



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:18 AM UTC

PDB ID : 4LTQ / pdb_00004ltq
Title : Bacterial sodium channel in low calcium, P42 space group
Authors : Shaya, D.; Findeisen, F.; Abderemane-Ali, F.; Arrigoni, C.; Wong, S.; Reddy
Nurva, S.; Loussouarn, G.; Minor, D.L.
Deposited on : 2013-07-23
Resolution : 5.50 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

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

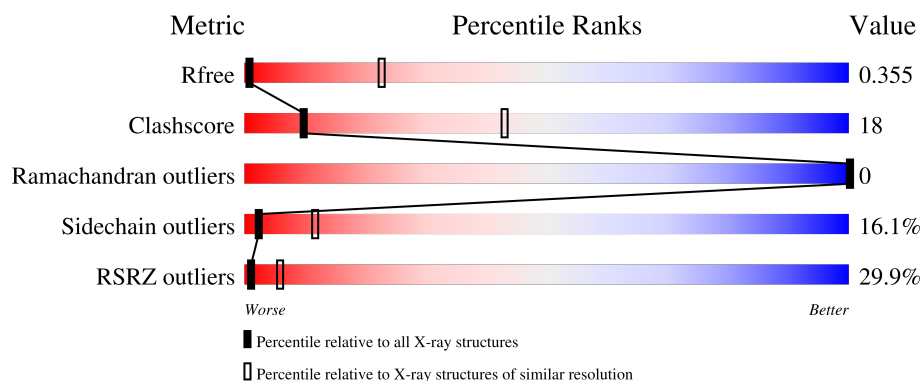
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.50 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}	180053	1088 (7.00-4.00)
Clashscore	190562	1147 (7.00-4.00)
Ramachandran outliers	187476	1012 (7.02-3.98)
Sidechain outliers	187428	1023 (7.04-3.96)
RSRZ outliers	180081	1081 (7.00-4.00)

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	152	
1	B	152	
1	C	152	
1	D	152	
1	H	152	

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Mol	Chain	Length	Quality of chain
1	I	152	19% 55% 30% 5% 11%
1	J	152	41% 54% 29% 7% 11%
1	K	152	22% 55% 30% 5% 11%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8086 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 Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	136	Total	C	N	O	S	0	0	0
			1018	680	154	178	6			
1	B	136	Total	C	N	O	S	0	0	0
			1014	680	153	175	6			
1	C	136	Total	C	N	O	S	0	0	0
			1012	678	155	173	6			
1	D	136	Total	C	N	O	S	0	0	0
			999	671	153	169	6			
1	H	136	Total	C	N	O	S	0	0	0
			1018	680	154	178	6			
1	I	136	Total	C	N	O	S	0	0	0
			1014	680	153	175	6			
1	J	136	Total	C	N	O	S	0	0	0
			1012	678	155	173	6			
1	K	136	Total	C	N	O	S	0	0	0
			999	671	153	169	6			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	137	GLY	-	expression tag	UNP Q0ABW0
A	138	PRO	-	expression tag	UNP Q0ABW0
A	139	SER	-	expression tag	UNP Q0ABW0
A	140	SER	-	expression tag	UNP Q0ABW0
A	141	PRO	-	expression tag	UNP Q0ABW0
A	142	SER	-	expression tag	UNP Q0ABW0
B	137	GLY	-	expression tag	UNP Q0ABW0
B	138	PRO	-	expression tag	UNP Q0ABW0
B	139	SER	-	expression tag	UNP Q0ABW0
B	140	SER	-	expression tag	UNP Q0ABW0
B	141	PRO	-	expression tag	UNP Q0ABW0
B	142	SER	-	expression tag	UNP Q0ABW0
C	137	GLY	-	expression tag	UNP Q0ABW0

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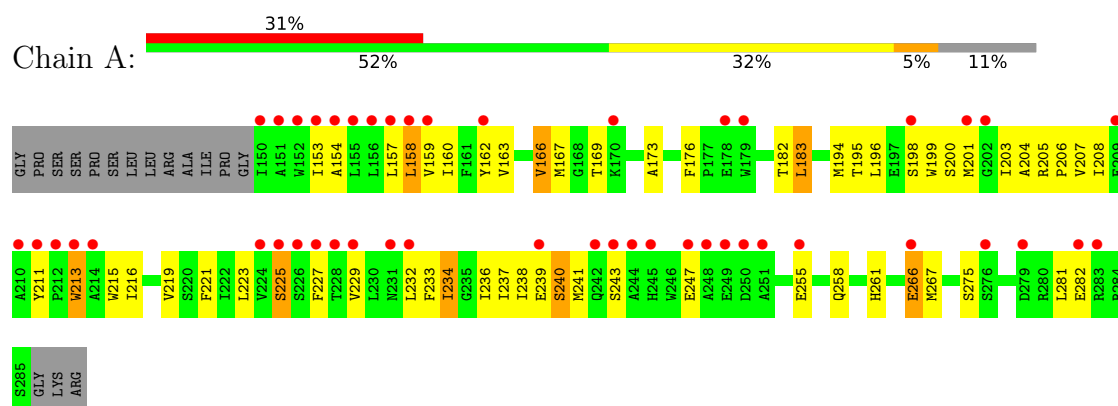
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Chain	Residue	Modelled	Actual	Comment	Reference
C	138	PRO	-	expression tag	UNP Q0ABW0
C	139	SER	-	expression tag	UNP Q0ABW0
C	140	SER	-	expression tag	UNP Q0ABW0
C	141	PRO	-	expression tag	UNP Q0ABW0
C	142	SER	-	expression tag	UNP Q0ABW0
D	137	GLY	-	expression tag	UNP Q0ABW0
D	138	PRO	-	expression tag	UNP Q0ABW0
D	139	SER	-	expression tag	UNP Q0ABW0
D	140	SER	-	expression tag	UNP Q0ABW0
D	141	PRO	-	expression tag	UNP Q0ABW0
D	142	SER	-	expression tag	UNP Q0ABW0
H	137	GLY	-	expression tag	UNP Q0ABW0
H	138	PRO	-	expression tag	UNP Q0ABW0
H	139	SER	-	expression tag	UNP Q0ABW0
H	140	SER	-	expression tag	UNP Q0ABW0
H	141	PRO	-	expression tag	UNP Q0ABW0
H	142	SER	-	expression tag	UNP Q0ABW0
I	137	GLY	-	expression tag	UNP Q0ABW0
I	138	PRO	-	expression tag	UNP Q0ABW0
I	139	SER	-	expression tag	UNP Q0ABW0
I	140	SER	-	expression tag	UNP Q0ABW0
I	141	PRO	-	expression tag	UNP Q0ABW0
I	142	SER	-	expression tag	UNP Q0ABW0
J	137	GLY	-	expression tag	UNP Q0ABW0
J	138	PRO	-	expression tag	UNP Q0ABW0
J	139	SER	-	expression tag	UNP Q0ABW0
J	140	SER	-	expression tag	UNP Q0ABW0
J	141	PRO	-	expression tag	UNP Q0ABW0
J	142	SER	-	expression tag	UNP Q0ABW0
K	137	GLY	-	expression tag	UNP Q0ABW0
K	138	PRO	-	expression tag	UNP Q0ABW0
K	139	SER	-	expression tag	UNP Q0ABW0
K	140	SER	-	expression tag	UNP Q0ABW0
K	141	PRO	-	expression tag	UNP Q0ABW0
K	142	SER	-	expression tag	UNP Q0ABW0

