



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 24, 2017 – 09:20 AM EDT

PDB ID : 4YO3  
Title : Enteroaggregative Escherichia Coli TssA N-terminal fragment  
Authors : Durand, E.; Zoued, A.; Spinelli, S.; Douzi, B.; Brunet, Y.R.; Bebeacua, C.;  
Legrand, P.; Journet, L.; Mignot, T.; Cambillau, C.; Cascales, E.  
Deposited on : unknown  
Resolution : 3.37 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

<http://wwpdb.org/validation/2016/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  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

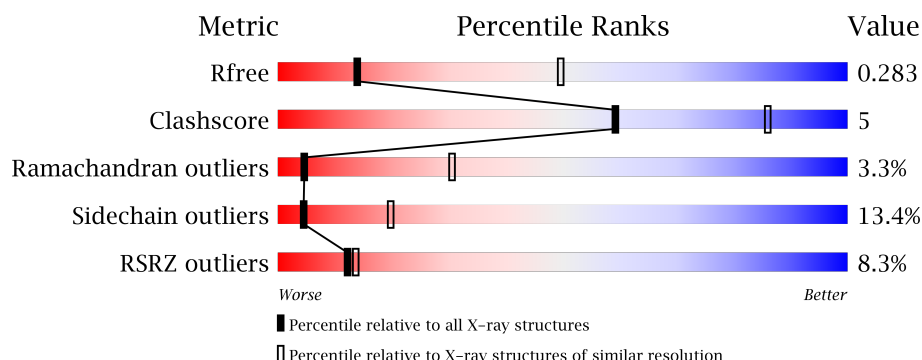
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.37 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.





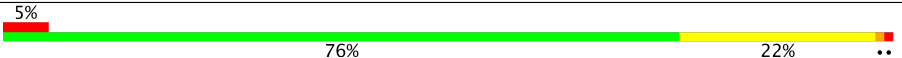
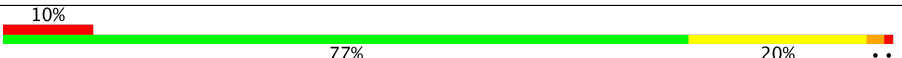
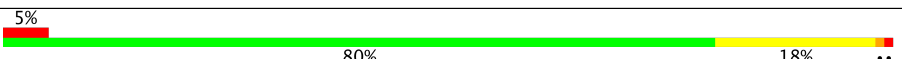
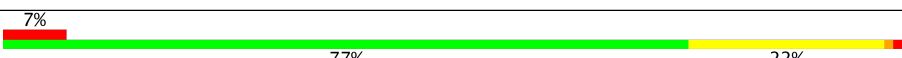

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	1241 (3.46-3.30)
Clashscore	112137	1319 (3.46-3.30)
Ramachandran outliers	110173	1298 (3.46-3.30)
Sidechain outliers	110143	1297 (3.46-3.30)
RSRZ outliers	101464	1251 (3.46-3.30)

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. 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	157	<div> <div>3%</div> <div>75%</div> <div>22%</div> <div>..</div> </div>
1	B	157	<div> <div>4%</div> <div>74%</div> <div>23%</div> <div>..</div> </div>
1	C	157	<div> <div>4%</div> <div>74%</div> <div>23%</div> <div>..</div> </div>
1	D	157	<div> <div>4%</div> <div>77%</div> <div>21%</div> <div>..</div> </div>
1	E	157	<div> <div>2%</div> <div>77%</div> <div>20%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	157	
1	G	157	
1	H	157	
1	I	157	
1	J	157	
1	K	157	
1	L	157	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14496 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.

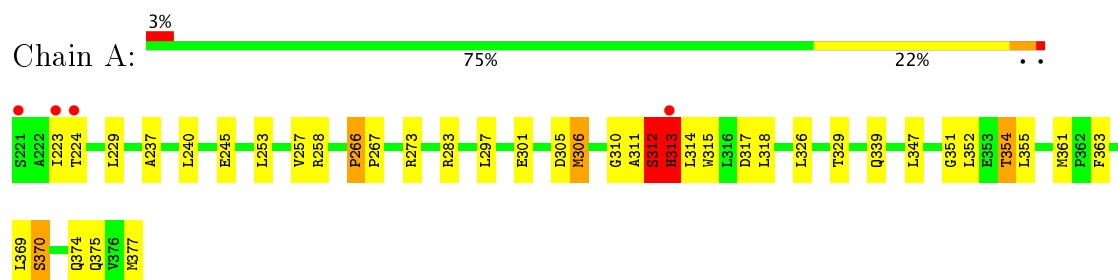
- Molecule 1 is a protein called TssA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	B	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	C	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	D	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	E	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	F	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	G	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	H	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	I	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	J	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	K	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			
1	L	157	Total	C	N	O	S	Se	0	0	0
			1208	774	210	219	1	4			

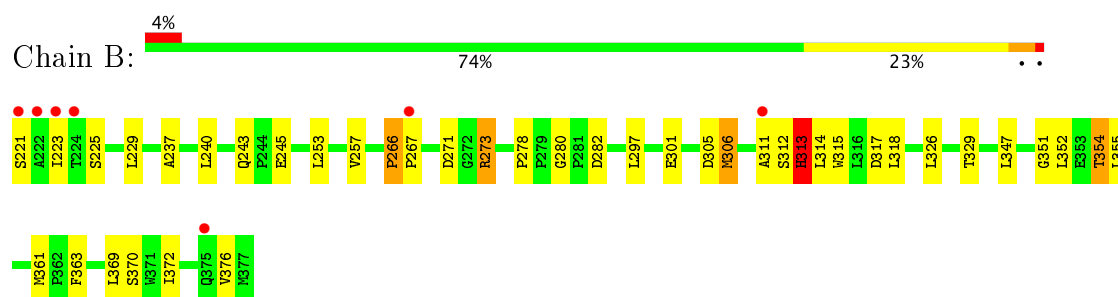
### 3 Residue-property plots [i](#)

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.

