



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 28, 2026 – 01:01 AM UTC

PDB ID : 4TRH / pdb_00004trh
Title : The Legionella effector SidC defines a unique family of ubiquitin ligases important for bacterial phagosomal remodeling
Authors : Hsu, F.S.; Luo, X.; Qiu, J.; Teng, Y.; Jin, J.; Smolka, M.B.; Luo, Z.Q.; Mao, Y.
Deposited on : 2014-06-16
Resolution : 2.03 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
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

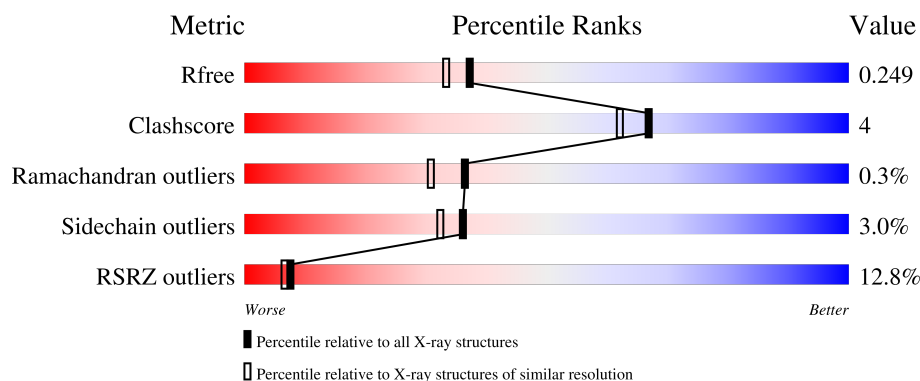
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

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	542	12% 84% 9% 6%
1	B	542	12% 82% 11% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8496 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 SidC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	509	Total	C	N	O	S	0	3	0
			4143	2618	704	815	6			
1	B	508	Total	C	N	O	S	0	1	0
			4120	2603	700	812	5			

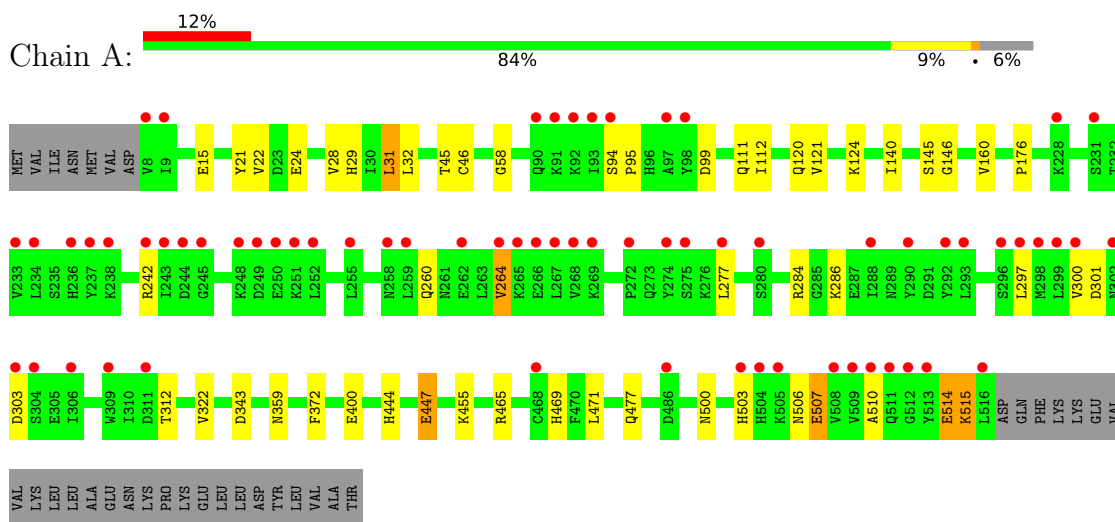
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	165	Total	O	0	0
			165	165		
2	B	68	Total	O	0	0
			68	68		