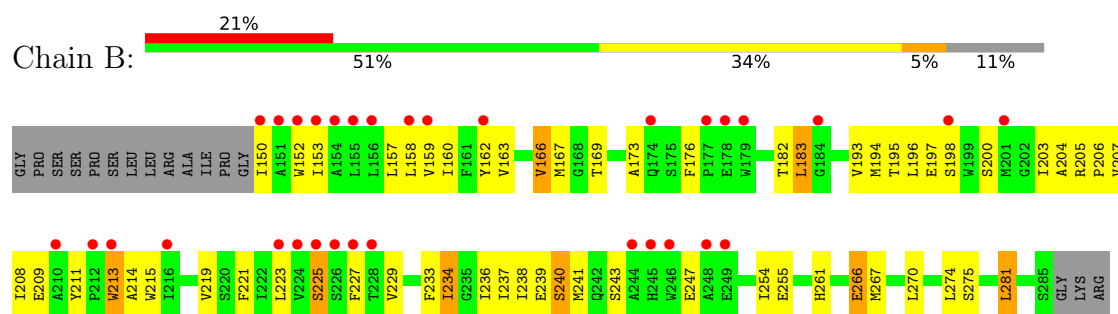
3 Residue-property plots [i](#)

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.

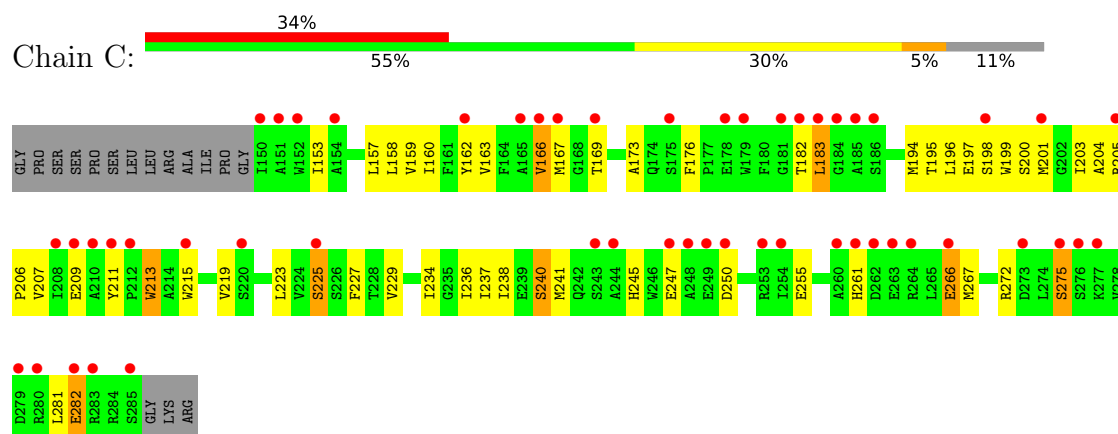
• Molecule 1: Ion transport protein



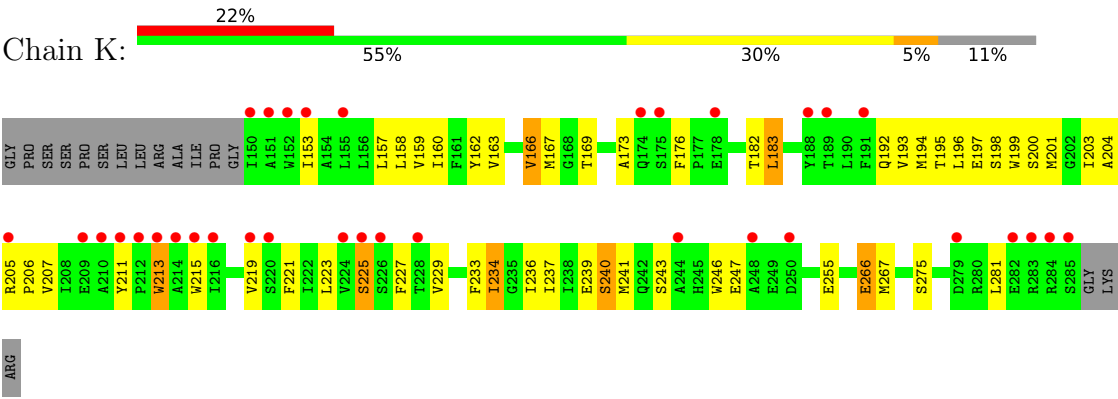
• Molecule 1: Ion transport protein



• Molecule 1: Ion transport protein



- Molecule 1: Ion transport protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α , β , γ	181.14Å 181.14Å 94.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 5.50 15.00 – 5.50	Depositor EDS
% Data completeness (in resolution range)	96.9 (15.00-5.50) 96.9 (15.00-5.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 5.42Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.266 , 0.294 0.319 , 0.355	Depositor DCC
R_{free} test set	449 reflections (4.43%)	wwPDB-VP
Wilson B-factor (Å ²)	377.2	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 426.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.30$, $\langle L^2 \rangle = 0.14$	Xtriage
Estimated twinning fraction	0.326 for h,-k,-l	Xtriage
Reported twinning fraction	0.598 for H, K, L 0.402 for -H, K, -L	Depositor
Outliers	0 of 9776 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8086	wwPDB-VP
Average B, all atoms (Å ²)	292.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.70	0/1045	1.08	2/1431 (0.1%)
1	B	0.72	0/1041	1.09	2/1426 (0.1%)
1	C	0.73	0/1040	1.09	2/1425 (0.1%)
1	D	0.73	0/1026	1.07	2/1407 (0.1%)
1	H	0.72	0/1045	1.09	2/1431 (0.1%)
1	I	0.67	0/1041	1.06	1/1426 (0.1%)
1	J	0.68	0/1040	1.07	2/1425 (0.1%)
1	K	0.72	0/1026	1.09	1/1407 (0.1%)
All	All	0.71	0/8304	1.08	14/11378 (0.1%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	247	GLU	N-CA-C	-6.48	105.95	114.31
1	K	247	GLU	N-CA-C	-6.36	106.10	114.31
1	I	247	GLU	N-CA-C	-6.33	106.19	114.04
1	B	247	GLU	N-CA-C	-6.30	106.23	114.04
1	J	247	GLU	N-CA-C	-6.16	106.40	114.04
1	D	247	GLU	N-CA-C	-5.75	106.90	114.31
1	A	261	HIS	N-CA-C	-5.71	105.81	112.89
1	B	261	HIS	N-CA-C	-5.69	105.84	112.89
1	A	247	GLU	N-CA-C	-5.53	107.19	114.04
1	C	247	GLU	N-CA-C	-5.27	107.50	114.04
1	J	261	HIS	N-CA-C	-5.05	106.63	112.89
1	H	261	HIS	N-CA-C	-5.03	106.65	112.89
1	C	261	HIS	N-CA-C	-5.03	106.65	112.89
1	D	261	HIS	N-CA-C	-5.02	105.91	112.23