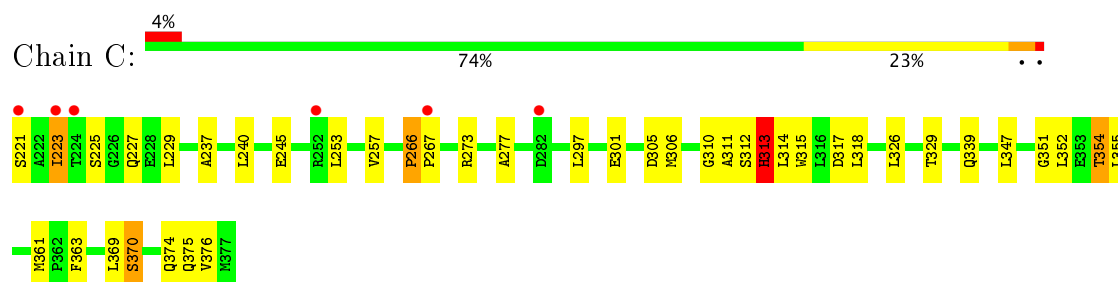
#### • Molecule 1: TssA



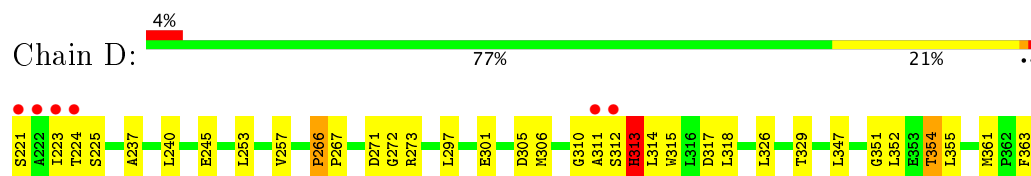
#### • Molecule 1: TssA



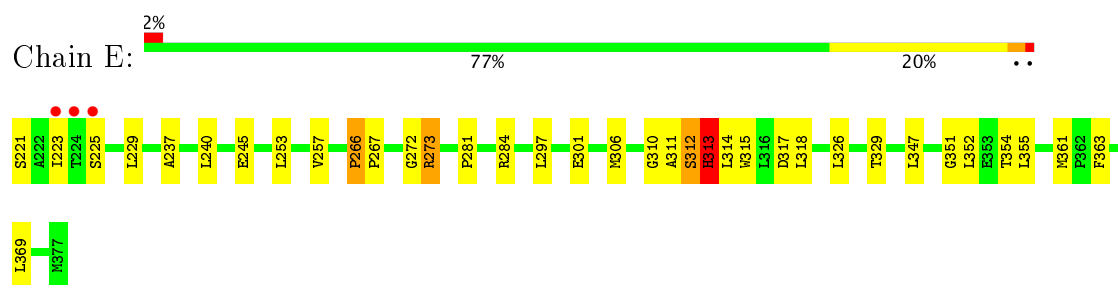
#### • Molecule 1: TssA



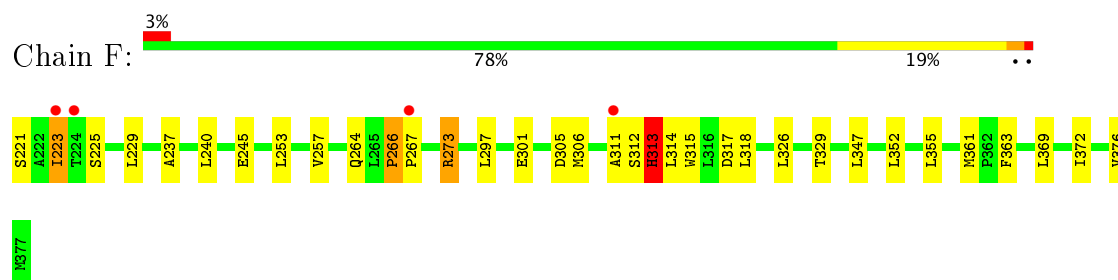
#### • Molecule 1: TssA



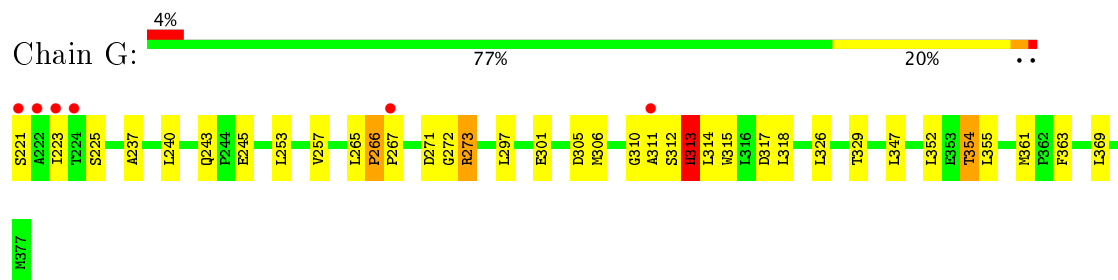
#### • Molecule 1: TssA



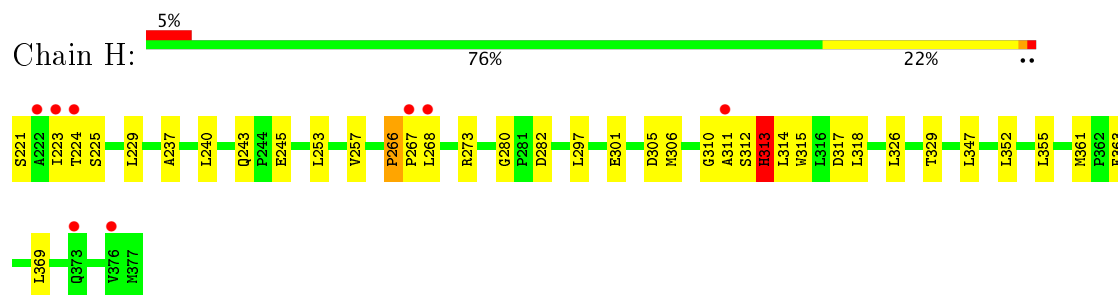
- Molecule 1: TssA



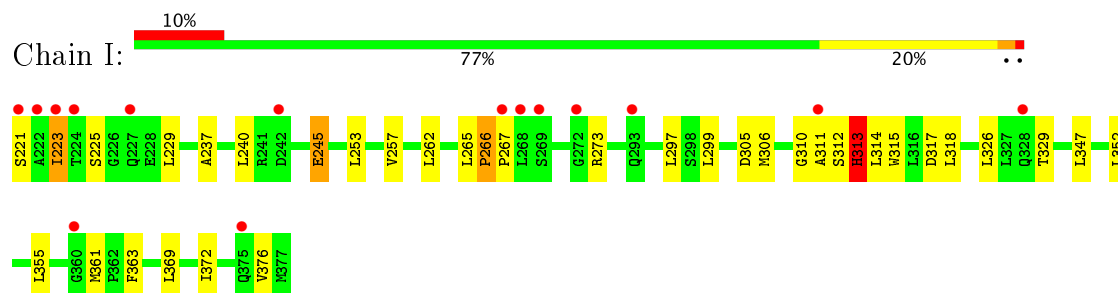
- Molecule 1: TssA



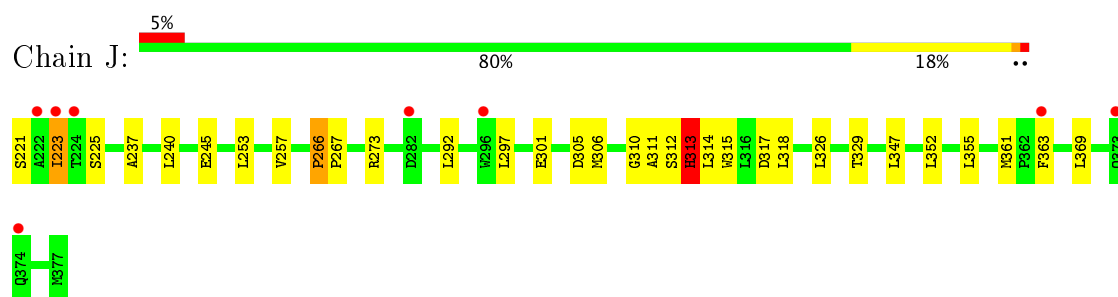
- Molecule 1: TssA



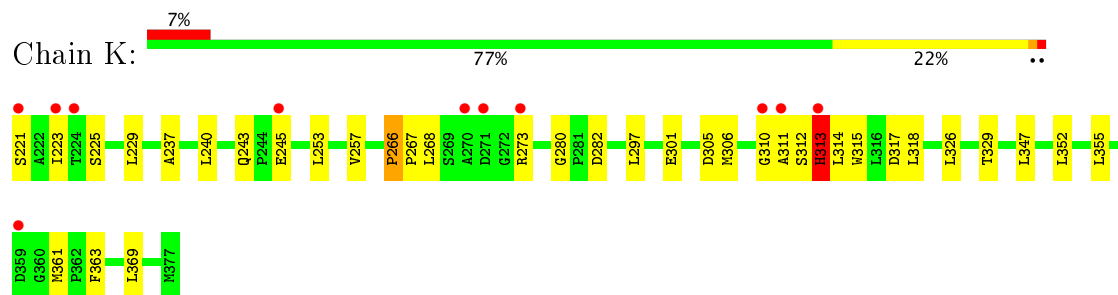
- Molecule 1: TssA



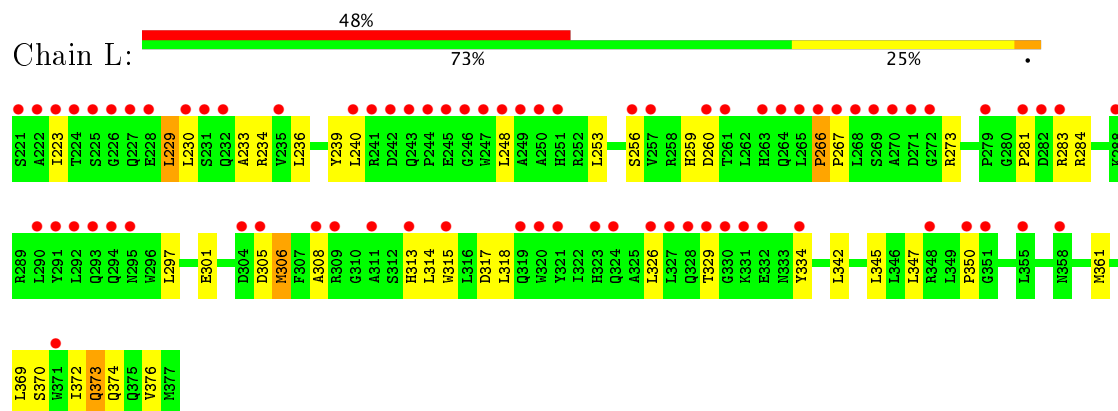
- Molecule 1: TssA



- Molecule 1: TssA



- Molecule 1: TssA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.13Å 178.05Å 106.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.39 – 3.37 28.16 – 3.37	Depositor EDS
% Data completeness (in resolution range)	100.0 (28.39-3.37) 100.0 (28.16-3.37)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.37 (at 3.39Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, $R_{free}$	0.250 , 0.261 0.275 , 0.283	Depositor DCC
$R_{free}$ test set	1836 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	94.3	Xtriage
Anisotropy	0.584	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 69.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	14496	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.48% 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

### 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	0.52	0/1232	0.75	1/1673 (0.1%)
1	B	0.52	0/1232	0.72	0/1673
1	C	0.49	0/1232	0.72	0/1673
1	D	0.49	0/1232	0.72	0/1673
1	E	0.48	0/1232	0.70	1/1673 (0.1%)
1	F	0.47	0/1232	0.70	0/1673
1	G	0.50	0/1232	0.72	0/1673
1	H	0.47	0/1232	0.69	0/1673
1	I	0.47	0/1232	0.71	0/1673
1	J	0.47	0/1232	0.69	0/1673
1	K	0.46	0/1232	0.69	0/1673
1	L	0.54	0/1232	0.74	0/1673
All	All	0.49	0/14784	0.71	2/20076 (0.0%)