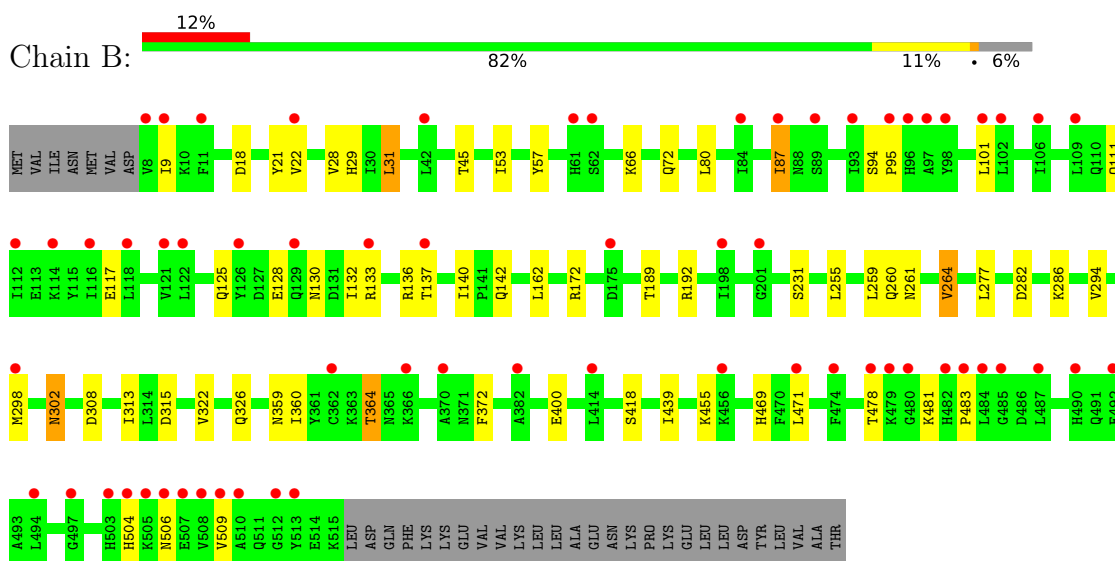
3 Residue-property plots [i](#)

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: SidC



• Molecule 1: SidC



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.23Å 132.69Å 171.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.90 – 2.03 35.90 – 2.03	Depositor EDS
% Data completeness (in resolution range)	94.8 (35.90-2.03) 95.1 (35.90-2.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.213 , 0.249 0.220 , 0.249	Depositor DCC
R_{free} test set	4501 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.132	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8496	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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	1.25	9/4230 (0.2%)	1.09	9/5709 (0.2%)
1	B	1.15	9/4207 (0.2%)	1.05	9/5679 (0.2%)
All	All	1.20	18/8437 (0.2%)	1.07	18/11388 (0.2%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	286	LYS	N-CA	7.29	1.54	1.46
1	B	261	ASN	N-CA	6.78	1.54	1.46
1	A	145	SER	C-O	-6.75	1.16	1.24
1	B	282	ASP	CA-C	6.44	1.60	1.52
1	B	255	LEU	N-CA	6.05	1.53	1.46
1	A	120	GLN	CD-NE2	-5.90	1.20	1.33
1	B	259	LEU	CA-C	-5.73	1.45	1.52
1	B	231	SER	CA-C	-5.61	1.45	1.52
1	A	176	PRO	C-O	-5.60	1.17	1.23
1	B	45	THR	C-O	-5.45	1.19	1.24
1	B	313	ILE	C-O	5.43	1.30	1.24
1	A	455	LYS	CA-C	-5.33	1.46	1.52
1	A	140	ILE	C-O	-5.32	1.17	1.24
1	A	447	GLU	N-CA	5.30	1.52	1.46
1	A	465	ARG	CD-NE	-5.11	1.39	1.46
1	A	32	LEU	N-CA	-5.07	1.38	1.46
1	B	308	ASP	CA-C	5.06	1.59	1.52
1	A	45	THR	CA-C	5.04	1.59	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	400	GLU	CA-C-N	-6.87	112.62	119.56
1	B	400	GLU	C-N-CA	-6.87	112.62	119.56
1	A	400	GLU	CA-C-N	-6.67	112.82	119.56
1	A	400	GLU	C-N-CA	-6.67	112.82	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	ASP	N-CA-C	6.38	117.90	111.07
1	A	94	SER	CA-C-N	6.21	127.60	119.84
1	A	94	SER	C-N-CA	6.21	127.60	119.84
1	B	439	ILE	N-CA-C	6.04	117.97	112.29
1	B	504	HIS	N-CA-C	5.96	117.86	111.36
1	B	94	SER	CA-C-N	5.56	126.78	119.84
1	B	94	SER	C-N-CA	5.56	126.78	119.84
1	B	31	LEU	CA-CB-CG	-5.45	97.23	116.30
1	A	112	ILE	CB-CA-C	-5.43	104.93	111.88
1	B	298	MET	CG-SD-CE	-5.18	89.50	100.90
1	B	294	VAL	CB-CA-C	-5.11	105.50	111.94
1	A	31	LEU	CA-CB-CG	-5.05	98.62	116.30
1	A	343	ASP	CB-CA-C	-5.04	102.97	110.88
1	A	58	GLY	CA-C-O	-5.01	118.23	122.29