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	1018	0	946	46	0
1	B	1014	0	947	45	0
1	C	1012	0	939	39	0
1	D	999	0	926	47	0
1	H	1018	0	946	42	0
1	I	1014	0	947	41	0
1	J	1012	0	939	45	0
1	K	999	0	926	44	0
All	All	8086	0	7516	274	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 18.

All (274) 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:234:ILE:HD11	1:D:237:ILE:HA	1.50	0.92
1:J:245:HIS:CE1	1:K:246:TRP:CB	2.54	0.91
1:H:234:ILE:HD11	1:K:237:ILE:HA	1.52	0.90
1:J:195:THR:HB	1:K:196:LEU:HD13	1.54	0.89
1:C:195:THR:HB	1:D:196:LEU:HD13	1.56	0.87
1:I:195:THR:HB	1:J:196:LEU:HD13	1.57	0.87
1:A:195:THR:HB	1:B:196:LEU:HD13	1.58	0.86
1:H:195:THR:HB	1:I:196:LEU:HD13	1.58	0.85
1:C:205:ARG:O	1:C:209:GLU:HG2	1.81	0.80
1:H:196:LEU:HD13	1:K:195:THR:HB	1.62	0.80
1:A:223:LEU:O	1:A:227:PHE:HB2	1.83	0.79
1:J:213:TRP:HD1	1:J:213:TRP:H	1.31	0.79
1:J:213:TRP:H	1:J:213:TRP:CD1	2.02	0.78
1:H:223:LEU:O	1:H:227:PHE:HB2	1.85	0.77
1:K:213:TRP:HD1	1:K:213:TRP:H	1.31	0.77
1:B:195:THR:HB	1:C:196:LEU:HD13	1.65	0.76
1:K:213:TRP:H	1:K:213:TRP:CD1	2.03	0.76
1:I:236:ILE:O	1:I:240:SER:HB2	1.86	0.76
1:B:236:ILE:O	1:B:240:SER:HB2	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:223:LEU:O	1:D:227:PHE:HB2	1.87	0.75
1:A:213:TRP:CD1	1:A:213:TRP:H	2.05	0.75
1:K:236:ILE:O	1:K:240:SER:HB2	1.86	0.74
1:K:223:LEU:O	1:K:227:PHE:HB2	1.87	0.74
1:A:213:TRP:H	1:A:213:TRP:HD1	1.34	0.74
1:A:205:ARG:HB2	1:A:206:PRO:HD3	1.68	0.74
1:D:213:TRP:HD1	1:D:213:TRP:H	1.34	0.74
1:A:196:LEU:HD13	1:D:195:THR:HB	1.69	0.74
1:I:223:LEU:O	1:I:227:PHE:HB2	1.88	0.74
1:B:213:TRP:HD1	1:B:213:TRP:H	1.35	0.73
1:J:223:LEU:O	1:J:227:PHE:HB2	1.88	0.73
1:B:223:LEU:O	1:B:227:PHE:HB2	1.88	0.73
1:C:223:LEU:O	1:C:227:PHE:HB2	1.89	0.73
1:H:213:TRP:CD1	1:H:213:TRP:H	2.06	0.73
1:C:213:TRP:HD1	1:C:213:TRP:H	1.37	0.73
1:D:236:ILE:O	1:D:240:SER:HB2	1.87	0.73
1:I:213:TRP:HD1	1:I:213:TRP:H	1.36	0.73
1:B:213:TRP:H	1:B:213:TRP:CD1	2.07	0.72
1:B:281:LEU:HD13	1:C:282:GLU:HG2	1.71	0.72
1:H:205:ARG:HB2	1:H:206:PRO:HD3	1.71	0.72
1:C:213:TRP:H	1:C:213:TRP:CD1	2.07	0.72
1:I:205:ARG:HB2	1:I:206:PRO:HD3	1.71	0.72
1:B:205:ARG:HB2	1:B:206:PRO:HD3	1.72	0.72
1:D:205:ARG:HB2	1:D:206:PRO:HD3	1.71	0.72
1:C:236:ILE:O	1:C:240:SER:HB2	1.89	0.71
1:J:245:HIS:HE1	1:K:246:TRP:CB	2.02	0.71
1:I:213:TRP:H	1:I:213:TRP:CD1	2.07	0.71
1:A:233:PHE:CE2	1:D:233:PHE:HZ	2.08	0.71
1:D:213:TRP:H	1:D:213:TRP:CD1	2.05	0.71
1:H:236:ILE:O	1:H:240:SER:HB2	1.91	0.71
1:H:213:TRP:H	1:H:213:TRP:HD1	1.35	0.71
1:A:236:ILE:O	1:A:240:SER:HB2	1.91	0.71
1:J:236:ILE:O	1:J:240:SER:HB2	1.91	0.71
1:J:205:ARG:O	1:J:209:GLU:HG2	1.90	0.70
1:J:205:ARG:HB2	1:J:206:PRO:HD3	1.73	0.70
1:D:200:SER:HA	1:D:204:ALA:HB3	1.73	0.70
1:C:205:ARG:HB2	1:C:206:PRO:HD3	1.74	0.70
1:K:205:ARG:HB2	1:K:206:PRO:HD3	1.74	0.70
1:C:245:HIS:NE2	1:D:246:TRP:CB	2.55	0.69
1:B:200:SER:HA	1:B:204:ALA:HB3	1.74	0.69
1:K:200:SER:HA	1:K:204:ALA:HB3	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:200:SER:HA	1:I:204:ALA:HB3	1.75	0.68
1:I:205:ARG:O	1:I:209:GLU:HG3	1.94	0.68
1:J:200:SER:HA	1:J:204:ALA:HB3	1.75	0.67
1:A:200:SER:HA	1:A:204:ALA:HB3	1.76	0.67
1:C:200:SER:HA	1:C:204:ALA:HB3	1.76	0.66
1:H:200:SER:HA	1:H:204:ALA:HB3	1.77	0.66
1:A:200:SER:HB3	1:D:192:GLN:HG3	1.79	0.65
1:H:233:PHE:CE2	1:K:233:PHE:HZ	2.14	0.64
1:C:211:TYR:HB3	1:C:213:TRP:CD1	2.32	0.64
1:H:176:PHE:CZ	1:H:207:VAL:HA	2.33	0.64
1:H:211:TYR:HB3	1:H:213:TRP:CD1	2.32	0.64
1:I:211:TYR:HB3	1:I:213:TRP:CD1	2.33	0.64
1:A:234:ILE:HD11	1:D:237:ILE:CA	2.26	0.64
1:C:176:PHE:CZ	1:C:207:VAL:HA	2.34	0.63
1:A:176:PHE:CZ	1:A:207:VAL:HA	2.33	0.63
1:A:211:TYR:HB3	1:A:213:TRP:CD1	2.34	0.63
1:A:215:TRP:O	1:A:219:VAL:HG23	1.98	0.63
1:B:194:MET:HG3	1:B:225:SER:OG	1.98	0.62
1:D:194:MET:HG3	1:D:225:SER:OG	1.99	0.62
1:K:176:PHE:CZ	1:K:207:VAL:HA	2.35	0.61
1:J:211:TYR:HB3	1:J:213:TRP:CD1	2.35	0.61
1:H:234:ILE:HD11	1:K:237:ILE:CA	2.28	0.61
1:H:238:ILE:HG12	1:K:241:MET:HG2	1.81	0.61
1:D:211:TYR:HB3	1:D:213:TRP:CD1	2.36	0.61
1:D:176:PHE:CZ	1:D:207:VAL:HA	2.35	0.60
1:H:200:SER:HB3	1:K:192:GLN:HG3	1.82	0.60
1:A:194:MET:HG3	1:A:225:SER:OG	2.01	0.60
1:J:245:HIS:NE2	1:K:246:TRP:CB	2.63	0.60
1:I:281:LEU:HD13	1:J:282:GLU:HG2	1.83	0.60
1:H:215:TRP:O	1:H:219:VAL:HG23	2.01	0.60
1:B:176:PHE:CZ	1:B:207:VAL:HA	2.36	0.60
1:B:266:GLU:HG3	1:B:267:MET:N	2.16	0.59
1:B:225:SER:O	1:B:229:VAL:HG23	2.02	0.59