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	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	2
1	J	0	1
1	K	0	1
1	L	0	1
All	All	0	13

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	312	SER	C-N-CA	5.09	134.42	121.70
1	E	312	SER	C-N-CA	5.02	134.24	121.70

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	266	PRO	Peptide
1	B	266	PRO	Peptide
1	C	266	PRO	Peptide
1	D	266	PRO	Peptide
1	E	266	PRO	Peptide
1	F	266	PRO	Peptide
1	G	266	PRO	Peptide
1	H	266	PRO	Peptide
1	I	265	LEU	Peptide
1	I	266	PRO	Peptide
1	J	266	PRO	Peptide
1	K	266	PRO	Peptide
1	L	266	PRO	Peptide

## 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	1208	0	1151	14	0
1	B	1208	0	1151	17	0
1	C	1208	0	1151	16	0
1	D	1208	0	1151	13	0
1	E	1208	0	1151	16	0
1	F	1208	0	1151	12	0
1	G	1208	0	1151	13	0
1	H	1208	0	1151	13	0
1	I	1208	0	1151	12	0
1	J	1208	0	1151	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K	1208	0	1151	12	0
1	L	1208	0	1151	18	0
All	All	14496	0	13812	152	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 5.

All (152) 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:B:306:MSE:SE	1:B:306:MSE:CE	2.18	1.41
1:L:236:LEU:HD23	1:L:253:LEU:HD11	1.49	0.95
1:L:236:LEU:CD2	1:L:253:LEU:HD11	2.23	0.67
1:C:370:SER:O	1:C:374:GLN:HG2	1.95	0.66
1:G:311:ALA:C	1:G:313:HIS:H	1.99	0.65
1:L:240:LEU:HD22	1:L:253:LEU:HD12	1.78	0.64
1:L:259:HIS:HB3	1:L:345:LEU:HD13	1.80	0.62
1:D:310:GLY:HA3	1:D:313:HIS:CE1	2.35	0.62
1:B:282:ASP:HA	1:E:272:GLY:CA	2.32	0.60
1:D:311:ALA:C	1:D:313:HIS:H	2.05	0.59
1:J:311:ALA:C	1:J:313:HIS:H	2.06	0.59
1:B:282:ASP:HA	1:E:272:GLY:HA3	1.84	0.58
1:D:221:SER:N	1:D:225:SER:HG	2.01	0.58
1:I:311:ALA:C	1:I:313:HIS:H	2.07	0.57
1:F:311:ALA:C	1:F:313:HIS:H	2.07	0.57
1:H:311:ALA:C	1:H:313:HIS:H	2.06	0.57
1:K:311:ALA:C	1:K:313:HIS:H	2.07	0.57
1:E:311:ALA:C	1:E:313:HIS:H	2.09	0.56
1:B:311:ALA:C	1:B:313:HIS:H	2.07	0.55
1:G:310:GLY:HA3	1:G:313:HIS:CE1	2.41	0.55
1:C:311:ALA:C	1:C:313:HIS:H	2.09	0.54
1:A:310:GLY:HA3	1:A:313:HIS:CE1	2.42	0.54
1:A:311:ALA:C	1:A:313:HIS:H	2.11	0.54
1:F:352:LEU:HA	1:F:355:LEU:HD12	1.91	0.53
1:E:352:LEU:HA	1:E:355:LEU:HD12	1.91	0.52
1:J:352:LEU:HA	1:J:355:LEU:HD12	1.92	0.52
1:C:352:LEU:HA	1:C:355:LEU:HD12	1.93	0.51
1:G:221:SER:N	1:G:225:SER:HG	2.07	0.51
1:K:352:LEU:HA	1:K:355:LEU:HD12	1.93	0.51
1:L:248:LEU:HB2	1:L:334:TYR:CE1	2.45	0.51
1:L:342:LEU:HD23	1:L:376:VAL:HG21	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:352:LEU:HA	1:H:355:LEU:HD12	1.91	0.51
1:K:310:GLY:HA3	1:K:313:HIS:CE1	2.45	0.51
1:L:372:ILE:HA	1:L:376:VAL:HG22	1.92	0.51
1:D:272:GLY:CA	1:K:282:ASP:HA	2.40	0.51
1:A:352:LEU:HA	1:A:355:LEU:HD12	1.93	0.50
1:E:221:SER:N	1:E:225:SER:HG	2.09	0.50
1:D:352:LEU:HA	1:D:355:LEU:HD12	1.93	0.50
1:I:352:LEU:HA	1:I:355:LEU:HD12	1.92	0.50
1:H:243:GLN:HE22	1:I:223:ILE:HD12	1.77	0.50
1:L:281:PRO:HA	1:L:284:ARG:HG2	1.94	0.50
1:A:339:GLN:HE22	1:A:375:GLN:HG3	1.76	0.50
1:L:283:ARG:HD3	1:L:306:MSE:HG2	1.92	0.50
1:G:352:LEU:HA	1:G:355:LEU:HD12	1.92	0.50
1:C:221:SER:N	1:C:225:SER:HG	2.10	0.49
1:J:223:ILE:HD12	1:K:243:GLN:HE22	1.77	0.49
1:I:221:SER:N	1:I:225:SER:HG	2.09	0.49
1:C:310:GLY:HA3	1:C:313:HIS:CE1	2.48	0.49
1:D:354:THR:HG23	1:K:280:GLY:HA2	1.94	0.49
1:J:221:SER:N	1:J:225:SER:HG	2.11	0.49
1:B:352:LEU:HA	1:B:355:LEU:HD12	1.94	0.49
1:L:370:SER:O	1:L:374:GLN:HG2	2.13	0.48
1:A:370:SER:O	1:A:374:GLN:HG2	2.13	0.48
1:B:221:SER:N	1:B:225:SER:HG	2.11	0.48
1:G:354:THR:HG23	1:H:280:GLY:HA2	1.97	0.47
1:H:221:SER:N	1:H:225:SER:HG	2.12	0.47
1:D:326:LEU:HA	1:D:329:THR:HG22	1.97	0.47
1:B:326:LEU:HA	1:B:329:THR:HG22	1.96	0.47
1:J:310:GLY:HA3	1:J:313:HIS:CE1	2.48	0.47
1:B:315:TRP:CD1	1:B:318:LEU:HD13	2.50	0.47
1:F:221:SER:N	1:F:225:SER:HG	2.12	0.47
1:C:277:ALA:HB2	1:L:373:GLN:CD	2.35	0.47
1:L:326:LEU:HA	1:L:329:THR:HG22	1.97	0.46
1:C:326:LEU:HA	1:C:329:THR:HG22	1.97	0.46
1:J:315:TRP:CD1	1:J:318:LEU:HD13	2.51	0.46
1:B:355:LEU:HB2	1:B:363:PHE:CE2	2.50	0.46
1:C:227:GLN:NE2	1:L:350:PRO:HG3	2.31	0.46
1:L:315:TRP:O	1:L:318:LEU:HB2	2.15	0.46
1:G:326:LEU:HA	1:G:329:THR:HG22	1.98	0.46
1:F:223:ILE:HD12	1:G:243:GLN:HE22	1.81	0.45
1:F:315:TRP:CD1	1:F:318:LEU:HD13	2.51	0.45