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	4143	0	4082	26	0
1	B	4120	0	4055	37	0
2	A	165	0	0	2	1
2	B	68	0	0	1	1
All	All	8496	0	8137	60	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 4.

All (60) 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:469:HIS:HD2	1:A:471:LEU:H	1.33	0.77
1:B:302:ASN:HD22	1:B:302:ASN:H	1.34	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:481:LYS:O	1:B:483:PRO:HD3	1.89	0.73
1:B:469:HIS:HD2	1:B:471:LEU:H	1.39	0.69
1:B:9:ILE:HD11	1:B:87:ILE:CD1	2.24	0.67
1:B:364:THR:HG23	1:B:455:LYS:HE2	1.76	0.66
1:A:146:GLY:H	1:A:477:GLN:HE22	1.44	0.64
1:B:359:ASN:ND2	1:B:372:PHE:H	1.97	0.63
1:A:15:GLU:OE1	1:A:510:ALA:HB2	2.01	0.61
1:A:301:ASP:OD1	1:A:303:ASP:OD1	2.18	0.61
1:B:125:GLN:HE21	1:B:125:GLN:HA	1.66	0.61
1:A:359:ASN:ND2	1:A:372:PHE:H	2.03	0.57
1:B:360:ILE:O	1:B:364:THR:HB	2.04	0.57
1:A:242:ARG:NH1	1:A:303:ASP:O	2.38	0.56
1:A:46[B]:CYS:SG	2:A:730:HOH:O	2.52	0.55
1:A:284:ARG:HD3	1:B:53:ILE:HD13	1.89	0.55
1:A:300:VAL:HG13	1:A:312:THR:HG21	1.88	0.54
1:A:146:GLY:H	1:A:477:GLN:NE2	2.05	0.54
1:B:302:ASN:H	1:B:302:ASN:ND2	2.06	0.54
1:A:503:HIS:HE1	1:A:507:GLU:OE1	1.93	0.52
1:B:125:GLN:HA	1:B:125:GLN:NE2	2.24	0.52
1:B:260:GLN:O	1:B:264:VAL:HG13	2.09	0.51
1:B:364:THR:HG23	1:B:455:LYS:CE	2.39	0.51
1:A:29:HIS:ND1	1:A:469:HIS:HE1	2.09	0.50
1:B:9:ILE:HD11	1:B:87:ILE:HD13	1.92	0.50
1:A:260:GLN:O	1:A:264:VAL:HG13	2.11	0.50
1:B:364:THR:HG23	1:B:455:LYS:CD	2.41	0.50
1:B:57:TYR:CD1	1:B:136:ARG:HD3	2.47	0.50
1:B:133:ARG:HG2	1:B:133:ARG:HH11	1.78	0.49
1:B:506:ASN:HB2	1:B:509:VAL:CG1	2.42	0.49
1:B:28:VAL:H	1:B:111:GLN:NE2	2.11	0.48
1:B:66:LYS:HA	2:B:664:HOH:O	2.14	0.48
1:B:481:LYS:O	1:B:483:PRO:CD	2.61	0.48
1:A:28:VAL:H	1:A:111:GLN:NE2	2.12	0.48
1:A:28:VAL:H	1:A:111:GLN:HE22	1.62	0.48
1:A:359:ASN:HD21	1:A:372:PHE:H	1.62	0.47
1:B:18:ASP:HB2	1:B:72:GLN:NE2	2.29	0.47
1:B:359:ASN:HD21	1:B:372:PHE:H	1.63	0.47
1:B:28:VAL:H	1:B:111:GLN:HE22	1.62	0.46
1:B:364:THR:HG23	1:B:455:LYS:HD2	1.98	0.46
1:B:130:ASN:ND2	1:B:133:ARG:HH21	2.13	0.45
1:A:444:HIS:HE1	1:B:315:ASP:OD2	2.00	0.45
1:A:444:HIS:HD2	2:A:704:HOH:O	2.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:29:HIS:ND1	1:B:469:HIS:HE1	2.14	0.45
1:A:297:LEU:HD22	1:B:140:ILE:HG13	1.98	0.45
1:B:18:ASP:HB2	1:B:72:GLN:HE22	1.83	0.44
1:A:469:HIS:CD2	1:A:471:LEU:H	2.24	0.43
1:B:21:TYR:HA	1:B:506:ASN:HD21	1.84	0.43
1:B:302:ASN:ND2	1:B:302:ASN:N	2.66	0.43
1:A:284:ARG:CZ	1:A:286:LYS:HE3	2.48	0.43
1:A:21:TYR:HA	1:A:506:ASN:HD21	1.85	0.42
1:B:22:VAL:H	1:B:506:ASN:ND2	2.18	0.42
1:A:515:LYS:CD	1:A:515:LYS:N	2.83	0.42
1:A:22:VAL:H	1:A:506:ASN:ND2	2.17	0.42
1:A:160:VAL:O	1:A:447:GLU:HA	2.20	0.42
1:B:142:GLN:OE1	1:B:172:ARG:CZ	2.67	0.42
1:B:364:THR:CG2	1:B:455:LYS:HE2	2.45	0.42
1:B:189:THR:O	1:B:192:ARG:NH1	2.52	0.41
1:A:515:LYS:N	1:A:515:LYS:HD2	2.36	0.40
1:B:87:ILE:HA	1:B:87:ILE:HD12	1.77	0.40