1:K:211:TYR:HB3	1:K:213:TRP:CD1	2.39	0.58
1:K:194:MET:HG3	1:K:225:SER:OG	2.04	0.58
1:B:211:TYR:HB3	1:B:213:TRP:CD1	2.38	0.58
1:J:194:MET:HG3	1:J:225:SER:OG	2.04	0.58
1:C:194:MET:HG3	1:C:225:SER:OG	2.05	0.57
1:H:194:MET:HG3	1:H:225:SER:OG	2.03	0.57
1:A:236:ILE:HG22	1:B:234:ILE:HD13	1.87	0.57
1:A:198:SER:HA	1:D:197:GLU:OE1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:SER:O	1:C:229:VAL:HG23	2.04	0.57
1:I:215:TRP:O	1:I:219:VAL:HG23	2.04	0.57
1:B:215:TRP:O	1:B:219:VAL:HG23	2.06	0.55
1:K:215:TRP:O	1:K:219:VAL:HG23	2.06	0.55
1:A:238:ILE:HG12	1:D:241:MET:HG2	1.88	0.55
1:A:266:GLU:HG3	1:A:267:MET:N	2.21	0.55
1:D:266:GLU:HG3	1:D:267:MET:N	2.21	0.55
1:I:194:MET:HG3	1:I:225:SER:OG	2.06	0.55
1:I:270:LEU:HD21	1:J:272:ARG:CG	2.37	0.55
1:J:203:ILE:O	1:J:207:VAL:HG23	2.06	0.55
1:C:237:ILE:HA	1:D:234:ILE:HD11	1.89	0.55
1:J:176:PHE:CZ	1:J:207:VAL:HA	2.42	0.55
1:C:215:TRP:O	1:C:219:VAL:HG23	2.07	0.55
1:I:203:ILE:O	1:I:207:VAL:HG23	2.08	0.54
1:B:197:GLU:OE2	1:C:200:SER:HB3	2.07	0.54
1:C:266:GLU:HG3	1:C:267:MET:N	2.20	0.54
1:I:270:LEU:HD21	1:J:272:ARG:HG2	1.90	0.54
1:J:197:GLU:OE2	1:K:200:SER:HB3	2.07	0.54
1:J:225:SER:O	1:J:229:VAL:HG23	2.08	0.54
1:B:281:LEU:CD1	1:C:282:GLU:HG2	2.36	0.54
1:K:225:SER:O	1:K:229:VAL:HG23	2.07	0.54
1:I:176:PHE:CZ	1:I:207:VAL:HA	2.43	0.54
1:B:205:ARG:O	1:B:209:GLU:HG3	2.07	0.54
1:H:237:ILE:HA	1:I:234:ILE:HD11	1.89	0.54
1:K:266:GLU:HG3	1:K:267:MET:N	2.22	0.53
1:C:197:GLU:HG3	1:D:199:TRP:CD1	2.44	0.52
1:H:162:TYR:O	1:H:166:VAL:HG23	2.09	0.52
1:J:213:TRP:CD1	1:J:213:TRP:N	2.76	0.52
1:H:225:SER:O	1:H:229:VAL:HG23	2.09	0.52
1:I:225:SER:O	1:I:229:VAL:HG23	2.09	0.52
1:J:215:TRP:O	1:J:219:VAL:HG23	2.09	0.52
1:A:237:ILE:O	1:A:241:MET:HB2	2.09	0.52
1:I:266:GLU:HG3	1:I:267:MET:N	2.25	0.52
1:I:237:ILE:HA	1:J:234:ILE:HD11	1.92	0.52
1:C:237:ILE:O	1:C:241:MET:HB2	2.10	0.52
1:D:215:TRP:O	1:D:219:VAL:HG23	2.10	0.52
1:I:197:GLU:HG3	1:J:199:TRP:CD1	2.45	0.52
1:A:166:VAL:HG22	1:A:183:LEU:HD21	1.92	0.51
1:B:197:GLU:HG3	1:C:199:TRP:CD1	2.46	0.51
1:I:197:GLU:OE2	1:J:200:SER:HB3	2.10	0.51
1:H:198:SER:HA	1:K:197:GLU:OE1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:162:TYR:O	1:K:166:VAL:HG23	2.11	0.51
1:B:237:ILE:HA	1:C:234:ILE:HD11	1.93	0.50
1:B:240:SER:HB3	1:C:238:ILE:HD11	1.92	0.50
1:A:233:PHE:CE2	1:D:233:PHE:CZ	2.94	0.50
1:B:221:PHE:O	1:B:225:SER:HB3	2.12	0.50
1:A:225:SER:O	1:A:229:VAL:HG23	2.11	0.50
1:A:159:VAL:O	1:A:163:VAL:HG23	2.12	0.50
1:J:237:ILE:HA	1:K:234:ILE:HD11	1.93	0.50
1:D:225:SER:O	1:D:229:VAL:HG23	2.11	0.50
1:C:197:GLU:OE2	1:D:200:SER:HB3	2.11	0.50
1:D:208:ILE:HA	1:D:211:TYR:O	2.12	0.49
1:D:213:TRP:CD1	1:D:213:TRP:N	2.79	0.49
1:J:197:GLU:HG3	1:K:199:TRP:CD1	2.47	0.49
1:H:237:ILE:O	1:H:241:MET:HB2	2.11	0.49
1:D:203:ILE:O	1:D:207:VAL:HG23	2.12	0.49
1:A:213:TRP:CD1	1:A:213:TRP:N	2.79	0.49
1:J:266:GLU:HG3	1:J:267:MET:N	2.27	0.49
1:I:213:TRP:CD1	1:I:213:TRP:N	2.80	0.49
1:B:162:TYR:O	1:B:166:VAL:HG23	2.13	0.48
1:C:198:SER:HB2	1:D:201:MET:HG3	1.94	0.48
1:H:233:PHE:CE2	1:K:233:PHE:CZ	3.00	0.48
1:C:203:ILE:O	1:C:207:VAL:HG23	2.13	0.48
1:D:166:VAL:HG22	1:D:183:LEU:HD21	1.95	0.48
1:A:201:MET:HG2	1:D:192:GLN:NE2	2.27	0.48
1:C:213:TRP:CD1	1:C:213:TRP:N	2.81	0.48
1:A:157:LEU:HA	1:A:160:ILE:HD12	1.94	0.48
1:A:237:ILE:HA	1:B:234:ILE:HD11	1.96	0.48
1:I:162:TYR:O	1:I:166:VAL:HG23	2.13	0.48
1:D:193:VAL:O	1:D:196:LEU:HD23	2.13	0.48
1:H:239:GLU:O	1:H:243:SER:HB3	2.14	0.48
1:K:203:ILE:O	1:K:207:VAL:HG23	2.14	0.48
1:J:198:SER:HB2	1:K:201:MET:HG3	1.96	0.48
1:H:157:LEU:HA	1:H:160:ILE:HD12	1.97	0.47
1:C:197:GLU:OE1	1:D:198:SER:HA	2.14	0.47
1:D:157:LEU:HA	1:D:160:ILE:HD12	1.95	0.47
1:K:159:VAL:O	1:K:163:VAL:HG23	2.15	0.47
1:A:162:TYR:O	1:A:166:VAL:HG23	2.14	0.47
1:I:169:THR:O	1:I:173:ALA:HB2	2.14	0.47
1:I:240:SER:HB3	1:J:238:ILE:HD11	1.97	0.47
1:J:162:TYR:O	1:J:166:VAL:HG23	2.15	0.47
1:H:201:MET:HG3	1:K:198:SER:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:237:ILE:O	1:J:241:MET:HB2	2.14	0.47
1:H:169:THR:O	1:H:173:ALA:HB2	2.14	0.47
1:A:219:VAL:O	1:A:223:LEU:HG	2.15	0.47
1:B:208:ILE:HA	1:B:211:TYR:O	2.15	0.47
1:D:162:TYR:O	1:D:166:VAL:HG23	2.15	0.46
1:H:266:GLU:HG3	1:H:267:MET:N	2.30	0.46
1:B:166:VAL:HG22	1:B:183:LEU:HD21	1.98	0.46
1:C:169:THR:O	1:C:173:ALA:HB2	2.16	0.46
1:H:213:TRP:CD1	1:H:213:TRP:N	2.79	0.46
1:I:208:ILE:HD11	1:I:215:TRP:HA	1.97	0.46