1:F:326:LEU:HA	1:F:329:THR:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:264:GLN:HE22	1:J:310:GLY:N	2.15	0.45
1:G:315:TRP:CD1	1:G:318:LEU:HD13	2.51	0.45
1:K:221:SER:N	1:K:225:SER:HG	2.15	0.45
1:A:326:LEU:HA	1:A:329:THR:HG22	1.99	0.45
1:G:355:LEU:HB2	1:G:363:PHE:CE2	2.52	0.45
1:C:315:TRP:CD1	1:C:318:LEU:HD13	2.52	0.45
1:H:326:LEU:HA	1:H:329:THR:HG22	1.99	0.45
1:A:355:LEU:HB2	1:A:363:PHE:CE2	2.52	0.44
1:H:315:TRP:CD1	1:H:318:LEU:HD13	2.53	0.44
1:K:315:TRP:CD1	1:K:318:LEU:HD13	2.52	0.44
1:B:278:PRO:HG2	1:E:354:THR:HG21	1.99	0.44
1:C:374:GLN:HG3	1:C:375:GLN:N	2.33	0.44
1:D:355:LEU:HB2	1:D:363:PHE:CE2	2.53	0.44
1:E:315:TRP:CD1	1:E:318:LEU:HD13	2.52	0.44
1:B:355:LEU:HB2	1:B:363:PHE:CD2	2.53	0.44
1:D:315:TRP:CD1	1:D:318:LEU:HD13	2.52	0.44
1:E:326:LEU:HA	1:E:329:THR:HG22	2.00	0.44
1:B:280:GLY:HA2	1:E:354:THR:HG23	2.00	0.44
1:F:237:ALA:HA	1:F:240:LEU:HD12	1.99	0.44
1:G:272:GLY:CA	1:H:282:ASP:HA	2.48	0.44
1:B:273:ARG:H	1:B:273:ARG:HG2	1.55	0.43
1:F:273:ARG:HG2	1:F:273:ARG:H	1.61	0.43
1:I:310:GLY:HA3	1:I:313:HIS:CE1	2.53	0.43
1:L:230:LEU:HA	1:L:233:ALA:HB3	2.01	0.43
1:A:315:TRP:CD1	1:A:318:LEU:HD13	2.53	0.43
1:B:243:GLN:HE22	1:C:223:ILE:HD12	1.82	0.43
1:J:326:LEU:HA	1:J:329:THR:HG22	1.99	0.43
1:E:310:GLY:HA3	1:E:313:HIS:CE1	2.54	0.43
1:I:355:LEU:HB2	1:I:363:PHE:CE2	2.54	0.43
1:B:237:ALA:HA	1:B:240:LEU:HD12	2.00	0.43
1:B:351:GLY:O	1:B:354:THR:HG22	2.19	0.43
1:H:237:ALA:HA	1:H:240:LEU:HD12	2.00	0.43
1:A:311:ALA:C	1:A:313:HIS:N	2.72	0.43
1:I:326:LEU:HA	1:I:329:THR:HG22	1.99	0.43
1:J:355:LEU:HB2	1:J:363:PHE:CE2	2.54	0.43
1:B:372:ILE:HA	1:B:376:VAL:HG22	2.01	0.43
1:E:355:LEU:HB2	1:E:363:PHE:CE2	2.54	0.43
1:I:237:ALA:HA	1:I:240:LEU:HD12	2.01	0.43
1:K:326:LEU:HA	1:K:329:THR:HG22	2.00	0.43
1:L:229:LEU:O	1:L:233:ALA:HB2	2.19	0.43
1:D:224:THR:HG22	1:D:225:SER:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:237:ALA:HA	1:D:240:LEU:HD12	2.00	0.42
1:G:273:ARG:HG2	1:G:273:ARG:H	1.56	0.42
1:K:237:ALA:HA	1:K:240:LEU:HD12	2.01	0.42
1:C:355:LEU:HB2	1:C:363:PHE:CE2	2.54	0.42
1:H:355:LEU:HB2	1:H:363:PHE:CE2	2.55	0.42
1:C:237:ALA:HA	1:C:240:LEU:HD12	2.01	0.42
1:E:237:ALA:HA	1:E:240:LEU:HD12	2.01	0.42
1:E:273:ARG:HG2	1:E:273:ARG:H	1.59	0.42
1:E:351:GLY:O	1:E:354:THR:HG22	2.20	0.42
1:A:237:ALA:HA	1:A:240:LEU:HD12	2.02	0.42
1:I:315:TRP:CD1	1:I:318:LEU:HD13	2.54	0.42
1:K:355:LEU:HB2	1:K:363:PHE:CD2	2.55	0.42
1:H:310:GLY:HA3	1:H:313:HIS:CE1	2.55	0.42
1:K:355:LEU:HB2	1:K:363:PHE:CE2	2.54	0.42
1:F:372:ILE:HA	1:F:376:VAL:HG22	2.02	0.42
1:L:256:SER:HA	1:L:260:ASP:OD2	2.20	0.42
1:E:355:LEU:HB2	1:E:363:PHE:CD2	2.55	0.41
1:G:237:ALA:HA	1:G:240:LEU:HD12	2.02	0.41
1:J:355:LEU:HB2	1:J:363:PHE:CD2	2.55	0.41
1:A:351:GLY:O	1:A:354:THR:HG22	2.20	0.41
1:G:355:LEU:HB2	1:G:363:PHE:CD2	2.55	0.41
1:H:355:LEU:HB2	1:H:363:PHE:CD2	2.55	0.41
1:C:339:GLN:HE21	1:C:376:VAL:HG12	1.85	0.41
1:C:351:GLY:O	1:C:354:THR:HG22	2.21	0.41
1:F:355:LEU:HB2	1:F:363:PHE:CE2	2.56	0.41
1:D:351:GLY:O	1:D:354:THR:HG22	2.21	0.41
1:I:355:LEU:HB2	1:I:363:PHE:CD2	2.56	0.41
1:A:283:ARG:CD	1:A:306:MSE:HE3	2.51	0.40
1:A:355:LEU:HB2	1:A:363:PHE:CD2	2.56	0.40
1:E:281:PRO:HA	1:E:284:ARG:HG2	2.03	0.40
1:F:355:LEU:HB2	1:F:363:PHE:CD2	2.56	0.40
1:L:234:ARG:HD3	1:L:308:ALA:HB1	2.03	0.40
1:A:258:ARG:NH2	1:A:312:SER:H	2.19	0.40
1:C:355:LEU:HB2	1:C:363:PHE:CD2	2.56	0.40
1:D:355:LEU:HB2	1:D:363:PHE:CD2	2.56	0.40
1:H:224:THR:HG22	1:H:225:SER:H	1.87	0.40
1:I:372:ILE:HA	1:I:376:VAL:HG22	2.03	0.40
1:J:237:ALA:HA	1:J:240:LEU:HD12	2.02	0.40
1:I:262:LEU:HA	1:I:262:LEU:HD13	1.98	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	155/157 (99%)	140 (90%)	10 (6%)	5 (3%)	5	31
1	B	155/157 (99%)	141 (91%)	9 (6%)	5 (3%)	5	31
1	C	155/157 (99%)	140 (90%)	10 (6%)	5 (3%)	5	31
1	D	155/157 (99%)	141 (91%)	9 (6%)	5 (3%)	5	31
1	E	155/157 (99%)	142 (92%)	8 (5%)	5 (3%)	5	31
1	F	155/157 (99%)	141 (91%)	9 (6%)	5 (3%)	5	31
1	G	155/157 (99%)	140 (90%)	9 (6%)	6 (4%)	3	26
1	H	155/157 (99%)	141 (91%)	9 (6%)	5 (3%)	5	31
1	I	155/157 (99%)	141 (91%)	8 (5%)	6 (4%)	3	26
1	J	155/157 (99%)	141 (91%)	9 (6%)	5 (3%)	5	31
1	K	155/157 (99%)	141 (91%)	9 (6%)	5 (3%)	5	31
1	L	155/157 (99%)	138 (89%)	13 (8%)	4 (3%)	6	35
All	All	1860/1884 (99%)	1687 (91%)	112 (6%)	61 (3%)	4	30