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)
2:A:608:HOH:O	2:B:603:HOH:O[4_555]	2.06	0.14

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	510/542 (94%)	503 (99%)	5 (1%)	2 (0%)	30	22
1	B	507/542 (94%)	498 (98%)	8 (2%)	1 (0%)	43	40
All	All	1017/1084 (94%)	1001 (98%)	13 (1%)	3 (0%)	36	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	PRO
1	A	514	GLU
1	B	95	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	463/491 (94%)	452 (98%)	11 (2%)	43	41
1	B	460/491 (94%)	443 (96%)	17 (4%)	30	24
All	All	923/982 (94%)	895 (97%)	28 (3%)	36	32

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	GLU
1	A	31	LEU
1	A	121	VAL
1	A	124	LYS
1	A	264	VAL
1	A	277	LEU
1	A	322	VAL
1	A	500	ASN
1	A	507	GLU
1	A	514	GLU
1	A	515	LYS
1	B	31	LEU
1	B	80	LEU
1	B	87	ILE
1	B	101	LEU
1	B	117	GLU
1	B	128	GLU
1	B	132	ILE
1	B	137	THR
1	B	162	LEU

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Mol	Chain	Res	Type
1	B	264	VAL
1	B	277	LEU
1	B	302	ASN
1	B	322	VAL
1	B	326	GLN
1	B	364	THR
1	B	418	SER
1	B	478	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	111	GLN
1	A	120	GLN
1	A	221	ASN
1	A	260	GLN
1	A	273	GLN
1	A	359	ASN
1	A	365	ASN
1	A	381	HIS
1	A	444	HIS
1	A	469	HIS
1	A	477	GLN
1	A	495	GLN
1	A	500	ASN
1	A	503	HIS
1	A	504	HIS
1	A	506	ASN
1	B	71	HIS
1	B	72	GLN
1	B	88	ASN
1	B	96	HIS
1	B	111	GLN
1	B	125	GLN
1	B	130	ASN
1	B	142	GLN
1	B	221	ASN
1	B	273	GLN
1	B	302	ASN
1	B	359	ASN
1	B	365	ASN

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Mol	Chain	Res	Type
1	B	381	HIS
1	B	411	HIS
1	B	469	HIS
1	B	491	GLN
1	B	506	ASN
1	B	511	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 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

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	509/542 (93%)	0.40	67 (13%) 7 6	14, 38, 103, 149	6 (1%)
1	B	508/542 (93%)	0.94	63 (12%) 8 7	21, 56, 110, 157	2 (0%)
All	All	1017/1084 (93%)	0.67	130 (12%) 7 6	14, 49, 109, 157	8 (0%)