1:A:203:ILE:O	1:A:207:VAL:HG23	2.16	0.46
1:A:258:GLN:O	1:A:258:GLN:HG2	2.16	0.46
1:I:159:VAL:O	1:I:163:VAL:HG23	2.16	0.46
1:C:166:VAL:HG22	1:C:183:LEU:HD21	1.98	0.46
1:H:240:SER:HB3	1:I:238:ILE:HD11	1.97	0.46
1:B:270:LEU:HD21	1:C:272:ARG:CG	2.46	0.45
1:I:208:ILE:HA	1:I:211:TYR:O	2.16	0.45
1:K:193:VAL:O	1:K:196:LEU:HD23	2.17	0.45
1:I:198:SER:HB2	1:J:201:MET:HG3	1.97	0.45
1:I:263:GLU:OE2	1:J:261:HIS:CE1	2.69	0.45
1:J:169:THR:O	1:J:173:ALA:HB2	2.17	0.45
1:J:208:ILE:HA	1:J:211:TYR:O	2.17	0.45
1:B:198:SER:HB2	1:C:201:MET:HG3	1.98	0.44
1:I:166:VAL:HG22	1:I:183:LEU:HD21	2.00	0.44
1:J:221:PHE:O	1:J:225:SER:HB3	2.17	0.44
1:K:213:TRP:CD1	1:K:213:TRP:N	2.77	0.44
1:D:154:ALA:O	1:D:158:LEU:HD12	2.18	0.44
1:H:203:ILE:O	1:H:207:VAL:HG23	2.16	0.44
1:H:236:ILE:HG22	1:I:234:ILE:HD13	1.99	0.44
1:D:159:VAL:O	1:D:163:VAL:HG23	2.17	0.44
1:H:233:PHE:HZ	1:I:233:PHE:CE2	2.35	0.44
1:D:239:GLU:O	1:D:243:SER:HB3	2.18	0.44
1:H:221:PHE:O	1:H:225:SER:HB3	2.18	0.44
1:J:166:VAL:HG22	1:J:183:LEU:HD21	1.98	0.44
1:H:208:ILE:HA	1:H:211:TYR:O	2.17	0.44
1:K:237:ILE:O	1:K:241:MET:HB2	2.17	0.44
1:D:169:THR:O	1:D:173:ALA:HB2	2.18	0.44
1:A:199:TRP:H	1:D:197:GLU:HG3	1.83	0.43
1:H:197:GLU:OE1	1:I:198:SER:HA	2.18	0.43
1:B:274:LEU:CD1	1:C:275:SER:HA	2.48	0.43
1:I:274:LEU:CD1	1:J:275:SER:HA	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:274:LEU:HD12	1:J:274:LEU:HA	1.90	0.43
1:H:241:MET:HB3	1:K:241:MET:HE1	2.01	0.43
1:A:169:THR:O	1:A:173:ALA:HB2	2.18	0.43
1:A:241:MET:HB3	1:D:241:MET:HE1	2.00	0.43
1:C:162:TYR:O	1:C:166:VAL:HG23	2.17	0.43
1:A:208:ILE:HD11	1:A:215:TRP:HA	2.01	0.43
1:B:157:LEU:HA	1:B:160:ILE:HD12	2.00	0.43
1:B:208:ILE:HD11	1:B:215:TRP:HA	2.00	0.43
1:D:221:PHE:O	1:D:225:SER:HB3	2.18	0.43
1:K:239:GLU:O	1:K:243:SER:HB3	2.18	0.43
1:B:203:ILE:O	1:B:207:VAL:HG23	2.18	0.43
1:B:274:LEU:HD12	1:B:274:LEU:HA	1.91	0.43
1:C:157:LEU:HA	1:C:160:ILE:HD12	2.00	0.43
1:D:237:ILE:O	1:D:241:MET:HB2	2.19	0.43
1:J:197:GLU:OE1	1:K:198:SER:HA	2.18	0.42
1:I:237:ILE:O	1:I:241:MET:HB2	2.19	0.42
1:A:233:PHE:CD2	1:D:233:PHE:HZ	2.37	0.42
1:K:157:LEU:HA	1:K:160:ILE:HD12	2.00	0.42
1:H:199:TRP:H	1:K:197:GLU:HG3	1.84	0.42
1:B:213:TRP:CD1	1:B:213:TRP:N	2.80	0.42
1:C:159:VAL:O	1:C:163:VAL:HG23	2.19	0.42
1:H:201:MET:HG2	1:K:192:GLN:NE2	2.34	0.42
1:J:239:GLU:O	1:J:243:SER:HB3	2.20	0.42
1:J:157:LEU:HA	1:J:160:ILE:HD12	2.02	0.42
1:A:233:PHE:HZ	1:B:233:PHE:CE2	2.37	0.42
1:B:237:ILE:O	1:B:241:MET:HB2	2.19	0.42
1:H:159:VAL:O	1:H:163:VAL:HG23	2.20	0.42
1:A:239:GLU:O	1:A:243:SER:HB3	2.20	0.41
1:A:201:MET:HG3	1:D:198:SER:HB2	2.02	0.41
1:B:270:LEU:HD21	1:C:272:ARG:HG3	2.01	0.41
1:B:239:GLU:O	1:B:243:SER:HB3	2.21	0.41
1:K:169:THR:O	1:K:173:ALA:HB2	2.19	0.41
1:A:208:ILE:HA	1:A:211:TYR:O	2.21	0.41
1:B:159:VAL:O	1:B:163:VAL:HG23	2.19	0.41
1:K:221:PHE:O	1:K:225:SER:HB3	2.21	0.41
1:H:166:VAL:HG22	1:H:183:LEU:HD21	2.01	0.41
1:A:221:PHE:O	1:A:225:SER:HB3	2.20	0.41
1:A:240:SER:HB3	1:B:238:ILE:HD11	2.02	0.41
1:B:169:THR:O	1:B:173:ALA:HB2	2.19	0.41
1:B:207:VAL:HG12	1:B:214:ALA:CB	2.51	0.41
1:K:166:VAL:HG22	1:K:183:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:ILE:N	1:B:152:TRP:HD1	2.19	0.41
1:I:239:GLU:O	1:I:243:SER:HB3	2.21	0.41
1:H:234:ILE:HA	1:H:237:ILE:HD12	2.04	0.40
1:I:270:LEU:HD21	1:J:272:ARG:HG3	2.03	0.40
1:A:232:LEU:O	1:A:236:ILE:HG13	2.20	0.40
1:B:193:VAL:O	1:B:196:LEU:HD23	2.21	0.40
1:D:208:ILE:HD11	1:D:215:TRP:HA	2.02	0.40
1:A:154:ALA:O	1:A:158:LEU:HD12	2.21	0.40
1:D:232:LEU:O	1:D:236:ILE:HG13	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
1	B	134/152 (88%)	130 (97%)	4 (3%)	0	100	100
1	C	134/152 (88%)	128 (96%)	6 (4%)	0	100	100
1	D	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
1	H	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
1	I	134/152 (88%)	130 (97%)	4 (3%)	0	100	100
1	J	134/152 (88%)	128 (96%)	6 (4%)	0	100	100
1	K	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
All	All	1072/1216 (88%)	1032 (96%)	40 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	95/131 (72%)	79 (83%)	16 (17%)	2	11
1	B	94/131 (72%)	79 (84%)	15 (16%)	2	12
1	C	93/131 (71%)	78 (84%)	15 (16%)	2	12
1	D	90/131 (69%)	75 (83%)	15 (17%)	2	11
1	H	95/131 (72%)	80 (84%)	15 (16%)	2	12
1	I	94/131 (72%)	78 (83%)	16 (17%)	2	10
1	J	93/131 (71%)	79 (85%)	14 (15%)	3	13
1	K	90/131 (69%)	76 (84%)	14 (16%)	2	12
All	All	744/1048 (71%)	624 (84%)	120 (16%)	2	12