All (61) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	PRO
1	A	267	PRO
1	B	223	ILE
1	B	266	PRO
1	B	267	PRO
1	C	223	ILE
1	C	266	PRO
1	C	267	PRO
1	D	223	ILE
1	D	266	PRO
1	D	267	PRO
1	E	266	PRO

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Mol	Chain	Res	Type
1	E	267	PRO
1	F	266	PRO
1	F	267	PRO
1	G	266	PRO
1	G	267	PRO
1	H	266	PRO
1	H	267	PRO
1	I	245	GLU
1	I	266	PRO
1	I	267	PRO
1	J	223	ILE
1	J	266	PRO
1	J	267	PRO
1	K	266	PRO
1	K	267	PRO
1	L	266	PRO
1	L	267	PRO
1	A	223	ILE
1	A	313	HIS
1	B	313	HIS
1	C	313	HIS
1	D	313	HIS
1	E	223	ILE
1	E	313	HIS
1	F	223	ILE
1	F	313	HIS
1	G	223	ILE
1	G	312	SER
1	G	313	HIS
1	H	223	ILE
1	H	313	HIS
1	I	223	ILE
1	I	313	HIS
1	J	313	HIS
1	K	223	ILE
1	K	313	HIS
1	L	223	ILE
1	A	312	SER
1	D	312	SER
1	E	312	SER
1	F	312	SER
1	H	312	SER

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Mol	Chain	Res	Type
1	J	312	SER
1	K	312	SER
1	L	313	HIS
1	B	312	SER
1	C	312	SER
1	I	312	SER
1	G	265	LEU

### 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	118/129 (92%)	99 (84%)	19 (16%)	3	13
1	B	118/129 (92%)	100 (85%)	18 (15%)	3	15
1	C	118/129 (92%)	101 (86%)	17 (14%)	4	17
1	D	118/129 (92%)	102 (86%)	16 (14%)	4	19
1	E	118/129 (92%)	104 (88%)	14 (12%)	6	24
1	F	118/129 (92%)	103 (87%)	15 (13%)	5	22
1	G	118/129 (92%)	102 (86%)	16 (14%)	4	19
1	H	118/129 (92%)	102 (86%)	16 (14%)	4	19
1	I	118/129 (92%)	103 (87%)	15 (13%)	5	22
1	J	118/129 (92%)	103 (87%)	15 (13%)	5	22
1	K	118/129 (92%)	102 (86%)	16 (14%)	4	19
1	L	118/129 (92%)	105 (89%)	13 (11%)	7	29
All	All	1416/1548 (92%)	1226 (87%)	190 (13%)	4	20