All (130) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	243	ILE	6.4
1	B	508	VAL	6.1
1	B	513	TYR	6.0
1	B	509	VAL	4.7
1	A	516	LEU	4.6
1	A	510	ALA	4.4
1	B	126	TYR	4.4
1	B	503	HIS	4.4
1	A	513	TYR	4.1
1	A	93	ILE	4.0
1	B	9	ILE	4.0
1	A	237	TYR	3.9
1	A	268	VAL	3.8
1	B	487	LEU	3.8
1	B	478	THR	3.8
1	B	8	VAL	3.8
1	A	309	TRP	3.7
1	B	61	HIS	3.6
1	B	84	ILE	3.6
1	B	106	ILE	3.6
1	A	288	ILE	3.5
1	B	480	GLY	3.5
1	A	302	ASN	3.5
1	B	102	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	22	VAL	3.5
1	B	507	GLU	3.4
1	A	508	VAL	3.4
1	A	238	LYS	3.3
1	A	303	ASP	3.3
1	A	298	MET	3.3
1	B	510	ALA	3.3
1	B	121	VAL	3.3
1	A	9	ILE	3.3
1	A	245	GLY	3.2
1	A	251	LYS	3.2
1	B	133	ARG	3.1
1	A	503	HIS	3.1
1	B	504	HIS	3.1
1	A	512	GLY	3.1
1	A	97	ALA	3.1
1	B	112	ILE	3.1
1	B	506	ASN	3.0
1	B	11	PHE	3.0
1	B	93	ILE	3.0
1	A	242	ARG	3.0
1	B	62	SER	3.0
1	A	259	LEU	3.0
1	B	483	PRO	2.9
1	B	505	LYS	2.9
1	B	98	TYR	2.9
1	B	479	LYS	2.9
1	B	414	LEU	2.8
1	B	512	GLY	2.8
1	A	233	VAL	2.8
1	A	306	ILE	2.8
1	A	8	VAL	2.8
1	A	509	VAL	2.8
1	A	231	SER	2.7
1	A	277	LEU	2.7
1	A	468	CYS	2.7
1	A	293	LEU	2.7
1	B	482	HIS	2.7
1	B	484	LEU	2.7
1	B	101	LEU	2.6
1	B	456	LYS	2.6
1	A	297	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	96	HIS	2.5
1	A	258	ASN	2.5
1	A	244	ASP	2.5
1	A	311	ASP	2.5
1	A	90	GLN	2.5
1	A	272	PRO	2.5
1	A	290	TYR	2.5
1	A	252	LEU	2.5
1	A	505	LYS	2.5
1	A	264	VAL	2.4
1	A	267	LEU	2.4
1	B	95	PRO	2.4
1	A	299	LEU	2.4
1	B	490	HIS	2.4
1	A	250	GLU	2.4
1	A	300	VAL	2.4
1	A	274	TYR	2.4
1	B	109	LEU	2.4
1	B	198	ILE	2.4
1	B	362	CYS	2.4
1	A	511	GLN	2.3
1	B	42	LEU	2.3
1	B	471	LEU	2.3
1	B	175	ASP	2.3
1	A	228	LYS	2.3
1	A	248	LYS	2.3
1	A	94	SER	2.3
1	B	89	SER	2.3
1	A	98	TYR	2.3
1	A	292	TYR	2.3
1	B	122	LEU	2.3
1	B	201	GLY	2.3
1	B	114	LYS	2.2
1	B	298	MET	2.2
1	A	234	LEU	2.2
1	A	255	LEU	2.2
1	A	504	HIS	2.2
1	A	265	LYS	2.2
1	B	137	THR	2.2
1	B	97	ALA	2.2
1	A	486	ASP	2.2
1	B	129	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	494	LEU	2.1
1	A	91	LYS	2.1
1	A	262	GLU	2.1
1	B	116	ILE	2.1
1	A	236	HIS	2.1
1	B	370	ALA	2.1
1	A	280	SER	2.1
1	B	492	GLU	2.1
1	B	497	GLY	2.1
1	B	366	LYS	2.1
1	B	474	PHE	2.1
1	A	266	GLU	2.0
1	A	275	SER	2.1
1	A	296	SER	2.1
1	B	382	ALA	2.1
1	B	118	LEU	2.0
1	A	249	ASP	2.0
1	A	269	LYS	2.0
1	B	87	ILE	2.0
1	A	304	SER	2.0
1	A	92	LYS	2.0
1	B	485	GLY	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.