All (120) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ILE
1	A	158	LEU
1	A	166	VAL
1	A	167	MET
1	A	182	THR
1	A	183	LEU
1	A	213	TRP
1	A	216	ILE
1	A	225	SER
1	A	234	ILE
1	A	240	SER
1	A	255	GLU
1	A	266	GLU
1	A	275	SER
1	A	281	LEU
1	A	282	GLU
1	B	153	ILE
1	B	158	LEU
1	B	166	VAL

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Mol	Chain	Res	Type
1	B	167	MET
1	B	182	THR
1	B	183	LEU
1	B	213	TRP
1	B	225	SER
1	B	234	ILE
1	B	240	SER
1	B	254	ILE
1	B	255	GLU
1	B	266	GLU
1	B	275	SER
1	B	281	LEU
1	C	153	ILE
1	C	158	LEU
1	C	166	VAL
1	C	167	MET
1	C	182	THR
1	C	183	LEU
1	C	213	TRP
1	C	225	SER
1	C	240	SER
1	C	250	ASP
1	C	255	GLU
1	C	266	GLU
1	C	275	SER
1	C	281	LEU
1	C	282	GLU
1	D	153	ILE
1	D	158	LEU
1	D	166	VAL
1	D	167	MET
1	D	182	THR
1	D	183	LEU
1	D	213	TRP
1	D	215	TRP
1	D	225	SER
1	D	240	SER
1	D	255	GLU
1	D	266	GLU
1	D	269	GLN
1	D	275	SER
1	D	281	LEU