All (190) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	THR
1	A	229	LEU
1	A	245	GLU

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Mol	Chain	Res	Type
1	A	253	LEU
1	A	257	VAL
1	A	273	ARG
1	A	297	LEU
1	A	301	GLU
1	A	305	ASP
1	A	306	MSE
1	A	313	HIS
1	A	314	LEU
1	A	317	ASP
1	A	347	LEU
1	A	354	THR
1	A	361	MSE
1	A	369	LEU
1	A	370	SER
1	A	377	MSE
1	B	229	LEU
1	B	245	GLU
1	B	253	LEU
1	B	257	VAL
1	B	271	ASP
1	B	273	ARG
1	B	297	LEU
1	B	301	GLU
1	B	305	ASP
1	B	306	MSE
1	B	313	HIS
1	B	314	LEU
1	B	317	ASP
1	B	347	LEU
1	B	354	THR
1	B	361	MSE
1	B	369	LEU
1	B	370	SER
1	C	229	LEU
1	C	245	GLU
1	C	253	LEU
1	C	257	VAL
1	C	273	ARG
1	C	297	LEU
1	C	301	GLU
1	C	305	ASP

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Mol	Chain	Res	Type
1	C	306	MSE
1	C	313	HIS
1	C	314	LEU
1	C	317	ASP
1	C	347	LEU
1	C	354	THR
1	C	361	MSE
1	C	369	LEU
1	C	370	SER
1	D	245	GLU
1	D	253	LEU
1	D	257	VAL
1	D	271	ASP
1	D	273	ARG
1	D	297	LEU
1	D	301	GLU
1	D	305	ASP
1	D	306	MSE
1	D	313	HIS
1	D	314	LEU
1	D	317	ASP
1	D	347	LEU
1	D	354	THR
1	D	361	MSE
1	D	369	LEU
1	E	229	LEU
1	E	245	GLU
1	E	253	LEU
1	E	257	VAL
1	E	273	ARG
1	E	297	LEU
1	E	301	GLU
1	E	306	MSE
1	E	313	HIS
1	E	314	LEU
1	E	317	ASP
1	E	347	LEU
1	E	361	MSE
1	E	369	LEU
1	F	229	LEU
1	F	245	GLU
1	F	253	LEU

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Mol	Chain	Res	Type
1	F	257	VAL
1	F	273	ARG
1	F	297	LEU
1	F	301	GLU
1	F	305	ASP
1	F	306	MSE
1	F	313	HIS
1	F	314	LEU
1	F	317	ASP
1	F	347	LEU
1	F	361	MSE
1	F	369	LEU
1	G	245	GLU
1	G	253	LEU
1	G	257	VAL
1	G	271	ASP
1	G	273	ARG
1	G	297	LEU
1	G	301	GLU
1	G	305	ASP
1	G	306	MSE
1	G	313	HIS
1	G	314	LEU
1	G	317	ASP
1	G	347	LEU
1	G	354	THR
1	G	361	MSE
1	G	369	LEU
1	H	229	LEU
1	H	245	GLU
1	H	253	LEU
1	H	257	VAL
1	H	268	LEU
1	H	273	ARG
1	H	297	LEU
1	H	301	GLU
1	H	305	ASP
1	H	306	MSE
1	H	313	HIS
1	H	314	LEU
1	H	317	ASP
1	H	347	LEU

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Mol	Chain	Res	Type
1	H	361	MSE
1	H	369	LEU
1	I	229	LEU
1	I	245	GLU
1	I	253	LEU
1	I	257	VAL
1	I	273	ARG
1	I	297	LEU
1	I	299	LEU
1	I	305	ASP
1	I	306	MSE
1	I	313	HIS
1	I	314	LEU
1	I	317	ASP
1	I	347	LEU
1	I	361	MSE
1	I	369	LEU
1	J	245	GLU
1	J	253	LEU
1	J	257	VAL
1	J	273	ARG
1	J	292	LEU
1	J	297	LEU
1	J	301	GLU
1	J	305	ASP
1	J	306	MSE
1	J	313	HIS
1	J	314	LEU
1	J	317	ASP
1	J	347	LEU
1	J	361	MSE
1	J	369	LEU
1	K	229	LEU
1	K	245	GLU
1	K	253	LEU
1	K	257	VAL
1	K	268	LEU
1	K	273	ARG
1	K	297	LEU
1	K	301	GLU
1	K	305	ASP
1	K	306	MSE

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Mol	Chain	Res	Type
1	K	313	HIS
1	K	314	LEU
1	K	317	ASP
1	K	347	LEU
1	K	361	MSE
1	K	369	LEU
1	L	229	LEU
1	L	239	TYR
1	L	273	ARG
1	L	297	LEU
1	L	301	GLU
1	L	305	ASP
1	L	306	MSE
1	L	314	LEU
1	L	317	ASP
1	L	347	LEU
1	L	361	MSE
1	L	369	LEU
1	L	373	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	313	HIS
1	A	339	GLN
1	B	243	GLN
1	B	339	GLN
1	B	374	GLN
1	C	227	GLN
1	C	339	GLN
1	D	339	GLN
1	E	339	GLN
1	F	243	GLN
1	F	264	GLN
1	F	339	GLN
1	G	243	GLN
1	G	313	HIS
1	G	339	GLN
1	H	243	GLN
1	H	339	GLN
1	I	339	GLN
1	J	243	GLN

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Mol	Chain	Res	Type
1	J	339	GLN
1	K	243	GLN
1	K	339	GLN
1	L	323	HIS

