	A	120	ASN
1	A	126	THR
1	A	129	ASN
1	A	135	ASN
1	A	161	ASN
1	A	162	ASN
1	B	61	LYS
1	B	71	MET
1	B	73	SER
1	B	86	LYS
1	B	87	LEU
1	B	88	GLU
1	B	96	LEU
1	B	100	GLN
1	B	103	PRO
1	B	115	VAL
1	B	117	LEU
1	B	127	LEU
1	B	130	LYS
1	B	131	SER
1	B	149	ASP
1	B	154	SER
1	B	159	LEU
1	B	160	LYS
1	C	65	LEU
1	C	71	MET
1	C	74	SER
1	C	79	VAL
1	C	87	LEU
1	C	91	GLN
1	C	94	LEU
1	C	96	LEU
1	C	113	PHE
1	C	116	ARG
1	C	126	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	132	LYS
1	C	135	ASN
1	C	149	ASP
1	C	150	LEU
1	C	163	THR
1	C	168	ILE
1	C	169	LEU
1	C	172	ASN
1	D	71	MET
1	D	73	SER
1	D	74	SER
1	D	81	LYS
1	D	82	VAL
1	D	91	GLN
1	D	94	LEU
1	D	100	GLN
1	D	104	ASN
1	D	115	VAL
1	D	116	ARG
1	D	117	LEU
1	D	128	THR
1	D	129	ASN
1	D	135	ASN
1	D	154	SER
1	D	172	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	100	GLN
1	A	120	ASN
1	A	125	GLN
1	A	129	ASN
1	A	134	GLN
1	A	161	ASN
1	A	162	ASN
1	B	100	GLN
1	C	91	GLN
1	C	92	ASN
1	C	134	GLN
1	C	135	ASN
1	C	143	HIS

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Mol	Chain	Res	Type
1	C	172	ASN
1	D	91	GLN
1	D	104	ASN
1	D	120	ASN
1	D	135	ASN
1	D	162	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

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	102/133 (76%)	0.98	17 (16%) <b>1</b> <b>1</b>	30, 52, 71, 78	0
1	B	113/133 (84%)	0.18	7 (6%) 20 21	18, 30, 51, 57	0
1	C	100/133 (75%)	0.05	4 (4%) 38 41	18, 34, 58, 61	0
1	D	112/133 (84%)	0.33	13 (11%) <b>4</b> <b>4</b>	17, 33, 58, 67	0
All	All	427/532 (80%)	0.38	41 (9%) <b>8</b> <b>7</b>	17, 36, 62, 78	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	113	PHE	6.3
1	A	66	PRO	5.5
1	D	128	THR	4.4
1	A	102	ALA	4.2
1	A	153	ASN	4.2
1	D	105	ALA	3.8
1	A	160	LYS	3.8
1	D	114	GLU	3.7
1	A	128	THR	3.6
1	C	113	PHE	3.3
1	B	96	LEU	3.1
1	B	74	SER	3.1
1	A	130	LYS	3.1
1	D	103	PRO	3.1
1	B	73	SER	2.9
1	C	174	GLN	2.9
1	D	104	ASN	2.9
1	D	74	SER	2.6
1	D	158	VAL	2.6
1	A	121	LYS	2.6
1	C	139	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	137	GLY	2.5
1	A	152	PHE	2.5
1	A	161	ASN	2.4
1	C	103	PRO	2.4
1	A	139	THR	2.4
1	D	129	ASN	2.3
1	A	136	VAL	2.3
1	B	138	GLY	2.3
1	B	75	GLU	2.3
1	A	97	ILE	2.3
1	A	75	GLU	2.2
1	B	139	THR	2.2
1	D	156	HIS	2.2
1	D	116	ARG	2.2
1	D	138	GLY	2.1
1	A	162	ASN	2.1
1	A	85	TRP	2.1
1	D	97	ILE	2.0
1	A	99	GLY	2.0
1	D	73	SER	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.