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Mol	Chain	Res	Type
1	H	153	ILE
1	H	166	VAL
1	H	167	MET
1	H	182	THR
1	H	183	LEU
1	H	213	TRP
1	H	225	SER
1	H	234	ILE
1	H	240	SER
1	H	255	GLU
1	H	266	GLU
1	H	275	SER
1	H	279	ASP
1	H	281	LEU
1	H	282	GLU
1	I	153	ILE
1	I	158	LEU
1	I	166	VAL
1	I	167	MET
1	I	182	THR
1	I	183	LEU
1	I	213	TRP
1	I	225	SER
1	I	234	ILE
1	I	240	SER
1	I	250	ASP
1	I	254	ILE
1	I	255	GLU
1	I	266	GLU
1	I	275	SER
1	I	281	LEU
1	J	153	ILE
1	J	166	VAL
1	J	167	MET
1	J	182	THR
1	J	183	LEU
1	J	209	GLU
1	J	213	TRP
1	J	225	SER
1	J	234	ILE
1	J	240	SER
1	J	255	GLU

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Mol	Chain	Res	Type
1	J	266	GLU
1	J	275	SER
1	J	281	LEU
1	K	153	ILE
1	K	158	LEU
1	K	166	VAL
1	K	167	MET
1	K	182	THR
1	K	183	LEU
1	K	213	TRP
1	K	225	SER
1	K	234	ILE
1	K	240	SER
1	K	255	GLU
1	K	266	GLU
1	K	275	SER
1	K	281	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	245	HIS

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 ⓘ

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	136/152 (89%)	1.73	47 (34%) 1 5	195, 287, 353, 409	0
1	B	136/152 (89%)	1.11	32 (23%) 2 7	210, 282, 370, 454	0
1	C	136/152 (89%)	1.56	52 (38%) 1 4	219, 285, 372, 395	0
1	D	136/152 (89%)	1.18	31 (22%) 2 7	187, 283, 371, 449	0
1	H	136/152 (89%)	1.25	38 (27%) 1 6	211, 285, 363, 437	0
1	I	136/152 (89%)	1.13	29 (21%) 2 8	209, 282, 355, 402	0
1	J	136/152 (89%)	2.02	62 (45%) 0 3	202, 288, 362, 437	0
1	K	136/152 (89%)	1.19	34 (25%) 2 7	206, 285, 354, 439	0
All	All	1088/1216 (89%)	1.40	325 (29%) 1 6	187, 285, 364, 454	0

All (325) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	228	THR	11.1
1	J	151	ALA	8.9
1	J	248	ALA	8.0
1	H	225	SER	7.9
1	A	151	ALA	7.9
1	A	231	ASN	7.5
1	A	225	SER	7.0
1	H	243	SER	7.0
1	J	225	SER	7.0
1	D	151	ALA	6.8
1	A	154	ALA	6.8
1	J	247	GLU	6.8
1	H	226	SER	6.7
1	B	154	ALA	6.6
1	J	252	LYS	6.6
1	H	228	THR	6.5

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Mol	Chain	Res	Type	RSRZ
1	A	243	SER	6.5
1	B	151	ALA	6.4
1	A	150	ILE	6.2
1	J	231	ASN	6.2
1	A	152	TRP	6.1
1	J	228	THR	5.9
1	K	152	TRP	5.9
1	J	214	ALA	5.8
1	J	154	ALA	5.8
1	K	284	ARG	5.8
1	A	247	GLU	5.7
1	A	153	ILE	5.6
1	A	156	LEU	5.6
1	J	226	SER	5.5
1	I	213	TRP	5.5
1	K	209	GLU	5.5
1	K	282	GLU	5.2
1	J	250	ASP	5.1
1	D	154	ALA	5.0
1	C	209	GLU	5.0
1	A	155	LEU	5.0
1	H	245	HIS	5.0
1	J	283	ARG	5.0
1	A	244	ALA	4.9
1	D	152	TRP	4.8
1	J	220	SER	4.8
1	J	209	GLU	4.7
1	H	244	ALA	4.7
1	K	150	ILE	4.7
1	K	151	ALA	4.7
1	A	214	ALA	4.7
1	J	249	GLU	4.6
1	C	244	ALA	4.5
1	K	214	ALA	4.5
1	K	220	SER	4.5
1	J	284	ARG	4.5
1	A	212	PRO	4.5
1	J	282	GLU	4.4
1	C	283	ARG	4.4
1	J	285	SER	4.4
1	I	154	ALA	4.4
1	I	228	THR	4.4