### 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	153/157 (97%)	0.02	4 (2%) 56 57	54, 76, 109, 162	0
1	B	153/157 (97%)	0.03	7 (4%) 33 34	57, 81, 116, 175	0
1	C	153/157 (97%)	0.11	6 (3%) 40 41	63, 102, 138, 171	0
1	D	153/157 (97%)	0.14	6 (3%) 40 41	65, 98, 130, 168	0
1	E	153/157 (97%)	0.07	3 (1%) 65 67	57, 95, 135, 170	0
1	F	153/157 (97%)	0.11	4 (2%) 56 57	69, 106, 145, 160	0
1	G	153/157 (97%)	0.07	6 (3%) 40 41	66, 89, 119, 176	0
1	H	153/157 (97%)	0.12	8 (5%) 28 29	74, 109, 149, 167	0
1	I	153/157 (97%)	0.57	15 (9%) 8 9	76, 134, 169, 181	0
1	J	153/157 (97%)	0.35	8 (5%) 28 29	93, 125, 159, 178	0
1	K	153/157 (97%)	0.39	11 (7%) 16 18	92, 122, 157, 178	0
1	L	153/157 (97%)	2.86	75 (49%) 0 0	121, 184, 211, 221	0
All	All	1836/1884 (97%)	0.40	153 (8%) 12 14	54, 106, 182, 221	0

All (153) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	264	GLN	13.4
1	L	221	SER	13.3
1	L	266	PRO	12.5
1	L	291	TYR	10.9
1	L	222	ALA	10.3
1	L	267	PRO	9.9
1	L	328	GLN	9.5
1	L	223	ILE	9.4
1	L	246	GLY	9.1
1	L	244	PRO	9.1
1	L	225	SER	8.9

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Mol	Chain	Res	Type	RSRZ
1	L	323	HIS	8.3
1	L	265	LEU	8.1
1	L	293	GLN	7.8
1	E	223	ILE	7.5
1	L	249	ALA	7.4
1	G	223	ILE	7.0
1	L	231	SER	6.9
1	L	327	LEU	6.8
1	L	245	GLU	6.8
1	L	235	VAL	6.7
1	L	292	LEU	6.7
1	L	330	GLY	6.5
1	B	223	ILE	6.1
1	K	223	ILE	6.1
1	L	243	GLN	6.1
1	K	311	ALA	6.0
1	L	224	THR	5.8
1	I	224	THR	5.8
1	E	224	THR	5.6
1	J	223	ILE	5.5
1	L	305	ASP	5.3
1	L	294	GLN	5.1
1	F	223	ILE	5.1
1	L	263	HIS	5.0
1	I	223	ILE	4.9
1	D	223	ILE	4.9
1	L	269	SER	4.8
1	L	251	HIS	4.8
1	L	250	ALA	4.7
1	G	222	ALA	4.6
1	C	223	ILE	4.5
1	L	321	TYR	4.5
1	I	311	ALA	4.5
1	L	279	PRO	4.5
1	L	242	ASP	4.4
1	L	282	ASP	4.3
1	D	222	ALA	4.2
1	D	224	THR	4.2
1	I	328	GLN	4.2
1	H	223	ILE	4.1
1	L	309	ARG	4.1
1	L	308	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	224	THR	3.9
1	L	247	TRP	3.9
1	L	329	THR	3.9
1	L	331	LYS	3.8
1	K	221	SER	3.7
1	L	313	HIS	3.7
1	L	295	ASN	3.6
1	L	228	GLU	3.6
1	C	282	ASP	3.6
1	L	271	ASP	3.5
1	L	261	THR	3.5
1	L	311	ALA	3.4
1	K	224	THR	3.4
1	L	351	GLY	3.4
1	D	311	ALA	3.4
1	L	281	PRO	3.3
1	L	232	GLN	3.3
1	L	283	ARG	3.2
1	L	227	GLN	3.2
1	L	350	PRO	3.2
1	K	270	ALA	3.2
1	G	224	THR	3.2
1	K	359	ASP	3.2
1	L	358	ASN	3.2
1	K	271	ASP	3.2
1	L	256	SER	3.1
1	L	288	LYS	3.1
1	L	272	GLY	3.1
1	L	268	LEU	3.1
1	B	222	ALA	3.0
1	K	310	GLY	3.0
1	F	311	ALA	3.0
1	L	270	ALA	3.0
1	L	334	TYR	2.9
1	I	222	ALA	2.9
1	L	319	GLN	2.8
1	D	221	SER	2.8
1	I	293	GLN	2.8
1	B	224	THR	2.8
1	L	240	LEU	2.8
1	I	267	PRO	2.7
1	L	304	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	J	282	ASP	2.6
1	H	376	VAL	2.6
1	I	272	GLY	2.6
1	L	326	LEU	2.6
1	L	320	TRP	2.6
1	I	375	GLN	2.6
1	L	371	TRP	2.6
1	H	373	GLN	2.6
1	K	245	GLU	2.5
1	L	226	GLY	2.5
1	H	224	THR	2.5
1	L	260	ASP	2.5
1	I	269	SER	2.5
1	K	313	HIS	2.5
1	H	222	ALA	2.5
1	I	268	LEU	2.5
1	B	375	GLN	2.4
1	A	223	ILE	2.4
1	A	224	THR	2.4
1	B	267	PRO	2.4
1	B	221	SER	2.4
1	I	227	GLN	2.4
1	C	221	SER	2.3
1	J	222	ALA	2.3
1	J	224	THR	2.3
1	G	267	PRO	2.3
1	C	252	ARG	2.3
1	L	315	TRP	2.3
1	J	363	PHE	2.3
1	L	257	VAL	2.3
1	L	230	LEU	2.2
1	L	348	ARG	2.2
1	L	332	GLU	2.2
1	H	268	LEU	2.2
1	I	221	SER	2.2
1	K	273	ARG	2.2
1	I	242	ASP	2.2
1	I	360	GLY	2.2
1	L	355	LEU	2.2
1	A	313	HIS	2.2
1	J	374	GLN	2.2
1	F	224	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	312	SER	2.2
1	F	267	PRO	2.2
1	A	221	SER	2.1
1	G	311	ALA	2.1
1	G	221	SER	2.1
1	B	311	ALA	2.1
1	L	324	GLN	2.1
1	L	290	LEU	2.1
1	J	296	TRP	2.1
1	H	267	PRO	2.1
1	J	373	GLN	2.1
1	C	267	PRO	2.1
1	L	248	LEU	2.0
1	L	241	ARG	2.0
1	E	225	SER	2.0
1	H	311	ALA	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.