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Mol	Chain	Res	Type	RSRZ
1	K	285	SER	4.4
1	I	245	HIS	4.3
1	D	282	GLU	4.3
1	J	251	ALA	4.3
1	A	226	SER	4.3
1	A	248	ALA	4.3
1	J	254	ILE	4.3
1	I	225	SER	4.2
1	J	239	GLU	4.2
1	A	227	PHE	4.2
1	D	155	LEU	4.2
1	D	167	MET	4.1
1	K	178	GLU	4.1
1	C	210	ALA	4.1
1	C	151	ALA	4.1
1	H	155	LEU	4.0
1	D	153	ILE	4.0
1	A	211	TYR	4.0
1	D	179	TRP	4.0
1	A	282	GLU	4.0
1	H	153	ILE	4.0
1	B	174	GLN	3.9
1	C	201	MET	3.9
1	C	182	THR	3.9
1	J	212	PRO	3.9
1	K	228	THR	3.8
1	J	150	ILE	3.8
1	H	154	ALA	3.8
1	H	227	PHE	3.8
1	J	178	GLU	3.8
1	I	183	LEU	3.8
1	I	153	ILE	3.8
1	B	212	PRO	3.7
1	C	275	SER	3.7
1	D	198	SER	3.7
1	I	244	ALA	3.7
1	J	153	ILE	3.7
1	H	282	GLU	3.7
1	B	228	THR	3.7
1	C	198	SER	3.7
1	D	150	ILE	3.7
1	C	250	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	167	MET	3.6
1	H	231	ASN	3.6
1	J	215	TRP	3.6
1	I	150	ILE	3.6
1	J	244	ALA	3.6
1	H	151	ALA	3.6
1	J	263	GLU	3.6
1	A	245	HIS	3.5
1	K	189	THR	3.5
1	J	216	ILE	3.5
1	A	198	SER	3.5
1	B	201	MET	3.5
1	A	213	TRP	3.5
1	K	191	PHE	3.5
1	C	212	PRO	3.5
1	J	255	GLU	3.5
1	A	242	GLN	3.5
1	K	188	TYR	3.5
1	K	213	TRP	3.5
1	J	242	GLN	3.5
1	H	224	VAL	3.4
1	J	253	ARG	3.4
1	C	282	GLU	3.4
1	H	209	GLU	3.4
1	J	269	GLN	3.4
1	C	225	SER	3.4
1	K	248	ALA	3.4
1	D	228	THR	3.4
1	K	224	VAL	3.3
1	C	279	ASP	3.3
1	A	159	VAL	3.3
1	J	266	GLU	3.3
1	J	152	TRP	3.3
1	B	227	PHE	3.3
1	A	266	GLU	3.3
1	C	247	GLU	3.3
1	I	151	ALA	3.3
1	K	210	ALA	3.3
1	C	285	SER	3.3
1	A	224	VAL	3.3
1	B	150	ILE	3.3
1	K	225	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	162	TYR	3.3
1	B	245	HIS	3.2
1	J	235	GLY	3.2
1	K	216	ILE	3.2
1	C	211	TYR	3.2
1	C	215	TRP	3.2
1	C	248	ALA	3.2
1	A	158	LEU	3.2
1	C	205	ARG	3.2
1	H	152	TRP	3.2
1	H	212	PRO	3.2
1	B	158	LEU	3.2
1	K	279	ASP	3.2
1	K	211	TYR	3.1
1	A	179	TRP	3.1
1	J	246	TRP	3.1
1	I	243	SER	3.1
1	D	156	LEU	3.1
1	B	249	GLU	3.1
1	A	239	GLU	3.1
1	J	279	ASP	3.1
1	K	212	PRO	3.1
1	C	208	ILE	3.1
1	B	213	TRP	3.1
1	D	216	ILE	3.1
1	K	153	ILE	3.1
1	I	226	SER	3.1
1	J	243	SER	3.1
1	A	232	LEU	3.1
1	H	248	ALA	3.0
1	K	215	TRP	3.0
1	A	279	ASP	3.0
1	B	153	ILE	3.0
1	J	232	LEU	3.0
1	D	215	TRP	3.0
1	D	279	ASP	3.0
1	H	195	THR	3.0
1	D	170	LYS	3.0
1	K	283	ARG	3.0
1	I	212	PRO	3.0
1	A	249	GLU	3.0
1	C	260	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	I	174	GLN	2.9
1	I	152	TRP	2.9
1	J	198	SER	2.9
1	A	210	ALA	2.9
1	B	244	ALA	2.9
1	B	178	GLU	2.9
1	I	285	SER	2.9
1	D	178	GLU	2.9
1	B	198	SER	2.8
1	C	179	TRP	2.8
1	D	231	ASN	2.8
1	I	279	ASP	2.8
1	B	224	VAL	2.8
1	I	155	LEU	2.8
1	A	209	GLU	2.8
1	A	157	LEU	2.8
1	A	229	VAL	2.8
1	A	283	ARG	2.8
1	A	251	ALA	2.8
1	C	162	TYR	2.8
1	H	229	VAL	2.8
1	C	276	SER	2.8
1	A	255	GLU	2.7
1	B	248	ALA	2.7
1	H	210	ALA	2.7
1	J	210	ALA	2.7
1	C	273	ASP	2.7
1	H	279	ASP	2.7
1	J	262	ASP	2.7
1	I	276	SER	2.7
1	C	264	ARG	2.7
1	K	205	ARG	2.7
1	H	175	SER	2.7
1	B	225	SER	2.7
1	H	156	LEU	2.7
1	C	175	SER	2.7
1	C	166	VAL	2.7
1	I	184	GLY	2.7
1	J	240	SER	2.7
1	I	248	ALA	2.6
1	C	152	TRP	2.6
1	I	211	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	J	211	TYR	2.6
1	J	208	ILE	2.6
1	C	154	ALA	2.6
1	K	219	VAL	2.6
1	C	263	GLU	2.6
1	D	255	GLU	2.6
1	B	179	TRP	2.6
1	B	184	GLY	2.6
1	H	283	ARG	2.6
1	C	277	LYS	2.6
1	J	270	LEU	2.6
1	A	178	GLU	2.5
1	D	214	ALA	2.5
1	I	182	THR	2.5
1	J	261	HIS	2.5
1	J	187	MET	2.5
1	B	246	TRP	2.5
1	A	202	GLY	2.5
1	I	283	ARG	2.5
1	J	179	TRP	2.5
1	C	261	HIS	2.5
1	J	221	PHE	2.5
1	J	222	ILE	2.4
1	B	210	ALA	2.4
1	C	150	ILE	2.4
1	H	184	GLY	2.4
1	H	182	THR	2.4
1	B	162	TYR	2.4
1	C	178	GLU	2.4
1	C	243	SER	2.4
1	I	270	LEU	2.4
1	D	174	GLN	2.4
1	K	244	ALA	2.4
1	J	273	ASP	2.3
1	B	156	LEU	2.3
1	K	155	LEU	2.3
1	H	240	SER	2.3
1	J	177	PRO	2.3
1	K	226	SER	2.3
1	I	249	GLU	2.3
1	D	227	PHE	2.3
1	C	185	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	J	219	VAL	2.3
1	K	174	GLN	2.3
1	C	165	ALA	2.3
1	K	250	ASP	2.3
1	C	186	SER	2.3
1	B	177	PRO	2.3
1	B	159	VAL	2.3
1	B	223	LEU	2.3
1	D	166	VAL	2.3
1	C	249	GLU	2.2
1	C	266	GLU	2.2
1	D	211	TYR	2.2
1	H	158	LEU	2.2
1	J	256	GLN	2.2
1	B	155	LEU	2.2
1	I	171	LEU	2.2
1	A	250	ASP	2.2
1	D	258	GLN	2.2
1	H	222	ILE	2.2
1	B	152	TRP	2.2
1	H	177	PRO	2.2
1	J	206	PRO	2.2
1	H	198	SER	2.2
1	J	227	PHE	2.2
1	C	183	LEU	2.2
1	C	280	ARG	2.2
1	D	193	VAL	2.2
1	D	224	VAL	2.2
1	D	218	PHE	2.1
1	C	181	GLY	2.1
1	A	170	LYS	2.1
1	H	223	LEU	2.1
1	J	224	VAL	2.1
1	J	217	TYR	2.1
1	C	184	GLY	2.1
1	C	254	ILE	2.1
1	C	169	THR	2.1
1	H	256	GLN	2.1
1	H	178	GLU	2.1
1	H	255	GLU	2.1
1	J	245	HIS	2.1
1	D	202	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	201	MET	2.1
1	H	157	LEU	2.1
1	D	212	PRO	2.1
1	I	229	VAL	2.1
1	J	229	VAL	2.1
1	C	262	ASP	2.1
1	B	216	ILE	2.1
1	I	231	ASN	2.1
1	D	285	SER	2.1
1	C	253	ARG	2.0
1	H	239	GLU	2.0
1	K	175	SER	2.0
1	B	226	SER	2.0
1	C	220	SER	2.0
1	A	276	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 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.